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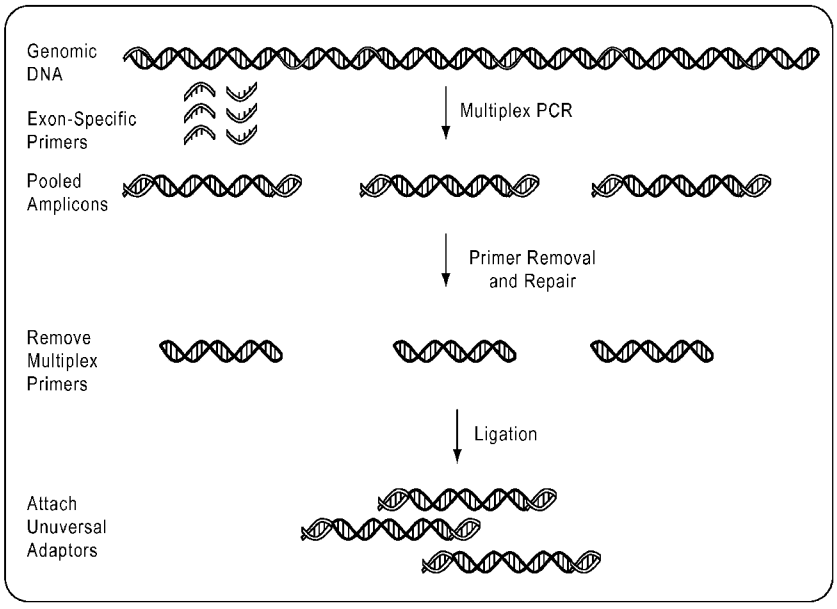


FIG. 2

(57) Abstract: The present invention provides methods, compositions, kits, systems and apparatus that are useful for multiplex PCR of one or more nucleic acids present in a sample. In particular, various target-specific primers are provided that allow for the selective amplification of one or more target sequences. In one aspect, the invention relates to target-specific primers useful for the selective amplification of one or more target sequences associated with cancer or inherited disease. In some aspects, amplified target sequences obtained using the disclosed methods, kits, systems and apparatuses can be used in various downstream processes including nucleic acid sequencing and used to detect the presence of genetic variants.

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METHODS AND COMPOSITIONS FOR MULTIPLEX PCR

[0001] CROSS REFERENCE TO RELATED APPLICATIONS

[0002] This application claims benefit of priority under 35 U.S.C. §119(e) to U.S. Provisional Application No. 61/479,952, filed April 28, 2011, U.S. Provisional Application No. 61/531,583, filed September 6, 2011, U.S. Provisional Application No. 61/531,574, filed September 6, 2011, U.S. Provisional Application No. 61/538,079, filed September 22, 2011, U.S. Provisional Application No. 61/564,763, filed November 29, 2011, U.S. Provisional Application No. 61/578,192, filed December 20, 2011, U.S. Provisional Application No. 61/594,160 filed February 2, 2012, U.S. Provisional Application No. 61/598,881 filed February 14, 2012, U.S. Provisional Application No. 61/598,892 filed February 14, 2012, U.S. Provisional Application No. 61/625,596 filed April 17, 2012, and U.S. Provisional Application No. 61/639,017 filed April 26, 2012 entitled "METHODS AND COMPOSITIONS FOR MULTIPLEX PCR", the disclosures of which are incorporated herein by reference in their entireties.

[0003] SEQUENCE LISTING

[0004] This application hereby incorporates by reference the material of the electronic Sequence Listing filed concurrently herewith. The material in the electronic Sequence Listing is submitted as a text (.txt) file entitled "2012_04_25 LT00503 PCT_ST25.txt" created on April 25, 2012, which has a file size of 18943 KB, and is herein incorporated by reference in its entirety.

[0005] TECHNICAL FIELD

[0006] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for amplifying one or more target sequences within a sample containing a plurality of target sequences. Optionally, a plurality of target sequences, for example at least 10, 50, 100, 500, 1000, 2500, 5000, 7500, 10000, 25000, 50000 or 100000, are amplified within a single amplification reaction. In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for amplifying one or more target sequences from a single source, such as genomic DNA or formalin-fixed paraffin-embedded (FFPE) DNA. In particular, methods, kits, systems apparatuses and compositions useful for amplifying one or more target sequences using primers having a cleavable group are disclosed.

[0007] BACKGROUND

[0008] Several biological applications involve the selective amplification of nucleic acid molecules within a population. For example, next-generation sequencing methods can involve the analysis of

selected targets within a large population of nucleic acid molecules. For such applications, it can be useful to increase the total number of targets that can be selectively amplified from a population within a single amplification reaction. Such selective amplification is typically achieved through use of one or more primers that can selectively hybridize to, or selectively promote the amplification of, a particular target nucleic acid molecule. Such selective amplification can be complicated by the formation of amplification artifacts, such as primer-dimers and the like. The formation of such amplification artifacts (also referred to herein as nonspecific amplification products) can consume critical amplification reagents, e.g., nucleotides, polymerase, primers, etc. Furthermore, such artifacts can frequently have shorter length relative to the intended product and in such situations can amplify more efficiently than the intended products and dominate the reaction output. Selective amplification can also be complicated by the formation of 'superamplicons', i.e., the formation of a extended amplicon, which can occur when extension of a first primer is extended through an adjacent target nucleic acid sequence, thereby creating a long non-specific amplification product, which can act as a template for extension with a second primer. The formation of such artifacts in amplification reactions, even when only a single pair of primers is employed, can complicate downstream applications such as qPCR, cloning, gene expression analysis and sample preparation for next-generation sequencing. In some downstream applications, including several next-generation sequencing methods, this problem can be compounded by the requirement to practice a secondary amplification step, since the artifacts can be further amplified during the secondary amplification. For example, downstream sequencing applications can involve the generation of clonally amplified nucleic acid populations that are individually attached to separate supports, such as beads, using emulsion PCR ("emPCR") and enrichment for clonal amplicons performed via positive selection. In such applications, the artifacts can be carried all the way through the library generation process to the emPCR stage, producing DNA capture beads that include non-specific amplification products. These artifact-containing beads can be selected for during the enrichment process with the template containing beads but are genetically non-informative.

[0009] Nucleic acid molecules amplified in a multiplex PCR reaction can be used in many downstream analysis or assays with, or without, further purification or manipulation. For example, the products of a multiplex PCR reaction (amplicons) when obtained in sufficient yield can be used for single nucleotide polymorphism (SNP) analysis, genotyping, copy number variation analysis, epigenetic analysis, gene expression analysis, hybridization arrays, analysis of gene mutations including but not limited to detection, prognosis and/or diagnosis of disease states, detection and

analysis of rare or low frequency allele mutations, nucleic acid sequencing including but not limited to *de novo* sequencing or targeted resequencing, and the like.

[0010] Exemplary next-generation sequencing systems include the Ion Torrent PGM™ sequencer (Life Technologies) and the Ion Torrent Proton™ Sequencer (Life Technologies), which are ion-based sequencing systems that sequence nucleic acid templates by detecting ions produced as a byproduct of nucleotide incorporation. Typically, hydrogen ions are released as byproducts of nucleotide incorporations occurring during template-dependent nucleic acid synthesis by a polymerase. The Ion Torrent PGM™ sequencer and Ion Proton ™ Sequencer detect the nucleotide incorporations by detecting the hydrogen ion byproducts of the nucleotide incorporations. The Ion Torrent PGM™ sequencer and Ion Torrent Proton™ sequencer include a plurality of nucleic acid templates to be sequenced, each template disposed within a respective sequencing reaction well in an array. The wells of the array are each coupled to at least one ion sensor that can detect the release of H^+ ions or changes in solution pH produced as a byproduct of nucleotide incorporation. The ion sensor comprises a field effect transistor (FET) coupled to an ion-sensitive detection layer that can sense the presence of H^+ ions or changes in solution pH. The ion sensor provides output signals indicative of nucleotide incorporation which can be represented as voltage changes whose magnitude correlates with the H^+ ion concentration in a respective well or reaction chamber. Different nucleotide types are flowed serially into the reaction chamber, and are incorporated by the polymerase into an extending primer (or polymerization site) in an order determined by the sequence of the template. Each nucleotide incorporation is accompanied by the release of H^+ ions in the reaction well, along with a concomitant change in the localized pH. The release of H^+ ions is registered by the FET of the sensor, which produces signals indicating the occurrence of the nucleotide incorporation. Nucleotides that are not incorporated during a particular nucleotide flow will not produce signals. The amplitude of the signals from the FET may also be correlated with the number of nucleotides of a particular type incorporated into the extending nucleic acid molecule thereby permitting homopolymer regions to be resolved. Thus, during a run of the sequencer multiple nucleotide flows into the reaction chamber along with incorporation monitoring across a multiplicity of wells or reaction chambers permit the instrument to resolve the sequence of many nucleic acid templates simultaneously. Further details regarding the compositions, design and operation of the Ion Torrent PGM™ sequencer can be found, for example, in U.S. Patent Application Ser. No. 12/002781, now published as U.S. Patent Publication No. 2009/0026082; U.S. Patent Application Ser. No. 12/474897, now published as U.S. Patent Publication No. 2010/0137143; and

U.S. Patent Application Ser. No. 12/492844, now published as U.S. Patent Publication No. 2010/0282617, all of which applications are incorporated by reference herein in their entireties. In some embodiments, amplicons can be manipulated or amplified through bridge amplification or emPCR to generate a plurality of clonal templates that are suitable for a variety of downstream processes including nucleic acid sequencing. In one embodiment, nucleic acid templates to be sequenced using the Ion Torrent PGM™ or Ion Torrent Proton™ system can be prepared from a population of nucleic acid molecules using one or more of the target-specific amplification techniques outlined herein. Optionally, following target-specific amplification a secondary and/or tertiary amplification process including, but not limited to a library amplification step and/or a clonal amplification step such as emPCR can be performed.

[0011] As the number of nucleic acid targets desired to be amplified within a sample nucleic acid population increases, the challenge of selectively amplifying these targets while avoiding the formation of undesirable amplification artifacts can correspondingly increase. For example, the formation of artifacts including primer-dimers and superamplicons can be a greater issue in multiplex PCR reactions where PCR primer pairs for multiple targets are combined in a single reaction tube and co-amplified. In multiplex PCR, the presence of additional primer pairs at elevated concentrations relative to the template DNA makes primer-primer interactions, and the formation of primer-dimers and other artifacts, more likely.

[0012] Current methods for avoiding or reducing the formation of artifacts, such as primer-dimers, during nucleic acid amplification center around the primer design process and often utilize dedicated software packages (e.g., DNAsoftwares's Visual OMP, MultiPLX, ABI's Primer Express, etc.) to design primer pairs that are predicted to exhibit minimal interaction between the other primers in the pool during amplification. Through the use of such software, primers can be designed to be as target-specific or amplicon-specific as possible, and often are grouped into subsets to minimize primer-primer interactions, primer-dimer formation and superamplicons. Stringent design parameters, however, limit the number of amplicons that can be co-amplified simultaneously and in some cases may prevent the amplification of some amplicons altogether. Other current methods require the use of multiple PCR primer pools to segregate primers into non-overlapping pools to minimize or prevent primer artifacts during the amplification step. Other methods include the use of multiple primer pools or single plex reactions to enhance the overall yield of amplification product per reaction. In a multiplex PCR reaction, each primer pair competes in the amplification reaction with additional primer pairs for a finite amount of dNTPs, polymerase and other reagents. There is

therefore a need for improved methods, compositions, systems, apparatuses and kits that allow for the selective amplification of multiple target nucleic acid molecules within a population of nucleic acid molecules while avoiding, or minimizing, the formation of artifacts (also referred to as non-specific amplification products), including primer dimers. There is also a need for improved methods, compositions, systems, apparatuses and kits that allow for the selective amplification of multiple target nucleic acid molecules from a single nucleic acid sample, such as genomic DNA and/or formalin-fixed paraffin embedded (FFPE) DNA while avoiding, or minimizing, the formation of artifacts. There is also a need in the art for improved methods, compositions, systems and kits that allow for the simultaneous amplification of thousands of target-specific nucleic acid molecules in a single reaction, which can be used in any applicable downstream assay or analysis.

[0013] The practice of the present subject matter may employ, unless otherwise indicated, conventional techniques and descriptions of organic chemistry, molecular biology (including recombinant techniques), cell biology, and biochemistry, which are within the skill of the art. Such conventional techniques include, but are not limited to, preparation of synthetic polynucleotides, polymerization techniques, chemical and physical analysis of polymer particles, preparation of nucleic acid libraries, nucleic acid sequencing and analysis, and the like. Specific illustrations of suitable techniques can be used by reference to the examples provided herein. Other equivalent conventional procedures can also be used. Such conventional techniques and descriptions can be found in standard laboratory manuals such as *Genome Analysis: A Laboratory Manual Series* (Vols. I-IV), *PCR Primer: A Laboratory Manual, and Molecular Cloning: A Laboratory Manual* (all from Cold Spring Harbor Laboratory Press), Hermanson, Bioconjugate Techniques, Second Edition (Academic Press, 2008); Merkus, Particle Size Measurements (Springer, 2009); Rubinstein and Colby, Polymer Physics (Oxford University Press, 2003); and the like.

[0014] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art to which these inventions belong. All patents, patent applications, published applications, treatises and other publications referred to herein, both *supra* and *infra*, are incorporated by reference in their entirety. If a definition and/or description is set forth herein that is contrary to or otherwise inconsistent with any definition set forth in the patents, patent applications, published applications, and other publications that are herein incorporated by reference, the definition and/or description set forth herein prevails over the definition that is incorporated by reference.

[0015] As used herein, the terms "comprises," "comprising," "includes," "including," "has," "having" or any other variation thereof, are intended to cover a non-exclusive inclusion. For example, a process, method, article, or apparatus that comprises a list of features is not necessarily limited only to those features but may include other features not expressly listed or inherent to such process, method, article, or apparatus. Further, unless expressly stated to the contrary, "or" refers to an inclusive-or and not to an exclusive-or. For example, a condition A or B is satisfied by any one of the following: A is true (or present) and B is false (or not present), A is false (or not present) and B is true (or present), and both A and B are true (or present).

[0016] BRIEF DESCRIPTION OF THE DRAWINGS

[0017] The accompanying drawings, which are incorporated into and form a part of the specification, illustrate one or more exemplary embodiments and serve to explain the principles of various exemplary embodiments. The drawings are exemplary and explanatory only and are not to be construed as limiting or restrictive in any way.

[0018] FIG. 1 is a schematic outlining an exemplary embodiment of a method utilizing degradable amplification primers according to the disclosure.

[0019] FIG. 2 is a schematic outlining an exemplary embodiment of a method obtaining a target-specific amplicon library according to the disclosure.

[0020] FIG. 3 shows examples of elution profiles for exemplary unmodified and modified primer pools. FIG. 3A shows a significant and predominant production of primer-dimers when using an exemplary set of standard multiplex primers. FIG. 3B shows a decrease in primer-dimers and an overall increase in expected amplicon product (104 bp) when using an exemplary set of modified multiplex primers as exemplified by the application.

[0021] FIG. 4 shows the effect of increasing amplicon GC content in both an exemplary 94-plex and an exemplary 380-plex reaction.

[0022] FIG. 5 shows quantification of the abundance and reproducibility of an exemplary multiplex reaction on genomic DNA using primer set HSMv12. The data is averaged across individual 3 runs performed on an Ion Torrent PGM™ Sequencer (Life Technologies). The level of coverage per amplicon is provided as Log of Counts.

[0023] FIG. 6 shows quantification of the abundance and reproducibility of an exemplary multiplex reaction on genomic DNA when analyzed using an Ion Torrent PGM™ Sequencer (Life Technologies). The data shows the number of reads per amplicon for both the forward (FIG. 6A) and reverse primers (FIG. 6B) in the primer pool.

[0024] FIG. 7 shows quantification of the abundance and reproducibility of an exemplary 384-plex reaction on a genomic DNA sample across 7 individual runs on an Ion Torrent PGM™ Sequencer (Life Technologies). The average number of reads per amplicon is 400.

[0025] FIG. 8 shows quantification of the abundance and reproducibility of an exemplary 411-plex PCR of genomic DNA across 7 individual runs on an Ion Torrent PGM™ Sequencer (Life Technologies) . The average number of reads per amplicon is 400.

[0026] FIG. 9 shows an image of agarose gel electrophoresis visualizing exemplary amplification products (lanes 2 and 4) after performing a multiplex PCR and library amplification on an FFPE sample according to an exemplary embodiment.

[0027] FIG. 10 shows quantification of the abundance and reproducibility of data obtained from an FFPE DNA sample (10 ng) in an exemplary 384-plex PCR obtained using an Ion Torrent PGM™ Sequencer (Life Technologies). The average number of reads per amplicon is 400.

[0028] FIG. 11 shows quantification of the abundance and reproducibility of data obtained from a FFPE DNA sample (10 ng) after an exemplary 94-plex reaction. The data shows the number of reads per amplicon for both the forward (FIG. 11A) and reverse primers (FIG. 11B) in the primer pool.

[0029] FIG. 12 shows a graph reporting the detection of mutations in codon 12 and codon 13 of the KRAS gene obtained by performing multiplex PCR and library amplification of control DNA and sequencing on an Ion Torrent PGM™ Sequencer (Life Technologies).

[0030] FIG. 13 shows sequencing alignment data identifying 6 mutations of the cystic fibrosis (CFTR) gene in a sample when using exemplary modified multiplex primers and exemplary library amplification process according to the disclosure.

[0031] FIG. 14 shows the frequencies of twelve different amplicons obtained for a region of the CLTCL1 gene in several DNA samples containing known copy number variation. The amplicons were obtained according to exemplary embodiments of the disclosure.

[0032] FIG. 15 shows the frequencies of four different amplicons obtained for a region of the IKZF1 gene in several DNA samples containing known copy number variation. The amplicons were obtained according to exemplary embodiments of the multiplex PCR methods disclosed herein.

[0033] FIG. 17 illustrates a system for designing primers or assays according to an exemplary embodiment.

[0034] FIG. 18 illustrates a system for designing primers or assays according to an exemplary embodiment.

[0035] FIG. 19 illustrates an amplicon sequence including an insert sequence surrounded by a pair of primers designed according to an exemplary embodiment.

[0036] FIG. 20 illustrates PCR amplification of an amplicon sequence (which may be referred to as "tile" herein) including an insert surrounded by a pair of primers designed according to an exemplary embodiment.

[0037] FIG. 21 illustrates a set of candidate amplicons for a given target region, each including an insert surrounded by a pair of primers, for tiling and pooling according to an exemplary embodiment.

[0038] FIG. 22 illustrates a method according to an exemplary embodiment.

[0039] FIG. 23 illustrates a method for tiling a plurality of amplicons for one or more given targets according to an exemplary embodiment.

[0040] FIG. 24 illustrates a method for determining tiles for one or more given targets and candidate amplicons according to an exemplary embodiment.

[0041] FIG. 25A illustrates a set of candidate amplicons for covering a given target region, each including an insert surrounded by a pair of primers, for tiling and pooling according to an exemplary embodiment.

[0042] FIG. 25B illustrates a set of vertices for generating a graph according to an exemplary embodiment.

[0043] FIG. 26A illustrates the 15 candidate amplicons of FIG. 25A, except that three "initial" amplicons having at least some overlap between their insert and the beginning of the target region are highlighted.

[0044] FIG. 26B illustrates the connection of a source vertex to three vertices corresponding to the initial amplicons of FIG. 26A with edges.

[0045] FIG. 27A illustrates the 15 candidate amplicons of FIG. 25A, except that three "terminal" amplicons having at least some overlap between their insert and the end of the target region are highlighted.

[0046] FIG. 27B illustrates the connection of a sink vertex to three vertices corresponding to the terminal amplicons of FIG. 27A with edges.

[0047] FIG. 28A illustrates the 15 candidate amplicons of FIG. 25A, except that various amplicons for building internal edges are highlighted.

[0048] FIG. 28B illustrates the connection of some amplicon insert vertices to subsequent, proper, overlaps according to an exemplary embodiment.

[0049] FIG. 29A illustrates the connection of additional amplicon insert vertices to subsequent, proper, overlaps according to an exemplary embodiment.

[0050] FIG. 29B illustrates the 15 candidate amplicons of FIG. 25A, along with the basis for the gap shown in FIG. 29A according to an exemplary embodiment.

[0051] FIG. 30A illustrates three possible additional edges that could be used from source to sink to tile the target in this example according to an exemplary embodiment.

[0052] FIG. 30B illustrates an exemplary definition of an edge cost function assigning a cost to each one of the graph's edges linking amplicon vertices according to an exemplary embodiment.

[0053] FIG. 30C illustrates the least-cost path from source to sink in the example of FIG. 30B according to an exemplary embodiment.

[0054] FIG. 31 illustrates the 15 candidate amplicons of FIG. 25A, except that the five amplicons corresponding to the vertices forming the least-cost path shown in FIG. 30C are highlighted.

[0055] FIG. 32 illustrates three amplicons assigned to a first pool and two amplicons assigned to a second pool according to an exemplary embodiment.

[0056] FIG. 33A illustrates a minimal distance between amplicons according to an exemplary embodiment.

[0057] FIGS. 33B-D illustrate several problems, including primer "race condition," preferential amplification of sub amplicons, and super amplicons that may be ameliorated by using a minimal distance as illustrated in FIG. 33A.

[0058] FIG. 34 illustrates a method for pooling amplicons across a plurality of pools according to an exemplary embodiment.

[0059] FIG. 35 illustrates a method according to an exemplary embodiment.

[0060] **SUMMARY**

[0061] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for performing multiplex amplification of nucleic acids. In some embodiments, the method includes amplifying a plurality of target sequences within a sample including two or more target sequences. Optionally, multiple target sequences of interest from a sample can be amplified using one or more target-specific primers in the presence of a polymerase under amplification conditions to produce a plurality of amplified target sequences. The amplifying optionally includes contacting a nucleic acid molecule including at least one target sequence with one or more target-specific primers and at least one polymerase under amplification conditions. The contacting can produce one or more amplified target sequences.

[0062] In some embodiments, the disclosed methods (and related compositions, systems, apparatuses and kits) can include ligating at least one adapter to at least one of the amplified target sequences to produce one or more adapter-ligated amplified target sequences. The adapter can include at least one sequence that is substantially non-complementary to the target sequence, to the amplified target sequence, and/or to the nucleic acid molecule.

[0063] In some embodiments, the amplifying can produce least two amplified target sequences that are less than 50 % complementary to each other. In some embodiments, at least one amplified target sequence is substantially non-complementary to another target sequence in the sample. In some embodiments, an amplified target sequence can be substantially noncomplementary to any one or more nucleic acid molecules in the sample that does not include the target sequence.

[0064] In some embodiments, the disclosed methods (as well as related compositions, systems, apparatuses and kits) can involve reamplifying at least one of the amplified target sequences c. For example, an adapter-ligated amplified target sequence can be reamplified to produce at least one reamplified adapter-ligated amplified target sequence. In some embodiments, at least one of the adapter-ligated amplified target sequences can be contacted with one or more adapters or their complement, and a polymerase under amplification conditions to produce at least one reamplified adapter-ligated amplified target sequence. In some embodiments, at least one adapter or its complement is substantially non-complementary to at least one amplified target sequence.

[0065] In some embodiments, the disclosure relates generally to compositions (as well as related methods, kits, apparatuses and systems using such compositions) comprising one or more target-specific primers useful for hybridizing to, and optionally amplifying, at least one target sequence in a sample. In some embodiments, the composition can include a plurality of target-specific primers useful for amplifying one, two or more target sequences in a sample. The compositions can further include one or more adapters.

[0066] In some embodiments, a target sequence includes one or more mutational hotspots, single nucleotide polymorphisms (SNPs), short tandem repeats (STRs), coding regions, exons and genes. In some embodiments, the number of target sequences amplified by one or more of the methods using the compositions (and related kits, apparatuses and systems) disclosed herein can be dozens, hundreds or thousands of target sequences in a single reaction. In some embodiments, the number of different targets amplified in a single multiplex amplification can be at least 100, 300, 500, 750, 1000, 2500, 5000, 7500, 10000, 12500, 15000 or greater.

[0067] In some embodiments, a target-specific primer, adapter, amplified target sequence or nucleic acid molecule can include one or more cleavable moieties, also referred to herein as cleavable groups. Optionally, the methods can further include cleaving at least one cleavable group of the target-specific primer, adapter, amplified target sequence or nucleic acid molecule. The cleaving can be performed before or after any of the other steps of the disclosed methods. In some embodiments, the cleavage step occurs after the amplifying and prior to the ligating. In one embodiment, the cleaving includes cleaving at least one amplified target sequence prior to the ligating. The cleavable moiety can be present in a modified nucleotide, nucleoside or nucleobase. In some embodiments, the cleavable moiety can include a nucleobase not naturally occurring in the target sequence of interest. In some embodiments, uracil or uridine can be incorporated into a DNA-based nucleic acid as a cleavable group. In one exemplary embodiment, a uracil DNA glycosylase can be used to cleave the cleavable group from the nucleic acid. In another embodiment, inosine can be incorporated into a DNA-based nucleic acid as a cleavable group. In one exemplary embodiment, EndoV can be used to cleave near the inosine residue and a further enzyme such as Klenow can be used to create blunt-ended fragments capable of blunt-ended ligation. In another exemplary embodiment, the enzyme hAAG can be used to cleave inosine residues from a nucleic acid creating abasic sites that can be further processed by one or more enzymes such as Klenow to create blunt-ended fragments capable of blunt-ended ligation.

[0068] In some embodiments, the methods disclosed herein (as well as related kits, compositions, apparatuses and systems) can include amplifying at least two target sequences of the sample (e.g., a first target sequence and a second target sequence) that are different from each other. In some embodiments, the methods disclosed herein (as well as related kits, compositions, apparatuses and systems) include simultaneously amplifying a first target sequence and a second target sequence that are less than 50% complementary to each other. In some embodiments, the first target sequence and a second target sequence are substantially non-complementary to each other.

[0069] In some embodiments, the methods disclosed herein (as well as related kits, compositions, apparatuses and systems) can include amplifying using at least two target-specific primers (e.g., a first target-specific primer and a second target-specific primer) that are different from each other. In some embodiments, a first target-specific primer can be at least 50% complementary to at least some portion of a first target sequence. In some embodiments, the first target-specific primer can be substantially noncomplementary to another target sequence in the sample. For example, the first target-specific primer can be substantially noncomplementary to a second target sequence.

Optionally, the first target-specific primer can be substantially complementary to a first target sequence within a sample and can be substantially noncomplementary to any portion of any other nucleic acid molecule within the sample other than the first target sequence.

[0070] Optionally, methods of multiplex amplification disclosed herein include amplifying at least a portion of a target sequence in a sample using at least one target-specific primer that is substantially complementary to at least some portion of a nucleic acid molecule that includes a corresponding target sequence. In some embodiments, the at least one target-specific primer is substantially complementary to at least some portion of the corresponding target sequence. In some embodiments, the amplifying can include using a primer pair including a target-specific forward primer and a target-specific reverse primer. In some embodiments, the target-specific primer can include at least one sequence that is substantially complementary or substantially identical to at least some portion of a nucleic acid molecule that includes the corresponding target sequence or its complement. Optionally, the target-specific primer is not substantially complementary to any other nucleic acid molecule present in the sample. In some embodiments, the target-specific primer can include at least one sequence that is substantially complementary or substantially identical to at least some portion of a corresponding target sequence or its complement. In some embodiments, the target-specific primer can include at least one sequence that is complementary or identical to at least some portion of a corresponding target sequence or its complement. In some embodiments, a target-specific primer does not include any nucleic acid sequence that is at least 5 contiguous nucleotides, 8 nucleotides, 10 contiguous nucleotides, or 15 contiguous nucleotides in length, and that is substantially noncomplementary to at least some portion of its corresponding target sequence. In some embodiments, a target-specific primer can hybridize under stringent conditions to at least some portion of a corresponding target sequence in the sample. In some embodiments, at least one of the target-specific primers is not substantially complementary to any nucleic acid sequence present in the sample other than its corresponding target sequence.

[0071] In some embodiments, one or more target-specific primers can be designed to exclude one or more sequence motifs. For example, at least one of the target-specific primers may be designed to not include a triplet nucleotide motif that is repeated 5 or more times in the target-specific primer. Optionally, at least one of the target-specific primers may be designed to not include the nucleotide sequence “ACA”, repeated 3 or more times. Further, at least one of the target-specific primers may be designed to not include a homopolymer greater than 8 nucleotides in length. Optionally, at least

one of the target-specific primers of the methods disclosed herein may be designed to possess a GC content of less than 85%.

[0072] In some embodiments, one or more of the methods of amplifying disclosed herein includes performing a target-specific amplification. Performing the target-specific amplification can include amplifying one or more target sequences using one or more exclusively target-specific primers, i.e., primers that do not include any shared or universal sequence motifs. Typically, one or more of the target-specific primers are substantially complementary to at least some portion of their corresponding target sequence, or to some portion of the nucleic acid molecule including the corresponding target sequence. In some embodiments, one, some or all of the target-specific primers are substantially complementary to at least some portion of their corresponding target sequence, or to some portion of the nucleic acid molecule including the corresponding target sequence, across their (i.e., the primers') entire length. .

[0073] In some embodiments, a nucleic acid molecule in a sample, an amplified target sequence, an adapter or a target-specific primer includes a 5' end and a 3' end. The 5' end can include a free 5' phosphate group or its equivalent; the 3' end can include a free 3' hydroxyl group or its equivalent. Optionally, the ends of an amplified target sequence can be substantially non-complementary to the ends of another amplified target sequence. In some embodiments, the 3' end can include about 30 nucleotides, or about 15 nucleotides from the 3' hydroxyl group. In some embodiments, the 5' end can include about 30 nucleotides, or about 15 nucleotides, from the 5' phosphate group. In some embodiments, any one amplified target sequence having a 3' end and 5'end can be substantially non-complementary to any portion of any other amplified target sequence.

[0074] Optionally, the disclosed methods can further include ligating one or more adapters including a universal priming sequence to the amplified product formed as a result of such target-specific amplification. For example, in some embodiments, one or more adapters can be ligated to an amplified target sequence. Optionally, an adapter that is ligated to an amplified target sequence is susceptible to exonuclease digestion. In some embodiments, an adapter susceptible to exonuclease digestion can be ligated to the 3' end of an amplified target sequence. In some embodiments, an adapter ligated to an amplified target sequence does not include a protecting group. In some embodiments, the adapter does not include a protecting group that can prevent nucleic acid degradation or digestion under degrading or digesting conditions. Subsequent enzymatic digestion of the adapter-ligated amplified target sequence in the presence of nucleic acids that do not include a

protecting group, offers a means for selective digestion of the unprotected nucleic acids. In some embodiments, an adapter can include a DNA barcode or tagging sequence.

[0075] In some embodiments, the methods disclosed herein (as well as related kits, systems, apparatuses and compositions) can include contacting an amplified target sequence having a 3' end and a 5'end with a ligation reaction mixture. In some embodiments, a ligation reaction mixture can include one or more adapters and a ligase to produce at least one adapter-ligated amplified target sequence. In some embodiments, none of the adapters in a ligation mixture, prior to the ligating, includes a target-specific sequence. In some embodiments, none of the adapters in the ligation mixture, prior to ligating, includes a sequence that is substantially complementary to a 3' end or a 5' end of an amplified target sequence. Optionally, the 3' end or the 5' end of an amplified target sequence includes about 30 nucleotides, and in some instances refers to about 15 nucleotides from the 3' end or the 5' end of an amplified target sequence. In some embodiments, none of the adapters in a ligation mixture, prior to ligating, can hybridize under high stringency, to some portion of an amplified target sequence. In some embodiments, ligating can include direct ligation of one or more adapters to one or more amplified target sequences. In one embodiment, ligating can include performing a blunt-ended ligation. For example, the process of blunt-ended ligation can include ligating a substantially blunt-end double-stranded amplified target sequence to a substantially blunt-ended double-stranded adapter. In some embodiments, ligating does not include one or more additional oligonucleotide adapters prior to ligating an adapter to an amplified target sequence.

[0076] In some embodiments, the disclosure relates generally to methods for performing amplification of a target sequence (as well as related compositions, systems, apparatuses and kits using the disclosed methods) and can include a digestion step. In some embodiments, the methods also include a ligating step, and the digestion step is performed prior to a ligating step. In some embodiments, an amplified target sequence can be partially digested prior to performing a ligation step. For example, an amplified target sequence can be digested by enzymatic, thermal or chemical means. In some embodiments, an amplified target sequence can be digested prior to ligating to produce a blunt-end amplified target sequence. In some embodiments, a blunt-ended amplified target sequence can include a 5' phosphate group at the 5' end of the digested amplified target sequence.

[0077] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for performing multiplex nucleic acid amplification. In some embodiments, the methods (as well as related compositions, kits, apparatuses and systems using such methods) include amplifying one or more target sequences using one or more target-specific primers in the presence of

polymerase under amplification conditions to produce an amplified target sequence and, ligating an adapter to the amplified target sequence. Further, the method can include reamplifying an adapter-ligated amplified target sequence to form a reamplified adapter-ligated amplified target sequence. In some embodiments, a reamplified adapter-ligated amplified target sequence can be produced using no more than two rounds of target-specific selection.

[0078] In some embodiments, one or more target-specific primers, target sequences or adapters can include a cleavable group. Furthermore, a cleavable group can be located at a nucleotide position at, or near, the terminus of a target-specific primer, target sequence or adapter. In some embodiments, a cleavable group can be located within 15 nucleotides of the 3' end or 5' end of the nucleic acid having the cleavable group. In some embodiments, a cleavable group can be located at or near a central nucleotide in a target-specific primer. In some embodiments, one or more cleavable groups can be present in a target-specific primer or adapter. In some embodiments, cleavage of one or more cleavable groups in a target-specific primer or an adapter can generate a plurality of nucleic acid fragments with differing melting temperatures. In one embodiment, the placement of one or more cleavable groups in a target-specific primer or adapter can be regulated or manipulated by determining a comparable maximal minimum melting temperature for each nucleic acid fragment, after cleavage of the cleavable group. In some embodiments the cleavable group can be a uracil or uridine moiety. In some embodiments the cleavable group can be an inosine moiety. In some embodiments, at least 50% of the target-specific primers can include at least one cleavable group. In some embodiments, each target-specific primer includes at least one cleavable group.

[0079] In one embodiment, a multiplex nucleic acid amplification method is disclosed herein that includes a) amplifying one or more target sequences using one or more target-specific primers in the presence of polymerase to produce an amplified target sequence, and b) ligating an adapter to the amplified target sequence to form an adapter-ligated amplified target sequence. In some embodiments, amplifying can be performed in solution such that an amplified target sequence or a target-specific primer is not linked to a solid support or surface. In some embodiments, ligating can be performed in solution such that an amplified target sequence or an adapter is not linked to a solid support or surface. In another embodiment, amplifying and ligating can be performed in solution such that an amplified target sequence, a target-specific primer or an adapter is not linked to a solid support or surface.

[0080] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for synthesizing two or more target sequences within a sample. In one

embodiment, the synthesizing method includes a) synthesizing two or more target sequences using a plurality of target-specific primers in the presence of polymerase under polymerizing conditions to produce a plurality of synthesized target sequences. In some embodiments, the method further includes ligating one or more adapters to the synthesized target sequences. In some embodiments, a target sequence of interest includes one or more mutational hotspots, single nucleotide polymorphisms (SNPs), short tandem repeats (STRs), coding regions, exons and genes. In some embodiments, the number of target sequences that can be synthesized in a multiplex reaction using the compositions (and related methods, kits, apparatuses and systems) disclosed herein can be dozens, hundreds or thousands of target sequences in a single sample. Optionally, multiple target sequences of interest from a sample can be synthesized using one or more target-specific primers in the presence of a polymerase under polymerizing conditions to produce a plurality of synthesized target sequences. In some embodiments, a synthesized target sequence can be less than 50 % complementary to another synthesized target sequence. In some embodiments, a synthesized target sequence can be substantially non-complementary to another target sequence in the sample. In some embodiments, a synthesized target sequence can be substantially noncomplementary to any one or more nucleic acid molecules in the sample that is not a target sequence of interest. In some embodiments, synthesizing a target sequence can include ligating an adapter to a synthesized target sequence, thereby producing an adapter-ligated synthesized target sequence.

[0081] In some embodiments, the disclosure relates generally to synthesizing a target sequence from a plurality of target sequences. For example, a method of synthesizing can include synthesizing a target sequence using a plurality of target-specific primers in the presence of polymerase under polymerizing conditions to produce a plurality of synthesized target sequences. Synthesizing can further include resynthesizing at least one adapter-ligated synthesized target sequence. In some embodiments, resynthesizing can include contacting at least one adapter-ligated synthesized target sequence with at least one adapter or its complement and a polymerase under polymerizing conditions to produce a plurality of resynthesized adapter-ligated synthesized target sequences. In some embodiments, a resynthesized adapter-ligated synthesized target sequence can be produced using no more than two rounds of target-specific selection.

[0082] In some embodiments, a method for synthesizing target sequences can include a synthesizing and a ligating step. In some embodiments, ligating does not include an adapter that is substantially complementary to a portion of a synthesized target sequence. In some embodiments, an adapter is not substantially complementary to about 30 contiguous nucleotides, or about 20 contiguous

nucleotides, from a 3' end or a 5' end of a synthesized target sequence. In some embodiments, an adapter can include at least one sequence that is substantially complementary, or substantially identical, to at least a portion of a universal primer.

[0083] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for performing multiplex nucleic acid amplification. In one embodiment, the method includes amplifying one or more target sequences using one or more target-specific primers in the presence of polymerase under amplification conditions to produce an amplified target sequence; ligating an adapter to the amplified target sequence; and reamplifying at least one adapter-ligated amplified target sequence. In some embodiments, reamplifying includes contacting an adapter-ligated amplified target sequence with one or more adapters (or their complements) and a polymerase under amplification conditions to produce at least one reamplified adapter-ligated amplified target sequence. In some embodiments, an amplified target sequence can be less than 50 % complementary to another amplified target sequence. In some embodiments, an amplified target sequence can be substantially non-complementary to another target sequence in the sample. In some embodiments, an amplified target sequence can be substantially noncomplementary to any one or more nucleic acid molecules in the sample that is not a target sequence of interest. In some embodiments, an amplified target sequence can be ligated to at least one adapter, or their complement, to produce one or more adapter-ligated amplified target sequences. In some embodiments, an adapter-ligated amplified target sequence can be reamplified to produce at least one reamplified adapter-ligated amplified target sequence. In some embodiments, an adapter or their complement is not substantially complementary to any portion of any other nucleic acid molecule within the sample. In some embodiments, an adapter or their complement is not substantially complementary to at least one amplified target sequence. In one embodiment, one or more of the adapters or their complement during the reamplifying step can be a universal primer. In one embodiment, the ligating step can further include ligating a DNA barcode or DNA tagging sequence to an amplified target sequence prior to ligating an adapter to an amplified target sequence.

[0084] In some embodiments, amplifying and synthesizing methods of the disclosure can be performed as "addition-only" processes. In some embodiments, an addition-only process excludes the removal of all, or a portion of a first reaction mixture including the amplifying or synthesizing compositions, for further manipulation during the amplification or synthesizing steps. In some embodiments, an addition-only process can be automated for example for use in high-throughput processing.

[0085] In some embodiments, the disclosure generally relates to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) for performing nucleic acid amplification and nucleic acid synthesis. In some embodiments, one or more of the compositions disclosed herein (as well as related methods, kits, systems and apparatuses) can include at least one target-specific primer and/or at least one adapter. In some embodiments, the compositions include a plurality of target-specific primers or adapters that are about 15 to about 40 nucleotides in length. In some embodiments, the compositions include one or more target-specific primers or adapters that include one or more cleavable groups. In some embodiments, one or more types of cleavable groups can be incorporated into a target-specific primer or adapter. In some embodiments, a cleavable group can be located at, or near, the 3' end of a target-specific primer or adapter. In some embodiments, a cleavable group can be located at a terminal nucleotide, a penultimate nucleotide, or any location that corresponds to less than 50% of the nucleotide length of the target-specific primer or adapter. In some embodiments, a cleavable group can be incorporated at, or near, the nucleotide that is central to the target-specific primer or the adapter. For example, a target specific primer of 40 bases can include a cleavage group at nucleotide positions 15-25. Accordingly, a target-specific primer or an adapter can include a plurality of cleavable groups within its 3' end, its 5' end or at a central location. In some embodiments, the 5' end of a target-specific primer includes only non-cleavable nucleotides. In some embodiments, the cleavable group can include a modified nucleobase or modified nucleotide. In some embodiments, the cleavable group can include a nucleotide or nucleobase that is not naturally occurring in the corresponding nucleic acid. For example, a DNA nucleic acid can include a RNA nucleotide or nucleobase. In one example, a DNA based nucleic acid can include uracil or uridine. In another example, a DNA based nucleic acid can include inosine. In some embodiments, the cleavable group can include a moiety that can be cleaved from the target-specific primer or adapter by enzymatic, chemical or thermal means. In some embodiments, a uracil or uridine moiety can be cleaved from a target-specific primer or adapter using a uracil DNA glycosylase. In some embodiments, a inosine moiety can be cleaved from a target-specific primer or adapter using hAAG or EndoV.

[0086] In some embodiments, the disclosure relates generally to compositions including a target-specific primer of about 15 to about 40 nucleotides in length having a cleavable group located near the terminus of the target-specific primer, hybridized to a first strand of a double-stranded target sequence. In some embodiments, the primer is substantially complementary to the first strand of the double-stranded target sequence. In some embodiments, the disclosure relates generally to

compositions including a target-specific primer of about 15 to about 40 nucleotides in length having a cleavable group located near the terminus of the target-specific primer, hybridized to a first strand of a double-stranded target sequence, and a second target-specific primer of about 15 to about 40 nucleotides in length having a cleavable group located near the terminus of the second target-specific primer, hybridized to a second strand of the double-stranded target sequence. In some embodiments, the second target-specific primer is substantially complementary to the second strand of the double-stranded target sequence.

[0087] In some embodiments, the disclosure generally relates to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) for performing nucleic acid amplification and nucleic acid synthesis. In some embodiments, the compositions include a target-specific primer of about 15 to about 40 nucleotides in length having a uracil nucleotide located near the terminus of the target-specific primer and a second uracil nucleotide located near the central nucleotide of the target-specific primer. In some embodiments, the disclosure generally relates to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) for performing nucleic acid amplification and nucleic acid synthesis. In some embodiments, the compositions include a target-specific primer of about 15 to about 40 nucleotides in length having an inosine nucleotide located near the 3' terminus of the target-specific primer and at least a second inosine nucleotide located near the central nucleotide of the target-specific primer.

[0088] In some embodiments, the disclosure relates generally to a composition comprising at least one target-specific primer or at least one target-specific primer pair. In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers. Optionally, the composition can include at least 100, 200, 300, 500, 750, 1000, 1250, 1500, 1750, 2000, 2500, 3000, 4000, 5000, 7500 or 10,000 target-specific primers or target-specific primer pairs. In some embodiments, the composition comprising a plurality of target-specific primers includes at least one of the target-specific primers disclosed herein. In some embodiments, the composition comprising a plurality of target-specific primers includes at least one target-specific primer that is at least 90% identical to any one of the nucleic acid sequences provided herein or in the concurrently filed sequencing listing. In some embodiments, the composition comprising a plurality of target-specific primers includes one or more target-specific primer pairs disclosed herein or one or more primer pairs having at least 90% identity to any one of the primer pair nucleic acid sequences provided herein. In some embodiments, the composition comprising a plurality of target-specific primers can include a percentage identity of at least 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or

99% identity to any one or more of the nucleic acid sequences disclosed herein or in the concurrently filed sequence listing. In some embodiments, the composition comprising a plurality of target-specific primers can include any one or more target-specific primers selected from Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the composition comprising a plurality of target-specific primers can include any one or more target-specific primer pairs selected from Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the composition comprising a plurality of target-specific primers generally relates to any one or more nucleic acid sequences selected from SEQ ID NOs: 1-103,143 or includes at least 15 contiguous nucleotides from any one nucleic acid sequence selected from SEQ ID NOs: 1-103,143. In some embodiments, the composition is generally directed to an isolated nucleic acid sequence consisting of any one or more of the nucleic acid sequences set forth in SEQ ID NOs: 1-103,143.

[0089] In some embodiments, the disclosure relates generally to a composition comprising a target-specific primer of about 15 nucleotides to about 40 nucleotides in length. In some embodiments, the disclosure relates generally to a composition comprising a plurality of at least 2 target-specific primers of about 15 nucleotides to about 40 nucleotides in length. In some embodiments, the composition comprises a plurality of target-specific primer pairs of about 15 nucleotides to about 40 nucleotides in length designed using the primer selection criteria or primer selection methods outlined herein.

[0090] In some embodiments, the composition includes at least one target-specific primer that is substantially complementary across its entire length to at least one target sequence in a sample. In some embodiments, the composition includes a plurality of target-specific primers, where substantially all of the plurality of target-specific primers include a complementary nucleic acid sequence across their entire primer lengths to one or more target sequences in a sample. In some embodiments, the composition includes at least one target-specific primer that is complementary across its entire length to at least one target sequence in a sample. In some embodiments, the composition includes a plurality of target-specific primers, where substantially all of the plurality of target-specific primers include a complementary nucleic acid sequence across their entire primer lengths to one or more target sequences in a sample.

[0091] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having a cleavable group located at a 3' end of at least one of the plurality of the target-specific primers. In some embodiments, the composition includes a cleavable group located at a 3' end of substantially all of the plurality of target-specific primers. In some

embodiments, the cleavable group can include a uracil nucleobase, an inosine nucleoside or an analog thereof. In some embodiments, the 3' end of one or more target-specific primers can include more than one cleavable group and/or more than one species of cleavable group. For example, a composition having a cleavable group at the 3' end of one target-specific primer can include one uracil moiety and an inosine moiety in the 3' end of the same target-specific primer. In some embodiments, the composition can include at least one target-specific primer that includes a non-cleavable at the 3' terminal nucleotide. For example, a target-specific primer can include a cleavable group at the 3' end of the target-specific primer except for the terminal nucleotide at the 3' end of the target-specific primer. In some embodiments, the composition can include a plurality of target-specific primers where substantially all of the target-specific primers include a cleavable group at the 3' end except for the terminal nucleotide location.

[0092] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having a cleavable group located near or about a central nucleotide of at least one of the target-specific primers. In some embodiments, the composition includes a cleavable group located near or about a central nucleotide of substantially all of the plurality of the target-specific primers. For example, in a target-specific primer of 40 nucleotides, a cleavable group can be located near the central nucleotide, for example at the 15th nucleotide through the 25th nucleotide. In some instances, 'near' a central nucleotide can refer to a percentage of the length of the entire target-specific primer. For example in a 40 nucleotide target-specific primer, the location of a central cleavable group can include any location from about 40% to about 60% of the length of the target-specific primer. In some embodiments, a central nucleotide of an odd numbered target-specific primer includes the central nucleotide of the target-specific primer. In an even numbered target-specific primer a central nucleotide can include one nucleotide either side of the central nucleotide location. For example, in a 20 nucleotide target-specific primer, the central nucleotide can include nucleotide position 10, nucleotide position 11, or both.

[0093] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having at a 5' end only non-cleavable nucleotides. In some embodiments, the composition can include substantially all of the plurality of target-specific primers having only non-cleavable nucleotides at the 5' end. In some embodiments, the 5' end of the plurality of target-specific primers having only non-cleavable nucleotides can include fewer than 10 nucleotides from the 5' end. In some embodiments, the 5' end can include fewer than 8, 7, 6, 5, 4, 3 or 2 nucleotides from the 5' end. In some embodiments, the 5' end having non-cleavable nucleotides

can include less than 50% of the length of the target specific primer, less than 40% of the length of the target specific primer, less than 30% of the length of the target specific primer, less than 20% of the length of the target specific primer, or less than 10% of the length of the target-specific primer from the 5' end.

[0094] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers where at least one of the target-specific primers includes less than 20% of the nucleotides across the primer's entire length containing a cleavable group. In some embodiments, the composition comprises a plurality of target-specific primers where substantially all of the target-specific primers include less than 20% of the nucleotides across each primer's entire length containing a cleavable group. For example, a target-specific primer of 20 nucleotides in length can include 4 or fewer cleavage groups. In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers where at least one of the target-specific primers includes less than 10% of the nucleotides across the primer's entire length containing a cleavable group. In some embodiments, the composition comprises a plurality of target-specific primers where substantially all of the target-specific primers include less than 10% of the nucleotides across each primer's entire length containing a cleavable group. For example, a target-specific primer of 20 nucleotides in length can include 2 or fewer cleavage groups.

[0095] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having minimal cross-hybridization to at least one of the target-specific primers in the plurality of primers. In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having minimal cross-hybridization to substantially all of the target-specific primers in the plurality of primers. In some embodiments, minimal cross-hybridization to one or more target-specific primers in the plurality of primers can be evaluated by the formation of primer-dimers or dimer-dimers. In some embodiments, the composition can include fewer primer-dimers in a multiplex PCR amplification reaction as compared to a multiplex PCR amplification reaction of the prior art under corresponding amplification conditions.

[0096] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers, where at least one of the target-specific primers includes minimal cross-hybridization to non-specific sequences present in a sample. In some embodiments, the composition comprises a plurality of target-specific primers where substantially all of the target-specific primers include minimal cross-hybridization to non-specific sequences present in a sample.

In some embodiments, minimal cross-hybridization to non-specific sequences present in a sample can be evaluated by the presence of 'percent of reads off-target' or a decrease in 'percent of reads on target'. In some embodiments, the compositions as disclosed herein can provide fewer 'percent of reads off-target' or an increase in 'percent of reads on target' in multiplex PCR amplification reactions as compared to multiplex PCR amplification reactions of the prior art under corresponding amplification conditions. The "plex" of a given multiplex amplification refers generally to the number of different target-specific sequences that are amplified during a single multiplex amplification according to the disclosure. In some embodiments, the plex can be about 12-plex, 24-plex, 48-plex, 96-plex, 192-plex, 384-plex, 768-plex, 1536-plex, 3072-plex, 6144-plex or higher. In some embodiments, minimal cross-hybridization to non-specific sequences present in a sample can include less than 15%, less than 12%, or fewer than 10% reads off target. In some embodiments, the percent of reads on target per multiplex amplification can be greater than 85%, 88%, 90%, 92%, 94%, 95%, 96%, 97%, 98%, or more.

[0097] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having minimal self-complementarity. In some embodiments, the composition includes at least one target-specific primer that does not form a secondary structure, such as loops or hairpins. In some embodiments, the composition includes a plurality of target-specific primers where a majority (i.e., greater than 50%), or substantially all of the plurality of target-specific primers fail to form a secondary structure. The "plex" of a given multiplex amplification refers generally to the number of different target-specific sequences that are amplified during a single multiplex amplification according to the disclosure. In some embodiments, the plex can be about 12-plex, 24-plex, 48-plex, 96-plex, 192-plex, 384-plex, 768-plex, 1536-plex, 3072-plex, 6144-plex or higher. In some embodiments, minimal self-complementarity can include less than 10%, less than 8%, less than 5% or less than 3% of the plurality of target-specific primers possessing self-complementarity that allows a target-specific primer to form a secondary structure.

[0098] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers having minimal nucleotide sequence overlap at a 3' end or a 5' end. In some embodiments, the composition can include minimal overlap of nucleotide sequence in the 3' end of at least one target-specific primer. In some embodiments, the composition can include minimal overlap of nucleotide sequence in the 3' end of substantially all of the plurality of target-specific primers. In some embodiments, the composition can include minimal overlap of nucleotide sequence in the 5' end of at least one target-specific primer. In some embodiments, the composition

can include minimal overlap of nucleotide sequence in the 5' end of substantially all of the plurality of target-specific primers. In some embodiments, the composition can include minimal overlap of nucleotide sequence in the 3' end and the 5' end of at least one target-specific primer. In some embodiments, the composition can include minimal overlap of nucleotide sequence in the 3' end and the 5' end of substantially all of the plurality of target-specific primers. In some embodiments, the amount of nucleotide sequence overlap between one or more target-specific primers is less than 8 nucleotides. In some embodiments, the amount of nucleotide sequence overlap between one or more target-specific primers is less than 5 nucleotides. In some embodiments, the amount of nucleotide sequence between one or more target-specific primers of the plurality of primers is less than 8, 7, 6, 5, 4, 3, 2 or 1 nucleotide. In some embodiments, the composition can include a plurality of target-specific primers including a nucleotide sequence gap of one or more nucleotides. In some embodiments, the composition can include a nucleotide sequence gap of 1, 2, 3, 4, 5, 10, 15, 20 or more nucleotides between two or more of the plurality of target-specific primers. In some embodiments, the composition can include a nucleotide sequence gap of about 50 nucleotides between two or more target-specific primers in the plurality of target-specific primers. In some embodiments, the composition can include a nucleotide sequence gap of about 10, 20, 30, 40, or 50 nucleotides between substantially all of the target-specific primers in the plurality of target-specific primers.

[0099] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers of about 15 nucleotides to about 40 nucleotides in length having at least two or more following criteria,: a cleavable group located at a 3' end of substantially all of the plurality of primers, a cleavable group located near or about a central nucleotide of substantially all of the plurality of primers, substantially all of the plurality of primers at a 5' end including only non-cleavable nucleotides, minimal cross-hybridization to substantially all of the primers in the plurality of primers, minimal cross-hybridization to non-specific sequences present in a sample, minimal self-complementarity, and minimal nucleotide sequence overlap at a 3' end or a 5' end of substantially all of the primers in the plurality of primers. In some embodiments, the composition can include any 3, 4, 5, 6 or 7 of the above criteria.

[00100] In some embodiments, the disclosure relates generally to a composition comprising a plurality of at least 2 target-specific primers of about 15 nucleotides to about 40 nucleotides in length having two or more of the following criteria, a cleavable group located near or about a central nucleotide of substantially all of the plurality of primers, substantially all of the plurality of primers

at a 5' end including only non-cleavable nucleotides, substantially all of the plurality of primers having less than 20% of the nucleotides across the primer's entire length containing a cleavable group, at least one primer having a complementary nucleic acid sequence across its entire length to a target sequence present in a sample, minimal cross-hybridization to substantially all of the primers in the plurality of primers, minimal cross-hybridization to non-specific sequences present in a sample, and minimal nucleotide sequence overlap at a 3' end or a 5' end of substantially all of the primers in the plurality of primers. In some embodiments, the composition can include any 3, 4, 5, 6 or 7 of the above criteria.

[00101] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers designed according to the criteria disclosed here or including any one or more of the target-specific primers disclosed herein, where at least one of the plurality of target-specific primers is substantially complementary across its entire length to at last a portion of one or more genes selected from ABI1; ABL1; ABL2; ACSL3; ACSL6; AFF1; AFF3; AFF4;AKAP9; AKT1; AKT2; ALK; APC; ARHGAP26; ARHGEF12; ARID1A; ARNT; ASPSCR1; ASXL1; ATF1; ATIC; ATM; AXIN2; BAP1; BARD1; BCAR3; BCL10; BCL11A; BCL11B; BCL2; BCL3; BCL6; BCL7A;BCL9; BCR; BIRC3; BLM; BMPR1A; BRAF; BRCA1; BRCA2; BRD3; BRD4; BRIP1; BUB1B; CARD11; CARS; CASC5; CBFA2T3; CBFB; CBL; CBLB; CBLC; CCDC6; CCNB1IP1; CCND1; CCND2; CD74; CD79A; CDC73; CDH1; CDH11; CDK4; CDK6; CDKN2A; CDKN2B; CDKN2C; CDX2; CEBPA; CEP110; CHEK1; CHEK2; CHIC2; CHN1; CIC; CIITA; CLP1; CLTC; CLTCL1; COL1A1; CREB1; CREB3L2; CREBBP; CRTC1; CRTC3; CSF1R; CTNNB1; CXCR7; CYLD; CYTSB; DCLK3; DDB2; DDIT3; DDR2; DDX10; DDX5; DDX6; DEK; DGKG; DICER1; DNMT3A; EGFR; EIF4A2; ELF4; ELL; ELN; EML4;EP300; EPS15; ERBB2; ERBB4; ERC1; ERCC2; ERCC3; ERCC4; ERCC5; ERG; ETV1; ETV4; ETV5; ETV6; EWSR1; EXT1; EXT2; EZH2; FAM123B; FANCA; FANCC; FANCD2; FANCE; FANCF; FANCG; FAS; FBXW7; FCRL4; FGFR1; FGFR1OP; FGFR2; FGFR3; FH; FIP1L1; FLCN; FLI1; FLT1; FLT3; FNBP1; FOXL2; FOXO1; FOXO3; FOXO4; FOXP1; FUS; GAS7; GATA1; GATA2; GATA3; GMPS; GNAQ; GNAS; GOLGA5; GOPC; GPC3; GPHNGPR124; HIP1; HIST1H4I; HLF; HNF1A; HNRNPA2B1; HOOK3; HOXA11; HOXA13; HOXA9; HOXC11; HOXC13; HOXD13; HRAS; HSP90AA1; HSP90AB1; IDH1; IDH2; IKZF1; IL2; IL21R; IL6ST; IRF4; ITGA10; ITGA9; ITK; JAK1; JAK2; JAK3; KDM5A; KDM5C; KDM6A; KDR; KDSR; KIAA1549; KIT; KLF6; KLK2; KRAS; KTN1; LASP1; LCK; LCP1; LHFP; LIFR; LMO2; LPP; MAF; MALT1; MAML2; MAP2K1; MAP2K4; MDM2; MDM4;

MECOM; MEN1; MET; MITF; MKL1; MLH1; MLL; MLLT1; MLLT10; MLLT3; MLLT4; MLLT6; MN1; MPL; MRE11A; MSH2; MSH6; MSI2; MSN; MTCP1; MTOR; MUC1; MYB; MYC; MYCL1; MYCN; MYH11; MYH9; MYST3; MYST4; NACA; NBN; NCOA1; NCOA2; NCOA4; NEK9; NF1; NF2; NFE2L2; NFKB2; NIN; NKX2-1; NLRP1; NONO; NOTCH1; NOTCH2; NPM1; NR4A3; NRAS; NSD1; NTRK1; NTRK3; NUMA1; NUP214; NUP98; OLIG2; OMD; PAFAH1B2; PALB2; PATZ1; PAX3; PAX5; PAX7; PAX8; PBRM1; PBX1; PCM1;PDE4DIP; PDGFB; PDGFRA; PDGFRB; PER1; PHOX2B; PICALM; PIK3CA; PIK3R1; PIM1; PLAG1; PML; PMS1; PMS2; POU2AF1; POU5F1; PPARG; PPP2R1A; PRCC; PRDM16; PRF1; PRKAR1A; PRRX1; PSIP1; PTCH1; PTEN; PTPN11; RABEP1; RAD50; RAD51L1; RAF1; RANBP17; RAP1GDS1; RARA; RB1; RBM15; RECQL4; REL; RET; RHOH; RNF213; ROS1; RPN1; RPS6KA2; RUNX1; RUNX1T1; SBDS; SDHAF2; SDHB; SETD2; SFPQ; SFRS3; SH3GL1; SLC45A3; SMAD4; SMARCA4; SMARCB1; SMO; SOCS1; SRC; SRGAP3; SS18; SS18L1; STIL; STK11; STK36; SUFU; SYK; TAF15; TAF1L; TAL1; TAL2; TCF12; TCF3; TCL1A; TET1; TET2; TEX14; TFE3; TFEB; TFG; TFRC; THRAP3; TLX1; TLX3; TMPRSS2; TNFAIP3; TOP1; TP53; TPM3; TPM4; TPR; TRIM27; TRIM33; TRIP11; TSC1; TSC2; TSHR; USP6; VHL; WAS; WHSC1L1; WRN; WT1; XPA; XPC; ZBTB16; ZMYM2; ZNF331; ZNF384; and ZNF521.

[00102] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers designed according to the criteria disclosed here or including any one or more of the target-specific primers disclosed herein, where at least one of the plurality of target-specific primers is substantially complementary across its entire length to at last a portion of one or more genes selected from ABL1; AKT1; ALK; APC; ATM; BRAF; CDH1; CDKN2A; CSF1R; CTNNB1; EGFR; ERBB2; ERBB4; FBXW7; FGFR1; FGFR2; FGFR3; FLT3; GNAS; HNF1A; HRAS; IDH1; JAK2; JAK3; KDR; KIT; KRAS; MET; MLH1; MPL; NOTCH1; NPM1; NRAS; PDGFRA; PIK3CA; PTEN; PTPN11; RB1; RET; SMAD4; SMARCB1; SMO; SRC; STK11; TP53; and VHL.

[00103] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers designed according to the criteria disclosed here or including any one or more of the target-specific primers disclosed herein, where at least one of the plurality of target-specific primers is substantially complementary across its entire length to at last a portion of one or more genes selected from ABCA4; ABCC8; ABCD1; ACADVL; ACTA2; ACTC; ACTC1; ACVRL1; ADA; AIPL1; AIRE; ALK1; ALPL; AMT; APC; APP; APTX; AR; ARL6; ARSA; ASL;

ASPA; ASS; ASS1; ATL; ATM; ATP2A2; ATP7A; ATP7B; ATXN1; ATXN2; ATXN3; ATXN7; BBS6; BCKDHA; BCKDHB; BEST1; BMPR1A; BRCA1; BRCA2; BRIP1; BTD; BTK; C2orf25; CA4; CALR3; CAPN3; CAV3; CCDC39; CCDC40; CDH23; CEP290; CERKL; CFTR; CHAT; CHD7; CHEK2; CHM; CHRNA1; CHRNB1; CHRND; CHRNE; CLCN1; CNBP; CNGB1; COH1; COL11A1; COL11A2; COL1A1; COL1A2; COL2A1; COL3A1; COL4A5; COL5A1; COL5A2; COL7A1; COL9A1; CRB1; CRX; CTDP1; CTNS; CYP21A2; CYP27A1; DAX1; DBT; DCX; DES; DHCR7; DJ1; DKC1; DLD; DMD; DMPK; DNAAF1; DNAAF2; DNAH11; DNAH5; DNAI1;DNAI2; DNAL1;DNM2; DOK7; DSC2; DSG2; DSP; DYSF; DYT1; EMD; ENG; EYA1; EYS; F8; F9; FANCA; FANCC; FANCF; FANCG;FANCJ; FANDC2; FBN1; FBXO7; FGFR1; FGFR3; FMO3; FMR1; FOXL2; FRG1; FRMD7; FSCN2; FXN; GAA; GALT; GBA; GBE1; GCSH; GDF5; GJB2; GJB3; GJB6; GLA; GLDC; GNE; GNPTAB; GPC3; GPR143; GUCY2D; HBA1; HBA2; HBB; HD; HERG; HEXA; HFE; HHF; HIBCH; HLA-B27; HMBS; HPLH1; HPRP3; HR; HTNB; HTT; IKBKAP; IKBKG; IL2RG; IMPDH1; ITGB4; JAG1; JPH3; KCNE1; KCNE2; KCNH2; KCNQ1; KCNQ4; KIAA0196; KLHL7; KRAS; KRT14; KRT5; L1CAM; LAMB3; LAMP2; LDB3; LMNA; LMX18; LRAT; LRRK2; MAPT; MC1R; MECP2; MED12; MEN1; MERTK; MFN2; MKKS; MLH1; MMAA; MMAB; MMACHC; MMADHC; MPZ; MSH2; MTM1; MTND5; MTTG; MTTI; MTTK; MTTL1; MTTQ; MUT; MYBPC3; MYH11; MYH6; MYH7; MYL2; MYL3; MYLK2; MYO7A; ND5; ND6; NEMO; NF1; NF2; NIPBL; NR0B1; NR2E3; NRAS; NSD1; OCA2; OCRL; OPA1; OTC; PABPN1; PAFAH1B1; PAH; PARK2; PARK7; PARKIN; PAX3; PAX6; PCDH15; PEX1; PEX2; PEX10; PEX13; PEX14; PEX19; PEX26; PEX3; PEX5; PINK1; PKD1; PKD2; PKD3; PKHD1; PKP2; PLEC1; PLOD1; PMM2; PMP22; POLG; PPT1; PRCD; PRKAG2; PRNP; PROM1; PRPF3; PRPF8; PRPH2; PRPN; PSEN1; PSEN2; PTCH1; PTPN11; RAB7A; RAF1; RAI1; RAPSN; RB1; RDH12; RDS; RECQL3; RET; RHO; ROR2; RP1; RP2; RP9; RPE65; RPGR; RPGRIP1; RPL11; RPL35A; RPS10; RPS17; RPS19; RPS24; RPS26; RPS6KA3; RPS7; RPSL5; RS1; RSPH4A; RSPH9; RYR1; RYR2; SALL4; SCA3; SCN5A; SCN9A; SEMA4A; SERPINA1; SERPING1; SGCD; SH3BP2; SHOX; SIX1; SIX5; SLC25A13; SLC25A4; SLC26A4; SMAD4; SMN1; SNCA; SNRNP200; SOD1; SOS1; SOX9;SP110; SPAST; SPATA7; SPG3A; SPG4; SPG7; TAF1; TBX5; TCOF1; TGFBR1; TGFBR2; TNFRSC13C; TNNC1; TNNI3; TNNT1; TNNT2; TNXB; TOPORS; TOR1A; TP53; TPM1; TRNG; TRNI; TRNK; TRNL1; TRNQ; TSC1; TSC2; TTN; TTPA; TTR; TULP1; TWIST1; TXNDC3; TYR; USH1C; USH1H; USH2A; VCL; VHL; VPS13B; WAS; WRN; WT1; and ZNF9.

[00104] In some embodiments, the disclosure relates generally to a composition comprising a plurality of target-specific primers designed according to the criteria disclosed here or including any one or more of the target-specific primers disclosed herein, where at least one of the plurality of target-specific primers is substantially complementary across its entire length to at last a portion of one or more genes associated with breast cancer selected from AIM1, AR, ATM, BARD1, BCAS1, BRIP1, CCND1, CCND2, CCNE1, CDH1, CDK3,CDK4,CDKN2A, CDKN2B, CAMK1D, CHEK2, DIRAS3, EGFR, ERBB2, EPHA3, ERBB4, ETV6, GNRH1, KCTD9, CDCA2, EBF2, EMSY, BNIP3L, PNMA2, DPYSL2, ADRA1A, STMN4, TRIM35, PAK1, AQP11, CLSN1A, RSF1, KCTD14, THRSP, NDUFC2, ALG8, KCTD21, USP35, GAB2, DNAH9, ZNF18, MYOCD, STK11, TP53, JAK1, JAK2, MET, PDGFRA, PML, PTEN, RET, TMPRSS2, WNK1, FGFR1, IGF1R, PPP1R12B, PTPRT, GSTM1, IPO8, MYC, ZNF703, MDM1, MDM2, MDM4,MKK4, P14KB, NCOR1, NBN, PALB2, RAD50, RAD51, PAK1,RSF1, INTS4, ZMIZ1, SEPHS1, FOXM1, SDCCAG1, IGF1R, TSHZ2, RPSK6K1, PPP2R2A, MTAP, MAP2K4, AURKB, BCL2, BUB1, CDCA3, CDCA4, CDC20, CDC45, CHEK1, FOXM1, HDAC2, IGF1R, KIF2C, KIFC1, KRAS, RB1, SMAD4, NCOR1, UTX, MTHDFD1L, RAD51AP1, TTK and UBE2C.

[00105] In some embodiments, the disclosure is generally related to a combination of polynucleotides, where the combination of polynucleotides includes at least one polynucleotide selected from Tables 2, 3, 13, 14, 15, 17 and 19, and one or more additional polynucleotides independent of the polynucleotides disclosed herein. In some embodiments, the disclosure is generally related to a combination of polynucleotides, where the combination of polynucleotides includes a polynucleotide having at least 90% identity to one or more polynucleotides selected from Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the disclosure relates to 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 500, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10,000 or more polynucleotides selected from Tables 2, 3, 13, 14, 15, 17 and 19.

[00106] In some embodiments, the disclosure is generally related to a combination of polynucleotides, where the combination of polynucleotides includes at least one polynucleotide selected from Tables 2, 3, 13, 14, 15, 17 and 19, and one or more additional polynucleotides independent of the polynucleotides disclosed herein. In some embodiments, the disclosure is generally related to a combination of polynucleotides, where the combination of polynucleotides includes at least one polynucleotide having at least 90% identity to one or more polynucleotides selected from Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the disclosure relates to 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 500, 1000, 2000, 3000, 4000, 5000, 6000,

7000, 8000, 9000, 10,000 or more polynucleotides selected from Tables 2, 3, 13, 14, 15, 17 and 19 or one or more polynucleotides having at least 90% identity thereto.

[00107] In some embodiments, the disclosure is generally related to a pair of polynucleotides that specifically anneal to a portion of at least one gene selected from EGFR, BRAF or KRAS. In one embodiment, a pair of polynucleotides that specifically anneal to a portion of the EGFR gene includes any one or more of the following Amplicon IDs: 229910389, 227801665, 229055506, 230397881, 230175199, 230195609, 228630698, 230632980, 227722022, 232978808, 231616816, 230481741, 231198336, 229919273, 227816834, 228030652, 230679876, 229747025, 228741519, 228636601, 230635054, 230738160, 232984355, 228941652, 230495367, 231212482, 229608278, 230461276, 228035285, 230683371, 230173849, 330137554, 228857751, 230742871, 232237229, 228956984, 228732632, 231222418, 231493149, 229630617, 229052979, 230392156, 230683680, 230187475, 228709018, 230628101, 227716821, 227830783, 232260099, 230075336, 231314233, and 231239581. In one embodiment, a pair of polynucleotides that specifically anneal to a portion of the BRAF gene includes any one or more of the following Amplicon IDs: 222636793, 223460541, 223967627, 326913823, 223739184, 223944056, 224404546, 222922922, 224119138, 223519358, 223465859, 223971374, 222680486, 223741661, 223950351, 224410546, 222935598, 224119999, 222629880, 223175118, 223719489, 225222024, 222684242, 223700378, 222258987, 222895407, 223103332, 222635553, 223177865, 223960162, 326889377, 223588249, 223708886, 222259284, 222903910, and 223104608. In one embodiment, a pair of polynucleotides that specifically anneal to a portion of the KRAS gene includes any one or more of the following Amplicon IDs: 233361228, 234355242, 234355242, 233466735, 233466735, 231132733, 231132733, 234764991, 234764991, 233467720, 233467720, 231133990, 231133990, 233356818, 326772204, and 326772204.

[00108] In some embodiments, the disclosure is generally related to kits (as well as related compositions, methods, apparatuses and systems using such kits) for amplifying one or more target sequences in a sample. In some embodiments, the kits for amplifying one or more target sequences in a sample include at least one target-specific primer that can amplify the at least one target sequence in the sample. In some embodiments, the kit can include at least two target-specific primers that can amplify at least one target sequence in the sample. In another embodiment, the kit can include a plurality of target-specific primers for amplifying at least two target sequences in a sample, where the kit includes a) a first target-specific primer having at least 90% identity to a nucleic acid sequence selected from SEQ ID NOs: 1-103,143 being substantially complementary to the first target sequence in a sense direction; b) a second target-specific primer having at least 90%

identity to a nucleic acid sequence selected from SEQ ID NOs: 1-103,143 being substantially complementary to the first target sequence in a antisense direction; c) a third target-specific primer having at least 90% identity to a nucleic acid sequence selected from SEQ ID NOs: 1-103,143 being substantially complementary to the second target sequence in a sense direction; and, d) a fourth target-specific primer having at least 90% identity to a nucleic acid sequence selected from SEQ ID NOs: 1-103,143 being substantially complementary to the second target sequence in a antisense direction. In some embodiments, the sample can be an environmental, aquatic, microbiological, entomological, plant, fungi, animal or mammalian nucleic acid containing sample. In some embodiments, the sample can include a clinical, surgical, physician, forensic or laboratory obtained nucleic acid sample.

[00109] In some embodiments, the disclosure relates generally to a method for amplifying a plurality of target sequences in a sample comprising contacting at least some portion of the sample with at least one target-specific primer as disclosed herein, or designed using the primer selection criteria disclosed herein, and a polymerase under amplification conditions thereby producing at least one amplified target sequence. In some embodiments, the method further includes ligating at least one adapter to at least one amplified target sequence, thereby producing at least one adapter-ligated amplified target sequence. In some embodiments, the method includes any one or more of the target-specific primers provided in Tables 2, 3, 13, 14, 15, 17 and 19 or any nucleic acid sequence having at least 90% identity to any one or more of the target-specific primers provided in Tables 2, 3, 13, 14, 15, 17 and 19.

[00110] In some embodiments, the disclosure is generally related to an amplification product generated by amplifying at least one target sequence present in a sample with one or more target-specific primers disclosed herein or one or more target-specific primers designed using the primer selection criteria disclosed herein. In some embodiments, the disclosure is generally related to an amplification product generated by contacting at least one target sequence in a sample with one or more target-specific primers disclosed herein or one or more target-specific primers designed using the primer selection criteria disclosed herein under amplification conditions. In some embodiments, the amplification product can include one or more mutations associated with cancer or inherited disease. For example, a sample suspected of containing one or more mutations associated with at least one cancer can be subjected to any one of the amplification methods disclosed herein. The amplification products obtained from the selected amplification method can optionally be compared to a normal or matched sample known to be noncancerous with respect to the at least one cancer, and

can therefore be used as a reference sample. In some embodiments, the amplification products obtained by the methods disclosed herein can be optionally sequenced using any suitable nucleic acid sequencing platform to determine the nucleic acid sequence of the amplification products, and optionally compared to sequencing information from the normal or non-cancerous sample. In some embodiments, amplification products can include one or more markers associated with antibiotic resistance, pathogenicity or genetic modification. In some embodiments, nucleic acid sequences of one or more amplification products obtained by contacting at least one target sequence with at least one target-specific primer under amplification conditions can be used to determine the presence or absence of a genetic variant within the one or more amplification products.

[00111] In some embodiments, the disclosure generally relates to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) for performing nucleic acid amplification and nucleic acid synthesis. In some embodiments, the composition includes a plurality of target-specific primer pairs, at least one target-specific primer pair including a target-specific forward primer and a target-specific reverse primer. In some embodiments, the composition includes at least 100, 200, 500, 750, 1000, 2500, 5000, 7500, 10000, 12000, 15000, 17500, 20000 or 50000 different primer pairs, some or all of which can be target-specific. Optionally at least two of the different target-specific primer pairs are directed to (i.e., are specific for) different target sequences.

[00112] In some embodiments, the composition includes at least one target-specific primer pair that can be specific for at least one amplified target sequence. In some embodiments, the composition includes a plurality of target-specific primer pairs, at least two target-specific primer pairs being specific for at different amplified target sequences. In some embodiments, the composition includes a target-specific primer pair, which each member of the primer pair includes a target-specific primer that can hybridize to at least a portion of a first amplified sequence or its complement, and that is substantially non-complementary to the 3' end or the 5' end of any other amplified sequence in the sample. In some embodiments, the composition includes at least one target-specific primer pair that can be substantially non-complementary to a portion of any other nucleic acid molecule in the sample. In some embodiments, the compositions include a plurality of target-specific primer pairs that include one or more cleavable groups at one or more locations within the target-specific primer pair.

[00113] In some embodiments, the composition includes one or more target-specific primer pairs that can amplify a short tandem repeat, single nucleotide polymorphism, gene, exon, coding

region, exome, or portion thereof. For example, a plurality of target-specific primer pairs can uniformly amplify one gene, exon, coding region, exome or portion thereof. In some embodiments, the compositions include target-specific primer pairs designed to minimize overlap of nucleotide sequences amplified using the one or more target-specific primer pairs. In some embodiments, the nucleotide sequence overlap between one or more target-specific primers can be minimized at the 3' end, the 5' end, or both. In some embodiments, at least one primer in a plurality of target-specific primers includes less than 5 nucleotides of nucleotide sequence overlap at the 3' end, 5' end or both. In some embodiments, at least one target-specific primer of a plurality of target-specific primers includes a nucleotide sequence gap of at least one nucleotide, as compared to the plurality of target-specific primers. In some embodiments, the compositions include one or more target-specific primer pairs designed to comprehensively amplify one or more genes or exons. For example, a plurality of target-specific primer pairs can be designed to uniformly amplify (i.e., provide 100% representation of all nucleotides) in a single gene or exon.

[00114] In some embodiments, at least two pairs of target-specific primers are capable of hybridizing to locations on a template nucleic acid and serving as substrates for template-dependent primer extension by a polymerase. In some embodiments, the template-dependent primer extension can include amplification of the region of template located between the sites of hybridization of the primers of the at least two pairs of primers, resulting in formation of an amplified region or "amplicon". Typically, the sequence of the amplicon includes the sequence of the template located between the sites of hybridization of the primers, as well as at least part of the sequence of the primers themselves. In some embodiments, the amplification reaction can include at least about 5, 10, 25, 50, 100, 150, 200, 250, 400, 500, 750, 1000, 1200, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 5000, 7500 or 10,000 different primer pairs. In some embodiments, the amplification reaction can result in the generation of at least about 5, 10, 25, 50, 100, 150, 200, 250, 400, 500, 750, 1000, 1200, 1250, 1500, 1750, 2000, 2250, 2500, 2750, 3000, 5000, 7500 or 10,000 different amplicons. In some embodiments, at least about 75%, 80%, 90%, 95%, 97% or 99% of the amplicons generated during the amplification reaction are similarly sized, for example, the amplicons differ in size from each other by no more than 5, 10, 25, 50, 75, 100, 500, 1000 or 2000 nucleotides. In some embodiments, the difference in length between any two amplicons is no greater than 1%, 5%, or 10% of average amplicon length in the amplification reaction mixture. Optionally, the average amplicon length is about 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 200, 250, 500,

1000, 2000, 10,000 nucleotides or greater. In some embodiments, the standard deviation in length among amplicons in a mixture is no greater than 0.1, 0.25, 0.4, 0.5, 0.75, 1, 1.5, 2.0, 2.4 or 3.0

[00115] In some embodiments, the compositions include target-specific primer pairs designed to generate amplified target sequences that overlap with an adjacent amplified target sequence by a single nucleotide. In some embodiments, the compositions include target-specific primer pairs designed to generate an amplified target sequence that does not overlap with an adjacent amplified target sequence. For example, target-specific primer pairs can be designed to generate amplified target sequences that are separated by one or more nucleotides. In some embodiments, the composition includes target-specific primer pairs designed to separate amplified target sequences by about 50 nucleotides.

[00116] In some embodiments, the composition includes a plurality of exon- or gene-specific, target-specific primer pairs that can be substantially complementary to an individual exon or gene. In some embodiments, the composition includes a plurality of exon- or gene-specific, target-specific primer pairs that can be substantially complementary to one or more exons or genes. In some embodiments, the composition includes a plurality of substantially complementary exon- or gene-specific, target-specific primer pairs and that no two primer pairs amplify greater than 10% of the same target sequence. In some embodiments, no two target-specific primer pairs amplify the same exon or gene. In some embodiments, the target-specific primer pairs amplify about 100 to about 600 nucleotides of a target sequence. In some embodiments, the target-specific primer pairs can be used to amplify about 25% to 100% of an exon, gene or coding region. In some embodiments, the compositions includes a plurality of target-specific primer pairs to generate a plurality of amplified target sequences and that no individual amplified target sequence is overexpressed by more than 50% as compared to the other amplified target sequences. In some embodiments, the compositions includes a plurality of target-specific primer pairs designed to generate a plurality of amplified target sequences that are substantially homogenous (i.e., homogenous with respect to GC content, melting temperature, or amplified target sequence length). In some embodiments, the plurality of target-specific primer pairs overlap in sequence by no more than five nucleotides.

[00117] In some embodiments, the disclosure generally relates to a method for preventing or eliminating non-specific amplification products in a multiplex PCR reaction. In some embodiments, the method includes (as well as related compositions, kits, systems and apparatuses used using the disclosed methods) hybridizing one or more target-specific primer pairs to a target sequence in a sample having a plurality of target sequences, extending the hybridized target-specific primers to

form a plurality of amplified target sequences, denaturing and annealing the amplified target sequences to form a plurality of double-stranded amplified target sequences and performing a digesting step on the sample containing the double-stranded amplified target sequences to eliminate non-specific amplification products. In some embodiments, the method includes one or more cleavable groups at one or more locations in one or more target-specific primer pairs. In some embodiments, each target-specific primer pair includes at least one cleavable group. In some embodiments, each target-specific primer of the primer pairs includes a cleavable group. In some embodiments, the digestion is an enzymatic or chemical digestion. In some embodiments, the digestion step includes partial digestion of a target-specific primer of an amplified target sequence. In some embodiments, the method includes a thermostable polymerase. In some embodiments, the thermostable polymerase can be optionally reactivated by heat or chemical treatment.

[00118] In some embodiments, the composition includes a plurality of target-specific primer pairs directed to one or more diseases or disorders. In some embodiments, a target-specific primer pair can be substantially complementary to a target sequence correlated or associated with one or more cancers. In some embodiments, a target-specific primer pair can be substantially complementary to a target sequence correlated with or associated with one or more congenital or inherited disorders. In some embodiments, one or more target-specific primer pairs can be associated with one or more neurological, metabolic, neuromuscular, developmental, cardiovascular or autoimmune disorders. In some embodiments, one or more target-specific primer pairs can be associated with one or more genes or exons associated with one or more neurological, metabolic, neuromuscular, developmental, cardiovascular or autoimmune disorders. In some embodiments, the plurality of target-specific primers can include a gene or gene fragment associated with neoplastic development in mammals.

[00119] In some embodiments, the disclosure relates generally to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) comprising any, some or all of the primers disclosed herein, including in the Examples and in the related appendices, supplements and tables attached hereto. In some embodiments, the disclosure relates generally to compositions (as well as related kits, methods, systems and apparatuses using the disclosed compositions) comprising any of the primer pools used in the Examples, or any subset thereof. For example, in some embodiments the disclosure relates generally to compositions including one or more target-specific primers selected from the primers listed in Tables 2, 3, 13, 14, 15, 17 and 19, which include sets of primers designed and selected using the design methods and selection criteria

of the disclosure, and which have been used to perform highly multiplex amplification according to the methods disclosed herein. It will be readily appreciated by one of ordinary skill in the art that any subsets of each of the primer sets set forth in Tables 2, 3, 13, 14, 15, 17 and 19 can also be expected to support multiplex amplification, since the entire set of primers of each table has been demonstrated to support such multiplex amplification and removal of particular primer pairs from the pool will not be expected to significantly alter the performance of the remaining primers for purposes of multiplex amplification. In some embodiments, the disclosure relates generally to compositions including any 1, 2, 5, 10, 25, 50, 100, 250, 500, 750, 1000, 2500, 5000, 7500, 10000, 12500, 50000, 100000 or more different target-specific primer pairs set forth in Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the disclosure relates to a composition including at least 1, 2, 5, 10, 25, 50, 100, 250, 500, 750, 1000, 2500, 5000, 7500, 10000, 12500, 50000, 100000 or more primers selected from Tables 2, 3, 13, 14, 15,17 and 19, or their complements. In some embodiments, the disclosure relates to a composition including at least 1, 2, 5, 10, 25, 50, 100, 250, 500, 750, 1000, 2500, 5000, 7500, 10000, 12500, 50000, 100000 or more primers that are at least 85% identical or complementary to any primer of Tables 2, 3, 13, 14, 15, 17 and 19. In some embodiments, the composition includes at least one 1, 2, 5, 10, 25, 50, 100, 250, 500, 750, 1000, 2500, 5000, 7500, 10000, 12500, 50000, 100000 or more primers selected from Tables 2, 3, 13, 14, 15, 17 and 19, or their complements, wherein at least one primer includes at least one nucleotide substitution. A nucleotide substitution includes replacement of any nucleotide residue or nucleobase of any primer with any other nucleotide or nucleobase, and can include, for example, purine to purine substitutions, pyrimidine to pyrimidine substitutions, purine to pyrimidine substitutions, and pyrimidine to purine substitutions. In some embodiments, the at least one primer of the composition can include any one, two, three, four or more nucleotide substitutions. In some embodiments, the at least one primer of the composition includes at least one primer in which any one, some or all of the uracil-containing nucleotide residues or nucleobases of the primer are replaced with a thymine-containing nucleotide residue or nucleobase. In some embodiments, the at least one primer of the composition includes at least one primer in which any one, two, three, four, five or more uracil-containing nucleotide residues or nucleobases of the primer are replaced with a thymine-containing nucleotide residue or nucleobase.

[00120] In some embodiments, a target-specific primer pair can include a nucleic acid sequence including a somatic or germline mutation. In some embodiments, the germline or somatic mutation can be found in any one or more of the genes provided in Tables 1, 4, 16 or 18. In some

embodiments, the target-specific primer pairs can be used to amplify a target sequence that can be used to detect the presence of mutations at less than 5% allele frequency. In some embodiments, the plurality of target-specific primers includes at least 500, at least 1000, at least 3000, at least 6000, at least 10000, at least 12000, or more target-specific primer pairs.

[00121] In some embodiments, the disclosure relates generally to a kit for performing multiplex nucleic acid amplification or multiplex nucleic acid synthesis. In some embodiments, the kit comprises a plurality of target-specific primers. In some embodiments, the kit can further include a polymerase, at least one adapter and/or a cleaving reagent. In some embodiments, the kit can also include dATP, dCTP, dGTP, dTTP and/or an antibody. In some embodiments, the cleaving reagent is any reagent that can cleave one or more cleaving groups present in one or more target-specific primers. In some embodiments the cleaving reagent can include an enzyme or chemical reagent. In some embodiments, the cleaving reagent can include an enzyme with an affinity for apurinic bases. In some embodiments, the cleaving reagent can include a first enzyme with an affinity for a first cleavable group and can further include a second enzyme with an affinity for a second cleavable group. In some embodiments, the kit can further include an enzyme with an affinity for abasic sites. In some embodiments, the polymerase is a thermostable polymerase. In some embodiments, the kits can include one or more preservatives, adjuvants or nucleic acid sequencing barcodes.

[00122] In some embodiments, the disclosure relates generally to methods (as well as related compositions, systems, kits and apparatuses) for determining copy number variation comprising performing any of the amplification methods disclosed herein.

[00123] **DETAILED DESCRIPTION**

[00124] The following description of various exemplary embodiments is exemplary and explanatory only and is not to be construed as limiting or restrictive in any way. Other embodiments, features, objects, and advantages of the present teachings will be apparent from the description and accompanying drawings, and from the claims.

[00125] As used herein, "amplify", "amplifying" or "amplification reaction" and their derivatives, refer generally to any action or process whereby at least a portion of a nucleic acid molecule (referred to as a template nucleic acid molecule) is replicated or copied into at least one additional nucleic acid molecule. The additional nucleic acid molecule optionally includes sequence that is substantially identical or substantially complementary to at least some portion of the template nucleic acid molecule. The template nucleic acid molecule can be single-stranded or double-stranded and the additional nucleic acid molecule can independently be single-stranded or double-stranded. In

some embodiments, amplification includes a template-dependent in vitro enzyme-catalyzed reaction for the production of at least one copy of at least some portion of the nucleic acid molecule or the production of at least one copy of a nucleic acid sequence that is complementary to at least some portion of the nucleic acid molecule. Amplification optionally includes linear or exponential replication of a nucleic acid molecule. In some embodiments, such amplification is performed using isothermal conditions; in other embodiments, such amplification can include thermocycling. In some embodiments, the amplification is a multiplex amplification that includes the simultaneous amplification of a plurality of target sequences in a single amplification reaction. At least some of the target sequences can be situated on the same nucleic acid molecule or on different target nucleic acid molecules included in the single amplification reaction. In some embodiments, "amplification" includes amplification of at least some portion of DNA- and RNA-based nucleic acids alone, or in combination. The amplification reaction can include single or double-stranded nucleic acid substrates and can further including any of the amplification processes known to one of ordinary skill in the art. In some embodiments, the amplification reaction includes polymerase chain reaction (PCR).

[00126] As used herein, "amplification conditions" and its derivatives, generally refers to conditions suitable for amplifying one or more nucleic acid sequences. Such amplification can be linear or exponential. In some embodiments, the amplification conditions can include isothermal conditions or alternatively can include thermocyling conditions, or a combination of isothermal and themocycling conditions. In some embodiments, the conditions suitable for amplifying one or more nucleic acid sequences includes polymerase chain reaction (PCR) conditions. Typically, the amplification conditions refer to a reaction mixture that is sufficient to amplify nucleic acids such as one or more target sequences, or to amplify an amplified target sequence ligated to one or more adapters, e.g., an adapter-ligated amplified target sequence. Generally, the amplification conditions include a catalyst for amplification or for nucleic acid synthesis, for example a polymerase; a primer that possesses some degree of complementarity to the nucleic acid to be amplified; and nucleotides, such as deoxyribonucleotide triphosphates (dNTPs) to promote extension of the primer once hybridized to the nucleic acid. The amplification conditions can require hybridization or annealing of a primer to a nucleic acid, extension of the primer and a denaturing step in which the extended primer is separated from the nucleic acid sequence undergoing amplification. Typically, but not necessarily, amplification conditions can include thermocycling; in some embodiments, amplification conditions include a plurality of cycles where the steps of annealing, extending and separating are

repeated. Typically, the amplification conditions include cations such as Mg^{++} or Mn^{++} (e.g., $MgCl_2$, etc) and can also include various modifiers of ionic strength.

[00127] As used herein, "target sequence" or "target sequence of interest" and its derivatives, refers generally to any single or double-stranded nucleic acid sequence that can be amplified or synthesized according to the disclosure, including any nucleic acid sequence suspected or expected to be present in a sample. In some embodiments, the target sequence is present in double-stranded form and includes at least a portion of the particular nucleotide sequence to be amplified or synthesized, or its complement, prior to the addition of target-specific primers or appended adapters. Target sequences can include the nucleic acids to which primers useful in the amplification or synthesis reaction can hybridize prior to extension by a polymerase. In some embodiments, the term refers to a nucleic acid sequence whose sequence identity, ordering or location of nucleotides is determined by one or more of the methods of the disclosure.

[00128] As defined herein, "sample" and its derivatives, is used in its broadest sense and includes any specimen, culture and the like that is suspected of including a target. In some embodiments, the sample comprises DNA, RNA, PNA, LNA, chimeric, hybrid, or multiplex-forms of nucleic acids. The sample can include any biological, clinical, surgical, agricultural, atmospheric or aquatic-based specimen containing one or more nucleic acids. The term also includes any isolated nucleic acid sample such a genomic DNA, fresh-frozen or formalin-fixed paraffin-embedded nucleic acid specimen.

[00129] As used herein, "contacting" and its derivatives, when used in reference to two or more components, refers generally to any process whereby the approach, proximity, mixture or commingling of the referenced components is promoted or achieved without necessarily requiring physical contact of such components, and includes mixing of solutions containing any one or more of the referenced components with each other. The referenced components may be contacted in any particular order or combination and the particular order of recitation of components is not limiting. For example, "contacting A with B and C" encompasses embodiments where A is first contacted with B then C, as well as embodiments where C is contacted with A then B, as well as embodiments where a mixture of A and C is contacted with B, and the like. Furthermore, such contacting does not necessarily require that the end result of the contacting process be a mixture including all of the referenced components, as long as at some point during the contacting process all of the referenced components are simultaneously present or simultaneously included in the same mixture or solution. For example, "contacting A with B and C" can include embodiments wherein C is first contacted

with A to form a first mixture, which first mixture is then contacted with B to form a second mixture, following which C is removed from the second mixture; optionally A can then also be removed, leaving only B. Where one or more of the referenced components to be contacted includes a plurality (e.g, "contacting a target sequence with a plurality of target-specific primers and a polymerase"), then each member of the plurality can be viewed as an individual component of the contacting process, such that the contacting can include contacting of any one or more members of the plurality with any other member of the plurality and/or with any other referenced component (e.g., some but not all of the plurality of target specific primers can be contacted with a target sequence, then a polymerase, and then with other members of the plurality of target-specific primers) in any order or combination.

[00130] As used herein, the term "primer" and its derivatives refer generally to any polynucleotide that can hybridize to a target sequence of interest. In some embodiments, the primer can also serve to prime nucleic acid synthesis. Typically, the primer functions as a substrate onto which nucleotides can be polymerized by a polymerase; in some embodiments, however, the primer can become incorporated into the synthesized nucleic acid strand and provide a site to which another primer can hybridize to prime synthesis of a new strand that is complementary to the synthesized nucleic acid molecule. The primer may be comprised of any combination of nucleotides or analogs thereof, which may be optionally linked to form a linear polymer of any suitable length. In some embodiments, the primer is a single-stranded oligonucleotide or polynucleotide. (For purposes of this disclosure, the terms 'polynucleotide" and "oligonucleotide" are used interchangeably herein and do not necessarily indicate any difference in length between the two). In some embodiments, the primer is single-stranded but it can also be double-stranded. The primer optionally occurs naturally, as in a purified restriction digest, or can be produced synthetically. In some embodiments, the primer acts as a point of initiation for amplification or synthesis when exposed to amplification or synthesis conditions; such amplification or synthesis can occur in a template-dependent fashion and optionally results in formation of a primer extension product that is complementary to at least a portion of the target sequence. Exemplary amplification or synthesis conditions can include contacting the primer with a polynucleotide template (e.g., a template including a target sequence), nucleotides and an inducing agent such as a polymerase at a suitable temperature and pH to induce polymerization of nucleotides onto an end of the target-specific primer. If double-stranded, the primer can optionally be treated to separate its strands before being used to prepare primer extension products. In some embodiments, the primer is an oligodeoxyribonucleotide or an oligoribonucleotide. In some

embodiments, the primer can include one or more nucleotide analogs. The exact length and/or composition, including sequence, of the target-specific primer can influence many properties, including melting temperature (Tm), GC content, formation of secondary structures, repeat nucleotide motifs, length of predicted primer extension products, extent of coverage across a nucleic acid molecule of interest, number of primers present in a single amplification or synthesis reaction, presence of nucleotide analogs or modified nucleotides within the primers, and the like. In some embodiments, a primer can be paired with a compatible primer within an amplification or synthesis reaction to form a primer pair consisting or a forward primer and a reverse primer. In some embodiments, the forward primer of the primer pair includes a sequence that is substantially complementary to at least a portion of a strand of a nucleic acid molecule, and the reverse primer of the primer of the primer pair includes a sequence that is substantially identical to at least of portion of the strand. In some embodiments, the forward primer and the reverse primer are capable of hybridizing to opposite strands of a nucleic acid duplex. Optionally, the forward primer primes synthesis of a first nucleic acid strand, and the reverse primer primes synthesis of a second nucleic acid strand, wherein the first and second strands are substantially complementary to each other, or can hybridize to form a double-stranded nucleic acid molecule. In some embodiments, one end of an amplification or synthesis product is defined by the forward primer and the other end of the amplification or synthesis product is defined by the reverse primer. In some embodiments, where the amplification or synthesis of lengthy primer extension products is required, such as amplifying an exon, coding region, or gene, several primer pairs can be created than span the desired length to enable sufficient amplification of the region. In some embodiments, a primer can include one or more cleavable groups. In some embodiments, primer lengths are in the range of about 10 to about 60 nucleotides, about 12 to about 50 nucleotides and about 15 to about 40 nucleotides in length. Typically, a primer is capable of hybridizing to a corresponding target sequence and undergoing primer extension when exposed to amplification conditions in the presence of dNTPS and a polymerase. In some instances, the particular nucleotide sequence or a portion of the primer is known at the outset of the amplification reaction or can be determined by one or more of the methods disclosed herein. In some embodiments, the primer includes one or more cleavable groups at one or more locations within the primer.

[00131] As used herein, "target-specific primer" and its derivatives, refers generally to a single stranded or double-stranded polynucleotide, typically an oligonucleotide, that includes at least one sequence that is at least 50% complementary, typically at least 75% complementary or at least

85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% or at least 99% complementary, or identical, to at least a portion of a nucleic acid molecule that includes a target sequence. In such instances, the target-specific primer and target sequence are described as "corresponding" to each other. In some embodiments, the target-specific primer is capable of hybridizing to at least a portion of its corresponding target sequence (or to a complement of the target sequence); such hybridization can optionally be performed under standard hybridization conditions or under stringent hybridization conditions. In some embodiments, the target-specific primer is not capable of hybridizing to the target sequence, or to its complement, but is capable of hybridizing to a portion of a nucleic acid strand including the target sequence, or to its complement. In some embodiments, the target-specific primer includes at least one sequence that is at least 75% complementary, typically at least 85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% complementary, or more typically at least 99% complementary, to at least a portion of the target sequence itself; in other embodiments, the target-specific primer includes at least one sequence that is at least 75% complementary, typically at least 85% complementary, more typically at least 90% complementary, more typically at least 95% complementary, more typically at least 98% complementary, or more typically at least 99% complementary, to at least a portion of the nucleic acid molecule other than the target sequence. In some embodiments, the target-specific primer is substantially non-complementary to other target sequences present in the sample; optionally, the target-specific primer is substantially non-complementary to other nucleic acid molecules present in the sample. In some embodiments, nucleic acid molecules present in the sample that do not include or correspond to a target sequence (or to a complement of the target sequence) are referred to as "non-specific" sequences or "non-specific nucleic acids". In some embodiments, the target-specific primer is designed to include a nucleotide sequence that is substantially complementary to at least a portion of its corresponding target sequence. In some embodiments, a target-specific primer is at least 95% complementary, or at least 99% complementary, or identical, across its entire length to at least a portion of a nucleic acid molecule that includes its corresponding target sequence. In some embodiments, a target-specific primer can be at least 90%, at least 95% complementary, at least 98% complementary or at least 99% complementary, or identical, across its entire length to at least a portion of its corresponding target sequence. In some embodiments, a forward target-specific primer and a reverse target-specific primer define a target-specific primer pair that can be used to amplify the target sequence via

template-dependent primer extension. Typically, each primer of a target-specific primer pair includes at least one sequence that is substantially complementary to at least a portion of a nucleic acid molecule including a corresponding target sequence but that is less than 50% complementary to at least one other target sequence in the sample. In some embodiments, amplification can be performed using multiple target-specific primer pairs in a single amplification reaction, wherein each primer pair includes a forward target-specific primer and a reverse target-specific primer, each including at least one sequence that substantially complementary or substantially identical to a corresponding target sequence in the sample, and each primer pair having a different corresponding target sequence. In some embodiments, the target-specific primer can be substantially non-complementary at its 3' end or its 5' end to any other target-specific primer present in an amplification reaction. In some embodiments, the target-specific primer can include minimal cross hybridization to other target-specific primers in the amplification reaction. In some embodiments, target-specific primers include minimal cross-hybridization to non-specific sequences in the amplification reaction mixture. In some embodiments, the target-specific primers include minimal self-complementarity. In some embodiments, the target-specific primers can include one or more cleavable groups located at the 3' end. In some embodiments, the target-specific primers can include one or more cleavable groups located near or about a central nucleotide of the target-specific primer. In some embodiments, one of more targets-specific primers includes only non-cleavable nucleotides at the 5' end of the target-specific primer. In some embodiments, a target specific primer includes minimal nucleotide sequence overlap at the 3'end or the 5' end of the primer as compared to one or more different target-specific primers, optionally in the same amplification reaction. In some embodiments 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more, target-specific primers in a single reaction mixture include one or more of the above embodiments. In some embodiments, substantially all of the plurality of target-specific primers in a single reaction mixture includes one or more of the above embodiments.

[00132] As used herein, "polymerase" and its derivatives, generally refers to any enzyme that can catalyze the polymerization of nucleotides (including analogs thereof) into a nucleic acid strand. Typically but not necessarily, such nucleotide polymerization can occur in a template-dependent fashion. Such polymerases can include without limitation naturally occurring polymerases and any subunits and truncations thereof, mutant polymerases, variant polymerases, recombinant, fusion or otherwise engineered polymerases, chemically modified polymerases, synthetic molecules or assemblies, and any analogs, derivatives or fragments thereof that retain the ability to catalyze such

polymerization. Optionally, the polymerase can be a mutant polymerase comprising one or more mutations involving the replacement of one or more amino acids with other amino acids, the insertion or deletion of one or more amino acids from the polymerase, or the linkage of parts of two or more polymerases. Typically, the polymerase comprises one or more active sites at which nucleotide binding and/or catalysis of nucleotide polymerization can occur. Some exemplary polymerases include without limitation DNA polymerases and RNA polymerases. The term "polymerase" and its variants, as used herein, also refers to fusion proteins comprising at least two portions linked to each other, where the first portion comprises a peptide that can catalyze the polymerization of nucleotides into a nucleic acid strand and is linked to a second portion that comprises a second polypeptide. In some embodiments, the second polypeptide can include a reporter enzyme or a processivity-enhancing domain. Optionally, the polymerase can possess 5' exonuclease activity or terminal transferase activity. In some embodiments, the polymerase can be optionally reactivated, for example through the use of heat, chemicals or re-addition of new amounts of polymerase into a reaction mixture. In some embodiments, the polymerase can include a hot-start polymerase or an aptamer based polymerase that optionally can be reactivated.

[00133] As used herein, the term "nucleotide" and its variants comprises any compound, including without limitation any naturally occurring nucleotide or analog thereof, which can bind selectively to, or can be polymerized by, a polymerase. Typically, but not necessarily, selective binding of the nucleotide to the polymerase is followed by polymerization of the nucleotide into a nucleic acid strand by the polymerase; occasionally however the nucleotide may dissociate from the polymerase without becoming incorporated into the nucleic acid strand, an event referred to herein as a "non-productive" event. Such nucleotides include not only naturally occurring nucleotides but also any analogs, regardless of their structure, that can bind selectively to, or can be polymerized by, a polymerase. While naturally occurring nucleotides typically comprise base, sugar and phosphate moieties, the nucleotides of the present disclosure can include compounds lacking any one, some or all of such moieties. In some embodiments, the nucleotide can optionally include a chain of phosphorus atoms comprising three, four, five, six, seven, eight, nine, ten or more phosphorus atoms. In some embodiments, the phosphorus chain can be attached to any carbon of a sugar ring, such as the 5' carbon. The phosphorus chain can be linked to the sugar with an intervening O or S. In one embodiment, one or more phosphorus atoms in the chain can be part of a phosphate group having P and O. In another embodiment, the phosphorus atoms in the chain can be linked together with intervening O, NH, S, methylene, substituted methylene, ethylene, substituted ethylene, CNH_2, C(O),

$C(CH_2)$, CH_2CH_2, or $C(OH)CH_2R$ (where R can be a 4-pyridine or 1-imidazole). In one embodiment, the phosphorus atoms in the chain can have side groups having O, BH_3, or S. In the phosphorus chain, a phosphorus atom with a side group other than O can be a substituted phosphate group. In the phosphorus chain, phosphorus atoms with an intervening atom other than O can be a substituted phosphate group. Some examples of nucleotide analogs are described in Xu, U.S. Patent No. 7,405,281. In some embodiments, the nucleotide comprises a label and referred to herein as a "labeled nucleotide"; the label of the labeled nucleotide is referred to herein as a "nucleotide label". In some embodiments, the label can be in the form of a fluorescent dye attached to the terminal phosphate group, i.e., the phosphate group most distal from the sugar. Some examples of nucleotides that can be used in the disclosed methods and compositions include, but are not limited to, ribonucleotides, deoxyribonucleotides, modified ribonucleotides, modified deoxyribonucleotides, ribonucleotide polyphosphates, deoxyribonucleotide polyphosphates, modified ribonucleotide polyphosphates, modified deoxyribonucleotide polyphosphates, peptide nucleotides, modified peptide nucleotides, metallonucleosides, phosphonate nucleosides, and modified phosphate-sugar backbone nucleotides, analogs, derivatives, or variants of the foregoing compounds, and the like. In some embodiments, the nucleotide can comprise non-oxygen moieties such as, for example, thio- or borano- moieties, in place of the oxygen moiety bridging the alpha phosphate and the sugar of the nucleotide, or the alpha and beta phosphates of the nucleotide, or the beta and gamma phosphates of the nucleotide, or between any other two phosphates of the nucleotide, or any combination thereof. "Nucleotide 5'-triphosphate" refers to a nucleotide with a triphosphate ester group at the 5' position, and are sometimes denoted as "NTP", or "dNTP" and "ddNTP" to particularly point out the structural features of the ribose sugar. The triphosphate ester group can include sulfur substitutions for the various oxygens, *e.g.* .alpha.-thio-nucleotide 5'-triphosphates. For a review of nucleic acid chemistry, see: Shabarova, Z. and Bogdanov, A. Advanced Organic Chemistry of Nucleic Acids, VCH, New York, 1994.

[00134] The term "extension" and its variants, as used herein, when used in reference to a given primer, comprises any in vivo or in vitro enzymatic activity characteristic of a given polymerase that relates to polymerization of one or more nucleotides onto an end of an existing nucleic acid molecule. Typically but not necessarily such primer extension occurs in a template-dependent fashion; during template-dependent extension, the order and selection of bases is driven by established base pairing rules, which can include Watson-Crick type base pairing rules or alternatively (and especially in the case of extension reactions involving nucleotide analogs) by some

other type of base pairing paradigm. In one non-limiting example, extension occurs via polymerization of nucleotides on the 3'OH end of the nucleic acid molecule by the polymerase.

[00135] The term "portion" and its variants, as used herein, when used in reference to a given nucleic acid molecule, for example a primer or a template nucleic acid molecule, comprises any number of contiguous nucleotides within the length of the nucleic acid molecule, including the partial or entire length of the nucleic acid molecule.

[00136] The terms "identity" and "identical" and their variants, as used herein, when used in reference to two or more nucleic acid sequences, refer to similarity in sequence of the two or more sequences (e.g., nucleotide or polypeptide sequences). In the context of two or more homologous sequences, the percent identity or homology of the sequences or subsequences thereof indicates the percentage of all monomeric units (e.g., nucleotides or amino acids) that are the same (i.e., about 70% identity, preferably 75%, 80%, 85%, 90%, 95%, 98% or 99% identity). The percent identity can be over a specified region, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection. Sequences are said to be "substantially identical" when there is at least 85% identity at the amino acid level or at the nucleotide level. Preferably, the identity exists over a region that is at least about 25, 50, or 100 residues in length, or across the entire length of at least one compared sequence. A typical algorithm for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al, Nuc. Acids Res. 25:3389-3402 (1977). Other methods include the algorithms of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), and Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), etc. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent hybridization conditions.

[00137] The terms "complementary" and "complement" and their variants, as used herein, refer to any two or more nucleic acid sequences (e.g., portions or entireties of template nucleic acid molecules, target sequences and/or primers) that can undergo cumulative base pairing at two or more individual corresponding positions in antiparallel orientation, as in a hybridized duplex. Such base pairing can proceed according to any set of established rules, for example according to Watson-Crick base pairing rules or according to some other base pairing paradigm. Optionally there can be "complete" or "total" complementarity between a first and second nucleic acid sequence where each nucleotide in the first nucleic acid sequence can undergo a stabilizing base pairing interaction with a

nucleotide in the corresponding antiparallel position on the second nucleic acid sequence. “Partial” complementarity describes nucleic acid sequences in which at least 20%, but less than 100%, of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. In some embodiments, at least 50%, but less than 100%, of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. In some embodiments, at least 70%, 80%, 90%, 95% or 98%, but less than 100%, of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. Sequences are said to be "substantially complementary" when at least 85% of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. In some embodiments, two complementary or substantially complementary sequences are capable of hybridizing to each other under standard or stringent hybridization conditions. “Non-complementary” describes nucleic acid sequences in which less than 20% of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. Sequences are said to be "substantially non-complementary" when less than 15% of the residues of one nucleic acid sequence are complementary to residues in the other nucleic acid sequence. In some embodiments, two non-complementary or substantially non-complementary sequences cannot hybridize to each other under standard or stringent hybridization conditions. A "mismatch" is present at any position in the two opposed nucleotides are not complementary. Complementary nucleotides include nucleotides that are efficiently incorporated by DNA polymerases opposite each other during DNA replication under physiological conditions. In a typical embodiment, complementary nucleotides can form base pairs with each other, such as the A-T/U and G-C base pairs formed through specific Watson-Crick type hydrogen bonding, or base pairs formed through some other type of base pairing paradigm, between the nucleobases of nucleotides and/or polynucleotides in positions antiparallel to each other. The complementarity of other artificial base pairs can be based on other types of hydrogen bonding and/or hydrophobicity of bases and/or shape complementarity between bases.

[00138] As used herein, “amplified target sequences” and its derivatives, refers generally to a nucleic acid sequence produced by the amplification of/amplifying the target sequences using target-specific primers and the methods provided herein. The amplified target sequences may be either of the same sense (the positive strand produced in the second round and subsequent even-numbered rounds of amplification) or antisense (i.e., the negative strand produced during the first and subsequent odd-numbered rounds of amplification) with respect to the target sequences. For the

purposes of this disclosure, the amplified target sequences are typically less than 50% complementary to any portion of another amplified target sequence in the reaction.

[00139] As used herein, the terms "ligating", "ligation" and their derivatives refer generally to the act or process for covalently linking two or more molecules together, for example, covalently linking two or more nucleic acid molecules to each other. In some embodiments, ligation includes joining nicks between adjacent nucleotides of nucleic acids. In some embodiments, ligation includes forming a covalent bond between an end of a first and an end of a second nucleic acid molecule. In some embodiments, for example embodiments wherein the nucleic acid molecules to be ligated include conventional nucleotide residues, the litgation can include forming a covalent bond between a 5' phosphate group of one nucleic acid and a 3' hydroxyl group of a second nucleic acid thereby forming a ligated nucleic acid molecule. In some embodiments, any means for joining nicks or bonding a 5'phosphate to a 3' hydroxyl between adjacent nucleotides can be employed. In an exemplary embodiment, an enzyme such as a ligase can be used. Generally for the purposes of this disclosure, an amplified target sequence can be ligated to an adapter to generate an adapter-ligated amplified target sequence.

[00140] As used herein, "ligase" and its derivatives, refers generally to any agent capable of catalyzing the ligation of two substrate molecules. In some embodiments, the ligase includes an enzyme capable of catalyzing the joining of nicks between adjacent nucleotides of a nucleic acid. In some embodiments, the ligase includes an enzyme capable of catalyzing the formation of a covalent bond between a 5' phosphate of one nucleic acid molecule to a 3' hydroxyl of another nucleic acid molecule thereby forming a ligated nucleic acid molecule. Suitable ligases may include, but not limited to, T4 DNA ligase, T4 RNA ligase, and *E. coli* DNA ligase.

[00141] As used herein, "ligation conditions" and its derivatives, generally refers to conditions suitable for ligating two molecules to each other. In some embodiments, the ligation conditions are suitable for sealing nicks or gaps between nucleic acids. As defined herein, a "nick" or "gap" refers to a nucleic acid molecule that lacks a directly bound 5' phosphate of a mononucleotide pentose ring to a 3' hydroxyl of a neighboring mononucleotide pentose ring within internal nucleotides of a nucleic acid sequence. As used herein, the term nick or gap is consistent with the use of the term in the art. Typically, a nick or gap can be ligated in the presence of an enzyme, such as ligase at an appropriate temperature and pH. In some embodiments, T4 DNA ligase can join a nick between nucleic acids at a temperature of about 70-72°C.

[00142] As used herein, "blunt-end ligation" and its derivatives, refers generally to ligation of two blunt-end double-stranded nucleic acid molecules to each other. A "blunt end" refers to an end of a double-stranded nucleic acid molecule wherein substantially all of the nucleotides in the end of one strand of the nucleic acid molecule are base paired with opposing nucleotides in the other strand of the same nucleic acid molecule. A nucleic acid molecule is not blunt ended if it has an end that includes a single-stranded portion greater than two nucleotides in length, referred to herein as an "overhang". In some embodiments, the end of nucleic acid molecule does not include any single stranded portion, such that every nucleotide in one strand of the end is based paired with opposing nucleotides in the other strand of the same nucleic acid molecule. In some embodiments, the ends of the two blunt ended nucleic acid molecules that become ligated to each other do not include any overlapping, shared or complementary sequence. Typically, blunted-end ligation excludes the use of additional oligonucleotide adapters to assist in the ligation of the double-stranded amplified target sequence to the double-stranded adapter, such as patch oligonucleotides as described in Mitra and Varley, US2010/0129874, published May 27, 2010. In some embodiments, blunt-ended ligation includes a nick translation reaction to seal a nick created during the ligation process.

[00143] As used herein, the terms "adapter" or "adapter and its complements" and their derivatives, refers generally to any linear oligonucleotide which can be ligated to a nucleic acid molecule of the disclosure. Optionally, the adapter includes a nucleic acid sequence that is not substantially complementary to the 3' end or the 5' end of at least one target sequences within the sample. In some embodiments, the adapter is substantially non-complementary to the 3' end or the 5' end of any target sequence present in the sample. In some embodiments, the adapter includes any single stranded or double-stranded linear oligonucleotide that is not substantially complementary to an amplified target sequence. In some embodiments, the adapter is substantially non-complementary to at least one, some or all of the nucleic acid molecules of the sample. In some embodiments, suitable adapter lengths are in the range of about 10-100 nucleotides, about 12-60 nucleotides and about 15-50 nucleotides in length. Generally, the adapter can include any combination of nucleotides and/or nucleic acids. In some aspects, the adapter can include one or more cleavable groups at one or more locations. In another aspect, the adapter can include a sequence that is substantially identical, or substantially complementary, to at least a portion of a primer, for example a universal primer. In some embodiments, the adapter can include a barcode or tag to assist with downstream cataloguing, identification or sequencing. In some embodiments, a single-stranded adapter can act as a substrate for amplification when ligated to an amplified target

sequence, particularly in the presence of a polymerase and dNTPs under suitable temperature and pH.

[00144] As used herein, "reamplifying" or "reamplification" and their derivatives refer generally to any process whereby at least a portion of an amplified nucleic acid molecule is further amplified via any suitable amplification process (referred to in some embodiments as a "secondary" amplification or "reamplification", thereby producing a reamplified nucleic acid molecule. The secondary amplification need not be identical to the original amplification process whereby the amplified nucleic acid molecule was produced; nor need the reamplified nucleic acid molecule be completely identical or completely complementary to the amplified nucleic acid molecule; all that is required is that the reamplified nucleic acid molecule include at least a portion of the amplified nucleic acid molecule or its complement. For example, the reamplification can involve the use of different amplification conditions and/or different primers, including different target-specific primers than the primary amplification.

[00145] As defined herein, a "cleavable group" generally refers to any moiety that once incorporated into a nucleic acid can be cleaved under appropriate conditions. For example, a cleavable group can be incorporated into a target-specific primer, an amplified sequence, an adapter or a nucleic acid molecule of the sample. In an exemplary embodiment, a target-specific primer can include a cleavable group that becomes incorporated into the amplified product and is subsequently cleaved after amplification, thereby removing a portion, or all, of the target-specific primer from the amplified product. The cleavable group can be cleaved or otherwise removed from a target-specific primer, an amplified sequence, an adapter or a nucleic acid molecule of the sample by any acceptable means. For example, a cleavable group can be removed from a target-specific primer, an amplified sequence, an adapter or a nucleic acid molecule of the sample by enzymatic, thermal, photo-oxidative or chemical treatment. In one aspect, a cleavable group can include a nucleobase that is not naturally occurring. For example, an oligodeoxyribonucleotide can include one or more RNA nucleobases, such as uracil that can be removed by a uracil glycosylase. In some embodiments, a cleavable group can include one or more modified nucleobases (such as 7-methylguanine, 8-oxo-guanine, xanthine, hypoxanthine, 5,6-dihydrouracil or 5-methylcytosine) or one or more modified nucleosides (i.e., 7-methylguanosine, 8-oxo-deoxyguanosine, xanthosine, inosine, dihydrouridine or 5-methylcytidine). The modified nucleobases or nucleotides can be removed from the nucleic acid by enzymatic, chemical or thermal means. In one embodiment, a cleavable group can include a moiety that can be removed from a primer after amplification (or synthesis) upon exposure to ultraviolet light (i.e.,

bromodeoxyuridine). In another embodiment, a cleavable group can include methylated cytosine. Typically, methylated cytosine can be cleaved from a primer for example, after induction of amplification (or synthesis), upon sodium bisulfite treatment. In some embodiments, a cleavable moiety can include a restriction site. For example, a primer or target sequence can include a nucleic acid sequence that is specific to one or more restriction enzymes, and following amplification (or synthesis), the primer or target sequence can be treated with the one or more restriction enzymes such that the cleavable group is removed. Typically, one or more cleavable groups can be included at one or more locations with a target-specific primer, an amplified sequence, an adapter or a nucleic acid molecule of the sample.

[00146] As used herein, "cleavage step" and its derivatives, generally refers to any process by which a cleavable group is cleaved or otherwise removed from a target-specific primer, an amplified sequence, an adapter or a nucleic acid molecule of the sample. In some embodiments, the cleavage steps involves a chemical, thermal, photo-oxidative or digestive process.

[00147] As used herein, the term "hybridization" is consistent with its use in the art, and generally refers to the process whereby two nucleic acid molecules undergo base pairing interactions. Two nucleic acid molecule molecules are said to be hybridized when any portion of one nucleic acid molecule is base paired with any portion of the other nucleic acid molecule; it is not necessarily required that the two nucleic acid molecules be hybridized across their entire respective lengths and in some embodiments, at least one of the nucleic acid molecules can include portions that are not hybridized to the other nucleic acid molecule. The phrase "hybridizing under stringent conditions" and its variants refers generally to conditions under which hybridization of a target-specific primer to a target sequence occurs in the presence of high hybridization temperature and low ionic strength. In one exemplary embodiment, stringent hybridization conditions include an aqueous environment containing about 30 mM magnesium sulfate, about 300 mM Tris-sulfate at pH 8.9, and about 90 mM ammonium sulfate at about 60-68°C., or equivalents thereof. As used herein, the phrase "standard hybridization conditions" and its variants refers generally to conditions under which hybridization of a primer to an oligonucleotide (i.e., a target sequence), occurs in the presence of low hybridization temperature and high ionic strength. In one exemplary embodiment, standard hybridization conditions include an aqueous environment containing about 100 mM magnesium sulfate, about 500 mM Tris-sulfate at pH 8.9, and about 200 mM ammonium sulfate at about 50-55°C., or equivalents thereof.

[00148] As used herein, "triple nucleotide motif" and its derivatives, refers generally to any nucleotide sequence that is repeated contiguously over three nucleotides e.g., AAA or CCC. Generally, a triple nucleotide motif is not repeated more than five times in a target-specific primer (or adapter) of the disclosure.

[00149] As used herein, "an ACA nucleotide motif" and its derivatives, refers generally to the nucleotide sequence "ACA". Generally, this motif is not repeated three or more times in a target-specific primer (or adapter) of the disclosure.

[00150] As used herein, "homopolymer" and its derivatives, refers generally to any repeating nucleotide sequence that is eight nucleotides or greater in length e.g., AAAAAAAA or CCCCCCCC. Generally, a homopolymer as defined herein is not present in a target-specific primer (or adapter) of the disclosure.

[00151] As used herein, "GC content" and its derivatives, refers generally to the cytosine and guanine content of a nucleic acid molecule. Generally, the GC content of a target-specific primer (or adapter) of the disclosure is 85% or lower. More typically, the GC content of a target-specific primer or adapter of the disclosure is between 15-85%.

[00152] As used herein, the term "end" and its variants, when used in reference to a nucleic acid molecule, for example a target sequence or amplified target sequence, can include the terminal 30 nucleotides, the terminal 20 and even more typically the terminal 15 nucleotides of the nucleic acid molecule. A linear nucleic acid molecule comprised of linked series of contiguous nucleotides typically includes at least two ends. In some embodiments, one end of the nucleic acid molecule can include a 3' hydroxyl group or its equivalent, and can be referred to as the "3' end" and its derivatives. Optionally, the 3' end includes a 3' hydroxyl group that is not linked to a 5' phosphate group of a mononucleotide pentose ring. Typically, the 3' end includes one or more 5' linked nucleotides located adjacent to the nucleotide including the unlinked 3' hydroxyl group, typically the 30 nucleotides located adjacent to the 3' hydroxyl, typically the terminal 20 and even more typically the terminal 15 nucleotides. Generally, the one or more linked nucleotides can be represented as a percentage of the nucleotides present in the oligonucleotide or can be provided as a number of linked nucleotides adjacent to the unlinked 3' hydroxyl. For example, the 3' end can include less than 50% of the nucleotide length of the oligonucleotide. In some embodiments, the 3' end does not include any unlinked 3' hydroxyl group but can include any moiety capable of serving as a site for attachment of nucleotides via primer extension and/or nucleotide polymerization. In some embodiments, the term "3' end" for example when referring to a target-specific primer, can include

the terminal 10 nucleotides, the terminal 5 nucleotides, the terminal 4, 3, 2 or fewer nucleotides at the 3'end. In some embodiments, the term "3' end" when referring to a target-specific primer can include nucleotides located at nucleotide positions 10 or fewer from the 3' terminus.

[00153] As used herein, "5' end", and its derivatives, generally refers to an end of a nucleic acid molecule, for example a target sequence or amplified target sequence, which includes a free 5' phosphate group or its equivalent. In some embodiments, the 5' end includes a 5' phosphate group that is not linked to a 3' hydroxyl of a neighboring mononucleotide pentose ring. Typically, the 5' end includes to one or more linked nucleotides located adjacent to the 5' phosphate, typically the 30 nucleotides located adjacent to the nucleotide including the 5' phosphate group, typically the terminal 20 and even more typically the terminal 15 nucleotides. Generally, the one or more linked nucleotides can be represented as a percentage of the nucleotides present in the oligonucleotide or can be provided as a number of linked nucleotides adjacent to the 5' phosphate. For example, the 5' end can be less than 50% of the nucleotide length of an oligonucleotide. In another exemplary embodiment, the 5' end can include about 15 nucleotides adjacent to the nucleotide including the terminal 5' phosphate. In some embodiments, the 5' end does not include any unlinked 5' phosphate group but can include any moiety capable of serving as a site of attachment to a a 3' hydroxyl group, or to the 3'end of another nucleic acid molecule. In some embodiments, the term "5' end" for example when referring to a target-specific primer, can include the terminal 10 nucleotides, the terminal 5 nucleotides, the terminal 4, 3, 2 or fewer nucleotides at the 5'end. In some embodiments, the term "5' end" when referring to a target-specific primer can include nucleotides located at positions 10 or fewer from the 5' terminus. In some embodiments, the 5' end of a target-specific primer can include only non-cleavable nucleotides, for example nucleotides that do not contain one or more cleavable groups as disclosed herein, or a cleavable nucleotide as would be readily determined by one of ordinary skill in the art.

[00154] As used herein, "protecting group" and its derivatives, refers generally to any moiety that can be incorporated into an adapter or target-specific primer that imparts chemical selectivity or protects the target-specific primer or adapter from digestion or chemical degradation. Typically, but not necessarily, a protecting group can include modification of an existing functional group in the target-specific primer r adapter to achieve chemical selectivity. Suitable types of protecting groups include alcohol, amine, phosphate, carbonyl, or carboxylic acid protecting groups. In an exemplary embodiment, the protecting group can include a spacer compound having a chain of carbon atoms.

[00155] As used herein, "DNA barcode" or "DNA tagging sequence" and its derivatives, refers generally to a unique short (6-14 nucleotide) nucleic acid sequence within an adapter that can act as a 'key' to distinguish or separate a plurality of amplified target sequences in a sample. For the purposes of this disclosure, a DNA barcode or DNA tagging sequence can be incorporated into the nucleotide sequence of an adapter.

[00156] As used herein, the phrases "two rounds of target-specific hybridization" or "two rounds of target-specific selection" and their derivatives refers generally to any process whereby the same target sequence is subjected to two consecutive rounds of hybridization-based target-specific selection, wherein a target sequence is hybridized to a target-specific sequence. Each round of hybridization based target-specific selection can include multiple target-specific hybridizations to at least some portion of a target-specific sequence. In one exemplary embodiment, a round of target-specific selection includes a first target-specific hybridization involving a first region of the target sequence and a second target-specific hybridization involving a second region of the target sequence. The first and second regions can be the same or different. In some embodiments, each round of hybridization-based target-specific selection can include use of two target specific oligonucleotides (e.g., a forward target-specific primer and a reverse target-specific primer), such that each round of selection includes two target-specific hybridizations.

[00157] As used herein, "comparable maximal minimum melting temperatures" and its derivatives, refers generally to the melting temperature (Tm) of each nucleic acid fragment for a single adapter or target-specific primer after cleavage of the cleavable groups. The hybridization temperature of each nucleic acid fragment generated by a single adapter or target-specific primer is compared to determine the maximal minimum temperature required preventing hybridization of any nucleic acid fragment from the target-specific primer or adapter to the target sequence. Once the maximal hybridization temperature is known, it is possible to manipulate the adapter or target-specific primer, for example by moving the location of the cleavable group along the length of the primer, to achieve a comparable maximal minimum melting temperature with respect to each nucleic acid fragment.

[00158] As used herein, "addition only" and its derivatives, refers generally to a series of steps in which reagents and components are added to a first or single reaction mixture. Typically, the series of steps excludes the removal of the reaction mixture from a first vessel to a second vessel in order to complete the series of steps. Generally, an addition only process excludes the manipulation

of the reaction mixture outside the vessel containing the reaction mixture. Typically, an addition-only process is amenable to automation and high-throughput.

[00159] As used herein, "synthesizing" and its derivatives, refers generally to a reaction involving nucleotide polymerization by a polymerase, optionally in a template-dependent fashion. Polymerases synthesize an oligonucleotide via transfer of a nucleoside monophosphate from a nucleoside triphosphate (NTP), deoxynucleoside triphosphate (dNTP) or dideoxynucleoside triphosphate (ddNTP) to the 3′ hydroxyl of an extending oligonucleotide chain. For the purposes of this disclosure, synthesizing includes to the serial extension of a hybridized adapter or a target-specific primer via transfer of a nucleoside monophosphate from a deoxynucleoside triphosphate.

[00160] As used herein, "polymerizing conditions" and its derivatives, refers generally to conditions suitable for nucleotide polymerization. In typical embodiments, such nucleotide polymerization is catalyzed by a polymerase. In some embodiments, polymerizing conditions include conditions for primer extension, optionally in a template-dependent manner, resulting in the generation of a synthesized nucleic acid sequence. In some embodiments, the polymerizing conditions include polymerase chain reaction (PCR). Typically, the polymerizing conditions include use of a reaction mixture that is sufficient to synthesize nucleic acids and includes a polymerase and nucleotides. The polymerizing conditions can include conditions for annealing of a target-specific primer to a target sequence and extension of the primer in a template dependent manner in the presence of a polymerase. In some embodiments, polymerizing conditions can be practiced using thermocycling. Additionally, polymerizing conditions can include a plurality of cycles where the steps of annealing, extending, and separating the two nucleic strands are repeated. Typically, the polymerizing conditions include a cation such as $MgCl_2$. Generally, polymerization of one or more nucleotides to form a nucleic acid strand includes that the nucleotides be linked to each other via phosphodiester bonds, however, alternative linkages may be possible in the context of particular nucleotide analogs.

[00161] As used herein, the term "nucleic acid" refers to natural nucleic acids, artificial nucleic acids, analogs thereof, or combinations thereof, including polynucleotides and oligonucleotides. As used herein, the terms "polynucleotide" and "oligonucleotide" are used interchangeably and mean single-stranded and double-stranded polymers of nucleotides including, but not limited to, 2'-deoxyribonucleotides (nucleic acid) and ribonucleotides (RNA) linked by internucleotide phosphodiester bond linkages, *e.g.* 3'-5' and 2'-5', inverted linkages, *e.g.* 3'-3' and 5'-5', branched structures, or analog nucleic acids. Polynucleotides have associated counter ions,

such as H^+, NH_4^+, trialkylammonium, Mg^{2+}, Na^+ and the like. An oligonucleotide can be composed entirely of deoxyribonucleotides, entirely of ribonucleotides, or chimeric mixtures thereof. Oligonucleotides can be comprised of nucleobase and sugar analogs. Polynucleotides typically range in size from a few monomeric units, *e.g.* 5-40, when they are more commonly frequently referred to in the art as oligonucleotides, to several thousands of monomeric nucleotide units, when they are more commonly referred to in the art as polynucleotides; for purposes of this disclosure, however, both oligonucleotides and polynucleotides may be of any suitable length. Unless denoted otherwise, whenever a oligonucleotide sequence is represented, it will be understood that the nucleotides are in 5' to 3' order from left to right and that "A" denotes deoxyadenosine, "C" denotes deoxycytidine, "G" denotes deoxyguanosine, "T" denotes thymidine, and "U' denotes deoxyuridine. Oligonucleotides are said to have "5' ends" and "3' ends" because mononucleotides are typically reacted to form oligonucleotides via attachment of the 5' phosphate or equivalent group of one nucleotide to the 3' hydroxyl or equivalent group of its neighboring nucleotide, optionally via a phosphodiester or other suitable linkage.

[00162] As defined herein, the term "nick translation" and its variants comprise the translocation of one or more nicks or gaps within a nucleic acid strand to a new position along the nucleic acid strand. In some embodiments, a nick can be formed when a double stranded adapter is ligated to a double stranded amplified target sequence. In one example, the primer can include at its 5' end, a phosphate group that can ligate to the double stranded amplified target sequence, leaving a nick between the adapter and the amplified target sequence in the complementary strand. In some embodiments, nick translation results in the movement of the nick to the 3' end of the nucleic acid strand. In some embodiments, moving the nick can include performing a nick translation reaction on the adapter-ligated amplified target sequence. In some embodiments, the nick translation reaction can be a coupled 5' to 3' DNA polymerization/degradation reaction, or coupled to a 5' to 3' DNA polymerization/strand displacement reaction. In some embodiments, moving the nick can include performing a DNA strand extension reaction at the nick site. In some embodiments, moving the nick can include performing a single strand exonuclease reaction on the nick to form a single stranded portion of the adapter-ligated amplified target sequence and performing a DNA strand extension reaction on the single stranded portion of the adapter-ligated amplified target sequence to a new position. In some embodiments, a nick is formed in the nucleic acid strand opposite the site of ligation.

[00163] As used herein, the term "polymerase chain reaction" ("PCR") refers to the method of K. B. Mullis U.S. Pat. Nos. 4,683,195 and 4,683,202, hereby incorporated by reference, which describe a method for increasing the concentration of a segment of a polynucleotide of interest in a mixture of genomic DNA without cloning or purification. This process for amplifying the polynucleotide of interest consists of introducing a large excess of two oligonucleotide primers to the DNA mixture containing the desired polynucleotide of interest, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded polynucleotide of interest. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the polynucleotide of interest molecule. Following annealing, the primers are extended with a polymerase to form a new pair of complementary strands. The steps of denaturation, primer annealing and polymerase extension can be repeated many times (i.e., denaturation, annealing and extension constitute one "cycle"; there can be numerous "cycles") to obtain a high concentration of an amplified segment of the desired polynucleotide of interest. The length of the amplified segment of the desired polynucleotide of interest (amplicon) is determined by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of repeating the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired amplified segments of the polynucleotide of interest become the predominant nucleic acid sequences (in terms of concentration) in the mixture, they are said to be "PCR amplified". As defined herein, target nucleic acid molecules within a sample including a plurality of target nucleic acid molecules are amplified via PCR. In a modification to the method discussed above, the target nucleic acid molecules can be PCR amplified using a plurality of different primer pairs, in some cases, one or more primer pairs per target nucleic acid molecule of interest, thereby forming a multiplex PCR reaction. Using multiplex PCR, it is possible to simultaneously amplify multiple nucleic acid molecules of interest from a sample to form amplified target sequences. It is also possible to detect the amplified target sequences by several different methodologies (e.g., quantitation with a bioanalyzer or qPCR, hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of ^{32}P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified target sequence). Any oligonucleotide sequence can be amplified with the appropriate set of primers, thereby allowing for the amplification of target nucleic acid molecules from genomic DNA, cDNA, formalin-fixed paraffin-embedded DNA, fine-needle biopsies and various other sources. In particular, the amplified

target sequences created by the multiplex PCR process as disclosed herein, are themselves efficient substrates for subsequent PCR amplification or various downstream assays or manipulations.

[00164] As defined herein "multiplex amplification" refers to selective and non-random amplification of two or more target sequences within a sample using at least one target-specific primer. In some embodiments, multiplex amplification is performed such that some or all of the target sequences are amplified within a single reaction vessel. The "plexy" or "plex" of a given multiplex amplification refers generally to the number of different target-specific sequences that are amplified during that single multiplex amplification. In some embodiments, the plexy can be about 12-plex, 24-plex, 48-plex, 96-plex, 192-plex, 384-plex, 768-plex, 1536-plex, 3072-plex, 6144-plex or higher.

[00165] In some embodiments, the disclosure relates generally to methods, compositions, systems, apparatuses and kits for avoiding or reducing the formation of amplification artifacts (for example primer-dimers) during selective amplification of one or more target nucleic acid molecules in a population of nucleic acid molecules.

[00166] In some embodiments, the disclosure relates generally to the amplification of multiple target-specific sequences from a population of nucleic acid molecules. In some embodiments, the method comprises hybridizing one or more target-specific primer pairs to the target sequence, extending a first primer of the primer pair, denaturing the extended first primer product from the population of nucleic acid molecules, hybridizing to the extended first primer product the second primer of the primer pair, extending the second primer to form a double stranded product, and digesting the target-specific primer pair away from the double stranded product to generate a plurality of amplified target sequences. In some embodiments, the digesting includes partial digesting of one or more of the target-specific primers from the amplified target sequence. In some embodiments, the amplified target sequences can be ligated to one or more adapters. In some embodiments, the adapters can include one or more DNA barcodes or tagging sequences. In some embodiments, the amplified target sequences once ligated to an adapter can undergo a nick translation reaction and/or further amplification to generate a library of adapter-ligated amplified target sequences.

[00167] In some embodiments, the disclosure relates generally to the preparation and formation of multiple target-specific amplicons. In some embodiments, the method comprises hybridizing one or more target-specific primer pairs to a nucleic acid molecule, extending a first primer of the primer, pair, denaturing the extended first primer from the nucleic acid molecule,

hybridizing to the extended first primer product, a second primer of the primer pair and extending the second primer, digesting the target-specific primer pairs to generate a plurality of target-specific amplicons. In some embodiments, adapters can be ligated to the ends of the target-specific amplicons prior to performing a nick translation reaction to generate a plurality of target-specific amplicons suitable for nucleic acid sequencing. In some embodiments, the one or more target specific amplicons can be amplified using bridge amplification or emPCR to generate a plurality of clonal templates suitable for nucleic acid sequencing. In some embodiments, the disclosure generally relates to methods for preparing a target-specific amplicon library, for use in a variety of downstream processes or assays such as nucleic acid sequencing or clonal amplification. In one embodiment, the disclosure relates to a method of performing target-specific multiplex PCR on a nucleic acid sample having a plurality of target sequences using primers having a cleavable group.

[00168] In one embodiment, nucleic acid templates to be sequenced using the Ion Torrent PGM™ or Ion Torrent Proton™ system can be prepared from a population of nucleic acid molecules using the target-specific amplification techniques as outlined herein. Optionally, following target-specific amplification a secondary and/or tertiary amplification process including, but not limited to, a library amplification step and/or a clonal amplification step such as emPCR can be performed.

[00169] In some embodiments, the disclosure relates to a composition comprising a plurality of target-specific primer pairs, each containing a forward primer and a reverse primer having at least one cleavable group located at either a) the 3' end or the 5' end, and/or b) at about the central nucleotide position of the target-specific primer, and wherein the target-specific primer pairs can be substantially non-complementary to other primer pairs in the composition. In some embodiments, the composition comprises at least 1000, 2000, 3000, 4000, 6000, 9000, 12000, or more target-specific primer pairs. In some embodiments, the target-specific primer pairs comprise about 15 nucleotides to about 40 nucleotides in length, wherein at least one nucleotide is replaced with a cleavable group. In some embodiments the cleavable group can be a uridine nucleotide. In some embodiments, the target-specific primer sets are designed to amplify an exon, gene, exome or region of the genome associated with a clinical or pathological condition, e.g., the amplification of one or more single nucleotide mutations (SNPs) associated with cancer, such as colon cancer, or the amplification of mutations associated with an inherited disease such as cystic fibrosis. In some embodiments, the target-specific primer pairs when hybridized to a target sequence and amplified as outlined herein can generate a library of adapter-ligated amplified target sequences that are about 100 to about 500 base pairs in length. In some embodiments, no one adapter-ligated amplified target

sequence is overexpressed in the library by more than 30% as compared to the remainder of the adapter-ligated amplified target sequences in the library. In some embodiments, the adapter-ligated amplified target sequence library is substantially homogenous with respect to GC content, amplified target sequence length or melting temperature (Tm).

[00170] In some embodiments, the disclosure relates generally to a kit for performing multiplex PCR comprising a plurality of target-specific primers having a cleavable group, a DNA polymerase, an adapter, dATP, dCTP, dGTP and dTTP. In some embodiments, the cleavable group can be a uracil nucleotide. The kit can further include one or more antibodies, nucleic acid barcodes, purification solutions or columns.

[00171] In some embodiments, the disclosure relates to a kit for generating a target-specific amplicon library comprising a plurality of target-specific primers having a cleavable group, a DNA polymerase, an adapter, dATP, dCTP, dGTP, dTTP, and a cleaving reagent. In some embodiments, the kit further comprises one or more antibodies, nucleic acid barcodes, purification solutions or columns.

[00172] In one embodiment, the disclosure generally relates to the amplification of multiple target-specific sequences from a single nucleic acid source or sample. In another embodiment, the disclosure relates generally to the target-specific amplification of two or more target sequences from two or more nucleic acid sources, samples or species. For example, it is envisioned by the disclosure that a single nucleic acid sample can include genomic DNA or fixed-formalin paraffin-embedded (FFPE) DNA. It is also envisioned that the sample can be from a single individual, a collection of nucleic acid samples from genetically related members, multiple nucleic acid samples from genetically unrelated members, multiple nucleic acid samples (matched) from a single individual such as a tumor sample and normal tissue sample, or genetic material from a single source that contains two distinct forms of genetic material such as maternal and fetal DNA obtained from a maternal subject, or the presence of contaminating bacteria DNA in a sample that contains plant or animal DNA. In some embodiments, the source of nucleic acid material can include nucleic acids obtained from a newborn, for example as typically procured as a blood sample for newborn screening.

[00173] The nucleic acid sample can include high molecular weight material such as genomic DNA or cDNA. The sample can include low molecular weight material such as nucleic acid molecules obtained from FFPE or archived DNA samples. In another embodiment, low molecular weight material includes enzymatically or mechanically sheared DNA. The sample can include cell-

free circulating DNA such as material obtained from a maternal subject. In some embodiments, the sample can include nucleic acid molecules obtained from biopsies, tumors, scrapings, swabs, blood, mucus, urine, plasma, semen, hair, laser capture micro-dissections, surgical resections, and other clinical or laboratory obtained samples. In some embodiments, the sample can be an epidemiological, agricultural, forensic or pathogenic sample.

[00174] In some embodiments, the sample can include nucleic acid molecules obtained from an animal such as a human or mammalian source. In another embodiment, the sample can include nucleic acid molecules obtained from a non-mammalian source such as a plant, bacteria, virus or fungus. In some embodiments, the source of the nucleic acid molecules may be an archived or extinct sample or species.

[00175] In some embodiments, the disclosure relates generally to the selective amplification of at least one target sequence in a normal or diseased containing tissue, biopsy, core, tumor or other sample. In some embodiments, the disclosure generally relates to the selective amplification of at least one target sequence and the detection and/or identification of mutations in the diseased tissue, core, biopsy or tumor sample. In some embodiments, the diseased or normal sample can include whole genomic DNA, formalin-fixed paraffin-embedded tissue (FFPE), sheared or enzymatically treated DNA. In some embodiments, the disclosure is directed to the selective amplification of at least one target sequence and detection and/or identification of clinically actionable mutations. In some embodiments, the disclosure is directed to the detection and/or identification of mutations associated with drug resistance or drug susceptibility. In some embodiments, the disclosure is generally directed to the identification and/or quantitation of genetic markers associated with organ transplantation or organ rejection.

[00176] In some embodiments, the disclosure relates generally to the selective amplification of at least one target sequence in cell-free circulating DNA. In some embodiments, the selective amplification of at least one target sequence in a sample includes a mixture of different nucleic acid molecules. The selective amplification can optionally be accompanied by detection and/or identification of mutations observed in circulating DNA. In some embodiments, the selective amplification can optionally be accompanied by detection and/or identification of mutations associated with cancer or an inherited disease such as metabolic, neuromuscular, developmental, cardiovascular, autoimmune or other inherited disorder.

[00177] In some embodiments, the target-specific primers and primer pairs are target-specific sequences that can amplify specific regions of a nucleic acid molecule. In some embodiments, the

target-specific primers can amplify genomic DNA or cDNA. In some embodiments, the target-specific primers can amplify mammalian DNA, such as human DNA. In some embodiments, the amount of DNA required for selective amplification can be from about 1 ng to 1 microgram. In some embodiments, the amount of DNA required for selective amplification of one or more target sequences can be about 1 ng, about 5 ng or about 10 ng. In some embodiments, the amount of DNA required for selective amplification of target sequence is about 10 ng to about 200 ng.

[00178] In some embodiments, selective amplification of at least one target sequence further includes nucleic acid sequencing of the amplified target sequence. Optionally, the method further includes detecting and/or identifying mutations present in the sample identified through nucleic acid sequencing of the amplified target sequence.

[00179] In some embodiments, target sequences or amplified target sequences are directed to mutations associated with cancer. In some embodiments, the target sequences or amplified target sequences are directed to mutations associated with one or more cancers selected from the group consisting of head and neck cancers, brain cancer, breast cancer, ovarian cancer, cervical cancer, colorectal cancer, endometrial cancer, gallbladder cancer, gastric cancer, bladder cancer, prostate cancer, testicular cancer, liver cancer, lung cancer, kidney (renal cell) cancer, esophageal cancer, pancreatic cancer, thyroid cancer, bile duct cancer, pituitary tumor, wilms tumor, kaposi sarcoma, osteosarcoma, thymus cancer, skin cancer, heart cancer, oral and larynx cancer, leukemia, neuroblastoma and non-hodgkin lymphoma. In one embodiment, the mutations can include substitutions, insertions, inversions, point mutations, deletions, mismatches and translocations. In one embodiment, the mutations can include variation in copy number. In one embodiment, the mutations can include germline or somatic mutations. In one embodiment, the mutations associated with cancer are located in at least one of the genes provided in Tables 1 or 4, or provided in Table 7 of US Application No. 61/598,881 hereby incorporated by reference in its entirety. In some embodiments, the mutations can be any of the genomic coordinates provided in Table 18, or provided in Table 7 of US Application 61/598,881 hereby incorporated by reference in its entirety. In some embodiments, the target sequences directed to mutations associated with cancer can include any one or more of the mutations provided in Table 10. In some embodiments, the mutations can be found within any one or more of the genomic coordinates provided in Table 16 or Table 18.

[00180] In some embodiments, the mutations associated with cancer are located in at least one of the genes selected from ABI1; ABL1; ABL2; ACSL3; ACSL6; AFF1; AFF3; AFF4;AKAP9; AKT1; AKT2; ALK; APC; ARHGAP26; ARHGEF12; ARID1A; ARNT; ASPSCR1; ASXL1;

ATF1; ATIC; ATM; AXIN2; BAP1; BARD1; BCAR3; BCL10; BCL11A; BCL11B; BCL2; BCL3; BCL6; BCL7A;BCL9; BCR; BIRC3; BLM; BMPR1A; BRAF; BRCA1; BRCA2; BRD3; BRD4; BRIP1; BUB1B; CARD11; CARS; CASC5; CBFA2T3; CBFB; CBL; CBLB; CBLC; CCDC6; CCNB1IP1; CCND1; CCND2; CD74; CD79A; CDC73; CDH1; CDH11; CDK4; CDK6; CDKN2A; CDKN2B; CDKN2C; CDX2; CEBPA; CEP110; CHEK1; CHEK2; CHIC2; CHN1; CIC; CIITA; CLP1; CLTC; CLTCL1; COL1A1; CREB1; CREB3L2; CREBBP; CRTC1; CRTC3; CSF1R; CTNNB1; CXCR7; CYLD; CYTSB; DCLK3; DDB2; DDIT3; DDR2; DDX10; DDX5; DDX6; DEK; DGKG; DICER1; DNMT3A; EGFR; EIF4A2; ELF4; ELL; ELN; EML4;EP300; EPS15; ERBB2; ERBB4; ERC1; ERCC2; ERCC3; ERCC4; ERCC5; ERG; ETV1; ETV4; ETV5; ETV6; EWSR1; EXT1; EXT2; EZH2; FAM123B; FANCA; FANCC; FANCD2; FANCE; FANCF; FANCG; FAS; FBXW7; FCRL4; FGFR1; FGFR1OP; FGFR2; FGFR3; FH; FIP1L1; FLCN; FLI1; FLT1; FLT3; FNBP1; FOXL2; FOXO1; FOXO3; FOXO4; FOXP1; FUS; GAS7; GATA1; GATA2; GATA3; GMPS; GNAQ; GNAS; GOLGA5; GOPC; GPC3; GPHNGPR124; HIP1; HIST1H4I; HLF; HNF1A; HNRNPA2B1; HOOK3; HOXA11; HOXA13; HOXA9; HOXC11; HOXC13; HOXD13; HRAS; HSP90AA1; HSP90AB1; IDH1; IDH2; IKZF1; IL2; IL21R; IL6ST; IRF4; ITGA10; ITGA9; ITK; JAK1; JAK2; JAK3; KDM5A; KDM5C; KDM6A; KDR; KDSR; KIAA1549; KIT; KLF6; KLK2; KRAS; KTN1; LASP1; LCK; LCP1; LHFP; LIFR; LMO2; LPP; MAF; MALT1; MAML2; MAP2K1; MAP2K4; MDM2; MDM4; MECOM; MEN1; MET; MITF; MKL1; MLH1; MLL; MLLT1; MLLT10; MLLT3; MLLT4; MLLT6; MN1; MPL; MRE11A; MSH2; MSH6; MSI2; MSN; MTCP1; MTOR; MUC1; MYB; MYC; MYCL1; MYCN; MYH11; MYH9; MYST3; MYST4; NACA; NBN; NCOA1; NCOA2; NCOA4; NEK9; NF1; NF2; NFE2L2; NFKB2; NIN; NKX2-1; NLRP1; NONO; NOTCH1; NOTCH2; NPM1; NR4A3; NRAS; NSD1; NTRK1; NTRK3; NUMA1; NUP214; NUP98; OLIG2; OMD; PAFAH1B2; PALB2; PATZ1; PAX3; PAX5; PAX7; PAX8; PBRM1; PBX1; PCM1;PDE4DIP; PDGFB; PDGFRA; PDGFRB; PER1; PHOX2B; PICALM; PIK3CA; PIK3R1; PIM1; PLAG1; PML; PMS1; PMS2; POU2AF1; POU5F1; PPARG; PPP2R1A; PRCC; PRDM16; PRF1; PRKAR1A; PRRX1; PSIP1; PTCH1; PTEN; PTPN11; RABEP1; RAD50; RAD51L1; RAF1; RANBP17; RAP1GDS1; RARA; RB1; RBM15; RECQL4; REL; RET; RHOH; RNF213; ROS1; RPN1; RPS6KA2; RUNX1; RUNX1T1; SBDS; SDHAF2; SDHB; SETD2; SFPQ; SFRS3; SH3GL1; SLC45A3; SMAD4; SMARCA4; SMARCB1; SMO; SOCS1; SRC; SRGAP3; SS18; SS18L1; STIL; STK11; STK36; SUFU; SYK; TAF15; TAF1L; TAL1; TAL2; TCF12; TCF3; TCL1A; TET1; TET2; TEX14; TFE3; TFEB; TFG; TFRC; THRAP3; TLX1; TLX3; TMPRSS2; TNFAIP3; TOP1; TP53; TPM3; TPM4; TPR; TRIM27;

TRIM33; TRIP11; TSC1; TSC2; TSHR; USP6; VHL; WAS; WHSC1L1; WRN; WT1; XPA; XPC; ZBTB16; ZMYM2; ZNF331; ZNF384; and ZNF521.

[00181] In some embodiments, the mutations associated with cancer are located in at least one of the genes selected from ABL1; AKT1; ALK; APC; ATM; BRAF; CDH1; CDKN2A; CSF1R; CTNNB1; EGFR; ERBB2; ERBB4; FBXW7; FGFR1; FGFR2; FGFR3; FLT3; GNAS; HNF1A; HRAS; IDH1; JAK2; JAK3; KDR; KIT; KRAS; MET; MLH1; MPL; NOTCH1; NPM1; NRAS; PDGFRA; PIK3CA; PTEN; PTPN11; RB1; RET; SMAD4; SMARCB1; SMO; SRC; STK11; TP53; and VHL.

[00182] In some embodiments, the amplified target sequences are directed to any one of more of the genomic coordinates provided in Table 18. In some embodiments, any one or more of the cancer target-specific primers provided in Tables 2, 3 or 17 can be used to amplify a target sequence present in a sample as disclosed by the methods described herein.

[00183] In some embodiments, the cancer target-specific primers from Tables 2, 3 or 17 can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 40, 60, 80, 100, 150, 200, 400, 500, 800, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10,000, 11,000, 12,000, 13,000 or more, target-specific primers. In some embodiments, the amplified target sequences can include any one or more of the amplified target sequences generated at the genomic coordinates (using amplicon ID target-specific primers) provided in Tables 10 or 18. In some embodiments, at least one of the target-specific primers associated with cancer is at least 90% identical to at least one nucleic acid sequence selected from SEQ ID NOs: 1-103,143. In some embodiments, at least one of the target-specific primers associated with cancer is complementary across its entire length to at least one target sequence in a sample. In some embodiments, at least one of the target-specific primers associated with cancer includes a non-cleavable nucleotide at the 3' end. In some embodiments, the non-cleavable nucleotide at the 3' end includes the terminal 3' nucleotide. In one embodiment, the amplified target sequences are directed to individual exons having a mutation associated with cancer. In some embodiments, the disclosure relates generally to the selective amplification of more than one target sequences in a sample and the detection and/or identification of mutations associated with cancer. In some embodiments, the amplified target sequences include two or more nucleotide sequences provided in Table 2. In some embodiments, the amplified target sequences can include any one or more the amplified target sequences generated at the genomic coordinates using the amplicon ID target-specific primers provided in Table 18, or provided in Table 7 of US Application 61/598,881 hereby incorporated by reference in its entirety. In one embodiment, the amplified target sequences include 100, 200, 500,

1000, 2000, 3000, 6000, 8000, 10,000, 12,000, or more amplicons from Tables1-5, or Tables 6 and 7 of US Application 61/598,881 hereby incorporated by reference in their entireties. In some embodiments, the disclosure relates generally to the detection and optionally, the identification of clinically actionable mutations. As defined herein, the term "clinically actionable mutations" includes mutations that are known or can be associated by one of ordinary skill in the art with, but not limited to, prognosis for the treatment of cancer. In one embodiment, prognosis for the treatment of cancer includes the identification of mutations associated with responsiveness or non-responsiveness of a cancer to a drug, drug combination, or treatment regime. In one embodiment, the disclosure relates generally to the amplification of a plurality of target sequences from a population of nucleic acid molecules linked to, or correlated with, the onset, progression or remission of cancer.

[00184] In some embodiments, target-specific primers are designed using the primer criteria disclosed herein. In some embodiments, target-specific primers are designed using the primer criteria disclosed herein and directed to one or more genes associated with breast cancer. In some embodiments, target-specific primers associated with breast cancer include at least one target-specific primer selected from one or more genes selected from the group consisting of AIM1, AR, ATM, BARD1, BCAS1, BRIP1, CCND1, CCND2, CCNE1, CDH1, CDK3,CDK4,CDKN2A, CDKN2B, CAMK1D, CHEK2, DIRAS3, EGFR, ERBB2, EPHA3, ERBB4, ETV6, GNRH1, KCTD9, CDCA2, EBF2, EMSY, BNIP3L, PNMA2, DPYSL2, ADRA1A, STMN4, TRIM35, PAK1, AQP11, CLSN1A, RSF1, KCTD14, THRSP, NDUFC2, ALG8, KCTD21, USP35, GAB2, DNAH9, ZNF18, MYOCD, STK11, TP53, JAK1, JAK2, MET, PDGFRA, PML, PTEN, RET, TMPRSS2, WNK1, FGFR1, IGF1R, PPP1R12B, PTPRT, GSTM1, IPO8, MYC, ZNF703, MDM1, MDM2, MDM4,MKK4, P14KB, NCOR1, NBN, PALB2, RAD50, RAD51, PAK1,RSF1, INTS4, ZMIZ1, SEPHS1, FOXM1, SDCCAG1, IGF1R, TSHZ2, RPSK6K1, PPP2R2A, MTAP, MAP2K4, AURKB, BCL2, BUB1, CDCA3, CDCA4, CDC20, CDC45, CHEK1, FOXM1, HDAC2, IGF1R, KIF2C, KIFC1, KRAS, RB1, SMAD4, NCOR1, UTX, MTHDFD1L, RAD51AP1, TTK and UBE2C.

[00185] In some embodiments, the disclosure relates generally to the amplification of target sequences directed to mutations associated with a congenital or inherited disease. In some embodiments, the disclosure can include the amplification of target sequences directed to somatic or germline mutations. In some embodiments, the mutations can be autosomal dominant or autosomal recessive. In one embodiment, the mutations associated with a congenital or inherited disease are located in at least one of the genes or diseases provided in Table 4. In some embodiments, the disclosure relates to the amplification of target sequences in a sample associated with one or more

inherited diseases selected from the group consisting of Adenosine Aminohydrolase Deficiency (ADA); Agammaglobulinemia, X-linked, Type 1; Alagille Syndrome; All Hypertrophic and Dilated Cardiomyopathy; Alopecia Universalis Congenita (ALUNC); Alpers Syndrome; Alpha-1-Antitrypsin Deficiency; Alpha-Thalassemia - Southeast Asia; Amyotrophic Lateral Sclerosis - Lou Gehrig's Disease; Androgen Insensitivity Syndrome; Aniridia; Ankylosing spondylitis; APC-Associated Polyposis Conditions; Argininosuccinate Lyase Deficiency; Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy; Ataxia with Oculomotor Apraxia Type 2; Ataxia with Vitamin E Deficiency; Ataxia-Telangiectasia; Autoimmune Polyendocrine Syndrome; Beta-Hydroxyisobutyryl CoA Deacylase deficiency (HIBCH deficiency); Biotinidase Deficiency; Blepharophimosis-ptosis-epicanthus inversus; Bloom Syndrome; Brachydactyly; Brachydactyly - Hypertension Syndrome; Brachydactyly Type B1; Branchiootorenal Spectrum Disorders; BRCA1; Campomelic Dysplasia; Canavan; Cerebrotendinous Xanthomatosis; Ceroid-lipofuscinoses-Batton; Charcot-Marie-Tooth Disease Type 2B; Charcot-Marie-Tooth Neuropathy Type 1B; Charcot-Marie-Tooth Neuropathy Type 2A2 ; Charge Syndrome; Cherubism; Choroideremia; Citrin Deficiency; Citrullinemia Type I; Coffin-Lowry Syndrome; Cohen Syndrome; Collagen 4A5; Common Variable Immune Deficiency; Congenital Adrenal Hyperplasia; Congenital Cataracts, Facial Dysmorphism, and Neuropathy; Congenital Disorder of Glycosylation Type 1a; Congenital Myasthenic Syndromes; Cornelia de Lange Syndrome; Cystic fibrosis; Cystinosis; Darier Disease; Desmin Storage Myopathy; DFNA2 Nonsyndromic Hearing Loss; Diamond-Blackfan Anemia; Double Cortex Syndrome; Duane Syndrome; Duchenne/Becker muscular dystrophy; Dysferlinopathy; Dyskeratosis Congenita; Early-Onset Familial Alzheimer Disease; Early-Onset Primary Dystonia (DYT1); Ehlers Danlos; Ehlers-Danlos Syndrome, Classic Type; Ehlers-Danlos Syndrome, Hypermobility Type; Ehlers-Danlos Syndrome, Kyphoscoliotic Form; Emery-Dreifuss Muscular Dystrophy X linked; Epidermolysis Bullosa Simplex; Fabry Disease; Facioscapulohumeral Muscular Dystrophy; Familial Dysautonomia (HSAN III); Familial Hyperinsulinism (FHI); Familial Hypertrophic Cardiomyopathy; Familial Transthyretin Amyloidosis; Fanconi Anemia; Fragile X; Friedreich Ataxia; FRMD7-Related Infantile Nystagmus; Fryns Syndrome; Galactosemia; Gaucher Disease; Glycine Encephalopathy; Glycogen Storage Disease Type VI; Hemophagocytic Lymphohistiocytosis; Hemophilia A; Hemophilia B; Hepatic Veno-Occlusive Disease with Immunodeficiency; Hereditary Hemorrhagic Telangiectasia; Hereditary Neuropathy with Liability to Pressure Palsies; Hereditary Nonpolyposis Colon Cancer; Hexosaminidase A Deficiency; HFE-Associated Hereditary Hemochromatosis; Holt-Oram Syndrome; Huntington Disease; Hydroxymethylbilane Synthase (HMBS) Deficiency;

Hypophosphatasia; Inclusion Body Myopathy 2; Incontinentia Pigmenti; Juvenile Polyposis Syndrome; Kallmann Syndrome; Leber Congenital Amaurosis; Leber congenital amaurosis 10; Li-Fraumeni Syndrome; Limb-Girdle Muscular Dystrophy Type 2A Calpainopathy; LIS1-Associated Lissencephaly; Long QT Syndrome; Lowe Syndrome; Malignant Hyperthermia Susceptibility; Maple Syrup Urine Disease; MAPT-Related Disorders; McKusick-Kaufman Syndrome; MECP2-Rett Syndrome; Menkes; Metachromatic Leukodystrophy; Methylmalonic Acidemia; Mucolipidosis II; Multiple Endocrine Neoplasia Type 1; Multiple Endocrine Neoplasia Type 2; Myotonia Congenita; Myotonic Dystrophy Type 1; Myotonic Dystrophy Type 2; Nail-Patella Syndrome; Nemaline Myopathy; Neurofibromatosis 1; Neurofibromatosis 2; Noonan Syndrome; Ocular Albinism, X-Linked; Oculocutaneous Albinism Type 1; Oculocutaneous Albinism Type 2; Oculopharyngeal Muscular Dystrophy; Optic Atrophy Type 1; Ornithine Transcarbamylase Deficiency; Osteogenesis Imperfecta; Parkinson Disease; Pendred Syndrome; Peroxisome Biogenesis, Zellweger; Phenylketonuria; Polycystic Kidney Disease; Pompe Disease -GSD II; Primary Ciliary Dyskinesia; Retinitis Pigmentosa; Retinoblastoma; Saethre-Chotzen Syndrome; SCN9A-Related Inherited Erythromelalgia; SHOX-Related Haploinsufficiency; Sickle Cell Disease; Smith-Lemli-Opitz Syndrome; Smith-Magenis Syndrome; Sotos Syndrome; Spastic Paraplegia 3A; Spastic Paraplegia 7; Spastic Paraplegia 8; Spastic Paraplegia Type 1; Spastic Paraplegia Type 4; Spinal Muscular Atrophy; Spinocerebellar Ataxia 2; Spinocerebellar Ataxia 3; Spinocerebellar Ataxia 7; Spinocerebellar Ataxia Type 1; Stickler Syndrome; Thanatophoric Dysplasia; Thoracic Aortic Aneurysms and Aortic Dissections; Treacher Collins Syndrome; Trimethylaminuria; Tuberous Sclerosis Complex; Udd Distal Myopathy; Usher Syndrome type 1; Very Long Chain Acyl-Coenzyme A Dehydrogenase Deficiency; von Hippel-Lindau; Waardenburg Syndrome, Type 1; Werner Syndrome; Wilms Tumor; Wilson Disease; Wiskott-Aldrich; X-Linked Adrenal Hypoplasia Congenita; X-Linked Adrenoleukodystrophy; X-Linked Dystonia-Parkinsonism; X-linked Juvenile Retinoschisis; X-linked myotubular Myopathy; X-Linked SCIDS; and Zellweger Syndrome.

[00186] In one embodiment, the mutations associated with a congenital or inherited disease can include substitutions, insertions, inversions, point mutations, deletions, mismatches and translocations. In some embodiments, the mutations associated with an inherited or congenital disease includes copy number variation. In some embodiments, the disclosure relates generally to the selective amplification of at least one target sequence and the detection and/or identification of mutations associated with an inherited disease. In some embodiments, the mutations associated with a congenital or inherited disease can be located in one or more of the genes selected from the group

consisting of ABCA4; ABCC8; ABCD1; ACADVL; ACTA2; ACTC; ACTC1; ACVRL1; ADA; AIPL1; AIRE; ALK1; ALPL; AMT; APC; APP; APTX; AR; ARL6; ARSA; ASL; ASPA; ASS; ASS1; ATL; ATM; ATP2A2; ATP7A; ATP7B; ATXN1; ATXN2; ATXN3; ATXN7; BBS6; BCKDHA; BCKDHB; BEST1; BMPR1A; BRCA1; BRCA2; BRIP1; BTD; BTK; C2orf25; CA4; CALR3; CAPN3; CAV3; CCDC39; CCDC40; CDH23; CEP290; CERKL; CFTR; CHAT; CHD7; CHEK2; CHM; CHRNA1; CHRNB1; CHRND; CHRNE; CLCN1; CNBP; CNGB1; COH1; COL11A1; COL11A2; COL1A1; COL1A2; COL2A1; COL3A1; COL4A5; COL5A1; COL5A2; COL7A1; COL9A1; CRB1; CRX; CTDP1; CTNS; CYP21A2; CYP27A1; DAX1; DBT; DCX; DES; DHCR7; DJ1; DKC1; DLD; DMD; DMPK; DNAAF1; DNAAF2; DNAH11; DNAH5; DNAI1;DNAI2; DNAL1;DNM2; DOK7; DSC2; DSG2; DSP; DYSF; DYT1; EMD; ENG; EYA1; EYS; F8; F9; FANCA; FANCC; FANCF; FANCG;FANCJ; FANDC2; FBN1; FBXO7; FGFR1; FGFR3; FMO3; FMR1; FOXL2; FRG1; FRMD7; FSCN2; FXN; GAA; GALT; GBA; GBE1; GCSH; GDF5; GJB2; GJB3; GJB6; GLA; GLDC; GNE; GNPTAB; GPC3; GPR143; GUCY2D; HBA1; HBA2; HBB; HD; HERG; HEXA; HFE; HHF; HIBCH; HLA-B27; HMBS; HPLH1; HPRP3; HR; HTNB; HTT; IKBKAP; IKBKG; IL2RG; IMPDH1; ITGB4; JAG1; JPH3; KCNE1; KCNE2; KCNH2; KCNQ1; KCNQ4; KIAA0196; KLHL7; KRAS; KRT14; KRT5; L1CAM; LAMB3; LAMP2; LDB3; LMNA; LMX18; LRAT; LRRK2; MAPT; MC1R; MECP2; MED12; MEN1; MERTK; MFN2; MKKS; MLH1; MMAA; MMAB; MMACHC; MMADHC; MPZ; MSH2; MTM1; MTND5; MTTG; MTTI; MTTK; MTTL1; MTTQ; MUT; MYBPC3; MYH11; MYH6; MYH7; MYL2; MYL3; MYLK2; MYO7A; ND5; ND6; NEMO; NF1; NF2; NIPBL; NR0B1; NR2E3; NRAS; NSD1; OCA2; OCRL; OPA1; OTC; PABPN1; PAFAH1B1; PAH; PARK2; PARK7; PARKIN; PAX3; PAX6; PCDH15; PEX1; PEX2; PEX10; PEX13; PEX14; PEX19; PEX26; PEX3; PEX5; PINK1; PKD1; PKD2; PKD3; PKHD1; PKP2; PLEC1; PLOD1; PMM2; PMP22; POLG; PPT1; PRCD; PRKAG2; PRNP; PROM1; PRPF3; PRPF8; PRPH2; PRPN; PSEN1; PSEN2; PTCH1; PTPN11; RAB7A; RAF1; RAI1; RAPSN; RB1; RDH12; RDS; RECQL3; RET; RHO; ROR2; RP1; RP2; RP9; RPE65; RPGR; RPGRIP1; RPL11; RPL35A; RPS10; RPS17; RPS19; RPS24; RPS26; RPS6KA3; RPS7; RPSL5; RS1; RSPH4A; RSPH9; RYR1; RYR2; SALL4; SCA3; SCN5A; SCN9A; SEMA4A; SERPINA1; SERPING1; SGCD; SH3BP2; SHOX; SIX1; SIX5; SLC25A13; SLC25A4; SLC26A4; SMAD4; SMN1; SNCA; SNRNP200; SOD1; SOS1; SOX9;SP110; SPAST; SPATA7; SPG3A; SPG4; SPG7; TAF1; TBX5; TCOF1; TGFBR1; TGFBR2; TNFRSC13C; TNNC1; TNNI3; TNNT1; TNNT2; TNXB; TOPORS; TOR1A; TP53;

TPM1; TRNG; TRNI; TRNK; TRNL1; TRNQ; TSC1; TSC2; TTN; TTPA; TTR; TULP1; TWIST1; TXNDC3; TYR; USH1C; USH1H; USH2A; VCL; VHL; VPS13B; WAS; WRN; WT1; and ZNF9.

[00187] In some embodiments, target-specific primers directed to one or more inherited diseases or congenital disorders can be selected from any one or more of the target-specific primers provided in Table 15. In some embodiments, the target-specific primers from Table 15 can include 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 40, 60, 80, 100, 150, 200, 400, 500, 800, 1000, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000, 10,000, 11,000, 12,000, 13,000 or more target-specific primers. In some embodiments, the amplified target sequences can include any one or more of the amplified target sequences generated at the genomic coordinates (using amplicon ID target-specific primers) provided in Table 16. In some embodiments, at least one of the target-specific primers associated with a congenital disease or disorder is at least 90% identical to at least one nucleic acid sequence selected from SEQ ID NOs: 1-103,143. In some embodiments, at least one of the target-specific primers associated with a congenital disease or disorder is complementary across its entire length to at least one target sequence in a sample. In some embodiments, at least one of the target-specific primers associated with a congenital disease or disorder includes a non-cleavable nucleotide at the 3' end. In some embodiments, the non-cleavable nucleotide at the 3' end includes the terminal 3' nucleotide. In one embodiment, target sequences or resulting amplified target sequences are directed to individual exons having a mutation associated with an inherited disease. In some embodiments, congenital or inherited disease amplified target sequences can include two or more target-specific primers provided in Table 15 (or table 8 of US Application 61/598,881 hereby incorporated by reference in its entirety). In some embodiments, the amplified target sequences can include any one or more of the amplified target sequences generated at the genomic coordinates using the amplicon ID target-specific primers provided in Table 16 (or table 9 of US Application 61/598,881 hereby incorporated by reference in its entirety). In some embodiments, congenital or inherited disease amplified target sequences can include two or more target-specific primers provided in Table 15. In some embodiments, the amplified target sequences can include any one or more of the amplified target sequences generated at the genomic coordinates using the amplicon ID target-specific primers provided in Table 16. In one embodiment, the congenital or inherited disease target-specific primers can include any one or more of the target-specific primers provided in Table 8 of US Application 61/598,881 hereby incorporated by reference in its entirety. In some embodiments, any one or more target-specific primers can be designed using the target-specific primer selection criteria outlined herein. In some embodiments, the disclosure relates generally to the selective amplification of more

than one target sequence in a sample and the detection and/or identification of mutations associated with a congenital or inherited disease. In one embodiment, the disclosure relates generally to the amplification of a plurality of target sequences linked to, or correlated with a congenital or inherited disease.

[00188] In some embodiments, the target-specific primers are prepared to amplify regions or fragments of the human genome associated with a congenital or inherited disease. In some embodiments, the target-specific primers can be prepared to amplify regions of the human genome associated with heredity disorders, such as cystic fibrosis, Alagille syndrome, Alpers syndrome, Alpha-Thalassemia, Amyotrophic Lateral Sclerosis, Anklosing spondylitis, Ataxia-Telangiectasia, congential Myasthenic syndromes, Darier disease, Diamond-Blackfan anemia, early onset familial Alzheimer disease, Ehlers-Danlos syndrome, Epidermolysis Bullosa Simplex, familial Hypertrophic Cardiomyopathy, Fanconi anemia, Glycine Encephalopathy, Hereditary Hemorrhagic Telangiectasia, Huntington Disease, Juvenile Polyposis syndrome, Leber Congential Amaurosis, Long QT syndrome, Maple Syrup Urine Disease, Marfan syndrome, Mitochondrial Encephalomyopathy, Methylmalonic Acidemia, Multiple Endocrine Neoplasia Type 2, Noonan syndrome, Parkinson disease, Peroxisome Biogenesis, Primary Cilary Dyskineasia, Retinitis Pigmentosa, Stickler syndrome, Thoracic Aortic Aneurysms and Aortic Dissections, Tuberous Sclerosis Complex, Usher syndrome, Werner syndromw, Wilson disease and Zellweger syndrome. In some embodiments, the target-specific primers can be prepared from any one or more of the genes provided in Table 4.

[00189] In some embodiments, the disclosure relates generally to detecting the presence of a target sequence or amplified target sequence associated with one or more newborn disorders. In some embodiments, the disclosure relates generally to detecting the presence of an amplified target sequence obtained by amplifying a sample containing at least one target sequence associated with a newborn disorder with one or more target-specific primers disclosed herein. In some embodiments, the disclosure relates generally to detecting the presence of an amplified target sequence obtained by amplifying a sample containing at least one target sequence associated with a newborn disorder and a target-specific primer designed according to the primer criteria provided herein.

[00190] In some embodiments, the one or more newborn disorders can include 2-methyl-3-hydroxybutyric aciduria (2M3HBA); 2-methylbutyryl-CoA dehydrogenase (2MBG); 3-methylglutaconic aciduria (3MGA); argininemia (ARG); defects of biopterin cofactor biosynthesis (BIOPT-BS); defects of biopterin cofactor regeneration (BIOPT-REG); carnitine acylcarnitine translocase (CACT); methylmalonic acidemia (CBL-C,D); citrullinemia type II (CIT-II); carnitine

palmitoyltransferase I (CPT-Ia); carnitine palmitoyltransferase II (CPT-II); Dienoyl-CoA reductase (De-Red); Glutaric acidemia type II (GA-II); galactose epimerase (GALE); galactokinase (GALK); benign hyperphenylalaninemia (H-PHE); isobutyryl-CoA dehydrogenase (IBG); medium/short chain L-3-hydroxy acyl-CoA dehydrogenase (M/SCHAD); malonic acidemia (MAL); medium chain ketoacyl-CoA thiolase (MCKAT); hypermethioninemia (MET); short chain acyl-CoA dehydrogenase (SCAD); Tyrosinemia type II (TYR-II); tyrosinemia type III (TYR-III); Biotinidase (BIO); Cystic fibrosis (CF); Transferase deficient galactosemia (GALT); Sickle - C disease (HB S/C); Congenital adrenal hyperplasia (CAH); Congenital hypothyroidism (CH); Sickle cell anemia (HB S/S); S-βeta thalassemia(HB S/A); (SCID) Severe Combined Immunodeficiency; 5-oxoprolinuria (pyroglutamic aciduria)(5-OXO); Glucose 6 phosphate dehydrogenase (G6PD); Nonketotic hyperglycinemia (NKH); Carbamoylphosphate synthetase (CPS); Hyperammonemia/ornithinemia/citrullinemia (Ornithine transporter defect) (HHH); Prolinemia (PRO); Ethylmalonic encephalopathy (EMA); Human immunodeficiency virus (HIV); Toxoplasmosis (TOXO); 3-Methylcrotonyl-CoA carboxylase (3-MCC); Carnitine uptake defect (CUD); Long-chain L-3-hydroxyacyl-CoA dehydrogenase (LCHAD); Phenylketonuria/ Hyperphenylalaninemia (PKU); Argininosuccinate aciduria (ASA); Glutaric acidemia type 1 (GA-1); Medium-chain acyl-CoA dehydrogenase (MCAD); Propionic acidemia (Propionyl-CoA carboxylase)(PROP); Beta ketothiolase (mitochondrial acetoacetyl-CoA thiolase; short-chain ketoacyl thiolase; T2)(BKT); Homocystinuria (cystathionine beta synthase)(HCY); Multiple carboxylase (Holocarboxylase synthetase)(MCD); Trifunctional protein deficiency (TFP); Methylmalonic academia (Vitamin B12 Disorders) (CBL A,B); 3-Hydroxy 3-methylglutaric aciduria (3-Hydroxy 3-methylglutaryl-CoA lyase)(HMG); Maple syrup urine disease (branched-chain ketoacid dehydrogenase)(MSUD); Tyrosinemia Type 1 (TYR-1); Citrullinemia type I (Argininosuccinate synthetase)(CIT I); Isovaleric acidemia (Isovaleryl-CoA dehydrogenase)(IVA); Methylmalonic Acidemia (methylmalonyl-CoA mutase)(MUT); and very long-chain acyl-CoA dehydrogenase (VLCAD).

[00191] In some embodiments, the disclosure relates generally to target-specific primers for the detection of newborn screening disorders. In some embodiments, target-specific primers for newborn disorders including the disorders provided above can be prepared using the primer criteria disclosed herein. In some embodiments, the disclosure relates generally to detecting a newborn disorder by contacting a sample that may contain one or more target sequences for one or more newborn disorders and amplifying the one or more target sequences in the sample, thereby obtaining at least one amplified target sequence associated with at least one newborn disorder. In some

embodiments, a plurality of target-specific primers can be designed to amplify a plurality of target sequences from a sample, thereby providing a means to detect a plurality of newborn disorders optionally, in a single method or procedure. In some embodiments, target-specific primers designed to amplify a plurality of amplified target sequences associated with one or more newborn disorders can be pooled and provided as a newborn screening panel.

[00192] In some embodiments, target sequences or amplified target sequences are directed to nucleic acids obtained from a forensic sample. In one embodiment, forensic samples can include nucleic acids obtained from a crime scene, nucleic acids obtained from a missing persons DNA database, nucleic acids obtained from a laboratory associated with a forensic investigation or include forensic samples obtained by law enforcement agencies, one or more military services or any such personnel. In some embodiments, target sequences can be present in one or more bodily fluids including but not limited to, blood, sputum, plasma, semen, urine and serum. In some embodiments, target sequences can be obtained from hair, skin, tissue samples, autopsy or remains of a victim. In some embodiments, nucleic acids including one or more target sequences can be obtained from a deceased animal or human. In some embodiments, target sequences can include nucleic acids obtained from non-human DNA such a microbial, plant or entomological DNA. In some embodiments, target sequences or amplified target sequences are directed to purposes of human identification. In some embodiments, the disclosure relates generally to methods for identifying a nucleic acid sample from an animal, including a human. In some embodiments, the disclosure relates generally to methods for identifying characteristics of a forensic sample. In some embodiments, the disclosure relates generally to human identification methods using one or more target-specific primers disclosed herein or one or more target-specific primers prepared using the primer criteria outlined herein.

[00193] In one embodiment, a forensic or human identification sample containing at least one target sequence can be amplified using any one or more of the target-specific primers discloser herein or using the primer criteria outlined herein. In some embodiments, a forensic or human identification sample containing one or more target sequences can be identified by amplifying the at least one or more target sequences with any one or more target-specific primers provided in Tables 13 and 14. Table 13 provides a plurality of target-specific primers, provided as primer pairs, directed to single nucleotide polymorphisms (SNPs) associated with human identification. Table 14 provides a plurality of target-specific primers, provided as primer pairs, directed to short tandem repeats (STRs) associated with human identification. An individual inherits one copy of an STR from each parent,

which may or may not have similar repeat sizes. The number of repeats in STR markers can be highly variable among individuals, which makes STRs effective for human identification purposes. In some embodiments, targets-specific primers such as those provided in Table 14, or target-specific primers prepared as disclosed herein, that are directed to the gene amelogenin (AMG) can be used to determine the sex of the individual providing the sample. For example, primers to the amelogenin gene can be prepared using the criteria disclosed herein that are specific, for example, to intron 1. Once a sample is amplified using such target-specific primers, the amplification product from a male sample versus a female sample will generally result in amplification products (amplified target sequences) that differ by in length by several nucleotides and therefore provides a simple method by which to determine the sex of the individual providing the sample.

[00194] In one embodiment, a sample containing one or more target sequences can be amplified using any one or more of the target-specific primers disclosed herein. In another embodiment, amplified target sequences obtained using the methods (and associated compositions, systems, apparatuses and kits) disclosed herein, can be coupled to a downstream process, such as but not limited to, nucleic acid sequencing. For example, once the nucleic acid sequence of an amplified target sequence is known, the nucleic acid sequence can be compared to one or more reference samples such as Hg19 genome. The Hg19 genome is commonly used in the genomics field as a reference genome sample for humans. In some embodiments, a sample suspected of containing one or more SNPs and/or STRs can be identified by amplifying the sample suspected of containing the SNP or STR with any one or more of the target-specific primers provided in Tables 13 and 14. Consequently, the output from the amplification procedure can be optionally analyzed for example by nucleic acid sequencing to determine if the expected amplification product based on the target-specific primers is present in the amplification output. The identification of an appropriate SNP or STR amplification product can in some instances provide additional information regarding the source of the sample or it characteristics (e.g., a male or female sample or a sample of particular ancestral origin).

[00195] It is envisaged that one of ordinary skill in the art can readily prepare one or more target-specific primers using the primer criteria disclosed herein without undue experimentation. It is also envisaged that one of ordinary skill in the art can readily prepare one or more target-specific primers using the criteria disclosed herein, to identify at least one medically relevant polymorphism. In some instances, a medically relevant polymorphism can be used in forensic or human identification purposes. Generally, a medically relevant polymorphism includes a polymorphism that

is associated with at least one disease state in multiple populations (e.g., a European Caucasian population). In some embodiments, a medically relevant polymorphism includes any one or more of the polymorphisms outlined below.

Polymorphism	Caucasian MAF	Chromosome	Gene	Disease Associated with Polymorphism
rs1137101	0.449	1p31	LEPR	Obesity, Insulin Resistance, Non-Hodgkin's lymphoma
rs486907	0.408	1q25	RNASEL	Prostate cancer
rs1042031	0.208	2p24	APOB	Cardiovascular disease, Dislipidemia
rs231775	0.379	2q33	CTLA4	Multiple Sclerosis, Autoimmune Disease
rs5186	0.348	3q21	AGTR1	Metabolic syndrome, Aortic aneurism, Left-ventricular hypertrophy
rs6280	0.35	3q13.3	DRD3	Schizophrenia
rs1693482	0.477	4q21	ADH1C	Alcohol dependence, Coronary heart disease
rs1799883	0.373	4q28	FABP2	Metabolic syndrome, Type 2 diabetes
rs4444903	0.392	4q25	EGF	Cancer
rs4961	0.208	4p16.3	ADD1	Hypertension, Coronary artery disease
rs1042714	0.467	5q31	ADRB2	Obesity, COPD
rs351855	0.283	5q35.1	FGFR4	Cancer
rs5370	0.242	6p24	EDN1	Asthma, sleep apnea
rs6296	0.322	6q13	HTR1B	Substance abuse
rs2227983	0.25	7p12.3	EGFR	Cancer
rs213950	0.492	7q31.2	CFTR	Cystic fibrosis
rs7493	0.237	7q21.3	PON2	Myocardial infarction
rs328	0.273	8p22	LPL	Left ventricular hypertrophy
rs2383206	0.475	9p21		Coronary artery disease
rs1800861	0.25	10q11.2	RET	Hirschsprung disease, Thyroid cancer
rs1801253	0.283	10q24	ADRB1	Insulin Resistance
rs2227564	0.341	10q24	PLAU	Alzheimer's disease, Asthma
rs1799750	0.433	11q22.3	MMP1	Endometriosis, Osteolysis, Rheumatoid arthritis
rs1063856	0.342	12p13.3	VWF	Hypertension
rs6313	0.438	13q14	HTR2A	Psychiatric disorders
rs2236225	0.396	14q24	MTHFD1	Neural tube defects
rs1800588	0.333	15q21	LIPC	Coronary artery disease
rs243865	0.198	16q13	MMP2	Cancer
rs4673	0.342	16q24	CYBA	Coronary artery disease
rs708272	0.478	16q21	CETP	Coronary artery disease
rs1800012	0.188	17q21.3	COL1A1	Osteoporosis
rs4291	0.354	17q23	ACE	Depression, Alzheimer's disease
rs4792311	0.331	17p11	ELAC2	Prostate cancer
rs16430	0.37	18p11.3	ENOSF1/TYMS	Cancer
rs601338	0.391	19q13.3	FUT2	Infection susceptibility

rs688	0.45	19p13.2	LDLR	Alzheimer's disease, Coronary artery disease
rs7121	0.458	20q13.3	GNAS	Obesity, Cancer
rs234706	0.333	21q22	CBS	Oral cleft defects
rs4680	0.483	22q11.21	COMT	Schizophrenia, ADHD
AMG	0.5	Xp22.3	AMG	Sex Marker

[00196] In some embodiments, a medically relevant polymorphism can be present within a single exon of the corresponding disease associated gene. In some embodiments, the disclosure relates generally to the selective amplification of at least one target sequence in a sample and the detection and/or identification of a medically relevant polymorphism. In some embodiments, the disclosure relates generally to the selective amplification of at least one target sequence in a sample and the detection and/or identification of a SNP or STR. In some embodiments, amplified target sequences can be generated by amplifying a sample with one or more target-specific primers of Tables 13 or 14. In some embodiments, the amplified target sequences can include any one or more of the amplified target sequences generated at the genomic coordinates provided in the polymorphism table above. In one embodiment, an amplified target sequence can be prepared using one or more of the target-specific primers from Tables 13 or 14. In some embodiments, any one or more target-specific primers corresponding to SEQ ID NOs: 50354-50451 can be used to selectively amplify at least one target sequence present in a sample. In some embodiments, at least one target-specific primer selected from SEQ ID NOs: 50354-50451 can be used to amplify a target sequence from a sample for the purposes of forensic or human identification.

[00197] In some embodiments, target-specific primers directed to human identification can be selected from any one or more of the target-specific primers provided in Tables 13 or 14. In some embodiments, the target-specific primers from Tables 13 or 14 can include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 22, 25, 27, 30, 35, 38, 40, 42, 45 or more target-specific primers. In some embodiments, at least one of the target-specific primers associated with human identification is at least 90% identical to at least one of the target-specific primers provided in Tables 13 or 14. In some embodiments, at least one of the target-specific primers associated with human identification is complementary across its entire length to at least one target sequence in a sample. In some embodiments, at least one of the target-specific primers associated with human identification includes a non-cleavable nucleotide at the 3' end. In some embodiments, the non-cleavable nucleotide at the 3' end includes the terminal 3' nucleotide.

[00198] In some embodiments, the disclosure relates generally to methods (and associated compositions, systems, apparatuses and kits) for reducing the formation of amplification artifacts in a multiplex PCR. In some embodiments, primer-dimers or non-specific amplification products are obtained in lower number or yield as compared to standard multiplex PCR of the prior art. In some embodiments, the reduction in amplification artifacts is in part, governed by the use of target-specific primer pairs in the multiplex PCR reaction. In one embodiment, the number of target-specific primer pairs in the multiplex PCR reaction can be greater than 1000, 3000, 5000, 10000, 12000, or more. In some embodiments, the disclosure relates generally to methods (and associated compositions, systems, apparatuses and kits) for performing multiplex PCR using target-specific primers that contain a cleavable group. In one embodiment, target-specific primers containing a cleavable group can include one or more cleavable moieties per primer of each primer pair. In some embodiments, a target-specific primer containing a cleavable group includes an nucleotide neither normally present in a non-diseased sample nor native to the population of nucleic acids undergoing multiplex PCR. For example, a target-specific primer can include one or more non-native nucleic acid molecules such as, but not limited to thymine dimers, 8-oxo-2'-deoxyguanosine, inosine, deoxyuridine, bromodeoxyuridine, apurinic nucleotides, and the like.

[00199] In some embodiments, the disclosed methods (and associated compositions, systems, etc.,) involve performing a primary amplification of target sequecnes from a population of nucleic acids, optionally using target-specific primers. In some embodiments, the disclosed methods involve amplifying target sequences using target-specific forward and reverse primer pairs. The target-specific forward and reverse primer pairs can optionally include one or more intron-specific and/or exon specific forward and reverse primer pairs. In some embodiments, each primer pair is directed to a single or discrete exon. In some embodiments, the disclosed methods involve amplifying target sequences using exon-specific forward and reverse primer pairs containing at least one cleavable group. In some embodiments, the target-specific forward and reverse primer pairs contain a uracil nucleotide as the one or more cleavable groups. In one embodiment, a target-specific primer pair can include a uracil nucleotide in each of the forward and reverse primers of each primer pair. In one embodiment, a target-specific forward or reverse primer contains one, two, three or more uracil nucleotides. In some embodiments, the disclosed methods involve amplifying at least 10, 50, 100, 200, 500, 1000, 2000, 3000, 5000, 6000, 8000, 10000, 12000 or more, target sequences from a population of nucleic acids having a plurality of target sequences using target-specific forward and reverse primer pairs containing at least two uracil nucleotides.

[00200] In some embodiments, target-specific primers (including but not limited to intron-specific and exon-specific primers, which can be forward and/or reverse primers) can be designed *de novo* using algorithms that generate oligonucleotide sequences according to specified design criteria. For example, the primers may be selected according to any one or more of criteria specified herein. In some embodiments, one or more of the target-specific primers are selected or designed to satisfy any one or more of the following criteria: (1) inclusion of two or more modified nucleotides within the primer sequence, at least one of which is included near or at the termini of the primer and at least one of which is included at, or about the center nucleotide position of the primer sequence; (2) primer length of about 15 to about 40 bases in length; (3) T_m of from about 60°C to about 70°C; (4) low cross-reactivity with non-target sequences present in the target genome or sample of interest; (5) for each primer in a given reaction, the sequence of at least the first four nucleotides (going from 3' to 5' direction) are not complementary to any sequence within any other primer present in the same reaction; and (6) no amplicon includes any consecutive stretch of at least 5 nucleotides that is complementary to any sequence within any other amplicon.

[00201] In some embodiments, the target-specific primers include one or more primer pairs designed to amplify target sequences from the sample that are about 100 base pairs to about 500 base pairs in length. In some embodiments, the target-specific primers include a plurality of primer pairs designed to amplify target sequences, where the amplified target sequences are predicted to vary in length from each other by no more than 50%, typically no more than 25%, even more typically by no more than 10%, or 5%. For example, if one target-specific primer pair is selected or predicted to amplify a product that is 100 nucleotides in length, then other primer pairs are selected or predicted to amplify products that are between 50-150 nucleotides in length, typically between 75-125 nucleotides in length, even more typically between 90-110 nucleotides, or 95-105 nucleotides, or 99-101 nucleotides in length.

[00202] In some embodiments, at least one primer pair in the amplification reaction is not designed *de novo* according to any predetermined selection criteria. For example, at least one primer pair can be an oligonucleotide sequence selected or generated at random, or previously selected or generated for other applications. In one exemplary embodiment, the amplification reaction can include at least one primer pair selected from the TaqMan® probe reagents (Roche Molecular Systems). The TaqMan® reagents include labeled probes and can be useful, *inter alia*, for measuring the amount of target sequence present in the sample, optionally in real time. Some examples of

TaqMan technology are disclosed in U.S. Pat. Nos. 5,210,015, 5,487,972, 5,804,375, 6,214,979, 7,141,377 and 7,445,900, hereby incorporated by reference in their entireties.

[00203] In some embodiments, at least one primer within the amplification reaction can be labeled, for example with an optically detectable label, to facilitate a particular application of interest. For example, labeling may facilitate quantification of target template and/or amplification product, isolation of the target template and/or amplification, product, and the like.

[00204] In some embodiments, one or more of the primers within the amplification reaction can be useful in genotyping of a nucleic acid sample.

[00205] In some embodiments, the target-specific primers can be provided as a set of target-specific primer pairs in a single amplification vessel. In some embodiments, the target-specific primers can be provided in one or more aliquots of target-specific primer pairs that can be pooled prior to performing the multiplex PCR reaction in a single amplification vessel or reaction chamber. In one embodiment, the target-specific primers can be provided as a pool of target-specific forward primers and a separate pool of target-specific reverse primers. In another embodiment, target-specific primer pairs can be pooled into subsets such as non-overlapping target-specific primer pairs. In some embodiments, the pool of target-specific primer pairs can be provided in a single reaction chamber or microwell, for example on a PCR plate to perform multiplex PCR using a thermocycler. In some embodiments, the target-specific forward and reverse primer pairs can be substantially complementary to the target sequences.

[00206] In some embodiments, the method of performing multiplex PCR amplification includes contacting a plurality of target-specific primer pairs having a forward and reverse primer, with a population of target sequecnes to form a plurality of template/primer duplexes; adding a DNA polymerase and a mixture of dNTPs to the plurality of template/primer duplexes for sufficient time and at sufficient temperature to extend either (or both) the forward or reverse primer in each target-specific primer pair via template-dependent synthesis thereby generating a plurality of extended primer product/template duplexes; denaturing the extended primer product/template duplexes; annealing to the extended primer product the complementary primer from the target-specific primer pair; and extending the annealed primer in the presence of a DNA polymerase and dNTPs to form a plurality of target-specific double-stranded nucleic acid molecules. In some embodiments, the steps of the amplification PCR method can be performed in any order. In some instances, the methods disclosed herein can be further optimized to remove one or more steps and still obtain sufficient amplified target sequences to be used in a variety of downstream processes. For example, the

number of purification or clean-up steps can be modified to include more or less steps than disclose herein, providing the amplified target sequences are generated in sufficient yield.

[00207] In some embodiments, the target-specific primer pairs do not contain a common extension (tail) at the 3' or 5' end of the primer. In another embodiment, the target-specific primers do not contain a Tag or universal sequence. In some embodiments, the target-specific primer pairs are designed to eliminate or reduce interactions that promote the formation of non-specific amplification.

[00208] In one embodiment, the target-specific primer pairs comprise at least one cleavable group per forward and reverse target-specific primer. In one embodiment, the cleavable group can be a uracil nucleotide. In one embodiment, the target-specific primer pairs are partially or substantially removed after generation of the amplified target sequence. In one embodiment, the removal can include enzymatic, heat or alkali treatment of the target-specific primer pairs as part of the amplified target sequence. In some embodiments, the amplified target sequences are further treated to form blunt-ended amplification products, referred to herein as, blunt-ended amplified target sequences.

[00209] In some embodiments, any one or more of the target-specific primers disclosed in the methods, compositions, kits, systems and apparatuses may be designed using the following primer selection criteria.

[00210] There is a need for new methods, computer readable media, and systems for identifying or designing products or kits that use PCR to enrich one or more genomic regions of interest (which may be, for example, cumulative regions of 1 kb to 1 Mb) for subsequent sequencing.

[00211] There is a need for new methods, computer readable media, and systems for identifying or designing products or kits including primers or assays that maximize coverage of one or more genomic regions or targets of interest while minimizing one or more of off-target hybridization, a number of primers, and a number of primer pools.

[00212] In accordance with the teachings and principles embodied in this application, new methods, computer readable media, and systems are provided that identify or design products or kits that use PCR to enrich one or more genomic regions or targets of interest for subsequent sequencing and/or that include primers or assays that maximize coverage of one or more genomic regions or targets of interest while minimizing one or more of off-target hybridization, a number of primers, and a number of primer pools.

[00213] FIG. 17 illustrates a system for designing primers or assays according to an exemplary embodiment. The system includes a data receiving module 1701, a primer providing

module 1702, a scoring (in silico PCR) module 1703, a scoring (SNP overlap) module 1704, a filtering module 1705, a pooling module 1706, and a reporting module 1707. The system also includes a database 1708, which may include data regarding genetic annotations, SNP-related data, or other genetic data such as identification of a repeat, chromosome, position, direction, etc., for example, or any other type of information that could be related to a genomic region or target of interest, and a database 1709, which may include primer-related data such as a melting temperature (Tm), a chromosome, a position, a direction, and SNP overlap information, etc., for example, or any other type of information that could be related to primers. The system may be implemented in or using one or more computers and/or servers using one or more software components, which may not be accessible or released to customers who may be ordering custom primers or assays that may be designed using such a system. Customers may order custom primers or assays at least in part through a web-accessible data portal by providing one or more genomic regions or targets of interest in any suitable format. In an exemplary embodiment, there is provided a method performing steps including the general steps associated with modules 1701-1707 and databases 1708 and 1709 (e.g., receiving data, providing primers, scoring primers and/or amplicons, filtering primers and/or amplicons, pooling primers and/or amplicons, reporting results, and querying databases).

[00214] FIG. 18 illustrates a system for designing primers or assays according to an exemplary embodiment. The system includes a target generator module, which may generate one or more coordinate-based genomic regions or targets of interest and which may query and/or receive information from an annotation database (which may include data regarding genetic annotations, SNP-related data, or other genetic data such as identification of a repeat, chromosome, position, direction, etc., for example, as well as information regarding primers or any other type of information that could be related to a genomic region or target of interest); a designing module, which may design one or more primers or assays and determine and/or apply various scoring and filtering procedures for the primers or assays and which may perform various quality control procedures; a loader module, which may load the primers or assays and/or related information (such as quality control results, for example) to a primer database (which may be in communication with or comprised within the annotation database and which may include primer-related data such as a melting temperature (Tm), a chromosome, a position, a direction, and SNP overlap information, etc., for example, or any other type of information that could be related to primers); a SNP overlap/repeat overlap module; a driver module; a tiler module, which may determine a subset of amplicons or tiles maximizing a coverage of a genomic region or target of interest; a pooler module, which may

determine a pooling of the amplicons or tiles into one or more pools of amplicons; and a report generator module. The system may be implemented in or using one or more computers and/or servers using one or more software components, which may not be accessible or released to customers who may be ordering custom primers or assays that may be designed using such a system. Customers may order custom primers or assays at least in part through a web-accessible data portal by providing one or more genomic regions or targets of interest in any suitable format. In an exemplary embodiment, there is provided a method performing steps including the general steps associated with these modules and databases.

[00215] FIG. 19 illustrates an amplicon sequence including an insert sequence surrounded by a pair of primers designed according to an exemplary embodiment. The amplicon may include a forward primer and a reverse primer surrounding the insert sequence. The two primers may together form an assay, which may be customized and ordered. The primer component of an amplicon may be a copy of a spiked-in primer, rather than the underlying sample, and one or more inserts may be selected to cover the target.

[00216] FIG. 20 illustrates PCR amplification of an amplicon sequence (which may be referred to as "tile" herein) including an insert surrounded by a pair of primers designed according to an exemplary embodiment. Shown are denaturation, annealing, and elongation steps ultimately leading to exponential growth of the amplicon.

[00217] FIG. 21 illustrates a set of candidate amplicons for a given target region, each including an insert surrounded by a pair of primers, for tiling and pooling according to an exemplary embodiment. The dotted lines indicate the boundaries of a target region (on chromosome 19 in this example). There are 112 candidate amplicons for covering the target region in this example, but the number of candidate amplicons could of course be different, including much lower or much higher, and may be selected by taking into account computational resources, the length of the target region, and any other relevant factor.

[00218] According to various exemplary embodiments, there are provided methods for designing primers using a design pipeline that allows design of oligonucleotide primers across genomic areas of interest while incorporating various design criteria and considerations including amplicon size, primer composition, potential off-target hybridization, and SNP overlap of the primers. In an embodiment, the design pipeline includes several functional modules that may be sequentially executed as discussed next.

[00219] First, in an embodiment, a sequence retrieval module may be configured to retrieve sequences based on instructions of an operator regarding a final product desired by a customer. The operator may request a design of primer pairs for genomic regions which may be specified by chromosome and genome coordinates or by a gene symbol designator. In the latter case, the sequence retrieval module may retrieve the sequence based on the exon coordinates. The operator may also specify whether to include a 5' UTR sequence (untranslated sequence).

[00220] Second, in an embodiment, an assay design module may be configured to design primer pairs using a design engine, which may be a public tool such as Primer3 or another primer design software that can generate primer pairs across the entire sequence regions retrieved by the sequence retrieval module, for example. The primers pairs may be selected to tile densely across the nucleotide sequence. The primer design may be based on various parameters, including: (1) the melting temperature of the primer (which may be calculated using the nearest neighbor algorithm set forth in John SantaLucia, Jr., "A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics," Proc. Natl. Acad. Sci. USA, vol. 95, 1460-1465 (1998), the contents of which is incorporated by reference herein in its entirety), (2) the primer composition (e.g., nucleotide composition such as GC content may be determined and filtered and penalized by the software, as may be primer hairpin formation, composition of the GC content in the 3' end of primer, and specific parameters that may be evaluated are stretches of homopolymeric nucleotides, hairpin formation, GC content, and amplicon size), (3) scores of forward primer, reverse primer and amplicon (the scores may be added up to obtain a probe set score, and the score may reflect how close the amplicon confirms with the intended parameters), and (4) conversion of some of the T's to U's (T's may be placed such that the predicted Tm of the T delimited fragments of a primer have a minimum average Tm.)

[00221] Third, in an embodiment, a primer mapping module may be configured to use a mapping software (e.g., e-PCR (NCBI), see Rotmistrovsky et al., "A web server for performing electronic PCR," Nucleic Acids Research, vol. 32, W108-W112 (2004), and Schuler, "Sequence Mapping by Electronic PCR," Genome Research, vol. 7, 541-550 (1997), which are both incorporated by reference herein in their entirety, or other similar software) to map primers to a genome. The primers mapping may be scored using a mismatch matrix. In an embodiment, a perfect match may receive a score of 0, and mismatched primers may receive a score of greater than 0. The mismatch matrix takes the position of the mismatch and the nature of the mismatch into account. For example, the mismatch matrix may assign a mismatch score to every combination of a particular

motif (e.g., AA, AC, AG, CA, CC, CT, GA, GG, GT, TC, TG, TT, A-, C-, G-, T-, -A, -C, -G, and –T, where '-' denotes an ambiguous base or gap) with a particular position (e.g., base at 3' end, second base from 3' end, third base from 3' end, third base from 5' end, second base from 5' end, base at 5' end, and positions therebetween), which may be derived empirically and may be selected to reflect that mismatches closer to the 3'end tend to weaker PCR reactions more than mismatches closer to the 5' end and may therefore be generally larger. The mismatch scores for motifs with an ambiguous base or gap may be assigned an average of scores of other motifs consistent therewith (e.g., A- may be assigned an average of the scores of AA, AC, and AG). Based on the number of hits with a certain score threshold, an amplicon cost may be calculated.

[00222] Fourth, in an embodiment, a SNP module may be configured to determine underlying SNPs and repeat regions: SNPs may be mapped to the primers and based on the distance of a SNP from the 3' end, primers may be filtered as potential candidates. Similarly, if a primer overlaps to a certain percentage with a repeat region, the primer might be filtered.

[00223] Fifth, in an embodiment, a tiler module may be configured to use a function based on the amplicon cost (see primer mapping) and the number of primers necessary to select a set of primers covering the target while ensuring that selection of tiling primers for a target is independent of other targets that may be in a customer's request so that the same set of primers for a target will be selected whether the customer requested only that target or additional targets and whether amplicons are to help cover on that target or additional targets.

[00224] Sixth, in an embodiment, a pooler module may be configured to use a pooling algorithm that prevents amplicon overlaps, and ensures that the average number of primers in a pool does not deviate by more than a preset value.

[00225] FIG. 22 illustrates a method according to an exemplary embodiment. In step 2201, a module or other hardware and/or software component receives one or more genomic regions or sequences of interest. In step 2202, a module or other hardware and/or software component determines one or more target sequences for the received one or more genomic regions or sequences of interest. In step 2203, a module or other hardware and/or software component provides one or more primer pairs for each of the determined one or more target sequences. In step 2204, a module or other hardware and/or software component scores the one or more primer pairs, wherein the scoring comprises a penalty based on the performance of in silico PCR for the one or more primer pairs, and wherein the scoring further comprises an analysis of SNP overlap for the one or more primer pairs. In step 2205, a module or other hardware and/or software component filters the one or

more primer pairs based on a plurality of factors, including at least the penalty and the analysis of SNP overlap, to identify a filtered set of primer pairs corresponding to one or more candidate amplicon sequences for the one or more genomic regions or sequences of interest.

[00226] According to an exemplary embodiment, there is provided a method, comprising: (1) receiving one or more genomic regions or sequences of interest; (2) determining one or more target sequences for the received one or more genomic regions or sequences of interest; (3) providing one or more primer pairs for each of the determined one or more target sequences; (4) scoring the one or more primer pairs, wherein the scoring comprises a penalty based on the performance of in silico PCR for the one or more primer pairs, and wherein the scoring further comprises an analysis of SNP overlap for the one or more primer pairs; and (5) filtering the one or more primer pairs based on a plurality of factors, including at least the penalty and the analysis of SNP overlap, to identify a filtered set of primer pairs corresponding to one or more candidate amplicon sequences for the one or more genomic regions or sequences of interest.

[00227] In various embodiments, receiving one or more genomic regions or sequences of interest may comprise receiving a list of one or more gene symbols or identifiers. Receiving one or more genomic regions or sequences of interest may comprise receiving a list of one or more genomic coordinates or other genomic location identifiers. Receiving one or more genomic regions or sequences of interest may comprise receiving a list of one or more BED coordinates.

[00228] In various embodiments, determining one or more target sequences may comprise determining one or more exons or coding regions that correspond to each of the one or more genomic regions or sequences of interest. Determining one or more target sequences may comprise querying an amplicon or other genomic sequence database for a presence therein of the one or more genomic regions or sequences of interest and information related thereto.

[00229] In various embodiments, providing one or more primer pairs may comprise designing one or more primer pairs. Providing one or more primer pairs may comprise querying an amplicon or other genomic sequence database for a presence therein of the one or more genomic regions or sequences of interest or of the one or more primer pairs and information related thereto.

[00230] In various embodiments, the performance of in silico PCR may comprise performing in silico PCR against a reference or previously sequenced genome of any species. The performance of in silico PCR may comprise performing in silico PCR against an hg19 reference genome. The performance of in silico PCR against a reference genome may comprise determining a number of off-target hybridizations for each of the one or more primer pairs. The performance of in silico PCR

against a reference genome may comprise determining a worst case attribute or score for each of the one or more primer pairs. The performance of in silico PCR may comprise determining one or more genomic coordinates for each of the one or more primer pairs. The performance of in silico PCR may comprise determining one or more predicted amplicon sequences for each of the one or more primer pairs. The performance of in silico PCR may comprise querying an amplicon or other genomic sequence database for a presence therein of the one or more genomic regions or sequences of interest or of in silico PCR results for the one or more primer pairs and information related thereto.

[00231] In various embodiments, the analysis of SNP overlap may comprise determining a SNP class for each of the one or more primer pairs. The analysis of SNP overlap may comprise querying an amplicon or other genomic sequence database for a presence therein of the one or more genomic regions or sequences of interest or of SNP overlap results for the one or more primer pairs and information related thereto.

[00232] In various embodiments, the plurality of factors may include one or more of an indication of forward SNP overlap, an indication of a reverse SNP overlap, an indication of a frequency of forward repeats, an indication of a frequency of reverse repeats, an indication of an off-target hybridization of each of the one or more primer pairs, and a composition of each of the one or more primer pairs. The plurality of factors may include one or more of a forward triplet factor, a reverse triplet factor, a forward A run factor, a reverse A run factor, a forward C run factor, a reverse C run factor, a forward G run factor, a reverse G run factor, a forward T run factor, and a reverse T run factor. The plurality of factors may include one or more of an indication of an extent to which each of the one or more primer pairs includes one or more homopolymers. The plurality of factors may include an indication of an extent to which each of the one or more primer pairs includes one or more repeating sequences. The plurality of factors may include a length of the one or more primer pairs, wherein a score for the one or more primer pairs decreases as the length gets shorter than a minimal length threshold and decreases as the length gets longer than a maximal length threshold. The plurality of factors may include a maximal number of a given base in the one or more primer pairs, wherein a score for the one or more primer pairs decreases as the number of instances of the given base exceeds a maximal base inclusion threshold. The plurality of factors may include a maximal number of contiguous instances of a given base, wherein a score for the one or more primer pairs decreases as the number of contiguous instances of the given base exceeds a maximal contiguous base inclusion threshold.

[00233] The plurality of factors may include a maximal percentage of a set of two given bases, wherein a score for the one or more primer pairs decreases as the percentage of the two given bases increases. The plurality of factors may include a maximal percentage of G and C bases, wherein a score for the one or more primer pairs decreases as the percentage of G and C bases increases. The plurality of factors may include a deviation of a predicted melting temperature for the one or more primer pairs relative to minimal and maximal melting temperature thresholds. The plurality of factors may include a number of primer-dimer inclusions for the one or more primer pairs. The plurality of factors may include a level of local complementarity for the one or more primer pairs. The plurality of factors may include an indication of a complexity level of each of the one or more primer pairs. The plurality of factors may include an indication of SNP overlap of each of the one or more primer

[00234] In various embodiments, the method may comprise selecting a subset of the one or more candidate amplicon sequences that substantially covers the one or more genomic regions or sequences of interest while minimizing a cost function associated with the candidate amplicon sequences. Minimizing the cost function may include generating an overlap graph comprising a source vertex, one or more amplicon vertices, and a sink vertex.

[00235] In various embodiments, the method may comprise assembling the primer pairs in the filtered set of primer pairs that correspond with the selected subset of the one or more candidate amplicon sequences into a plurality of separate pools of primer pairs. Assembling the primer pairs may include limiting an inclusion of one or more primer pairs in the filtered set of primer pairs that correspond with the selected subset of the one or more candidate amplicon sequences into a given pool based at least on a minimal threshold distance between amplicon sequences in the given pool. The minimal threshold distance may be between about 5 base pairs and about 100 base pairs, or between about 15 base pairs and about 90 base pairs, or between about 25 base pairs and about 75 base pairs, or between about 40 base pairs and about 60 base pairs, for example. In some embodiments, the minimum threshold distance between amplicons may include any integer, including a negative one. For example, a value of 0 can mean that any two amplicons are allowed to "touch," and a value of -8 can mean that any two amplicons can overlap by up to 8 bases.

[00236] In various embodiments, assembling the filtered set of primer pairs into a plurality of separate pools of primer pairs may comprise splitting the primer pairs between tubes so as to prevent amplicon overlap within any given tube. Assembling the primer pairs may include limiting an inclusion of one or more primer pairs in the filtered set of primer pairs that correspond with the

selected subset of the one or more candidate amplicon sequences into a given pool based at least on a pre-determined amplicon capacity of the given pool. Assembling the primer pairs may include limiting an inclusion of one or more primer pairs in the filtered set of primer pairs that correspond with the selected subset of the one or more candidate amplicon sequences into a given pool based at least on an inequality relating a size of the given pool with a product between a balance factor and a maximum value of the sizes of the separate pools.

[00237] In various embodiments, the method may comprise providing a report reporting on any one or more element of information of data used or generated by any one or more of the receiving, providing, scoring, filtering, selecting, and assembling steps.

[00238] According to an exemplary embodiment, there is provided a non-transitory machine-readable storage medium comprising instructions which, when executed by a processor, cause the processor to perform a method comprising: (1) receiving one or more genomic regions or sequences of interest; (2) determining one or more target sequences for the received one or more genomic regions or sequences of interest; (3) providing one or more primer pairs for each of the determined one or more target sequences; (4) scoring the one or more primer pairs, wherein the scoring comprises a penalty based on the performance of in silico PCR for the one or more primer pairs, and wherein the scoring further comprises an analysis of SNP overlap for the one or more primer pairs; and (5) filtering the one or more primer pairs based on a plurality of factors, including at least the penalty and the analysis of SNP overlap, to identify a filtered set of primer pairs corresponding to one or more candidate amplicon sequences for the one or more genomic regions or sequences of interest.

[00239] In various embodiments, such a non-transitory machine-readable storage medium may comprise instructions which, when executed by a processor, cause the processor to perform a method further comprising: (6) selecting a subset of the one or more candidate amplicon sequences that substantially covers the one or more genomic regions or sequences of interest while minimizing a cost function associated with the candidate amplicon sequences; and (7) assembling the primer pairs in the filtered set of primer pairs that correspond with the selected subset of the one or more candidate amplicon sequences into a plurality of separate pools of primer pairs.

[00240] According to an exemplary embodiment, there is provided a system, comprising: (1) a machine-readable memory; and (2) a processor configured to execute machine-readable instructions, which, when executed by the processor, cause the system to perform steps including: (a) receiving one or more genomic regions or sequences of interest; (b) determining one or more target

sequences for the received one or more genomic regions or sequences of interest; (c) providing one or more primer pairs for each of the determined one or more target sequences; (d) scoring the one or more primer pairs, wherein the scoring comprises a penalty based on the performance of in silico PCR for the one or more primer pairs, and wherein the scoring further comprises an analysis of SNP overlap for the one or more primer pairs; and (e) filtering the one or more primer pairs based on a plurality of factors, including at least the penalty and the analysis of SNP overlap, to identify a filtered set of primer pairs corresponding to one or more candidate amplicon sequences for the one or more genomic regions or sequences of interest.

[00241] In various embodiments, the processor of such a system may further be configured to execute machine-readable instructions, which, when executed by the processor, cause the system to perform steps including: (f) selecting a subset of the one or more candidate amplicon sequences that substantially covers the one or more genomic regions or sequences of interest while minimizing a cost function associated with the candidate amplicon sequences; and (g) assembling the primer pairs in the filtered set of primer pairs that correspond with the selected subset of the one or more candidate amplicon sequences into a plurality of separate pools of primer pairs.

[00242] According to various exemplary embodiment, various parameters or criteria may be used to select primers and/or amplicons.

[00243] In an embodiment, a forward SNP score may be used and may be given a numerical attribute/score of 1 if there is no SNP within a given length of base pairs of the forward primer (such as 4, for example) or a numerical attribute of 0 if there is one or more SNPs within a length of 4 base pairs. In one embodiment, the forward SNP score may be given a numerical attribute/score of 1 if there is no SNP within a given length of base pairs from the 3' end of the forward primer. In some embodiments, a SNP can include one or more SNPs found on UCSC's Genome Browser Web Page including but not limited to, the SNP reference table referred to as "dbSNP132 common". An attribute/score of 1 may be a minimal attribute/score such that failure to achieve that attribute/score would result in disqualification. The base length threshold for the attribute/score determination could be lower or higher than 4, and could be 5, 6, 7, 8, 9, 10, 15, 20, for example, or more generally any positive integer larger than 4. The attribute/score could be other than binary and could be a more complex linear or non-linear function of the number of SNPs within the given length of base pairs.

[00244] In an embodiment, a reverse SNP score may be used and may be given a numerical attribute/score of 1 if there is no SNP within a given length of base pairs of the reverse primer (such as 4, for example) or a numerical attribute of 0 if there is one or more SNPs within a length of 4 base

pairs. In one embodiment, the reverse SNP score may be given a numerical attribute/score of 1 if there is no SNP within a given length of base pairs from the 3' end of the reverse primer. In some embodiments, a SNP can include one or more SNPs found on UCSC's Genome Browser Web Page including but not limited to, the SNP reference table referred to as "dbSNP132 common". An attribute/score of 1 may be a minimal attribute/score such that failure to achieve that attribute/score would result in disqualification. The base length threshold for the attribute/score determination could be lower or higher than 4, and could be 5, 6, 7, 8, 9, 10, 15, 20, for example, or more generally any positive integer larger than 4. The attribute/score could be other than binary and could be a more complex linear or non-linear function of the number of SNPs within the given length of base pairs.

[00245] In an embodiment, a forward repeat score may be used and may be given a numerical attribute/score of 1 if there is no repeat within a given length of base pairs of the forward primer (such as 4, for example) or a numerical attribute of 0 if there is one or more repeats within a length of 4 base pairs. In one embodiment, the forward repeat score may be given a numerical attribute/score of 1 if there is less than 30% overlap of the forward primer with known repeats. In some embodiments, known repeats may include one or more repeats reported by UCSC's Genome Browser, for example repeat regions as provided by the repeat masked hg19 genome from UCSC. An attribute/score of 1 may be a minimal attribute/score such that failure to achieve that attribute/score would result in disqualification. The base length threshold for the attribute/score determination could be lower or higher than 4, and could be 5, 6, 7, 8, 9, 10, 15, 20, for example, or more generally any positive integer larger than 4. The attribute/score could be other than binary and could be a more complex linear or non-linear function of the number of repeats within the given length of base pairs.

[00246] In an embodiment, a reverse repeat score may be used and may be given a numerical attribute/score of 1 if there is no repeat within a given length of base pairs of the reverse primer (such as 4, for example) or a numerical attribute of 0 if there is one or more repeats within a length of 4 base pairs. In one embodiment, the reverse repeat score may be given a numerical attribute/score of 1 if there is less than 30% overlap of the reverse primer with known repeats. In some embodiments, known repeats may include one or more repeats reported by UCSC's Genome Browser, for example repeat regions as provided by the repeat masked hg19 genome from UCSC. An attribute/score of 1 may be a minimal attribute/score such that failure to achieve that attribute/score would result in disqualification. The base length threshold for the attribute/score determination could be lower or higher than 4, and could be 5, 6, 7, 8, 9, 10, 15, 20, for example, or more generally any positive

integer larger than 4. The attribute/score could be other than binary and could be a more complex linear or non-linear function of the number of repeats within the given length of base pairs.

[00247] In various embodiments, one or more of a forward triplet score, a reverse triplet score, a forward A run score, a reverse A run score, a forward C run score, a reverse C run score, a forward G run score, a reverse G run score, a forward T run score, and a reverse T run score, may be used and may be given a numerical attribute/score equal to the number of forward triplets, reverse triplets, forward A runs, reverse A runs, forward C runs, reverse C runs, forward G runs, reverse G runs, forward T runs, and reverse T runs within the entire primer. An attribute/score of 3 may be a maximal attribute/score for the triplets such that failure to remain at or below that attribute/score would result in disqualification. An attribute/score of 5 may be a maximal attribute/score for the runs such that failure to remain at or below that attribute/score would result in disqualification. The attribute/score could be other than binary and could be a more complex linear or non-linear function of the number of triplets/runs.

[00248] In an embodiment, a length of the primers may be limited by a minimum primer length threshold and a maximum primer length, and a length score for the primers may be set so as to decrease as the length gets shorter than the minimum primer length threshold and to decrease as the length gets longer than the maximum primer length threshold. In an embodiment, the minimum primer length threshold may be 16. In other embodiments, the minimum primer length threshold may be 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, or 5, for example, and may also be 17, 18, 19, 20, 21, 22, 23, and 24, for example. In an embodiment, the maximum primer length threshold may be 28. In other embodiments, the maximum primer length threshold may be 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, and 40, for example, and may also be 27, 26, 25, 24, 23, 22, 21, and 20, for example. In an embodiment, the primer length criterion may be given a score of 1.0 if the length thresholds are satisfied, for example, and that score may go down to 0.0 as the primer length diverges from the minimum or maximum length threshold. For example, if the maximum primer length threshold were set to 28, then the score could be set to 1.0 if the length does not exceed 28, to 0.7 if the length is 29, to 0.6 if the length is 30, to 0.5 if the length is 31, to 0.3 if the length is 32, to 0.1 if the length is 33, and to 0.0 if the length is 34 or more. The attribute/score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increase difference relative to the threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from length thresholds.

[00249] In an embodiment, a number of G bases (or of A, C, or T bases) in the primers may be limited by a maximum threshold, and corresponding score for the primers may be set so as to decrease as the number of G bases (or of A, C, or T bases) exceeds the maximum threshold. In an embodiment, the maximum threshold may be 3. In other embodiments, the maximum threshold may be 2, 4, 5, 6, 7, 8, 9, and 10, for example. In an embodiment, the number of G bases (or of A, C, or T bases) criterion may be given a score of 1.0 if the maximum threshold is satisfied, for example, and that score may go down to 0.0 as the number of G bases (or of A, C, or T bases) diverges from the maximum threshold. For example, if the maximum threshold were set to 4, then the score could be set to 1.0 if the number of G bases (or of A, C, or T bases) does not exceed 4, to 0.9 if the number is 5, to 0.8 if the number is 6, to 0.6 if the number is 7, to 0.4 if the number is 8, to 0.2 if the number is 9, and to 0.0 if the number is 10 or more. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the number of G bases (or of A, C, or T bases) and the maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the maximum threshold.

[00250] In an embodiment, the numbers of contiguous and total matches in a loop (e.g., hairpin) in the primers may be limited by a maximum threshold, and corresponding scores for the primers may be set so as to decrease as the numbers of contiguous and total matches in a loop exceed the maximum threshold. In an embodiment, the maximum threshold for contiguous matches may be 3 and the maximum threshold for total matches may be 5. In other embodiments, the maximum threshold for contiguous matches may be 2, 4, 5, 6, 7, 8, 9, and 10, for example, and the maximum threshold for total matches may be 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 14, and 15, for example. In an embodiment, the numbers of contiguous and total matches in a loop criteria may be given a score of 1.0 if the maximum threshold is satisfied, for example, and that score may go down to 0.0 as the number of the numbers of contiguous and total matches in a loop diverge from the corresponding maximum threshold. For example, if the maximum threshold for contiguous matches were set to 3, then the score could be set to 1.0 if the number of contiguous matches does not exceed 3, to 0.9 if the number is 4, to 0.7 if the number is 5, to 0.4 if the number is 6, to 0.2 if the number is 7, to 0.1 if the number is 8, and to 0.0 if the number is 9 or more. For example, if the maximum threshold for total matches were set to 5, then the score could be set to 1.0 if the number of total matches does not exceed 5, to 0.9 if the number is 6, to 0.8 if the number is 7, to 0.6 if the number is 8, to 0.4 if the number is 9, to 0.2 if the number is 10, to 0.1 if the number is 11, and to 0.0 if the number is 12 or

more. The scores could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the scores vary with an increased difference between the number of contiguous/total matches and the corresponding maximum thresholds could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the maximum threshold.

[00251] In an embodiment, a number of G and C bases (or any two of the A, C, G, and T bases) in the last five bases of the primers may be limited by a maximum threshold, and corresponding score for the primers may be set so as to decrease as the number of G and C bases (or any two of the A, C, G, and T bases) exceeds the maximum threshold. In an embodiment, the maximum threshold may be 2. In other embodiments, the maximum threshold may be 3, 4, and 5, for example. In an embodiment, the number of G and C bases (or any two of the A, C, G, and T bases) criterion may be given a score of 1.0 if the maximum threshold is satisfied, for example, and that score may go down to 0.0 as the number of G and C bases (or any two of the A, C, G, and T bases) diverges from the maximum threshold. For example, if the maximum threshold were set to 2, then the score could be set to 1.0 if the number of G and C bases (or any two of the A, C, G, and T bases) does not exceed 2, to 0.8 if the number is 3, to 0.4 if the number is 4, and to 0.1 if the number is 5. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the number of G and C bases (or any two of the A, C, G, and T bases) and the maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the maximum threshold. In other embodiments, this criterion could consider the number of G and C bases (or any two of the A, C, G, and T bases) in a larger window of bases, such as in the last six bases, the last seven bases, the last eight bases, etc., for example.

[00252] In an embodiment, a percentage of G and C bases (or any two of the A, C, G, and T bases) in the primers may be limited by minimum and maximum thresholds, and corresponding score for the primers may be set so as to decrease as the percentage of G and C bases (or any two of the A, C, G, and T bases) diverges from the minimum or maximum threshold. In an embodiment, the minimum threshold may be 0.2 (20%) and the maximum threshold may be 0.8 (80%). In other embodiments, the minimum threshold may be any percentage between about 0.2 (20%) and about 0.5 (50%) and the maximum threshold may be any percentage between about 0.8 (80%) and 0.5 (50%), for example. In an embodiment, the percentage of G and C bases (or any two of the A, C, G, and T bases) criterion may be given a score of 1.0 if the minimum and maximum thresholds are satisfied,

for example, and that score may go down to 0.0 if either of the thresholds is not satisfied. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the percentage of G and C bases (or any two of the A, C, G, and T bases) and the minimum or maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the minimum or maximum threshold.

[00253] In an embodiment, a melting temperature (Tm) of the primers may be limited by minimum and maximum thresholds, and corresponding score for the primers may be set so as to decrease as the melting temperature diverges from the minimum or maximum threshold. In an embodiment, the minimum threshold may be 60 and the maximum threshold may be 67 with a target melting temperature of 62. In other embodiments, the minimum threshold may be a value between about 55 and about 65 and the maximum threshold may be a value between about 62 and about 72, for example. In an embodiment, the melting temperature criterion may be given a score of 1.0 if the minimum and maximum thresholds are satisfied, for example, and that score may go down to 0.0 if either of the thresholds is not satisfied. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the melting temperature and the minimum or maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the minimum or maximum threshold. The melting temperature of a primer may be calculated using the teachings set forth in John SantaLucia, Jr., "A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics," Proc. Natl. Acad. Sci. USA, vol. 95, 1460-1465 (1998), the contents of which is incorporated by reference herein in its entirety.

[00254] In an embodiment, a primer-dimer propensity in the primers may be limited by a maximum threshold of contiguous primer-dimers at the 3' end and a maximum threshold of total contiguous matches over the full length, and corresponding score for the primers may be set so as to decrease as the primer-dimer propensity diverges from the maximum thresholds. In an embodiment, the maximum threshold of contiguous primer-dimers at the 3' end may be 4 and the maximum threshold of total contiguous matches over the full length may be 8. In other embodiments, the maximum threshold of contiguous primer-dimers at the 3' end may be a value between about 2 and about 6 and the maximum threshold of total contiguous matches over the full length may be a value between about 4 and 10, for example. In an embodiment, the primer-dimer propensity criteria may be given a score of 1.0 if the threshold is satisfied, for example, and that score may go down to 0.0 if

the threshold is not satisfied. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the primer-dimer propensity and the maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for primer that further diverge from the maximum threshold.

[00255] In an embodiment, a percentage of G and C bases (or any two of the A, C, G, and T bases) in an amplicon sequence may be limited by minimum and maximum thresholds, and corresponding score for the amplicons may be set so as to decrease as the percentage of G and C bases (or any two of the A, C, G, and T bases) diverges from the minimum or maximum threshold. In an embodiment, the minimum threshold may be 0.0 (0%) and the maximum threshold may be 1.0 (100%). In other embodiments, the minimum threshold may be any percentage between about 0.1 (10%) and about 0.25 (25%) and the maximum threshold may be any percentage between about 0.75 (75%) and 0.9 (90%), for example. In an embodiment, the percentage of G and C bases (or any two of the A, C, G, and T bases) criterion may be given a score of 1.0 if the minimum and maximum thresholds are satisfied, for example, and that score may go down to 0.0 if either of the thresholds is not satisfied. The score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increased difference between the percentage of G and C bases (or any two of the A, C, G, and T bases) and the minimum or maximum threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for amplicons that further diverge from the minimum or maximum threshold.

[00256] In an embodiment, a length of the amplicons may be limited by a minimum amplicon length threshold and a maximum amplicon length, and a length score for the amplicons may be set so as to decrease as the length gets shorter than the minimum amplicon length threshold and to decrease as the length gets longer than the maximum amplicon length threshold. In an embodiment, the minimum amplicon length threshold may be 110. In other embodiments, the minimum primer length threshold may be a value between about 80 and about 140, for example. In an embodiment, the maximum amplicon length threshold may be 240. In other embodiments, the maximum amplicon length threshold may be a value between about 200 and about 280, for example. In an embodiment, the amplicon length criterion may be given a score of 1.0 if the length thresholds are satisfied and of 0.0 if either is not satisfied. In another embodiment, that score may go down to 0.0 as the amplicon length diverges from the minimum or maximum length threshold. For example, if the maximum amplicon length threshold were set to 240, then the score could be set to 1.0 if the length does not

exceed 240, to 0.8 if the length is at least 250, to 0.6 if the length is at least 260, to 0.4 if the length is at least 270, to 0.1 if the length is at least 280, and to 0.0 if the length is at least 290. The attribute/score could be scaled between values other than 0.0 and 1.0, of course, and the function defining how the score varies with an increase difference relative to the threshold could be any other or more complex linear or non-linear function that does not lead to increases in score for amplicons that further diverge from length thresholds.

[00257] According to an exemplary embodiment, there is provided a method for selecting a subset (which may be referred to as "tiling" herein) of amplicons (which may be referred to as "tiles" herein) from a plurality of candidate amplicons for covering one or more specific desired (e.g., customized) genomic regions or targets using one or more pools of amplicons. The method may include receiving as input a set of one or more targets and a set of candidate amplicons, and may include outputting as output a subset of the candidate amplicons and an assignment of each of the amplicons in the subset to a pool in which that amplicon can be multiplexed. Amplicons of any suitable sizes may be used. In an embodiment, an assay or primer design may accommodate 200 bp amplicons and 150 bp amplicons, for example, which may be especially useful for certain challenging samples such as FFPE, for example. In an embodiment, an assay or primer design may be adapted to be compatible with one or more specific library kits, such as, for example, the Ion AmpliSeq™ Library Kit 2.0.

[00258] According to an exemplary embodiment, there is provided a method for tiling and pooling, comprising (1) selecting a subset of amplicons (which may be referred to as "tiling" herein) from a set of input amplicons such that the subset of amplicons (i) covers as much of each target as do the amplicons in the set of input amplicons, (ii) has many fewer amplicons than the set of input amplicons, and (iii) maximizes a quality of the amplicons; and (2) assigns each amplicon or tile in the subset of amplicons or tiling to a pool so as to allow each pool to be multiplexed.

[00259] FIG. 23 illustrates a method for tiling a plurality of amplicons for one or more given targets according to an exemplary embodiment. In step 2301, a module or other hardware and/or software component sorts the one or more given targets by their start positions (or ensures that the given targets were already pre-sorted in such a manner when provided as input). In step 2302, a module or other hardware and/or software component sorts the amplicons by insert start (or ensures that the amplicons were already pre-sorted in such a manner when provided as input). In step 2303, a module or other hardware and/or software component merges overlapping targets present in the sorted one or more targets. In step 2304, for each merged overlapping target, a module or other

hardware and/or software component (i) determines what amplicons have inserts overlapping the target and identifies such amplicons as candidate amplicons, and (ii) determines tiles using a function of the one or more given targets and the candidate amplicons. In step 2305, a module or other hardware and/or software component outputs the determined tiles. In some embodiments, targets may or may not be merged ahead of gathering any target amplicons, amplicons may be gathered for unmerged targets, and, if two targets share at least one amplicon, such two targets may be merged together (and one of the two targets may already represent a set of merged input amplicons).

[00260] According to an exemplary embodiment, there is provided a method for tiling a plurality of amplicons for one or more given targets, comprising: (1) sorting the one or more given targets by their start positions or ensuring that the given targets were already pre-sorted in such a manner when provided as input; (2) sorting the amplicons by insert start or ensuring that the amplicons were already pre-sorted in such a manner when provided as input; (3) merging overlapping targets present in the sorted one or more targets; (4) for each merged overlapping target, (i) determining what amplicons have inserts overlapping the target and identifying such amplicons as candidate amplicons and (ii) determining the tiles using a function of the one or more given targets and the candidate amplicons; and (5) outputting the tiles.

[00261] FIG. 24 illustrates a method for determining tiles for one or more given targets and candidate amplicons according to an exemplary embodiment. In step 2401, a module or other hardware and/or software component creates an overlap graph of candidate inserts, the graph including a source vertex, one or more amplicon vertices, and a sink vertex along with one or more edges linking vertices. In step 2402, a module or other hardware and/or software component defines an edge cost function or uses a defined edge cost function. In step 2403, a module or other hardware and/or software component finds a least cost path for such an edge cost function from the source vertex to the sink vertex. In step 2404, a module or other hardware and/or software component extracts the tiles from the least-cost path from source to sink. In step 2405, a module or other hardware and/or software component returns the extracted tiles.

[00262] According to an exemplary embodiment, there is provided a method for determining tiles for one or more given targets and candidate amplicons, comprising: (1) creating an overlap graph of candidate inserts, the overlap graph comprising a set of vertices V and a set of edges E (e.g., a graph G = (V,E)), such creating including (i) letting V equal the union of the set of candidate amplicons (each of which being assigned a corresponding vertex) and the set consisting of a source element and a sink element (e.g., $V = \{amplicons\} \cup \{source,sink\}$), (ii) connecting the source vertex

to all initial vertices and the sink vertex to all terminal vertices, (iii) connecting each amplicon vertex to all subsequent, proper, overlaps, and (iv) connecting rightmost vertices on the left of a gap to leftmost vertices on the right of that gap; (2) defining an edge cost function or using a defined edge cost function; (3) finding a least cost path for such an edge cost function from the source vertex to each vertex; (4) extracting the tiles from the least-cost path from source to sink; and (5) returning the extracted tiles.

[00263] FIG. 25A illustrates a set of candidate amplicons for covering a given target region, each including an insert surrounded by a pair of primers, for tiling and pooling according to an exemplary embodiment. The dotted lines indicate the boundaries of the target region (on chromosome 19 in this example).

[00264] FIG. 25B illustrates a set of vertices for generating a graph. The vertices V includes 15 amplicon vertices (white) corresponding to the 15 candidate amplicons illustrated in FIG. 25A together with a source vertex (light gray or green, left) and a sink vertex (dark grey or red, right). FIG. 26A illustrates the 15 candidate amplicons of FIG. 25A, except that three "initial" amplicons having at least some overlap between their insert and the beginning of the target region are highlighted.

[00265] FIG. 26B illustrates the connection of a source vertex to three vertices corresponding to the initial amplicons of FIG. 26A with edges.

[00266] FIG. 27A illustrates the 15 candidate amplicons of FIG. 25A, except that three "terminal" amplicons having at least some overlap between their insert and the end of the target region are highlighted.

[00267] FIG. 27B illustrates the connection of a sink vertex to three vertices corresponding to the terminal amplicons of FIG. 27A with edges.

[00268] FIG. 28A illustrates the 15 candidate amplicons of FIG. 25A, except that various amplicons for building internal edges are highlighted.

[00269] FIG. 28B illustrates the connection of some amplicon insert vertices to subsequent, proper, overlaps according to an exemplary embodiment. Shown are arrows linking the 9767127 amplicon vertex to the 9767463 and 9767519 amplicon vertices (whose inserts overlap the insert of the 9767127 amplicon vertex) and arrows linking the 9767610 amplicon vertex to the 9767780 and 9767756 amplicon vertices (whose inserts overlap the insert of the 9767610 amplicon vertex).

[00270] FIG. 29A illustrates the connection of additional amplicon insert vertices to subsequent, proper, overlaps according to an exemplary embodiment. Also shown is a disconnect or gap that may arise if the candidate amplicons do not fully cover the target.

[00271] FIG. 29B illustrates the 15 candidate amplicons of FIG. 25A, along with the basis for the gap shown in FIG. 29A according to an exemplary embodiment.

[00272] FIG. 30A illustrates three possible additional edges that could be used from source to ink to tile the target in this example according to an exemplary embodiment. In an embodiment, of the possible paths the one with a least cost may be selected.

[00273] FIG. 30B illustrates an exemplary definition of an edge cost function assigning a cost to each one of the graph's edges linking amplicon vertices according to an exemplary embodiment.

[00274] FIG. 30C illustrates the least-cost path from source to ink in the example of FIG. 30B according to an exemplary embodiment.

[00275] FIG. 31 illustrates the 15 candidate amplicons of FIG. 25A, except that the five amplicons corresponding to the vertices forming the least-cost path shown in FIG. 30C are highlighted.

[00276] According to an exemplary embodiment, the least-cost path may be determined using an O(|V|+|E|) algorithm. The least-cost path may be determined as follows: (1) for each vertex v, (i) initialize D[v] to infinity (the least cost so far in the process) from the source vertex to v and initialize D[source] to zero, and (ii) initialize Pred[v] to null (the predecessor of v in the least-cost path from the source vertex to v); and (2) for each vertex u in topological order, for each vertex v in adj[u], if D[u] + cost(u,v) < D[v], then let D[v] = D[u] + cost(u,v) and Pred[v] = u. More information regarding algorithms for constructing paths on graphs may be found in Dijkstra, "A Note on Two Problems in Connexion with Graphs," Numerische Mathematik, vol. 1, 269-271 (1959), and Sniedovich, "Dijkstra's algorithm revisited: the dynamic programming connexion," Control and Cybernetics, vol. 35, 599-620 (2006), which are both incorporated by reference herein in their entirety.

[00277]

According to an exemplary embodiment, the cost of a path (e.g., amplicon plus "union" redundancy) may be the sum of the edges forming the path. In an embodiment, the cost of a path may be determined using Equation 1 below:

Equation 1: $$\text{cost}(path) = \sum_{(u,v)\in path} \text{cost}(u,v)$$

[00278] According to an exemplary embodiment, the cost of an edge forming a path may be a sum of an amplicon cost and an overlap cost weighed using a factor α selected to blend the two costs, e.g., $0 \leq \alpha \leq 1$. In an embodiment, the cost of an edge forming the path may be determined using Equation 2 below:

Equation 2: $$\text{cost}(u,v) = \alpha\text{cost}(v.\text{amplicon}) + (1-\alpha)\text{cost}(\text{overlap}(u,v))$$

[00279] According to an exemplary embodiment, there is provided a method for determining a cost associated with a tiling or subset of amplicons. In an embodiment, the cost of a tiling may be the sum of a cost of each amplicon in the tiling plus a cost of any one or more insert overlaps. The cost of an amplicon may be assigned any suitable value in any suitable predetermined range of values such that a low value imparts a low cost and a high value imparts a high cost so as to penalize various undesirable characteristics such as, for example, off-target amplification, primer-dimer propensity, etc. For example, the cost of an amplicon may be assigned a value from 1 to 10 such that a higher/lower cost is associated with a higher/lower level of undesirable characteristics (using any appropriate relationships, which may be linear/proportional or non-linear, for example). The cost of an insert overlap may also similarly be assigned any suitable value in any suitable predetermined range of values, for example, such that a low value imparts a low cost and a high value imparts a high cost so as to penalize various undesirable characteristics such as, for example, the redundancy introduced by overlapping inserts. For example, the cost of an insert overlap may also be assigned a value from 1 to 10. In an embodiment, one may opt to select a least-cost tiling from a set of candidate amplicons. In an embodiment, the cost of an insert overlap may be determined based on the redundancy introduced by overlapping inserts using Equation 3 below:

Equation 3: $$\text{redundancy}(\text{overlap}(u,v)) = \frac{\text{numBP}(\text{overlap}(u,v))}{\text{numBP}(\text{union}(u,v))}$$

[00280] According to an exemplary embodiment, the costs for amplicon and specificity may be used by a tiling hardware or software component of tiler to calculate the cost of an edge. In an embodiment, a cost system may be used that allows a scaled cost calculation for a vertex in the tiler. The cost of an amplicon may be a composite of the amplicon cost and the specificity cost. The amplicon cost may reflect the quality of PCR amplification and the specificity cost may reflect the propensity of the amplicon to amplify off-target nucleotides.

[00281] In an embodiment, the cost of an amplicon may be determined as follows: Initially, a threshold may be used to filter primers that allow potential off-target amplification. The filter may

be based on a program such as e-PCR2 (NCBI), see Rotmistrovsky et al., "A web server for performing electronic PCR," Nucleic Acids Research, vol. 32, W108-W112 (2004), and Schuler, "Sequence Mapping by Electronic PCR," Genome Research, vol. 7, 541-550 (1997), which are both incorporated by reference herein in their entirety, or other similar programs capable of being used for filtering primers. Various scoring strategies may be used for filtering. In various embodiments, the assays may be filtered that have a sum of score of forward and reverve primer less than a certain minimal score threshold (e.g., 150) or show more than 50 hits with a score less than some threshold (e.g., 200). Of course, numerical cut-offs may differ and will vary according to software used. In various embodiments, scores used for filtering may be converted to a cost using a conversion table such as illustrated below:

0-19	170+	10
20-39	150-169	9
40-59	130-149	8
60-79	110-129	7
80-99	90-109	6
100-119	70-89	5
120-149	50-69	4
150-179	30-49	3
180-210	10-29	2
210+	0-9	1

In this exemplary table, the first column represents sp_score, which is a specificity score; the second column represents sp_hits, which is the number of matches for the forward and reverse primers facing each other; and the third column is a corresponding cost. The first perfect match is free, since it is the self match. In an embodiment, Acost is the cost based on binning the sp_score values, Bcost is the cost based on sp_hits values, and the amplicon cost may be calculated using the formula: AmpliconCost = 0.9*Acost+0.1*Bcost.

[00282] FIG. 32 illustrates three amplicons assigned to a first pool and two amplicons assigned to a second pool according to an exemplary embodiment. The dotted lines indicate the boundaries of a target region (on chromosome 19 in this example). As illustrated, the amplicons in the first and second pools substantially cover the target regions, with the exception of the gaps.

[00283] According to an exemplary embodiment, there is provided a method for pooling amplicons into one or more pools of amplicons. In an embodiment, the method may pool the amplicons using one or more pooling criteria, which may related at least in part to pool sizes. In an embodiment, a number of pools may be limited to a pre-determined maximum number of pools, which may be 10 pools, for example, or which may be 50, 40, 30, 20, 9, 8, 7, 6, 5, 4, 3, 2, or 1, for example, or any other positive integer. In an embodiment, a capacity of each pool (e.g, a maximal size of a pool) may also be limited to a pre-determined maximal value, which may be any fixed number of amplicons, and which may be about 10,000, about 7,500, about 5,000, about 2,500, about 2,000, about 1,500, about 1,000, and about 500, or any value between those examples, for example, and which may be a maximum of 768 or 1,536 amplicons, for example. In an embodiment, a balance factor may be used, which may be a percentage between about 60% and 100%, or between about 65% and 95%, or between about 70% and 90%, or about 90%, for example. In an embodiment, the size of a pool p may be constrained by the inequality set forth in Equation 4 below:

Equation 4: $$size(p) \geq \left\lfloor balanceFactor \times \max_{q \in pools} \{size(q)\} \right\rfloor$$

[00284] According to an exemplary embodiment, an intra pool distance may be limited by a minimal threshold distance, which may be, for example, an integer number of base pairs (e.g., 50 base pairs, or 5, 10, 15, 20, etc., or any predetermined number of base pairs).

[00285] FIG. 33A illustrates a minimal distance between amplicons according to an exemplary embodiment. FIGS. 33B-D illustrate several problems, including primer "race condition" (see FIG. 33B), preferential amplification of sub amplicons (see FIG. 33C), and super amplicons (see FIG. 33D) that may be ameliorated by using a minimal distance as illustrated in FIG. 33A. In an embodiment, the distance may be determined using equation 5, for example. Such an approach may prevent or reduces "race condition," preferential amplification of sub amplicons, and super amplicons.

Equation 5: $$\text{dist}(a,b) = \max(a.\text{start},b.\text{start}) - \min(a.\text{end},b.\text{end}) - 1$$

[00286] According to an exemplary embodiment, amplicons may be disqualified from being added to a pool in certain circumstances. For example, an amplicon amp may not be added to a pool p if one or more of the following criteria are met: (1) the size of the pool p equals or exceeds the pool capacity limit; (2) the size of the pool p equals the size of the largest pool (e.g., size(p) = size(largest pool)) and the size of the smallest pool is less than a floor (rounded down) value of the product of (i) the size of the pool p plus 1 and (ii) a balance factor (e.g., size(smallest pool) < floor((size(p)+1)

balanceFactor)); and (3) the distance between amp and any other amplicon already in the pool is less than a minimum amplicon separation threshold (e.g., which distance may be determined using Equation 5, for example).

[00287] FIG. 34 illustrates a method for pooling amplicons across a plurality of pools according to an exemplary embodiment. In step 3401, a module or other hardware and/or software component sorts the amplicons by decreasing priority. In step 3402, a module or other hardware and/or software component starts a first available pool. In step 3403, a module or other hardware and/or software component empties all available pools. In step 3404, for each amplicon in the sorted amplicons, a module or other hardware and/or software component, (i) determines a list of compatible pools in which the amplicon could be multiplexed, (ii) if there is at least one compatible pool then places the amplicon in a first compatible pool that maximizes the minimum distance between the amplicon and any other amplicon in the compatible pool, (iii) if there is no compatible pool then if a new pool can be added adds a new pool and returns to step 3403, and (iv) if there is no compatible pool and none can be added then puts the amplicon in an overflow (unpooled) list of amplicons. In step 3405, a module or other hardware and/or software component outputs the pools.

[00288] According to an exemplary embodiment, a method for pooling amplicons across a plurality of pools comprises: (1) sorting the amplicons by decreasing priority; (2) starting a first available pool; (3) emptying all available pools; (4) for each amplicon in the sorted amplicons, (i) determining a list of compatible pools in which the amplicon could be multiplexed, (ii) if there is at least one compatible pool then placing the amplicon in a first compatible pool that maximizes the minimum distance between the amplicon and any other amplicon in the compatible pool, (iii) if there is no compatible pool then if a new pool can be added add a new pool and return to step (3), and (iv) if there is no compatible pool and none can be added then put the amplicon in an overflow (unpooled) list of amplicons. The method may further comprise outputting the amplicon pools.

[00289] Such a method may help ensure that the PCR pools cover as much of the targets as do the candidate amplicons supplied as input. It may generate a small number of PCR pools (e.g., 2, 4, etc.). The primers in a pool will not interact, which may help avoid undesired preferential amplification, "race condition" competition for primer hybridization, and super-amplicons. Further, such a method may run very quickly and using only a reasonable amount of memory.

[00290] FIG. 35 illustrates a method for tiling according to an exemplary embodiment. In step 3501, a module or other hardware and/or software component receives or provides as inputs a genomic target region and a set of candidate amplicons for the genomic target region. In step 3502, a

module or other hardware and/or software component generates a graph comprising a source vertex, a set of amplicon vertices arranged in correspondence with the set of candidate amplicons, and a sink vertex. In step 3503, a module or other hardware and/or software component determines a cost associated with one or more paths across the graph from the source vertex to the sink vertex via amplicon vertices. In step 3504, a module or other hardware and/or software component extracts the amplicon vertices from the one of the one or more paths across the graph having a least cost associated therewith. In some embodiments, such a method may be extended to a method for pooling amplicons across a plurality of pools by using as input the amplicons corresponding to the extracted vertices. For example, various steps such as described in FIG. 34 may be performed on amplicons corresponding to the extracted vertices to pool the amplicons.

[00291] According to an exemplary embodiment, there is provided a method comprising: (1) receiving or providing as inputs a genomic target region and a set of candidate amplicons for the genomic target region; (2) generating a graph comprising a source vertex, a set of amplicon vertices arranged in correspondence with the set of candidate amplicons, and a sink vertex; (3) determining a cost associated with one or more paths across the graph from the source vertex to the sink vertex via amplicon vertices; and (4) extracting the amplicon vertices from the one of the one or more paths across the graph having a least cost associated therewith.

[00292] In various embodiments, the one or more paths may comprise a sequence of amplicons wherein an ending portion of an insert of a first amplicon in the sequence of amplicons overlaps a beginning portion of an insert of a second amplicon in the sequence of amplicons. An ending portion of an insert of the second amplicon in the sequence of amplicons may overlap a beginning portion of an insert of a third amplicon in the sequence of amplicons. An ending portion of an insert of the third amplicon in the sequence of amplicons may overlap a beginning portion of an insert of a fourth amplicon in the sequence of amplicons.

[00293] In various embodiments, the one or more paths may comprise a sequence of N amplicons, N being a positive integer, wherein an ending portion of an insert of an amplicon amp in the sequence of amplicons overlaps a beginning portion of an insert of an amplicon amp+1 in the sequence of amplicons, wherein amp is an integer taking values 1, . . . , N-1. The one or more paths may comprise a sequence of L=N+M amplicons, N and M being positive integers, wherein an ending portion of an insert of an amplicon amp in the sequence of amplicons overlaps (which may include merely touching) a beginning portion of an insert of an amplicon amp+1 in the sequence of amplicons where amp is an integer taking values 1, . . . , N-1; wherein an ending portion of an insert

of an amplicon amp in the sequence of amplicons overlaps (which may include merely touching) a beginning portion of an insert of an amplicon amp+1 in the sequence of amplicons where amp is an integer taking values N+1, . . . , N+M-1; and wherein there is a gap between an ending portion of an insert of amplicon amp=N and a beginning portion of an insert of amplicon amp=N+1.

[00294] In various embodiments, the cost associated with each of the one or more paths may be a sum of the cost of every edge of the path linking two amplicon vertices. The cost associated with every edge of the path linking two amplicon vertices may be a sum of a first term related to the cost of the edge's destination amplicon vertex and a second term related to the cost of an overlap between an insert of the edge's destination amplicon and an insert of the edge's origin amplicon. The first term and the second term may be weighed by a blending factor such that the first term is multiplied by the blending factor or a function thereof and the second term is multiplied by one minus the blending factor or a function thereof. The cost of an amplicon vertex may be a numerical value along a scale between a first value representing a lower level of one or more undesirable characteristics selected from a group comprising at least a level of off-target amplification and a level of primer-dimer propensity and a second value representing a higher level of the one or more undesirable characteristics. The cost of an overlap between an insert of the edge's destination amplicon and an insert of the edge's origin amplicon may be determined based on a redundancy introduced by overlapping inserts. The cost of an overlap between an insert of the edge's destination amplicon and an insert of the edge's origin amplicon may be a function of a quotient between a number of base pairs in an overlap between the insert of the edge's destination amplicon and the insert of the edge's origin amplicon and a number of base pairs in a union of the insert of the edge's destination amplicon and the insert of the edge's origin amplicon.

[00295] In various embodiments, such a method may further comprise determining a pooling of amplicons corresponding to the extracted amplicons into one or more pools of amplicons. Determining a pooling of amplicons may comprise limiting a number of amplicon pools and a capacity of each amplicon pool. Determining a pooling of amplicons may comprise limiting the number of amplicon pools to a threshold number between about 2 and about 5 and limiting the capacity of each amplicon pool to a threshold capacity between about 500 amplicons and about 2,500 amplicons, for example. Determining a pooling of amplicons may comprise limiting a size of any of the one or more pools based on a maximum size of other pools.

[00296] In various embodiments, determining a pooling of amplicons may comprise limiting an inclusion of one or more into a given pool based at least on a minimal threshold distance between

amplicon sequences in the given pool. The minimal threshold distance may be between about 5 base pairs and about 100 base pairs, for example.

[00297] According to an exemplary embodiment, there is provided a non-transitory machine-readable storage medium comprising instructions which, when executed by a processor, cause the processor to perform a method comprising: (1) receiving or providing as inputs a genomic target region and a set of candidate amplicons for the genomic target region; (2) generating a graph comprising a source vertex, a set of amplicon vertices arranged in correspondence with the set of candidate amplicons, and a sink vertex; (3) determining a cost associated with one or more paths across the graph from the source vertex to the sink vertex via amplicon vertices; and (4) extracting the amplicon vertices from the one of the one or more paths across the graph having a least cost associated therewith. In some embodiments, such a method may be extended to a method for pooling amplicons across a plurality of pools by using as input the amplicons corresponding to the extracted vertices. For example, various steps such as described in FIG. 34 may be performed on amplicons corresponding to the extracted vertices to pool the amplicons.

[00298] In various embodiments, such a non-transitory machine-readable storage medium may comprise instructions which, when executed by a processor, cause the processor to perform a method further comprising determining a pooling of amplicons corresponding to the extracted amplicons into one or more pools of amplicons.

[00299] According to an exemplary embodiment, there is provided a system, comprising: (1) a machine-readable memory; and (2) a processor configured to execute machine-readable instructions, which, when executed by the processor, cause the system to perform steps including: (a) receiving or providing as inputs a genomic target region and a set of candidate amplicons for the genomic target region; (b) generating a graph comprising a source vertex, a set of amplicon vertices arranged in correspondence with the set of candidate amplicons, and a sink vertex; (c) determining a cost associated with one or more paths across the graph from the source vertex to the sink vertex via amplicon vertices; and (d) extracting the amplicon vertices from the one of the one or more paths across the graph having a least cost associated therewith. In some embodiments, such a system may be extended to a system for pooling amplicons across a plurality of pools by using as input the amplicons corresponding to the extracted vertices. For example, various steps such as described in FIG. 34 may be performed on amplicons corresponding to the extracted vertices to pool the amplicons.

[00300] In various embodiments, the processor of such a system may further be configured to execute machine-readable instructions, which, when executed by the processor, cause the system to perform steps including determining a pooling of amplicons corresponding to the extracted amplicons into one or more pools of amplicons.

[00301] According to various exemplary embodiments, one or more features of any one or more of the above-discussed teachings and/or exemplary embodiments may be performed or implemented using appropriately configured and/or programmed hardware and/or software elements. Determining whether an embodiment is implemented using hardware and/or software elements may be based on any number of factors, such as desired computational rate, power levels, heat tolerances, processing cycle budget, input data rates, output data rates, memory resources, data bus speeds, etc., and other design or performance constraints.

[00302] Examples of hardware elements may include processors, microprocessors, input(s) and/or output(s) (I/O) device(s) (or peripherals) that are communicatively coupled via a local interface circuit, circuit elements (e.g., transistors, resistors, capacitors, inductors, and so forth), integrated circuits, application specific integrated circuits (ASIC), programmable logic devices (PLD), digital signal processors (DSP), field programmable gate array (FPGA), logic gates, registers, semiconductor device, chips, microchips, chip sets, and so forth. The local interface may include, for example, one or more buses or other wired or wireless connections, controllers, buffers (caches), drivers, repeaters and receivers, etc., to allow appropriate communications between hardware components. A processor is a hardware device for executing software, particularly software stored in memory. The processor can be any custom made or commercially available processor, a central processing unit (CPU), an auxiliary processor among several processors associated with the computer, a semiconductor based microprocessor (e.g., in the form of a microchip or chip set), a macroprocessor, or generally any device for executing software instructions. A processor can also represent a distributed processing architecture. The I/O devices can include input devices, for example, a keyboard, a mouse, a scanner, a microphone, a touch screen, an interface for various medical devices and/or laboratory instruments, a bar code reader, a stylus, a laser reader, a radio-frequency device reader, etc. Furthermore, the I/O devices also can include output devices, for example, a printer, a bar code printer, a display, etc. Finally, the I/O devices further can include devices that communicate as both inputs and outputs, for example, a modulator/demodulator (modem; for accessing another device, system, or network), a radio frequency (RF) or other transceiver, a telephonic interface, a bridge, a router, etc.

[00303] Examples of software may include software components, programs, applications, computer programs, application programs, system programs, machine programs, operating system software, middleware, firmware, software modules, routines, subroutines, functions, methods, procedures, software interfaces, application program interfaces (API), instruction sets, computing code, computer code, code segments, computer code segments, words, values, symbols, or any combination thereof. A software in memory may include one or more separate programs, which may include ordered listings of executable instructions for implementing logical functions. The software in memory may include a system for identifying data streams in accordance with the present teachings and any suitable custom made or commercially available operating system (O/S), which may control the execution of other computer programs such as the system, and provides scheduling, input-output control, file and data management, memory management, communication control, etc.

[00304] According to various exemplary embodiments, one or more features of any one or more of the above-discussed teachings and/or exemplary embodiments may be performed or implemented using appropriately configured and/or programmed non-transitory machine-readable medium or article that may store an instruction or a set of instructions that, if executed by a machine, may cause the machine to perform a method and/or operations in accordance with the exemplary embodiments. Such a machine may include, for example, any suitable processing platform, computing platform, computing device, processing device, computing system, processing system, computer, processor, scientific or laboratory instrument, etc., and may be implemented using any suitable combination of hardware and/or software. The machine-readable medium or article may include, for example, any suitable type of memory unit, memory device, memory article, memory medium, storage device, storage article, storage medium and/or storage unit, for example, memory, removable or non-removable media, erasable or non-erasable media, writeable or re-writeable media, digital or analog media, hard disk, floppy disk, read-only memory compact disc (CD-ROM), recordable compact disc (CD-R), rewriteable compact disc (CD-RW), optical disk, magnetic media, magneto-optical media, removable memory cards or disks, various types of Digital Versatile Disc (DVD), a tape, a cassette, etc., including any medium suitable for use in a computer. Memory can include any one or a combination of volatile memory elements (e.g., random access memory (RAM, such as DRAM, SRAM, SDRAM, etc.)) and nonvolatile memory elements (e.g., ROM, EPROM, EEROM, Flash memory, hard drive, tape, CDROM, etc.). Moreover, memory can incorporate electronic, magnetic, optical, and/or other types of storage media. Memory can have a distributed architecture where various components are situated remote from one another, but are still accessed by

the processor. The instructions may include any suitable type of code, such as source code, compiled code, interpreted code, executable code, static code, dynamic code, encrypted code, etc., implemented using any suitable high-level, low-level, object-oriented, visual, compiled and/or interpreted programming language.

[00305] According to various exemplary embodiments, one or more features of any one or more of the above-discussed teachings and/or exemplary embodiments may be performed or implemented at least partly using a distributed, clustered, remote, or cloud computing resource.

[00306] According to various exemplary embodiments, one or more features of any one or more of the above-discussed teachings and/or exemplary embodiments may be performed or implemented using a source program, executable program (object code), script, or any other entity comprising a set of instructions to be performed. When a source program, the program can be translated via a compiler, assembler, interpreter, etc., which may or may not be included within the memory, so as to operate properly in connection with the O/S. The instructions may be written using (a) an object oriented programming language, which has classes of data and methods, or (b) a procedural programming language, which has routines, subroutines, and/or functions, which may include, for example, C, C++, Pascal, Basic, Fortran, Cobol, Perl, Java, and Ada.

[00307] According to various exemplary embodiments, one or more of the above-discussed exemplary embodiments may include transmitting, displaying, storing, printing or outputting to a user interface device, a computer readable storage medium, a local computer system or a remote computer system, information related to any information, signal, data, and/or intermediate or final results that may have been generated, accessed, or used by such exemplary embodiments. Such transmitted, displayed, stored, printed or outputted information can take the form of searchable and/or filterable lists of runs and reports, pictures, tables, charts, graphs, spreadsheets, correlations, sequences, and combinations thereof, for example.

[00308] Various additional exemplary embodiments may be derived by repeating, adding, or substituting any generically or specifically described features and/or components and/or substances and/or steps and/or operating conditions set forth in one or more of the above-described exemplary embodiments. Further, it should be understood that an order of steps or order for performing certain actions is immaterial so long as the objective of the steps or action remains achievable, unless specifically stated otherwise. Furthermore, two or more steps or actions can be conducted simultaneously so long as the objective of the steps or action remains achievable, unless specifically stated otherwise. Moreover, any one or more feature, component, aspect, step, or other characteristic

mentioned in one of the above-discussed exemplary embodiments may be considered to be a potential optional feature, component, aspect, step, or other characteristic of any other of the above-discussed exemplary embodiments so long as the objective of such any other of the above-discussed exemplary embodiments remains achievable, unless specifically stated otherwise.

[00309] Various additional exemplary embodiments may be derived by incorporating in the above described exemplary embodiments one or more of the features described in U.S. Pat. Appl. Publ. No. 2008/0228589 A1, published September 18, 2008, and U.S. Pat. Appl. Publ. No. 2004/0175733 A1, published September 9, 2004, the contents of both of which are incorporated by reference herein in their entireties.

[00310] In some embodiments, the amplified target sequences generated by the methods disclosed herein represent at least 60%, 70%, 80%, 90%, or more, of one or more exons amplified from the plurality of target sequences. In one embodiment, amplified target sequences of the present invention are about 90 to about 140 base pairs in length, about 100 to about 200 base pairs in length, about 100 to about 300 base pairs in length, or about 100 to about 400 base pairs in length. In one embodiment, the amplified target seqeunce includes the length of the forward primer and the length of the complementary reverse primer for each primer pair. In another embodiment, the amplified target sequence length includes the length of the reverse primer and the length of the complementary forward primer. In some embodiments, the length of the amplified target sequence minus the forward and reverse primer lengths is about 40 base pairs to about 350 base pairs. In some embodiments, the length of the amplified target sequences generated in the multiplex PCR reaction is substantially the same. As defined herein, "substantially the same" with respect to length of amplified target sequences generated via the methods disclosed herein refers to no more than 30% deviation in nucleotide length across the total number of amplified target sequences. In one embodiment, the percent GC content of an amplicon is less than 85%, less than 75%, less than 65 %, less than 60%, or less than 50%. In one embodiment, substantially all amplified target sequences within a reaction contain between 30% and less than 85% GC content. In one embodiment, where the nucleic acid molecules are obtained from an archived or FFPE DNA sample, the length of the amplified target sequence is typically about 100 to about 200 base pairs in length. In one embodiment, if the nucleic acid sample is derived or obtained from genomic DNA, the length of the amplified target sequence can be about 100 to about 500 base pairs in length.

[00311] In some embodiments, the amplified target sequences of the disclosed methods can be used in various downstream analysis or assays with, or without, further purification or

manipulation. For example, the amplified target sequences can be clonally amplified by techniques known in the art, such a bridge amplification or emPCR to generate a template library that can be used in next generation sequencing. In some embodiments, the amplified target sequences of the disclosed methods or the resulting template libraries can be used for single nucleotide polymorphism (SNP) analysis, genotyping or epigenetic analysis, copy number variation analysis, gene expression analysis, analysis of gene mutations including but not limited to detection, prognosis and/or diagnosis, detection and analysis of rare or low frequency allele mutations, nucleic acid sequencing including but not limited to *de novo* sequencing, targeted resequencing and synthetic assembly analysis. In one embodiment, amplified target sequences can be used to detect mutations at less than 5% allele frequency. In some embodiments, the methods disclosed herein can be used to detect mutations in a population of nucleic acids at less than 4%, 3%, 2% or at about 1% allele frequency. In another embodiment, amplified target sequences prepared as described herein can be sequenced to detect and/or identify germline or somatic mutations from a population of nucleic acid molecules.

[00312] In some embodiments, the forward and/or reverse target-specific primers in the target-specific primer pairs can be "complementary" or "substantially complementary" to the population of nucleic acid molecules. As termed herein "substantially complementary to the population of nucleic acid molecules" refers to percentage complementarity between the primer and the nucleic acid molecule to which the primer will hybridize. Generally, the term "substantially complementary" as used herein refers to at least 70% complementarity. Therefore, substantially complementary refers to a range of complementarity of at least 70% but less than 100% complementarity between the primer and the nucleic acid molecule. A complementary primer is one that possesses 100% complementarity to the nucleic acid molecule. In one embodiment, each target-specific primer pair is designed to minimize cross-hybridization to another primer (or primer pair) in the same multiple PCR reaction (i.e., reduce the prevalence of primer-dimers). In another embodiment, each target-specific primer pair is designed to minimize cross-hybridization to non-specific nucleic acid sequences in the population of nucleic acid molecules (i.e., minimize off-target hybridization). In one embodiment, each target-specific primer is designed to minimize self-complementarity, formation of hairpin structures or other secondary structures.

[00313] In some embodiments, the amplified target sequences are formed via polymerase chain reaction. Extension of target-specific primers can be accomplished using one or more DNA polymerases. In one embodiment, the polymerase can be any Family A DNA polymerase (also known as pol I family) or any Family B DNA polymerase. In some embodiments, the DNA

polymerase can be a recombinant form capable of extending target-specific primers with superior accuracy and yield as compared to a non-recombinant DNA polymerase. For example, the polymerase can include a high-fidelity polymerase or thermostable polymerase. In some embodiments, conditions for extension of target-specific primers can include 'Hot Start' conditions, for example Hot Start polymerases, such as Amplitaq Gold® DNA polymerase (Applied Biosciences), Platinum® Taq DNA Polymerase High Fidelity (Invitrogen) or KOD Hot Start DNA polymerase (EMD Biosciences). Generally, a 'Hot Start' polymerase includes a thermostable polymerase and one or more antibodies that inhibit DNA polymerase and 3'-5' exonuclease activities at ambient temperature. In some instances, 'Hot Start' conditions can include an aptamer.

[00314] In some embodiments, the polymerase can be an enzyme such as Taq polymerase (from *Thermus aquaticus*), Tfi polymerase (from *Thermus filiformis*), Bst polymerase (from *Bacillus stearothermophilus*), Pfu polymerase (from *Pyrococcus furiosus*), Tth polymerase (from *Thermus thermophilus*), Pow polymerase (from *Pyrococcus woesei*), Tli polymerase (from *Thermococcus litoralis*), Ultima polymerase (from *Thermotoga maritima*), KOD polymerase (from *Thermococcus kodakaraensis*), Pol I and II polymerases (from *Pyrococcus abyssi*) and Pab (from *Pyrococcus abyssi*). In some embodiments, the DNA polymerase can include at least one polymerase such as Amplitaq Gold ® DNA polymerase (Applied Biosciences), Stoffel fragment of Amplitaq® DNA Polymerase (Roche), KOD polymerase (EMD Biosciences), KOD Hot Start polymerase (EMD Biosciences), Deep Vent™ DNA polymerase (New England Biolabs), Phusion polymerase (New England Biolabs), Klentaq1 polymerase (DNA Polymerase Technology, Inc), Klentaq Long Accuracy polymerase (DNA Polymerase Technology, Inc), Omni KlenTaq™ DNA polymerase (DNA Polymerase Technology, Inc), Omni KlenTaq™ LA DNA polymerase (DNA Polymerase Technology, Inc), Platinum® Taq DNA Polymerase (Invitrogen), Hemo Klentaq™ (New England Biolabs), Platinum® Taq DNA Polymerase High Fidelity (Invitrogen), Platinum® *Pfx* (Invitrogen), Accuprime™ *Pfx* (Invitrogen), or Accuprime™ Taq DNA Polymerase High Fidelity (Invitrogen).

[00315] In some embodiments, the DNA polymerase can be a thermostable DNA polymerase. In some embodiments, the mixture of dNTPs can be applied concurrently, or sequentially, in a random or defined order. In some embodiments, the amount of DNA polymerase present in the multiplex reaction is significantly higher than the amount of DNA polymerase used in a corresponding single plex PCR reaction. As defined herein, the term "significantly higher" refers to an at least 3-fold greater concentration of DNA polymerase present in the multiplex PCR reaction as compared to a corresponding single plex PCR reaction.

[00316] In some embodiments, the amplification reaction does not include a circularization of amplification product, for example as disclosed by rolling circle amplification.

[00317] In some embodiments, the methods of the disclosure include selectively amplifying target sequences in a sample containing a plurality of nucleic acid molecules and ligating the amplified target sequences to at least one Adaptersadapters and/or barcode. Adapters and barcodes for use in molecular biology library preparation techniques are well known to those of skill in the art. The definitions of adapters and barcodes as used herein are consistent with the terms used in the art. For example, the use of barcodes allows for the detection and analysis of multiple samples, sources, tissues or populations of nucleic acid molecules per multiplex reaction. A barcoded and amplified target sequence contains a unique nucleic acid sequence, typically a short 6-15 nucleotide sequence, that identifies and distinguishes one amplified nucleic acid molecule from another amplified nucleic acid molecule, even when both nucleic acid molecules minus the barcode contain the same nucleic acid sequence. The use of adapters allows for the amplification of each amplified nucleic acid molecule in a uniformed manner and helps reduce strand bias. Adapters can include universal adapters or propriety adapters both of which can be used downstream to perform one or more distinct functions. For example, amplified target sequences prepared by the methods disclosed herein can be ligated to an adapter that may be used downstream as a platform for clonal amplification. The adapter can function as a template strand for subsequent amplification using a second set of primers and therefore allows universal amplification of the adapter-ligated amplified target sequence. In some embodiments, selective amplification of target nucleic acids to generate a pool of amplicons can further comprise ligating one or more barcodes and/or adapters to an amplified target seqeucne. The ability to incorporate barcodes enhances sample throughput and allows for analysis of multiple samples or sources of material concurrently. In one example, amplified target nucleic acid molecules prepared by the disclosed methods can be ligated to Ion Torrent™ Sequencing AdaptersAdapters (A and P1 Adaptersadapters, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) or Ion Torrent™ DNA Barcodes (Life Technologies, Part No. 4468654).

[00318] The methods disclosed herein are directed to the amplification of multiple target sequences via polymerase chain reaction (PCR). In some embodiments the multiplex PCR comprises hybridizing one or more target-specific primer pairs to a nucleic acid molecule, extending the primers of the target-specific primer pairs via template dependent synthesis in the presence of a DNA polymerase and dNTPs; repeating the hybridization and extension steps for sufficient time and sufficient temperature there generating a plurality of amplified target sequences. In some

embodiments, the steps of the multiplex amplification reaction method can be performed in any order.

[00319] The amount of nucleic acid material required for successful multiplex amplification can be about 1 ng. In some embodiments, the amount of nucleic acid material can be about 10 ng to about 50 ng, about 10 ng to about 100 ng, or about 1 ng to about 200 ng of nucleic acid material. Higher amounts of input material can be used, however one aspect of the disclosure is to selectively amplify a plurality of target sequence from a low (ng) about of starting material.

[00320] The multiplex PCR amplification reactions disclosed herein can include a plurality of "cycles" typically performed on a thermocycler. Generally, each cycle includes at least one annealing step and at least one extension step. In one embodiment, a mutliplex PCR amplification reaction is performed wherein target-specific primer pairs are hybridized to a target sequence; the hybridized primers are extended generating an extended primer product/nucleic acid duplex; the extended primer product/nucleic acid duplex is denatured allowing the complementary primer to hybridize to the extended primer product, wherein the complementary primer is extended to generate a plurality of amplified target sequences. In one embodiment, the methods disclosed herein have about 5 to about 18 cycles per preamplification reaction. The annealing temperature and/or annealing duration per cycle can be identical; can include incremental increases or decreases, or a combination of both. The extension temperature and/or extension duration per cycle can be identical; can include incremental increases or decreases, or a combination of both. For example, the annealing temperature or extension temperature can remain constant per cycle. In some embodiments, the annealing temperature can remain constant each cycle and the extension duration can incrementally increase per cycle. In some embodiments, increases or decreases in duration can occur in 15 second, 30 second, 1 minute, 2 minute or 4 minute increments. In some embodiments, increases or decrease in temperature can occur as 0.5, 1, 2, 3, or 4 Celsius deviations. In some embodiments, the amplification reaction can beconducted using hot-start PCR techniques. These techniques include the use of a heating step (>60°C) before polymerization begins to reduce the formation of undesired PCR products. Other techniques such as the reversible inactivation or physical separation of one or more critical reagents of the reaction, for example the magnesium or DNA polymerase can be sequestered in a wax bead, which melts as the reaction is heated during the denaturation step, releasing the reagent only at higher temperatures. The DNA polymerase can also be kept in an active state by binding to an aptamer or an antibody. This binding is disrupted at higher temperatures, releasing the functional DNA polymerase that can proceed with the PCR unhindered.

[00321] In some embodiments, the disclosed methods can optionally include destroying one or more primer-containing amplification artifacts, e.g., primer-dimers, dimer-dimers or superamplicons. In some embodiments, the destroying can optionally include treating the primer and/or amplification product so as to cleave specific cleavable groups present in the primer and/or amplification product. In some embodiments, the treating can include partial or complete digestion of one or more target-specific primers. In one embodiment, the treating can include removing at least 40% of the target specific primer from the amplification product. The cleavble treatment can include enzymatic, acid, alkali, thermal, photo or chemical activity. The cleavable treatment can result in the cleavage or other destruction of the linkages between one or more nucleotides of the primer, or between one or more nucleotides of the amplification product. The primer and/or the amplification product can optionally include one or more modified nucleotides or nucleobases. In some embodiments, the cleavage can selectively occur at these sites, or adjacent to the modified nucleotides or nucleobases. In some embodiments, the cleavage or treatment of the amplified target sequence can result in the formation of a phosphorylated amplified target sequence. In some embodiments, the amplified target sequence is phosphorylated at the 5' terminus.

[00322] In some embodiments, the template, primer and/or amplification product includes nucleotides or nucleobases that can be recognized by specific enzymes. In some embodiments, the nucleotides or nucleobases can be bound by specific enzymes. Optionally, the specific enzymes can also cleave the template, primer and/or amplification product at one or more sites. In some embodiments, such cleavage can occur at specific nucleotides within the template, primer and/or amplification product. For example, the template, primer and/or amplification product can include one or more nucleotides or nucleobases including uracil, which can be recognized and/or cleaved by enzymes such as uracil DNA glycosylase (UDG, also referred to as UNG) or formamidopyrimidine DNA glycosylase (Fpg). The template, primer and/or amplification product can include one or more nucleotides or nucleobases including RNA-specific bases, which can be recognized and/or cleaved by enzymes such as RNAseH. In some embodiments, the template, primer and/or amplification product can include one or more abasic sites, which can be recognized and/or cleaved using various proofreading polymerases or apyrase treatments. In some embodiments, the template, primer and/or amplification product can include 7,8-dihydro-8-oxoguanine (8-oxoG) nucleobases, which can be recognized or cleaved by enzymes such as Fpg. In some embodiments, one or more amplified target sequences can be partially digested by a FuPa reagent.

[00323] In some embodiments, the primer and/or amplification product includes one or more modified nucleotides including bases that bind, e.g., base pair, with other nucleotides, for example nucleotides in a complementary nucleic acid strand, via chemical linkages. In some embodiments, the chemical linkages are subject to specific chemical attack that selectively cleaves the modified nucleotides (or selectively cleaves one or more covalent linkages between the modified nucleotides and adjacent nucleotides within the primer and/or amplification product) but leaves the other nucleotides unaffected. For example, in some embodiments modified nucleotides can form disulfite linkages with other nucleotides in a complementary strand. Such disulfite linkages can be oxidized via suitable treatments. Similarly, certain modified nucleotides can base pair with other nucleotides in a complementary nucleic acid strand through linkages that can be selectively disrupted via alkali treatment. In some embodiments, the primer and/or amplification product includes one or more modified nucleotides that bind, e.g., base pair, with other nucleotides in a complementary nucleic acid strand through linkages exhibiting decreased thermal stability relative to typical base pairing linkages formed between natural bases. Such reduced-thermal stability linkages can be selectively disrupted through exposure of the primer and/or amplification product to elevated temperatures following amplification.

[00324] An exemplary embodiment is depicted in Figure 1, which depicts a schematic of degradable amplification primers. The amplification primers are bisulfite in design, with either a 5' universal forward amplification sequence linked to a 3' target-specific forward primer, or a 5' universal reverse amplification sequence linked to a 3' target-specific reverse primer. Both primers contain modified nucleotides.

[00325] In some embodiments, primers are synthesized that are complementary to, and can hybridize with, discrete segments of a nucleic acid template strand, including: a primer that can hybridize to the 5' region of the template, which encompasses a sequence that is complementary to either the forward or reverse amplification primer. In some embodiments, the forward primers, reverse primers, or both, share no common nucleic acid sequence, such that they hybridize to distinct nucleic acid sequences. For example, target-specific forward and reverse primers can be prepared that do not compete with other primer pairs within the primer pool to amplify the same nucleic acid sequence. In this example, primer pairs that do not compete with other primer pairs in the primer pool assist in the reduction of non-specific or spurious amplification products. In some embodiments, the forward and reverse primers of each primer pair are unique, in that the nucleotide sequence for each primer is non-complementary and non-identical to the other primer in the primer

pair. In some embodiments, the primer pair can differ by at least 10 %, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, or at least 90% nucleotide identity. In some embodiments, the forward and reverse primers in each primer pair are non-complementary or non-identical to other primer pairs in the primer pool or multiplex reaction. For example, the primer pairs within a primer pool or multiplex reaction can differ by at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, or at least 70% nucleotide identity to other primer pairs within the primer pool or multiplex reaction. Generally, primers are designed to minimize the formation of primer-dimers, dimer-dimers or other non-specific amplification products. Typically, primers are optimized to reduce GC bias and low melting temperatures (T_m) during the amplification reaction. In some embodiments, the primers are designed to possess a T_m of about 55°C to about 72°C. In some embodiments, the primers of a primer pool can possess a T_m of about 59°C to about 70°C, 60°C to about 68°C, or 60°C to about 65°C. In some embodiments, the primer pool can possess a T_m that does not deviate by more than 5°C.

[00326] In some embodiments, the target-specific primers do not contain a carbon-spacer or terminal linker. In some embodiments, the target-specific primers or amplified target sequences do not contain an enzymatic, magnetic, optical or fluorescent label.

[00327] The template can include a 3' region that contains the sequence for either the upstream or downstream regions surrounding a particular gene or region of interest, such that the region of interest is bracketed by a forward amplification/upstream gene-specific fusion, and a reverse amplification/downstream region of interest fusion primer. In some embodiments, an internal separator sequence can separate the template regions that can hybridize to the amplification and gene-specific primers, and this may act as a key or barcode for subsequent downstream applications such as sequencing, etc. In some embodiments, a barcode or key can be incorporated into each of the amplification products to assist with data analysis and for example, cataloging. In some embodiments, the barcodes can be Ion Torrent™ DNA barcodes (Life Technologies).

[00328] In some embodiments, the primer includes a sufficient number of modified nucleotides to allow functionally complete degradation of the primer by the cleavage treatment, but not so many as to interfere with the primer's specificity or functionality prior to such cleavage treatment, for example in the amplification reaction. In some embodiments, the primer includes at least one modified nucleotide, but no greater than 75% of nucleotides of the primer are modified.

[00329] In some embodiments, multiple different primers including at least one modified nucleotide can be used in a single amplification reaction. For example, multiplexed primers including modified nucleotides can be added to the amplification reaction mixture, where each primer (or set of primers) selectively hybridizes to, and promotes amplification of different target nucleic acid molecules within the nucleic acid population. In some embodiments, different primer combinations can be added to the amplification reaction at plexy of at least about 24, 96, 384, 768, 1000, 2000, 3000, 6000 or 10000, or more (where "plexy" indicates the total number of different targets that can theoretically be amplified in a sequence-specific manner in the amplification reaction). In some embodiments, the modified primers contain at least one modified nucleotide near or at the termini of the primer. In some embodiments, the modified primers contain two or more modified nucleotides within the primer sequence. In an exemplary embodiment, the primer sequence contains a uracil near, or at, the termini of the primer sequence. For the purposes of this disclosure "near" or "at the termini" of the primer sequences refers up to 10 nucleotides from the termini of the primer sequence. In some embodiments, the primer sequence contains a uracil located at, or about, the center nucleotide position of the primer sequence. For the purposes of this disclosure "at, or about the center nucleotide position of the primer sequence" refers to the incorporation of a uracil moiety at the center nucleotide of the primer sequence or within eight nucleotides, in either a 3' or 5' direction flanking the center nucleotide. In one embodiment, the target-specific primer sequence can contain a modified nucleocbase at or about the center nucleotide position and contain a modified nucleobase at the 3' and/or 5' terminus. In some embodiments, the length of the forward or reverse primer sequence can be about 15 to about 40 bases in length. In some embodiments, the T_m of the primer sequence used in the multiplex reaction can be about 55°C to about 72°C. In some embodiments, the primer pairs are designed to amplify sequences from the target nucleic acid molecules or amplicons that are about 100 base pairs to about 500 base pairs in length.

[00330] In some embodiments, the amplification reactions are conducted in parallel within a single reaction phase (for example, within the same amplification reaction mixture within a single tube). In some instances, an amplification reaction can generate a mixture of products including both the intended amplicon product as well as unintended, unwanted, nonspecific amplification artifacts such as primer-dimers. Post amplification, the reactions are then treated with any suitable agent that will selectively cleave or otherwise selectively destroy the nucleotide linkages of the modified nucleotides within the excess unincorporated primers and the amplification artifacts without cleaving or destroying the specification amplification products. For example, the primers can include uracil-

containing nucleobases that can be selectively cleaved using UNG/UDG (optionally with heat and/or alkali). In some embodiments, the primers can include uracil-containing nucleotides that can be selectively cleaved using UNG and Fpg. In some embodiments, the cleavage treatment includes exposure to oxidizing conditions for selective cleavage of dithiols, treatment with RNAseH for selective cleavage of modified nucleotides including RNA-specific moieties (e.g., ribose sugars, etc.), and the like. This cleavage treatment can effectively fragment the original amplification primers and non-specific amplification products into small nucleic acid fragments that include relatively few nucleotides each. Such fragments are typically incapable of promoting further amplification at elevated temperatures. Such fragments can also be removed relatively easily from the reaction pool through the various post-amplification cleanup procedures known in the art (e.g., spin columns, NaEtOH precipitation, etc).

[00331] In some embodiments, amplification products following cleavage or other selective destruction of the nucleotide linkages of the modified nucleotides are optionally treated to generate amplification products that possess a phosphate at the 5' termini. In some embodiments, the phosphorylation treatment includes enzymatic manipulation to produce 5' phosphorylated amplification products. In one embodiment, enzymes such as polymerases can be used to generate 5' phosphorylated amplification products. For example, T4 polymerase can be used to prepare 5' phosphorylated amplicon products. Klenow can be used in conjunction with one or more other enzymes to produce amplification products with a 5' phosphate. In some embodiments, other enzymes known in the art can be used to prepare amplification products with a 5' phosphate group. For example, incubation of uracil nucleotide containing amplification products with the enzyme UDG, Fpg and T4 polymerase can be used to generate amplification products with a phosphate at the 5' termini. It will be apparent to one of skill in the art that other techniques, other than those specifically described herein, can be applied to generate phosphorylated amplicons. It is understood that such variations and modifications that are applied to practice the methods, systems, kits, compositions and apparatuses disclosed herein, without resorting to undue experimentation are considered within the scope of the disclosure.

[00332] In some embodiments, primers that are incorporated in the intended (specific) amplification products, these primers are similarly cleaved or destroyed, resulting in the formation of "sticky ends" (e.g., 5' or 3' overhangs) within the specific amplification products. Such "sticky ends" can be addressed in several ways. For example, if the specific amplification products are to be cloned, the overhang regions can be designed to complement overhangs introduced into the cloning

vector, thereby enabling sticky ended ligations that are more rapid and efficient than blunt ended ligations. Alternatively, the overhangs may need to be repaired (as with several next-generation sequencing methods). Such repair can be accomplished either through secondary amplification reactions using only forward and reverse amplification primers (in the embodiment shown in Figure 1, this corresponds to A and P1 primers) comprised of only natural bases. In this manner, subsequent rounds of amplification rebuild the double-stranded templates, with nascent copies of the amplicon possessing the complete sequence of the original strands prior to primer destruction. Alternatively, the sticky ends can be removed using some forms of fill-in and ligation processing, wherein the forward and reverse primers are annealed to the templates. A polymerase can then be employed to extend the primers, and then a ligase, optionally a thermostable ligase, can be utilized to connect the resulting nucleic acid strands. This could obviously be also accomplished through various other reaction pathways, such as cyclical extend-ligation, etc. In some embodiments, the ligation step can be performed using one or more DNA ligases.

[00333] The amplification reaction can include any reaction that increases the copy number of a nucleic acid molecule, optionally in a cyclical fashion, and can include without limitation isothermal amplification (for example, rolling circle amplification or isothermal amplification as described in US Provisional Application Nos. 61/424,599, 61/445,324 and 61/451,919, hereby incorporated by reference in their entireties), amplification using thermocycling, and the like.

[00334] In some embodiments, the disclosure generally relates to methods for single-tube multiplex PCR. In some embodiments, the method for single-tube multiplex PCR can include target-specific or exon-specific primers. In some embodiments, the exon-specific or target-specific primers can include at least one uracil nucleotide. In some embodiments, single-tube multiplex PCR can include selective amplification of at least 1000, 2000, 3000, 4000, 5000, 6000 or more target nucleic acid molecules using target-specific or exon-specific uracil based primers.

[00335] In some embodiments, the disclosure relates generally to methods for generating a target-specific or exon-specific amplicon library. In some embodiments, the amplicon library generated using target-specific or exon-specific primers can be associated with mutations of human cancers. In some embodiments, the mutations can be in the KRAS, BRAF and/or EGFR genes. In some embodiments, the amplicon library can be generated from genomic DNA or formalin-fixed, paraffin-embedded (FFPE) tissue. In some embodiments, the amplicons of the amplicon library prepared using the methods disclosed herein can be about 100 to about 300 base pairs in length, about 100 to about 250 base pairs in length, about 120 to about 220 base pairs in length or about 135

to about 205 base pairs in length. In some embodiments, the amplicon library can be prepared using primer pairs that are targeted to cancer specific mutations. In some embodiments, the primer pairs can be directed to non-cancer related mutations, such as inherited diseases, e.g., cystic fibrosis and the like. In some embodiments, the primer pairs can be used to generate amplicons that once sequenced by any sequencing platform, including semi-conductor sequencing technology can be used to detect genetic mutations such as inversion, deletions, point mutations and variations in copy number.

[00336] In some embodiments, the primer pairs used to produce an amplicon library can result in the amplification of target-specific nucleic acid molecules possessing one or more of the following metrics: greater than 97% target coverage at 20x if normalized to 100x average coverage depth; greater than 97% of bases with greater than 0.2x mean; greater than 90% base without strand bias; greater than 95% of all reads on target; greater than 99% of bases with greater than 0.01x mean; and greater than 99.5% per base accuracy.

[00337] In some embodiments, the amplicon library can be used to detect and/or identify known mutations or *de novo* mutations in a sample.

[00338] In some embodiments, the amplicon library prepared using target–specific primer pairs can be used in downstream enrichment applications such as emulsion PCR or bridge PCR. In some embodiments, the amplicon library can be used in an enrichment application and a sequencing application. For example, an amplicon library can be sequenced using any suitable DNA sequencing platform. In some embodiments, an amplicon library can be sequenced using an Ion Torrent PGM Sequencer (Life Technologies). In some embodiments, a PGM sequencer can be coupled to server that applies parameters or software to determine the sequence of the amplified target nucleic acid molecules. In some embodiments, the amplicon library can be prepared, enriched and sequenced in less than 24 hours. In some embodiments, the amplicon library can be prepared, enriched and sequenced in approximately 9 hours. In some embodiments, an amplicon library can be a paired library, that is, a library that contains amplicons from a tumor sample and amplicons from a non-diseased sample. Each pair can be aligned, to detect and/or identify mutations present in the target nucleic acid molecules.

[00339] In some embodiments, methods for generating an amplicon library can include: amplifying genomic DNA targets using exon-specific or target-specific primers to generate amplicons; purifying the amplicons from the input DNA and primers; phosphorylating the amplicons; ligating Adaptersadapters to the phosphorylated amplicons; purifying the ligated

amplicons; nick-translating the amplified amplicons; and purifying the nick-translated amplicons to generate the amplicon library. In some embodiments, additional amplicon library manipulations can be conducted following the step of amplification of genomic DNA targets to generate the amplicons. In some embodiments, any combination of additional reactions can be conducted in any order, and can include: purifying; phosphorylating; ligating Adaptersadapters; nick-translating; amplification and/or sequencing. In some embodiments, any of these reactions can be omitted or can be repeated. It will be readily apparent to one of skill in the art that the method can repeat or omit any one or more of the above steps. It will also be apparent to one of skill in the art that the order and combination of steps may be modified to generate the required amplicon library, and is not therefore limited to the exemplary methods provided.

[00340] A phosphorylated amplicon can be joined to an adapter to conduct a nick translation reaction, subsequent downstream amplification (e.g., template preparation), or for attachment to particles (e.g., beads), or both. For example, an adapter that is joined to a phosphorylated amplicon can anneal to an oligonucleotide capture primer which is attached to a particle, and a primer extension reaction can be conducted to generate a complementary copy of the amplicon attached to the particle or surface, thereby attaching an amplicon to a surface or particle. AdaptersAdapters can have one or more amplification primer hybridization sites, sequencing primer hybridization sites, barcode sequences, and combinations thereof. In some embodiments, amplicons prepared by the methods disclosed herein can be joined to one or more Ion Torrent™ compatible Adaptersadapters to construct an amplicon library. Amplicons generated by such methods can be joined to one or more Adaptersadapters for library construction to be compatible with a next generation sequencing platform. For example, the amplicons produced by the teachings of the present disclosure can be attached to Adaptersadapters provided in the Ion Fragment Library Kit (Life Technologies, Catalog No. 4466464).

[00341] In some embodiments, amplification of genomic DNA targets (such as high molecular weight DNA) or FFPE samples can be conducted using a 2x AmpliSeq Hi Fi Master Mix. In some embodiments, the AmpliSeq Hi Fi Master Mix can include glycerol, dNTPs, and a DNA polymerase, such as Platinum® Taq DNA polymerase High Fidelity. In some embodiments, the 2x AmpliSeq Hi Fi Master Mix can further include at least one of the following: a preservative, magnesium sulfate, tris-sulfate and/or ammonium sulfate.

[00342] In some embodiments, amplification of genomic DNA targets (such as high molecular weight DNA) or FFPE samples can be conducted using a 5x Ion AmpliSeq Hi Fi Master

Mix. In some embodiments, the 5x Ion AmpliSeq Hi Fi Master Mix can include glycerol, dNTPs, and a DNA polymerase such as Platinum® Taq DNA polymerase High Fidelity. In some embodiments, the 5x Ion AmpliSeq Hi Fi Master Mix can further include at least one of the following: a preservative, magnesium chloride, magnesium sulfate, tris-sulfate and/or ammonium sulfate.

[00343] In some embodiments, phosphorylation of the amplicons can be conducted using a FuP reagent. In some embodiments, the FuP reagent can include a DNA polymerase, a DNA ligase, at least one uracil cleaving or modifying enzyme, and/or a storage buffer. In some embodiments, the FuP reagent can further include at least one of the following: a preservative and/or a detergent.

[00344] In some embodiments, phosphorylation of the amplicons can be conducted using a FuPa reagent. In some embodiments, the FuPa reagent can include a DNA polymerase, at least one uracil cleaving or modifying enzyme, an antibody and/or a storage buffer. In some embodiments, the FuPa reagent can further include at least one of the following: a preservative and/or a detergent. In some embodiments, the antibody is provided to inhibit the DNA polymerase and 3'-5' exonuclease activities at ambient temperature.

[00345] In some embodiments, the amplicon library produced by the teachings of the present disclosure are sufficient in yield to be used in a variety of downstream applications including the Ion Xpress™ Template Kit using an Ion Torrent™ PGM system (e.g., PCR-mediated addition of the nucleic acid fragment library onto Ion Sphere™ Particles)(Life Technologies, Part No. 4467389). For example, instructions to prepare a template library from the amplicon library can be found in the Ion Xpress Template Kit User Guide (Life Technologies, Part No. 4465884), hereby incorporated by reference in its entirety. Instructions for loading the subsequent template library onto the Ion Torrent™ Chip for nucleic acid sequencing are described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated by reference in its entirety. In some embodiments, the amplicon library produced by the teachings of the present disclosure can be used in paired end sequencing (e.g., paired-end sequencing on the Ion Torrent™ PGM system (Life Technologies, Part No. MAN0006191), hereby incorporated by reference in its entirety.

[00346] It will be apparent to one of ordinary skill in the art that numerous other techniques, platforms or methods for clonal amplification such as wildfire PCR and bridge amplification can be used in conjunction with the amplified target seqeucnes of the present disclosure. It is also envisaged that one of ordinary skill in art upon further refinement or optimization of the conditions provided

herein can proceed directly to nucleic acid sequencing (for example using the Ion Torrent PGM™ or Proton™ sequencers, Life Technologies) without performing a clonal amplification step.

[00347] In some embodiments, at least one of the amplified targets sequences to be clonally amplified can be attached to a support or particle. The support can be comprised of any suitable material and have any suitable shape, including, for example, planar, spheroid or particulate. In some embodiments, the support is a scaffolded polymer particle as described in U.S. Published App. No. 20100304982, hereby incorporated by reference in its entirety.

[00348] In some embodiments, nucleic acid sequencing of the amplified target sequences produced by the teachings of this disclosure include *de novo* sequencing or targeted resequencing. In some embodiments, nucleic acid sequencing further includes comparing the nucleic acid sequencing results of the amplified target sequences against a reference nucleic acid sample. In some embodiments, the reference sample can be normal tissue or well documented tumor sample. In some embodiments, nucleic acid sequencing of the amplified target sequences further includes determining the presence or absence of a mutation within the nucleic acid sequence. In some embodiments, the method further includes correlating the presence of a mutation with drug susceptibly, prognosis of treatment and/or organ rejection. In some embodiments, nucleic acid sequencing includes the identification of genetic markers associated with cancer and/or inherited diseases. In some embodiments, nucleic acid sequencing includes the identification of copy number variation in a sample under investigation.

[00349] In some embodiments, a kit is provided for amplifying multiple target sequences from a population of nucleic acid molecules in a single reaction. In some embodiments, the kit includes a plurality of target-specific primer pairs containing one or more cleavable groups, one or more DNA polymerases, a mixture of dNTPs and at least one cleaving reagent. In one embodiment, the cleavable group can be 8-oxo-deoxyguanosine, deoxyuridine or bromodeoxyuridine. In some embodiments, the at least one cleaving reagent includes RNaseH, uracil DNA glycosylase, Fpg or alkali. In one embodiment, the cleaving reagent can be uracil DNA glycosylase. In some embodiments, the kit is provided to perform multiplex PCR in a single reaction chamber or vessel. In some embodiments, the kit includes at least one DNA polymerase, which can be a thermostable DNA polymerase. In some embodiments, the concentration of the one or more DNA polymerases is present in a 3-fold excess as compared to a single PCR reaction. In some embodiments, the final concentration of each target-specific primer pair is present at about 25 nM to about 50 nM. In one embodiment, the final concentration of each target-specific primer pair can be present at a

concentration that is 50% lower than conventional single plex PCR reactions. In some embodiments, the kit provides amplification of at least 100, 500, 1000, 3000, 6000, 10000, 12000, or more, target sequences from a population of nucleic acid molecules in a single reaction chamber.

[00350] In some embodiments, the kit further comprises one or more adapters, barcodes, and/or antibodies.

[00351] The following description of various exemplary embodiments is exemplary and explanatory only and is not to be construed as limiting or restrictive in any way. Other embodiments, features, objects, and advantages of the present teachings will be apparent from the description and accompanying drawings, and from the claims.

[00352] Although the present description described in detail certain exemplary embodiments, other embodiments are also possible and within the scope of the present invention. Variations and modifications will be apparent to those skilled in the art from consideration of the specification and figures and practice of the teachings described in the specification and figures, and the claims.

[00353]

[00354] **Examples**

[00355] **Example 1. Library Preparation**

[00356] **PCR Amplify Genomic DNA Targets**

[00357] A multiplex polymerase chain reaction was performed to amplify 384 individual amplicons across a genomic DNA sample. A pool of greater than 32,000 primers was originally developed covering more than 300 genes. A representative list of genes that were incorporated for investigation while synthesizing the initial primer pool is provided in Table 1. A sub-set of the primer pool known as "HSMv12" was used to generate the data presented in Figure 5 (primers from HSMv12 are presented in Table 2). Each primer pair in the primer pool was designed to contain at least one uracil nucleotide near the terminus of each forward and reverse primer. Each primer pair was also designed to selectively hybridize to, and promote amplification of a specific gene or gene fragment of the genomic DNA sample.

[00358] To a single well of a 96-well PCR plate was added 5 microliters of HSMv12 Primer Pool containing 384 primer pairs at a concentration of 15 μM in TE, 10-50 ng genomic DNA and 10 microliters of an amplification reaction mixture (2x AmpliSeq HiFi Master Mix) that can include glycerol, dNTPs, and Platinum® Taq High Fidelity DNA Polymerase (Invitrogen, Catalog No. 11304) to a final volume of 20 microliters with DNase/RNase Free Water (Life Technologies, CA, Part No. 600004).

[00359] The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the preamplified amplicon library.

[00360] An initial holding stage was performed at 98°C for 2 minutes, followed by 16 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 4 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the purification step outlined below. A schematic of an exemplary library amplification process is shown in FIG. 2.

[00361] **Purify the Amplicons from input DNA and Primers**

[00362] Two rounds of Agencourt® AMPure® XP Reagent (Beckman Coulter, CA) binding, wash, and elution at 0.6x and 1.2x volume ratios were found to remove genomic DNA and unbound or excess primers. The amplification and purification step outlined herein produces amplicons of about 100 bp to about 600 bp in length.

[00363] In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the preamplified amplicon library (20 microliters) was combined with 12 microliters (0.6x volumes) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the preamplified amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00364] The tube containing the sample was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was transferred to a new tube, where 24 microliters (1.2x volume) of AgenCourt® AMPure® XP beads (Beckman Coulter, CA) were added to the supernatant. The mixture was pipetted to ensure the bead suspension mixed with the preamplified amplicon library. The sample was then pulse-spin and incubated at room temperature for 5 minutes. The tube containing the sample was placed on the magnetic rack for 2 minutes to capture the beads. Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. The desired preamplified amplicon library was now bound to the beads. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was

removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00365] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of DNase/RNase Free Water was added (Life Technologies, CA, Part No. 600004). The tube was vortexed and pipetted to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the eluted DNA was transferred to a new tube.

[00366] **Phosphorylate the Amplicons**

[00367] To the eluted DNA (~ 20 microliters), 3 microliters of DNA ligase buffer (Invitrogen, Catalog No. 15224041), 2 microliters dNTP mix, and 2 microliters of FuP reagent were added. The reaction mixture was mixed thoroughly to ensure uniformity and incubated at 37°C for 10 minutes.

[00368] **Ligate Adpaters to the Amplicons and Purify the Ligated Amplicons**

[00369] After incubation, the reaction mixture proceeded directly to a ligation step. Here, the reaction mixture now containing the phosphorylated amplicon library was combined with 1 microliter of A/P1 Adaptersadapters (20 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 1 microliter of DNA ligase (sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), and incubated at room temperature for 30 minutes.

[00370] After the incubation step, 52 microliters (1.8x sample volume) of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was pipetted thoroughly to mix the bead suspension with the ligated DNA. The mixture was pulse-spin and incubated at room temperature for 5 minutes. The samples underwent another pulse-spin and were placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for two minutes. After the solution had cleared, the supernatant was discarded. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00371] The pellet was resuspended in 20 microliters of DNase/RNase Free Water (Life Technologies, CA, Part No. 600004) and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the ligated DNA was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00372] **Nick Translate and Amplify the Amplicon Library and Purify the Library**

[00373] The ligated DNA (~20 microliters) was combined with 76 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 4 microliters of Library Amplification Primer Mix (5 μM each)(Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), the mixture was pipetted thoroughly to ensure a uniformed solution. The solution was applied to a single well of a 96-well PCR plate and sealed. The plate was loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00374] A nick-translation was performed at 72°C for 1 minute, followed by an enzyme activation stage at 98°C for 2 minutes, followed by 5-10 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00375] In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the final amplicon library (~100 microliters) was combined with 180 microliters (1.8x sample volume) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the final amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00376] The tube containing the final amplicon library was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. Without removing the tube from the magnetic rack, 400 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded.

Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00377] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of Low TE was added (Life Technologies, CA, Part No. 602-1066-01). The tube was pipetted and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the final amplicon library was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00378] Assess the Library Size Distribution and Determine the Template Dilution Factor

[00379] The final amplicon library was quantitated to determine the library dilution (Template Dilution Factor) that results in a concentration within the optimized target range for Template Preparation (e.g., PCR-mediated addition of library molecules onto Ion Sphere™ Particles). The final amplicon library is typically quantitated for downstream Template Preparation procedure using an Ion Library Quantitation Kit (qPCR) (Life Technologies, Part No. 4468802) and/or a Bioanalyzer™ (Agilent Technologies, Agilent 2100 Bioanalyzer) to determine the molar concentration of the amplicon library, from which the Template Dilution Factor is calculated. For example, instructions to determine the Template Dilution Factor by quantitative real-time PCR (qPCR) can be found in the Ion Library Quantitation Kit User Guide (Life Technologies, Part No. 4468986), hereby incorporated by reference in its entirety.

[00380] In this example, 1 microliter of the final amplicon library preparation was analyzed on the 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626) to generate peaks in the 135-205 bp size range and at a concentration of about 5 x 10^9 copies per microliter.

[00381] Proceed to Template Preparation

[00382] An aliquot of the final library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded

onto an Ion 314™ Chip (Life Technologies, Part No. 4462923) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety. The data obtained from this example is provided in Figure 5.

[00383] **Example 2. Optimizing multiplex reactions to minimize GC bias**

[00384] This example demonstrates that optimizing multiplex PCR reactions performed under the guidance of the exemplary library amplification process described in Example 1 help to minimize GC bias.

[00385] In this example, a low-plex sample containing 94 primer pairs of target-specific primers and a high-plex sample containing 380 primer pairs of target-specific primers were prepared from across the human genome. Each low-plex and high plex sample was subjected to library amplification as described in Example 1. The melting temperature of amplicon products was observed to correlate with GC content of the amplicon assay (FIG. 4). The high multiplex (384-plex) sample with high GC content (i.e., 80%) was observed to have a higher melting temperature than the corresponding 94-plex sample (FIG. 4). Additionally, high-plex samples with highest GC content (75% and 80%) were observed to possess a single predominant peak, the amplicon product (connected to X-axis via dotted line), in contrast to other non-specific amplification products (observed as additional peaks and noise across the X-axis). The low-plex samples containing highest GC content (75% and 80%) were found to form multiple peaks along the X-axis suggesting the formation of a substantial amount of non-specific amplification products in addition to the desired amplicons. This example demonstrates that high-multiplex PCR reactions (394-plex) can be successfully optimized, for example through primer design, to increase the melting temperature of the desired amplicon product, increase the amount of amplicon specific product generated, and decrease the formation of amplification artifacts.

[00386] **Example 3. Optimizing primer design to reduce non-specific amplification**

[00387] This example demonstrates that target-specific primers containing modified nucleotides generated substantially fewer primer-dimers than a corresponding non-modified primer pool. In this example, a population of non-modified primer pairs were prepared using conventional methods and subjected to the library amplification process as described in Example 1. A

corresponding primer set containing modified nucleotides were prepared and amplified as described in Example 1. The amount of amplicon product and non-specific amplification product generated for each primer pool was compared. The amount of primer-dimers observed in the non-modified primer pool was found to greatly exceed the amount of primer-dimers in the corresponding modified primer pool (FIGS. 3A and 3B). The production of amplification artifacts can cause significant, if not permanent, amplification issues in downstream amplification events such as those commonly used in next-generating sequencing assays. The use of modified primers as disclosed herein can be used to alleviate these issues and decrease the output of amplification artifacts per multiplex reaction.

[00388] Appendix A discloses the general state of the art for traditional multiplex PCR methods and highlights some of the disadvantages of these methods. Appendix A also discloses some of the high priority genes initially evaluated as targets for the HSM (hotspot mutation panel). Appendix A provides a schematic outlining the workflow of the multiplex PCR methods disclosed herein. The Appendix also provides a graph showing a reduction in non-specific amplification products using the methods and target-specific primers according to the disclosure as compared to standard multiplex primers (without a cleavable group). Appendix A also describes an exemplary method for obtaining DNA from an FFPE sample, for example using an Epicentre Quick Extract protocol. Results from studies performed using the exemplary methods and target-specific primers disclosed herein using Ion Torrent 314, 316, and 318 chips were performed generating exemplary data regarding number of reads, coverage and total number of amplicons amenable to each chip type are provided in Appendix A.

[00389] **Example 4. Generation of a 384-plex (multiplex) PCR reaction**

[00390] In this example, a multiplex polymerase chain reaction was performed to amplify 384 amplicons across genomic DNA. A primer pool containing modified forward and reverse primer pairs was cycled with genomic DNA and subjected to library amplification as described in Example 1. The data obtained from 3 individual runs on an Ion Torrent PGM™ Sequencer was averaged and is presented in FIG. 5. The data shows an average read rate of 1000 per amplicon.

[00391] **Example 5. Effect of forward and reverse primers on the coverage of a 384-plex multiplex PCR reaction**

[00392] In this example, a multiplex polymerase chain reaction was performed to amplify 411 amplicons across genomic DNA. The primer pool for the amplification reaction contained modified

forward and reverse primers and was subjected to library amplification as described in Example 1. The data obtained from a single run on an Ion Torrent PGM™ Sequencer shows the average read rate of about 400 for both the reverse and forward modified primers (FIGS. 6A and 6B).

[00393] **Example 6. Reproducibility of 384-multiplex reactions**

[00394] In this example, a multiplex polymerase chain reaction was performed to amplify 384 amplicons across genomic DNA. The primer pool contained modified forward and reverse primer pairs and was subjected to library amplification as described in Example 1. The data obtained from 7 individual runs on the Ion Torrent PGM™ Sequencer was averaged and is presented in FIG. 7. The data shows an average read rate of about 400 per amplicon.

[00395] **Example 7. Reproducibility of 411-multiplex reactions**

[00396] In this example, a multiplex polymerase chain reaction was performed to amplify 411 amplicons across genomic DNA. The primer pool contained modified forward and reverse primer pairs and was subjected to library amplification as described in Example 1. The data obtained from 7 individual runs on the Ion Torrent PGM™ Sequencer was averaged and is presented in FIG. 8. The data shows an average read rate of about 400 per amplicon.

[00397] **Example 8. FFPE samples as amendable substrates for low multiplex PCR**

[00398] In this example, a multiplex polymerase chain reaction was performed to amplify 96 amplicons from a Fresh-Frozen Paraffin-Embedded (FFPE) sample. Fresh-Frozen and FFPE samples are often problematic for amplification processes due to the small amount of DNA that can be extracted from such samples. Additionally, because of the harsh chemical treatment required to preserve these samples, the quality of DNA extracted from such a sample is generally very poor. DNA was extracted from a FFPE sample and loaded onto an agarose gel for visualization (lanes 1 and 3) or subjected to multiplex PCR and library amplification as described in Example 1 and then loaded onto the agarose gel for visualization (lanes 2 and 4). A 96-plex PCR reaction and library amplification was performed on 10 ng of FFPE DNA as described in Example 1. FIG. 9 shows a photograph of the agarose electrophoresis gel including FFPE DNA prior to and after library amplification as described in Example 1.

[00399] **Example 9. FFPE samples as amenable substrates for high multiplex PCR**

[00400] In this example, a multiplex polymerase chain reaction was performed to amplify 384 amplicons from a Fresh-Frozen Paraffin-Embedded (FFPE) sample. As discussed in Example 8, Fresh-Frozen and FFPE samples are often problematic for amplification due to low extracted DNA quantity and quality. In this example, 10 ng of DNA was extracted from a FFPE sample and subjected to a 384-plex PCR reaction and library amplification as described by Example 1. The data obtained from the Ion Torrent PGM™ Sequencer was averaged and is presented in FIG. 10. The data shows an average read rate of about 400 per amplicon. Further analysis of the read rate for some of the modified forward and reverse primer pairs used in the 384-plex reaction is presented in FIGS. 11A and 11B.

[00401] **Example 10. Detection of variants in control mix of KRAS codon 12 and codon 13 mutants**

[00402] In this example, a sample of DNA containing spiked amounts of mutations of the KRAS gene at codon 12 and codon 13 were provided as a blind test sample. The sample was amplified using target-specific modified primer pairs developed for the KRAS gene. The primer pool and samples were amplified as described in Example 1. The amplified library was prepared as a template and enriched. The enriched template was applied to an Ion 314™ Chip and analyzed using an Ion Torrent PGM™ Sequencer as described in Example 1. The data from 3 individual runs was averaged and is provided as FIG. 12. The amplicon products generated during the library amplification process correspond to the expected level of mutations present in the control DNA sample for the KRAS gene at codon 12 and codon 13.

[00403] **Example 11. Resequencing the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) gene coding region**

[00404] The CFTR protein is encoded by the CFTR gene which is approximately 200 kbp, spanning 27 exons. CFTR is an ABC transporter-class ion channel that transports chloride and thiocyanate ions across epithelial cell membranes. Mutations of the CFTR gene affect functioning of the chloride ion channels in these cell membranes, leading to cystic fibrosis and congenital absence of the vas deferens. As a consequence, a male carrier of the mutation in the CFTR gene can be infertile so the detection of the defect is key in IVD considerations.

[00405] In this example, genomic DNA (gDNA) was obtained containing mutations of the CFTR gene. The gDNA was prepared for library amplification, template preparation and applied to

Ion Torrent 314™ Chip as described in Example 1. Over 8947 bases were amplified during the multiplex PCR reaction. The resulting amplicon library contained 34 amplicons with an average amplicon length of 104 bp. Sequence analysis of the amplicon library was conducted against the CFTR gene sequence reference: NCBI gi|287325315|ref|NG_016465.1|, 195703 bp

[00406] The generated amplicon library was used to evaluate detection of the CFTR gene mutations in the sample. It was found that the library amplification process detected and identified 5 point mutations and 1 insertion/deletion at low coverage (4,001 reads)(FIG. 13). The naming system for the 6 mutations is as follows:

Naming system: CFMD (UMD)

c.869+11C>T (1001+ 11C/T)

c.1408A>G (M470V)

c.2562T>G (2694T/G)

c.4389G>A (4521G/A)

c.1-8G>C (125G/C)

c.1521_1523delCTT (ΔF508)

[00407] Most resequencing assays are based on amplicons that are greater than 100 bp. This example demonstrates the applicability and amenability of the library amplification process exemplified in Example 1, to generate amplicons of a length necessary for resequencing assays. The example also shows the accuracy of the Ion Torrent PGM™ Sequencer to correctly identify point mutations and insertions/deletion mutations in a given sample.

[00408] **Example 12. Generation of target-specific primers**

Table 2 provides a list of target-specific forward and reverse uracil containing primers that were used in the above examples to amplify target-specific regions of gDNA or DNA extracted from samples, such as FFPE samples. Table 2 provides the chromosome location of each primer pair, the nucleotide sequence of each forward and reverse primer in each primer pair. Table 2 also provides the coordinates of the 5' end of the upstream/forward primer, the length of each amplicon, the corresponding amplicon nucleotide sequence, the length of each forward and reverse primer, and the T_m for each forward or reverse primer. Tables 3a-3d also provide a list of distinct target-specific forward and reverse primer pairs that were used in example 13 to amplify target-specific regions of gDNA or DNA extracted from FFPE samples from the genes of Table 1 that are associated with cancer. The following primer pair was also included for coverage of a mutation in the AKT1 gene

(c.49G>A). Forward primer: GCCGCCAGGUCTTGATGUA and reverse primer: GCACAUCTGTCCUGGCACA.

[00409] **Example 13. Alternate Library Protocol**

[00410] **PCR Amplify Genomic DNA Targets**

[00411] In this example, a multiplex polymerase chain reaction was performed to amplify multiple individual amplicons across a genomic DNA sample or FFPE sample. A representative list of genes associated with cancers that were incorporated for investigation while synthesizing the primer pool is provided in Table 1. Each primer pair in the primer pool was designed to contain at least one uracil nucleotide in each of the forward and reverse primer (Tables 3a-3d). Each primer pair was also designed to selectively hybridize to, and promote amplification of a specific gene or gene fragment of the genomic DNA sample to reduce formation of non-specific amplification products.

[00412] To a single well of a 96-well PCR plate was added 4 microliters of 5X Primer Pool (containing the primer pairs) at a concentration of 250nm each in TE, 10 ng of genomic DNA and 10 microliters of an amplification reaction mixture (2x Stoffel HiFi Master Mix) that can include glycerol, dNTPs and Stoffel fragment of Amplitaq® DNA Polymerase (Invitrogen, Catalog No. N8080038) to a final volume of 20 microliters with nuclease free water (Life Technologies, CA, Part No. 600004).

[00413] The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile to generate the preamplified amplicon library. Variation to the number of cycles was performed based on the total plexy of the reaction mixture under investigation. For example, a plexy of 48-96 was run for 17 cycles; a plexy of 97-192 was run for 16 cycles; a plexy of 193-384 was run for 15 cycles; a plexy of 385-768 was run for 14 cycles; a plexy of 769-1536 was run for 13 cycles. Additionally, for reaction mixtures containing barcodes or pooled reaction mixtures the number of cycles was lowered by one or more additional cycles. For example, 2-3 barcodes per sample were subtracted by one cycle; 4-8 barcodes per sample were subtracted by 2 cycles, and 9-16 barcodes were subtracted by 3 cycles. An initial holding stage was performed at 99°C for 2 minutes, followed by X cycles (as determined above) of denaturing at 99°C for 15 seconds and an annealing and extending stage at 60°C for 4 minutes. After cycling, the

preamplified amplicon library was held at 4°C until proceeding to the digestion and phosphorylation step outlined below.

[00414] Digest/Phosphorylate/Heat Kill the Amplicons

[00415] To the preamplified library (~ 20 microliters), 2 microliters of FuPa reagent was added. Typically, the FuPa reagent comprises one or more uracil degradable enzymes such as UDG, FPG and the like, a DNA polymerase such as Pol I, T4PNK, Klenow and the like, and an antibody such as an anti-Taq antibody. In this example, the relative amount of each enzymatic component in the FuPa reagent was 1:1:1:1 but can be varied according to the number of required cycles, variations to the temperature profile, etc., as can be determined by one of ordinary skill in the art. The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 37°C for 5 minutes, followed by 55°C for 10 minutes and then 60°C for 20 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the ligation/nick translation step outlined below.

[00416] Ligate Adpaters to the Amplicons and Nick Translate

[00417] After phosphorylation, the amplicon preamplification library (~22 µl) proceeded directly to a ligation step. In this example, the preamplification library now containing the phosphorylated amplicon library was combined with 1 microliter of A/P1 Adaptersadapters (20 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), 2 microliters of 10x ligation buffer and 1 microliter of DNA ligase (sold as components of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464). The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 22°C for 30 minutes, followed by 65°C for 10 minutes and then held at 4°C until proceeding to the next step.

[00418] If the amplicon library is to contain barcodes (for example Ion DNA Barcoding 1-16 kit, Life Technologies, Part No. 4468654, incorporated herein in its entirety), the barcodes can be added at this step to the PCR plate essentially according to the manufacturer's instructions prior to proceeding to the next step

[00419] 1.8x AMPure XP Purification

[00420] 1.8x sample volume of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was mixed and incubated at room temperature for 5 minutes. After the solution had cleared, the supernatant was discarded. An ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed and the pellet was air-dried for about 5 minutes at room temperature. The pellet was resuspended in 20 microliters of DNase/RNase Free Water (Life Technologies, CA, Part No. 600004). In some instances, an optional library amplification step can be performed on the amplicon library, as outlined below.

[00421] Nick Translate and Amplify the Amplicon Library and Purify the Library

[00422] The ligated DNA (~20 microliters) was combined with 78 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 4 microliters of Library Amplification Primer Mix (5 μM each)(Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464). The solution was applied to a single well of a 96-well PCR plate and sealed. The plate was loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00423] A nick-translation was performed at 72°C for 1 minute, followed by an enzyme activation stage at 98°C for 2 minutes, followed by 7 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00424] The final amplicon library (~100 microliters) was combined with 1.8x sample volume of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The mixture was then incubated for 5 minutes at room temperature. The PCR plate containing the final amplicon library was washed with 70% ethanol and the supernatant discarded. Any remaining ethanol was removed and air-dried for about 5 minutes at room temperature. Once dry, the library was resuspended in 20 microliters of Low TE (Life Technologies, CA, Part No. 602-1066-01).

[00425] Assess the Library Size Distribution and Determine the Template Dilution Factor

[00426] The final amplicon library was quantitated to determine the library dilution (Template Dilution Factor) that results in a concentration within the optimized target range for Template Preparation (e.g., PCR-mediated addition of library molecules onto Ion Sphere™ Particles). The final amplicon library is typically quantitated for downstream Template Preparation procedure using an Ion Library Quantitation Kit (qPCR) (Life Technologies, Part No. 4468802) and/or a Bioanalyzer™ (Agilent Technologies, Agilent 2100 Bioanalyzer) to determine the molar concentration of the amplicon library, from which the Template Dilution Factor is calculated. For example, instructions to determine the Template Dilution Factor by quantitative real-time PCR (qPCR) can be found in the Ion Library Quantitation Kit User Guide (Life Technologies, Part No. 4468986), hereby incorporated by reference in its entirety.

[00427] In this example, 1 microliter of the final amplicon library preparation was analyzed on the 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626) to generate peaks in the 135-205 bp size range and at a concentration of about 5 x 10^9 copies per microliter.

[00428] **Proceed to Template Preparation**

[00429] An aliquot of the final library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 314™ Chip (Life Technologies, Part No. 4462923) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety.

[00430] **Example 14. Alternate Library Protocol**

[00431] **PCR Amplify Genomic DNA Targets**

[00432] In this example, a multiplex polymerase chain reaction was performed to amplify multiple individual amplicons across a genomic DNA sample. A representative list of genes associated with cancers that were incorporated for investigation while synthesizing the primer pool is provided in Table 1. Each primer pair in the primer pool was designed to contain at least one uracil

nucleotide in each of the forward and reverse primer (Table 2). Each primer pair was also designed to selectively hybridize to, and promote amplification of a specific gene or gene fragment of the genomic DNA sample to reduce formation of non-specific amplification products.

[00433] To a single well of a 96-well PCR plate was added 5 microliters of 4x HSM Primer Pool (containing the primer pairs of Table 2) at a concentration of 250nm each in TE, 50 ng of genomic DNA and 10 microliters of an amplification reaction mixture (2x PreAmp HiFi Master Mix) that can include glycerol, dNTPs and a DNA Polymerase (such as Taq DNA Polymerase, Invitrogen, Catalog No. N8080038) to a final volume of 20 microliters with nuclease free water (Life Technologies, CA, Part No. 600004).

[00434] The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile to generate the preamplified amplicon library. An initial holding stage was performed at 98°C for 2 minutes, followed by 16 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 4 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the purification step outlined below.

[00435] **Purify the Amplicons from input DNA and Primers**

[00436] Two rounds of Agencourt® AMPure® XP Reagent (Beckman Coulter, CA) binding, wash, and elution at 0.6x and 1.2x volume ratios were found to remove genomic DNA and unbound or excess primers. In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the preamplified amplicon library (20 microliters) was combined with 12 microliters (0.6x volumes) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the preamplified amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00437] The tube containing the sample was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was transferred to a new tube, where 24 microliters (1.2x volume) of AgenCourt® AMPure® XP beads (Beckman Coulter, CA) were added to the supernatant. The mixture was pipetted to ensure the bead suspension mixed with the preamplified amplicon library. The sample was then pulse-spin and incubated at room temperature for 5 minutes. The tube containing the sample was placed on the magnetic rack for 2 minutes to capture the beads.

Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. The desired preamplified amplicon library was now bound to the beads. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00438] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of DNase/RNase Free Water was added (Life Technologies, CA, Part No. 600004). The tube was vortexed and pipetted to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the eluted DNA was transferred to a new tube.

[00439] **Phosphorylate the Amplicons**

[00440] To the eluted DNA (~ 20 microliters), 3 microliters of DNA ligase buffer (Invitrogen, Catalog No. 15224041), 2 microliters dNTP mix (10 mm), and 2 microliters of FuP reagent were added. The reaction mixture was mixed thoroughly to ensure uniformity and incubated at 37°C for 10 minutes.

[00441] **Ligate Adpaters to the Amplicons and Purify the Ligated Amplicons**

[00442] After incubation, the reaction mixture proceeded directly to a ligation step. Here, the reaction mixture now containing the phosphorylated amplicon library was combined with 1 microliter of A/P1 adapters (20 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 1 microliter of DNA ligase (sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), and incubated at room temperature for 30 minutes.

[00443] After the incubation step, 52 microliters (1.8x sample volume) of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was pipetted thoroughly to mix the bead suspension with the ligated DNA. The mixture was pulse-spin and incubated at room temperature for 5 minutes. The samples underwent another pulse-spin and were placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No.

123-21D) for two minutes. After the solution had cleared, the supernatant was discarded. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00444] The pellet was resuspended in 20 microliters of DNase/RNase Free Water (Life Technologies, CA, Part No. 600004) and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the ligated DNA was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00445] **Nick Translate and Amplify the Amplicon Library and Purify the Library**

[00446] The ligated DNA (~20 microliters) was combined with 76 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 4 microliters of Library Amplification Primer Mix (5 μM each)(Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), the mixture was pipetted thoroughly to ensure a uniformed solution. The solution was applied to a single well of a 96-well PCR plate and sealed. The plate was loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00447] A nick-translation was performed at 72°C for 1 minute, followed by an enzyme activation stage at 98°C for 2 minutes, followed by 6 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00448] In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the final amplicon library (~100 microliters) was combined with 180 microliters (1.8x sample volume) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the final amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00449] The tube containing the final amplicon library was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. Without removing the tube from the magnetic rack, 400 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00450] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of Low TE was added (Life Technologies, CA, Part No. 602-1066-01). The tube was pipetted and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the final amplicon library was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00451] Assess the Library Size Distribution and Determine the Template Dilution Factor

[00452] The final amplicon library was quantitated to determine the library dilution (Template Dilution Factor) that results in a concentration within the optimized target range for Template Preparation (e.g., PCR-mediated addition of library molecules onto Ion Sphere™ Particles). The final amplicon library is typically quantitated for downstream Template Preparation procedure using an Ion Library Quantitation Kit (qPCR) (Life Technologies, Part No. 4468802) and/or a Bioanalyzer™ (Agilent Technologies, Agilent 2100 Bioanalyzer) to determine the molar concentration of the amplicon library, from which the Template Dilution Factor is calculated. For example, instructions to determine the Template Dilution Factor by quantitative real-time PCR (qPCR) can be found in the Ion Library Quantitation Kit User Guide (Life Technologies, Part No. 4468986), hereby incorporated by reference in its entirety.

[00453] In this example, 1 microliter of the final amplicon library preparation was analyzed on the 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626).

[00454] **Proceed to Template Preparation**

[00455] An aliquot of the final library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 314™ Chip (Life Technologies, Part No. 4462923) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety.

[00456] **Example 15 Alternate Library Protocol**

[00457] **PCR Amplify Genomic DNA Targets**

[00458] In this example, a multiplex polymerase chain reaction was performed to amplify multiple individual amplicons across a genomic DNA sample. A representative list of genes associated with cancers that were incorporated for investigation while synthesizing the primer pool is provided in Table 1. Each primer pair in the primer pool was designed to contain at least one uracil nucleotide in each of the forward and reverse primer (Table 2). Each primer pair was also designed to selectively hybridize to, and promote amplification of a specific gene or gene fragment of the genomic DNA sample to reduce formation of non-specific amplification products.

[00459] To a single well of a 96-well PCR plate was added 10 microliters of 2x Primer Pool (containing the primer pairs of Table 2) at a concentration of 250nm each, 10 ng of genomic DNA and 4 microliters of an amplification reaction mixture (5x Ion Ampliseq Master Mix) that can include glycerol, dNTPs and a DNA polymerase (for example, Stoffel fragment of Amplitaq® DNA Polymerase (Invitrogen Catalog No. N8080038)) to a final volume of 20 microliters with nuclease free water (Life Technologies, CA, Part No. 600004).

[00460] The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile to generate the preamplified amplicon library. Variation to the number of cycles was performed based on the total plexy of the reaction mixture under investigation. For example, a plexy of 48-96 was run for 17 cycles; a plexy of 97-192 was run for 16 cycles; a plexy of 193-384 was run for 15 cycles; a plexy of 385-768 was run for 14 cycles; a plexy

of 769-1536 was run for 13 cycles. Additionally, for reaction mixtures containing barcodes or pooled reaction mixtures the number of cycles was lowered by one or more additional cycles. For example, 2-3 barcodes per sample were subtracted by one cycle; 4-8 barcodes per sample were subtracted by 2 cycles, and 9-16 barcodes were subtracted by 3 cycles. For samples that contain fragmented DNA, e.g., enzymatically digested DNA, the number of cycles can be increased for up to 3 cycles. For selective amplification of one or more DNA samples using a starting input of 1 ng or less DNA, the number of cycles was increased by an additional 3 cycles. An initial holding stage was performed at 99°C for 2 minutes, followed by X cycles (as determined above) of denaturing at 99°C for 15 seconds and an annealing and extending stage at 60°C for 4 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the purification step outlined below.

[00461] Digest/Phosphorylate/Heat Kill the Amplicons

[00462] To the preamplified library (~ 20 microliters), 2 microliters of FuPa reagent was added. Typically, the FuPa reagent comprises one or more uracil degradable enzymes such as UDG, FPG and the like, a DNA polymerase such as Klenow fragment, and an antibody such as an anti-Taq antibody. In this example, the relative amount of each enzymatic component in the FuPa reagent was 1:1:1:2 but can be varied according to the number of required cycles, variations to the temperature profile, etc., as can be determined by one of ordinary skill in the art. The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 37°C for 10 minutes, followed by 55°C for 10 minutes and then 60°C for 20 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the ligation/nick translation step outlined below.

[00463] Ligate Adpaters to the Amplicons and Nick Translate

[00464] After phosphorylation, the amplicon preamplification library (~22 µl) proceeded directly to a ligation step. In this example, the preamplification library now containing the phosphorylated amplicon library was combined with 2 microliters of A/P1 Adaptersadapters (5 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), 4 microliters of 7.5x ligation buffer and 2 microliters of T4 DNA ligase (5u/µl). The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler

(Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 22°C for 30 minutes, followed by 60°C for 5 minutes and then held at 4°C until proceeding to the next step.

[00465] If the amplicon library is to contain barcodes (for example Ion DNA Barcoding 1-16 kit, Life Technologies, Part No. 4468654, incorporated herein in its entirety), the barcodes are added at this step to the PCR plate essentially according to the manufacturer's instructions prior to proceeding to the next step. Optionally, all the samples or barcodes can be pooled into a single tube at this step.

[00466] **1.6x AMPure XP Purification**

[00467] 1.6x sample volume of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was mixed and incubated at room temperature for 5 minutes. An ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed and air-dried for about 5 minutes at room temperature. The dry tube containing the library was resuspended in 20 microliters of Nuclease Free Water (Life Technologies, CA, Part No. 600004). In some instances, an optional nick translation/library amplification step can be performed on the amplicon library, as outlined below.

[00468] **Nick Translate and Amplify the Amplicon Library and Purify the Library**

[00469] The ligated DNA (~20 microliters) was combined with 78 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 4 microliters of Library Amplification Primer Mix (5 μM each)(Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464). The solution was applied to a single well of a 96-well PCR plate and sealed. The plate was loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00470] A nick-translation was performed at 72°C for 1 minute, followed by an enzyme activation stage at 98°C for 2 minutes, followed by 7 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00471] The final amplicon library (~100 microliters) was combined with 1.8x sample volume of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The mixture was then incubated for 5 minutes at room temperature. The final amplicon library was washed with 70% ethanol and the supernatant discarded. Any remaining ethanol was removed and air-dried for about 5 minutes at room temperature. Once dry, the library was resuspended in 20 microliters of Low TE (Life Technologies, CA, Part No. 602-1066-01). In this example, 1 microliter of the final amplicon library preparation was analyzed on the 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626).

[00472] **Example 16.**

[00473] In this example, an amplicon library was prepared using 2946 target-specific primer pairs. The primer pairs were prepared from the list of genes in Tables 1 and 18. Each primer pair was designed to selectively hybridize and promote amplification of the selected targeted region. The libraries were prepared according to Example 14 except that the primer pool was pooled into a single PCR tube, evaporated and resupsended in low TE and supplemented with 0.25 mM magnesium chloride prior to incubating with DNA and the amplification reaction mixture. In this example, both high molecular weight DNA or mechanically sheared DNA were applied as input DNA (10 ng input). The results from this sequencing experiment are provided in the Table below and demonstrated approximately 91-98% of all reads were on target, greater than 99% target coverage at 1 x when normalized to 100x, and greater than 98% base accuracy.

Plexity of PreAmp	2946	2946
Target DNA	Sheared	HMW

Percent greater than 0.01 mean reads per base	99.40%	99.29%
Percent greater than 0.1 mean reads per base	96.33%	95.16%
Percent greater than 0.2 mean reads per base	92.26%	89.40%
Percent no strand bias of all Amps	71.15%	72.98%
Percent no strand bias of all Amps >100 reads	73.31%	77.12%
Percent end to end read of on target reads	-1.00%	-1.00%
Per base accuracy	98.34%	98.59%
Percent of total reads mapped ontarget	99.10%	99.14%
Percent wells with read	35.94%	31.23%
Number of total reads	2277968	1979529
Number of mapped reads	2257427	1962501
Number of targets	2946	2946
Number of reads on target	2094328	1941916
Percent all reads on target	91.94%	98.10%
Percent mapped reads on target	92.78%	98.95%
Percent reads off target	7.16%	1.04%
Percent reads unmapped	0.90%	0.86%
Bases in targeted reference	327815	327815
Bases covered (at least 1x)	326642	326656
Total base reads on target	220235195	206585756
Average base coverage depth	671.83	630.19
Maximum base read depth	3070	2520
Average base read depth	674.23	632.43
Std.Dev base read depth	431.42	466.91
Target coverage at 1x	99.64%	99.65%
Target coverage at 10x	99.23%	99.12%
Target coverage at 20x	98.77%	98.42%
Target coverage at 1x - norm 100	99.40%	99.29%
Target coverage at 10x - norm 100	96.33%	95.16%
Target coverage at 20x - norm 100	92.26%	89.40%
Percent end to end read of on target reads	-1.00%	-1.00%
Percent forward end to end read of on target reads	-1.00%	-1.00%
Percent reverse end to end read of on target reads	-1.00%	-1.00%
Coverage needed for 99 percentile base with at least 1x coverage	52.2	48.96
Coverage needed for 98 percentile base with at least 10x coverage	207.65	247.24
Coverage needed for 95 percentile base with at least 20x coverage	145.33	203.58

[00474] **Example 17.**

[00475] In this example, an amplicon library was prepared using 6110 target-specific primer pairs. The library corresponds to approximately 450 cancer genes. The primer pairs were prepared from the list of genes in Tables 1 and 18. Each primer pair was designed to selectively hybridize and promote amplification of the selected targeted region using the target-specific selection criteria outline herein. The libraries were prepared according to Example 14 except that the primer pools were prepared as two tubes (3188-plex and 2946-plex) and supplemented with 0.5 mM magnesium chloride. The PCR preamplification cycling steps were also modified to increase the denaturing temperature to 99°C, included an extending step of 72°C for 5 minutes, after the 60°C annealing step, which was also extended to 10 minutes. After cycling, each tube containing the amplicon library was combined into a single emulsion for emulsion PCR enrichment. The amplicon library was used to

prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 316™ Chip (Life Technologies, Part No. 4466616) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety.

[00476] In this example, high molecular weight DNA was applied as the input DNA (10 ng). The results from this experiment are provided in the Table below and demonstrated approximately 95% of all reads were on target, approximately 95% of all reads (greater than 100 reads) showed no strand bias, and greater than 97% base accuracy.

Percent greater than 0.01 mean reads per base	81.58%
Percent greater than 0.1 mean reads per base	75.40%
Percent greater than 0.2 mean reads per base	69.73%
Percent no strand bias of all bases	92.16%
Percent no strand bias of all Amps	72.16%
Percent no strand bias of all Amps >100 reads	95.06%
Percent end to end read of on target reads	-1.00%
Per base accuracy	97.78%
Percent of total reads mapped to hg19	98.05%
Percent wells with read	34.51%
Number of total reads	2190638
Number of mapped reads	2147835
Number of targets	6110
Number of reads on target	2098176
Percent all reads on target	95.78%
Percent mapped reads on target	97.69%
Percent reads off target	2.27%
Percent reads unmapped	1.95%
Bases in targeted reference	677270
Bases covered (at least 1x)	556880
Total base reads on target	243058082
Average base coverage depth	358.88
Maximum base read depth	2402
Average base read depth	436.45
Std.Dev base read depth	371.45
Target coverage at 1x	82.22%
Target coverage at 10x	80.45%
Target coverage at 20x	78.41%
Target coverage at 100x	66.15%
Target coverage at 500x	29.11%
Target coverage at 1x - norm 100	81.58%
Target coverage at 10x - norm 100	75.40%
Target coverage at 20x - norm 100	69.73%
Target coverage at 100x - norm 100	40.40%
Target coverage at 500x - norm 100	0.34%
Percent end to end read of on target reads	-1.00%
Percent forward end to end read of on target reads	-1.00%
Percent reverse end to end read of on target reads	-1.00%
Coverage needed for 99 percentile base with at least 1x coverage	865.36
Coverage needed for 98 percentile base with at least 20x coverage	8653.57
Coverage needed for 95 percentile base with at least 350x coverage	60574.98
Percent priority 1 design covered	0
Percent priority 9 design covered	0

[00477] **Example 18.**

[00478] In this example, an amplicon library was prepared using approximately 1500 target-specific primer pairs. The primer pairs were prepared from genes in Table 1. Each primer pair was designed to selectively hybridize and promote amplification of the selected targeted region using the target-specific primer selection criteria outlined herein. The libraries were prepared according to Example 15 except that the number of preamplification PCR cycles was amended as follows: Plexy: 12-24=18 cycles; 25-48=17 cycles; 48-96=16 cycles; 97-192=15 cycles; 193-384=14 cycles; 385-768=13 cycles; 769-1536=12 cycles; 1537-3072=11 cycles. When using fragmented DNA, up to 2 additional cycles were added to the preamplification PCR process. Additionally, the annealing temperature (60°C) can be increased from 4 minutes to 8 minutes when using 1537+ plexy.

[00479] During the nick translation and library amplification step, the number of PCR cycles can be increased, for example to about 10, when necessary.

[00480] The amplicon library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 316™ Chip (Life Technologies, Part No. 4466616) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety.

[00481] In this example, 10 ng FFPE DNA was applied as the input DNA. The results from this experiment are provided in the Table below and demonstrated approximately 94% showed base without strand bias, greater than 98% per base accuracy, and 99% of bases with greater than 20x coverage when average coverage normalized to 100x.

Number of targets	1459
Per Base Accuracy	98.70%
Percent bases > 0.2x mean	99.20%
Target coverage at 20x if normalized to 100x average coverage depth	99.20%
Base without Strand Bias	94.12%
Percent of reads on target	80.54%
Coverage needed for 98 percentile base with at least 20x coverage	65.07
Percent bases > 0.01x mean	99.77%

Example 19. Multiplex PCR with 12,500 target specific primers

[00482] In this example, several amplicon libraries were prepared using approximately 12,000 target-specific primer pairs in a single reaction. The target-specific primer pairs were prepared from

genes associated with cancers, provided in Table 18. The target-specific primers were designed using the primer selection criteria outlined herein. In this example, primers from Table 6 of US Application 61/598,881 hereby incorporated by reference in its entirety were used as target-specific primers in the reaction. Each target-specific primer pair was designed to promote amplification of the intended target sequence outlined in Table 18. Each amplicon library was prepared according to the section of Example 13 titled PCR amplify genomic DNA targets, except that the concentration of target-specific primers in the primer pool was amended to 25 nM and the number of target-specific primers was about 12,000. Additionally, the preamplification PCR cycles was amended as follows: An initial holding stage was performed at 99°C for 2 minutes, followed by 11 cycles of denaturing at 99°C for 15 seconds; a first annealing stage at 60°C for 10 minutes; a second annealing stage at 63°C for 5 minutes; a third annealing stage at 66°C for 5 minutes; a fourth annealing stage at 69°C for 5 minutes; and an extending stage at 72°C for 5 minutes; followed by 5 cycles of denaturing at 99°C for 15 seconds; a first annealing stage at 60°C for 10 minutes; a second annealing stage at 63°C for 6 minutes; a third annealing stage at 66°C for 6 minutes; a fourth annealing stage at 69°C for 6 minutes; and an extending stage at 72°C for 6 minutes. After cycling, the preamplified amplicon library was held at 4°C until proceeding to the next step as outlined below.

[00483] Purify the Amplicons from input DNA and Primers

[00484] One round of Agencourt® AMPure® XP Reagent (Beckman Coulter, CA) binding, wash, and elution at 1.2x volume ratio was found to remove genomic DNA and unbound or excess primers.

[00485] In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the preamplified amplicon library (20 microliters) was combined with 24 microliters (1.2x volume) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the preamplified amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00486] The tube containing the sample was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was transferred to a new tube, where 13.3 ul of nuclease free water was added. Then, 48 microliters of AgenCourt® AMPure® XP beads (Beckman Coulter, CA) were added to the diluted supernatant. The mixture was pipetted to ensure the bead suspension mixed with the preamplified amplicon library. The sample was then pulse-spin and incubated at room temperature for 5 minutes. The tube containing the sample was placed on the

magnetic rack for 2 minutes to capture the beads. Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. The desired preamplified amplicon library was now bound to the beads. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00487] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of DNase/RNase Free Water was added (Life Technologies, CA, Part No. 600004). The tube was vortexed and pipetted to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the eluted DNA was transferred to a new tube.

[00488] **Phosphorylate the Amplicons**

[00489] To the eluted DNA (~ 20 microliters), 3 microliters of DNA ligase buffer (Invitrogen, Catalog No. 15224041), 2 microliters dNTP mix, and 2 microliters of FuP reagent were added. The reaction mixture was mixed thoroughly to ensure uniformity and incubated at 37°C for 13 minutes.

[00490] **Ligate Adpaters to the Amplicons and Purify the Ligated Amplicons**

[00491] After incubation, the reaction mixture proceeded directly to a ligation step. Here, the reaction mixture now containing the phosphorylated amplicon library was combined with 1.5 microliter of A/P1 adapters (20 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 1 microliter of DNA ligase (sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), and incubated at room temperature for 30 minutes.

[00492] After the incubation step, 52 microliters (1.8x sample volume) of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was pipetted thoroughly to mix the bead suspension with the ligated DNA. The mixture was pulse-spin and incubated at room temperature for 5 minutes. The samples underwent another pulse-spin and were placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No.

123-21D) for two minutes. After the solution had cleared, the supernatant was discarded. Without removing the tube from the magnetic rack, 200 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00493] The pellet was resuspended in 20 microliters of DNase/RNase Free Water (Life Technologies, CA, Part No. 600004) and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the ligated DNA was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00494] **Nick Translate and Amplify the Amplicon Library and Purify the Library**

[00495] The ligated DNA (~20 microliters) was combined with 76 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and 4 microliters of Library Amplification Primer Mix (5 μM each)(Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), the mixture was pipetted thoroughly to ensure a uniformed solution. The solution was applied to a single well of a 96-well PCR plate and sealed. The plate was loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00496] A nick-translation was performed at 72°C for 1 minute, followed by an enzyme activation stage at 98°C for 2 minutes, followed by 6 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00497] In a 1.5ml LoBind tube (Eppendorf, Part No. 022431021), the final amplicon library (~100 microliters) was combined with 180 microliters (1.8x sample volume) of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The bead suspension was pipetted up and down to thoroughly mix the bead suspension with the final amplicon library. The sample was then pulse-spin and incubated for 5 minutes at room temperature.

[00498] The tube containing the final amplicon library was placed on a magnetic rack such as a DynaMag™-2 spin magnet (Life Technologies, CA, Part No. 123-21D) for 2 minutes to capture the beads. Once the solution cleared, the supernatant was carefully discarded without disturbing the bead pellet. Without removing the tube from the magnetic rack, 400 microliters of freshly prepared 70% ethanol was introduced into the sample. The sample was incubated for 30 seconds while gently rotating the tube on the magnetic rack. After the solution cleared, the supernatant was discarded without disturbing the pellet. A second ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed by pulse-spinning the tube and carefully removing residual ethanol while not disturbing the pellet. The pellet was air-dried for about 5 minutes at room temperature.

[00499] Once the tube was dry, the tube was removed from the magnetic rack and 20 microliters of Low TE was added (Life Technologies, CA, Part No. 602-1066-01). The tube was pipetted and vortexed to ensure the sample was mixed thoroughly. The sample was pulse-spin and placed on the magnetic rack for two minutes. After the solution cleared, the supernatant containing the final amplicon library was transferred to a new Lobind tube (Eppendorf, Part No. 022431021).

[00500] Assess the Library Size Distribution and Determine the Template Dilution Factor

[00501] The final amplicon library was quantitated to determine the library dilution (Template Dilution Factor) that results in a concentration within the optimized target range for Template Preparation (e.g., PCR-mediated addition of library molecules onto Ion Sphere™ Particles). The final amplicon library is typically quantitated for downstream Template Preparation procedure using an Ion Library Quantitation Kit (qPCR) (Life Technologies, Part No. 4468802) and/or a Bioanalyzer™ (Agilent Technologies, Agilent 2100 Bioanalyzer) to determine the molar concentration of the amplicon library, from which the Template Dilution Factor is calculated. For example, instructions to determine the Template Dilution Factor by quantitative real-time PCR (qPCR) can be found in the Ion Library Quantitation Kit User Guide (Life Technologies, Part No. 4468986), hereby incorporated by reference in its entirety.

[00502] In this example, 1 microliter of the final amplicon library preparation was analyzed on the 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626) to generate peaks in the 135-205 bp size range and at a concentration of about 5 x 10^9 copies per microliter.

[00503] Proceed to Template Preparation

[00504] An aliquot of the final library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 314™ Chip (Life Technologies, Part No. 4462923) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety. The data obtained from this example is provided in the Table below.

Ampliseq 1.0 work flow mod				
Sample (50ng NA12878)				enrich unbound
Plexity	6,000	12,000	12,000	12,000
C450 oligo pool	pool 1+3	pool 1+2+3+4	pool 1+2+3+4	pool 1+2+3+4
PreAmp cycle (6hr = PA1, 9hr = PA2)	6hr	6hr	9hr	9hr
PA enzyme / load %	Taq/69%	Taq/82%	Stoffel/35%	Stoffel/83%
Percent greater than 0.01 mean reads per base	97.72%	79.15%	82.08%	78.42%
Percent greater than 0.1 mean reads per base	84.32%	54.28%	82.08%	54.22%
Percent greater than 0.2 mean reads per base	73.79%	44.86%	68.80%	45.45%
Percent no strand bias of all bases	80.42%	66.48%	45.19%	66.01%
Percent no strand bias of all Amps	81.23%	62.87%	32.68%	54.80%
Percent no strand bias of all Amps >100 reads	139.07%	229.75%	8126.00%	334.62%
Percent end to end read of on target reads	71.40%	69.05%	53.32%	77.87%
Per base accuracy	97.38%	97.47%	97.18%	98.87%
Percent of total reads mapped to hg19	98.17%	97.86%	97.85%	97.10%
Percent wells with read	25.93%	30.24%	1.62%	12.97%
Number of total reads	1643486	1916570	102468	821799
Number of mapped reads	1613468	1875619	100261	797953
Number of targets	6249	12489	12489	12489
Number of reads on target	1534973	1793835	93560	763982
Percent all reads on target	93.40%	93.60%	91.31%	92.96%
Percent mapped reads on target	95.14%	95.64%	93.32%	95.74%
Percent reads off target	4.78%	4.27%	6.54%	4.13%
Percent reads unmapped	1.83%	2.14%	2.15%	2.90%
Bases in targeted reference	668162	1249178	1249178	1249178
Bases covered (at least 1x)	661418	1076079	1025284	979584
Total base reads on target	156995237	189835759	9789500	80845870
Average base coverage depth	234.97	151.97	7.84	84.72
Maximum base read depth	2391	4284	339	3921
Average base read depth	237.32	178.23	9.52	82.48
Std Dev base read depth	277.21	351.91	16.09	157.73
Target coverage at 1x	98.99%	86.14%	82.08%	78.42%
Target coverage at 10x	93.38%	60.43%	22.25%	49.45%
Target coverage at 20x	86.73%	51.08%	9.49%	39.12%
Target coverage at 100x	57.38%	28.52%	0.44%	17.75%
Target coverage at 500x	14.24%	9.07%	0.00%	2.34%
Target coverage at 1x - norm 100	97.72%	79.15%	82.08%	78.42%
Target coverage at 10x - norm 100	84.32%	54.28%	82.08%	54.22%
Target coverage at 20x - norm 100	73.79%	44.86%	68.80%	45.45%
Target coverage at 100x - norm 100	33.67%	23.15%	27.68%	23.25%
Target coverage at 500x - norm 100	1.20%	5.22%	3.24%	5.22%
Percent end to end read of on target reads	71.40%	69.05%	53.32%	77.87%
Percent forward end to end read of on target reads	36.45%	35.07%	26.64%	39.40%
Percent reverse end to end read of on target reads	34.95%	33.98%	26.67%	38.47%
Coverage needed for 99 percentile base with at least 1x coverage	158.65	475.51	215.63	274.86

[00505] **Example 20. Assessment of relative copy number variation (CNV)**

[00506] In this example, several DNA samples were amplified using 3000 target-specific primer pairs. The target-specific primers were designed using the target-specific primer selection criteria outlined herein. The sequences of the selected target-specific primers used in this experiment can be found in Table 17 (or Table 6 of US Application 61/598,881 hereby incorporated by reference in its entirety). The DNA samples were barcoded during the library amplification process (as

outlined in Example 13). In this example, the DNA samples were obtained from a commercial source (Coriell DNA) and contained known variations in copy number to demonstrate that the multiplex amplification methods disclosed herein can be used to assess copy number variation.

[00507] Four DNA samples were purchased from Coriell DNA that contained a 3Mb deletion on chromosome 22 that was associated with DiGeorge Syndrome. An additional DNA sample was purchased from Coriell DNA that contained a 16 Mb deletion on chromosome 7 associated with Grieg Cephalopolysyndactyly Syndrome (GCPS). An amplicon library was prepared for each DNA sample including a barcode for the purposes of distinguishing one DNA sample from another. Each amplicon library was prepared according to the method outlined in Example 15, except in this example, 3000 target-specific primer pairs were used in a single preamplification reaction. The target-specific primer pairs were prepared from the genes in Table 18. Each amplicon library was prepared using 10 ng of DNA from the starting material. The libraries were prepared according to Example 15 except that the number of preamplification PCR cycles was amended as follows: Plexy: 12-24=18 cycles; 25-48=17 cycles; 48-96=16 cycles; 97-192=15 cycles; 193-384=14 cycles; 385-768=13 cycles; 769-1536=12 cycles; 1537-3072=11 cycles. When using fragmented DNA (e.g., FFPE DNA samples), up to 2 additional cycles can be added to the preamplification PCR process. Additionally, the annealing temperature (60°C) can be increased from 4 minutes to 8 minutes when using 1537+ plexy, if a higher yield is necessary.

[00508] If required, the number of PCR cycles can be increased during the nick translation and library amplification step, for example to about 10 cycles.

[00509] The amplicon library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 316™ Chip (Life Technologies, Part No. 4466616) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety.

[00510] In this example, 10 ng DNA was applied as the input DNA. The results from this experiment are provided in Figures 14-15.

[00511] Figure 14 shows that the multiplex PCR amplification methods disclosed herein can be used to assess copy number variation. Figure 14 shows the amplicon frequency data for 12 amplicons spanning part of the critical region of the gene CLTCL1 associated with DiGeorge Syndrome. The circles plotted at frequency 0 represent each amplicon of CLTCL1 amplified by the multiplex amplification method. The red (solo) circles are data points from a single DiGeorge Syndrome DNA sample obtained from Coriell DNA. Four DiGeorge Syndrome DNA samples were tested in this experiment and an average ratio of percent total reads filtered for DiGeorge samples compared to controls are plotted as circles with error bars. The dotted line at frequency 1.0 is the frequency expected for a normal sample (i.e., a sample not containing a variation in copy number). As is shown in Figure 14, the frequencies of the tested DiGeorge Syndrome samples are about 0.5, indicating that a deletion within the CLTCL1 gene has occurred and can be observed and detected using the amplification methods disclosed herein.

[00512] Figure 15 shows that the multiplex amplification methods disclosed herein can be used to assess copy number variation in a different chromosome. Figure 15 shows the amplicon frequency data for 4 amplicons spanning part of the gene IKZF1, associated with Greig Cephalopolysyndactyly Syndrome (GCPS). The circles plotted at frequency 0 represent each of the four amplicons of IKZF1 that were amplified by the multiplex PCR amplification method outlined in this example. Ratios were obtained for a single GCPS sample as compared to four control samples and their frequencies are plotted in FIG.15. GCPS DNA has only one copy of the GCPS gene, whereas normal (or control) DNA samples contain two copies of the gene. As noted in Figure 15, the control samples show 2x for copy number as compared to the expected frequency (dotted line). As is demonstrated by Figure 15, variation in copy number can be determined using the multiplex PCR amplification method disclosed herein.

[00513] **Example 21. Mutiplex Amplification with an Inosine Cleavable Group**

[00514] In this example, target-specific primers containing one or more cleavable groups denoted as an inosine were prepared according to the primer selection criteria disclosed herein. After an initial *in silico* evaluation of the primer pairs to proposed target sequences, the evaluated target-specific primers (disclosed in Table 19) were ordered from Integrated DNA Technologies (IDT)(Coravilla, IA). The inosine containing primers were received from IDT and subjected to multiplex amplification, performed according to the method of Example 15 with the following exceptions. The 2x Primer Pool (containing primer from Table 2) was replaced with the Inosine

containing primers (disclosed on Table 19, corresponding to SEQ ID NOs: 103122-103143). Additionally, after performing PCR amplification of genomic DNA targets, the samples was subjected to digestion with EndoV and FuPa.

[00515] In this example, an aliquot of the final library was used to prepare DNA templates that were clonally amplified on Ion Sphere™ Particles using emulsion PCR (emPCR). The preparation of template in the instant example was prepared according to the manufacturer's instructions using an Ion Xpress Template Kit (Life Technologies, Part No. 4466457), hereby incorporated by reference in its entirety. Once template-positive Ion Sphere Particles were enriched, an aliquot of the Ion Spheres were loaded onto an Ion 314™ Chip (Life Technologies, Part No. 4462923) as described in the Ion Sequencing User Guide (Part No. 4467391), hereby incorporated in its entirety, and subjected to analysis and sequencing as described in the Ion Torrent PGM Sequencer User Guide (Life Technologies, Part No. 4462917), hereby incorporated in its entirety. The data obtained from this example included a per base accuracy percentage of 97.17% and percent of reads on target were observed as 96.83%.

[00516] **Example 22. Alternative multiplex PCR protocol**

[00517] In this example, various alternative embodiments are presented over one or more of the prior multiplex PCR methods.

[00518] **PCR Amplify Genomic DNA Targets**

[00519] In this example, a multiplex polymerase chain reaction was performed to amplify multiple individual amplicons (target sequences) across a genomic DNA sample and an FFPE sample. A representative list of genes associated with cancers and inherited diseases that were incorporated for investigation while synthesizing the primer pool is provided in at least Tables 1 and 4. Each primer pair in the primer pool was designed to contain at least one uracil nucleotide in each of the forward and reverse primer (Table 2) or designed to contain at least one inosine residue in each of the forward and reverse primer (Table 19). Each primer pair was also designed to selectively hybridize to, and promote amplification of a specific gene or gene fragment of the genomic DNA or FFPE sample to reduce formation of non-specific amplification products.

[00520] To a single well of a 96-well PCR plate was added 10 microliters of 2x Primer Pool (containing the primer pairs of Table 2), 4 microliters of 5x Cancer Primer pool (containing the primer pairs of Table 17), 4 microliters of 5x IDP Primer pool (containing the primer pairs of Table 15) or 10 microliters of 2x HID Primer Pool (containing the primer pairs of Tables 13 and 14), at a

concentration of 200nm each for plexy under 96, or at a concentration of 50 nm for plexy above 96. 10 ng of genomic DNA or FFPE DNA and 4 microliters of an amplification reaction mixture (5x Ion Ampliseq HiFi Master Mix) was added to a final volume of 20 microliters with nuclease free water (Life Technologies, CA, Part No. 600004).

[00521] The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile to generate the preamplified amplicon library. Variation to the number of cycles was performed based on the total plexy of the reaction mixture under investigation. For example, a plexy of 12-24 was run for 20 cycles; a plexy of 25-48 was run for 19 cycles; a plexy of 48-96 was run for 18 cycles; a plexy of 97-192 was run for 17 cycles; a plexy of 193-384 was run for 16 cycles; a plexy of 385-768 was run for 15 cycles; a plexy of 769-1536 was run for 14 cycles; a plexy of 1537-3072 was run for 13 cycles; a plexy of 3073-6144 was run for 12 cycles. Additionally, for reaction mixtures containing barcodes or pooled reaction mixtures the number of cycles was lowered by one or more additional cycles. For example, 2-3 barcodes per sample were subtracted by one cycle; 4-8 barcodes per sample were subtracted by 2 cycles, and 9-16 barcodes were subtracted by 3 cycles. For samples that contain fragmented DNA, e.g., FFPE or enzymatically digested DNA, the number of cycles can be increased for up to 3 cycles.

[00522] An initial holding stage was performed at 99°C for 2 minutes, followed by X cycles (as determined above) of denaturing at 99°C for 15 seconds and an annealing and extending stage at 60°C for 4 minutes. For plexy above 1536, the annealing and extending stage was increase to 8 minutes at 60°C. After cycling, the preamplified amplicon library was held at 10°C until proceeding to the purification step outlined below.

[00523] **Digest/Phosphorylate/Heat Kill the Amplicons**

[00524] To the preamplified library (~ 20 microliters), 2 microliters of FuPa reagent was added. The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 50°C for 10 minutes, followed by 55°C for 10 minutes and then 65°C for 20 minutes. After cycling, the preamplified amplicon library was held at 10°C until proceeding to the ligation/nick translation step outlined below.

[00525] Ligate Adpaters to the Amplicons and Nick Translate

[00526] After phosphorylation, the amplicon preamplification library (~22 µl) proceeded directly to a ligation step. In this example, the preamplification library now containing the phosphorylated amplicon library was combined with 2 microliters of A/P1 Adapter (5 µm each)(sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464), 4 microliters of Switch Solution and 2 microliters of DNA ligase (5u/µl). The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperature profile. An initial holding stage was performed at 22°C for 30 minutes, followed by 72°C for 10 minutes and then held at 10°C until proceeding to the next step.

[00527] If the amplicon library is to contain barcodes (for example Ion DNA Barcoding 1-16 kit, Life Technologies, Part No. 4468654, incorporated herein in its entirety), the barcodes are added at this step to the PCR plate essentially according to the manufacturer's instructions prior to proceeding to the next step. Optionally, all the samples or barcodes can be pooled into a single tube at this step.

[00528] 1.5x AMPure XP Purification

[00529] 1.5x sample volume (45 microliters) of AgenCourt® AMPure® Reagent (Beckman Coulter, CA) was added to the ligated DNA. The mixture was mixed and incubated at room temperature for 5 minutes and then transferred to a magnet plate. Sample was incubated on the magnet plate for 2 minutes, and the supernatant discarded. An ethanol wash was performed and the supernatant discarded. Any remaining ethanol was removed and air-dried for about 5 minutes at room temperature. The dry tube containing the library was resuspended in 20 microliters of Nuclease Free Water (Life Technologies, CA, Part No. 600004) or low Tris-EDTA buffer. In some instances, an optional nick translation/library amplification step can be performed on the amplicon library, as outlined below.

[00530] Nick Translate and Amplify the Amplicon Library and Purify the Library

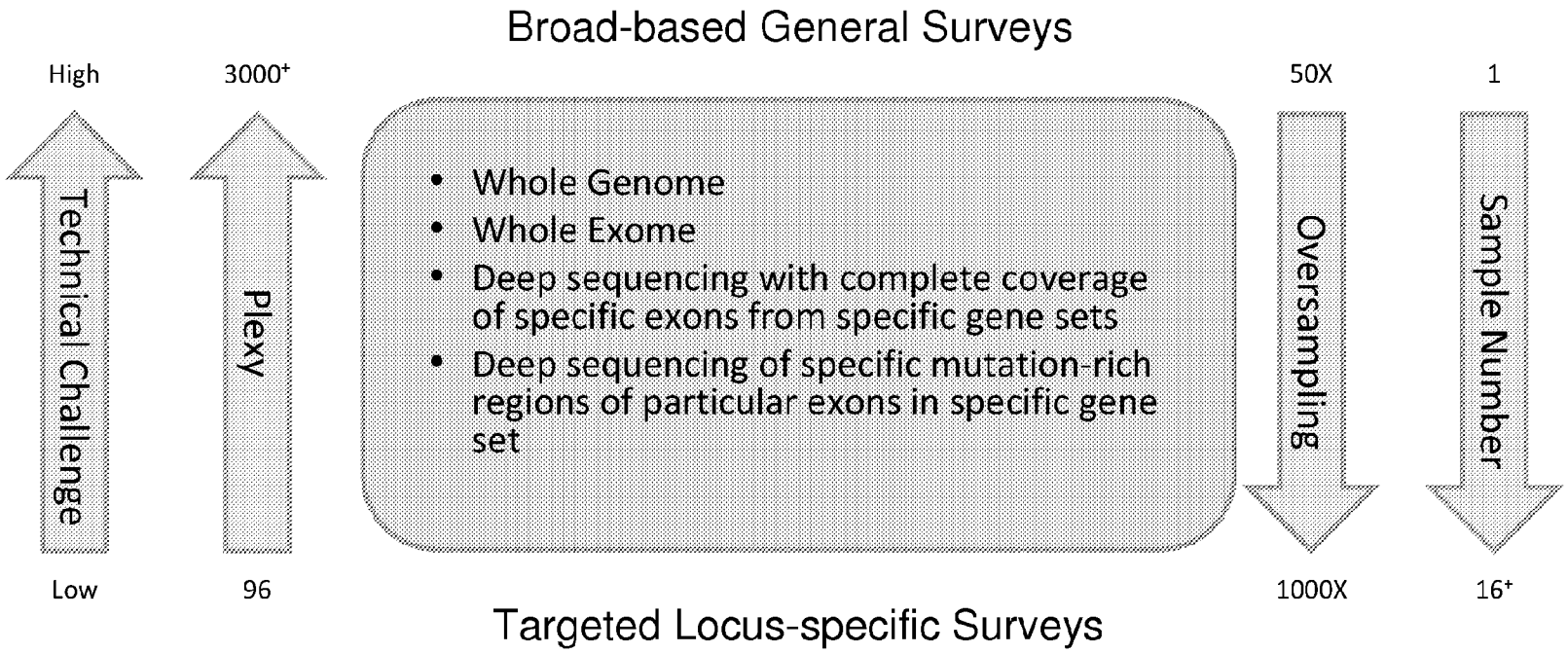
[00531] The ligated DNA (~20 microliters) was combined with 50 microliters of Platinum® PCR SuperMix High Fidelity (Life Technologies, CA, Part No. 12532-016, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464) and placed on a magnet plate for 2 minutes. 48 ul of the eluted amplicons in the PCR supermix were transferred to a new well of a 96-

well plate to which was added 2 microliters of Library Amplification Primer Mix (Life Technologies, CA, Part No. 602-1068-01, sold as a component of the Ion Fragment Library Kit, Life Technologies, Part No. 4466464). The PCR plate was sealed and loaded into a thermal cycler (GeneAmp® PCR system 9700 Dual 96-well thermal cycler (Life Technologies, CA, Part No. N8050200 and 4314445)) and run on the following temperate profile to generate the final amplicon library.

[00532] An enzyme activation stage at 98°C for 2 minutes, followed by 5 cycles of denaturing at 98°C for 15 seconds and an annealing and extending stage at 60°C for 1 minute. After cycling, the final amplicon library was held at 4°C until proceeding to the final purification step outlined below.

[00533] The final amplicon library (~100 microliters) was combined with 0.5x sample volume of Agencourt® AMPure® XP reagent (Beckman Coulter, CA). The mixture was then incubated for 5 minutes at room temperature. The sample was transferred to a magnet plate for 2 minutes and the supernatant (~75 microliters) removed to a new well. 1.2x volume of Agencourt® AMPure® XP reagent (Beckman Coulter, CA) was added and incubated at room temperature for 5 minutes. The sample was then placed on a magnet plate for 2 minutes and the supernatant discarded. The final amplicon library was washed with 70% ethanol and the supernatant discarded. Any remaining ethanol was removed and air-dried for about 5 minutes at room temperature. Once dry, the library was resuspended in 20 microliters of Low TE (Life Technologies, CA, Part No. 602-1066-01). In this example, 1 microliter of the final amplicon library preparation was analyzed on a 2100 Bioanalyzer™ with an Agilent High Sensitivity DNA Kit (Agilent Technologies, Part No. 5067-4626) or analyzed on a Qubit machine using the DSDNA HS Assay Kit (Part number Q32851).

Application Space



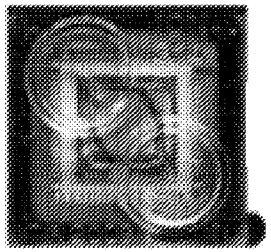
Successful occupation of application space requires balancing market requirements, PGM bandwidth, primer design and multiplex capabilities.

Amplicons and Coverage

Rough calculations: Mutations detectable at 5% frequency

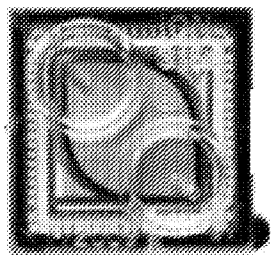
314

- Based on data to date, >400 amplicons
- 1172 reads per amplicon (est) to ensure 95% of amplicons covered at >450X coverage
- ~0.5M Reads
- Conclusion: One 314 per 400 amplicon panel



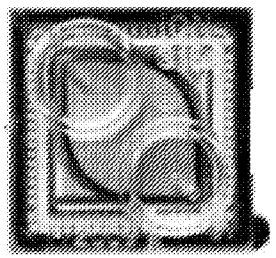
316

- Based on data to date, >1800 amplicons
- 1172 reads per amplicon (est) to ensure 95% of amplicons covered at >450X coverage
- ~2 M Reads
- Conclusion: One 316 per 1800 amplicon panel (or 4 barcoded 400 amplicon sets)



318

- Based on data to date, >3700 amplicons 1172 reads per amplicon (est) to ensure 95% of amplicons covered at >450X coverage
- ~4.5M Reads
- Conclusion: One 314 per 400 amplicon panel (or 9 barcoded 400 amplicon sets)



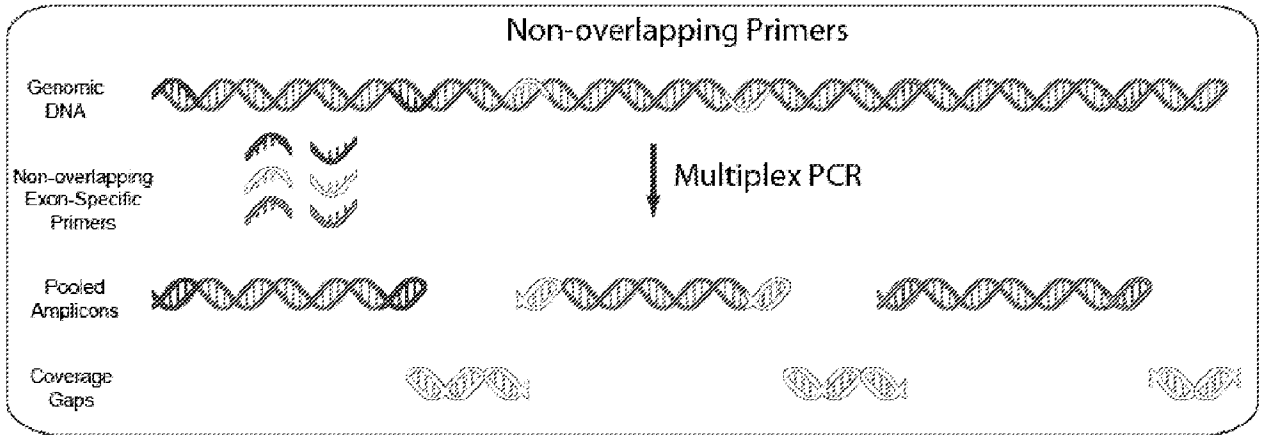
Loci were chosen from the following genes

MPL	KRAS	TP53	ERBB4	PIK3CA	CSF1R	JAK2
NRAS	PTPN11	ERBB2	SRC	FGFR3	NPM1	CDKN2A
RET	HNF1A	SMAD4	GNAS	PDGFRA	EGFR	ABL1
PTEN	FLT3	STK11	SMARCB1	KIT	MET	NOTCH1
FGFR2	RB1	JAK3	VHL	KDR	SMO	LOC100289474
HRAS	AKT1	ALK	MLH1	FBXW7	BRAF	
ATM	CDH1	IDH1	CTNNB1	APC	FGFR1	

83 High Priority Loci (from EGFR, KRAS, BRAF and PTEN)
483 Lower Priority Loci from remaining genes
One locus can contain multiple mutations

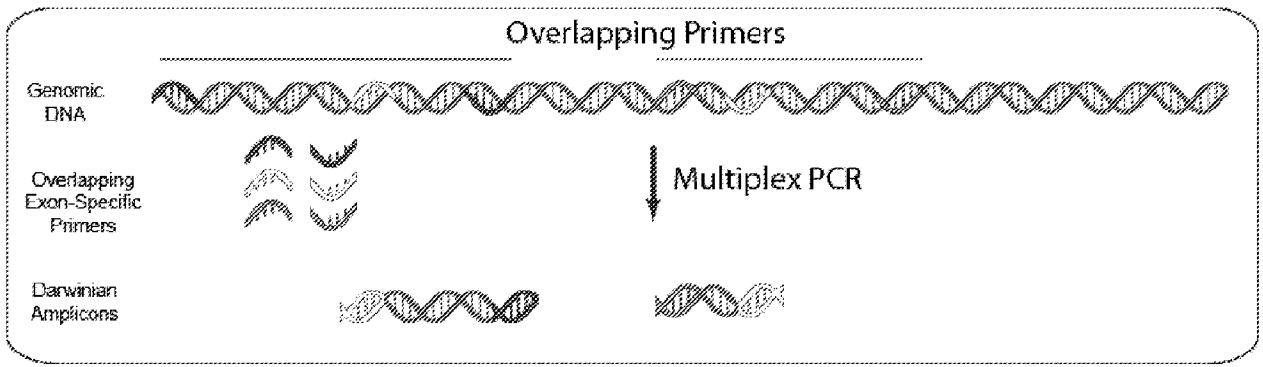
Challenges in Traditional Multiplex Amplification

Single Pool
Non-overlapping



Coverage Gaps result

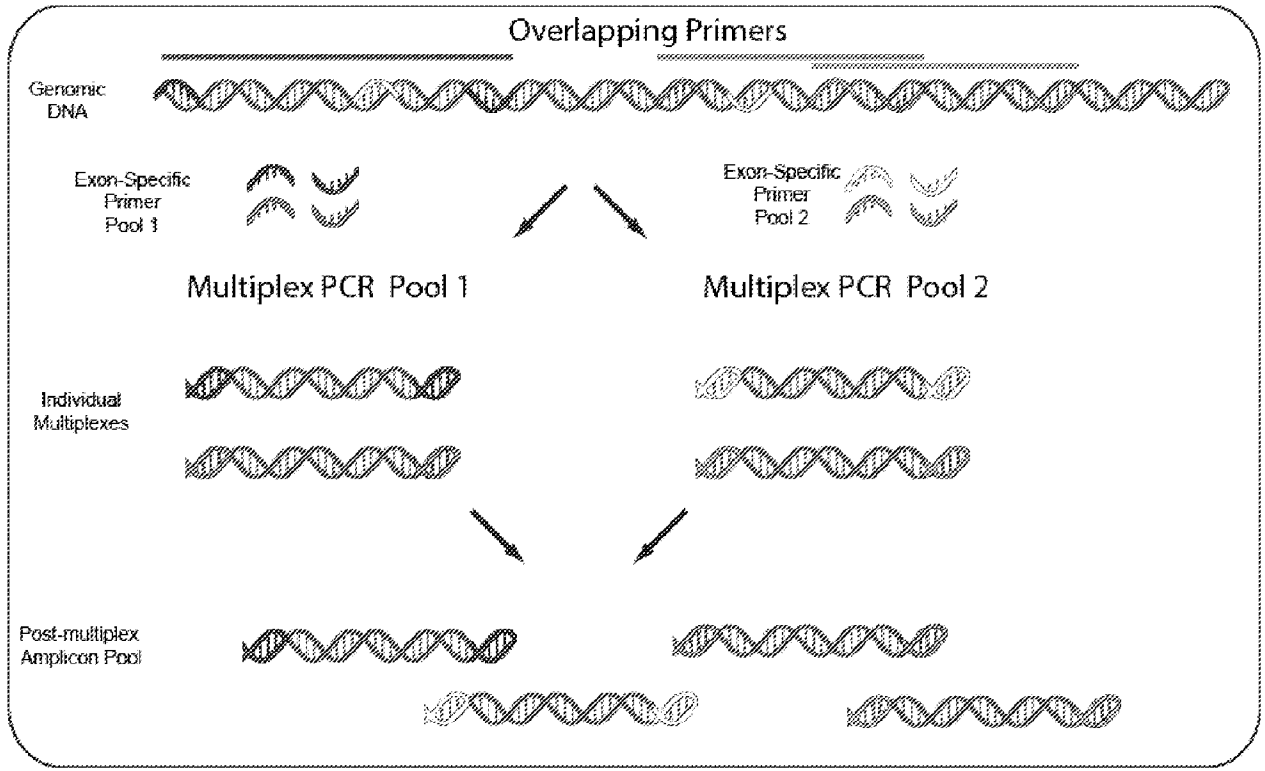
Single Pool
Overlapping



Darwinian PCR

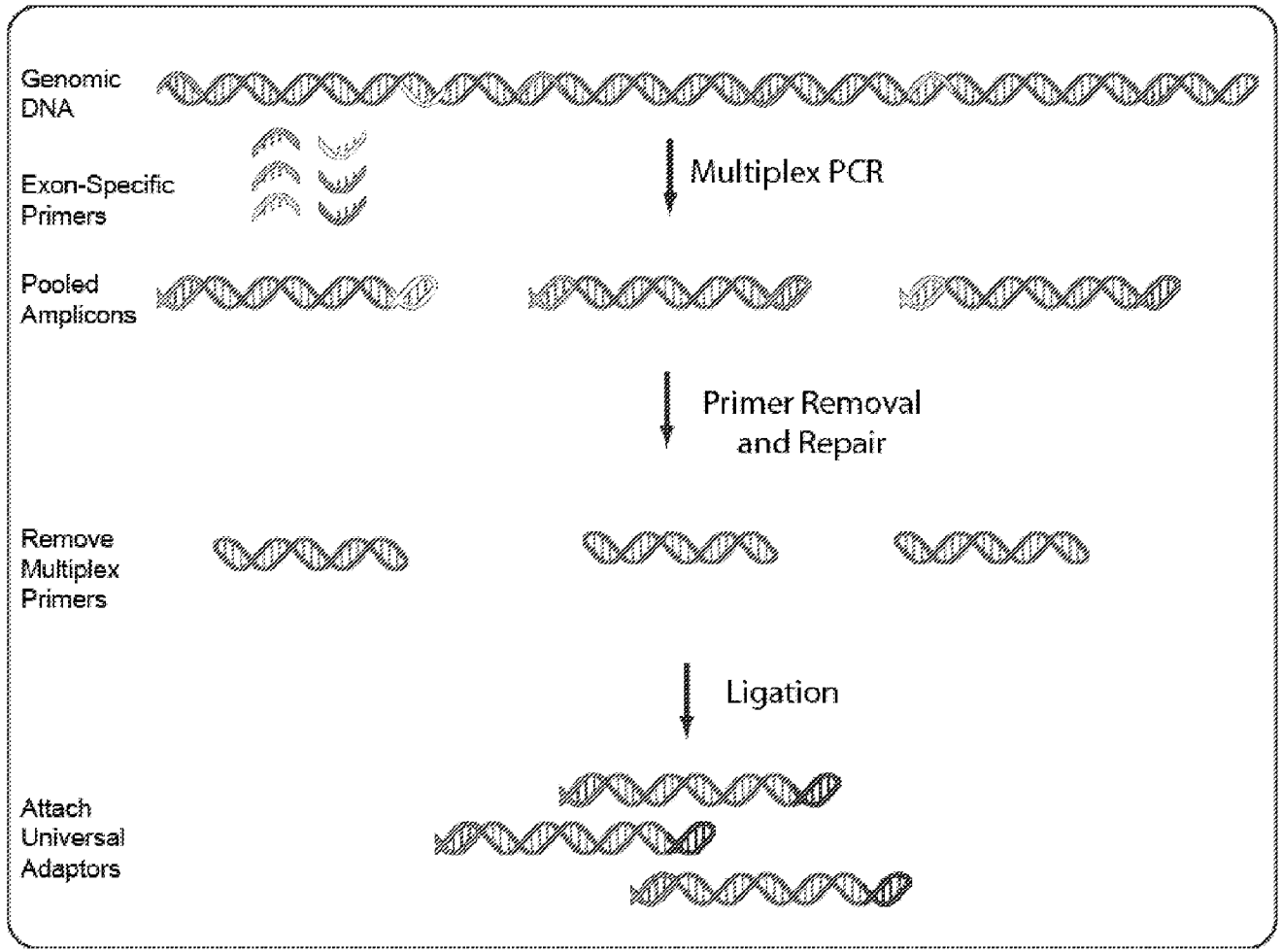
Smallest, fastest amplicon dominates

Multiplex Pooling



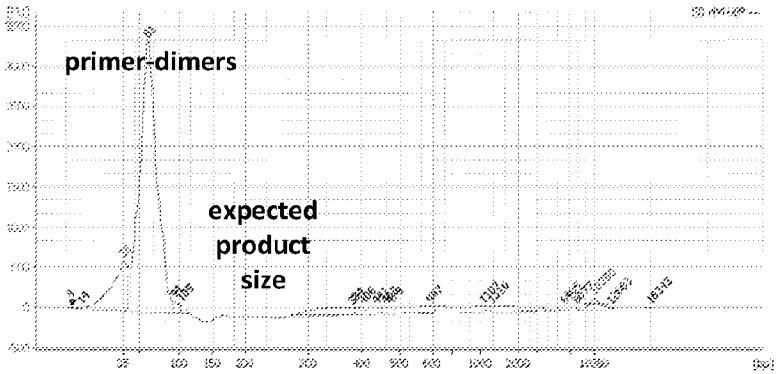
Pooling segregates primers into non-overlapping bins
Bioinformatically challenging, multiple pools, primer costs

Ion Multiplex Library Approach

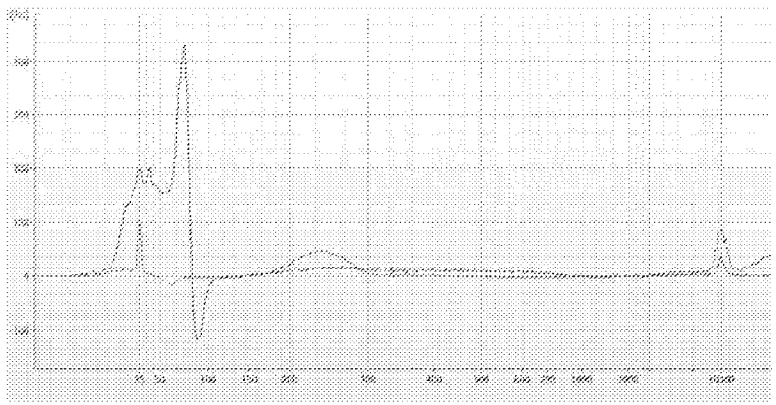


Modified Base destruction reduces dimers >99%

Standard Multiplex Primers:
Significant Dimers



Modified Multiplex Primers:
Blue - digested
Red – digested and Purelink purified



Modified Primers significantly remove dimers, enables permissive primer design

New Samples

- Cell cultures, with well characterized KRAS mutations
- FFPE preserved
- Received as paraffin slices, require treatment to release DNA
- Used Epicentre Quick-Extract (one of several possibilities)
  - Simple process, ~1 hour, PCR ready post-incubation

Benefits

- PCR-ready DNA in minutes, not days.
- No xylene or phenol extraction.
- No columns, transfers, or sample loss.
- Extracted DNA is compatible with both real-time and endpoint PCR.

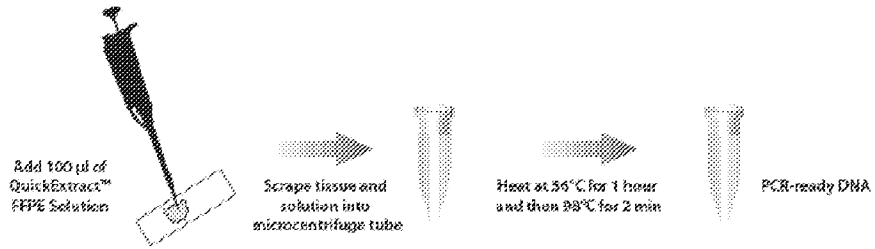


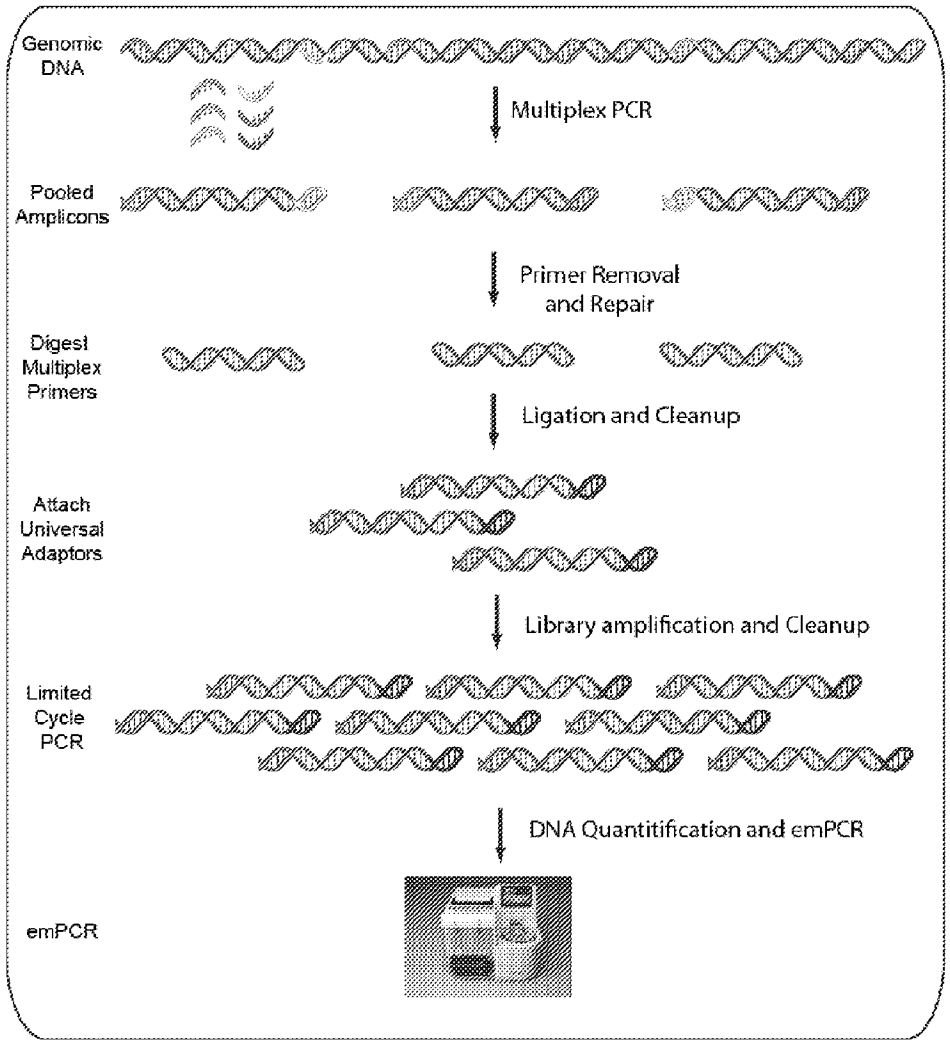
Figure 1. Overview of the QuickExtract™ FFPE DNA extraction procedure.

FFPE DNA

	Invitrogen gDNA extraction kit trial 1 total DNA (ng)		**Invitrogen gDNA extraction kit trial 2** total DNA (ng)	
Acrometrix contol	concentration (ng/ul)	total DNA (ng)	concentration (ng/ul)	total DNA (ng)
WT	2.32	58	2.75	68.75
G12A	3.19	79.75	3.48	87
G12C	2.99	74.75	3.19	79.75
G12D	8.42	210.5	8.6	215
G12R	2.67	66.75	2.38	59.5
G12S	7.99	199.75	5.44	136
G12V	1.12	28	1.05	26.25
G13D	0.653	16.325	0.449	11.225

To protect FFPE sample supply, 10 ng of input DNA is used (50 ng typical for wgDNA). This requires a few additional cycles of preamplification and library amplification.

Workflow (Process)



1.5 hours

0.5 hours

1 hour

0.5 hours

5 hours

Process Workflow

- ***Preamplification 20uL***
  - Input – 10-50 ng FFPE or gDNA
  - 16-20 cycle of PCR
- ***0.6x / 1.2x AMPure XP Purification***
  - 0.6x removes high MW DNA
  - 1.2x removed low MW DNA
- ***Phosphorylation***
- ***Ligation***
  - Ion forward and reverse primers
- ***1.8x AMPure XP Purification***
- ***Library Amplification***
  - Limited cycle PCR to increase library concentration
- ***1.8x AMPure XP Purification***
- ***Run on Agilent High Sensitivity DNA Chip to quantify***
  - Product should run at 150-200bp, yield should be ~5 x 10^9 copies per ul

Table 1. Representative list of genes from which loci were amplified and sequenced using the library preparation method disclosed.

ABL1	MET
AKT1	MLH1
ALK	MPL
APC	NOTCH1
ATM	NPM1
BRAF	NRAS
CDH1	PDGFRA
CDKN2A	PIK3CA
CSF1R	PTEN
CTNNB1	PTPN11
EGFR	RB1
ERBB2	RET
ERBB4	SMAD4
FBXW7	SMARCB1
FGFR1	SMO
FGFR2	SRC
FGFR3	STK11
FLT3	TP53
GNAS	VHL
HNF1A	IDH2
HRAS	GNAQ
IDH1	
JAK2	
JAK3	
KDR	
KIT	
KRAS	
LOC100289474	

TABLE 2

assay_id	SEQ ID	fwdUSeq	SEQ ID	revUSeq	chr	chr_start	chr_end	fwd_tm	fwd_size	rev_tm	rev_size	amp_len
30014	1	TTCGCCTGUCCTCATGTATUGG	2	AGTGGTTATAGAUGGTGAAACCTGTTUG	1	115256483	115256582	62.03	22	62.34	28	100
30373	4	CATCTACAAAGUGGTTCTGGATUAGCT	5	CTGGTGTGAAAUGACTGAGUACAAAC	1	115258691	115258791	61.9	27	61.46	26	101
31381	7	CCAACATGACTUACTTGATCCCCAUAA	8	GAGAAGCCATUATCTGCAAAAATAUCGC	2	209113079	209113181	61.91	27	61.7	28	103
31533	10	TGTAAACGTCAAUAGTGCAGAUGGG	11	ACCTTUGGAGGAAAACGCTATGAUG	2	212288895	212289003	62.47	25	61.94	25	109
32781	13	CATCGCCACAUAGGGUAGAACAT	14	CATGGCCTUCCAACTTGACUCT	2	212652695	212652797	61.68	23	62.18	22	103
32827	16	ACTTACGUGGACATTTCTUGACACA	17	CAAACCUTTGTCTACAAUCCAACCAC	2	212587112	212587211	62.02	25	61.91	26	100
33013	19	CCAAUGCAGCGAACAATGTTCUG	20	CCAGTTTAAGAUTTGCCCAGACUC	2	29443666	29443765	62.84	23	61.1	24	100
33555	22	GACAGTAACCCUACATATACAATUGCCT	23	GAAACTTTGGACUTCAAGAACTUGGAT	2	212812080	212812196	61.61	28	61.25	27	117
33659	25	CCAGTGACTAGAAAGAUCAAATTCCCAUT	26	GGCATUGGCACAGGATCATUG	2	212576784	212576893	62.25	29	61.99	21	110
33781	28	AAUCAAAUAGGGAAGGAAAGGAGAGC	29	TGACTGCUGCCATCGAGAAUG	2	212589743	212589861	61.84	26	62.53	21	119
34014	31	GAGGCAGTCUTTACTCACCTGUAG	32	CCAGAAACUGCCTCTTGACCUG	2	29432634	29432733	61.63	24	62.74	22	100
34860	34	GGTTTTTGCCCUTCCAGTGTAUACT	35	CCTGACGAUGTCCAGTCUCCT	3	10191454	10191553	62.39	25	62.78	21	100
35831	37	AAAAUGACAAAGAACAGCUCAAAGCA	38	CATTTTAGCACUTACCTGTGACUCCA	3	178936032	178936137	61.81	26	62.21	26	106
36101	40	ACATTTTCGUAAGTGTTACUCAAGAAGCA	41	GGTTGCCTACUGGTTCAATTACTTTUAA	3	178916816	178916935	62.52	29	61.19	28	120
36569	43	GGGAAGAAAAGUGTTTTGAAATGUGT	44	CAAACAAGTTUATATTTCCCCAUGCCA	3	178927906	178928013	60.36	26	61.63	27	108
37385	46	TGGATCTUCCACACAATUAAACAGCA	47	GCTGAGAGTTAUTAACAGTGCAGUGT	3	178952114	178952216	62.39	26	62.46	26	103
38772	49	TGACGTCGUCTTCTAGTTCUGGA	50	AGAGGCUGCAGAAATGCAUCAA	3	37067186	37067288	61.69	23	62.51	22	103
40184	52	TGTCTTTGAGTUCCATTCCACTTGUT	53	GATCTCTTGATACAUCAATCCGTGTTUG	4	153245417	153245521	62.28	26	61.42	28	105
40234	55	CCCTCCUGCCATCATATUGAACAC	56	TCTGCAGAGUTGTTAGCGGUT	4	153247262	153247390	62.79	24	61.73	21	129
41691	58	ACCATGACAAGAUTTTCCCTTACCTUT	59	ACTCAAAGUGTGGAAUGGAGAGA	4	153249337	153249452	61.99	27	61.62	23	116
41812	61	ACTGCTGACCAAACUTTTAAAGTGTUG	62	TTCTTATAGGTGCUGAAAGGACATGAUG	4	153250834	153250946	62.09	27	62.02	28	113
42297	64	CCTCTTUAGGGAGCAATGAAAUGAAGT	65	TGAACTCAUTGATAGTTGUGAACCAACA	4	153258953	153259053	62.34	27	62.23	28	101
43181	67	TGGGACTTTGGUAATTCACCAGTUAC	68	CTGCATCGGGUCCACATAAATATATUCA	4	55140963	55141091	62.17	26	62.17	28	129
43200	70	CCCATCTCCUAACGGCTTTTGUC	71	GGCTCAGGAAGCUATCCCTATUCT	4	55144499	55144612	62.9	23	62.59	24	114
43383	73	CAAGCTCTCATGUCTGAACTGAAGAUA	74	AAAATCCTCACUCCAGGTCAGUG	4	55144086	55144203	61.67	27	61.69	23	118
44733	76	CCATCCAUCCAGGAAAATCAGACTUAA	77	CTTATTCTCATTCGUTTCATCCAGGAUC	4	55561723	55561844	61.92	27	61.02	28	122
46166	79	TTTCGTAATCGUAGCTGGCAUGA	80	TCAGTCATUAGAGCACTCUGGAGAG	4	55593427	55593534	61.85	23	62.49	25	108
46436	82	CAACGATGUGGGCAAGACTUC	83	AGCCTAAACAUCCCCTTAAATTGGAUT	4	55592158	55592257	61.56	21	61.89	27	100
47704	85	GGAAGCCCUCATGTCTGAACUC	86	CAAUAAAAGGCAGCTUGGACACG	4	55594199	55594317	62.28	22	62.31	23	119
47725	88	CCTTCTACATGUCCCACTTGATUCAG	89	GCCTTGGTUGGGACAACAUAAGAA	4	55597443	55597559	62.31	26	62.81	24	117
48478	91	ACCTTCTTTCTAACCUTTTCTTATGTGCUT	92	CTGCTTTGAACAAAUAAATGAATCACGTUT	4	55595467	55595592	62.17	30	61.39	30	126
49160	94	CCTTACTCAUGGTCGGAUCACAAAG	95	GGACTGUCAAGCAGAGAAUGGG	4	55599271	55599387	62.52	25	62.54	22	117
49191	97	CTCGACUACCTGTGAAGUGGAT	98	ACAGCUCCCAAAGAAAAATCCCAUAG	4	55602665	55602766	60.85	22	62.51	26	102
49305	100	GGGTGTGGAUGCTTCCTTTUAA	101	AGCTGAUAGAGATTGGAGUGCAAAC	4	55946090	55946196	60.46	22	62.25	25	107
49402	103	AGCTTTAAAAGUTCTGCTTCCUCACT	104	TGGCATCUGAAGGCUCAAACC	4	55946193	55946298	62.11	26	62.71	21	106
50673	106	CAGTACCTGAUTCCTGCTGTGUT	107	GCAUGGAAGAGGATTCUGGACT	4	55953768	55953882	61.99	23	61.46	22	115
50695	109	CTGAGCATTAGCUTGCAAGAGATUT	110	GTGTTTTGCUTCTCTAGGUACCAGA	4	55955038	55955157	61.26	25	61.62	25	120
52170	112	CCAGTACCTTCCUCTTCTTCTACAUC	113	TTGGAGCAAUCCCTGTGGAUC	4	55960962	55961085	61.15	26	61.9	21	124
52189	115	GACCACAUTGAGATGGUGACCAAT	116	GTCCATACCTAUGATTTCCCTCTTUGT	4	55962427	55962549	62.38	24	61.48	27	123
52210	118	CGAAGAAGGGUATTCCCAGTUGA	119	TGTCATGGAATUGAAGTATGTGTUGGAG	4	55980296	55980400	61.49	23	61.77	28	105
52386	121	CTTCAATTTTAUTTCCTCCCUGGAAGT	122	GCGCTGTTAUCTCTTTCTTAUAGCCA	4	55972895	55973000	60.66	27	62.19	26	106
52394	124	AAAAATTTCUTCATCTCAGUCCCAGACT	125	TGCTTTGGAAGUTCAGTCAACTCUT	4	55979581	55979681	61.84	28	62.21	25	101
53695	127	GGAATTGGTCUAGGCAAGTACCAUC	128	ACTTCTTCCAUGACTTTGGCAAUCT	5	112173660	112173972	62.31	25	62.11	25	113
54189	130	TGTGTTTCUCCATACAGGUCACG	131	GACACAAAGACUGGCTTACATTTUGAT	5	112174583	112174682	61.97	23	61.56	27	100
59674	133	CACCATGACUTTGAGGTUGAGC	134	GTGUGTTCTGCTTUCCAGAGAGT	5	149452971	149453074	61.36	22	62.17	23	104
59934	136	CAGGTTCTUCCAGATGCTGAUACT	137	GTATAAATGGCUCATCGAGGCUCA	5	112175729	112175840	61.41	24	61.82	24	112
60049	139	GCAGCCUAAAGAATCAAAUGAAAACCAA	140	AGTATTTCAATATCAUCATCATCTGAATCAUCT	5	112175911	112176015	62.32	28	60	33	105
60239	142	TGGTACUCCCTGTCGUCAACT	143	GAGCTCTAGUGAGCACCUGAC	5	149433609	149433716	62.32	21	61.65	21	108
61096	145	ATACAGUCGGAGGTTCACUGC	146	AGTTGAUGAACCGGTCCTTUACAG	7	116339598	116339721	61.59	21	62.06	24	124
61118	148	GAACCAAUGGATCGATCUGCCA	149	TGCTGGAGACAUCTCACATTGTTTUT	7	116340201	116340301	62.36	22	62.61	26	101
62593	151	AGTGAATTAGUTCGCTACGAUGCAA	152	GAAAAGTAGCUCGGTAGTCTACAGAUT	7	116411911	116412037	62.23	25	61.24	27	127
62615	154	GTTACGCAGUGCTAACCAAGTUC	155	GCCACTTACUGTTCAAGGATTUCACA	7	116417406	116417532	61.75	23	62.87	26	127
64101	157	GTGGGCUACAAGAACTACCGAUAC	158	TTCACUCACCTCGGAUGAGGA	7	128846338	128846437	61.98	24	62.11	21	100
64212	160	GATTTTGGTCTUGCCAGAGACAUG	161	TTGAGTTUGCAGACTTUCCAAAGC	7	116423389	116423499	61.63	24	61.93	24	111
65601	163	ACATTACATACTUACCATGCCACTTUCC	164	GAGTGATGATUGGGAGATTCCUGA	7	140481361	140481470	62.44	28	61.17	24	110
67037	166	GTTATGTCCUCATTGCCCUCAAC	167	GCTAAGGCAUAGGAATTTTCGTAGUACA	7	55211017	55211116	61.04	23	62.06	28	100
67066	169	GACCAGACAACUGTATCCAGUGT	170	TTCCAGACCAGGGUGTTGTTUT	7	55232974	55233076	61.42	23	61.94	22	103
67641	172	CCTCTUACACCCAGUGGAGAAG	173	ACCTUATACACCGUGCCGAAC	7	55241623	55241738	61.38	22	62.19	21	116
68178	175	CCACGUACCAGATGGATGUGAAC	176	CAAGGATGCCUGACCAGTUAGAG	7	55221774	55221889	62.64	23	62.11	23	116
68572	178	TCTTCCTTCUCTCTCTGTCAUAGGG	179	TCGAGGATTUCCTTGTTGGCTUT	7	55242392	55242512	61.76	25	62.19	23	121
71564	181	CAGCATGTCAAGAUCACAGATTTUGG	182	ACCTAAAGCCACCUCCTTACTTUG	7	55259487	55259587	62.07	26	61.78	24	101
71577	184	ACATGAACUCCACGTTGCUACC	185	CTCCTCUCCCATCTUCCACAGA	8	38282134	38282238	62.47	22	62.27	22	105

TABLE 2

assay_id	SEQ ID	fwdUSeq	SEQ ID	revUSeq	chr	chr_start	chr_end	fwd_tm	fwd_size	rev_tm	rev_size	amp_len
71600	187	GGTTTGGTTUGGTGTTATCTGTTUCT	188	TGCCCCTUCTTCTTCCCAUAGAT	8	38285870	38285974	61.37	26	62.38	23	105
73075	190	CCCACUGAAAAGCACTTCCUGAA	191	CTTTCATGACUGCAGCTTCTTUCAA	9	133747461	133747567	62.69	23	61.6	25	107
73104	193	TGTTGAAGTCCUCGTTGTCTTGUT	194	GTAGTCCAGGAGGUTCCCGUA	9	133748218	133748317	62.12	24	62.18	21	100
73150	196	CCAACTACGACAAGUGGGAGAUG	197	CCGTCAGGCUGTATTTCTUCCAC	9	133738289	133738402	62.33	23	62.89	23	114
74598	199	GCAGCAAGUATGAUGAGCAAGCT	200	AGAAAGGCATUAGAAAGCCTGTAGTTUT	9	5073710	5073819	63.21	23	62.3	28	110
74743	202	GATTTTGGCCUGAGCAGGTUG	203	CGGACTTGAUGGAGAACTTGTTGUA	9	133750310	133750430	61.86	21	62.13	25	121
76043	205	GAGTATTTGGGCGAAUGCAGTTTUT	206	TGAUGAAGATGATUGGGAAACACAAGAA	10	123257972	123258071	62.17	25	62.3	28	100
76049	208	TTCTTCATUCGGCACAGGAUGA	209	CAATCUAGCGCCUGGAAGAGAA	10	123274713	123274841	61.65	22	61.76	22	129
77536	211	CCAGTTGTGGGUACCTTTAGATUCAG	212	GTGGAUCAAGCACGUGGAAAAG	10	123279456	123279565	62.26	26	61.92	22	110
78961	214	CTTCCAGGAGCGAUCGTTUG	215	CTGCTUCAGGACGTTGAACUCT	10	43613776	43613879	60.96	20	62.14	22	104
78994	217	GACTUGGCAGCCAGAAACAUC	218	TCCTCTTCACGUAGGAATCCTCUT	10	43615541	43615646	61.58	21	61.86	24	106
79119	220	CATCTTCTCTTUAGGGTCGGATUCC	221	AACACCCACACUTACACAUCACT	10	43617380	43617479	61.85	25	61.56	23	100
80635	223	TTTTTCTGUCCACCAGGGAGUAAC	224	TGCCACTGGUCTATAATCCAGAUGAT	10	89711859	89711958	61.96	24	62.43	26	100
81777	226	CCCAGACAUGACAGCCATCAUC	227	CCGCAGAAAUGGATACAGGUCAA	10	89624220	89624321	62.67	22	62.36	23	102
82011	229	CATTTGACCGUGGAGAAGTAGAAUCA	230	TCGTTTGCAUCACTAACACTACTAUCAG	11	108137917	108138043	62.03	26	61.99	28	127
82152	232	GACAGTUAAAGGCATTTCCTGUGAAA	233	GGTCCTGAATUGGAGGAATATATCTUCA	10	89717556	89717667	61.42	26	61.2	28	112
82652	235	AGGATTTGGUAATATTGCCGUCAAAGAA	236	ACAGGAAATTUCTAAATGTGACAUGACCT	11	108117791	108117894	62.43	28	62.16	29	104
82666	238	GAAGAAAAUAGAACTAGGCUGGGAAGT	239	GACACTGAAUGAGAAAATGGTAACACTUT	11	108119752	108119860	61.64	27	61.47	29	109
82758	241	ACATGGCTTTUGGTCTTCTAAGUGAA	242	GCAGCTTUACAGTTTTTCATAGUGAGAC	11	108123497	108123609	62.12	26	61.93	28	113
83478	244	TGTCAAAGUTCGAUCAGCAGCT	245	CTGTAGAUAGGCCAGCATUGGAT	11	108172375	108172492	62.15	22	61.44	23	118
83501	247	AGTCATTUAAAGCAGAATTTCGCTUAGC	248	AGGGAAGGCUCACCTUAACAA	11	108205736	108205849	61.99	28	60.79	21	114
83530	250	CTTAATTATTCUGAAGGGCCGTGAUGA	251	TCCTAGTTUCCGTGTTTCTCUGC	11	108206556	108206659	62.22	27	61.97	23	104
83554	253	CCTATGAGGGUACCAGAGACAGUG	254	GCCATACCTGTUTTCCCAATAAGTTTUC	11	108155103	108155207	62.74	24	62.16	28	105
83653	256	CTATATGTAGAGGCUGTTGGAAGCUG	257	CTTAAGGGCCUTGGTATAAGAUGCA	11	108170431	108170538	61.97	26	61.81	25	108
83779	259	GAAGUACCCAGATTUGACAAAGAAAACC	260	CACAAGTCAGTGUCTTTATCCAAATGUC	11	108173586	108173694	61.85	28	61.68	28	109
83902	262	GAGCAGUCAGCAGAACTTGTACAUA	263	GTAGGCAAACAACAUTCCATGAUGA	11	108218059	108218163	61.95	25	61.21	25	105
84622	265	TTCTGTTAAAGTUCATGGCTTTTGTGUT	266	CAGGGCTAAUTCATCCAACUCCA	11	108200890	108200989	61.71	28	61.82	23	100
84933	268	CCTCACTGAAACCUTTGTGTTTTUGT	269	GCCTTCTTCCACUCCTTTCAGUT	11	108236020	108236133	61.97	26	62.19	23	114
84984	271	GTCCACAAAAUGGTTCTGGAUCAG	272	CCTGAGGAGCGAUGACGGAATAUA	11	534233	534333	61.33	24	62.9	24	101
85006	274	GATGCTGUGAGAAAACCAUGGAAG	275	ATGAGATACACAGUCTACCTGGUAAGAA	11	108225537	108225662	61.63	24	61.73	28	126
85059	277	GGTGGACAAGUGAATTTGCTCAUAC	278	CATATACTGAAGAUCACACCCAAGCTUT	11	108236149	108236248	61.71	25	62.23	28	100
86500	280	GATGTTTCCTUCGTAGGTGTUGACT	281	GATAAATCGGUACTGTGCTTCTGUCT	12	112926812	112926922	62.13	25	61.86	26	111
87927	283	TCCTCATGUACTGGTCCCUCA	284	TGTTTCTCCCTUCTCAGGATTCCUA	12	25380238	25380363	61.5	21	61.9	25	126
87967	286	AGTAGGAAAUAGCAGCCTCACATUG	287	CCACGGGAAAGUGGTGAAGAUA	13	28592583	28592685	62.03	25	61.64	22	103
87993	289	GGUGATGAGCUACCAACCAAGA	290	GGGTTCTTCUGCCTCTCAUAGG	12	121431367	121431467	61.65	22	61.51	22	101
88109	292	GACAUAACAGTTATGATTTUGCAGAAAACAGA	293	CAGGCUCAGGACTUAGCAAGAAG	12	25378490	25378613	61.96	32	62.34	23	124
89417	295	GAAGTGGGTUACCTGACAGUGT	296	TGAAAGAGAGGCACUCATGUCAGAA	13	28602303	28602409	61.51	22	63.09	25	107
89439	298	GCAGAAACAUTTGGCACATUCCAT	299	ACCGGCTCCUCAGATAATGAGUA	13	28608189	28608312	62.36	24	61.89	23	124
89861	301	CTTCTTCCAGGUCCAAGATGGUAAT	302	ACGTTCTTTTCUATAGGGAAACCUCAAG	13	28610092	28610196	61.46	25	61.92	28	105
90401	304	GGTGACGUGTACCATCTGUAGCT	305	TTGTTTCGTCUATCTGCAGAACUGC	13	28608310	28608411	62.89	23	61.96	25	102
90912	307	GGUCGACAAAGGACAGCCTATTUT	308	GACCAAGAAAUGCATCTGTGGGTUA	16	68835593	68835709	62.6	24	61.93	25	117
91050	310	TGGTTCAAGCUGCTGACCTUC	311	GAATTACCGUGGTGGGATUGAAGAT	16	68846060	68846173	62.62	21	62.26	25	114
91174	313	TCTTCCTCAGACAUTCAAACGTGTUT	314	GGTGGAAGCAUACTGCAAAATATTTGUT	13	49039124	49039244	62.32	26	62.17	28	121
91406	316	GGCTAACGUCGTAAUCACCACA	317	GACAAATTGUCCACCATCATCATUCAAT	16	68847242	68847350	62.25	22	61.76	28	109
91827	319	TATTCTTTCCTTTGUAGTGTCCATAAATTCTUT	320	GCTGAAGAGUGCAAACAATACATCAUAC	13	48919199	48919324	60.67	33	62.03	28	126
91829	322	TCTGCATTGGUGCTAAAAGTTTCTUG	323	AGTCCAAAGGAAUGCCAATTTAATTATUAC	13	48923111	48923228	61.91	26	60.05	30	118
91909	325	GGCAACTUGACAAGAGAAATGAUAAAACA	326	TTGTTAGCCAUATGCACATGAAUGAAT	13	48955502	48955630	61.92	29	61.04	27	129
92464	328	GTCTACATGGGUGCTTCCCAUT	329	TGACATGGTUGGGACTCTUGAC	17	37881276	37881386	61.99	22	61.84	22	111
93379	331	CCTTGUCCCCAGGAAGCAUAC	332	GCCATAGGGCAUAAGCTGTGUC	17	37880967	37881083	62.23	21	62.99	22	117
94170	334	CTGGAGTCTUCCAGTGTGATGAUG	335	CCTAGGTUGGCTCTGACTGUAC	17	7577499	7577613	62.17	24	61.44	22	115
98573	337	TGGCCTGATCTUCACAAAAATGAACUA	338	CAACTCGTTCGUAGTGATATGGATUCA	18	48575107	48575215	62.24	27	61.97	27	109
98681	340	GAAGGATGAATAUGTGCATGACTTUGAG	341	CGATGCACGAUTACTTGGUGGAT	18	48581170	48581269	61.64	28	62.7	23	100
99638	343	CTCTAGGUCAGCCTGCCAGTAUA	344	CCAGTAAATCCAUTCTGCTGCUGT	18	48584489	48584591	62.2	23	62.67	24	103
101246	346	GTCTTTGATTUGCGTCAGTGUCAT	347	GAGCTATTCGCACGUAGTGATCGUG	18	48603008	48603137	61.56	24	61.28	24	130
103227	349	CTCTGACCUTAGCAGGAUCCAG	350	ACTTAGCUTGGAAGCUGACAAGT	19	17945654	17945757	61.25	22	61.62	23	104
103630	352	AGATGCCGGUACGACACTUG	353	CACAAAATTUGGGATTATTGGAGUGGA	19	17947973	17948089	62.1	20	61.37	27	117
103879	355	AACAUCACCACGGGTCTGUAC	356	CACCTTUCAGGAGGUCAGAGAG	19	1221216	1221342	61.8	21	62.21	22	127
104671	358	GAGATCCATUGACCTCAATTTTGTTUCA	359	GGTAACAGUTGGCTTACUGGAAGT	20	57484376	57484495	61.45	28	62.01	24	120
104720	361	GTGGGAAACUACCTCCGTATGUT	362	CAACTATTTTCUTCCTCTCTUCCACAGT	22	24133943	24134042	61.49	23	61.87	28	100
106398	364	TGTGATCCAUGAGAACGCATCUC	365	TGTACCATTCAUGTTCCAGGUGAAG	22	24145503	24145614	62.15	23	62.15	25	112
107255	367	GCUCCACAACCAUCAACAGGAA	368	GAGAACUAAGGCGGAAUCAGCA	22	24143208	24143320	62.69	22	62.02	22	113
110679	370	TGAGTUCCAAGGCCTCATUCAG	371	TGAACCATCTTTUAACTCAGGTACTGUG	17	7573976	7574097	61.91	22	62.07	28	122

TABLE 2

assay_id	SEQ ID	fwdUSeq	SEQ ID	revUSeq	chr	chr_start	chr_end	fwd_tm	fwd_size	rev_tm	rev_size	amp_len
116963	373	GAATTGGTGTUGATGACCTTCGUC	374	GGGCCCGGUGTAAGTGAAUT	18	48604644	48604775	61.61	24	62.36	20	132
117792	376	TCTTGTCCUGCTTGCTTACCUC	377	GGUAATCTACUGGGACGGAACAG	17	7577000	7577154	61.9	22	61.6	23	155
118631	379	GCCAGAACTACAAUCTTTTGATGACAUT	380	CAATCCAUTTTTGTTGUCCAGCCA	3	178951975	178952115	61.49	28	62	24	141
120430	382	GUTGTTGAUGGCAAACACACACA	383	GAAGCAGGUGGTCATTGAUGG	11	533798	533933	62.33	23	61.04	21	136
121852	385	GAGTATTGGTGTUCCATTGCTTACTTUG	386	GACAUTGGAGAGTUGACCCAAAC	18	48591798	48591947	61.94	28	61.16	23	150
122008	388	CTCTCUGCACAGCTCCAAUGA	389	CCAGGGCUTTGAAGGAAGUGT	7	128845979	128846109	61.87	21	62.31	21	131
133212	391	CAGAATGAGGUGCAGAACAUCAAG	392	CCTCTGUGAAGAGCGGGTUC	7	128845041	128845179	61.38	24	62.39	20	139
136501	394	CGTCTCCUCCGACCACUGT	395	GCTTATTTATTGGUCTCTCATTCUCCCA	10	123279612	123279745	63.22	19	61.82	28	134
136537	397	CCTCCAGGAAGCCUACGUGA	398	AATATTGTCTTTGUGTTCCCGGACAUA	7	55248979	55249129	63.01	20	61.86	27	151
142574	400	CAGTGTGTAUGCAGGCAUCCT	401	GGGAGAUCTTGUGCACGGT	4	1806091	1806227	62.22	21	61.96	19	137
143592	403	TTAAATACAGAAGGCAUAAATATUCCAGCAGA	404	TCAAGAGTTAATUGCAAATTACCTTAATTUCCA	11	108204603	108204717	61.91	32	61.43	33	115
145156	406	CCAGAUAGCCCUGGACAAACC	407	CAGCATTTACUGCAGCTTGCTUAG	5	112175561	112175714	62.23	21	62.2	24	154
147815	409	AACAAAACCATGTAAUAAAATTCTGACTACTUT	410	GAGGAAGATCCUTGTATGCTGTUAC	13	49037814	49037957	60.05	33	60.34	25	144
178642	412	CTAUTTTTCCCTTTCUCCCCACAGA	413	TGACCAAAACUCAGCCTGTTUCT	4	55593558	55593712	61.64	25	62.07	23	155
226369	415	CTCACCAUCGCTATCUGAGCAG	416	GTGCAGCUGTGGGTTGATUC	17	7578366	7578503	62.19	22	61.74	20	138
226460	418	CTTACCCTUGGGTGCAGTTUG	419	GCTCUCATTTTAAAGAUGGCCCAAA	2	212530043	212530180	61.18	21	61.45	25	138
226789	421	CCAGTUGCAAACCAGACCUCA	422	CTGATTCCTCACUGATTGCTCTUAGG	17	7578160	7578314	62.57	21	62.14	26	155
227540	424	TUTATCTTCAGAAUCAGCCAGGCA	425	CTGACAGAAGUACATCTGCTAAACAUGA	5	112175314	112175463	61.6	24	61.95	28	150
232121	427	GATAGGTCACCUTTGGCTCTUCAG	428	AGTACCUGGCAGTGTGATATUGG	3	10188193	10188325	62.18	24	61.56	23	133
234145	430	GCAGTGTGUCCACCGTGAUC	431	GTACACTGCCUTTCGACACATAGUT	4	55152004	55152134	63.27	20	62.4	25	131
236158	433	GATGTCTATGAAGUGTTGTGGTTCCUT	434	ACTGTUACAGAAATGAAAUAAGACGGAAA	5	170837476	170837628	62.27	27	60.63	29	153
255119	436	CAAATTGTAAATTTUCAGTATGTGAATGACTUC	437	GGAAAATTCATACCUAACTGGAGTGUGT	13	48942614	48942753	60.01	33	62.13	28	140
304699	439	CTGUTCAAACTGAUGGGACCCA	440	TGCTTGCTCTGAUAGGAAAATGAGAUC	7	140453099	140453250	62.12	22	62.22	27	152
309408	442	GAAGAAAUGGAGCTGUCACCCA	443	CTTTTAATUGCCCGTGATGTUCCA	12	112888121	112888252	62.17	22	61.57	24	132
310032	445	CACTCACAGTUTCCATAGGTCUGAAAAT	446	ATCCCCACUTTTCCTCTUGCA	17	7579832	7579962	62.33	28	61.43	21	131
320120	448	GTCATCAGCUGAAGATGAAATAGGAUGT	449	GCTGTGACACUGCTGGAACUT	5	112175131	112175276	62.07	28	62.88	21	146
329410	451	CCCCAAAUCTGAAUCCCGAGA	452	CGCTACTTCCUCCTCAAGAATGAUG	14	105246386	105246527	61.34	21	62.34	25	142
339432	454	CAGAGGTTUGGGCTGCTTTUG	455	ATCCTTCTTCTCCUGTTTGAGAATGUC	3	178938802	178938933	62.06	21	61.85	27	132
341576	457	GTGCGUCACGCTUGAAGAC	458	GGACTGUGCGGAGCATGUAC	9	139399312	139399466	61.95	19	63.06	20	155
379514	460	CAATTTTTAATGAUGCTTTCTGGCUGGA	461	CATACTTTTCTTAUCTGCATAGATTTCUGC	11	108180901	108181025	62.17	28	60.01	30	125
411633	463	CGAGGACAACGUGATGAAGAUCG	464	GGCGTCCUACTGGCAUGAC	4	1807819	1807950	62.94	23	62.74	19	132
416298	466	TGCTTACTAATGUGGTTTTAATTTCATCAUG	467	GATUAAGAGGACAAGCAGATUCAAGGT	13	49027088	49027213	60.37	31	62.12	27	126
416888	469	GCGTGCAGAUAATGACAAGGAATAUC	470	GTCAACAACCCCCACAAAAUGTTUAAT	10	89720770	89720911	61.56	26	62.17	27	142
421278	472	CGACGGGAAGACAAGUTCATGUA	473	TTCTCCCAATGAAAGUAAAGTACAAACCUT	10	89717672	89717803	62.02	23	62.12	30	132
423052	475	GCTGATTTGAUGGAGTTGGACAUG	476	CAGGATTGCCUTTACCACUCAGA	3	41266016	41266160	61.69	24	61.75	23	145
464386	478	ATGGTGGCTTTUTGTTTGTTTGTTTUG	479	CAAGCAGATAACTUTCACTTAATAGTTGTUT	10	89685236	89685387	62.03	27	60.08	31	152
482180	481	CAAGAAUCGCCCGAGCCTTCUG	482	CACCAGGUACGCCTCCAGAUGAG	7	128850264	128850386	65.37	22	65.89	23	123
482609	484	GAAUGCGGCCACGUCGGT	485	GGTCCCAGCCCCUCTCTGATUG	9	139397695	139397813	65.89	18	66.02	22	119
482833	487	GACACGTTCAUCCACCGCAUCG	488	CCGAGUCCAGCACCTCCTUCAC	19	1206979	1207120	65.84	22	66.41	22	142
483802	490	CACGGGUCGGGTGAGAGUGG	491	CACCCTGGCUCTGACCATTCUGT	9	21971112	21971242	66.62	20	65.81	23	131
484088	493	CACTCCTCTUCCAGGCGGAUGA	494	GAGAGGCGGCCCAAUCTTCUG	22	24176314	24176423	65.4	22	64.91	21	110
484297	496	CACTTTTGGGUAAATACATTCTTCAUACCAGGA	497	CACGCTCTAUACTGCAAATGCTAUCGA	10	89720663	89720774	63.79	33	64.12	27	112
484410	499	GAGAATGTGAAAAUTCCAGTGGCCAUCA	500	GGGTCCTUCCTGTCCTCCUAGCA	17	37880186	37880307	64.82	28	66.46	23	122
484618	502	CAGACTTGGCUGTCCCAGAAUGC	503	CCCUGCACCAGCAGCTCCUA	17	7579323	7579465	65.26	23	66.14	20	143
490549	505	CCAGUGCCCAUCCCACCGA	506	CACCGTGAAGUCCTGAGTGTAGAUGA	19	1223018	1223167	66.57	19	64.85	26	150
491413	508	ACATGGCCACUCAGATCTCGUCAG	509	CTCCACGCCCUGTGACUCCAT	9	133748364	133748473	65.53	24	66	21	110
492612	511	CCCCACCCACAGAUCCACUGT	512	TGGUAGCAGTGGAUGCAGAAGG	10	43609916	43610030	65.7	21	63.95	22	115
492615	514	GCCCAGCAUGTCACCAAGAUGGT	515	CCTTCCUCCAGAAGCTTGAACTCUCA	7	128851530	128851640	66.91	23	65.08	26	111
493041	517	TCCCCTGCAGCUGGTCCTTUG	518	CAGTUGGCGGGCTTGUCCAT	4	1808263	1808398	66.55	21	65.42	20	136
495041	520	TCCTTGGUGACCGCTCUGCAT	521	CCTGGUCCACCGCCAGTCUC	1	43814942	43815070	65.96	21	66.68	20	129
503320	523	TGCAUAGCCAGGGCATTGUGC	524	CCCCUAGCACGTGCCUACCT	19	1220407	1220522	65.76	21	65.56	20	116
504796	526	GGCUGCTGGACATUGACGAGACA	527	GTTCTCCCAUGGGCUAGACACCA	17	37881411	37881520	66.54	23	65.33	23	110
505293	529	GGGACGACUCCGTGTTUGCC	530	CTGCUAGGGACCCCTCACATUG	4	1808919	1809029	65.64	20	64.02	22	111
507582	532	TGUCCCCAUCACAGGCACAGG	533	GGCCCGCUGTACGTGUCCAT	12	121431990	121432119	66.27	21	67	20	130
508777	535	GGTGGCCCCUGAGCGUCAT	536	GCAGTGGAACUCCACGUCGCT	4	1803531	1803647	66.91	19	66.98	21	117
516350	538	CTTTTTTCTTCCUAAGGTTGCACAUAGGCA	539	ACTCTGUACAAAGACCGCGUGGT	18	48593373	48593482	64.71	30	65.65	23	110
552959	541	GAATTTTTGTTGTCTTUTCTTTAGGGCCTGUT	542	TTCAATCACCACTAAAUCAATCTAAATACAGGAAAUC	18	48586212	48586342	63.98	32	62.68	37	131
553293	544	ACCTCTATTGTUGGATCATATTCGUCCACAAA	545	TTTTTATTATAAGGCCUGCTGAAAATGACTGAATAUA	12	25398206	25398342	64.79	32	62.38	37	137
554194	547	AATGGAGAAACAUCTACAAAATCCCTTUGG	548	AAAATAATAAGCATCAGCAUTTGACTTTACCTTAUCA	3	178921473	178921607	62.9	30	62.85	37	135
555556	550	AGTAAAAATGACTAATTTTUCTTATTCCCACAGTGUA	551	GGGTGTGCUGGAAAAGGUCCA	13	49033791	49033925	62.38	37	66.64	22	135
559669	553	GGATTAAAGCUGGCTATGGCACCUG	554	GTGCTGTUGAGACCTCTGUGGG	10	43609046	43609184	65.07	25	64.67	22	139
613072	556	CGTCGTGCUGCCCGTAUGG	557	GCCCGTACCUCGGTAGCUGT	3	10183777	10183879	65.86	19	65.82	20	103

TABLE 2

assay_id	SEQ ID	fwdUSeq	SEQ ID	revUSeq	chr	chr_start	chr_end	fwd_tm	fwd_size	rev_tm	rev_size	amp_len
645344	559	GGCAAATGUCAGTGCAAGGTTUACACA	560	TTTTTTTTTAATCAGAUAACTTTGTGGTAGATUCCAGT	2	212578266	212578387	65.59	27	62.69	37	122
649396	562	GAGCGGCCCACCUTCGAGUA	563	CCGCCTGUGCCTAGAGGTUCT	20	36031693	36031792	66.1	20	65.73	21	100
658417	565	GGCAGGTCUTGGCCAGTUGG	566	CTGTTCACTTGUGCCCTGACTTUCAA	17	7578506	7578605	65.71	20	64.91	26	100

TABLE 2

assay_id	SEQ ID	amplicon
30014	3	ttcgcctgtcctcatgtattggTCTCTCATGGCACTGTACTCTTCTTGTCCAGCTGTATCCAGTATGTCCAAcaaacaggtttcaccatctataaccact
30373	6	catctacaaagtggttctggattagctGGATTGTCAGTGCGCTTTTCCCAACACCACCTGCTCCAACCACCACCAgtttgtactcagtcatttcacaccag
31381	9	ccaacatgacttacttgatccccataaGCATGACGACCTATGATGATAGGTTTTACCCATCCACTCACAAGCCGGgggatatttttgcagataatggctttctc
31533	12	tgtaaacgtcaatagtgcagatgggAGGCTGAGGCAAACGTTCTCCTTTCTCTAATAAATCAGGGATTTCTCGCGTTGGAATTCcatcataggggttttcctccaaaggt
32781	15	catcgccacatagggtagaacatTTTGAGAAATTAAAAAGAATAATTCTACTTACATCCTGAACTACCATTTGTTGACACAagagtcaagttggaaggccatg
32827	18	acttacgtggacatttcttgacacaGAATGCTCCATATGTGTACTTTGCATTGAAATTGTGCTCCAGTTGAAAGgtggttggattgtagacaaaggtttg
33013	21	ccaatgcagcgaacaatgttctgGTGGTTGAATTTGCTGCAGAGCAGAGAGGGATGTAACCAAAATTAACTGAGCTgagtctgggcaaatcttaaactgg
33555	24	gacagtaaccctacatatacaattgcctTATATTGATAATGAAAGCATATTTGCCATTTTGGATATATTCCTTACCTGTCAAGTTCTTTAatccaagttcttgaagtccaaagtttc
33659	27	ccagtgactagaaagatcaaattcccattGATCTTGGTACAGTTTATGAATTTGTCAATGTTACTGGAATCCACAGTCTGAGCTGACATcaatgatcctgtgccaatgcc
33781	30	aatcaaatagggaaggaaaggagagcAGGATAATAAAAGAGAGAAATCACAGACATACAAAGCAGTCTGTGTCCTTAGGTCCTGAGCAGCCTCCAGCAcattctcgatggcagcagtca
34014	33	gaggcagtctttactcacctgtagATGTCTCGGGCCATCCCGAAGTCTCCAATCTTGGCCACTCTTCCAGGGCCTGGAcaggtcaagaggcagtttctgg
34860	36	ggtttttgcccttccagtgtatactCTGAAAGAGCGATGCCTCCAGGTTGTCCGGAGCCTAGTCAAGCCTGAGAATTACaggagactggacatcgtcagg
35831	39	aaaatgacaaagaacagctcaaagcaATTTCTACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTTCTAtggagtcacaggtaagtgctaaaatg
36101	42	acattttcgtaagtgttactcaagaagcaGAAAGGGAAGAATTTTTTGATGAAACAAGACGACTTTGTGACCTTCGGCTTTTTCAACCCTTTttaaaagtaattgaaccagtaggcaacc
36569	45	gggaagaaaagtgttttgaaatgtgTTTATAATTTAGACTAGTGAATATTTTTCTTTGTTTTTTAAGGAACACTGTCCATtggcatggggaaatataaacttgtttg
37385	48	tggatcttccacacaattaaacagcaTGCATTGAACTGAAAAGATAACTGAGAAAATGAAAGCTCACTCTGGATTCCacactgcactgttaataactctcagc
38772	51	tgacctcgtcttctacttctggaAGTAGTGATAAGGTCTATGCCCACCAGATGGTTCGTACAGATTCCCGGGAACAGAAGCttgatgcatttctgcagcctct
40184	54	tgtctttgagttccattccacttgttAACGACTGGTGCCCTGTTAACGTGTGAATGCAATTCCCTGTCTCCACATCCcaaacacggattgatgtatcaagagatc
40234	57	ccctcctgccatcatattgaacacAGCGGACTGCTGCAACATGACCCATCAAAACATGTAAACACTGGCCTGTCTCAATATCCCAAACCCTAAGAGTGGCATCTCGAGaaccgctaacaactctgcaga
41691	60	accatgacaagattttccctaccttTTTCATGAAGATGCATACAACGCACAGTGGAAGTATGCCCATATAAGGTGTGTATACATTCTCCAGtctctgcattccacacttgagt
41812	63	actgctgaccaaacttttaaagtgttgTCATCAGAACCACTAACTATTCGGTTACCACAAAACTGTAAGCATGTGATCACATGATcatcatgtcctttcagcacctataagaa
42297	66	cctctttagggagcaatgaaatgaagtCTCGTTGAAACTGGGGTTCTATCACTTGCATCATATGTTTTACTTGtgttggttcacaactatcaatgagttca
43181	69	tgggactttggtaattcaccagttacCTGTCCTGGTCATTTATAGAAACCGAGGTATGAAATTCGCTGGAGGGTCATTGAATCAATCAGCCCAGATGGACAtgaatatatttatgtggacccgatgcag
43200	72	cccatctcctaacggcttttgtcCCCATAGGCCCCATTTACATCATCACAGAGTATTGCTTCTATGGAGATTTGGTCAACTATTTGCATAagaatagggatagcttcctgagcc
43383	75	caagctctcatgtctgaactgaagataATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGAGCCTGCACCAAGTCAGGTGGGCTcactgacctggagtgaggatttt
44733	78	ccatccatccaggaaaatcagacttaaTAGTCCGCGTGGGCGACGAGATTAGGCTGTTATGCACTGATCCGGGCTTTGTCAAATGGACTTTGAgatcctggatgaaacgaatgagaataag
46166	81	tttcgtaatcgtagctggcatgaTGTGCATTATTGTGATGATTCTGACCTACAAATATTTACAGGTAACCATTTATTTGTTCTctctccagagtgctctaatgactga
46436	84	caacgatgtgggcaagacttcTGCCTATTTTAACTTTGCATTTAAAGGTAACAACAAAGGTATATTTCTTTTTaatccaatttaaggggatgtttaggct
47704	87	ggaagccctcatgtctgaactcAAAGTCCTGAGTTACCTTGGTAATCACATGAATATTGTGAATCTACTTGGAGCCTGCACCATTGGAGGTAAAGCcgtgtccaagctgccttttatg
47725	90	ccttctacatgtcccacttgattcagTCATGACTTGTTTCATCTCTCCCAGCAGCGATAGTACTAATGAGTACATGGACATGAAACCTGGAGTttcttatgttgtcccaaccaaggc
48478	93	accttctttctaaccttttcttatgtgcttTTAGGGCCCACCCTGGTCATTACAGAATATTGTTGCTATGGTGATCTTTTGAATTTTTTGAGAAGAaaacgtgattcatttatttgttcaaagcag
49160	96	ccttactcatggtcggatcacaaagATTTGTGATTTTGGTCTAGCCAGAGACATCAAGAATGATTCTAATTATGTGGTTAAAGGAAACGTGAGTAcccattctctgcttgacagtcc
49191	99	ctcgactacctgtgaagtggatGGCACCTGAAAGCATTTTCAACTGTGTATACACGTTTGAAAGTGACGTCTGGTCctatgggatttttctttgggagctgt
49305	102	gggtgtggatgcttcctttttaaACAGGAGGAGAGCTCAGTGTGGTCCCCGAGTCAGGCTGGAGAATCTGGGCTGTGCTACCGgtttgcactccaatctctatcagct
49402	105	agctttaaaagttctgcttcctcactGGAGTACACGGTGGTGTCTGTGTCATCGGAGTGATATCCGGACTGGTAGCCGCTTGTCTggtttgagccttcagatgcca
50673	108	cagtacctgattcctgctgtgttGTCATAATGGAATTTGGGGTCACATACTTCCTCCTCCTCCATACAGGAAACAGGTGAGGTAGGCAGAGAGagtccagaatcctcttccatgc
50695	111	ctgagcattagcttgcaagagatttCCCAAATGTTCCACCAACTCTGAAAACGTGGGTCTCTGACTGGGCTCCCCGTGCCAGCAGTCCAGCATGGtctggtacctagagaagcaaaacac
52170	114	ccagtaccttcctcttcttctacatcACTGAGGGACTTCTCCTCCACAAATCCAGAGCTGGCTGAGCTCTGGCTACTGGTGATGCTGTCCAAGCGCCGTTTCAgatccacagggattgctccaa
52189	117	gaccacattgagatggtgaccaatATGAATGAGGATCTTGAGTTCAGACATGAGAGCTCGATGCTCACTGTGTGTTGCTCCTTCTACAAATACAGTacaaagagggaaatcataggtatggac
52210	120	cgaagaagggtattcccagttgaAGTCAATCCCCACATTTAGTTCAGTTCTTGCTGTACAATTTAAGACAAGCTTTTctccaacagatagttcaattccatgaga
52386	123	cttcaattttatttcctcccctggaagtCCTCCACACTTCTCCATTCTTCACAAGGGTATGGGTTTGTCACTGAGACAGCTtggctataagaaagagatataacagcgc
52394	126	aaaaatttcttcatctcactcccagactGGGTTTTTAGGTCTCGGTTTACAAGTTTCTTATGCTGATGCTGAAAAAaagagttgactgaacttccaaagca
53695	129	ggaattggtctaggcaactaccatcCAGCAACAGAAAATCCAGGAACTTCTTCAAAGCGAGGTTTGCAGATCTCCACCACTGCAGCCCagattgccaaagtcatggaagaagt
54189	132	tgtgtttctccatacaggtcacgGGGAGCCAATGGTTCAGAAACAAATCGAGTGGGTTCTAATCATGGAATTAatcaaaatgtaagccagtctttgtgtc
59674	135	caccatgactttgaggttgagcCCCTCCCCCACGGTCACCTCCTGGATGAGGTTCTGCTCAGAGCTCAAGTTCAAGTAGGCactctctggaaagcagaacacac
59934	138	caggttcttccagatgctgatactTTATTACATTTTGCCACGGAAAGTACTCCAGATGGATTTTCTTGTTCATCCAGCCTGAGTGCTCtgagcctcgatgagccatttatac
60049	141	gcagcctaaagaatcaaatgaaaaccaaGAGAAAGAGGCAGAAAAAACTATTGATTCTGAAAAGGACCTATTagatgattcagatgatgatgatattgaaatact
60239	144	tggtactccctgtcgtcaactCCTCAGCAGAACTGATAGTTGTTGGGCTGCAGCAAGGGCTGGGCGATATCCCCTTGCTCGCAGCAGgtcaggtgctcactagagctc
61096	147	atacagtcggaggttcactgcATATTCTCCCCACAGATAGAAGAGCCCAGCCAGTGTCCTGACTGTGTGGTGAGCGCCCTGGGAGCCAAAGTCCTTTCATctgtaaaggaccggttcatcaact
61118	150	gaaccaatggatcgatctgccaTGTGTGCATTCCCTATCAAATATGTCAACGACTTCTTCAACAAGATCGTCAACaaaaacaatgtgagatgtctccagca
62593	153	agtgaattagttcgctacgatgcaaGAGTACACACTCCTCATTTGGATAGGCTTGTAAGTGCCCGAAGTGTAAGCCCAACTACAGAAATGGTTTCAAATGaatctgtagactaccgagctacttttc
62615	156	gttacgcagtgctaaccaagttcTTTCTTTTGCACAGGGCATTTTGGTTGTGTATATCATGGGACTTTGTTGGACAATGATGGCAAGAAAATTCACTGTGCtgtgaaatccttgaacagtaagtggc
64101	159	gtgggctacaagaactaccgatacCGTGCGGGCTTCGTGCTGGCCCCAATCGGCCTGGTGCTCATCGTGGGAGGCTACTtcctcatccgaggtgagtgaa
64212	162	gattttggtcttgccagagacatgTATGATAAAGAATACTATAGTGTACACAACAAAACAGGTGCAAAGCTGCCAGTGAAGTGGATGgcttggaaagtctgcaaactcaa
65601	165	acattacatacttaccatgccactttccCTTGTAGACTGTTCCAAATGATCCAGATCCAATTCTTTGTCCCACTGTAATCTGCCCAtcaggaatctcccaatcatcactc
67037	168	gttatgtcctcattgccctcaacACAGTGGAGCGAATTCCTTTGGAAAACCTGCAGATCATCAGAGGAAATAtgtactacgaaaattcctatgccttagc
67066	171	gaccagacaactgtatccagtgtGCCCACTACATTGACGGCCCCCACTGCGTCAAGACCTGCCCGGCAGGAGTCATGGGAGaaaacaacaccctggtctggaa
67641	174	cctcttacacccagtggagaagCTCCCAACCAAGCTCTCTTGAGGATCTTGAAGGAAACTGAATTCAAAAAGATCAAAGTGCTGGGCTCCGGTGCgttcggcacggtgtataaggt
68178	177	ccacgtaccagatggatgtgaacCCCGAGGGCAAATACAGCTTTGGTGCCACCTGCGTGAAGAAGTGTCCCCGTGAGTCCTCCTCTGTGGGCCctctaactggtcaggcatccttg
68572	180	tcttccttctctctctgtcatagggACTCTGGATCCCAGAAGGTGAGAAAGTTAAAATTCCCGTCGCTATCAAGGAATTAAGAGAAGCAACATCTCCGaaagccaacaaggaaatcctcga
71564	183	cagcatgtcaagatcacagattttggGCTGGCCAAACTGCTGGGTGCGGAAGAGAAAGAATACCATGCAGAAGGAGGcaaagtaaggaggtggctttaggt
71577	186	acatgaactccacgttgctaccCAGGGCCACTGTTTTGTTGGCGGGCAACCCTGCTTGCAGGATGGGCCGGTGAGGGGACCGCtctgtggaagatgggagaggag

TABLE 2

assay_id	SEQ ID	amplicon
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73075	192	ccactgaaaagcactcctgaaATAATTTCACCTTCGTTTTTTTCCTTCTGCAGGAGCACACCATGGAGGTGTGGAAGAGTTCtgaaagaagtgcagtcatgaaag
73104	195	tgtgaagtcctcgttgtcttgtgtGGCAGGGGTCTGCACGCGGGAGCCCCCGTTCTATATCATCACTGAGTTCATGACCtacgggaacctctggactac
73150	198	ccaactacgacaagtgtgggagatgGAACGCACGGACATCACCATGAAGCACAAGCTGGGCGGGGGCCACTACGGGGAGGTGTACGAGGGGCGTgtggaagaaatacagcctgacgg
74598	201	gcagcaagtatgatggcaagctTTCTCACAAGCATTTGGTTTTAAATTATGGAGTATGTCTGTGGAGACGAGAGTAAGTaaaactacaggctttctaatgcctttct
74743	204	gatttggcctgagcaggttgATGACAGGGGACACCTACACAGCCCATGCTGGAGCCAAGTTCCCCATCAAATGGACTGTGCACCCGAGAGCCTGGCCtacaacaagttctccatcaagtccg
76043	207	gagtatttgggcgaatgcagttttCCTCCTACTCACCATCCTGTGTGCAGGCTCCAAGAAGATTTATGATAttctgttgtttccaatcatctcatca
76049	210	ttctfcattcggcacaggatgaCTGTTTACCACATACAGGCGATTAAGAAGCACCCTATGCAGTAAATGGCTATCTCCAGGTAGTCTGGGGAAGCTGTAATCTCCTTttctcttccaggcgctagattg
77536	213	ccagttgtgggtacctttagattcagAAAGTCCTCACCTTGAGAACCTTGAGGTAGGGCAGCCCGTCGGGCCCGTATTTACTGCCGTTctttttccagtgctgatccac
78961	216	cttccaggaggcgatcgttgCAACCTGCTGTGCTGCTCATTTCAGAGAACGCCTCCCCGAGTGAGCTGCGAGAACCTGCTGTCagagttcaagtccdgaagcag
78994	219	gacttggcagccagaaacatccTGGTAGCTGAGGGCGGAAGATGAAGATTTCGGATTTCGGCTTGTCCCGAGATGTTTATGaagaggattcctacgtgaagagga
79119	222	catcttctcttaggcgcggattccAGTTAAATGGATGGCAATTGAATCGCTTTTTGATCATATCTACACCACGCAAagtatgtgtaagtgtgggtgtt
80635	225	ttttctgtccacaggcgagtaacTATTCCCAGTCAGAGGCGCTATGTGTATTATTATAGCTACCTGTTAAAGAatcatctggattatagacccagtggca
81777	228	cccagacatgacagccatcatcAAAGAGATCGTTAGCAGAAACAAAAGGAGATCAAGAGGATGGATTCGACTTAGACtgacctgtatccatttctgcgg
82011	231	catttgaccgtggagaagtagaatcaATGGAAGATGATACTAATGGAAATCTAATGGAAGGTGAGAGGATCAGTCATCCATGAATCTATTTAACGATTACCctgatagtagtgttagtgatgcaaacga
82152	234	gacagttaaaggcatttcctgtgaaaTAATACTGGTATGTATTTAACCATGCACGATCCTCCAGTTTGTGGTCTGCCAGCTAAAGGtgaagatatatcctccaattcaggacc
82662	237	aggatttcgtaatatgccgtcaaagaaAATTTGATTGAATTGAATTGCAGGTACAGTAAGTaggtcatgtcacatttagaaatttcctgt
82666	240	gaagaaaatagaacctaggcgtgggaagtAATAAAAGATCACCTTCAGAAGTCACACAGAATGATTTTGATCTTGTGCGTTGGTaaagtgttaccatttttcttcaattcagtgtc
82758	243	acatggcttttgtcctaaggtcggattccAGTTTAAATGGATGGCAATTGAATCGCTTTTTGATCATATCTACACCACGCAAagtatgtgtaagtgtgggtgtt
83478	246	tgtcaaagttcgatcagcagctgTTACCTGTTTGAAAAACATTTTAGCGACACAAAGACTGGACATAGTTTCTGGGAGATTTATAACATGACAACAGatccaatgctggcctatctacag
83501	249	agtcatttaaagcagaatttggcttagcAGGAGGTGTAAATTTACCAAAAAATAATAGATTGTGTAGGTTCCGATGGCAAGGAGAGAGGAGACAGCAGGCttgtaaggtgaggccttccct
83530	252	cttaattattctgaagggcccgtgatgaCCTGAGACAAGATGCTGTCATGCAACAGGTCTTCCAGATGTGTATAATACATTACTgcagagaaaacacggaaactagga
83554	255	cctatgaggggtaccagaagacagtgGGATGGCACAGCAAAGAGAGCTGCTACGAAGGTCTATGATGATCGCTTAAAAGTgaaaacttatgggaaaacaggtatggc
83653	258	ctatatgtagaggctgttggaagctgcTTGGGAGAAGTGGGTCCTATAGATTTCTCTCACCATAGCTATACAAGATGTAAAGAtgcatcttatacccaggcccttaag
83779	261	gaagtaccccagtattgacaaagaaaaccCTTTTGAAGGCCTGGATGATATAAATCTGTGGATTCCTCTAAGTGAAAATCATgacattggatataaagacactgacttgtg
83902	264	gagcagtcagcagaactgtacatATAGATCTAGGTAAGTAATAAAATCTATGTATCTTTTTAGTAAATATTTGGtcatcatggaatgttgtttgcctac
84622	267	ttctgttaaagttcatggctttgtgttTTACCTTAATTATTCTATGCAAGATACACAGTAAAGGTTCAGCGAGATGGTCAGAGGTCAGGGATGGTCCagacagaagccagtaccgattatc
84933	270	cctcactgaaaccttgtgttttgtcCCTTAGTGATATTGACCAGAGTTTCAACAAAGTAGCTGAACGTGTCTTAATGAGACTACAAGAGAAactgaaaggagtggaagaaggc
84984	273	gtccacaaaalggttctggatcagCTGGATGGTCAGCGCACTCTTGCCCACACGCGGCGCCACCACCACGAGCTatattccgtcatcgctcctcagg
85006	276	gatgtgtgagaaaccatggaagTGATGAGAAACTCTGTTAACCATTGTAGAGGTAAAGTATTTTATAAGAAGAACTTTATTTTTTTtcttaccaggtagactgtgtatctcat
85059	279	ggtggacaagtgaatttgccatacAGCAGGCCATAGACCCCAAAAATCTCAGCCGACTTTTCCCAGGATGGaaagcttgggtgatctcagtatatg
86500	282	gatgttcctctgtaggtgttgacGCGATATTGACGTTCCCAAAACCATCCAGATGGTGCGGTCTCAGAGGTCAGGGATGGTTCCagacagaagccagtaccgattatc
87927	285	tcctcatgctcgtctcctcaTTGCACTGTACTCCTCTTGACCTGCTGTGTCGAGAATATCCCAAGAGACAGGTTTCTCCATCAATTACTACTTGCTTTCCTGTaggaatcctgagaaaggggagaaaca
87967	288	agtaggaaatagcagcctcacattgCCCCTGACAACATAGTTGGAATCACTCTGATATCTCGAGCCAATCCAAAGTCACATatcttcaccacttttccctgtgg
87993	291	ggtgatgagctaccaaccaagaAGGGGCGGAGGAACCGTTTCAAGTGGGGCCCAGCATCCCAGGCATGATCCTGTTCCAGGcctatgaggcagaagaaacc
88109	294	gacataacagttatagatttgcagaaaaacagaTCTGTATTTATTTCAGTGTTACCTGTTCTTTGTCTTTGCTGATGTTTCAATAAAAGGAATTCCATAActtgctaagtcctgagcctg
89417	297	gaagtgggttgctcacatgtGCACGCCCCAGCAGGTTGGCTTCCGCAGGTTGCATCATCTTGACAATatgatgatgtggtgcaatttgtc
89439	300	gcagaaacatttggcacatttcatTCTTACCAAACTCTCAAATTTTCTCTGTGAAACTCCCATTTGACATCATATTCATCTCTGAAATCAACGTAGAAGtactcatttatctgaggagccggt
89861	303	ctttctccaggtccaagatggtaatGGGTATCCATCGGAGAAACAGGACGCCTGACTTGCCGATGCTTCTGCGAGCActtgaggttccctatagaaaagaacgt
90401	306	ggtcacctgtacaatctgtagtGGCTTTCATACGCTAAATTGATACGCAGTTTAGGAATAGcgagttctgcgaatagaaggaaaga
90912	309	ggtcgacaaaggaacagcctatttTCCCTCGACACCCGATTCAAAGTGGGCACAGATGGTGTGATTACAGTCAAAAGGCCTCTACGGTTTCAtaacccacagatccatttctttggtc
91050	312	tggttcaagtcgtcgacctcAAGGTGAGGGGTTAAGCACAACAGCAGCTGTGATCACAGTCACTGACACCCAACGATAATCCCTCCGAtctctcaatcccaccacggtaatctc
91174	315	tcttcctcagacattcaaacgtgtttTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAaacaaatatttgcagtatgctcttcacc
91406	318	ggctaacgtctgtaatcaccacaTCGATGTCATGACGCCCCAATACCCCAGCGTGGGAGGCTGTATACACCATatgatgatgtggtgcaatttgtc
91827	321	tatctttccttgtagtgtccataaatttcttAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATATTTCAAATgtaataattaaattggcatttcctttggact
91829	324	tctgcattggtgctaaaagtttcttgGATCACATTTTTATTAGCTAAAGGTAAGTTCATTATATTTATTAAATGCTAATATTTCAAATgtaataattaaattggcatttcctttggact
91909	327	ggcaacttgacaaagaaatgataaaacaTTTAGAACGATGTGAACATCGATGAATCCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAAttcatgtgcataatggctaacaa
92464	330	gtdtacatggtgctcccatfCAGGGGATGAGCTACCTGGAGGATGTGCGGCTCGTACACAGGGCACTTGGCCGCTCGGAACGTGCTGgtcaagagtcccaacctgtca
93379	333	cctgtcccaggaagcatacGTGATGGCTGGTGTGGGCTCCCCATATGTCTCGCGCCTTCTGGGCATCTGCCTGACATCCAGCGGTGCAGCTGGTgacacagctatgccctatggc
94170	336	ctggagtcttccagtgtgatgatgCGAGGATGGGCCTCCGGTTCATGCCGCCCATGCACAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGgtacagtcagagccaacctagg
98573	339	tggcctgatcttccacaaaatgaaactaAAACATTGTCAGTTAAAATTGTGATAGTGTCTGTggaatccatcactacgaacgagttg
98661	342	gaaggatgaatatctgcatgacttggGGACAGCCATCGTTGTCCACTGAAGGACATTCCAATTCAAACCATCCAGCatccaccaagtaatcgtgcatcg
99638	345	ctctaggtcagcctgccagtataCTGGGGGGGCAGCCATAGTGAAGGACTGTTGCAGATAGCATCAGGGCCTCAGCCAGGaacagcagcagaatggatttactgg
101246	348	gtctttgattgcgtcagtgtcatCGACAGATGCAGCAGCGGCTATCGCACAAGCTGCAGCAGCAGCGTGGCCAGGGAAACATCCCCTGGCCcaggatcagtaggtggaaatagctc
102227	351	ctctgacctagcaggatccagGGCACTGATGGGCATCGGTGACGCCACTAAACACTTCCCAGAACCGTGGCGCCGAAGCCCCactgtcagcttcaagctaagt
103630	354	agatgccggtacgacattgGCTCATCAAGCTCGCTGCTTCCAGGAATGACTGGGGAAGGGAGAAGAATGCGTGGGTTTCTccactcaataatcccaaatttgtg
103879	357	aacatcacaccaggtctgtaaCCCTTCGAAGGGGACAACATCTACAAGTTGTTTGAAACATCGGGAAGGGAGACTACGCCATCCCGGGCGCTGTGGCCCCCGctctctgacctgtgaaaggtg
104671	360	gagatctcaattgttgtcaGGACCTGTCGCTGTCGGAACTTCTGGAACCAAGTTCCAGGTGGAACAAAGTTCCAAGGTGAGACAAAGTTCAactccagtaagcaaactgttacc
104720	363	gtgggaaactacctccgtatgttCCGAAGTTTCTCTGTACAAGAGATACCCCCTCACTCTGAGAGGCGACTAGCCactgtggaaagaggaggaaagaaatagttg
106398	366	tgtgatccatgagaagccatctcAGCCCGAGTGCTGGTCCCCATCCGGCTGGACATGGAGATGCGATGGGGCAGAAGCTGCCGAGACGCCttcacctggaacatgaatggttaca
107255	369	gctccacaaccatcaacaggaaCCGCATGGGCCGAAGCAAAGAAGCTCCCCCTTTGGTGTGGATGCATCGCTGCACTCACACCTCCGGtgatgattcgccttagttctc
110679	372	tgagttccaaggcctcattcagCTCTCGGAAGCATCTCGAAGGCGCTCACGCCCACGGATCTGCAGCAACAGAGGAGGGGGACAAGTTAAGTATATACacagtacctgagttaaaagatggttca

TABLE 2

assay_id	SEQ ID	amplicon
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117792	378	tcttgtccgtgcttgcttacttcGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCGCTTTCTTGCGGAGATTCTCTTCGCTCTGTGCGCCGGTCTCTCCCAGGAGACAGGCACAAACACGCACCTCAAAGctgttccgtcccagtagatttacc
118631	381	gccagaactacaatctttgatgacattGCATACATTCGAAAGACCCTAGCCTTAGATAAAACTGAGCAAGAGGCTTTGGAGTATTTCATGAAACAAATGAATGATGCACATCATGGtggctggacaacaaaaatggattg
120430	384	gttgttgatggcaaacacacacaaGGAAGCCCTCCCCGGTGCGCATGTACTGGTCCCGCATGGCGCTGTACTCCTCGTGGCCGGCGGTATCCAGAGATGTCCAACAGGCACGTCTCCccatcaatgaccactgcttc
121852	387	gagtattggttccattgcttacttgAAATGGATGTTCCAGGTATGGCCTATTGTTACTGTTGATGGATACGTGGACCCTCTGTGGAGGAGATCGCTTTTgtttgggtcaacttctccaatgtc
122008	390	ctctctgcacagctccaatgaGACTCTGTCTGCGTCATCATCTTTGTCATCGTGTGTGGTTTGGTTTGTGGTCCTCACCTATGCCTGGCaacacttcctcaaagccctgg
133212	393	cagaatgaggtgcagaacatcaagTTCAACAGTTCAGGCCAGTGGCAAGTGCCCTTGGTTCGGACAGACAACCCCAAGAGCTGGTACGAGGAGCGTGGAGGGCTGCGGCATCCAGTGCCAGaacccgctcttcacagagg
136501	396	cgtctcctccgaccactgtGAGGCATTCCGGCTTGAGGATGGGCCGGTGAGGCGATCGCTCTGGTGGAGAAGAGGAAGAAAGGAGGAGTGGGGATgtggagaatgagagcaaataaataagc
136537	399	cctccaggaagcctacgtgaTGGCCAGCGTGGACAACCCCCACGTGTCGCCTCACCTCCACCGTGCAGCTCATCACGCAGGTCGATGCCCTTCGGCTGCCTCCTGGACtatgtccgggaacacaaagacaatatt
142574	402	cagtgtgtatgcaggcatcctCAGCTACGGGGTGGGCTTCTTCCTGTTCATCCTGGTGGTGGCGGCTGTGACGCTCTGCCGCCTATGGCATCGTTGAAGTAAGAAAGGCCTGTGGCTCCCCCaccgtgcacaagatctccc
143592	405	ttaaatacagaaggcataaatattccagcagaCCAGCCAATTACTAAACTTAAGAATTTAGAAGATGTTGTTGTCCCTACTAtggaaattaaggtaatttgccaattaactctga
145156	408	ccagatagccctggacaaaccATGCCACCCAAGCAGCTGCTCAAACGAGCTGAAACCAAGCAGAAGTACGTAAAAATAAAGCACGTACTGCTGAAAAGAGAGAGGAGTGGACctaagcaagctgcagtaaatgctg
147815	411	aacaaaaccatgtaataaattctgactatttTACATCAATTTATTTACTAGATTATGATGTTGTTCCATGTATGGCATAATGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTgtaacagcatacaaggatcttcctc
178642	414	ctatttttccctttctcccccacagaAACCCATGTATGAAGGTTGTTGAGGAGATAAATGGAAACAAATTATGTTTACATAGACCCAACAACTTCCTTATGATCACAAATGGGAGTTTCCCagaaacaggctgagtttggtca
178642	414	ctatttttccctttctcccccacagaAACCCATGTATGAAGGTTGTTGAGGAGATAAATGGAAACAAATTATGTTTACATAGACCCAACAACTTCCTTATGATCACAAATGGGAGTTTCCCagaaacaggctgagtttggtca
226369	417	ctcaccatcgctatctgagcagCGCTCATGGTGGGGGCAGCGCCTCACAACCTCCGTCATGTGCTGTAGATGGCCATGGCGCGACGCGGTGCCGGGCGCGGGAGGTTGTGaaatcaacccacagctgcac
226460	420	cttacctcttggtgcagttgGATGGCATGGGTGGCACTCCCGATCTGCAGCATACTTGAAAATGAAACTGTTTGCCCCCTGTATAAGCCATCTGGACATTTTTCCACACAGttggccatcttaaaatgagc
226789	423	ccagttgcaaaccaggcctcaGGCGGCTCATAGGGCACCACCACACTATGTCGTCAAAAGTGTTTCGTCCACTCGGATAAGATGCTGAGGAGAGGGCCAGAcctaaggagcaatcagtgaggaatcag
227540	426	tttatctcagaatcagccaggcaCAAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCGCTCCAAAAGTGGTGCTCAGACACCAAAAGTCCACCTGAACACTATGTTCAGGAGACCCCACtcatgtttagcagatgtacttctgtcag
232121	429	gataggtcacctttgcctctcagAGATGCAGGGACACACGATGGGCTCTGGTTAACCAAACTGAATTATTTGTGCCATCTCTCAATGTTTGCGACGACACGCCTATTTTTGccaatatcacactgccaggtact
234145	432	gcagtgtgtccaccgtgatcTGGCTGCTGCTCGCACAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCACGAGACATCATGCATTGCAATTCAaaacaactattaagtgaaagttatctgcttg
236158	435	gatgtctatgaagtgttgtggttcctAACCACATTTCTTTTTTTTTTTTTTTCCAGGCTATTCAAGATCTCTGGCAGTGGAGGAAGTCTCTTTAAGAAAATAGTTTAAACAATTTCGTCTTATTTCAAGTTTCCgtaacatt
255119	438	caaattgtaaatttcagtatgtgaatgacttcACTTATTGTTATTTAGTTTCGAAACACAAGAGAACACCACCAGAAAAAGTAACCTTCGATGAAGAGGTGAATTGTCAGTTATAGTAAGAAAACAGTAgatcctttcc
304699	441	ctgttcaaactgatgggaccacTCCATGAGATTTCACTGTAGGTCTTCATGAAGGTTGCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAAACAGTAgatcctatttccatcagagcaaaca
309408	444	gaagaaatggagctgtcacccaCATCAAGATTCAGAACACTGGTGATTACTATGACCTGTATGGAGGGGAGAAATTTGCCACTTTGGCTGAGTTGGTCCAGTATTACAtggaacatcacgggcaattaaaag
310032	447	cactcacagtttccattagtgttgaaaatGTTTCCTGACTCAGAGGGGGCTCGACGCTAGGATCTGACTGCGGCTCCTCCATGGCAGTCGACCCGGAAGGCAGTCTGGCTGTGCagcaagaggaaaagtggggat
320120	450	gtcatcagctgaagatgaaatgagatgtAATACCCTGCAATAGCAGAAATAAAAGAAAGAGTTGGAAGTAGGTCAGCTGAAGATCCTGTGAGCGaagttccagcagtgtcacagc
329410	453	cccaaatctgaatccgagagaGGCCAAGGGAATACTTACGCGCCACAGAGAAGTTGTTGAGGGGAGCCTCACGTTGGTCCACATCCTCGCGGCCGCTCCTTGTAGCCAATGAAGGTGCcatcattctgaggcgaagtagcg
339432	456	cagaggtttggcctgctttgGAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAGCACCTGAATAGGCAAGTCGAGGGCAATGGAAAAGCTCATTAACTTAACTgacattctcaaacaggagaagaggat
341576	459	gtgcgtcacgcttgaagacCACGTTGGTGTGTGCAGCACGCGGCTGAAGTCCGCAGGAAGTGGAAGGAGCTGTTGCGCAGCAGCTGCTCCGGCGGCATCAGACCACCACACGCTGTGCCGGCCAGCCTCTGGtacatgctccgcacagtcc
379514	462	caatttttaatgatgcttctgcgTTTAAATTATCTAGAAGTTTGCCAAGGTTAGCTCTAGTCTTGATGCTACTCTATgcagaaatctatgcagataagaaaagtatg
411633	465	cgaggacaacgtgatgaagatcgCAGACTTCGGGGCTGGCCCGGGAGCGTGCACAACCTCGACTACTACAAGAAGACGACCAACGTGAGCCCGGCCTGGGGTGCGGGGGTGCGGGGTGTCGGGGTGTCGCGGCTGCGCgcc
416298	468	tgcttactaatgtggtttaatttcatgTTTCATATAGGATTCACCTTTATTTAAAGAATCAAAGGAGAAGGAGCAACTGATCacctgaatctgcttgtcctctaatc
416888	471	gcgttcaaatgatgggaccaCTCCATGAGATTTCACTGTAGGTCTTCATGAAGGTTGCTTCATGAAGAAATATATCTGAGGTGTAGTAAGTAAAGGAAAACAGTAgatcctatttccatcagagcaaaca
421278	474	cgacgggaaagacaagttcatgtacTTTGAGTTCCCTCAGCCGTTACCTGTGTGTGGTGATATCAAAGTAGAGTTCTTCCACAAACAGAAGCAGATGCTAAAAaggtttgtacttacttcattgggagaa
423052	477	gctgatttgatggagttggacatgGCCATGGAACCAGACAGAAAAGCGGCTGTTAGTCACTGGCAGCAACAGTCTTACCTGGAGTCTGGAATCCATTCTGGTGCCACTACCACACAGCTCCTTCtctgagtggtaaggcaatcctg
464386	480	atggtggctttttgtttgtttgTTTTTAAAGTTTTTGAATTCAAAGCATAAAAACCATTACAAGATATACAATCTGTAAGTATTTTCTTATTTGTATGCTTGCAAATATCTTCTAAaacaactattaagtgaaagttatctgcttg
482180	483	caagaatctgccgcgctcttgTGAGAAGATCTGTGAGAAGTCTGTGGTCTGGACAAGGCCACGCTGctcatctgaaggcgtacctdgtg
482609	486	gaatgcggcccacgtcggtGGCACTCTCGAAGCAGCGCCTGCACACACTGCCGGTTGTCAATCTCCAGGTAGACGATGGAGCTGCGGCCGCAAcaatcagagaggggctgggacc
482833	489	gacacgttcatccacggcatcgACTCCACCGAGGTCATCTACCAGCCGCGCGCAAGCGGGCCAAGCTCATCGGCGAAGTACCTGATGGGGGAAGGCTCTTACGGCGAAGgtgaaaggaggtgctggactcgg
483802	492	cacggatcgggtgaagtggCGGGGTCGGCGCAGTTGGGCTCCGGCCACTCGCCACTCATCATCACGTCGCGCAGCTGCCACATCGTACGCCTGCGCAGAGAGAAacagaatggtcagaggccaggctg
484088	495	cactcctctcaggcggatgaGCGCGTCTTGCCAACACGGCGCCCGCGCCTGGTAACCAGCCCATCAGCACACGGCTCCCACGCAGCATCTcagaagatttgggccgcctctc
484297	498	cacttttgggtaaatacattcttcataccaggaCCAGAGGAAACCTCAGAAAAAGTAGAAAATGGAAGTCTATGTGATCAAGAAATcgatagcatttgcagtatagagcgtg
484410	501	gagaatgtgaaaattccagtggccatcaAAGTGTTGAGGAAAACACATCCCCCAAAGCCAACAAAAGAAATCTTACAGACGTAAGCCCCTCCACCCTCTCCtgctaggaggacaggaaaggaccc
484618	504	cagacttggtgtccagaatgcAAGAAAGCCCAGACGGAAACCGTTAGCTGCGCTGGTAGGTTTTCTGGGAAAGGGACAGAAGATGACAGGGGCGCAGGAGGGCGGCTGGTGCAGGGGCCGCCGCGGG
490549	507	ccagtgccatcccaccgaGCCCAGACACCAAGGACCTGATGCTGGTGGCGCATCGTGGTGGAGGACCTGCACGGCGCGCGGAGCGAGGAGCACGATGGAGCTCTCTTCGACATCATGAGGATGACGAGTGGTG
491413	510	acatggccactcagatctgctcagCCATGGAGTACCTGGAGAAGAAAAACTTCATCCACAGGTAGGGGCCTGGCCAGGCAGCCTGCGCCatggagtcacagggcgtggag
492612	513	cccacccacgatccactgtGCGACGAGCCGCTGTCCCTTCATCGTCGGTGCTGCTGTCTGCcatttgcatccactgtacca
492615	516	gcccagcatgtcacccaagatggtGGCTCGGAGAGGAGCCATACTGCCCCAGGATATTTCTGTCACCCCTGTGGCAACTCCAGGTAtgaggttcaagcttctggaggaagg
493041	519	tcccctgcagctggtccttgGGGTCCTGCTCTGGGAGATCTTCACGCTGGGGGGCTCCCCGTACGCCGGCATCGCCTGTGGAGGAGCTCTTCAAGCTGCTGAAGGAGGGCCACGCatggacaagccccgccaacig
495041	522	tcctggtgaccgctctgcatCTAGTGCTGGGCCTCAGCGCCGTCCTGGCCTGCTGCTGAGGTGGCAGTTTCCTGCACACTACAGGTACCGCCCCCCGCCAGGCAGgagactggcggtggaccagg
503320	525	tgcatagccaggcatgtgCACAAGGACATCAAGGCAGCGGGAACCTGCTGCTCACCACGGTGGCACCGTCAAAATCTCGCAGCTGGGCGTGGCCGatggacacgtgctgtaggg
504796	528	ggctgctgcgacattgacgagacaGAGTACCATGCAGATGGGGCGCAAGGTTAGGTGAAGGACCAAGGAGCAGAGGAGGCTGGGGTGGAGtggttgtctagcccatgggagaac
505293	531	gggacgacccgtgttgccCACGACCTGCTGCCCCCGGCCCCACCCACGAGCAGTGGGGGGCTCGCCGACGTGAAGGGCCACTGGTCCCCAAccaatgtgagggtccctagcag
507582	534	tgtcccatcacaggcaaggGGCTGGGCTCCAACCTCGTCTACAACCTGGTTTGCCAACCGGCGCAAAGAAGAAGCCTTCCGGCACAAGCTGTGGCCatggacacgtacagcgggcc
508777	537	ggtggcccctgagcgtcatCTGCCCCCACAGAGCGCTCCCCGCAGCCCATCGTCGAGGCGGGGGCTGCCGGCCAACCAGACGGCGGTGTCGTGGCacgcacgtggagttccactgc
516350	540	cttttttcttcctaggttgcacataggcaAAGGTGTGCAGTTGCAAAGGTGATGTTTGGGTCCAGGTGCCTTAGTGaccacgcggtcttgtacagagt
552959	543	gaatttttgttgtctttcttaggcctgttCACAATGAGCTTGCATTCCAGCCTCGCCAATTTGCAAATCATCCTGGTAAGTGTATTTCAAAATTgatttcctgtatttagatgattagtgtgattgaa
553293	546	acctctattgttgatcatattgtccacaaaATTCTGCGTCAAGGCACTGTTGCCTAAGTCACAAGTTATCGCGTAAATTACGCAGCAAGTTTatattacgtcatttcacgcaggcctattaataaaaa
554194	549	aatggagaaacatctacaaaatcccttggGTTATAAATAGTGCACTCAGAATAAAAATTCTTTGTGCAACCTACGTGAAGTAAATTTCGAGACATgatcaaggtaaagtcaaatgctgatgctattatttt
555556	552	agtaaaaatgactaatttttcttattcccacagtgtaTGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCGTGgaccctttccagcacaccc
559669	555	ggattaaagctggctatggcaactgCAACTGCTTCGCCTGAGGAGAAGTGCTTCTGCAGGGTGAGTGGGTGGCGGCCGGGAGCCACGCACCACCCTCCCAGCccccacagaggttctcaaacagcaec
613072	558	cgtcgtgctgccgtatggcTCAACTTCGACGGCGAGCCGCAGCCCTACCCAACGCTGTGCCGCCTGGCACGGCGCCGCGCATCCacagctacccgaggtacgggc

TABLE 2

assay_id	SEQ ID	amplicon
645344	561	ggcaaatgtcagtgcaaggtttacacaTTTTAATCCCATTTTTCTTCTACTTCCATCTTGGAACTAGGGCAGGCACGCACACAAGAAactggaatctaccacaaagttatctgattaaaaaaaa
649396	564	gagcggcccaccttcgagtaCCTGCAGGCCTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGGaagaacctctaggcacaggcgg
658417	567	ggcaggtcttggccagttggCAAAACATCTTGTTGAGGGCAGGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGttgaaagtcagggcacaagtgaacag

TABLE 3a

WellPosition	Name	Sequence	SEQ ID
A01	30014-F	TTCGCCTGUCCTCATGTATUGG	568
A02	30373-F	CATCTACAAAGUGGTTCTGGATUAGCT	569
A03	31381-F	CCAACATGACTUACTTGATCCCCAUAA	570
A04	31533-F	TGTAAACGTCAAUAGTGCAGAUGGG	571
A05	32781-F	CATCGCCACAUAGGGUAGAACAT	572
A06	32827-F	ACTTACGUGGACATTTCTUGACACA	573
A07	33013-F	CCAAUGCAGCGAACAATGTTCUG	574
A08	33555-F	GACAGTAACCCUACATATACAATUGCCT	575
A09	33659-F	CCAGTGACTAGAAAGAUCAAATTCCCAUT	576
A10	33781-F	AAUCAAAUAGGGAAGGAAAGGAGAGC	577
A11	34014-F	GAGGCAGTCUTTACTCACCTGUAG	578
A12	34860-F	GGTTTTTGCCCUTCCAGTGTAUACT	579
B01	35831-F	AAAAUGACAAAGAACAGCUCAAAGCA	580
B02	36101-F	ACATTTTCGUAAGTGTTACUCAAGAAGCA	581
B03	36569-F	GGGAAGAAAAGUGTTTTGAAATGUGT	582
B04	37385-F	TGGATCTUCCACACAATUAAACAGCA	583
B05	38772-F	TGACCTCGUCTTCTACTTCUGGA	584
B06	40184-F	TGTCTTTGAGTUCCATTCCACTTGUT	585
B07	40234-F	CCCTCCUGCCATCATATUGAACAC	586
B08	41691-F	ACCATGACAAGAUTTTCCCTTACCTUT	587
B09	41812-F	ACTGCTGACCAAACUTTTAAAGTGTUG	588
B10	42297-F	CCTCTTUAGGGAGCAATGAAAUGAAGT	589
B11	43181-F	TGGGACTTTGGUAATTCACCAGTUAC	590
B12	43200-F	CCCATCTCCUAACGGCTTTTGUC	591
C01	43383-F	CAAGCTCTCATGUCTGAACTGAAGAUA	592
C02	44733-F	CCATCCAUCCAGGAAAATCAGACTUAA	593
C03	46166-F	TTTCGTAATCGUAGCTGGCAUGA	594
C04	46436-F	CAACGATGUGGGCAAGACTUC	595
C05	47704-F	GGAAGCCCUCATGTCTGAACUC	596
C06	47725-F	CCTTCTACATGUCCCACTTGATUCAG	597
C07	48478-F	ACCTTCTTTCTAACCUTTTCTTATGTGCUT	598
C08	49160-F	CCTTACTCAUGGTCGGAUCACAAAG	599
C09	49191-F	CTCGACUACCTGTGAAGUGGAT	600
C10	49305-F	GGGTGTGGAUGCTTCCTTTUAA	601
C11	49402-F	AGCTTTAAAAGUTCTGCTTCCUCACT	602
C12	50673-F	CAGTACCTGAUTCCTGCTGTGUT	603
D01	50695-F	CTGAGCATTAGCUTGCAAGAGATUT	604
D02	52170-F	CCAGTACCTTCCUCTTCTTCTACAUC	605
D03	52189-F	GACCACAUTGAGATGGUGACCAAT	606
D04	52210-F	CGAAGAAGGGUATTCCCAGTUGA	607
D05	52386-F	CTTCAATTTTAUTTCCTCCCUGGAAGT	608
D06	52394-F	AAAAATTTCUTCATCTCACUCCCAGACT	609
D07	53695-F	GGAATTGGTCUAGGCAACTACCAUC	610
D08	54189-F	TGTGTTTCUCCATACAGGUCACG	611
D09	59674-F	CACCATGACUTTGAGGTUGAGC	612
D10	59934-F	CAGGTTCTUCCAGATGCTGAUACT	613
D11	60049-F	GCAGCCUAAAGAATCAAAUGAAAACCAA	614
D12	60239-F	TGGTACUCCCTGTCGUCAACT	615
E01	61096-F	ATACAGUCGGAGGTTCACUGC	616
E02	61118-F	GAACCAAUGGATCGATCUGCCA	617
E03	62593-F	AGTGAATTAGUTCGCTACGAUGCAA	618
E04	62615-F	GTTACGCAGUGCTAACCAAGTUC	619
E05	64101-F	GTGGGCUACAAGAACTACCGAUAC	620
E06	64212-F	GATTTTGGTCTUGCCAGAGACAUG	621
E07	65601-F	ACATTACATACTUACCATGCCACTTUCC	622
E08	67037-F	GTTATGTCCUCATTGCCCUCAAC	623
E09	67066-F	GACCAGACAACUGTATCCAGUGT	624
E10	67641-F	CCTCTUACACCCAGUGGAGAAG	625
E11	68178-F	CCACGUACCAGATGGATGUGAAC	626
E12	68572-F	TCTTCCTTCUCTCTCTGTCAUAGGG	627
F01	71564-F	CAGCATGTCAAGAUCACAGATTTUGG	628
F02	71577-F	ACATGAACUCCACGTTGCUACC	629

TABLE 3a

WellPosition	Name	Sequence	SEQ ID
F03	71600-F	GGTTTGGTTUGGTGTTATCTGTTUCT	630
F04	73075-F	CCCACUGAAAAGCACTTCCUGAA	631
F05	73104-F	TGTTGAAGTCCUCGTTGTCTTGUT	632
F06	73150-F	CCAACTACGACAAGUGGGAGAUG	633
F07	74598-F	GCAGCAAGUATGAUGAGCAAGCT	634
F08	74743-F	GATTTTGGCCUGAGCAGGTUG	635
F09	76043-F	GAGTATTTGGGCGAAUGCAGTTTUT	636
F10	76049-F	TTCTTCATUCGGCACAGGAUGA	637
F11	77536-F	CCAGTTGTGGGUACCTTTAGATUCAG	638
F12	78961-F	CTTCCAGGAGCGAUCGTTUG	639
G01	78994-F	GACTUGGCAGCCAGAAACAUC	640
G02	79119-F	CATCTTCTCTTUAGGGTCGGATUCC	641
G03	80635-F	TTTTTCTGUCCACCAGGGAGUAAC	642
G04	81777-F	CCCAGACAUGACAGCCATCAUC	643
G05	82011-F	CATTTGACCGUGGAGAAGTAGAAUCA	644
G06	82152-F	GACAGTUAAAGGCATTTCCTGUGAAA	645
G07	82662-F	AGGATTTCGUAATATTGCCGUCAAAGAA	646
G08	82666-F	GAAGAAAAUAGAACTAGGCUGGGAAGT	647
G09	82758-F	ACATGGCTTTUGGTCTTCTAAGUGAA	648
G10	83478-F	TGTCAAAGUTCGAUCAGCAGCT	649
G11	83501-F	AGTCATTUAAAGCAGAATTTCGCTUAGC	650
G12	83530-F	CTTAATTATTCUGAAGGGCCGTGAUGA	651
H01	83554-F	CCTATGAGGGUACCAGAGACAGUG	652
H02	83653-F	CTATATGTAGAGGCUGTTGGAAGCUG	653
H03	83779-F	GAAGUACCCAGATTUGACAAAGAAAACC	654
H04	83902-F	GAGCAGUCAGCAGAACTTGTACAUA	655
H05	84622-F	TTCTGTTAAAGTUCATGGCTTTTGTGUT	656
H06	84933-F	CCTCACTGAAACCUTTGTGTTTTUGT	657
H07	84984-F	GTCCACAAAAUGGTTCTGGAUCAG	658
H08	85006-F	GATGCTGUGAGAAAACCAUGGAAG	659
H09	85059-F	GGTGGACAAGUGAATTTGCTCAUAC	660
H10	86500-F	GATGTTTCCTUCGTAGGTGTUGACT	661
H11	87927-F	TCCTCATGUACTGGTCCCUCA	662
H12	87967-F	AGTAGGAAAUAGCAGCCTCACATUG	663

TABLE 3b

WellPosition	Name	Sequence	SEQ ID
A01	87993-F	GGUGATGAGCUACCAACCAAGA	664
A02	88109-F	GACAUAACAGTTATGATTTUGCAGAAAACAGA	665
A03	89417-F	GAAGTGGGTUACCTGACAGUGT	666
A04	89439-F	GCAGAAACAUTTGGCACATUCCAT	667
A05	89861-F	CTTCTTCCAGGUCCAAGATGGUAAT	668
A06	90401-F	GGTCACCUGTACCATCTGUAGCT	669
A07	90912-F	GGUCGACAAAGGACAGCCTATTUT	670
A08	91050-F	TGGTTCAAGCUGCTGACCTUC	671
A09	91174-F	TCTTCCTCAGACAUTCAAACGTGTUT	672
A10	91406-F	GGCTAACGUCGTAAUCACCACA	673
A11	91827-F	TATTCTTTCCTTTGUAGTGTCCATAAATTCTUT	674
A12	91829-F	TCTGCATTGGUGCTAAAAGTTTCTUG	675
B01	91909-F	GGCAACTUGACAAGAGAAATGAUAAAACA	676
B02	92464-F	GTCTACATGGGUGCTTCCCAUT	677
B03	93379-F	CCTTGUCCCCAGGAAGCAUAC	678
B04	94170-F	CTGGAGTCTUCCAGTGTGATGAUG	679
B05	98573-F	TGGCCTGATCTUCACAAAAATGAACUA	680
B06	98681-F	GAAGGATGAATAUGTGCATGACTTUGAG	681
B07	99638-F	CTCTAGGUCAGCCTGCCAGTAUA	682
B08	101246-F	GTCTTTGATTUGCGTCAGTGUCAT	683
B09	103227-F	CTCTGACCUTAGCAGGAUCCAG	684
B10	103630-F	AGATGCCGGUACGACACTUG	685
B11	103879-F	AACAUCACCACGGGTCTGUAC	686
B12	104671-F	GAGATCCATUGACCTCAATTTTGTTUCA	687
C01	104720-F	GTGGGAAACUACCTCCGTATGUT	688
C02	106398-F	TGTGATCCAUGAGAACGCATCUC	689
C03	107255-F	GCUCCACAACCAUCAACAGGAA	690
C04	110679-F	TGAGTUCCAAGGCCTCATUCAG	691
C05	116963-F	GAATTGGTGTUGATGACCTTCGUC	692
C06	117792-F	TCTTGTCCUGCTTGCTTACCUC	693
C07	118631-F	GCCAGAACTACAAUCTTTTGATGACAUT	694
C08	120430-F	GUTGTTGAUGGCAAACACACACA	695
C09	121852-F	GAGTATTGGTGTUCCATTGCTTACTTUG	696
C10	122008-F	CTCTCUGCACAGCTCCAAUGA	697
C11	133212-F	CAGAATGAGGUGCAGAACAUCAAG	698
C12	136501-F	CGTCTCCUCCGACCACUGT	699
D01	136537-F	CCTCCAGGAAGCCUACGUGA	700
D02	142574-F	CAGTGTGTAUGCAGGCAUCCT	701
D03	143592-F	TTAAATACAGAAGGCAUAAATATUCCAGCAGA	702
D04	145156-F	CCAGAUAGCCCUGGACAAACC	703
D05	147815-F	AACAAAACCATGTAAUAAAATTCTGACTACTUT	704
D06	178642-F	CTAUTTTTCCCTTTCUCCCCACAGA	705
D07	226369-F	CTCACCAUCGCTATCUGAGCAG	706
D08	226460-F	CTTACCCTUGGGTGCAGTTUG	707
D09	226789-F	CCAGTUGCAAACCAGACCUCA	708
D10	227540-F	TUTATCTTCAGAAUCAGCCAGGCA	709
D11	232121-F	GATAGGTCACCUTTGGCTCTUCAG	710
D12	234145-F	GCAGTGTGUCCACCGTGAUC	711
E01	236158-F	GATGTCTATGAAGUGTTGTGGTTCCUT	712
E02	255119-F	CAAATTGTAAATTTUCAGTATGTGAATGACTUC	713
E03	304699-F	CTGUTCAAACTGAUGGGACCCA	714
E04	309408-F	GAAGAAAUGGAGCTGUCACCCA	715
E05	310032-F	CACTCACAGTUTCCATAGGTCUGAAAAT	716
E06	320120-F	GTCATCAGCUGAAGATGAAATAGGAUGT	717
E07	329410-F	CCCCAAAUCTGAAUCCCGAGA	718
E08	339432-F	CAGAGGTTUGGCCTGCTTTUG	719
E09	341576-F	GTGCGUCACGCTUGAAGAC	720
E10	379514-F	CAATTTTTAATGAUGCTTTCTGGCUGGA	721
E11	411633-F	CGAGGACAACGUGATGAAGAUCG	722
E12	416298-F	TGCTTACTAATGUGGTTTTAATTTCATCAUG	723
F01	416888-F	GCGTGCAGAUAATGACAAGGAATAUC	724
F02	421278-F	CGACGGGAAGACAAGUTCATGUA	725

TABLE 3b

WellPosition	Name	Sequence	SEQ ID
F03	423052-F	GCTGATTTGAUGGAGTTGGACAUG	726
F04	464386-F	ATGGTGGCTTTUTGTTTGTTTGTTTUG	727
F05	482180-F	CAAGAAUCGCCCGAGCCTTCUG	728
F06	482609-F	GAAUGCGGCCACGUCGGT	729
F07	482833-F	GACACGTTCAUCCACCGCAUCG	730
F08	483802-F	CACGGGUCGGGTGAGAGUGG	731
F09	484088-F	CACTCCTCTUCCAGGCGGAUGA	732
F10	484297-F	CACTTTTGGGUAAATACATTCTTCAUACCAGGA	733
F11	484410-F	GAGAATGTGAAAAUTCCAGTGGCCAUCA	734
F12	484618-F	CAGACTTGGCUGTCCCAGAAUGC	735
G01	490549-F	CCAGUGCCCAUCCCACCGA	736
G02	491413-F	ACATGGCCACUCAGATCTCGUCAG	737
G03	492612-F	CCCCACCCACAGAUCCACUGT	738
G04	492615-F	GCCCAGCAUGTCACCAAGAUGGT	739
G05	493041-F	TCCCCTGCAGCUGGTCCTTUG	740
G06	495041-F	TCCTTGGUGACCGCTCUGCAT	741
G07	503320-F	TGCAUAGCCAGGGCATTGUGC	742
G08	504796-F	GGCUGCTGGACATUGACGAGACA	743
G09	505293-F	GGGACGACUCCGTGTTUGCC	744
G10	507582-F	TGUCCCCAUCACAGGCACAGG	745
G11	508777-F	GGTGGCCCCUGAGCGUCAT	746
G12	516350-F	CTTTTTTCTTCCUAAGGTTGCACAUAGGCA	747
H01	552959-F	GAATTTTTGTTGTCTTUTCTTTAGGGCCTGUT	748
H02	553293-F	ACCTCTATTGTUGGATCATATTCGUCCACAAA	749
H03	554194-F	AATGGAGAAACAUCTACAAAATCCCTTUGG	750
H04	555556-F	AGTAAAAATGACTAATTTTUCTTATTCCCACAGTGUA	751
H05	559669-F	GGATTAAAGCUGGCTATGGCACCUG	752
H06	613072-F	CGTCGTGCUGCCCGTAUGG	753
H07	645344-F	GGCAAATGUCAGTGCAAGGTTUACACA	754
H08	649396-F	GAGCGGCCCACCUTCGAGUA	755
H09	658417-F	GGCAGGTCUTGGCCAGTUGG	756
H10			
H11			
H12			

TABLE 3c

WellPosition	Name	Sequence	SEQ ID
A01	30014-R	AGTGGTTATAGAUGGTGAAACCTGTTUG	757
A02	30373-R	CTGGTGTGAAAUGACTGAGUACAAAC	758
A03	31381-R	GAGAAGCCATUATCTGCAAAAATAUCCC	759
A04	31533-R	ACCTTUGGAGGAAAACCCTATGAUG	760
A05	32781-R	CATGGCCTUCCAACTTGACUCT	761
A06	32827-R	CAAACCUTTGTCTACAAUCCAACCAC	762
A07	33013-R	CCAGTTTAAGAUTTGCCCAGACUC	763
A08	33555-R	GAAACTTTGGACUTCAAGAACTUGGAT	764
A09	33659-R	GGCATUGGCACAGGATCATUG	765
A10	33781-R	TGACTGCUGCCATCGAGAAUG	766
A11	34014-R	CCAGAAACUGCCTCTTGACCUG	767
A12	34860-R	CCTGACGAUGTCCAGTCUCCT	768
B01	35831-R	CATTTTAGCACUTACCTGTGACUCCA	769
B02	36101-R	GGTTGCCTACUGGTTCAATTACTTTUAA	770
B03	36569-R	CAAACAAGTTUATATTTCCCCAUGCCA	771
B04	37385-R	GCTGAGAGTTAUTAACAGTGCAGUGT	772
B05	38772-R	AGAGGCUGCAGAAATGCAUCAA	773
B06	40184-R	GATCTCTTGATACAUCAATCCGTGTTUG	774
B07	40234-R	TCTGCAGAGUTGTTAGCGGUT	775
B08	41691-R	ACTCAAAGUGTGGAAUGCAGAGA	776
B09	41812-R	TTCTTATAGGTGCUGAAAGGACATGAUG	777
B10	42297-R	TGAACTCAUTGATAGTTGUGAACCAACA	778
B11	43181-R	CTGCATCGGGUCCACATAAATATATUCA	779
B12	43200-R	GGCTCAGGAAGCUATCCCTATUCT	780
C01	43383-R	AAAATCCTCACUCCAGGTCAGUG	781
C02	44733-R	CTTATTCTCATTCGUTTCATCCAGGAUC	782
C03	46166-R	TCAGTCATUAGAGCACTCUGGAGAG	783
C04	46436-R	AGCCTAAACAUCCCCTTAAATTGGAUT	784
C05	47704-R	CAAUAAAAGGCAGCTUGGACACG	785
C06	47725-R	GCCTTGGTUGGGACAACAUAAGAA	786
C07	48478-R	CTGCTTTGAACAAAUAAATGAATCACGTUT	787
C08	49160-R	GGACTGUCAAGCAGAGAAUGGG	788
C09	49191-R	ACAGCUCCCAAAGAAAAATCCCAUAG	789
C10	49305-R	AGCTGAUAGAGATTGGAGUGCAAAC	790
C11	49402-R	TGGCATCUGAAGGCUCAAACC	791
C12	50673-R	GCAUGGAAGAGGATTCUGGACT	792
D01	50695-R	GTGTTTTGCUTCTCTAGGUACCAGA	793
D02	52170-R	TTGGAGCAAUCCCTGTGGAUC	794
D03	52189-R	GTCCATACCTAUGATTTCCCTCTTUGT	795
D04	52210-R	TCTCATGGAATUGAACTATCTGTUGGAG	796
D05	52386-R	GCGCTGTTAUCTCTTTCTTAUAGCCA	797
D06	52394-R	TGCTTTGGAAGUTCAGTCAACTCUT	798
D07	53695-R	ACTTCTTCCAUGACTTTGGCAAUCT	799
D08	54189-R	GACACAAAGACUGGCTTACATTTUGAT	800
D09	59674-R	GTGUGTTCTGCTTUCCAGAGAGT	801
D10	59934-R	GTATAAATGGCUCATCGAGGCUCA	802
D11	60049-R	AGTATTTCAATATCAUCATCATCTGAATCAUCT	803
D12	60239-R	GAGCTCTAGUGAGCACCUGAC	804
E01	61096-R	AGTTGAUGAACCGGTCCTTUACAG	805
E02	61118-R	TGCTGGAGACAUCTCACATTGTTTUT	806
E03	62593-R	GAAAAGTAGCUCGGTAGTCTACAGAUT	807
E04	62615-R	GCCACTTACUGTTCAAGGATTUCACA	808
E05	64101-R	TTCACUCACCTCGGAUGAGGA	809
E06	64212-R	TTGAGTTUGCAGACTTUCCAAAGC	810
E07	65601-R	GAGTGATGATUGGGAGATTCCUGA	811
E08	67037-R	GCTAAGGCAUAGGAATTTTCGTAGUACA	812
E09	67066-R	TTCCAGACCAGGGUGTTGTTUT	813
E10	67641-R	ACCTUATACACCGUGCCGAAC	814
E11	68178-R	CAAGGATGCCUGACCAGTUAGAG	815
E12	68572-R	TCGAGGATTUCCTTGTTGGCTUT	816
F01	71564-R	ACCTAAAGCCACCUCCTTACTTUG	817
F02	71577-R	CTCCTCUCCCATCTUCCACAGA	818

TABLE 3c

WellPosition	Name	Sequence	SEQ ID
F03	71600-R	TGCCCCTUCTTCTTCCCAUAGAT	819
F04	73075-R	CTTTCATGACUGCAGCTTCTTUCAA	820
F05	73104-R	GTAGTCCAGGAGGUTCCCGUA	821
F06	73150-R	CCGTCAGGCUGTATTTCTUCCAC	822
F07	74598-R	AGAAAGGCATUAGAAAGCCTGTAGTTUT	823
F08	74743-R	CGGACTTGAUGGAGAACTTGTTGUA	824
F09	76043-R	TGAUGAAGATGATUGGGAAACACAAGAA	825
F10	76049-R	CAATCUAGCGCCUGGAAGAGAA	826
F11	77536-R	GTGGAUCAAGCACGUGGAAAAG	827
F12	78961-R	CTGCTUCAGGACGTTGAACUCT	828
G01	78994-R	TCCTCTTCACGUAGGAATCCTCUT	829
G02	79119-R	AACACCCACACUTACACAUCACT	830
G03	80635-R	TGCCACTGGUCTATAATCCAGAUGAT	831
G04	81777-R	CCGCAGAAAUGGATACAGGUCAA	832
G05	82011-R	TCGTTTGCAUCACTAACACTACTAUCAG	833
G06	82152-R	GGTCCTGAATUGGAGGAATATATCTUCA	834
G07	82662-R	ACAGGAAATTUCTAAATGTGACAUGACCT	835
G08	82666-R	GACACTGAAUGAGAAAATGGTAACACTUT	836
G09	82758-R	GCAGCTTUACAGTTTTTCATAGUGAGAC	837
G10	83478-R	CTGTAGAUAGGCCAGCATUGGAT	838
G11	83501-R	AGGGAAGGCUCACCTUAACAA	839
G12	83530-R	TCCTAGTTUCCGTGTTTCTCUGC	840
H01	83554-R	GCCATACCTGTUTTCCCAATAAGTTTUC	841
H02	83653-R	CTTAAGGGCCUTGGTATAAGAUGCA	842
H03	83779-R	CACAAGTCAGTGUCTTTATCCAAATGUC	843
H04	83902-R	GTAGGCAAACAACAUTCCATGAUGA	844
H05	84622-R	CAGGGCTAAUTCATCCAACUCCA	845
H06	84933-R	GCCTTCTTCCACUCCTTTCAGUT	846
H07	84984-R	CCTGAGGAGCGAUGACGGAATAUA	847
H08	85006-R	ATGAGATACACAGUCTACCTGGUAAGAA	848
H09	85059-R	CATATACTGAAGAUCACACCCAAGCTUT	849
H10	86500-R	GATAAATCGGUACTGTGCTTCTGUCT	850
H11	87927-R	TGTTTCTCCCTUCTCAGGATTCCUA	851
H12	87967-R	CCACGGGAAAGUGGTGAAGAUA	852

TABLE 3d

WellPosition	Name	Sequence	SEQ ID
A01	87993-R	GGGTTCTTCUGCCTCTCAUAGG	853
A02	88109-R	CAGGCUCAGGACTUAGCAAGAAG	854
A03	89417-R	TGAAAGAGAGGCACUCATGUCAGAA	855
A04	89439-R	ACCGGCTCCUCAGATAATGAGUA	856
A05	89861-R	ACGTTCTTTTCUATAGGGAAACCUCAAG	857
A06	90401-R	TTCTTTCCTCUATCTGCAGAACUGC	858
A07	90912-R	GACCAAGAAAUGGATCTGTGGGTUA	859
A08	91050-R	GAATTACCGUGGTGGGATUGAAGAT	860
A09	91174-R	GGTGGAAGCAUACTGCAAAATATTTGUT	861
A10	91406-R	GACAAATTGUCCACCATCATCATUCAAT	862
A11	91827-R	GCTGAAGAGUGCAAACAATACATCAUAC	863
A12	91829-R	AGTCCAAAGGAAUGCCAATTTAATTATUAC	864
B01	91909-R	TTGTTAGCCAUATGCACATGAAUGAAT	865
B02	92464-R	TGACATGGTUGGGACTCTUGAC	866
B03	93379-R	GCCATAGGGCAUAAGCTGTGUC	867
B04	94170-R	CCTAGGTUGGCTCTGACTGUAC	868
B05	98573-R	CAACTCGTTCGUAGTGATATGGATUCA	869
B06	98681-R	CGATGCACGAUTACTTGGUGGAT	870
B07	99638-R	CCAGTAAATCCAUTCTGCTGCUGT	871
B08	101246-R	GAGCTATTCCACCUACTGATCCUG	872
B09	103227-R	ACTTAGCUTGGAAGCUGACAAGT	873
B10	103630-R	CACAAAATTUGGGATTATTGGAGUGGA	874
B11	103879-R	CACCTTUCAGCAGGUCAGAGAG	875
B12	104671-R	GGTAACAGUTGGCTTACUGGAAGT	876
C01	104720-R	CAACTATTTTCUTCCTCTCTUCCACAGT	877
C02	106398-R	TGTACCATTCAUGTTCCAGGUGAAG	878
C03	107255-R	GAGAACUAAGGCGGAAUCAGCA	879
C04	110679-R	TGAACCATCTTTUAACTCAGGTACTGUG	880
C05	116963-R	GGGCCCGGUGTAAGTGAAUT	881
C06	117792-R	GGUAATCTACUGGGACGGAACAG	882
C07	118631-R	CAATCCAUTTTTGTTGUCCAGCCA	883
C08	120430-R	GAAGCAGGUGGTCATTGAUGG	884
C09	121852-R	GACAUTGGAGAGTUGACCCAAAC	885
C10	122008-R	CCAGGGCUTTGAAGGAAGUGT	886
C11	133212-R	CCTCTGUGAAGAGCGGGTUC	887
C12	136501-R	GCTTATTTATTGGUCTCTCATTCUCCCA	888
D01	136537-R	AATATTGTCTTTGUGTTCCCGGACAUA	889
D02	142574-R	GGGAGAUCTTGUGCACGGT	890
D03	143592-R	TCAAGAGTTAATUGCAAATTACCTTAATTUCCA	891
D04	145156-R	CAGCATTTACUGCAGCTTGCTUAG	892
D05	147815-R	GAGGAAGATCCUTGTATGCTGTUAC	893
D06	178642-R	TGACCAAAACUCAGCCTGTTUCT	894
D07	226369-R	GTGCAGCUGTGGGTTGATUC	895
D08	226460-R	GCTCUCATTTTAAAGAUGGCCCAAA	896
D09	226789-R	CTGATTCCTCACUGATTGCTCTUAGG	897
D10	227540-R	CTGACAGAAGUACATCTGCTAAACAUGA	898
D11	232121-R	AGTACCUGGCAGTGTGATATUGG	899
D12	234145-R	GTACACTGCCUTTCGACACATAGUT	900
E01	236158-R	ACTGTUACAGAAATGAAAUAAGACGGAAA	901
E02	255119-R	GGAAAATTCATACCUAACTGGAGTGUGT	902
E03	304699-R	TGCTTGCTCTGAUAGGAAAATGAGAUC	903
E04	309408-R	CTTTTAATUGCCCGTGATGTUCCA	904
E05	310032-R	ATCCCCACUTTTCCTCTUGCA	905
E06	320120-R	GCTGTGACACUGCTGGAACUT	906
E07	329410-R	CGCTACTTCCUCCTCAAGAATGAUG	907
E08	339432-R	ATCCTTCTTCTCCUGTTTGAGAATGUC	908
E09	341576-R	GGACTGUGCGGAGCATGUAC	909
E10	379514-R	CATACTTTTCTTAUCTGCATAGATTTCUGC	910
E11	411633-R	GGCGTCCUACTGGCAUGAC	911
E12	416298-R	GATUAAGAGGACAAGCAGATUCAAGGT	912
F01	416888-R	GTCAACAACCCCCACAAAAUGTTUAAT	913
F02	421278-R	TTCTCCCAATGAAAGUAAAGTACAAACCUT	914

TABLE 3d

WellPosition	Name	Sequence	SEQ ID
F03	423052-R	CAGGATTGCCUTTACCACUCAGA	915
F04	464386-R	CAAGCAGATAACTUTCACTTAATAGTTGTUT	916
F05	482180-R	CACCAGGUACGCCTCCAGAUGAG	917
F06	482609-R	GGTCCCAGCCCCUCTCTGATUG	918
F07	482833-R	CCGAGUCCAGCACCTCCTUCAC	919
F08	483802-R	CACCCTGGCUCTGACCATTCUGT	920
F09	484088-R	GAGAGGCGGCCCAAUCTTCUG	921
F10	484297-R	CACGCTCTAUACTGCAAATGCTAUCGA	922
F11	484410-R	GGGTCCTUCCTGTCCTCCUAGCA	923
F12	484618-R	CCCUGCACCAGCAGCTCCUA	924
G01	490549-R	CACCGTGAAGUCCTGAGTGTAGAUGA	925
G02	491413-R	CTCCACGCCCUGTGACUCCAT	926
G03	492612-R	TGGUAGCAGTGGAUGCAGAAGG	927
G04	492615-R	CCTTCCUCCAGAAGCTTGAACTCUCA	928
G05	493041-R	CAGTUGGCGGGCTTGUCCAT	929
G06	495041-R	CCTGGUCCACCGCCAGTCUC	930
G07	503320-R	CCCCUAGCACGTGCCUACCT	931
G08	504796-R	GTTCTCCCAUGGGCUAGACACCA	932
G09	505293-R	CTGCUAGGGACCCCTCACATUG	933
G10	507582-R	GGCCCGCUGTACGTGUCCAT	934
G11	508777-R	GCAGTGGAACUCCACGUCGCT	935
G12	516350-R	ACTCTGUACAAAGACCGCGUGGT	936
H01	552959-R	TTCAATCACCACTAAAUCAATCTAAATACAGGAAAUC	937
H02	553293-R	TTTTTATTATAAGGCCUGCTGAAAATGACTGAATAUA	938
H03	554194-R	AAAATAATAAGCATCAGCAUTTGACTTTACCTTAUCA	939
H04	555556-R	GGGTGTGCUGGAAAAGGGUCCA	940
H05	559669-R	GTGCTGTUGAGACCTCTGUGGG	941
H06	613072-R	GCCCGTACCUCGGTAGCUGT	942
H07	645344-R	TTTTTTTTAATCAGAUAACTTTGTGGTAGATUCCAGT	943
H08	649396-R	CCGCCTGUGCCTAGAGGTUCT	944
H09	658417-R	CTGTTCACTTGUGCCCTGACTTUCAA	945
H10			
H11			
H12			

TABLE 4

Disease	Gene Symbols
Collagen 4A5 - 1 Alport gene tested	COL4A5
21-Hydroxylase-Deficient Congenital Adrenal Hyperplasia	CYP21A2
Achondroplasia FGFR3	FGFR3
Adenosine Aminohydrolase Deficiency (ADA)	ADA
Agammaglobulinemia, X-linked, Type 1	BTK
Alagille Syndrome - Test 1 gene	**JAG1**
Alopecia Universalis Congenita; ALUNC	HR
All Hypertrophic and Dilated Cardiomyopathy	**MYH7, TNNT2, MYBPC3, TNNI3, TPM1, ACTC, MYL3, MYL2, LAMP2, PRKAG2, GLA, CAV3, MTTG, MTTI, MTTK, TTR, TNNC1, DES, SGCD, LMNA, LDB3**
Alpers Syndrome	POLG
Alpha-1-Antitrypsin Deficiency	SERPINA1
Alpha-Thalassemia - Southeast Asia	HBA1, HBA2
Amyloidosis	TTR
Amyotrophic Lateral Sclerosis - Lou Gehrig's Disease	SOD1
Androgen Insensitivity Syndrome	AR
Aniridia	PAX6
Ankylosing spondylitis	HLA-B27
APC-Associated Polyposis Conditions	APC
Angioedema, Hereditary	C1NH
Argininosuccinate Lyase Deficiency	ASL
Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy,	**PKP2, DSP, DSG2, DSC2, RYR2,**
Arylsulfatase A Deficiency	ARSA
Ataxia-Telangiectasia	ATM
Ataxia with Oculomotor Apraxia Type 2	APTX
Ataxia with Vitamin E Deficiency	TTPA
Autoimmune Polyendocrine Syndrome	AIRE
Basal Cell Nevus Syndrome aka gorlin	PTCH
Beta-Hydroxyisobutyryl CoA Deacylase deficiency (HIBCH deficiency)	HIBCH
Beta-Thalassemia - Southeast Asia and Meditedrranean	HBB
Biotinidase Deficiency	BTD
Blepharophimosis-ptosis-epicanthus inversus	FOXL2
Bloom Syndrome	RECQL3
Branchiootorenal Spectrum Disorders - 3 Genes, Test 2	EYA1, SIX5, SIX1
Brachydactyly	GDF5
Brachydactyly, Type B1; BDB1	ROR2
Brachydactyly - Hypertension Syndrome	HTNB
BRCA1	BRCA1

BRCA2	BRCA2
Brugada Syndrome	SCN5A
Campomelic Dysplasia	SOX9
Canavan	ASPA
Cerebrotendinous Xanthomatosis - 1 mutation	CYP27A1
Ceroid-lipofuscinoses-Batton	PPT1
Charcot-Marie-Tooth Disease Type 2B - DNM2 Gene (Type 2B or 2M??)	DNM2 (or RAB7A)
Charcot-Marie-Tooth Neuropathy Type 1A	PMP22
Charcot-Marie-Tooth Neuropathy Type 1B	MPZ
Charcot-Marie-Tooth Neuropathy Type 2A	MFN2
Charcot-Marie-Tooth Neuropathy Type 2A2 -Test 1 gene - 20%	MFN2
Charge Syndrome - 1 Gene	CHD7
Cherubism	SH3BP2
Choroideremia - CHM Gene	CHM
Citrin Deficiency	SLC25A13
Citrullinemia Type I	ASS
Coffin-Lowry Syndrome	RPS6KA3
Cohen Syndrome	COH1
Common Variable Immune Deficiency	TNFRSC13C
Congenital Adrenal Hyperplasia	CYP21A2
Congenital Cataracts, Facial Dysmorphism, and Neuropathy	CTDP1
Congenital Disorder of Glycosylation Type 1a - PMM2	PMM2
Congenital Myasthenic Syndromes - [testing 5 genes~45%]	**CHAT, DOK7, CHRNB1, CHRNE, RAPSN, CHRNA1, CHRND**
Cornelia de Lange Syndrome	**NIPBL**
Cystic fibrosis	CFTR
Cystinosis	CTNS
Darier Disease	ATP2A2
DFNA2 Nonsyndromic Hearing Loss -KCNQ4 Gene	KCNQ4
DFNB1 - connexin 26 and connexin 30-50% AR-Testing GJB2	GJB2, GJB3, GJB6
Desmin Storage Myopathy	DES
Diamond-Blackfan Anemia	**RPS19, RPSL5, RPL11, RPL35A, RPS24, RPS17, RPS7, RPS10, RPS26**
Double Cortex Syndrome	DCX
Duane Syndrome - autosomal dominant	SALL4
Duchenne/Becker muscular dystrophy	DMD
Dysferlinopathy	DYSF
Dyskeratosis Congenita	DKC1
Early-Onset Familial Alzheimer Disease	APP, PSEN1, PSEN2
Early-Onset Primary Dystonia (DYT1)	DYT1
Ehlers Danlos	COL3A1
Ehlers-Danlos Syndrome, Classic Type - test 1 gene- 46%	**COL5A1, COL5A2**

Ehlers-Danlos Syndrome, Hypermobility Type	TNXB
Ehlers-Danlos Syndrome, Kyphoscoliotic Form	PLOD1
Emery-Dreifuss Muscular Dys.- X linked	**EMD, LMNA**
Epidermolysis Bullosa Simplex - 2 Genes	**KRT5, KRT14, LAMB3, COL7A1, ITGB4, PLEC1**
Fabry Disease	GLA
Facioscapulohumeral Muscular Dystrophy -D4Z4 deletion	FRG1
Familial Dysautonomia (HSAN III)	IKBKAP
Familial Hyperinsulinism (FHI)	HHF
Familial Hypertrophic Cardiomyopathy - 6 Genes testable	**CAV3, SLC25A4, MYH7, MYLK2, MYBPC3, PRKAG2, TNNT2, TPM1, MYL2, ACTC1, MYL3, VCL, TTN, CALR3, MYH6**
Familial Transthyretin Amyloidosis	TTR
Fanconi Anemia	FANCA, FANCC, FANDC2, FANCF, FANCJ and FANCG
Fragile X	FMR1
Friedreich Ataxia	FXN
FRMD7-Related Infantile Nystagmus	FRMD7
Fryns Syndrome	MED12
Galactosemia	GALT
Gaucher Disease	GBA
Glycine Encephalopathy	AMT, GCSH, GLDC
Glycogen Storage Disease Type II	GAA
Glycogen Storage Disease Type VI	**GBE1**
Hemochromatosis	HFE
Hemophagocytic Lymphohistiocytosis	HPLH1
Hemophilia A	F8
Hemophilia B	F9
Hepatic Veno-Occlusive Disease with Immunodeficiency	SP110
Hereditary Hemorrhagic Telangiectasia - Test 2 Genes	**ENG, ALK1**
Hereditary Nonpolyposis Colon Cancer	MSH2, MLH1
Hereditary Neuropathy with Liability to Pressure Palsies	**PMP22**
Hexosaminidase A Deficiency	HEXA
HFE-Associated Hereditary Hemochromatosis	HFE
Holt-Oram Syndrome	TBX5
Huntington Disease – test later (most of the time)	HD, PRPN, JPH3
Hydrocephalus, X-linked	L1CAM
Hydroxymethylbilane Synthase (HMBS) Deficiency	HMBS
Hypochondroplasia	FGFR3
Hypophosphatasia - autosomal recessive	ALPL
Inclusion Body Myopathy 2	GNE
Incontinentia Pigmenti	NEMO
Juvenile Polyposis Syndrome	**BMPR1A, SMAD4**
Kallmann Syndrome	FGFR1

Leber Congenital Amaurosis - Test 4 Genes for 33% - 65%	**CRB1,CEP290, GUCY2D, RPGRIP1, RPE65, RDH12, IMPDH1, AIPL1,**
Leber Hereditary Optic Neuropathy	Mitochondria
Li-Fraumeni Syndrome	TP53, CHEK2
Limb-Girdle Muscular Dystrophy Type 2A – Calpainopathy	CAPN3
LIS1-Associated Lissencephaly	PAFAH1B1
Long QT Syndrome, Autosomal Dominant	KCNQ1, HERG, SCN5A, KCNE1, KCNE2
Low γ-GT Familial Intrahepatic Cholestasis	
Lowe Syndrome	OCRL
Malignant Hyperthermia Susceptibility 6 Genes, 1 Tested	RYR1
Maple Syrup Urine Disease	BCKDHA, BCKDHB, DBT, DLD
MAPT-Related Disorders	MAPT
Marfan Syndrome	FBN1
McKusick-Kaufman Syndrome	BBS6
MECP2-Rett Syndrome	MECP2
MELAS (Mitochondrial Encephalomyopathy)	MTTL1, ND6, MTND5, MTTQ
Menkes/ATP7A-Related Copper Transport Dis	ATP7A
Metachromatic Leukodystrophy	ARSA
Methylmalonic Acidemia - 3 Genes Tested	**MUT, MMACHC, MMAA, MMAB, C2orf25**
Mucolipidosis II	GNPTAB
Muenke Syndrome	FGFR3
Multiple Endocrine Neoplasia Type 1	MEN1, MEN2A, MEN2B
Multiple Endocrine Neoplasia Type 2	**RET**
Myotonia Congenita	CLCN1
Myotonic Dystrophy Type 1	DMPK
Myotonic Dystrophy Type 2	ZNF9
Myotubular Myopathy	MTM
Nail-Patella Syndrome - LMX18 Gene - 95%	LMX18
Nemaline Myopathy	TNNT1
Neurofibromatosis 1	**NF1**
Neurofibromatosis 2	NF2
Noonan Syndrome - 3 gene test	**PTPN11, KRAS, SOS1, RAF1, NRAS**
Ocular Albinism, X-Linked	GPR143
Oculocutaneous Albinism Type 1	TYR
Oculocutaneous Albinism Type 2	OCA2, MC1R
Oculocutaneous Albinism Type 2	OCA2, MC1R
Oculopharyngeal Muscular Dystrophy	PABPN1
Optic Atrophy Type 1	OPA1
Ornithine Transcarbamylase Deficiency	OTC
Osteogenesis Imperfecta	COL1A1, COL1A2
Parkinson Disease - Testing for 1 gene (PARK 2)-50% pickup	**SNCA**
Parkinson Disease - Testing for 1 gene PARK 8)	**SNCA, PARKIN, PINK1, DJ1, LRRK2, FBXO7**
Pendred Syndrome/DFNB4 - SLC26A4	SLC26A4

Peroxisome Biogenesis, Zellweger	PEX10, PEX14, PEX19, PEX13, PEX3, PEX1, PEX5, PEX26
Phenylketonuria (listed above)	PAH
Polycystic Kidney Disease, Autosomal Dominant and recessive	PKD1, PKD2, PKD3, PKHD1
Pompe Disease -GSD II	GAA
Primary Ciliary Dyskinesia – 2 Genes	DNAI1, DNAH5, TXNDC3, DNAH11, DNAI2, DNAAF2, RSPH4A, RSPH9, DNAAF1, CCDC39, CCDC40, DNAL1
Retinitis Pigmentosa	**RPGR, RP2**
Retinitis Pigmentosa	**RPGR, RHO, PRPH2, IMPDH1, PRPF31, CRB1, PRPF8, RPGR, HPRP3, RPE65, MERTK, RDS, USH2A, ARL6, RP1, RP2, RP9, TULP1, CA4, ABCA4, EYS, CERKL, FSCN2, TOPORS, SNRNP200, SEMA4A, PRCD, NR2E3, USH2A, PROM1, KLHL7, CNGB1, BEST1, PRPH2, LRAT, SPATA7, CRX**
Retinoblastoma	RB1
Rett	MeCP2
Saethre-Chotzen Syndrome - TWIST 1 Gene	TWIST1
SCN9A-Related Inherited Erythromelalgia	SCN9A
SHOX-Related Haploinsufficiency	SHOX
Sickle Cell Disease	HBB
Smith-Lemli-Opitz Syndrome	DHCR7
Smith-Magenis Syndrome	RAI1
Sotos Syndrome	NSD1
Spastic Paraplegia 3A	SPG3A
Spastic Paraplegia 7 - SPG7	SPG7
Spastic Paraplegia 8	KIAA0196
Spastic Paraplegia Type 1 - L1 Syndrome - LICAM gene	L1CAM
Spastic Paraplegia Type 4	SPG4
Spinal Muscular Atrophy	SMN1
Spinocerebellar Ataxia Type 1 - ATXN1	ATXN1
Spinocerebellar Ataxia 2	ATXN2
Spinocerebellar Ataxia 3	SCA3
Spinocerebellar Ataxia 7	ATXN7
Stickler Syndrome - Test 2 Genes	**COL2A1, COL9A1, COL11A1, COL11A2**
Thanatophoric Dysplasia - FGFR3	FGFR3
Thoracic Aortic Aneurysms and Aortic Dissections -5 Genes	TGFBR1, TGFBR2, MYH11, ACTA2, FBN1
Treacher Collins Syndrome	TCOF1
Trimethylaminuria -1 gene, 30 mutations	FMO3
Tuberous Sclerosis Complex	**TSC1, TSC2**
Udd Distal Myopathy	TTN
Usher Syndrome type 1 - [5 of 8 gene loci testable]	**MYO7A, USH1C, CDH23, PCDH15, USH1H,**
Very Long Chain Acyl-Coenzyme A Dehydrogenase Deficiency	ACADVL

von Hippel-Lindau	VHL
Waardenburg Syndrome, Type 1	PAX3
Werner Syndrome	WRN
Wilms Tumor	**WT1, BRCA2, GPC3**
Wilson Disease	ATP7B
Wiskott-Aldrich	WAS
X-Linked Adrenal Hypoplasia Congenita	DAX1
X-Linked Adrenoleukodystrophy	ABCD1
X-Linked Dystonia-Parkinsonism	TAF1
X-linked Junenile Retinoschisis	RS1
X-linked myotubular Myopathy MTM1 Gene	MTM1
X-Linked SCIDS	IL2RG
Zellweger Syndrome	**PEX1, PEX2**

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
BRAF	NM_004333	449	c.1391G>A	p.G464E	-	7:140481417-140481417
BRAF	NM_004333	450	c.1391G>T	p.G464V	-	7:140481417-140481417
BRAF	NM_004333	451	c.1397G>T	p.G466V	-	7:140481411-140481411
BRAF	NM_004333	452	c.1397G>C	p.G466A	-	7:140481411-140481411
BRAF	NM_004333	453	c.1397G>A	p.G466E	-	7:140481411-140481411
BRAF	NM_004333	455	c.1405G>C	p.G469R	-	7:140481403-140481403
BRAF	NM_004333	457	c.1405G>A	p.G469R	-	7:140481403-140481403
BRAF	NM_004333	458	c.1405_1406GG>TC	p.G469S	-	7:140481402-140481403
BRAF	NM_004333	459	c.1406G>T	p.G469V	-	7:140481402-140481402
BRAF	NM_004333	460	c.1406G>C	p.G469A	-	7:140481402-140481402
BRAF	NM_004333	461	c.1406G>A	p.G469E	-	7:140481402-140481402
BRAF	NM_004333	462	c.1742A>G	p.N581S	-	7:140453193-140453193
BRAF	NM_004333	463	c.1756G>A	p.E586K	-	7:140453179-140453179
BRAF	NM_004333	464	c.1760A>C	p.D587A	-	7:140453175-140453175
BRAF	NM_004333	465	c.1761C>G	p.D587E	-	7:140453174-140453174
BRAF	NM_004333	466	c.1781A>T	p.D594V	-	7:140453154-140453154
BRAF	NM_004333	467	c.1781A>G	p.D594G	-	7:140453154-140453154
BRAF	NM_004333	468	c.1785T>G	p.F595L	-	7:140453150-140453150
BRAF	NM_004333	469	c.1786G>C	p.G596R	-	7:140453149-140453149
BRAF	NM_004333	470	c.1789C>G	p.L597V	-	7:140453146-140453146
BRAF	NM_004333	471	c.1790T>G	p.L597R	-	7:140453145-140453145
BRAF	NM_004333	472	c.1796C>T	p.T599I	-	7:140453139-140453139
BRAF	NM_004333	473	c.1798_1799GT>AA	p.V600K	-	7:140453136-140453137
BRAF	NM_004333	474	c.1798_1799GT>AG	p.V600R	-	7:140453136-140453137
BRAF	NM_004333	475	c.1799_1800TG>AA	p.V600E	-	7:140453135-140453136
BRAF	NM_004333	476	c.1799T>A	p.V600E	-	7:140453136-140453136
BRAF	NM_004333	477	c.1799_1800TG>AT	p.V600D	-	7:140453135-140453136
BRAF	NM_004333	478	c.1801A>G	p.K601E	-	7:140453134-140453134
HRAS	NM_005343	480	c.34G>A	p.G12S	-	11:534289-534289
HRAS	NM_005343	481	c.34G>T	p.G12C	-	11:534289-534289
HRAS	NM_005343	482	c.34G>C	p.G12R	-	11:534289-534289
HRAS	NM_005343	483	c.35G>T	p.G12V	-	11:534288-534288
HRAS	NM_005343	484	c.35G>A	p.G12D	-	11:534288-534288
HRAS	NM_005343	485	c.35G>C	p.G12A	-	11:534288-534288
HRAS	NM_005343	486	c.37G>C	p.G13R	-	11:534286-534286
HRAS	NM_005343	487	c.37G>A	p.G13S	-	11:534286-534286
HRAS	NM_005343	488	c.37G>T	p.G13C	-	11:534286-534286
HRAS	NM_005343	489	c.38G>T	p.G13V	-	11:534285-534285
HRAS	NM_005343	490	c.38G>A	p.G13D	-	11:534285-534285
HRAS	NM_005343	496	c.181C>A	p.Q61K	-	11:533875-533875
HRAS	NM_005343	498	c.182A>T	p.Q61L	-	11:533874-533874
HRAS	NM_005343	499	c.182A>G	p.Q61R	-	11:533874-533874

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
HRAS	NM_005343	500	c.182A>C	p.Q61P	-	11:533874-533874
HRAS	NM_005343	501	c.182_183AG>GT	p.Q61R	-	11:533873-533874
HRAS	NM_005343	502	c.183G>T	p.Q61H	-	11:533873-533873
HRAS	NM_005343	503	c.183G>C	p.Q61H	-	11:533873-533873
KRAS	NM_004985	513	c.34_36GGT>TGC	p.G12C	-	12:25398283-25398285
KRAS	NM_004985	515	c.35_36GT>TC	p.G12V	-	12:25398283-25398284
KRAS	NM_004985	516	c.34G>T	p.G12C	-	12:25398285-25398285
KRAS	NM_004985	517	c.34G>A	p.G12S	-	12:25398285-25398285
KRAS	NM_004985	518	c.34G>C	p.G12R	-	12:25398285-25398285
KRAS	NM_004985	520	c.35G>T	p.G12V	-	12:25398284-25398284
KRAS	NM_004985	521	c.35G>A	p.G12D	-	12:25398284-25398284
KRAS	NM_004985	522	c.35G>C	p.G12A	-	12:25398284-25398284
KRAS	NM_004985	526	c.37_39GGC>CGT	p.G13R	-	12:25398280-25398282
KRAS	NM_004985	527	c.37G>T	p.G13C	-	12:25398282-25398282
KRAS	NM_004985	528	c.37G>A	p.G13S	-	12:25398282-25398282
KRAS	NM_004985	529	c.37G>C	p.G13R	-	12:25398282-25398282
KRAS	NM_004985	530	c.38_39GC>TG	p.G13V	-	12:25398280-25398281
KRAS	NM_004985	531	c.38_39GC>AT	p.G13D	-	12:25398280-25398281
KRAS	NM_004985	532	c.38G>A	p.G13D	-	12:25398281-25398281
KRAS	NM_004985	533	c.38G>C	p.G13A	-	12:25398281-25398281
KRAS	NM_004985	534	c.38G>T	p.G13V	-	12:25398281-25398281
KRAS	NM_004985	543	c.64C>A	p.Q22K	-	12:25398255-25398255
KRAS	NM_004985	546	c.175G>A	p.A59T	-	12:25380283-25380283
KRAS	NM_004985	549	c.181C>A	p.Q61K	-	12:25380277-25380277
KRAS	NM_004985	550	c.181C>G	p.Q61E	-	12:25380277-25380277
KRAS	NM_004985	551	c.182A>C	p.Q61P	-	12:25380276-25380276
KRAS	NM_004985	552	c.182A>G	p.Q61R	-	12:25380276-25380276
KRAS	NM_004985	553	c.182A>T	p.Q61L	-	12:25380276-25380276
KRAS	NM_004985	554	c.183A>C	p.Q61H	-	12:25380275-25380275
KRAS	NM_004985	555	c.183A>T	p.Q61H	-	12:25380275-25380275
NRAS	NM_002524	561	c.34G>C	p.G12R	-	1:115258748-115258748
NRAS	NM_002524	562	c.34G>T	p.G12C	-	1:115258748-115258748
NRAS	NM_002524	563	c.34G>A	p.G12S	-	1:115258748-115258748
NRAS	NM_002524	564	c.35G>A	p.G12D	-	1:115258747-115258747
NRAS	NM_002524	565	c.35G>C	p.G12A	-	1:115258747-115258747
NRAS	NM_002524	566	c.35G>T	p.G12V	-	1:115258747-115258747
NRAS	NM_002524	569	c.37G>C	p.G13R	-	1:115258745-115258745
NRAS	NM_002524	570	c.37G>T	p.G13C	-	1:115258745-115258745
NRAS	NM_002524	571	c.37G>A	p.G13S	-	1:115258745-115258745
NRAS	NM_002524	572	c.38_39GT>TC	p.G13V	-	1:115258743-115258744
NRAS	NM_002524	573	c.38G>A	p.G13D	-	1:115258744-115258744
NRAS	NM_002524	574	c.38G>T	p.G13V	-	1:115258744-115258744

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
NRAS	NM_002524	575	c.38G>C	p.G13A	-	1:115258744-115258744
NRAS	NM_002524	577	c.52G>A	p.A18T	-	1:115258730-115258730
NRAS	NM_002524	579	c.181_182CA>AG	p.Q61R	-	1:115256529-115256530
NRAS	NM_002524	580	c.181C>A	p.Q61K	-	1:115256530-115256530
NRAS	NM_002524	581	c.181C>G	p.Q61E	-	1:115256530-115256530
NRAS	NM_002524	582	c.182A>C	p.Q61P	-	1:115256529-115256529
NRAS	NM_002524	583	c.182A>T	p.Q61L	-	1:115256529-115256529
NRAS	NM_002524	584	c.182A>G	p.Q61R	-	1:115256529-115256529
NRAS	NM_002524	585	c.183A>T	p.Q61H	-	1:115256528-115256528
NRAS	NM_002524	586	c.183A>C	p.Q61H	-	1:115256528-115256528
FGFR1	NM_000604	601	c.374C>T	p.S125L	-	8:38285938-38285938
ERBB2	NM_004448	681	c.2335_2336ins9	p.S779_P780insVGS	+	17:37881006-37881007
ERBB2	NM_004448	682	c.2322_2323ins12	p.M774_A775insAYVM	+	17:37880993-37880994
ERBB2	NM_004448	683	c.2263_2264TT>CC	p.L755P	+	17:37880219-37880220
ERBB2	NM_004448	685	c.2326G>A	p.G776S	+	17:37880997-37880997
MET	NM_000245	690	c.3742T>C	p.Y1248H	+	7:116423413-116423413
MET	NM_000245	691	c.3803T>C	p.M1268T	+	7:116423474-116423474
MET	NM_000245	696	c.3334C>T	p.H1112Y	+	7:116417463-116417463
MET	NM_000245	699	c.3743A>G	p.Y1248C	+	7:116423414-116423414
MET	NM_000245	700	c.3757T>G	p.Y1253D	+	7:116423428-116423428
MET	NM_000245	703	c.3335A>G	p.H1112R	+	7:116417464-116417464
MET	NM_000245	706	c.504G>T	p.E168D	+	7:116339642-116339642
MET	NM_000245	707	c.3029C>T	p.T1010I	+	7:116411990-116411990
MET	NM_000245	710	c.1124A>G	p.N375S	+	7:116340262-116340262
FGFR3	NM_000142	714	c.742C>T	p.R248C	+	4:1803564-1803564
FGFR3	NM_000142	715	c.746C>G	p.S249C	+	4:1803568-1803568
FGFR3	NM_000142	719	c.1948A>G	p.K650E	+	4:1807889-1807889
FGFR3	NM_000142	720	c.1949A>T	p.K650M	+	4:1807890-1807890
FGFR3	NM_000142	721	c.1172C>A	p.A391E	+	4:1806153-1806153
FGFR3	NM_000142	726	c.1948A>C	p.K650Q	+	4:1807889-1807889
FGFR3	NM_000142	729	c.2381_2381T>GA	p.L794fs*23	+	4:1808949-1808949
FGFR3	NM_000142	731	c.1949A>C	p.K650T	+	4:1807890-1807890
PDGFRA	NM_006206	736	c.2525A>T	p.D842V	+	4:55152093-55152093
PDGFRA	NM_006206	737	c.2524_2535del12	p.D842_H845del	+	4:55152092-55152103
PDGFRA	NM_006206	739	c.1682T>A	p.V561D	+	4:55141036-55141036
PDGFRA	NM_006206	741	c.1678_1692del15	p.R560_S564del	+	4:55141032-55141046
PDGFRA	NM_006206	743	c.2021C>T	p.T674I	+	4:55144547-55144547
PIK3CA	NM_006218.1	746	c.263G>A	p.R88Q	+	3:178916876-178916876
PIK3CA	NM_006218.1	754	c.1035T>A	p.N345K	+	3:178921553-178921553
PIK3CA	NM_006218.1	757	c.1258T>C	p.C420R	+	3:178927980-178927980
PIK3CA	NM_006218.1	759	c.1616C>G	p.P539R	+	3:178936074-178936074
PIK3CA	NM_006218.1	760	c.1624G>A	p.E542K	+	3:178936082-178936082

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
PIK3CA	NM_006218.1	762	c.1625A>T	p.E542V	+	3:178936083-178936083
PIK3CA	NM_006218.1	763	c.1633G>A	p.E545K	+	3:178936091-178936091
PIK3CA	NM_006218.1	764	c.1634A>G	p.E545G	+	3:178936092-178936092
PIK3CA	NM_006218.1	765	c.1635G>T	p.E545D	+	3:178936093-178936093
PIK3CA	NM_006218.1	766	c.1636C>A	p.Q546K	+	3:178936094-178936094
PIK3CA	NM_006218.1	767	c.1637A>C	p.Q546P	+	3:178936095-178936095
PIK3CA	NM_006218.1	771	c.3073A>G	p.T1025A	+	3:178952018-178952018
PIK3CA	NM_006218.1	773	c.3129G>T	p.M1043I	+	3:178952074-178952074
PIK3CA	NM_006218.1	774	c.3139C>T	p.H1047Y	+	3:178952084-178952084
PIK3CA	NM_006218.1	775	c.3140A>G	p.H1047R	+	3:178952085-178952085
PIK3CA	NM_006218.1	776	c.3140A>T	p.H1047L	+	3:178952085-178952085
PIK3CA	NM_006218.1	777	c.3145G>A	p.G1049S	+	3:178952090-178952090
PIK3CA	NM_006218.1	778	c.2102A>C	p.H701P	+	3:178938860-178938860
FLT3	Z26652	783	c.2503G>T	p.D835Y	-	13:28592642-28592642
FLT3	Z26652	784	c.2504A>T	p.D835V	-	13:28592641-28592641
FLT3	Z26652	785	c.2503G>C	p.D835H	-	13:28592642-28592642
FLT3	Z26652	786	c.2039C>T	p.A680V	-	13:28602329-28602329
FLT3	Z26652	787	c.2505T>A	p.D835E	-	13:28592640-28592640
FLT3	Z26652	788	c.2505T>G	p.D835E	-	13:28592640-28592640
FLT3	Z26652	796	c.2503_2505delGAT	p.D835del	-	13:28592640-28592642
FLT3	Z26652	797	c.2506_2508delATC	p.I836del	-	13:28592637-28592639
FLT3	Z26652	850	c.2520_2521insGGATCC	p.S840_N841insGS	-	13:28592624-28592625
RB1	NM_000321	868	c.2242G>T	p.E748*	+	13:49039164-49039164
RB1	NM_000321	869	c.1980_1983delCCGG	p.L660fs*2	+	13:49033843-49033846
RB1	NM_000321	879	c.1072C>T	p.R358*	+	13:48942685-48942685
RB1	NM_000321	883	c.2117G>T	p.C706F	+	13:49037877-49037877
RB1	NM_000321	887	c.1654C>T	p.R552*	+	13:48955538-48955538
RB1	NM_000321	888	c.1666C>T	p.R556*	+	13:48955550-48955550
RB1	NM_000321	890	c.409G>T	p.E137*	+	13:48919244-48919244
RB1	NM_000321	892	c.1735C>T	p.R579*	+	13:49027168-49027168
RB1	NM_000321	915	c.596T>A	p.L199*	+	13:48923148-48923148
CSF1R	NM_005211	946	c.902T>A	p.L301*	-	5:149453044-149453044
CSF1R	NM_005211	947	c.2906A>G	p.Y969C	-	5:149433645-149433645
CSF1R	NM_005211	948	c.2906A>T	p.Y969F	-	5:149433645-149433645
CSF1R	NM_005211	949	c.2907T>G	p.Y969*	-	5:149433644-149433644
CSF1R	NM_005211	952	c.2905T>C	p.Y969H	-	5:149433646-149433646
CSF1R	NM_005211	954	c.902T>C	p.L301S	-	5:149453044-149453044
CSF1R	NM_005211	955	c.2907T>A	p.Y969*	-	5:149433644-149433644
RET	NM_020975	965	c.2753T>C	p.M918T	+	10:43617416-43617416
RET	NM_020975	966	c.1900T>C	p.C634R	+	10:43609948-43609948
RET	NM_020975	968	c.1894_1899delGAGCTG	p.E632_L633del	+	10:43609942-43609947
RET	NM_020975	974	c.1901G>A	p.C634Y	+	10:43609949-43609949

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
RET	NM_020975	975	c.1902C>G	p.C634W	+	10:43609950-43609950
RET	NM_020975	977	c.2647_2648GC>TT	p.A883F	+	10:43615568-43615569
RET	NM_020975	978	c.1892A>G	p.D631G	+	10:43609940-43609940
RET	NM_020975	981	c.2646_2648AGC>TTT	p.A883F	+	10:43615567-43615569
RET	NM_020975	982	c.1895_1897delAGC	p.E632_L633>V	+	10:43609943-43609945
RET	NM_020975	983	c.1893_1898delCGAGCT	p.D631_L633>E	+	10:43609941-43609946
RET	NM_020975	984	c.1834_1860del27	p.F612_C620del	+	10:43609078-43609104
SMARCB1	NM_003073.2	991	c.141C>A	p.Y47*	+	22:24133990-24133990
SMARCB1	NM_003073.2	992	c.472C>T	p.R158*	+	22:24143240-24143240
SMARCB1	NM_003073.2	993	c.601C>T	p.R201*	+	22:24145582-24145582
SMARCB1	NM_003073.2	1002	c.118C>T	p.R40*	+	22:24133967-24133967
RET	NM_020975	1049	c.1895_1918>TGCGGC	p.E632_A640>VRP	+	10:43609943-43609966
SMARCB1	NM_003073.2	1057	c.1148delC	p.P383fs*3	+	22:24176357-24176357
BRAF	NM_004333	1111	c.1390G>C	p.G464R	-	7:140481418-140481418
BRAF	NM_004333	1112	c.1396G>C	p.G466R	-	7:140481412-140481412
BRAF	NM_004333	1113	c.1405_1407GGA>AGC	p.G469S	-	7:140481401-140481403
BRAF	NM_004333	1119	c.1776A>G	p.I592M	-	7:140453159-140453159
BRAF	NM_004333	1120	c.1774A>G	p.I592V	-	7:140453161-140453161
BRAF	NM_004333	1121	c.1782T>A	p.D594E	-	7:140453153-140453153
BRAF	NM_004333	1123	c.1784T>C	p.F595S	-	7:140453151-140453151
BRAF	NM_004333	1125	c.1790T>A	p.L597Q	-	7:140453145-140453145
BRAF	NM_004333	1126	c.1789_1790CT>TC	p.L597S	-	7:140453145-140453146
BRAF	NM_004333	1127	c.1797_1799AGT>GAG	p.V600R	-	7:140453136-140453138
BRAF	NM_004333	1128	c.1797_1797A>TACTACG	p.T599_V600insTT	-	7:140453138-140453138
BRAF	NM_004333	1130	c.1798G>A	p.V600M	-	7:140453137-140453137
BRAF	NM_004333	1132	c.1803A>C	p.K601N	-	7:140453132-140453132
BRAF	NM_004333	1135	c.1813_1814AG>TT	p.S605F	-	7:140453121-140453122
BRAF	NM_004333	1136	c.1814G>A	p.S605N	-	7:140453121-140453121
KIT	NM_000222	1146	c.154G>A	p.D52N	+	4:55561764-55561764
KIT	NM_000222	1169	c.1651_1665del15	p.P551_V555del	+	4:55593585-55593599
KIT	NM_000222	1210	c.1667_1672delAGTGGA	p.W557_K558del	+	4:55593601-55593606
KIT	NM_000222	1216	c.1669T>A	p.W557R	+	4:55593603-55593603
KIT	NM_000222	1217	c.1669_1674delTGGAAG	p.W557_K558del	+	4:55593603-55593608
KIT	NM_000222	1219	c.1669T>C	p.W557R	+	4:55593603-55593603
KIT	NM_000222	1221	c.1669T>G	p.W557G	+	4:55593603-55593603
KIT	NM_000222	1234	c.1672_1680del9	p.K558_V560del	+	4:55593606-55593614
KIT	NM_000222	1239	c.1672_1686del15	p.K558_E562del	+	4:55593606-55593620
KIT	NM_000222	1247	c.1675_1677delGTT	p.V559del	+	4:55593609-55593611
KIT	NM_000222	1251	c.1675G>A	p.V559I	+	4:55593609-55593609
KIT	NM_000222	1252	c.1676T>A	p.V559D	+	4:55593610-55593610
KIT	NM_000222	1253	c.1676T>G	p.V559G	+	4:55593610-55593610
KIT	NM_000222	1255	c.1676T>C	p.V559A	+	4:55593610-55593610

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
KIT	NM_000222	1257	c.1679T>A	p.V560D	+	4:55593613-55593613
KIT	NM_000222	1260	c.1679T>G	p.V560G	+	4:55593613-55593613
KIT	NM_000222	1290	c.1727T>C	p.L576P	+	4:55593661-55593661
KIT	NM_000222	1294	c.1735_1737delGAT	p.D579del	+	4:55593669-55593671
KIT	NM_000222	1299	c.1755C>T	p.P585P	+	4:55593689-55593689
KIT	NM_000222	1304	c.1924A>G	p.K642E	+	4:55594221-55594221
KIT	NM_000222	1306	c.2143_2145delAGC	p.S715del	+	4:55597495-55597497
KIT	NM_000222	1310	c.2446G>T	p.D816Y	+	4:55599320-55599320
KIT	NM_000222	1311	c.2446G>C	p.D816H	+	4:55599320-55599320
KIT	NM_000222	1314	c.2447A>T	p.D816V	+	4:55599321-55599321
KIT	NM_000222	1321	c.2466T>A	p.N822K	+	4:55599340-55599340
KIT	NM_000222	1322	c.2466T>G	p.N822K	+	4:55599340-55599340
KIT	NM_000222	1323	c.2474T>C	p.V825A	+	4:55599348-55599348
KIT	NM_000222	1324	c.2515G>A	p.E839K	+	4:55602694-55602694
KIT	NM_000222	1326	c.1509_1510insGCCTAT	p.Y503_F504insAY	+	4:55592185-55592186
KIT	NM_000222	1332	c.1669_1683del15	p.W557_E561del	+	4:55593603-55593617
SRC	NM_005417	1369	c.1591C>T	p.Q531*	+	20:36031762-36031762
PTEN	NM_000314.4	4894	c.952_955delCTTA	p.L318fs*2	+	10:89720801-89720804
PTEN	NM_000314.4	4898	c.950_953delTACT	p.V317fs*3	+	10:89720799-89720802
PTEN	NM_000314.4	4903	c.954_957delTACT	p.L318fs*2	+	10:89720803-89720806
PTEN	NM_000314.4	4929	c.17_18delAA	p.K6fs*4	+	10:89624243-89624244
PTEN	NM_000314.4	4937	c.16_17delAA	p.K6fs*4	+	10:89624242-89624243
PTEN	NM_000314.4	4958	c.955_958delACTT	p.T319fs*1	+	10:89720804-89720807
PTEN	NM_000314.4	4986	c.741_742insA	p.P248fs*5	+	10:89717716-89717717
PTEN	NM_000314.4	4990	c.968_969insA	p.N323fs*2	+	10:89720817-89720818
PTEN	NM_000314.4	4994	c.963_964insA	p.T321fs*3	+	10:89720812-89720813
PTEN	NM_000314.4	5025	c.742_743insC	p.P248fs*5	+	10:89717717-89717718
PTEN	NM_000314.4	5026	c.742_743insA	p.P248fs*5	+	10:89717717-89717718
PTEN	NM_000314.4	5036	c.202T>C	p.Y68H	+	10:89685307-89685307
PTEN	NM_000314.4	5039	c.518G>A	p.R173H	+	10:89711900-89711900
PTEN	NM_000314.4	5089	c.517C>T	p.R173C	+	10:89711899-89711899
PTEN	NM_000314.4	5149	c.511C>T	p.Q171*	+	10:89711893-89711893
PTEN	NM_000314.4	5150	c.640C>T	p.Q214*	+	10:89717615-89717615
PTEN	NM_000314.4	5151	c.1003C>T	p.R335*	+	10:89720852-89720852
CTNNB1	NM_001904	5661	c.94G>T	p.D32Y	+	3:41266097-41266097
CTNNB1	NM_001904	5662	c.110C>T	p.S37F	+	3:41266113-41266113
CTNNB1	NM_001904	5663	c.133T>C	p.S45P	+	3:41266136-41266136
CTNNB1	NM_001904	5664	c.121A>G	p.T41A	+	3:41266124-41266124
CTNNB1	NM_001904	5666	c.110C>A	p.S37Y	+	3:41266113-41266113
CTNNB1	NM_001904	5667	c.134C>T	p.S45F	+	3:41266137-41266137
CTNNB1	NM_001904	5668	c.94G>C	p.D32H	+	3:41266097-41266097
CTNNB1	NM_001904	5669	c.98C>T	p.S33F	+	3:41266101-41266101

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Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
CTNNB1	NM_001904	5670	c.101G>T	p.G34V	+	3:41266104-41266104
CTNNB1	NM_001904	5671	c.101G>A	p.G34E	+	3:41266104-41266104
CTNNB1	NM_001904	5672	c.94G>A	p.D32N	+	3:41266097-41266097
CTNNB1	NM_001904	5673	c.98C>A	p.S33Y	+	3:41266101-41266101
CTNNB1	NM_001904	5675	c.109T>G	p.S37A	+	3:41266112-41266112
CTNNB1	NM_001904	5676	c.122C>T	p.T41I	+	3:41266125-41266125
CTNNB1	NM_001904	5677	c.98C>G	p.S33C	+	3:41266101-41266101
CTNNB1	NM_001904	5679	c.110C>G	p.S37C	+	3:41266113-41266113
CTNNB1	NM_001904	5681	c.95A>G	p.D32G	+	3:41266098-41266098
CTNNB1	NM_001904	5684	c.100G>C	p.G34R	+	3:41266103-41266103
CTNNB1	NM_001904	5685	c.133T>G	p.S45A	+	3:41266136-41266136
CTNNB1	NM_001904	5686	c.100G>A	p.G34R	+	3:41266103-41266103
CTNNB1	NM_001904	5687	c.109T>C	p.S37P	+	3:41266112-41266112
CTNNB1	NM_001904	5688	c.121A>C	p.T41P	+	3:41266124-41266124
CTNNB1	NM_001904	5689	c.134C>G	p.S45C	+	3:41266137-41266137
CTNNB1	NM_001904	5690	c.95A>C	p.D32A	+	3:41266098-41266098
CTNNB1	NM_001904	5691	c.95A>T	p.D32V	+	3:41266098-41266098
CTNNB1	NM_001904	5692	c.134C>A	p.S45Y	+	3:41266137-41266137
CTNNB1	NM_001904	5701	c.122C>G	p.T41S	+	3:41266125-41266125
CTNNB1	NM_001904	5706	c.65T>C	p.V22A	+	3:41266068-41266068
CTNNB1	NM_001904	5716	c.121A>T	p.T41S	+	3:41266124-41266124
CTNNB1	NM_001904	5738	c.61G>A	p.A21T	+	3:41266064-41266064
CTNNB1	NM_001904	5747	c.37G>A	p.A13T	+	3:41266040-41266040
PTEN	NM_000314.4	5775	c.1002_1003CC>TT	p.R335*	+	10:89720851-89720852
PTEN	NM_000314.4	5801	c.968delA	p.N323fs*21	+	10:89720817-89720817
PTEN	NM_000314.4	5816	c.867delA	p.V290fs*1	+	10:89720716-89720716
PTEN	NM_000314.4	5823	c.963delA	p.T321fs*23	+	10:89720812-89720812
PTEN	NM_000314.4	5888	c.723_724insTT	p.E242fs*15	+	10:89717698-89717699
CTNNB1	NM_001904	6050	c.64_114del51	p.V22_G38del	+	3:41266067-41266117
CTNNB1	NM_001904	6064	c.74_97del24	p.W25_D32del	+	3:41266077-41266100
BRAF	NM_004333	6137	c.1799T>G	p.V600G	-	7:140453136-140453136
PIK3CA	NM_006218.1	6147	c.1636C>G	p.Q546E	+	3:178936094-178936094
EGFR	NM_005228	6210	c.2240_2251del12	p.L747_T751>S	+	7:55242470-55242481
EGFR	NM_005228	6213	c.2582T>A	p.L861Q	+	7:55259524-55259524
EGFR	NM_005228	6218	c.2239_2247del9	p.L747_E749del	+	7:55242469-55242477
EGFR	NM_005228	6219	c.2248G>C	p.A750P	+	7:55242478-55242478
EGFR	NM_005228	6220	c.2238_2255del18	p.E746_S752>D	+	7:55242468-55242485
EGFR	NM_005228	6223	c.2235_2249del15	p.E746_A750del	+	7:55242465-55242479
EGFR	NM_005228	6224	c.2573T>G	p.L858R	+	7:55259515-55259515
EGFR	NM_005228	6225	c.2236_2250del15	p.E746_A750del	+	7:55242466-55242480
EGFR	NM_005228	6239	c.2156G>C	p.G719A	+	7:55241708-55241708
EGFR	NM_005228	6240	c.2369C>T	p.T790M	+	7:55249071-55249071

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Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
EGFR	NM_005228	6241	c.2303G>T	p.S768I	+	7:55249005-55249005
EGFR	NM_005228	6252	c.2155G>A	p.G719S	+	7:55241707-55241707
EGFR	NM_005228	6253	c.2155G>T	p.G719C	+	7:55241707-55241707
EGFR	NM_005228	6254	c.2239_2253del15	p.L747_T751del	+	7:55242469-55242483
EGFR	NM_005228	6255	c.2239_2256del18	p.L747_S752del	+	7:55242469-55242486
EGFR	NM_005228	6256	c.2254_2277del24	p.S752_I759del	+	7:55242484-55242507
BRAF	NM_004333	6262	c.1330C>T	p.R444W	-	7:140481478-140481478
BRAF	NM_004333	6265	c.1803A>T	p.K601N	-	7:140453132-140453132
EGFR	NM_005228	6268	c.2257C>T	p.P753S	+	7:55242487-55242487
TP53	NM_000546	6530	c.723delC	p.C242fs*5	-	17:7577558-7577558
TP53	NM_000546	6545	c.741_742CC>TT	p.R248W	-	17:7577539-7577540
TP53	NM_000546	6549	c.743G>T	p.R248L	-	17:7577538-7577538
TP53	NM_000546	6932	c.733G>A	p.G245S	-	17:7577548-7577548
TP53	NM_000546	10645	c.527G>T	p.C176F	-	17:7578403-7578403
TP53	NM_000546	10647	c.404G>T	p.C135F	-	17:7578526-7578526
TP53	NM_000546	10648	c.524G>A	p.R175H	-	17:7578406-7578406
TP53	NM_000546	10654	c.637C>T	p.R213*	-	17:7578212-7578212
TP53	NM_000546	10656	c.742C>T	p.R248W	-	17:7577539-7577539
TP53	NM_000546	10659	c.817C>T	p.R273C	-	17:7577121-7577121
TP53	NM_000546	10660	c.818G>A	p.R273H	-	17:7577120-7577120
TP53	NM_000546	10662	c.743G>A	p.R248Q	-	17:7577538-7577538
TP53	NM_000546	10663	c.916C>T	p.R306*	-	17:7577022-7577022
TP53	NM_000546	10667	c.646G>A	p.V216M	-	17:7578203-7578203
TP53	NM_000546	10670	c.469G>T	p.V157F	-	17:7578461-7578461
TP53	NM_000546	10690	c.473G>A	p.R158H	-	17:7578457-7578457
TP53	NM_000546	10704	c.844C>T	p.R282W	-	17:7577094-7577094
TP53	NM_000546	10705	c.586C>T	p.R196*	-	17:7578263-7578263
TP53	NM_000546	10709	c.722C>G	p.S241C	-	17:7577559-7577559
TP53	NM_000546	10710	c.892G>T	p.E298*	-	17:7577046-7577046
TP53	NM_000546	10714	c.473G>T	p.R158L	-	17:7578457-7578457
TP53	NM_000546	10716	c.329G>T	p.R110L	-	17:7579358-7579358
TP53	NM_000546	10722	c.853G>A	p.E285K	-	17:7577085-7577085
TP53	NM_000546	10731	c.707A>G	p.Y236C	-	17:7577574-7577574
TP53	NM_000546	10735	c.638G>A	p.R213Q	-	17:7578211-7578211
TP53	NM_000546	10742	c.578A>G	p.H193R	-	17:7578271-7578271
TP53	NM_000546	10758	c.659A>G	p.Y220C	-	17:7578190-7578190
TP53	NM_000546	10769	c.820G>T	p.V274F	-	17:7577118-7577118
TP53	NM_000546	10779	c.818G>T	p.R273L	-	17:7577120-7577120
TP53	NM_000546	10790	c.455C>T	p.P152L	-	17:7578475-7578475
TP53	NM_000546	10808	c.488A>G	p.Y163C	-	17:7578442-7578442
TP53	NM_000546	10810	c.725G>T	p.C242F	-	17:7577556-7577556
TP53	NM_000546	10812	c.722C>T	p.S241F	-	17:7577559-7577559

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
TP53	NM_000546	10813	c.394A>G	p.K132E	-	17:7578536-7578536
TP53	NM_000546	10817	c.747G>T	p.R249S	-	17:7577534-7577534
TP53	NM_000546	10863	c.833C>T	p.P278L	-	17:7577105-7577105
TP53	NM_000546	10889	c.536A>G	p.H179R	-	17:7578394-7578394
TP53	NM_000546	10891	c.814G>A	p.V272M	-	17:7577124-7577124
TP53	NM_000546	10893	c.824G>A	p.C275Y	-	17:7577114-7577114
TP53	NM_000546	10939	c.832C>T	p.P278S	-	17:7577106-7577106
TP53	NM_000546	11063	c.711G>T	p.M237I	-	17:7577570-7577570
TP53	NM_000546	11073	c.1024C>T	p.R342*	-	17:7574003-7574003
TP53	NM_000546	11081	c.733G>T	p.G245C	-	17:7577548-7577548
TP53	NM_000546	11148	c.476C>T	p.A159V	-	17:7578454-7578454
TP53	NM_000546	11196	c.734G>T	p.G245V	-	17:7577547-7577547
TP53	NM_000546	11218	c.464C>A	p.T155N	-	17:7578466-7578466
TP53	NM_000546	11224	c.394A>C	p.K132Q	-	17:7578536-7578536
TP53	NM_000546	11232	c.842A>G	p.D281G	-	17:7577096-7577096
TP53	NM_000546	11249	c.537T>G	p.H179Q	-	17:7578393-7578393
TP53	NM_000546	11291	c.1006G>T	p.E336*	-	17:7574021-7574021
TP53	NM_000546	11305	c.809T>C	p.F270S	-	17:7577129-7577129
TP53	NM_000546	11606	c.31G>C	p.E11Q	-	17:7579882-7579882
EGFR	NM_005228	12366	c.2572C>A	p.L858M	+	7:55259514-55259514
EGFR	NM_005228	12367	c.2237_2254del18	p.E746_S752>A	+	7:55242467-55242484
EGFR	NM_005228	12369	c.2240_2254del15	p.L747_T751del	+	7:55242470-55242484
EGFR	NM_005228	12370	c.2240_2257del18	p.L747_P753>S	+	7:55242470-55242487
EGFR	NM_005228	12376	c.2307_2308ins9	p.V769_D770insASV	+	7:55249009-55249010
EGFR	NM_005228	12377	c.2319_2320insCAC	p.H773_V774insH	+	7:55249021-55249022
EGFR	NM_005228	12378	c.2310_2311insGGT	p.D770_N771insG	+	7:55249012-55249013
EGFR	NM_005228	12381	c.2319_2320ins9	p.H773_V774insNPH	+	7:55249021-55249022
EGFR	NM_005228	12382	c.2239_2248TTAAGAGAAG>C	p.L747_A750>P	+	7:55242469-55242478
EGFR	NM_005228	12383	c.2239_2251>C	p.L747_T751>P	+	7:55242469-55242481
EGFR	NM_005228	12384	c.2237_2255>T	p.E746_S752>V	+	7:55242467-55242485
EGFR	NM_005228	12387	c.2239_2258>CA	p.L747_P753>Q	+	7:55242469-55242488
PDGFRA	NM_006206	12396	c.2524G>T	p.D842Y	+	4:55152092-55152092
PDGFRA	NM_006206	12397	c.2524_2526GAC>TAT	p.D842Y	+	4:55152092-55152094
PDGFRA	NM_006206	12398	c.2524_2525GA>AT	p.D842I	+	4:55152092-55152093
PDGFRA	NM_006206	12399	c.2536G>T	p.D846Y	+	4:55152104-55152104
PDGFRA	NM_006206	12400	c.2527_2538del12	p.I843_D846del	+	4:55152095-55152106
PDGFRA	NM_006206	12401	c.2524_2532del9	p.D842_M844del	+	4:55152092-55152100
PDGFRA	NM_006206	12402	c.2530_2541del12	p.M844_S847del	+	4:55152098-55152109
PDGFRA	NM_006206	12405	c.2521_2526delAGAGAC	p.R841_D842del	+	4:55152089-55152094
PDGFRA	NM_006206	12407	c.2528_2539del12	p.I843_S847>T	+	4:55152096-55152107
PDGFRA	NM_006206	12408	c.2526_2538>G	p.D842_D846>E	+	4:55152094-55152106
PDGFRA	NM_006206	12411	c.2524_2536>A	p.D842_D846>N	+	4:55152092-55152104

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
PDGFRA	NM_006206	12412	c.2525_2538>GA	p.D842_D846>G	+	4:55152093-55152106
PDGFRA	NM_006206	12414	c.2525_2535>TT	p.D842_H845>V	+	4:55152093-55152103
PDGFRA	NM_006206	12415	c.2526_2541>GGCC	p.D842_S847>EA	+	4:55152094-55152109
EGFR	NM_005228	12419	c.2238_2252>GCA	p.L747_T751>Q	+	7:55242468-55242482
EGFR	NM_005228	12422	c.2238_2248>GC	p.L747_A750>P	+	7:55242468-55242478
EGFR	NM_005228	12429	c.2573_2574TG>GT	p.L858R	+	7:55259515-55259516
PIK3CA	NM_006218.1	12458	c.1634A>C	p.E545A	+	3:178936092-178936092
PIK3CA	NM_006218.1	12459	c.1637A>G	p.Q546R	+	3:178936095-178936095
PIK3CA	NM_006218.1	12461	c.3062A>G	p.Y1021C	+	3:178952007-178952007
PIK3CA	NM_006218.1	12464	c.3204_3205insA	p.N1068fs*4	+	3:178952149-178952150
CDKN2A	NM_000077	12473	c.172C>T	p.R58*	-	9:21971186-21971186
ERBB2	NM_004448	12552	c.2326_2327insTTT	p.G776>VC	+	17:37880997-37880998
ERBB2	NM_004448	12553	c.2326_2327insTGT	p.G776>VC	+	17:37880997-37880998
ERBB2	NM_004448	12556	c.2340_2341ins9	p.P780_Y781insGSP	+	17:37881011-37881012
ERBB2	NM_004448	12558	c.2325_2326ins12	p.A775_G776insYVMA	+	17:37880996-37880997
ABL1	X16416	12560	c.944C>T	p.T315I	+	9:133748283-133748283
ABL1	X16416	12573	c.763G>A	p.E255K	+	9:133738363-133738363
ABL1	X16416	12574	c.764A>T	p.E255V	+	9:133738364-133738364
ABL1	X16416	12575	c.951C>G	p.F317L	+	9:133748290-133748290
ABL1	X16416	12576	c.757T>C	p.Y253H	+	9:133738357-133738357
ABL1	X16416	12577	c.749G>A	p.G250E	+	9:133738349-133738349
ABL1	X16416	12578	c.1052T>C	p.M351T	+	9:133748391-133748391
PIK3CA	NM_006218.1	12591	c.3127A>G	p.M1043V	+	3:178952072-178952072
PIK3CA	NM_006218.1	12597	c.3145G>C	p.G1049R	+	3:178952090-178952090
JAK2	ENST00000381652	12600	c.1849G>T	p.V617F	+	9:5073770-5073770
ABL1	X16416	12602	c.827A>G	p.D276G	+	9:133747520-133747520
ABL1	X16416	12604	c.1187A>G	p.H396R	+	9:133750356-133750356
ABL1	X16416	12605	c.1075T>G	p.F359V	+	9:133748414-133748414
ABL1	X16416	12608	c.730A>G	p.M244V	+	9:133738330-133738330
ABL1	X16416	12609	c.756G>C	p.Q252H	+	9:133738356-133738356
ABL1	X16416	12610	c.758A>T	p.Y253F	+	9:133738358-133738358
ABL1	X16416	12611	c.1064A>G	p.E355G	+	9:133748403-133748403
ABL1	X16416	12631	c.742C>G	p.L248V	+	9:133738342-133738342
ABL1	X16416	12632	c.756G>T	p.Q252H	+	9:133738356-133738356
EGFR	NM_005228	12678	c.2237_2251del15	p.E746_T751>A	+	7:55242467-55242481
KRAS	NM_004985	12703	c.57G>C	p.L19F	-	12:25398262-25398262
KIT	NM_000222	12706	c.1961T>C	p.V654A	+	4:55594258-55594258
KIT	NM_000222	12708	c.2009C>T	p.T670I	+	4:55595519-55595519
KRAS	NM_004985	12721	c.38_39GC>TT	p.G13V	-	12:25398280-25398281
NRAS	NM_002524	12725	c.181_182CA>TT	p.Q61L	-	1:115256529-115256530
EGFR	NM_005228	12728	c.2236_2253del18	p.E746_T751del	+	7:55242466-55242483
KRAS	NM_004985	12729	c.180_181TC>CA	p.Q61K	-	12:25380277-25380278

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
NRAS	NM_002524	12730	c.180_181AC>TA	p.Q61K	-	1:115256530-115256531
CDKN2A	NM_000077	12731	c.171_172CC>TT	p.R58*	-	9:21971186-21971187
NOTCH1	NM_017617.2	12771	c.4802T>C	p.L1601P	-	9:139399344-139399344
NOTCH1	NM_017617.2	12772	c.4724T>C	p.L1575P	-	9:139399422-139399422
ATM	NM_000051	12791	c.7996A>G	p.T2666A	+	11:108204681-108204681
ATM	NM_000051	12792	c.5380C>T	p.L1794L	+	11:108173640-108173640
ATM	NM_000051	12793	c.2542G>C	p.E848Q	+	11:108137973-108137973
ERBB4	NM_005235	12833	c.908C>A	p.S303Y	-	2:212578349-212578349
FGFR1	NM_000604	12834	c.754C>A	p.P252T	-	8:38282209-38282209
STK11	NM_000455	12924	c.842delC	p.P281fs*6	+	19:1221319-1221319
STK11	NM_000455	12925	c.109C>T	p.Q37*	+	19:1207021-1207021
ATM	NM_000051	12951	c.7325A>C	p.Q2442P	+	11:108200958-108200958
EGFR	NM_005228	12986	c.2429G>A	p.G810D	+	7:55249131-55249131
EGFR	NM_005228	12988	c.2125G>A	p.E709K	+	7:55241677-55241677
PTPN11	NM_002834.3	13000	c.226G>A	p.E76K	+	12:112888210-112888210
EGFR	NM_005228	13003	c.2310_2311insAAC	p.D770_N771insN	+	7:55249012-55249013
EGFR	NM_005228	13004	c.2310_2311insGGC	p.D770_N771insG	+	7:55249012-55249013
PTPN11	NM_002834.3	13011	c.181G>T	p.D61Y	+	12:112888165-112888165
PTPN11	NM_002834.3	13013	c.205G>A	p.E69K	+	12:112888189-112888189
PTPN11	NM_002834.3	13014	c.214G>A	p.A72T	+	12:112888198-112888198
PTPN11	NM_002834.3	13016	c.226G>C	p.E76Q	+	12:112888210-112888210
PTPN11	NM_002834.3	13017	c.227A>G	p.E76G	+	12:112888211-112888211
PTPN11	NM_002834.3	13019	c.218C>T	p.T73I	+	12:112888202-112888202
PTPN11	NM_002834.3	13020	c.1504T>C	p.S502P	+	12:112926884-112926884
PTPN11	NM_002834.3	13022	c.182A>T	p.D61V	+	12:112888166-112888166
PTPN11	NM_002834.3	13025	c.227A>T	p.E76V	+	12:112888211-112888211
PTPN11	NM_002834.3	13026	c.227A>C	p.E76A	+	12:112888211-112888211
PTPN11	NM_002834.3	13027	c.1508G>C	p.G503A	+	12:112926888-112926888
PTPN11	NM_002834.3	13028	c.179G>T	p.G60V	+	12:112888163-112888163
PTPN11	NM_002834.3	13035	c.215C>A	p.A72D	+	12:112888199-112888199
NOTCH1	NM_017617.2	13042	c.4781T>C	p.L1594P	-	9:139399365-139399365
NOTCH1	NM_017617.2	13046	c.4757T>C	p.L1586P	-	9:139399389-139399389
NOTCH1	NM_017617.2	13047	c.4735_4737delGTG	p.V1579del	-	9:139399409-139399411
NOTCH1	NM_017617.2	13048	c.5036T>C	p.L1679P	-	9:139397768-139397768
NOTCH1	NM_017617.2	13053	c.4796G>C	p.R1599P	-	9:139399350-139399350
APC	NM_000038	13113	c.3927_3931delAAAGA	p.E1309fs*4	+	5:112175218-112175222
APC	NM_000038	13121	c.4099C>T	p.Q1367*	+	5:112175390-112175390
APC	NM_000038	13125	c.3340C>T	p.R1114*	+	5:112174631-112174631
APC	NM_000038	13127	c.4348C>T	p.R1450*	+	5:112175639-112175639
SMO	NM_005631.3	13145	c.595C>T	p.R199W	+	7:128845101-128845101
SMO	NM_005631.3	13146	c.1604G>T	p.W535L	+	7:128850341-128850341
SMO	NM_005631.3	13147	c.970G>A	p.A324T	+	7:128846040-128846040

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
SMO	NM_005631.3	13148	c.1210G>A	p.V404M	+	7:128846374-128846374
SMO	NM_005631.3	13150	c.1918A>G	p.T640A	+	7:128851593-128851593
ERBB2	NM_004448	13170	c.2305G>C	p.D769H	+	17:37880261-37880261
EGFR	NM_005228	13180	c.2188C>T	p.L730F	+	7:55242418-55242418
EGFR	NM_005228	13181	c.2198C>T	p.P733L	+	7:55242428-55242428
EGFR	NM_005228	13182	c.2203G>A	p.G735S	+	7:55242433-55242433
EGFR	NM_005228	13183	c.2225T>C	p.V742A	+	7:55242455-55242455
EGFR	NM_005228	13184	c.2236G>A	p.E746K	+	7:55242466-55242466
EGFR	NM_005228	13186	c.2255C>A	p.S752Y	+	7:55242485-55242485
EGFR	NM_005228	13188	c.2281G>A	p.D761N	+	7:55242511-55242511
EGFR	NM_005228	13192	c.2428G>A	p.G810S	+	7:55249130-55249130
CDKN2A	NM_000077	13281	c.205G>T	p.E69*	-	9:21971153-21971153
EGFR	NM_005228	13427	c.2126A>C	p.E709A	+	7:55241678-55241678
EGFR	NM_005228	13428	c.2311_2312ins9	p.D770_N771insSVD	+	7:55249013-55249014
EGFR	NM_005228	13432	c.2193G>A	p.W731*	+	7:55242423-55242423
EGFR	NM_005228	13433	c.2318A>G	p.H773R	+	7:55249020-55249020
CDKN2A	NM_000077	13486	c.181G>T	p.E61*	-	9:21971177-21971177
EGFR	NM_005228	13549	c.2235_2251>AG	p.E746_T751>A	+	7:55242465-55242481
EGFR	NM_005228	13551	c.2235_2252>AAT	p.E746_T751>I	+	7:55242465-55242482
EGFR	NM_005228	13553	c.2572_2573CT>AG	p.L858R	+	7:55259514-55259515
EGFR	NM_005228	13554	c.2312_2315ACCC>GCGTGGACAACCG	p.N771_P772>SVDNR	+	7:55249014-55249017
EGFR	NM_005228	13556	c.2253_2276del24	p.S752_I759del	+	7:55242483-55242506
APC	NM_000038	13728	c.3907C>T	p.Q1303*	+	5:112175198-112175198
APC	NM_000038	13864	c.4393_4394delAG	p.S1465fs*3	+	5:112175684-112175685
SMAD4	NM_005359.3	14057	c.733C>T	p.Q245*	+	18:48584560-48584560
ERBB2	NM_004448	14060	c.2264T>C	p.L755S	+	17:37880220-37880220
ERBB2	NM_004448	14062	c.2329G>T	p.V777L	+	17:37881000-37881000
ERBB2	NM_004448	14064	c.2329G>A	p.V777M	+	17:37881000-37881000
ERBB2	NM_004448	14065	c.2524G>A	p.V842I	+	17:37881332-37881332
SMAD4	NM_005359.3	14096	c.1333C>T	p.R445*	+	18:48603032-48603032
SMAD4	NM_005359.3	14105	c.1394_1395insT	p.A466fs*28	+	18:48603093-48603094
SMAD4	NM_005359.3	14110	c.989A>C	p.E330A	+	18:48591826-48591826
SMAD4	NM_005359.3	14111	c.1028C>G	p.S343*	+	18:48591865-48591865
SMAD4	NM_005359.3	14113	c.1490G>A	p.R497H	+	18:48604668-48604668
SMAD4	NM_005359.3	14115	c.1569C>G	p.C523W	+	18:48604747-48604747
SMAD4	NM_005359.3	14118	c.502G>T	p.G168*	+	18:48581198-48581198
SMAD4	NM_005359.3	14121	c.1015_1029del15	p.F339_S343del	+	18:48591852-48591866
SMAD4	NM_005359.3	14122	c.1082G>A	p.R361H	+	18:48591919-48591919
SMAD4	NM_005359.3	14124	c.1341_1365del25	p.Q448fs*20	+	18:48603040-48603064
SMAD4	NM_005359.3	14129	c.1543A>T	p.R515*	+	18:48604721-48604721
SMAD4	NM_005359.3	14134	c.1576G>T	p.E526*	+	18:48604754-48604754
SMAD4	NM_005359.3	14135	c.1051G>C	p.D351H	+	18:48591888-48591888

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
SMAD4	NM_005359.3	14163	c.931C>T	p.Q311*	+	18:48586262-48586262
SMAD4	NM_005359.3	14174	c.1072G>T	p.G358*	+	18:48591909-48591909
SMAD4	NM_005359.3	14177	c.1546_1553delCAGAGCAT	p.S517fs*7	+	18:48604724-48604731
KRAS	NM_004985	14209	c.35_36GT>AC	p.G12D	-	12:25398283-25398284
SMAD4	NM_005359.3	14216	c.363_364insA	p.C123fs*2	+	18:48575169-48575170
EGFR	NM_005228	14243	c.2234A>G	p.K745R	+	7:55242464-55242464
SMAD4	NM_005359.3	14249	c.1156G>C	p.G386R	+	18:48593405-48593405
PTPN11	NM_002834.3	14271	c.1508G>T	p.G503V	+	12:112926888-112926888
VHL	NM_000551.2	14305	c.266T>A	p.L89H	+	3:10183797-10183797
VHL	NM_000551.2	14311	c.499C>T	p.R167W	+	3:10191506-10191506
VHL	NM_000551.2	14346	c.266T>C	p.L89P	+	3:10183797-10183797
VHL	NM_000551.2	14368	c.473T>A	p.L158Q	+	3:10191480-10191480
VHL	NM_000551.2	14407	c.388G>C	p.V130L	+	3:10188245-10188245
VHL	NM_000551.2	14410	c.440delT	p.F148fs*11	+	3:10188297-10188297
PIK3CA	NM_006218.1	17442	c.1624G>C	p.E542Q	+	3:178936082-178936082
NPM1	NM_002520.4	17559	c.863_864insTCTG	p.W288fs*12	+	5:170837547-170837548
NPM1	NM_002520.4	17571	c.863_864insCATG	p.W288fs*12	+	5:170837547-170837548
NPM1	NM_002520.4	17573	c.863_864insCCTG	p.W288fs*12	+	5:170837547-170837548
VHL	NM_000551.2	17612	c.481C>T	p.R161*	+	3:10191488-10191488
VHL	NM_000551.2	17658	c.286C>T	p.Q96*	+	3:10183817-10183817
VHL	NM_000551.2	17735	c.444delT	p.F148fs*11	+	3:10188301-10188301
EGFR	NM_005228	18419	c.2200G>A	p.E734K	+	7:55242430-55242430
EGFR	NM_005228	18425	c.2156G>A	p.G719D	+	7:55241708-55241708
EGFR	NM_005228	18441	c.2154_2155GG>TT	p.G719C	+	7:55241706-55241707
EGFR	NM_005228	18442	c.2241_2244AAGA>CCCG	p.L747_R748>FP	+	7:55242471-55242474
BRAF	NM_004333	18443	c.1799T>C	p.V600A	-	7:140453136-140453136
APC	NM_000038	18561	c.4666_4667insA	p.T1556fs*3	+	5:112175957-112175958
ERBB2	NM_004448	18609	c.2327G>T	p.G776V	+	17:37880998-37880998
STK11	NM_000455	18652	c.996G>A	p.W332*	+	19:1223059-1223059
KIT	NM_000222	18681	c.2467T>G	p.Y823D	+	4:55599341-55599341
APC	NM_000038	18701	c.3926_3930delAAAAG	p.E1309fs*4	+	5:112175217-112175221
APC	NM_000038	18702	c.3964G>T	p.E1322*	+	5:112175255-112175255
APC	NM_000038	18704	c.4312delA	p.T1438fs*35	+	5:112175603-112175603
APC	NM_000038	18719	c.3923_3924insA	p.E1309fs*6	+	5:112175214-112175215
APC	NM_000038	18758	c.4108A>T	p.K1370*	+	5:112175399-112175399
APC	NM_000038	18760	c.3916G>T	p.E1306*	+	5:112175207-112175207
APC	NM_000038	18764	c.3921_3925delAAAAG	p.E1309fs*4	+	5:112175212-112175216
APC	NM_000038	18775	c.3925G>T	p.E1309*	+	5:112175216-112175216
APC	NM_000038	18783	c.4316delC	p.P1439fs*34	+	5:112175607-112175607
APC	NM_000038	18834	c.4135G>T	p.E1379*	+	5:112175426-112175426
APC	NM_000038	18838	c.4391_4394delAGAG	p.E1464fs*8	+	5:112175682-112175685
APC	NM_000038	18852	c.2626C>T	p.R876*	+	5:112173917-112173917

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
APC	NM_000038	18861	c.4128T>A	p.Y1376*	+	5:112175419-112175419
APC	NM_000038	18862	c.4132C>T	p.Q1378*	+	5:112175423-112175423
APC	NM_000038	18873	c.4385_4386delAG	p.S1465fs*3	+	5:112175676-112175677
KIT	NM_000222	18896	c.1673_1687del15	p.K558_E562del	+	4:55593607-55593621
MPL	NM_005373.1	18918	c.1544G>T	p.W515L	+	1:43815009-43815009
APC	NM_000038	18931	c.4392_4393delGA	p.S1465fs*3	+	5:112175683-112175684
APC	NM_000038	18960	c.3880C>T	p.Q1294*	+	5:112175171-112175171
APC	NM_000038	19021	c.4330C>T	p.Q1444*	+	5:112175621-112175621
APC	NM_000038	19072	c.3871C>T	p.Q1291*	+	5:112175162-112175162
APC	NM_000038	19098	c.4463delT	p.L1488fs*19	+	5:112175754-112175754
APC	NM_000038	19099	c.3949G>C	p.E1317Q	+	5:112175240-112175240
APC	NM_000038	19127	c.4394_4395delGT	p.S1465fs*3	+	5:112175685-112175686
APC	NM_000038	19145	c.3925_3929delGAAAA	p.E1309fs*4	+	5:112175216-112175220
MPL	NM_005373.1	19193	c.1543_1544TG>AA	p.W515K	+	1:43815008-43815009
APC	NM_000038	19236	c.4333delA	p.T1445fs*28	+	5:112175624-112175624
APC	NM_000038	19263	c.3922_3926delAAAGA	p.E1309fs*4	+	5:112175213-112175217
APC	NM_000038	19332	c.4391_4392delAG	p.S1465fs*3	+	5:112175682-112175683
APC	NM_000038	19349	c.4479_4480delGG	p.E1494fs*19	+	5:112175770-112175771
KRAS	NM_004985	19404	c.436G>A	p.A146T	-	12:25378562-25378562
FLT3	Z26652	19522	c.1775T>C	p.V592A	-	13:28608281-28608281
APC	NM_000038	19664	c.3919delA	p.I1307fs*1	+	5:112175210-112175210
FLT3	Z26652	19686	c.2508C>G	p.I836M	-	13:28592637-28592637
APC	NM_000038	19688	c.4386_4387delGA	p.S1465fs*3	+	5:112175677-112175678
FLT3	Z26652	19692	c.2525A>G	p.Y842C	-	13:28592620-28592620
APC	NM_000038	19695	c.4660_4661insA	p.T1556fs*3	+	5:112175951-112175952
FLT3	Z26652	19737	c.1803_1804ins81	p.L601_K602ins27	-	13:28608252-28608253
CDH1	NM_004360.2	19748	c.1108G>C	p.D370H	+	16:68846137-68846137
CDH1	NM_004360.2	19761	c.1196_1199delCTGA	p.T399fs*17	+	16:68847274-68847277
FLT3	Z26652	19790	c.1807_1808ins18	p.K602_W603insYEYDLK	-	13:28608248-28608249
FLT3	Z26652	19836	c.2508_2510delCAT	p.I836del	-	13:28592635-28592637
ERBB4	NM_005235	20392	c.419C>T	p.T140I	-	2:212812157-212812157
ATM	NM_000051	20404	c.7328G>A	p.R2443Q	+	11:108200961-108200961
KRAS	NM_004985	20818	c.57G>T	p.L19F	-	12:25398262-25398262
STK11	NM_000455	20857	c.787_790delTTGT	p.F264fs*22	+	19:1221264-1221267
STK11	NM_000455	20871	c.837delC	p.P281fs*6	+	19:1221314-1221314
STK11	NM_000455	20874	c.180C>G	p.Y60*	+	19:1207092-1207092
STK11	NM_000455	20957	c.581A>T	p.D194V	+	19:1220488-1220488
ERBB2	NM_004448	20959	c.2324_2325ins12	p.A775_G776insYVMA	+	17:37880995-37880996
KDR	NM_002253	21091	c.743C>G	p.A248G	-	4:55980348-55980348
STK11	NM_000455	21212	c.169delG	p.E57fs*7	+	19:1207077-1207077
RET	NM_020975	21338	c.2304G>C	p.E768D	+	10:43613840-43613840
STK11	NM_000455	21355	c.842C>T	p.P281L	+	19:1221319-1221319

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
STK11	NM_000455	21359	c.595G>A	p.E199K	+	19:1220502-1220502
STK11	NM_000455	21360	c.1062C>G	p.F354L	+	19:1223125-1223125
HNF1A	NM_000545.3	21471	c.617G>T	p.W206L	+	12:121431413-121431413
HNF1A	NM_000545.3	21477	c.817A>G	p.K273E	+	12:121432070-121432070
HNF1A	NM_000545.3	21478	c.618G>T	p.W206C	+	12:121431414-121431414
BRAF	NM_004333	21609	c.1761C>A	p.D587E	-	7:140453174-140453174
BRAF	NM_004333	21612	c.1783T>C	p.F595L	-	7:140453152-140453152
ATM	NM_000051	21624	c.9139C>T	p.R3047*	+	11:108236203-108236203
ATM	NM_000051	21626	c.9023G>A	p.R3008H	+	11:108236087-108236087
ATM	NM_000051	21636	c.8084G>C	p.G2695A	+	11:108205769-108205769
ATM	NM_000051	21642	c.9022C>T	p.R3008C	+	11:108236086-108236086
EGFR	NM_005228	21683	c.323G>A	p.R108K	+	7:55211080-55211080
EGFR	NM_005228	21687	c.866C>T	p.A289V	+	7:55221822-55221822
EGFR	NM_005228	21690	c.1793G>T	p.G598V	+	7:55233043-55233043
ATM	NM_000051	21825	c.1229T>C	p.V410A	+	11:108119823-108119823
ATM	NM_000051	21826	c.2572T>C	p.F858L	+	11:108138003-108138003
ATM	NM_000051	21918	c.5224G>C	p.A1742P	+	11:108172421-108172421
ATM	NM_000051	21919	c.5041A>G	p.I1681V	+	11:108170476-108170476
ATM	NM_000051	21920	c.5044G>T	p.D1682Y	+	11:108170479-108170479
ATM	NM_000051	21922	c.5821G>C	p.V1941L	+	11:108180945-108180945
ATM	NM_000051	21924	c.1058_1059delGT	p.C353fs*5	+	11:108117847-108117848
ATM	NM_000051	21930	c.8839A>T	p.T2947S	+	11:108225590-108225590
PDGFRA	NM_006206	21973	c.1659_1664delGAGGTA	p.R554_Y555del	+	4:55141013-55141018
EGFR	NM_005228	21984	c.2281G>T	p.D761Y	+	7:55242511-55242511
ERBB2	NM_004448	21985	c.2632C>T	p.H878Y	+	17:37881440-37881440
PDGFRA	NM_006206	22413	c.2472C>T	p.V824V	+	4:55152040-55152040
PDGFRA	NM_006206	22416	c.1975A>T	p.N659Y	+	4:55144146-55144146
ATM	NM_000051	22481	c.8174A>T	p.D2725V	+	11:108206594-108206594
ATM	NM_000051	22485	c.8668C>G	p.L2890V	+	11:108218089-108218089
ATM	NM_000051	22499	c.1810C>T	p.P604S	+	11:108123551-108123551
ATM	NM_000051	22507	c.3925G>A	p.A1309T	+	11:108155132-108155132
FBXW7	NM_033632.1	22932	c.1393C>T	p.R465C	-	4:153249385-153249385
FBXW7	NM_033632.1	22965	c.1394G>A	p.R465H	-	4:153249384-153249384
FBXW7	NM_033632.1	22971	c.832C>T	p.R278*	-	4:153258983-153258983
FBXW7	NM_033632.1	22973	c.1177C>T	p.R393*	-	4:153250883-153250883
FBXW7	NM_033632.1	22974	c.1436G>A	p.R479Q	-	4:153247366-153247366
FBXW7	NM_033632.1	22975	c.1513C>T	p.R505C	-	4:153247289-153247289
FBXW7	NM_033632.1	22979	c.1745C>T	p.S582L	-	4:153245446-153245446
FBXW7	NM_033632.1	23000	c.1514G>T	p.R505L	-	4:153247288-153247288
EGFR	NM_005228	23571	c.2238_2252del15	p.L747_T751del	+	7:55242468-55242482
APC	NM_000038	23598	c.4483delA	p.S1495fs*12	+	5:112175774-112175774
PTEN	NM_000314.4	23626	c.962_963insA	p.N323fs*2	+	10:89720811-89720812

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
FLT3	Z26652	24531	c.2509_2510AT>CC	p.M837P	-	13:28592635-28592636
BRAF	NM_004333	24642	c.1411G>T	p.V471F	-	7:140481397-140481397
NOTCH1	NM_017617.2	24673	c.4724T>C	p.L1575P	-	9:139399422-139399422
FGFR3	NM_000142	24802	c.2089G>T	p.G697C	+	4:1808331-1808331
FGFR3	NM_000142	24842	c.1138G>A	p.G380R	+	4:1806119-1806119
EGFR	NM_005228	24869	c.2235_2252del18	p.E746_T751del	+	7:55242465-55242482
APC	NM_000038	24946	c.4291delA	p.M1431fs*42	+	5:112175582-112175582
PIK3CA	NM_006218.1	25041	c.1637A>T	p.Q546L	+	3:178936095-178936095
STK11	NM_000455	25229	c.595G>T	p.E199*	+	19:1220502-1220502
FLT3	Z26652	25248	c.2492G>A	p.G831E	-	13:28592653-28592653
APC	NM_000038	25827	c.4048A>T	p.K1350*	+	5:112175339-112175339
JAK2	ENST00000381652	25834	c.1848_1849TG>CT	p.V617F	+	9:5073769-5073770
STK11	NM_000455	25847	c.580G>A	p.D194N	+	19:1220487-1220487
MLH1	NM_000249.2	26085	c.1151T>A	p.V384D	+	3:37067240-37067240
PIK3CA	NM_006218.1	27133	c.1633G>C	p.E545Q	+	3:178936091-178936091
STK11	NM_000455	27322	c.180delC	p.Y60fs*1	+	19:1207092-1207092
PIK3CA	NM_006218.1	27374	c.1635G>C	p.E545D	+	3:178936093-178936093
GNAS	NM_000516.3	27887	c.601C>T	p.R201C	+	20:57484420-57484420
GNAS	NM_000516.3	27895	c.602G>A	p.R201H	+	20:57484421-57484421
FLT3	Z26652	27906	c.1796A>T	p.Y599F	-	13:28608260-28608260
KIT	NM_000222	27909	c.1656_1673del18	p.Y553_K558>	+	4:55593590-55593607
BRAF	NM_004333	27912	c.1405_1407GGA>AGT	p.G469S	-	7:140481401-140481403
FLT3	Z26652	27979	c.1788_1789ins36	p.E596_Y597ins12	-	13:28608267-28608268
KIT	NM_000222	28026	c.1621A>C	p.M541L	+	4:55593464-55593464
FLT3	Z26652	28042	c.1352C>T	p.S451F	-	13:28610138-28610138
FLT3	Z26652	28044	c.1715A>G	p.Y572C	-	13:28608341-28608341
FLT3	Z26652	28047	c.2501G>A	p.R834Q	-	13:28592644-28592644
PDGFRA	NM_006206	28053	c.1694_1695insA	p.S566fs*6	+	4:55141048-55141049
ALK	NM_004304	28055	c.3522C>A	p.F1174L	-	2:29443695-29443695
ALK	NM_004304	28056	c.3824G>A	p.R1275Q	-	2:29432664-29432664
STK11	NM_000455	28298	c.841_842>T	p.P281fs*6	+	19:1221318-1221319
IDH1	NM_005896.2	28746	c.395G>A	p.R132H	-	2:209113112-209113112
IDH1	NM_005896.2	28747	c.394C>T	p.R132C	-	2:209113113-209113113
IDH1	NM_005896.2	28748	c.394C>A	p.R132S	-	2:209113113-209113113
IDH1	NM_005896.2	28749	c.394C>G	p.R132G	-	2:209113113-209113113
FLT3	Z26652	28771	c.1811_1812ins30	p.W603_E604insDREYEYDLKW	-	13:28608244-28608245
FLT3	Z26652	28921	c.1798_1799ins45	p.Y599_D600ins15	-	13:28608257-28608258
CDH1	NM_004360.2	28934	c.240_241insGGTG	p.V82fs*13	+	16:68835649-68835650
APC	NM_000038	29331	c.4063delT	p.S1355fs*60	+	5:112175354-112175354
SMARCB1	NM_003073.2	29382	c.1143delG	p.A382fs*5	+	22:24176352-24176352
FGFR3	NM_000142	29438	c.1921G>A	p.D641N	+	4:1807862-1807862
BRAF	NM_004333	30594	c.1801_1803delAAA	p.K601del	-	7:140453132-140453134

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
PTEN	NM_000314.4	30622	c.795delA	p.K267fs*9	+	10:89717770-89717770
NRAS	NM_002524	30646	c.182_183AA>TG	p.Q61L	-	1:115256528-115256529
KDR	NM_002253	32294	c.2617G>A	p.G873R	-	4:55962507-55962507
KDR	NM_002253	32339	c.824G>T	p.R275L	-	4:55979623-55979623
NRAS	NM_002524	33693	c.182_183AA>GG	p.Q61R	-	1:115256528-115256529
HRAS	NM_005343	33695	c.182_183AG>GA	p.Q61R	-	11:533873-533874
BRAF	NM_004333	33808	c.1798G>T	p.V600L	-	7:140453137-140453137
JAK3	NM_000215	34213	c.2164G>A	p.V722I	-	19:17945696-17945696
JAK3	NM_000215	34214	c.1715C>T	p.A572V	-	19:17948009-17948009
FGFR2	NM_000141.2	36901	c.929A>G	p.K310R	-	10:123279503-123279503
FGFR2	NM_000141.2	36902	c.1647T>G	p.N549K	-	10:123258034-123258034
FGFR2	NM_000141.2	36903	c.755C>G	p.S252W	-	10:123279677-123279677
FGFR2	NM_000141.2	36904	c.1124A>G	p.Y375C	-	10:123274794-123274794
FGFR2	NM_000141.2	36905	c.1115C>G	p.S372C	-	10:123274803-123274803
FGFR2	NM_000141.2	36906	c.1144T>C	p.C382R	-	10:123274774-123274774
FGFR2	NM_000141.2	36912	c.1647T>A	p.N549K	-	10:123258034-123258034
AKT1	ENST00000349310	36918	c.145G>A	p.E49K	-	14:105246455-105246455
APC	NM_000038	41618	c.4463_4466delTATT	p.L1488fs*18	+	5:112175754-112175757
PTEN	NM_000314.4	43098	c.969delT	p.N323fs*21	+	10:89720818-89720818
TP53	NM_000546	43559	c.517G>T	p.V173L	-	17:7578413-7578413
TP53	NM_000546	43657	c.569C>T	p.P190L	-	17:7578280-7578280
TP53	NM_000546	43683	c.758C>T	p.T253I	-	17:7577523-7577523
TP53	NM_000546	43827	c.581T>C	p.L194P	-	17:7578268-7578268
TP53	NM_000546	43836	c.475G>C	p.A159P	-	17:7578455-7578455
TP53	NM_000546	43989	c.596G>A	p.G199E	-	17:7578253-7578253
TP53	NM_000546	43990	c.610G>A	p.E204K	-	17:7578239-7578239
TP53	NM_000546	44017	c.869G>A	p.R290H	-	17:7577069-7577069
TP53	NM_000546	44037	c.322G>A	p.G108S	-	17:7579365-7579365
TP53	NM_000546	44151	c.535C>A	p.H179N	-	17:7578395-7578395
TP53	NM_000546	44162	c.635_636delTT	p.F212fs*3	-	17:7578213-7578214
TP53	NM_000546	44241	c.592G>T	p.E198*	-	17:7578257-7578257
TP53	NM_000546	44539	c.584T>G	p.I195S	-	17:7578265-7578265
TP53	NM_000546	44613	c.455C>A	p.P152Q	-	17:7578475-7578475
TP53	NM_000546	44673	c.284C>T	p.S95F	-	17:7579403-7579403
TP53	NM_000546	44769	c.755T>C	p.L252P	-	17:7577526-7577526
TP53	NM_000546	44782	c.520A>T	p.R174W	-	17:7578410-7578410
TP53	NM_000546	44877	c.584T>A	p.I195N	-	17:7578265-7578265
TP53	NM_000546	44908	c.743_744GG>AA	p.R248Q	-	17:7577537-7577538
TP53	NM_000546	45286	c.475G>T	p.A159S	-	17:7578455-7578455
TP53	NM_000546	45307	c.309C>A	p.Y103*	-	17:7579378-7579378
ERBB4	NM_005235	48361	c.2804A>T	p.K935I	-	2:212288942-212288942
ERBB4	NM_005235	48362	c.2791G>T	p.D931Y	-	2:212288955-212288955

TABLE 10

Gene	accession number	COSMIC id	cds_mut_syntax	aa_mut_syntax	Strand	hg19 coordinates
ERBB4	NM_005235	48363	c.1853A>C	p.H618P	-	2:212530066-212530066
ERBB4	NM_005235	48364	c.1784A>T	p.D595V	-	2:212530135-212530135
ERBB4	NM_005235	48365	c.1042G>T	p.V348L	-	2:212576857-212576857
ERBB4	NM_005235	48366	c.916C>A	p.R306S	-	2:212578341-212578341
ERBB4	NM_005235	48367	c.854A>G	p.Y285C	-	2:212587147-212587147
ERBB4	NM_005235	48368	c.731C>G	p.T244R	-	2:212589811-212589811
ERBB4	NM_005235	48369	c.542A>G	p.N181S	-	2:212652764-212652764
KDR	NM_002253	48460	c.3629C>T	p.P1210L	-	4:55953807-55953807
KDR	NM_002253	48461	c.3434G>A	p.G1145E	-	4:55955111-55955111
KDR	NM_002253	48462	c.3418C>A	p.L1140M	-	4:55955127-55955127
KDR	NM_002253	48463	c.2951G>C	p.S984T	-	4:55960989-55960989
KDR	NM_002253	48464	c.2917G>T	p.A973S	-	4:55961023-55961023
KDR	NM_002253	48465	c.1426G>T	p.V476L	-	4:55972964-55972964
STK11	NM_000455	48786	c.587G>T	p.G196V	+	19:1220494-1220494
KDR	NM_002253	48875	c.3922G>T	p.G1308*	-	4:55946257-55946257
KDR	NM_002253	48977	c.4063_4065delCCT	p.P1355del	-	4:55946114-55946116
ABL1	X16416	49074	c.949T>C	p.F317L	+	9:133748288-133748288
HRAS	NM_005343	52978	c.182_183AG>TA	p.Q61L	-	11:533873-533874
HRAS	NM_005343	52979	c.181_182CA>AG	p.Q61R	-	11:533874-533875
BRAF	NM_004333	53198	c.1785T>A	p.F595L	-	7:140453150-140453150
NRAS	NM_002524	53223	c.181_183CAA>AAG	p.Q61K	-	1:115256528-115256530
PTEN	NM_000314.4	53243	c.964_964delA	p.N323fs*21	+	10:89720813-89720813
KRAS	NM_004985	87281	c.36_37TG>AT	p.G13C	-	12:25398282-25398283
KRAS	NM_004985	87298	c.180_181TC>AA	p.Q61K	-	12:25380277-25380278
PTEN	NM_000314.4	87314	c.797_797delA	p.K267fs*9	+	10:89717772-89717772

TABLE 13

Chromosome	Insert start	Insert stop	Amplicon ID	SEQ ID NO	fwd_Uprimer	SEQ ID NO	rev_Uprimer
chr18	9749779	9749891	224824531	50354	ACTTTTAAUAGCTTGGACUGCACACA	50355	CATGCTGGGACCUGTTCACUT
chr20	51296041	51296164	224824951	50356	GAGTUAGAAGCCCCCAAAGUGA	50357	TGTGATCACCUAATAGCCAGCGAUA
chr19	39559693	39559818	224825327	50358	CCTGAGGGUGCTGTTAUAGAAGG	50359	ATGATAGUGGCAAAGGAGAGAGTUG
chr12	6945797	6945924	224825605	50360	GGGACTCCUCTATTCTTGGCUCA	50361	GGCTGGAAUCCCGCTTACUAA
chr18	55225666	55225789	224826815	50362	AAAAATGTGGUCCTGAGTCTUAGCA	50363	GGACAGTUAAGAGAAGGCTGCTTUT
chr9	27985817	27985939	224828811	50364	CAGAGCAGAAGAAAGGUGAATGAAGAUA	50365	AGTGAGAAGUGTCTTGGGTUGG
chr6	152697597	152697715	224829413	50366	CTTGGCGGUAGTGATTTTTGCAUT	50367	CAACTTTATCGCUTTTTCCTGCCATUA
chr7	137029730	137029850	224829586	50368	TCCCCCTUCCCAAACTCTTCAUA	50369	AGGTGAAATCTGAUTAAAACAAGCACUG
chr1	160786573	160786699	224829592	50370	AATGTCTCAUGGAGAAGCAGUGAAA	50371	TCAGTCAGGAUGCAAACTCTUGG
chr22	33559416	33559523	224830378	50372	TTTCAATACUCCAGAATGAAGUGAAGGT	50373	CCATGCCATCGUCTGTATTAAGTCTUAT
chr6	12059860	12059966	224830857	50374	GGTTCTCCUCGCCTACTGUG	50375	CAACCCAUCCCAGCTGAGTAUT
chr14	104769094	104769199	224836140	50376	CACCAGAATUTAAACAACGCUGACA	50377	GAUACAAGAGCTUCCGGAGACC
chr8	144656729	144656826	224841974	50378	CTGCCTGUGGCTTTGTAGTTCUA	50379	GATTTGCAUCCCAGUGAAAGCAC
chr5	136633267	136633358	224848875	50380	TGTTTTAAGGAGACUATGAGGTGTGUCT	50381	GTTACTTTCTUCCTGCCTTTGUCC
chr8	28410972	28411081	224850970	50382	GTAATCACAGUAAAACACAATGCUGAGG	50383	CCCGCAAACUAACTAGGATAAATCUCT
chr10	17193312	17193384	224851112	50384	ACAATAATAATCCUCAAAAACAAAGAAACAUGG	50385	TGTGACTGGUGGTGTGTATTCUG
chr10	118506777	118506904	224853634	50386	GGCCAGAGGAAAUTATTGCUCCA	50387	GGGTTTGAGCAGUTCTGAGAAUGT
chr15	39313286	39313402	224858176	50388	CCAACTCAAUGGCCCTCCTTTUA	50389	TGCAGUGCAAAAATGCAGUAAGG
chr12	130761571	130761697	224859704	50390	GCATCCCAGGAUAACGCUGT	50391	CTTATCTGCTAUGTGGCATACTUGGA
chr2	182413146	182413261	224860927	50392	GCTTACTAGGACCUGTAAGAGTCUGT	50393	TGATGATGUGCAAGAAAGGTAGGUAAAA
chr4	169663561	169663664	224862488	50394	CCCAGGGAAGGAAUAAGTACATTUGA	50395	CAGGCATUTGACCTTCUAGCCA
chr5	17374818	17374914	224864543	50396	AAATTTGCACCUGGTGTTATTTTUGGT	50397	GCCCCCATTAUAACATTGGAGAGAAUA
chr17	80461808	80461937	224864743	50398	CACCAGTTUGAGCACAGAGAUT	50399	GUGAGAAGAGCCUCAAGGACAG
chr13	100038132	100038253	224865079	50400	GGCCAGAGGACUCTGCAGUA	50401	TGTTCTTCUCCATCCCATTUCACC
chr16	5868664	5868750	224866641	50402	GATAGGACCCUTGTTTTCAAAAAGTUGT	50403	ATTAGCUGCAGGCAGCAGUAA
chr9	137417232	137417349	224868250	50404	GGACCUGCGAAAUCCCAAAA	50405	ACCCCGUCGTATCUAGCAGAG
chr3	193207278	193207393	224869380	50406	ACCTTTGGAUGTTGTTCUGGCT	50407	TCCGTAGTAAAUGAGAGCAAGTTUGT
chr11	5708914	5709034	224869774	50408	TCAGTTTTTCTAUTGGCCCACGUT	50409	CTTCCATAGATCUCATAGCCATCCTTUT
chr16	78016931	78017056	224870413	50410	GGAGGGAGUAGAGUGGAAGACA	50411	CCTTCCATUAAACCCAGCACCUAC
chr1	14155318	14155402	224870656	50412	CTGCAAUGGAGGAUCCAGCA	50413	GCTGATGTGTUTGGTGAGCTGUA
chr7	4310259	4310370	224872319	50414	GCACAGGCGGCUTAGAAGAUT	50415	GGCTAACTAGTUGCGTTTACAACTUT
chr5	178690622	178690736	224879644	50416	TCTCTACCAGCUGTGCUCGT	50417	CCTTCTGTCUCACCTTCTTUCGT

TABLE 14

Chromosome	Name	SEQ ID NO	Forward Primer	SEQ ID NO	Reverse Primer	Insert Start	Insert Stop	Insert Size
8	D8_A	50418	GGCAACTTATATGUATTTTTGTATTTCATGUG	50419	TGCCTTAATTTATTTACCUATCCTGTAGATTAUT	125907097	125907172	75
21	D21_A	50420	CATAAATATGUGAGTCAATUCCCCAAG	50421	AGACAGACTAAUAGGAGGTAGATAGACUGGA	20554281	20554428	147
7	D7_A	50422	TGATAGAACACUTGTCATAGTTUAGAACGA	50423	TGCACCAAATATUGGTAATTAAATGTTUAC	83789599	83789500	99
5	CSF_A	50424	GTCTCAGTTTUCCTACCTGTAAAAUGAAG	50425	GACAGCATUTCCTGTGUCAGACC	149455981	149455869	112
3	D3_A	50426	TTTGGGGGCAUCTCTTATACUCA	50427	CCACTGCAGUCCAATCUGGGT	45582206	45582316	110
11	TH_A	50428	CACAGGGCUTCCGAGUGC	50429	AATTCAAAGGGUATCTGGGCUCT	2192289	2192384	95
13	D13_A	50430	ACTCTGACCCAUCTAACGCCTAUC	50431	AGTTGGTCAAAUCTCCTCCTUCAA	82722143	82722263	120
16	D16_A	50432	CAGATCCCAAGCUCTTCCTCTUC	50433	TGTGTGCATCTGUAAGCATGTATCTAUC	86386278	86386378	100
2	D2_A	50434	GAGCCAGUGGATTUGGAAACAG	50435	AGGTGGCCCAUAATCATGAGTUA	218879687	218879556	131
19	D19_A	50436	GCCTGGGCAACAGAAUAAGATUCT	50437	CCATTACCCGAAUAAAAATCTTCTCUCT	30417209	30417130	79
12	VWA_A	50438	AGATGTGAAAGCCCUAGTGGAUG	50439	GATAGGACAGAUGATAAATACATAGGAUGGA	6093241	6093131	110
2	TP_A	50440	ACUGGCACAGAACAGGCACTUA	50441	TGGTCTTACUCCTGTTCCCTUCC	1493411	1493497	86
18	D18_A	50442	TTCATGCCACUGCACTUCACT	50443	TTCTCTGGTGUGTGGAGATGTCUT	60948873	60949025	152
5	D5_A	50444	CAAGGGTGAUTTTCCTCTTUGGT	50445	AAGTGATUCCAATCAUAGCCACAG	123111313	123111206	107
4	FG_A	50446	TAACCAAAATAAAAUTAGGCATATTUACAAGC	50447	GCTGCTGAGUGATTTGTCTGTAATUG	155508978	155508865	113
Y	Amelogenin	50448	CAACTUCAGCTATGAGGUAATTTTTCUC	50449	AUCAGAGCTUAAACTGGGAAGCUG	6738034	6737912	122
X	Amelogenin	50450	CAACTUCAGCTATGAGGUAATTTTTCUC	50451	AUCAGAGCTUAAACTGGGAAGCUG	11314959	11315075	116

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256119708	50452	TTTTGCCAGUGCCTUAACAACAG	50453	TTGATACAAGTCCUACTGTACTCACUGA
263795899	50454	GAACAAGAUAGAGCCAAAGTACAUACACT	50455	GCACGCTCUGTCACTGCTUAA
255499283	50456	CCTGCAAGCUTCAACAGAGGUT	50457	ACAGACTTGUGTGTCATTTUAAAGGGA
263702910	50458	CCTGGACCUCCAGTGAGTCUT	50459	CCTTTCAUACCAGGGAATCCAGGUA
269250723	50460	CAGGAGCCGCCUGATCTUC	50461	ACTCCCTAUGAACCAAGTTCUACCA
267539236	50462	GTTCGTGTCAAGAUACCCGTGTAUT	50463	CCAUATCTCTATTTCUAGGGACCCCAAG
264621653	50464	ACAAATATGTCAAUATGACCAGCAUCCA	50465	CUTCAACTGCATAUCAGCAACAAACT
315715085	50466	ATTATATCTCAAAUCTGTCAGGAUCCAAAAT	50467	CCAGAAACCTUATGTTGCACTTATUCA
268331213	50468	GAGUGGAUGGCAAACACACAA	50469	AGCUGGAGCCTCUAGGACAA
267942384	50470	GAGGCTCUGGCTGGGAAUAG	50471	CAGAAATGTTCUTAGCCGCGAUG
261499125	50472	GGAGAUGATGGAAUACCGACACC	50473	GCATCCAACUGGAATCCACTUGT
239908636	50474	GGGCCAGTUCCTCCCTAGTAUAA	50475	TGTTTTGTTCUTCTGTGCTTTUAGCC
235285155	50476	TCACAAACCUCAGAAATAACTCATUGGA	50477	CAAGATCCUGTGCAGGUACCA
268641959	50478	TGAUCCGGCACCTGTTUCAA	50479	CTATCCTGGUACTGGAAAGCCAUC
261694880	50480	AGAGATTGTGCUGGAGAACAAGUT	50481	CACGAAGCCGUAGTGGUAGAC
258063012	50482	CATTAAGAGCUACCTGATCGAGAUCC	50483	GCAGCCCCUGTGAAGAAGUC
237170982	50484	GTCCTCUGCCTCTTTCCTUAAAAAG	50485	TTCTACTCAUGCCCCTCAAACTTATTUT
237416684	50486	AACGAGGTTTTUCTTACTGAACCCUAA	50487	GTGTGGCTTCUGTTTGTCTTGUC
332401799	50488	CTCTTCUACCGACCCCTGUG	50489	AGGGAGUGCAGAGTCCAAAATUG
233386372	50490	CTTCAAAAGCCCUAGAUAACACCAAGT	50491	CAATGTGTUCCACAGTCCACTUC
313153338	50492	CTACCUGGGCACGAGGTTUA	50493	GACTCCAAUGGCTGCAUCAAC
256553931	50494	ATCTGATCCGUGCTGCACUT	50495	ACCTGAATAAUGACAGTCCAGTTTTUCA
319788579	50496	GACTAAAACACAGCAUCCAGAGUGA	50497	CAGGTAATGAAUTTGGGCATCCUG
317534939	50498	TTCTTCCAACCACCAUCTTATGTTUGA	50499	TTCTTGAACATTAUGATTCTTGAGAUAGAGCC
332113039	50500	CAAGACCAUTTTCATGTTAAUCCCCAAG	50501	CATGAATGTUCACCCCACGUT
332143448	50502	GAGCAGTUCTTGCTTTUGGCT	50503	GGAATCCGUGCTTGTGAUGAGT
323747558	50504	CCUGGAGGAGCCATGGUCT	50505	GAAGAUGGGACCGAAGTUGGA
259456459	50506	GCATACAATTUTACTGCACCUGCT	50507	AGAAGGCACAUAGTAAAAACAGTGAUGA
328551274	50508	GCACCUGGTGCATGUGGA	50509	GGTCTCUGAAGCTCUCACAGT
329263011	50510	CCTCTGAGUCCTTGGATGUCCAT	50511	AAGTCCTTCCACUCAAACACCUG
328759634	50512	AGGUCAUCGCGCAGCAT	50513	CGGGCGGGUGTTGTUGA
324843744	50514	TCCUGGACUCAGCCCCAT	50515	CAGCCCCUGCTTCCUACAC
263994324	50516	GTCGGCTCUTGGTGGAGTUT	50517	GGAGATGCCUCGGACGAUG
318050204	50518	GAGCCAAGTAGCUGTCATAATTCATUCT	50519	GCATTTGGTTUGTGACATTCTUGGA
321277528	50520	AACAAUGCAATACTUGGCAACACA	50521	CGTACTGAGTUGCAAAATGAGTGACUA
320695289	50522	TCATAGAGTUGCCAAATGCTUGGT	50523	CTAACAGCAGGUTCTCATAGAAGAUGA
318289946	50524	GGGCGAUATCAACTTUGCAGAGA	50525	GGACAUAAAGTGUGAGAGAAAAGAGAAGA
321606176	50526	GACAAGCACUTTGTCCCTCUGT	50527	GCGGTGTTTUCAGCTCATGACUA
326463773	50528	CCATACCTUGCCCAACTGGUC	50529	ACCACCCTUTAATCTGTTGTUGCT
332498539	50530	TGGATAACTGGTTAUAATCTGCTTCTAATCTUC	50531	AGTGCCACAGCUAGAGGAGUAA
333343659	50532	GAAGCAAAGUGTGTTTATTCAAUCCAGT	50533	CCATCTCTTTUTACCTCTTGAUCAGGAT
333752416	50534	ATTTAGCUGAAGACCGTCAUGCT	50535	CATCATCACCAGUCGGACTCUG
332916893	50536	GCTCTCAGAUCTAGACACCTCUGT	50537	CTTGTGGCCCCUTCTTCUGAT
333236271	50538	ACAGCACAGUATTGCTAUGCAGAA	50539	GCCTTGAGUCATATCATTAGGUACACA
314517491	50540	AGGGAGAAAUGGCATAAAGCACUT	50541	GCCTGATGTAUGCATTCATATCTCTUG
269318002	50542	GCATCATGUACAAGCTCAGTTTCTAUG	50543	ACAAAACTACCUAATTTCCGTTTACUGCT
267459045	50544	GCTTTCGAATUCCCTATCACAGUCA	50545	CTTGGCAGGUGAAAAAGAAAGAUGG
268508956	50546	CTCTCCCCAUGGACCTGAGUAT	50547	GTATGTGGAAAUGTAGCTGGTCTTUG
264152214	50548	CTTTCAAAGAGCCAGUGAACTUACC	50549	ATCTAAGTGTGCUTTGTTACCTTGTUCT
267825536	50550	GGCGTGCUGCTCATTTCTTCUA	50551	GGGAACATACGUAACTGAGAATCTTUAA
289962110	50552	CTTCAUCAGGCAGGAAGAGUGG	50553	CTCTTTGAAAGCUCAGGATCAGACUT
289950371	50554	GGCAAUGTTACUCAGGAGACAAAGAAA	50555	GGTTTAAGGGAACUTCTTGATTTGUCC
290675367	50556	GGGAAGAUGAAATCCAACAATUACAAAA	50557	CATGCTACCUCCCAATTTTCTUAAACC
290491925	50558	AGCCCCTAATUTAGATGATGGCUA	50559	GCTGAAACCUCCCCTTCTTCTUC
223604539	50560	GATTAATTTGCAGGUTATTGCGAGTGUT	50561	AGGTACCUTTTTAACTTCUAAAGCACAT
222792899	50562	GTCATCAGCUGAAGATGAAATAGGAUGT	50563	TGAAGATAAACUAGAACCCTGCAGUCT
224589069	50564	CCAGCCCAGACUGCTUCAAA	50565	GGGATTCGATUGTTAGATCACTUAGAGAT
222745390	50566	AAGAAAATUGGAGGAATCTGCTUCAT	50567	CTTTGCTGGTCUTCCATCATTATACUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
327868677	50568	AGACAGGGCCUGCAGTUG	50569	TGUGGAGACAGGAGCUGGAT
327240472	50570	GTCCAGGUCAAGGCUGAAAAG	50571	AAAACCCAUGCTCTGCCUGA
326527027	50572	GUAGAGAGGAGGACCAGUCACT	50573	CCACAGAUGGCACAGAUGCT
235784231	50574	GCCAGUCACAGAGGAUGAGAGT	50575	CCGTCCACTTCAUTTCTTTGCTTATTUT
257613968	50576	CGTTUAAACCAAAGGCGCACUA	50577	CGTGGCCCAGCUGAATCUAAG
238129827	50578	CCGAGTGATUGGCTGAACAUCT	50579	TCCCGGGAUCGTGTTCUACA
235147797	50580	TGTATACATTTGGAUACCAGTGTCCUT	50581	GTAACAGUGAAAACAGCATTTCCCAUT
259143743	50582	CATCAAGGAGAAGGAGUACGAGATUG	50583	TTTTGGAATCAUCCTCTTTTTGCAUGG
268522908	50584	CTTCGAUGACCGUCAGCAGAT	50585	AAGGCGACAUCTTTUGGCAAAAA
268536789	50586	TGACCCCAACACUGAAGAAAATCUT	50587	GGCCTCCUGAACAGACATTTCTUT
331947955	50588	CCCGUCCCTGTCCTUGT	50589	CTCTCTCUCCCTCCTTCUCCA
331600001	50590	CACATTTTCUAGGGCTGTCTUCCA	50591	TCACCGUGCAGUACAAGGAC
331637833	50592	TGGTUACCCCGAGACUCCAA	50593	GCTUCGACTCCTUCACCGT
268624743	50594	GGTCAAGAGGUCAAGCAUGGAT	50595	ACCGTCTCTTUCTTGTTCCTCATUT
263943182	50596	TCTGATATUCCCCACATCTCATTCUCT	50597	GCAATGACACCUATTTCTGTTCCUCT
267432272	50598	GGCAAAACAUCACCCCAUCCT	50599	CCTGTGTCCUTGTCTCTGCTTUC
264857634	50600	GTCAGCCAUCTCATCUGGAAAGA	50601	GCCATGACUCCTTCCTCCUGT
262131111	50602	CCUGTGACCTAGUGAAGCCAAC	50603	TGACCCUGAGCCTCTTTGUCT
271078092	50604	TGGCACCAAUAGATTCATUCAGCAA	50605	CTTACCCAUCAGGCAAAUCACCA
272476013	50606	CCCAGTCCUCAATCAATTTCTTCUCA	50607	GCCTTCAATGTCUGACTAAAGTACTUCT
269753164	50608	AATGGCCACACAGUTGAUGAGAT	50609	ATGTGTCCAGTUTTCTTATTTTGCTTUCA
320172451	50610	ATTCAGATATTGUGCATTAGACCAGCUT	50611	CAGCCAATUACCGTCAAGATTACUGA
317084126	50612	GAATGACAGAGUGGAGTACCAGUT	50613	CCTGCAGUTTAATGAAATGUGGCA
317377491	50614	GACUGAAGACATUGAGACCAACCA	50615	GAAGCAGAGAATUGAGTGGTATCATGTUA
316353242	50616	TTTCAAATGATUGCGACACCAUCT	50617	GCAAGAACAATUCCACCTGTACUGA
315988468	50618	CAGCTTCATGUTGACACTCATTTUCT	50619	TTCGTTGCTAUAGATTTGTGCAAAUGG
257715638	50620	TCAATTCAGGCUGTGTACTUGCT	50621	GCTGAAAGTTUAAAGATGCGGAAGUT
264393994	50622	CATAACCTTUAAAGAAGGCAGUGAGGAT	50623	TTAATTTTTAGGGUGCCTCTGGUGAA
258901983	50624	AGTGAGGGUGTGAAGGACTAUGA	50625	ACTCCTGTTTCAGUCATTTTTCTTCUCT
319226234	50626	CACAGTACCAAAUGCTTTTCTTTTCUCT	50627	CCTCCUGAGGGAAAGAACAATGUC
257531266	50628	CAAGATGCCAGGUTTTGTTTCTUCT	50629	ACAACGCAGGUAACTCTCCAAAUAA
257302636	50630	GGTCCTGTTTUACTTCACAAGATAUGGAA	50631	CTGGCCUGGCTCTCTACTTUA
268016381	50632	CCCTTGGTTAAAUTCAGTGCCATAAAUG	50633	ACAGTTACAGUCCTCACAACTCUGA
268865493	50634	ACCACCAAGAUCCTTTCAAGCUC	50635	GATCTGCAAUGCTGTCGAAAAGUT
268067125	50636	GGTTGTCAGUCCCCAAGCTUT	50637	GGTTGTUTTTCCTATCUGGACGGA
313921568	50638	GGTGGAAGCCAAUGGCCUAAT	50639	GTCTTTTGACATCUCCTACAGAGCTUA
325672900	50640	TGAGGCAUGTAAGTTGCAUGGAT	50641	CCATGCTGTTTAUACCTGTTCCCTUT
327008511	50642	GCAGAGCAAUGCAACCTTTATUCA	50643	GACTATCTATTTUGAAGAACTGACAGGTUGT
326764729	50644	AGGCTGCAGUGTTCTGTCTTUAG	50645	CTTATTCCAAACUGGGCUCGGAT
253831987	50646	CATGCUGCCTCCUAGGAAGT	50647	CACCATACUGCTCCACACUGT
228373527	50648	GAUGACTGGTCUGGGAAGAACT	50649	GGGAUCTTGGGUGCCCAAC
222446484	50650	TTGCCTCTUATATTTCAGGTUGAACAGT	50651	GCCCAAATAAAAUGCCACACCUT
224318500	50652	GAUTTGATTGATUACAGCACGGGAAA	50653	GCATATTTCTCUAGTCTGGTAAGCAUCA
321171784	50654	GCCTCUAGCACAATAUGCACCA	50655	ACATATTUCAGTGCGUCCAACACA
318263228	50656	GCCTGGCCCCAAUTCATTCTTATAAUT	50657	TGGAACCCCUCUCAGCAGAT
267316875	50658	AAACTATGGAAUCAAACCACAACAAUGG	50659	ACATAAGAGGCAUTACAAGCTTUCAGT
267250083	50660	GACUTCTTTCTACUGCAGCAGACA	50661	TCAATCAAGTGCUTAAAAACAGTGCTUC
267193567	50662	GAATGTATATAGUCCTCAAACUGGCCAT	50663	GGCUGACCAAAGGCAGTATUGT
326099105	50664	AGUATTTTTGTGCTAUAGGCAGGCT	50665	GCCAAGTACCUCACTATGAAUCCA
266091526	50666	CTTTGCAAGUGGCACTCCUC	50667	GCATAGAGCAGUCCTGGTTTTACUAAA
258162971	50668	GGCCATGTGCUTTTCAAACTAATUGT	50669	GACAGGAGUACCAAGAAGUGAGAAAT
265804838	50670	CGATCTGUGAGCCGAGTCTTUA	50671	TCATCTTTCTUCACGTGTGAATTCUCAA
313997688	50672	GTGAAGUAGAGCGCCGUCA	50673	GTTCTTGCTCAUGTGCACCTUT
320652276	50674	TGCCCCTUGGTGCTGAATTUA	50675	CGAATATCAGCUCTGCCTGTUGT
321150664	50676	TTGCTATUGTGCCCUCACCAT	50677	ACCGACACACUATGCUCCCT
319485331	50678	GTCCAGCGUTAACCGCTUC	50679	GCGGUTAUGGACACCAAGAAGAAAA
317777450	50680	GGTUGACCAGAAAUCCCCAAGT	50681	TGTAGTTGAAAAUGCTTTGTCCTCTCUC
316013587	50682	CAGGGUCCAGCAGCUCAC	50683	GAAAGTCCAUGCCCCAUCCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316429463	50684	GCTCCCUCTCCCCTGUGT	50685	TGGCCUCCTTCCTTUCCCA
239080303	50686	GGTCAATGTGTTUCTGAATTTAAAATTACUGT	50687	CCTTCAATTCCUACACCTGCCTTUT
229657918	50688	GACATCTCCUCGGGCTUACAG	50689	GAGGCGGAGAAGCUCUAACA
228565350	50690	GAGAGGCCUTGGGACTGAUAC	50691	CCAAGTAAATGAGUCTCAACGTGTUC
264219588	50692	TTTGTACCCAGUGACTTAAAAGGUGT	50693	CCTCACAGATTUTAATGGCTCCAAUG
256131247	50694	GTTGCUCAGCAGCCTTAAUGG	50695	CCCTGCTUTGCCTTAAAUCGT
266506040	50696	GCCTCCTTGUTCACACTGAUGT	50697	GAGGAAAACAAACCUATCAGAAUCAGGT
258857273	50698	ATTCTAGGTTTGUCAGCTCCTGUG	50699	CTCTCCAGGUCCACCCTCUAA
326707214	50700	TTCCTCTTAGCAUTGTTGAATTCUACACA	50701	ACUCCATCCGUAGCCAAGAAGAT
231368074	50702	ACAACGTCCUCCCCGTTAUG	50703	CCAACTTTGATGTUTCTATTCCCCTCUT
231381890	50704	CCTCGAUGGCCGCTAGAAUG	50705	CCUTGGGATCAATUGGAAAACGAG
313200445	50706	GTAAGAAGATGTUCCTAGGGCCUT	50707	GGAATCCAATCUGCAAGTATGTCAGUT
326648858	50708	CAATTGCCTUGATGGCTCAGUT	50709	CAATAGAAGCUGAATTTGGTGTGCUG
256650597	50710	TGTTCACCTATAUTACTCCATCACTUCCA	50711	TGGTTCTTTGTUGCATTTGTGTTUAACT
268714192	50712	TGGGAGAGCAGGCUTAGACUT	50713	CACAGCUTGAGCUGGAAGAAGA
315854058	50714	ATGACCCTCUCAACCCTCUGT	50715	GGGAUAUGACCCAGAAGGAGGT
317215892	50716	CCTAATCCCCUAGAGTGGTGUCT	50717	CACAATGTCACAUTTCGGAAGTCTTUAA
324651976	50718	AAATGGTCACUGTGGTAAGAUCAGG	50719	CCCTGGTGCUTTACGCAGAAUAAA
296625166	50720	AGATGGCTGUGTGCATGCTUAT	50721	AGCTCTAACAGACUTTGTGTGTTTCUT
327519579	50722	TGGGTCACUCATTAGTGCCTAUCA	50723	CCTCTCCAAACUTCTCCAAAUCGAC
326663583	50724	TTGGTAAAGAAGAAUGGAACTTGCTGUA	50725	GCAAGTTTAAGCUGAGTTTCAGCAAUG
317316210	50726	ATCAAATCTUACTGACAGCTUACACAT	50727	GTCACTTCCAGAAAUTTGGACTCTUACT
317188474	50728	CCUCATTTCACATTUAAAGCAGCACAT	50729	GATGACCAUAGACCACAAGTTACCUG
261911938	50730	CTGTCTAACUGGAGCAGGAACUC	50731	AGACAGGTCCAUGTCTTTCTTUCC
265431699	50732	AGACGCTUCTCCCATAGUCGT	50733	GGGTGCUCAGATTCCATGGUA
262375665	50734	CTGCTTCUGCTTTTTCTTCTUCAAGT	50735	TTCCTATATTCUGGCTGGTCTGTAUCT
242274630	50736	GCACCUCCTUCAAGGACAGAA	50737	AGGAAGTGATCUAACTTTGCTGCAAAUA
239601827	50738	GCUCAGGACAAGTUGCACAGT	50739	AAGTATCATCCAUTGCCCTTTTCTUGA
268927981	50740	CTTCCCTTTCUGGCTCTTTCUCC	50741	TGGGAGCACCAAGAUATACATUGAGA
266483732	50742	CTTCCCTCUCAAGGGCAACUC	50743	TGACCCACCCUTGGGATCTUA
262372483	50744	GCTCCAGGAAAGCUCATCUCT	50745	CAAAGCCAUGAAAAGGTTGGUCA
332262640	50746	CTATTTTTCCUCTCCTGUCCACCT	50747	GGACAATGGGAGCUTGGAAGTUAAT
321219523	50748	AAAAATTGGUCACAGTTTTGTCATUGGT	50749	GGAGTCCAUGATTGACAGUAAGAACA
320945675	50750	ATGTGCTGUCATCTGTUAAGCCA	50751	TGCCAGUATTTTTGAAGUGGAAGAAGA
318844220	50752	ATGCACATGTAAAUAACAGCTTTGAGUG	50753	CGTCAATATUCAAGTGATGGAUGCAAAT
259569694	50754	CACGTCUCTGCTUGACCGA	50755	GCTCATTCUCACAAAGCCUCACA
253841374	50756	CCAUGACCGAGACUCAGGAC	50757	TCACACAAUGGUGAGGCCAAAT
264440524	50758	AAAGCCACCCUCCCCCUA	50759	CAACCCCAGUCCCTGTCAUC
262619695	50760	CACTTACACCACCUGCCTCUT	50761	TGGCUAGAGGCCACTCAUGT
265738461	50762	CCACUGCCCGGGCTUAC	50763	GGCCAAGCUGACGTCUCA
326824613	50764	TGTGTTACCGUGTTTGCTAGTUGT	50765	GCTCCAACAUGGACAATCCTUAAAAA
327790236	50766	AAACCAAGGCAUAGAGGAAGCTUT	50767	GGGATTTTGCUTATTTCTCCACUAAGA
325821034	50768	CAGGAAGAGAGAUGCACAGAUGT	50769	CTGACCAGUGCCCTCUCC
333621038	50770	CCUTGAAGCAGAUCAGCCACT	50771	CACATCGGTUCCGAGTCTGAUT
314374660	50772	CTGGAAGAUCTACAUCCGGAAGG	50773	CAAGCCAAAUGCATGGUGAGA
314753698	50774	CCCACAGACGACAGUGCAUC	50775	GCCCAGAGUAACUGACACAGAAA
312974728	50776	CGTCGACCCUGAGCTCTUC	50777	GCTCTTCTCUCTGGGCCTTTUA
327822070	50778	CCTGCTCUGGCCTCACUC	50779	GGTGCUCCCTGCCTCUCT
318496369	50780	ACACTGAAAAGAUGCCCAGAGAAAUAA	50781	GAAAUAGAACATCCTTUACCCAAGAGCA
319826801	50782	GTCTGCCCGUTCAACAUCCT	50783	GACACTACCATTUGGTTTGATTTTGGUT
320028156	50784	CGTCGCGAGUCCCTGUG	50785	TTTTCTTGCUAACAGAGCCCCATAUT
240486609	50786	AGAGAATCAUGAAATCAACCCUAGCC	50787	TGAGATCCCCTUTTCCAGTATCATTTUC
333450293	50788	GTCCTGAAACACCACUGGTTGUA	50789	CCAGAGGGAAACUCAATUGCAAAAAC
314478027	50790	CTTGTGCCTUCTAGGGCTCUC	50791	GCCTGTGGUCAAGTGGTUCAA
261380877	50792	GGAGCAUCCTGATTUCAGGGT	50793	TUCAGCCAGCCAACAUAGAAGAA
259716484	50794	GGATAUGCCAGAGAUCCCCGAA	50795	GCAGTGAUGGAACCCUAGGAA
265276441	50796	CAGGAUCCATGUCCCAGACAAAT	50797	GACATCUGGGCCAAGACUCC
313025492	50798	GGGTACACUGACGTCCTCUT	50799	GATCTCCCAGUTCTCGGTGUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314676616	50800	CCAGCGCAUCATCCAGTUC	50801	AGGGTGAUGCATGGACACUC
328304872	50802	TGTTTAACAUGAGGGTGTTTTGUACAGA	50803	GCTGAAATUGGCAGCTTTAUCCA
225123514	50804	CAGCTGAUGTAGTAATCUAAGCAAGGT	50805	GGCTTGTGTUGAGGCTGATACAUT
222740341	50806	AGCAAGCAGCUGAAACAAATAATGUT	50807	AAACAGGAAGAACAGGAUAGAAAGACUG
224426408	50808	AAACCCTTTUGAAGGCCUGGAT	50809	GTGCAGTAUCACAGCACTCTTTAGAUAA
222547018	50810	CTTTGACTTATCUCACAGCAAAGAAGUAGA	50811	CAAGTTTUCAGAAAAGAAGCCAUGACAT
222179007	50812	TTGGATGAAUTAGCCCUGCGT	50813	ACAGGGTAGAAUATTGGGCUGAGT
329137616	50814	GTTGAGGCACTUTGTGATGCTTATAUT	50815	GGGAATGCUGAAGCCAUCAGAT
333338723	50816	AGCAGCAGCUAGAAGAGGAUCT	50817	CGGTCAAAGUTCTGTGCUGAC
332896818	50818	CACCAGATUGGGCTGCTCUA	50819	GAAAAUCACCAGCCAGUAGAAGACA
332527749	50820	CCCTCCTUGGCATCTGUAGGA	50821	AGCUGATGAAGUAGAAGACAGCAAAG
319280642	50822	GTGGAGCUGGGAAAAACTCCUA	50823	CTGTGGAACCUGTACCTTTCTUCT
318590158	50824	GCTCCACGGUCACCUACCA	50825	TCGTTGAUCTGCCCAUCCC
318921884	50826	GCAGACAGAGACAGGUCCAUT	50827	CTGCCGGAACUTCTUCAGG
319649825	50828	GGAATGAGGGCUGAACTUGGG	50829	CTTCCTAUCACCCCTCUGAGGAT
320987407	50830	GCAGCGACCUCCTACUGA	50831	GGCAGAAGCCAGAUGAAGGUG
319709989	50832	CTGCTGCUGCGCTUCAC	50833	GAACUGCCGCUGCAACC
264104950	50834	CATGTACCCCAAGAAUAAAACTGATGUG	50835	CCCUTTCUACAGAGGACAACAGA
259620070	50836	GCAGATCTTCCUCCCCTCCUC	50837	GGGTGTAUCCACCAAATGUGAA
324313690	50838	CCCTCAGCUGTGAGTGTATUGA	50839	CAAACCCTGTAUGTCCTTGTGACUA
317489585	50840	CGCCGTCUGCATCGTACUC	50841	AGGTUGGGTGCUGAAGCC
320769670	50842	GGCUTGGGCAUGAAGGAAAC	50843	GGCCUTTCCTTCUGCAGGAC
260105752	50844	GCGGTCUCAGTTCCTGTGUC	50845	ATGTTGCUAAAGGCCATCTCTUCT
265685001	50846	TCTTTCCACCCUTGCCAUGAG	50847	GGTAGAGTAACACUGGCTTCTGATUG
255708348	50848	AAGAGCTUGAAGAAGTCCACGUT	50849	CAGTTTCTAGUGTTGCCTCTTCUCC
268216720	50850	GACCAAUCAGGCCAATUAAACCAG	50851	TCCAGTTAGGUGATGAGAAGGAGAUT
269196827	50852	TGTACCTTUGCACCTTCTTTUCCT	50853	TGTTTTTGAGTUTGTGTTATCTTUGCCA
314633928	50854	CGCACACAUCAGUCACCGA	50855	CAAACGUACAGCAGTCTCTCTUCT
327756169	50856	TGTACACATGCCUTGTTAGTTTCTUCAT	50857	CTGCUTCAACTGTUGCAGCAAA
328049885	50858	GCTGTTGCUGGCAGTTACUGT	50859	CCAAATGGCCAGAUCAGAAGTTAUGA
326440772	50860	TCTGATCAATTUCCCTTCTCTCTTTUC	50861	GAATGTGCCUGGGTCGTTTATUC
327073046	50862	GTGCATGCUTGGACTCUGAAG	50863	TCACATCAAGAGUGCTTGCTTTCTUAA
328437214	50864	CTGTCCTCACTAUAGGCTTTCAGAAUG	50865	AGAACTGCCATTUTCCCTATTTTCTCUT
326893980	50866	CACTCTGCTCUTTTCCCTGGUA	50867	CCCTTTATGCGAUACTAATCCCTUACT
327302963	50868	CCAGCTGTTAUACACGTTGATTUGT	50869	GCCTATTTCUTTGACTTTAAUGGCACAT
326556784	50870	GCTTCAGGAUTCAACCGUGAC	50871	GTCCTTACAGUCTCCCTCTUGACT
327178801	50872	GGGACCTAUGAAAGCTTATACCUACA	50873	GCUGCAUCACACCAGACAAGAA
325623944	50874	TTTGATUGACAGGCATCTCTUGGA	50875	CATTAGGGACGUCCGCUCAT
323703454	50876	GTGCATTGGTTUGTCACTACTTATUCAA	50877	GTTGTCCATTAAUTCGGAACGAGAUG
324383153	50878	ACACACAAUTTTACCTTCUAAGAGGCT	50879	ACTGGGCTATUAGCAATGGGACUAT
325288675	50880	CTTTTATTCTTCAUTGCTGTCCTUCACA	50881	GTCTCAUAGGAACCCUCCCAAC
327622864	50882	CTTCATCAGUGCCTTTGGTTAAACUT	50883	CAATTTCCAGCUAAGACTTTTCAAGGUA
326858187	50884	TGGCATTTGACUTAACTACAAGTUCACA	50885	CCAGUACCACAGATGTTUGCAGT
327047005	50886	GGAAGTGGGATAUTCCTGGACATAAUT	50887	CAACAAAUCCCTAGAAAUAGAACCACGA
319347340	50888	GTGCCATGUCGGAGAACAUCT	50889	GGGAGAGGGAAUCACAUCCAAA
332383389	50890	ATCATTTGCATGTAUTGATACAAATACAAAUGG	50891	TTCTCAATCGCUTTTCAGCTGAUACT
332573108	50892	TGGCTTAUTATTCCTCAUGGAGACAC	50893	GCTCCTTGCAUGATAGTACAATGTTUAC
332636933	50894	GTAATAAAGGCCAUTACCCAAUACAGGA	50895	TACTCCTUCAACTCAAAACUCCAGAA
332640005	50896	GACATAAGAACTUCCTGCAAGAGCUA	50897	TGTGCATGUCTGTGAAAUAGCAGAA
278512567	50898	CTGAAGAAGTUGATAGTCAGGCUGAA	50899	TTAAGAGUCCGGGTTUGAGCAG
279477864	50900	GCAACTGACUGAATTTGTUGAGAACA	50901	ATTTAAATGCUACTTACAAGGAAUCGCT
313491413	50902	CTTGTAAGUGGAGGTGGCAUGAA	50903	CCTGGAAAACTUCCTTTGATGAAGAAUG
279395161	50904	CACCTGAATGUTTTGGAGTTAAUGCAG	50905	AAATGCTTCAGTUTTCAAGTGTCTTAUG
268672488	50906	GCCCCCAUTACTGAGUGAGGA	50907	GGCCTTTTGCCUCTTCCTTCUA
269334895	50908	GGGAAGGCGGCUTTTACUGAAT	50909	ATTCTTCUCTGAGCCUGAGACCT
268129907	50910	GGAACGGACUCAGAGGAGUG	50911	CAAACCTCCUGAGGGCTUGAG
267736345	50912	ACAGACTGGATUAACATAGCATTGCUT	50913	TGTTTGATCTAAUGAGTGTTTGAGUGACA
315577990	50914	TCAGTAAATGCUGAGGTAGATGGTTTUC	50915	TGGCTCTTAGAAAGUTTGATGCACTUAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317019785	50916	AGCATGTCGAAUTATTGGATTGUCACT	50917	GAAAACAGAGGAAAAAUGCCCAGTUAA
317937320	50918	GGTGACTTCAGUTAATACCAAACCAAUG	50919	AAAAGAACTGACCAUAAGTCCTGCAUAT
315895895	50920	CTCTTGAGAGGAAAUCAAAATGCTUACC	50921	AGCAAACCGUCTTGGTUACAGT
319553261	50922	AGTGAACAAGUACATTGCUCCAAGT	50923	GTACTCAGGACGUTGCCTTCUC
265870858	50924	CCCTGAUGCTGAACTGAUCGT	50925	ACAACAGCGCAUTTCCCCUAT
260059731	50926	GCTGAAGUGAAAGCTACUCACCAA	50927	TCCACTTCUCACACTTCAGATTUCAAC
264797954	50928	ATCCTGACTAAACAUGATCTAAGCAAUGT	50929	GGAATCTATGCAAAUATGAGGATGGTUCA
237941495	50930	CCTGGAGGAGGUGCACCAUA	50931	AGUGGGTAGGUAAAAGCAAGCC
327810400	50932	CGACCTTGAGUGCAGATGUGAA	50933	CCAAGGACTCUATCCCCTCAUCAG
327438482	50934	CACACTCACCUTTCCTCTUGGT	50935	TCGAGCTCUCTCCACCTCAUC
241362320	50936	GTCATAATGTTTTTCUTTTCAGGACATGUGA	50937	AGCCTGCTAUAATCGATCAAACUAACC
240782641	50938	TTGAGGGAAUGTAGAGACAAGUGG	50939	TCTGAAGGTUGATCACTTGCUGAAT
333085048	50940	GAGAAGGGUCATGGAGGGAAUG	50941	CGGCATTGTAAUCGCAATGATTGTUT
332405368	50942	AAAGCCGGUAAGTATGUGGGAAA	50943	AGGGTAAAAACACCUAGCTATGATCCUA
332911079	50944	ACTTGTCTACTCUGCTTTCATCACUAGA	50945	CTGTTTGATCCAACACUCTCTTTCTCUT
320132837	50946	GGACTGGUCGAGGGUGAC	50947	TCGGGCCCCUTGTAGUGA
313031432	50948	AAAACAGGAGAUGGCAGGAAUGA	50949	AGTTCCCTCACUCTGTCCCAUT
314775459	50950	CGGAGAGACACUGGTCUGGAT	50951	GCTCAATGCUTTTCCTGCTCUG
315433331	50952	AGAGGAAGGGAAGUGGGAAAAUG	50953	AACCUGCAGCGGGUGAA
314408000	50954	CGGGAAACCUCCTCTUGAGA	50955	CUCCCTAGTCAUGGCCAACAC
313330338	50956	CATCACCUGGTCCTCCTUCAC	50957	GAGCACTAUTGCCCTGUCACT
324536536	50958	GGTGATCUCCATTAACACUGACCT	50959	TGGAAAGCAAAGAUCTGTGTCUCA
330399475	50960	GTTTCAGTCTGAUTTCTCCTCCACUT	50961	AACCAATTATGGAUAGAAGTCAGGTCCUA
326742589	50962	GGGACAGCUGAGACUAAAAACAT	50963	GCCACCAACAGAUTATTCTUCACAG
326512754	50964	GACTGTUCGAGCGACATAUAAAACAAAA	50965	CUTTCACTTCUCCCACCACCA
319917974	50966	TCTGATACACACUAACTGTTGCTTUGG	50967	GTGGCATCAAUGTCCTCTUCCT
320943836	50968	AGATGTAGGCUTTCTTCATUCACCAAA	50969	GCCATCTGGTUGCTAATTTTAGCTGAUA
264845461	50970	AAGTGACAGCGUTTGCCCUAA	50971	CAGATCTCCAACUTTGTGAAATGGUAGA
261030440	50972	GAGGACGAUGACCCTGAUGAC	50973	GTCCTCCCUGGGAAAGTATGUT
254454776	50974	TTCCTGUACAACGCCUCCAAG	50975	TGGGCCAUGTGAGCTTTUAGAA
317379247	50976	CCTCAGCTGUGCAATTCAACCUA	50977	CTGTGAGAUCTGCCCTTUCCAG
316644505	50978	TTAGTCCAAAUTGCCACATGUGA	50979	CTGAATGAAGAUACACGAGTGTGUGA
333263738	50980	GCGGAGAUGAGCTTGAGGUC	50981	GGCTTCCCCUGTAGGCTTUAC
333255483	50982	AGGAAGUGCUCCGGGAGT	50983	CGGCUCCCACACCAUCAG
333260574	50984	GTGGTGGGUGAGGGCTAUG	50985	CCTCAACUCCGGCGUCT
333430109	50986	GUGGATUGGGACACGGGAA	50987	GAGCAGUACATGTCCTTUCACAAG
315961512	50988	CGGCTCUGCCCAGGTUA	50989	CGTGATCCUCTGCCCUGA
242589478	50990	CTTGTCTGCCUCAGGGAUCAG	50991	GCAGTCCTUCAGCTCGAUGA
320111961	50992	CACCTGGUCGAAGCTAGUGA	50993	CTGTTCGCCGUGCACUT
318582247	50994	CGCTAAAGGCUGCTCTCUCAA	50995	GCTGGAGCGUGTGACTGAUG
320904924	50996	TTTAGGCTGUTTATCTATGTUGCCCAA	50997	CAGCCATUCACCAAAGATATTUCAGAAA
240392505	50998	TCCGATGAUAGTTCGCTAUGAAAAAGG	50999	CAACAAAATGCUCAAAGCCGAAAUG
235102341	51000	CTCCTGCUGAAGCCTGTTCUT	51001	CCTCUCACCCTACCCUGGAC
235850442	51002	CTCCAGCAUCCATTCCUCCAC	51003	AGGGATCCACUGCCCTCTUT
269336554	51004	CCCACAUACAGUCAGACCCAAG	51005	CGTGGCAGGAUTTTCCCTTTUT
327846959	51006	CTGCCCATTUCCTGATTCTCUCT	51007	ACCATCCATTUCTACCAGAAGCUG
318860805	51008	AGGCGGCCCAGAUTCTTTTUA	51009	CTGGCTTGAUTGTGCTTTTUGGA
262010354	51010	GGGCUCAGAACTTGUAACAGAAA	51011	GCAACCTTTUGTATATGTTCTUCAGCAA
264495586	51012	GGACGAGGUTAGUACGAAGCC	51013	GAGGAGGAACGGUGATGUCAT
263012989	51014	GTGAUGAGGCCAAGTCUGACAA	51015	AGACTGGTUTTGGGAGCUGAG
268352590	51016	GGUCAACGTCATUGCCCCAT	51017	GCTGAAGCCCAAUCTATGAUGCT
267272880	51018	ACUTTCATCATCTUCACCAGCGT	51019	AGTATCACCAAACUCTCACTTCAACUG
258551994	51020	TGAGTCUGCCAGCTTATTUGAAGT	51021	CTGACCTCCUTGTCCAGGTTUC
269378442	51022	TCTCAGGCACCCAGUGTCUA	51023	GCCCCAACCAUGGAGGAUG
261042748	51024	CCCAGGUTGGTUGGAACAGT	51025	CAGGCAAGAAACUCCAGGTGUAA
325553386	51026	CCTGGAAGCUGAGGAGGAGUA	51027	GACTCGGUGCCCACTGUAG
236201515	51028	CCATTCACACCAUGCACATATGAUT	51029	GTTTGCGCACUTTCATCTUCAACT
333462205	51030	GGGCGACCUGTUCCAAAAGT	51031	CAGAAGACCUGGCUGAAAGGAG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332690380	51032	CAGTCGCATGAUGAAGCATGTATAUCT	51033	CCCCUGCUCAACAAGAACAAC
314504319	51034	TGGTGGCAGUAACTTTUCCCAA	51035	CTTCAGCTUCCTCTAAGATUCAAGAGA
226986629	51036	GGGATUACCGGCAUCCAAG	51037	TGGCAGCCUTTCTCAAACCAUT
225654024	51038	GGGAAACCUCTCTCGCCCUA	51039	GGTTTTGCUCACTGTCTGTUCCT
226496635	51040	ACCCUGCACAGAGAGAACACUA	51041	CCTAACCCUGAGTTCCCCTTUG
225839989	51042	CCUAAGGAUGGGAGGCACGA	51043	CCAAGTCCCACUCATACCTCUCT
226440627	51044	CCAGGCAAUGAGGGUGGA	51045	CUGAGGCUGGCACAGGAT
265913086	51046	CGGGAGAUGCGGCUGAA	51047	GGCCCCUACAGGCACUG
266861544	51048	CTGGUGGCAATGGGUGAGAT	51049	GTGCGTCCUGTGTTGTTCUG
316741168	51050	CAGCAGUACCTGGACGTUGT	51051	GGTCATGTTCUCCACCACCUG
331437922	51052	ATGGCATAGCUAATTACAACGGUGA	51053	CTTTGUATCGTGAAAGTUAGGGAGAAGT
330845783	51054	AAGCTGAGCAUTACCAGTUCACA	51055	CCTTACTCTAACUGTTGCCTACUCC
267128373	51056	GCTTCUCAACGGACATAGUGAAACT	51057	TTGCAACAACUCCAGAUGGGT
267349216	51058	CAAAGATACUGGAGAACTGAATGTUACCA	51059	CGTAACCTGTUAGCTGAAATCAUGACAT
269281421	51060	GGGTGCAGUCAGGUGAAG	51061	TTGACCACGUGCAGGUGT
321489824	51062	GACTGGCUGGGCCTCUT	51063	CGCAGAUGCGGAAGGCUA
333845075	51064	CCCCUTTACCGUCACCCA	51065	GGGACAGGCAUGCTTUGAC
324609045	51066	GGGATCTGUGCTTATTCTGTUCC	51067	GGCAGCTCAGAUACTAGGGTTGUA
325262487	51068	AGAGGAGGCUGACCTGUGT	51069	CACCCACCUTCTTCTUGAGCA
324663247	51070	CACCACGCAGUACAGCAAAUG	51071	TCCAGAGAUGCAGTCCAUCAAAG
325396407	51072	GACTGAUGCAGGAGGCUCAT	51073	GTGCAGCAGCUGAGCTUG
325129747	51074	CTCATAAAAGCCUTCAGCAUGACC	51075	GAGGGUCCTCAGTGAUCAGAGT
325112384	51076	CTUCACCCGGTTTUCCCAGAA	51077	TGAAATCTTCCUCTCTGTCUCCCA
324046920	51078	TGGCUGGAGAGTCUGGAGAAT	51079	CATGCGGUCCTCAAAACTGUG
324935836	51080	GGGAGGUGTATGCUGAGACCA	51081	GGCTTCTCUGAACCTCTTTACTGUT
256244881	51082	AGGGCCGGAUCTCCTTCUAC	51083	TCCTGGAAGAACACUCAGAAAAACUAAA
259150188	51084	CACACTTGAGUGCCCCAUCA	51085	GGGAGGGAAGGAGAUGAUCCC
257530320	51086	GCCTTATCACCUGATGTTGCAUCT	51087	GGGTGGTCCUGTTTATCCCAGUA
325911476	51088	GCCUGCAAAGTCUGCAAGA	51089	CCCAAAGUTGCAAAACAUGGCT
319411377	51090	GGGTGAUACAGGCTTCTTTTUGA	51091	AGAAGGAGAUAUACCCAGCCACAA
326487987	51092	GAAGAGACGUGAGAGGCTGUT	51093	GCTCCTAACGCCUTCTCTTCUG
316360319	51094	CGAACUGCCTTGCCAUCGAA	51095	CAATCTTACACGUGTGTGGGTTTTUAA
320420438	51096	CACACGAUAGTGGATGAGUGCT	51097	TTTTACTTAGGGCUAAGACCGCTUT
316126438	51098	ACTGGTCCAUTCCCGGAUGA	51099	TGTGATCTGAUCCCAAGCCTAUCT
315859914	51100	GGGTGAUAAATGGACACUAAAAGCA	51101	GCGTGACCUGTGATGACTACUACT
316217559	51102	GGCCTCCUTCCCGAGUAGT	51103	CACATACTUCAAAGTGTGCCUCAAG
333227533	51104	CATGTCAUGGACACCCCTCUT	51105	CCTGACTCUTCTCTCCAUCCAC
333687139	51106	AGAGAGAGAGGGAUAGGUCCCA	51107	GGCCAAGGAUGAGGCUAGT
332835623	51108	CCTCTTCGAGACAUATGCCATCTUC	51109	GGTGACTGCUGATGTCTCUCC
264623509	51110	GCAAGTTCTTUGCTTGACGTTCUG	51111	CTAGTGGGAGGUCAAATATTCTUCAGAT
261315252	51112	TGCAAACTTCAUCCCTACTTUGGT	51113	ATGATUGGAGCCAGCTCTUCC
328348940	51114	GGTAAATCAGCUGTTTTCTTTGTUCAGA	51115	CAAGUATGGGUCACCAGCACA
260630068	51116	GATCTGUCACCCGCTGUCT	51117	GUGGCCATGUGGACAGGA
264160391	51118	GGGTUACCCTGGGUGAAGAA	51119	CCAGGTATGUGCAGTGCTUG
317021360	51120	GCAGTGTUGGGAAGGUGAGAAC	51121	GGACACAGACACAGUCAGTCTTUT
324673873	51122	CGGAUGAAGCGGGAGAUGAT	51123	CACCCGCAAACUGCTTTAACUAC
324730207	51124	GCCAUCCACACAAAGACAACUGT	51125	GGCTTTTTGTUATTACTTCTCTTUGGCT
324089359	51126	TGCAGGTTUAAATGGCGGAUGA	51127	CCAUTTTTGATAGGUGCAGGACCA
257506837	51128	CGCAGAUTCAGGCTUCCCAAT	51129	GCTTCATTTTTGTUTTGCCTTTTTGGUA
268500478	51130	CCUCACCACCATTCUCCAACAA	51131	CCGGTGTUGGGATAATTTAGUCCAAAA
268060893	51132	GGATGGCTUCAATGCTCACTUG	51133	AGGACATTCAUGGACAATTCACTGUT
323567697	51134	GTAAGAGCTGUATCCTGCGUCA	51135	GTGGCACAAAUGATCCTUAAAGAAAACA
319486861	51136	CAATGAATCACCAUAGTACATGGGTCUT	51137	TCAGATCTGCUGATAGCCATAGCAUA
263059537	51138	ACCAUCCAACACACACACAGAUT	51139	GGTATCGUGAACTCGTGATGUCAG
316917782	51140	GAAUCTCACUGACGAGGCAGA	51141	TCTTTTACTTCCUGCCCCTAATUGAC
291569419	51142	AGGTTTTTCCUGAGGGCATTTGUA	51143	GTCACUGCCCCACUAGCAAA
291811929	51144	TGCTTTCCTUCACCCTTAGCUAC	51145	GGGATGGGUCCTAACATGTTTCUAT
291894593	51146	CGGAGGAGACACUTGGGATCUT	51147	TCATCCCCCUAGTCTCACAAUCC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326870162	51148	GAATGCGACACUCCTTTGTTTCUC	51149	TCAGCTCACGGUGCTTCTUC
299798177	51150	CCCACTGCCCUGAGAATCTUT	51151	GTGTTGGTTUGTTTGGAATCTUCACA
301986569	51152	GAGTGAAAGUGGAAGTGACTCUGA	51153	CAACATCAUAGCTGGGCACUGAT
257488386	51154	CTTTAGAGAATAGGUCTGCCATTGUGA	51155	GATGAGCUGGAGGGAGAGTTUG
254837958	51156	TGAATGACCUTGCATTAUCAGAACAGT	51157	GCAAGCCTTCAAUATTGGTGACTUT
256025597	51158	TTGCTCAGTTAUGTTTCACGTACUCAT	51159	TTGCTTCACTTUAGCAACCTTGUG
254227094	51160	GGTTGCAAAGUGTGAATTTTCCCAUT	51161	CTAATGCAACAAGUCCTGAAUCCCT
253815806	51162	CTAAGGCCAAGUCCTTGATATCTUGAA	51163	ACACAGGUGAACUCCAGAAAGAAG
268737550	51164	TCAAGGTATUCCCGGATGCAAUG	51165	AAGACCTGAAGACACUATATCCCTTCUT
259449291	51166	GGAAATGCTGUCCCTTAGTGCUA	51167	CTGAGGCAUAATTTACCUGGAGGAC
268759094	51168	GGGCTTTCAUATTGGCAGAUGT	51169	CCAGTGTCAGTGUGTATTAGTTTGGTUAG
312684956	51170	GCGTACTGUGAAATTCATCUGCCA	51171	AGTGGTGGGUAGAGCTTGTTTTUAA
318273188	51172	ACCACCGTCAUACTGACTCTCUT	51173	CTGATCCAGUCCCCCUGAAC
318412149	51174	GTCTTTATTCUGAGACCCCTTTGATUCT	51175	CCAAAGTTGUAGGGAAGGTCTACUCT
317639416	51176	CTATGTGGACUTGTCCTTTCCUCT	51177	ACAAGCTGTAAGUTTTCTGGTAAUCACA
333044804	51178	AGCCAACCCACACAGUATACCUA	51179	CTGAAGCATTUTCGATTCCGUGAC
312909638	51180	CCTGTUGGCAGGTCATUCCT	51181	CAACTGTCCUTCAACCTUCGG
313182255	51182	CCCACAAUCCCACACGAACUC	51183	CAGAGGTUCCAGGGCATCUAC
314295419	51184	CAGGGAGAAGGUGAGGAGGUA	51185	CCGCCGGGAAAGAUGGUC
313791416	51186	CCCTCUCCCAGTTACCGUGAA	51187	GTTCCTTGTGUCTTTCTGTTTGUCC
333551238	51188	GGAGCGCCUGACCTCUC	51189	GTCCCGAAUCCTCGCCTUT
333093464	51190	GAGGGUTTTGCTTCUAGGAGAACAA	51191	GAACACCTTUCCCCTCATTCUCT
327707968	51192	CGAATTTCUGCCATAAATGCTTTUACCA	51193	TCAGAGAACTUAGAGCATTTCACAUCAAA
237654990	51194	TTUAAGGAGCAAAGAATCUGCAGAGT	51195	GGATGCCTTATTUCCAGCTCTATTCTUAT
235692642	51196	AACCGGUTGTUGAAAGGCAAA	51197	CACAGTTTAGGUTTTGAGATAAATAUGACAGA
320297825	51198	TGTTCTGCCCGUTGTGTCTUA	51199	CTCACAGCCUGAAGAAUCCCA
320495266	51200	GTAGGAAAACGGUGGAATCAAGUAAAG	51201	GTTCAACUGCAGGCAAACAUGA
267758272	51202	GGGATCTAACUCTCTGGGCUAGT	51203	ACACCCTTAUCACCCCAUAGAGG
262817997	51204	GTCTTGTCUTGGTCCCTUGGT	51205	TGTCGAUGAGCACGTCTUCC
327585373	51206	TCATTTTAGGAAGGAGGUCTGTGCUA	51207	GCCUACTUCACCCGGAGAC
327597765	51208	ACAGCACACAGGGAUTGAACUG	51209	CTTGGACTGTUCAGTGATTGGUCT
313004422	51210	CACACAGTGAUGCTAGCGGUAA	51211	AGGTGTUAAAAATCATGACUGAGCCA
314318895	51212	GAGGAGGATTCUGAATTAGTGGTGAAUT	51213	CGACATCTTUGGCTTTTGTTAGAAAUCT
324500199	51214	TGGTTTTAGTTCUTTAAGTGCATTTGUCAA	51215	GGATTGTCAGUTCTGCGATCATUCA
267149356	51216	CGGTCACCAGGGUTCATCUT	51217	TGAAGUCAGACCAGGAGTCUAACA
268438419	51218	GATGATGACGUTGACGATGAAGUAGA	51219	ACCTGCCUGGGATTUCCAAAC
260651291	51220	GCCACCAUCCTGGGTGATTUAA	51221	CGCCCAGACCUTGTTCTCTAUAAC
264015527	51222	GGAACAACTTGAUGGTGCTACTTUG	51223	CCCCUCTTTGUGAGGAGAAGAAAG
268610928	51224	CCTTATTTUCAGGGCCCUCCAG	51225	TTTTCTTCUGGGATTCTGACAUAAAGCA
263092761	51226	AACTGACUTCTTTACTUCAGGGCAT	51227	CACACUCAAGGAUAGGCCAACA
267384422	51228	CCCTACAAGACCACUGGAACTTTUT	51229	GTAACTTACTGGUTCCCCAGGUT
258732323	51230	CCTCTTCATAGAGUTCCTGGTTTUCAAA	51231	TCTCAAATGCAGCUTTTATACAGGTUGA
264204951	51232	GGATCTCCTGGUGGCAAGGTAUA	51233	TGGGAACUCACACTTTCTCCUCT
265563779	51234	GTGACAAAGGUGAAACAGGUGAAC	51235	AGCCTTCAAATCCAUTTCTCATCTCTUC
238348183	51236	GCACACAAGCAAAUGGAATGTUCT	51237	ACAAAGGAGAGUGATTGATTTTCTUCCT
235208252	51238	CCTGTGGUGCTATAGGUGGGT	51239	CCTCTTCCCAAUCTGGCTGTTUT
333524168	51240	TGTAGAGAAGGCAUCTGCCGUA	51241	AUGGGCAGAGACCACGUAAG
263507800	51242	GCTCCAGCGCCUGAGUT	51243	CTGCCTCAAAGUAGAGGTTGTGUT
233350901	51244	TGGATTCACUATCTTAAGACCUCGCT	51245	CAGAGACCCACUCCCAGATTTUG
325228091	51246	CCATGTTGAUGAGGCTTATCTGGUT	51247	TCAACATGTACAUTGCCATCAUCCT
324116439	51248	TTGGCCAAGAUGTTGATTTTCUCA	51249	GAGCACTTUCCATTTGCCTCUC
323845966	51250	GGGTAGGTGAAAUAAATGAGTGAGUAG	51251	CTTGCTTGUTATGGTCATUGGCA
325020162	51252	CCAGGCAUATCCCTCUAGCCT	51253	TCTCGTGTGUGAATTTCCCTUGT
315332933	51254	GCATGAAGGCUTCCTTGAACUCT	51255	TTTUAAGCCGGGCATCUGAGT
262150561	51256	GAAGCTGGAAUGGCATGAGTUAG	51257	GTCAGCAAGAUGCCCTTTGUG
332132264	51258	CAGGTGGCUTCTCCAAGACUG	51259	TTTGAATAACAGTUCCTGCAACTTGUG
332181134	51260	AGGAAACGGCCAGUGCAAUA	51261	GCAUCAAGTACAUGCGGCAGA
332033567	51262	GTACAGAGGCCCCUTCTUCC	51263	AGCAGAAGCUGCAAGATGTUCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258979370	51264	GTTTGCTTTTGUTCTTCCTCATGUCT	51265	GCCAAGAUCAACAAAGCUGAAAAAGAAA
253907061	51266	TTGGCTAAGTUACATGAAGCTTCTUGAT	51267	CTGTAACAGGAUTTTCACATUCAACAAGT
329114344	51268	CGCATGTTUCCAAGTGGAACTUC	51269	GGGAGCACUGCGTCUACAC
328887349	51270	CTTTTGCUGGTGCACGUGT	51271	ACTUGGAGCCCACGTGUT
229322652	51272	CCTTCAGGCUGTTCCCGAAUAAG	51273	CGGTGGACGUCACGGUAAG
264404761	51274	ACACGCUGGCCATTGUCT	51275	CCCATCTUCCTGCACGGUT
319401936	51276	CCCTAGAAAAUGGCTATCCUGAAACT	51277	TGCTGTCATCATUTTAATGCTTCTACUCA
321240057	51278	CCAGAGAGATAGUATTCCCAGTCTUCAT	51279	TTCTAGTTAUAAGTTGGAAAUCAACCAGAAA
320897773	51280	AGATATGCACUAGTTCAAAGAGAAUGCC	51281	GGCACCAAGTUCTACCTCATGTUT
319950349	51282	TTGATGTCTTCUCTCTCTTACAGCUCT	51283	AACTGAGCAUACGCTAGGAAAATAAUGA
320088692	51284	TGCAAAAGGAGAAUACACUAAACCAAGT	51285	TTTCAGAACCUCAGGAAGCATGAUT
332620477	51286	GAAGGGTTUTACTCCCCUGCAT	51287	GCTCUCACATTCCTTUCAGAGAAGT
333151738	51288	GCTAUGCGAGGAUGCAGACAC	51289	GATGACTAAGUGGGAGGTTTAUCAGAAA
332893511	51290	AGACTCAACUGGGCTAGUGAACT	51291	TGTGCTGTTTCUGTGTACTCTGUG
333733556	51292	CAAAACCUCAGGGAGTCATUAGAAGT	51293	TUTCCAGAGAGUCACGGCAAG
333738533	51294	CGGATGCUCAACTTAACUCCCA	51295	GACCTGGUGAGTGTGGAAAAAUCT
333708576	51296	GATGAAAGTAGUAGTGCCCUGGAA	51297	ACATGCGUAGCACAGGGAAUC
333015093	51298	TGGGCCCAUCTCAGGATGUA	51299	GTGCAGTGCAUAACTCCTCTUGA
332891056	51300	TCTTTAAAGTAGAAAUGCTTGCCUCAGA	51301	TGCTTTTTCAAAACCUCCAAATGGUG
312830998	51302	CGTACTTUGCGCCGUACCT	51303	TCTCCAGTAGUAAAGACACCACCUC
312861938	51304	GCCUACGGAGCTAACAUCCT	51305	GGTGCCATAUCTGCAGTAGGUC
262980434	51306	GCTTCGUCCCTGUGCAAAAGA	51307	GCACCAUCATCAUGAGCGAAAA
268762116	51308	GCTAGAAAAUCACACAGAGGCCUA	51309	AGATCCUGGTGTCCUGACAGAA
262375703	51310	GGTAGGAAGCAUTTTAATCTTGGTCAUC	51311	GCAAACCCTAUGCTATAATGCTTTUCA
267966225	51312	CCTCTGCCUTCTGATTGGGUAA	51313	TCATAATATTUCAGGGCATTGUGGCA
264614871	51314	CTGTGCCCUCCATCAUCAAGT	51315	GAGAACAGCAGUTTCCATGTAACATTUT
292277995	51316	CTTTTGAATUCCAACACTTTACCTGUCA	51317	GGAGTUCCTTCACTUCCAGCAG
290973786	51318	GCAGAAGAAAAUGAAATUAGGCAAGGA	51319	ACACCAGAAATCAUATCCTCTTGCUG
293179375	51320	ACAACCCCAGACUTCTGTGGUA	51321	GCCCAGATGAUGAAGTGGTAATAAUGAG
290376636	51322	CTAAATGTTCTACCCAUAAGCAGAGAGUA	51323	CTGGTCTTATUATTGAGTGAGCUAGGT
319675139	51324	GCTTAGTGTGCUAATTTTGGCTUCT	51325	TGTTCGCATAGCUGTTTCATAAGAGUT
291335296	51326	AAAATAAGACCCCAGCUCATGGUT	51327	CGCATGUGAACTCTAAATTUAAAGCACT
320084568	51328	CAGTGCTTTCUGGATTTAAGCUGAA	51329	GGGTCUGTGCCCAUAGCA
289619978	51330	AAAACAGACGUGACTATGCTCTUGT	51331	CCTGCACTTUGACAGATGGATTAAGAAUA
223859952	51332	TGGCTGCAGCUTCATATGAUCAG	51333	CCTCAAGTTUACAAGAGGGAATACUGAA
222403679	51334	CTGTTTCTTACUAGGAATCAACCCUCAA	51335	CCGGUAAGTAAGAGUGCCAACC
222834771	51336	CAGAUAGCCCUGGACAAACCA	51337	CTTTCCGUGGCAAAATGTAAUAAAGT
224547648	51338	CTCAAGAAACAGTUCTCTCAGTTCTCUT	51339	CCACCCATATTUCTGGGACTATGUT
224604761	51340	GTGGAACGUACCCCATUCAGT	51341	ACTTTGGGTUCCACTGGATTCUG
327016505	51342	CAAGGTGATUAAACCCCCTCUGA	51343	CTCCCACCACUGCAUAAGGG
242511339	51344	AGCTTCTGATTUCATCTCCCTTTUCC	51345	CTTTGACCCCUTGGGAACAUCAT
257634097	51346	GGATATATCTGAUACGCAGGCCTCUA	51347	GGGUTTATTCTTCTCUCGAGAACACT
257653064	51348	CTTCATCCAAATUGCGAGATGCTUT	51349	CAGTACAGCAUCAAGAGUCACACT
237718489	51350	CCTGCTGCTUTTCATCGTGAAUG	51351	AGAGGATGGUAAAAGAGATGAGTGCUAT
257727566	51352	TCCACCCAGAGAUTTTGAAGUGAC	51353	AGAGCCAGCTAUTCCATTTCTCTTCUA
235239700	51354	CACAGTCTUGCTGGTCUGCT	51355	GCAGCTTGTTUGTTCATGTGACAUT
259065883	51356	GGCGCCUCTCTTTGTCTTUGT	51357	CGATCCTUCGGTAGATATTTUGAAGACT
267670757	51358	GCTTTCAUGCAGGCTCACCUA	51359	ATCAATGCACUTGGTGATCUGAAGA
268529626	51360	AGGCGTAAGCUGGAGGATUC	51361	TCATAGAGCUGCATTGCTGUCA
261235055	51362	CCCTTTTUAACAGAGCCGTTCUT	51363	ATTTGTTCCCTUCCTTCTTCCTCUC
331721880	51364	CTGUACCAGGAAGGAGUCAAAGG	51365	GGCCGCUAAGAAATGCUCACT
331561127	51366	CCUGCUCAGGAGGAGCCA	51367	GTGGGCCCCAUCTCUGT
331756947	51368	ATCCCTGUCCTTGTACUGCAC	51369	AGCCCTTTAUGCCTCTATCTCTUCT
268268277	51370	ACTGTCAAUACCCCATCCCCUT	51371	TGACCCTGACUCTTATTCTCCATCUG
315120604	51372	GGGATTGTGCUAACAGAAAAGAUGA	51373	CGAATGAUCGAATGGTGAGUGG
272215900	51374	TCTATAAGCCUCGACAGCCAGAAUA	51375	GGAAAAACAGAAGUCACATTCTTGCUT
271043537	51376	CCAAACTGUGAAGCTCUGGAAC	51377	AGATTCCATCTACCUTCATTCTCCCUAA
271336549	51378	ATCTTCTTCCAUGTCAACTUAGCCAA	51379	CCTAGACACAGUGCTGGCTTUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
271522375	51380	TCCTCAUGAGAACCAATCTUGCAAT	51381	TGGTCATTCTTACCUCAGTTTGTCTTTUC
317467204	51382	GTCTGTATTTGUGTCCAGAGAACUCA	51383	AGTTCCGTUCAACTTCGCUACAA
316096232	51384	AAACAAACAGCCUGCCAATCTUAC	51385	TCCCAGAGTTCUCTTTCTCTCCTUC
317956870	51386	TGGCCTTCCUTCCACAAGAAAUAAA	51387	CCAACCCCCUAAATCATTAGTCTTUGAT
317261163	51388	CTGATATUGCACACTAGGCUGAAGT	51389	ACAGGCTCAGUGCCTGATTUT
315537396	51390	GTTGCACATGTTUGGCTTAATTCTCTUA	51391	GATTGCUCAGCCCCUCGAT
317103933	51392	CACCTGUTTGTCAGAUCCACACA	51393	AAACTTGCCAUGCTACAATTAGTUGAAG
266708416	51394	CCCCTGTUGGCCCTGTTAUC	51395	AGCATGAGTTATTUTGGATGTTGCATUT
268149036	51396	AGGACACCAAGUTCATGTAAUGCT	51397	GTTTGCTAGAAUAACATTTGGTGTGCTUT
263146612	51398	ACCATACCAGAUGTCATCAACTTATTUC	51399	GGAGAACCUGGTGUGCCT
266065911	51400	ACCTAGTTGGAAUCCTGAAGTCTACAUT	51401	TTCCCATTCTAUAGGGTTTGATCTGAUCT
323720729	51402	GGGTTCCAGAGAUTCAGAATAUACCC	51403	GCTTAACTAAUCACAGAAATGGCTTUGT
333190531	51404	CTCTCGACCACUTAAAACTUCAGACT	51405	AGAGGTTGUAGCAGAACTUCAGAGA
318277408	51406	TGATGCCAGAUGAAGAAACTCCATUAG	51407	CAATCACTTACCUTTCAAGAGACUCAGA
319424031	51408	ACAAAACTUAGAGCTGAATTCAUCGCT	51409	ACATTAGCAGCAAAGUCTTTCACTUG
265303956	51410	AGACATGAAGUCTCACCTCUCCAT	51411	TGCCTGCTTUGCCTGATCAUT
258107535	51412	CCAUAGTGGCCUACGAGGAAA	51413	AGCAAGCTTACAUCTTGAAGTTCCTTUA
268172565	51414	GTTGAAGTGAAGGGUCTTATTAGCUGT	51415	CCTTCAGCAACUAACAAGATTUCACAGA
267760050	51416	CAACGCCGCAUCAGCATTTUA	51417	GGAAGATCTTUCAAGAAATGTGTTGGUT
267500618	51418	GTCAATCCATTAAGUCCTTTGAAGCUC	51419	AATGTGATCTUTCTACCTGCUGACAA
264425864	51420	CCTGTGTAUAGAACCAAACUGAGAGG	51421	AGTTAGAAUAATGTGCAUGGGAACAGT
313040147	51422	GGGCTATUAGGATACATUCCACAGT	51423	AACACACATTTTCUTCACAGGTTCAAUC
230328840	51424	GTCTGCAGGUACGATGGCUA	51425	GCATGGAGAGGGCUCTGTUC
223433634	51426	AGCACAAGACAGUCCGACUC	51427	GAGUAGCAAAUCAAAAGCCACAGAAAAT
333094468	51428	TGCAGATUGATAAGGGTAUGGAGAGAA	51429	TCTCTTTGTCTUCTGCATTTACTUCACA
222546482	51430	GTGTCAATGAGUATAGCATTTGCUCAAC	51431	AGTCTGAAAACCAAUTTGATCCTGUGAT
222669592	51432	CCATGATTTCCAGUTTAGTTTGATGTUGT	51433	CAGCAAAACCACUCCUCACAAG
333621352	51434	GGACTGCAUTACCAACTCTUGGG	51435	TTCATACTGCUGAGCTCCACTUG
222174893	51436	AAGGACAGCGACUACAAGGAAUC	51437	GCTGCAGTGCUTTCCTTAAAAATATCUA
223658806	51438	CTAGAGAGCAGGGUGAATGTTTTCTUA	51439	AGCAGCAGGUATTTCTTCTGGUAAA
223471061	51440	GGCAATTGTGAAAUTTGACATTTGTUCT	51441	TGCTATTTTGACUTCACCTTGATUCAGT
265488160	51442	GGGACAGACAUCTTCAGAAUGACA	51443	AGCACCACCGAUGUCCAAAG
324816963	51444	TTCGTGTGCUTTTTGTTCTTTUGGAT	51445	GAGAACAAGCUCACAGGUGGA
268113363	51446	GGTGACTTGTTUACTGGAAACTTTTGUT	51447	CTTTGUGAGCCAGCATUGGAC
259708645	51448	GGTCCCACUTTTTATTCTTTUGCAGAG	51449	CACCTATTCACCAGAUTTCGTAGTCUT
264223416	51450	TCAAAGAAUGGCACCAGTGUGA	51451	TGTCCATAGUCCTTTTAAGCTTGUAACAA
265597349	51452	ATCCAGATCGAUGGTGTGTCTUG	51453	CCTATGAGAAAACUGCACUGGAGAAAAA
266968374	51454	AGCUCAAAACACACCACAGGUT	51455	CAATGATGACAUGTGCCCTCUC
262605305	51456	GTCCAGUGAGTGCUGCAGA	51457	CCCAGCTCAUTTCACTGTCUCAA
267170040	51458	ACGGTGGACUAAAGGAAACTUCAG	51459	GTGCTGTTTCCUCTTTACCATGUG
267843763	51460	GCCCAAGGAGAGAUTGGTTCUG	51461	TTGATTACAGGGAAGUGGGAATGTUT
261061318	51462	GGGCUAACCCACCATGCTUT	51463	GCTCTGGAGUCGACTTCTUCCT
316428020	51464	GGCTCTTCUGAGGTTGCCTUA	51465	CAAGCACCUGCTCAGUGG
238374239	51466	TGAAGTCAAATAAUGAAGTCCCAAGUGA	51467	GGCTTTTTGUACTTGTTTGTCCUCAA
238709446	51468	GGGATGAAAUAGAAAGTCAAUGAGGAGAA	51469	ACCTGAGTCUCCTGCTCTUGT
239400853	51470	GGCAACCTUCCACCTTCCTUT	51471	ACCATGTTUAAGGATCTCAATUGCCA
328650290	51472	CAGGCAGGGAGCAAUGTUAGT	51473	CUATGCTTGCGUAACCAGCAG
256928921	51474	CCATUGTCCACAAUCCCCAAC	51475	GACCUTCCCAAGUCACCAAGA
262200502	51476	AACAAAAGCTGCUTTACATTCTGCUT	51477	AGATAGGTGTUCGAATGGGACTTCTUA
258002990	51478	CCAGATGAUGGTAGGTACATTUAGCA	51479	CGGATCTUCCGTAGCAGCUC
316644218	51480	AAAACAAATGAGACAAGAUGCACCAUC	51481	AGTTCAAGCACUGTCACATTAGGTUAC
229560074	51482	GTAAGAGACAUGTCCAGATTCCUCAC	51483	GATTGCTTGTUTGGCTTGTGTUCT
312873674	51484	TCCCTTTUGCACACATGATAATUACCA	51485	TGTTCATTCCAGGACUATTAGACAGUGAT
312855912	51486	CATCCACAGUAGCAATAAGGGUAAGT	51487	GCTCAGCGTGUCACAGTACTATUC
313607301	51488	GAGTAATAUAAACGGCCACCCCTUT	51489	GCAAGCAGATAUGCTACTGTCAGUG
316988683	51490	GAGTAGCTCATUTCTGTGTATCGUAAGG	51491	GCTGTGATTAUCTGTGCTAACUGGAT
326780372	51492	TGGTCAAAGGCUGCCATGTUAA	51493	GTCCCCUGGTTAAAACGUGAACT
257958770	51494	ACAAACCCAAAUTCCTAATCCUGAAGT	51495	AAGAACATCUCAGGAAGCACUGG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
254295476	51496	GCAUGAAAGCAGCGTCATUCA	51497	CGTCACUGGTCGCGAUACA
268741840	51498	GTGGCCAUTTACAACCUCAAGAAG	51499	TGACCTGAUGGTACCUGCCAT
316036961	51500	ACCACACUCCGGCTCCUAT	51501	CCTAGCCCCAGGAUCCTACTUG
296710247	51502	GGCCATCUGCATTGGGAUCT	51503	CCAGUGAGCAATGUGAGCAAC
280404001	51504	AAACACAGTAAAUAGGAGGAGACTCUCT	51505	CCAGTGACUAGAAGTTTTCCTTCCUAAA
317152186	51506	ATTCACAGAAUCTATCTGTTTAAUGAAGGT	51507	GAATGCAUGAGAAAGCTGAGAAUCAAT
257791753	51508	GACCACCCCAUGAUCGACAT	51509	CUGACCAACAGAGACGGUGAC
267671441	51510	GGTTCAGGGUGCATAGAUGCT	51511	CATCGTCAUGCCTGTGTCUCA
268605716	51512	CGGGCAAAUACAAGCATAGACUCT	51513	CCCTACCTUCCAGGCATUGG
268269270	51514	AGGCCGGAGAAGUAACCCUT	51515	GGUTTAAAGUGACAACCGCAAAGAC
260776656	51516	GGUCCCAGGGUAGAGAACAACA	51517	CTCTTCCUGAACTGCTCCUCA
264247313	51518	GGACTCGCUGGACATGATUGA	51519	CGCTTGCCUACTCACTCUCT
261408848	51520	ACCATGTGCCAUTCATCCTUCAT	51521	GCAGCCUCACTGGTTTCCUG
319725248	51522	CTCTTCAGGGAUATCTTGAGCTUCAG	51523	AAUCCACAGAGUCAGAAGGAGAAAAAG
318022350	51524	GCTCCAAGTTUCAGGCTTTTGUT	51525	GGTGTATCTGAAGAUGCAAGAATGTTUAC
319793577	51526	AAAAAGGTGAAGCUCTGGGTCUT	51527	CCACGATATAGGUCACCATCTTTUGAAT
320728526	51528	ATTAGCTTGGAUTATGACAAAGUAGCGA	51529	CATGTCATCTCUAACTTCCAAGAGGAUT
320125880	51530	AAATCCTGGCUCGCTCUAAAGG	51531	TCAGATCAGCUTTGAGTGAACTTUGA
264826015	51532	GAGCAGGUGCCAGACUGT	51533	CAUGCGGAAGGCCATGUC
255396070	51534	CAGGTCTTTCUCCTCATACTTUGGA	51535	GTTGTTGUCATTGATGUCCACGAT
257235485	51536	GTATGUGGCCTTCCTUGGACA	51537	CCACCACGGUCAGACUGAAC
315089751	51538	GGCTGTCCUTCTGGGTGUAAC	51539	CCCTCCTGCUCTGCCTCTUA
315229185	51540	GGAGGCCUAACGTGCTGUC	51541	AGCCCTUCACGCACATGUA
327238087	51542	AGCAGAUGGCCACUGCAA	51543	TGTTTTGTGTTUCTTGCTCTGCUC
327601892	51544	GGAGTGTGUGGCAGAGAUCAAA	51545	CTGGACTGCUGTGGTCTGUC
241656493	51546	ATTCTTCCCAUCCACCAAAUGCT	51547	AGATCCATGCAUGCTCCATUCC
266345890	51548	GCACGUCGGAGCCCAUT	51549	CGGCTUCCACGTGTGUC
313411071	51550	GGCTCACCAUGGTCTTCTUGT	51551	TGACCCAACUGGGTCTGUCT
315379835	51552	CCCCAGUCGAGACCCUGAA	51553	CCCCATCTCUCCACCCTTUGA
323495463	51554	GGTTTCCGAUCTCGGTCAUGAT	51555	TCTGCTUCGCTGACAUCCAC
313765951	51556	GTCCACCCACAUGACUCCAAA	51557	TCTTGTTGGTAUACTGGCGGAUG
223775985	51558	TTTTACAGACAGUGATGTGTGTTCUGA	51559	GGCGCTTAAATUTCTCAACTTCTTUCT
223526382	51560	TATTTTTAGAGTACTAUGGAAATGATGGTGAUT	51561	GGAGACAGCUCACAGTTAGGUAAAC
223558072	51562	TGAGCAAAUACAAGCTGAAAACTTUGG	51563	TGTAAGTCAGACAUAATGCATGCUGAA
224369561	51564	GCTTAATTATTCUGAAGGGCCGUGA	51565	CCCAACCAAAUGGCATCTTTTATATGUT
333290794	51566	CCUCCAGCGACAGGGTUAC	51567	GCGGTGCUGATTGGAGUAGAC
316753118	51568	GGAAAGGAACAGUGACUGCCT	51569	TCCAAAAGGAUCCGTCACTCTTCUA
333495105	51570	ACCAAGCAGCAGUAAGACTUCAG	51571	AGAAGAGGAUCAGGTTGGUGAAGA
318167710	51572	GCACCTUACAGGTCCTTGUGAA	51573	CGTGTTAGCUACAGGCUGCT
320184951	51574	GTGAACACCUGCCTCTGUCAA	51575	TGGUCCAAGAGGGTGUCCAT
314990984	51576	GTTCCTCCUCAGCCTCTTTCTUT	51577	GAAATGGAAACCUGGTGCCTUC
315316343	51578	GCAGAGAGGCUCTTGCTCTTUA	51579	CGCCAGAUACCAGAAUCAGAGGA
313733448	51580	GATGTGCCAUCTGCTAGGAUCT	51581	CAAGAGGACCUGTTGCUCCAT
316025167	51582	GTATACGUGGTGGCUGCAGA	51583	GCCACGUGCAGGAUGAC
314027322	51584	CTGATCACCGCCUGGTACAUC	51585	GCTCAACCCUGAGUCAGGAGT
314893401	51586	GCTCTGGCUAACTTGGCTCUC	51587	GGTCATTGAAGCUCCAGCTCTTUT
314188172	51588	GGGAAATGGAGUCGAAGCUGAC	51589	GCCAATCATAUATTTCGCCCUAGAACA
261250178	51590	GAAAGAAUGACCAAGAGGTCUGGT	51591	CAAGGAGCAGCUCUCAGAGAT
263060775	51592	CCAGCCCCUTAGACTTUCGAG	51593	CAACAAAACAGAGCUTGGGTTAGATUT
263224151	51594	GGGAAAGGAACCAAAGUATUCAAGAT	51595	GAGCAUCGTCTUGGAGAAGGAG
256390256	51596	GGGATGTAGGGAUTCTTGTTTCTUC	51597	CAACTTCGACUGGAGGGACATATUT
287501982	51598	ACTGCAGAGGUAATGTAGTATUGGT	51599	AAUTGGUGAGCCGGGACAA
264439090	51600	TGCAGAGAGAAUACGGTGGTGUA	51601	ACUAGGGCUCACCAGGAGAAC
267436171	51602	GGCGUCCACACACTCTATGAUT	51603	GGAUTACCAGGATAUCCAGGAAGACA
317123673	51604	GCGGACATTGUGGTGAGTACUG	51605	GGCCGGAUCATTCATGACCTUT
315262670	51606	GGCCUCCCAGGAACTAATTCUG	51607	AGAATAAGTCTTCUCCAGCTCCTUCT
312716650	51608	GCCTGAGUGGTCAGUCCCA	51609	GUGACACUGGAGGCAGAAGAG
318841018	51610	ATCCCCUCCCCATCCCTUAA	51611	ACACACACCAUGTCTCTTGTCUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
327216385	51612	CCCTTGCCUTGGTCCTGUG	51613	CACCCCAGUGTTCCAUGCT
327139431	51614	CCAAAACACACACAGCUACTTCUAC	51615	CCCTTTGTACCUGCACTGACTTUT
327359301	51616	GGCTCTTTGUGGATTTTTCTTTGUAGT	51617	GCCAGAGAUGACAAAAATGCTTUCT
328043179	51618	ACUGACGGCCCAAAGATCUG	51619	CCTATAGGCTUCAAAGGAATGAAAUGCT
328049808	51620	CCCCAAGCUTTTCCCUCGAAG	51621	CCTCAGCCUCTGUGGACAGAT
327853848	51622	AAGGTTUGAATCAGAGUCCAAGGG	51623	TCAGAGAATGACUTTCCAGCAATATUGT
326812376	51624	GCATTTUCAGCAGCTTCUCACT	51625	GCACTGTGAUAAGAGGGTCUCAC
327392837	51626	CTCCATTACAGCAUTTCTGGCUCT	51627	AGCCTCAGTTTUCTTCCCTTTTTCTAUT
327325072	51628	CCTTGTAGCATTUAGCTCTTCTCCUA	51629	CGCAACCCUCTTTTGTCCCUT
327039688	51630	AGGCTATTACAGAUGTGATTAACUGCAC	51631	TGGGAATTAGUGCCTTGGTAGAGTAUT
332644279	51632	CCAGACATACUGCGGTGCUT	51633	TCCAGATCAUACCCAGGGTCAUT
333335858	51634	TTAGCCCATGTUCATTTTCTCTCAUCA	51635	GATTTCATGUCAACAAGTGGCTTCAAUA
332701115	51636	CTCCAGAGACUCTTGCAATCAUCA	51637	CTCTGAATCACCUTCTCCACCUC
333163390	51638	GTTCAGTTGGUCAAGTAGAGTUGCT	51639	CCTTGGTTUGAGCTTGTCATCTTUT
326180820	51640	GGGTGTAUGGTTGACAUGAACGA	51641	GCTTCCTTGUGCTGCAAACTUAAAAA
325449072	51642	GCCCAGGUTTAAGGCAACUCAA	51643	ACATCTTCGGUGAGTCTUGCAG
324357251	51644	GGAAGTCATACUGCCCATGCTUT	51645	GGGTACAATGUCTTCTTCCAGTUC
325600362	51646	AGTGAGAGAUAAACAGGGACATAUCCT	51647	GAGAATCATCUCCACGTTGTUGGA
326295274	51648	AGCTGAGTGTGUATTTCAAAGTTCUGT	51649	GCATCCGUGAATTTGGAATTTUGAAAAA
327598740	51650	CTCAATAATTCGACUCACCACAGCUA	51651	TCACCCTGAAUGTGTCTTCTCTAUAGT
328113147	51652	GGAGUAAAAGAACAGGAACUGCCT	51653	TCACCTUACACCCAATAGAAATUGCT
320127738	51654	GCCACCTCUCAGTCCATCUCT	51655	AGCCAGAAAUGAGACTATGGAGUCA
318504412	51656	GCGGUACACACCAGCCTAUG	51657	CCATTCUCAGGACCCTTCAGUCT
333158752	51658	CCGGAGAAUGACAGACTUGGT	51659	TTTTCCTTCTGCUGATTCTCTTCTTTUCT
332918824	51660	ATGACATAGCAAUGGAAGCCAACUAA	51661	CACCAAGAAUCCATCTCATTCTGUAGT
332968765	51662	GGGTTTCATUCACACGCTGAACUA	51663	GGACTCCATCUATATGGCTTGCAAUG
319266356	51664	GAAGTGAAAGUGTGTTGCGCUT	51665	GGTTTGGAATCUGGCTGAATCUGT
321591682	51666	CTGCCGUCAGGTAGTTCUCC	51667	GATATGCTCGUTCCGAGAUCGT
278048187	51668	ATGAGTGGCAAUGTCAGGTGTTAUAAT	51669	CTAAGAAACTCACCUAATGTAAGCCTAUGG
279559748	51670	CCCTGGATGUGGCCAACAAUAG	51671	TCAAACTGGCAUGAATAACCACUAAAAGA
278706503	51672	GTGACACACTATUGGTAGCTGTTCTUA	51673	CTTCTGGAAUACAGGAAAATTTGTTCUGA
279631766	51674	CGGTCTTTAGAUATGAGCAGCAAUGA	51675	GGCAATAATCGTCUTACCTCTTTCAGTUT
278300258	51676	CTGGAGGTAGAAUAGTAGAGGGTTUGAA	51677	CATCTGTTTAAGGAAUTAAGCATACAACUACAA
278502182	51678	GTCUGACGAGACGCATTTTATUACCT	51679	GATTTACCUCAGAAGTGTATCCTUCAGT
279956162	51680	AATCCACAAATUCAACGGAAAGAAAUGT	51681	AAAATAACTTACAGTUGGCTTGTTCTTGUC
268642882	51682	GTACACAGGGAGUCAGTGGGAUA	51683	GGTTGGTGGGUTAGTGGGAUG
267018825	51684	TGACTCCAGAGAUGTCAGUGGAA	51685	GACUTTGCUACCCCAGGAGAG
323353481	51686	GCCCGACAGGCAUTTAAAUAGGT	51687	ACAGTAATGTAGCUTCACATACAGCTUG
317024156	51688	TGGCAAAAAGCCCAAGUAACTAUCT	51689	AAAAGAAAAGCCCCCAUCTCUGAT
314405406	51690	GCTGCTACUTCCCACAGAUGA	51691	GATGTGAAATGCUGCTCAAGGTTUAG
312952543	51692	TGCGTGAGAGCUTCACATUCA	51693	ACAGAATCTTAAUTTGGGTGGCUAAACA
264207230	51694	TGGGCATGAAAUTAGACATACTTCTUCC	51695	AACTCTCCUGCAGGGAAUAAAGAAAAT
235141692	51696	TGTGAAAGAACAACAUGAACCCAUAGT	51697	GCTCTCCCCUTTGTCAUCACC
236206807	51698	TGAATGAACAAAACUTGGACUAGGCT	51699	GGUCAGAAAACACTGUGAAAAGCAAA
240073649	51700	ACAGGCCAUTTTCCATGTUGGT	51701	GAGCATACTCAUCAGGCCAGTAUT
332423362	51702	CTGAAAGAAUAAGAAGAGTGAGCTAUAGCA	51703	AGCTCCCTAGAGUTCTGAATCCTATUT
314951847	51704	GGTCAGAUCCGACTCCATCTUC	51705	AAACGATCAATAGUCTAAAAGTGGGCUT
314524914	51706	CCCAGGUGAGGGAGAAGUG	51707	TTGAGCTTTCUGGCCCTCUG
315397536	51708	GCTCCAGCTUGACCTTAGACUT	51709	CCATAGATGUCTCCAGGCUGGT
313381853	51710	GCGTCCGUCTCATACTUGGT	51711	GGAGAAAGCUGAACCCACCUC
257353942	51712	ACTCAGGGAACCUTTGATAGUCAGT	51713	AGAACTCGTAUGCTAATTGAGUCAAACA
255929020	51714	GGAGAAUACCGAGAGCUGGGA	51715	GCTTGTATCUGGGCAGGTCAUA
326391633	51716	AAGATATTTGUGAAAGTCCACCATUCCT	51717	TCAGCUCCAAGACTCTCUGCT
324531519	51718	AGTGCACAAAGUTCTGTTTTTCTTUCC	51719	GCAAAGGCAGUTTCAGAGACUGA
326045363	51720	GGTGATCTUGTTGAAGGTUGGGT	51721	ATCCCTGAUCACTGGGAGUCAT
254803496	51722	CAGAAGCAUACAGGGAUAGCACT	51723	CGAGCATGGUATCATCACCAACUG
261655982	51724	GGGAGUCCCGTTGTCUCAAAG	51725	ACTGGGCACCCUGTATGTUG
315597478	51726	AGACAAAGGAAACACAAUTACCTUCCA	51727	GGCAGAGUAACAACTAAAGATTCCUGAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317164234	51728	AGTAGCGAUGAAAACAAAACUCAGA	51729	GCAACCCUGGCTACCATUCA
315729502	51730	CTCCCTGTGAAGUTATATGACAGCUT	51731	TCAGAACTGCAAAGUCTGGATATTGTUA
316115445	51732	AATTCTTTUGCAGGAAAAGCTGACAUT	51733	CGAATCAAGUCCTTGCATTAAUGGA
327391814	51734	GGGTGTCUTATGTATGAAUGCGT	51735	ATGTCTGGGTUGCAGTTAAACCUAA
270068977	51736	CAGAAAGCAAGCACAAUCCACAUT	51737	GCAGACCTCGUCCTTCTTCATAUT
315805537	51738	CCUCAGCAATUCACAGCGGAA	51739	GGGAAUACAGGGCCCAATCUG
319654530	51740	GGGCTAGGUGAGAGTUCAAGT	51741	CCTTTGCUGAGCGCTTACTAAUG
318115999	51742	GCTCTUGGGAGTCCACAUCAG	51743	TGTGGAATTUCAGCAGTGCUGT
262269489	51744	GGAGAGGUTTCATGCCUGGAT	51745	CCCATCAAGCUCGCCTGUC
240070744	51746	GACGATAGCCUGAAAAACCUCCA	51747	CUAGAAGACAGGGAGCGUGAA
264188845	51748	CACCCTGUGCGTGGGAUT	51749	GGGCCTUCCTGAACACUGG
321284910	51750	CCCAGCUCCTGCACGUA	51751	GCGUCUACGCCAAGGACA
320244116	51752	CTGAGAGGUGCACAGTGTCUT	51753	GCAGCAGGUGCUGGACA
321337364	51754	GGGTGGUAAATGGCUCGGA	51755	GCCGACUGCACCAUGGA
319590329	51756	AGCACGGUCAGGAGGUACT	51757	CAGCCCUCAGTGCTGCUA
238723188	51758	CCAGGUCCCCTGGATGAUGT	51759	CCCTTCUAGAGGCTTTGACUAACCA
237032059	51760	AGGCCACACACGUGUACAAG	51761	TCAACUACACCAACGAGAAGCUG
235871594	51762	CACCGAGCUGTACCUCAAAGAT	51763	GCCCATTGAGAAUAACCGGGTUC
265881533	51764	GGCACCAAAAGGUGTACCUGA	51765	CACTTGGCCGGUATGTATGUCT
262268930	51766	CCACCACCACACCUACCUC	51767	GCTGATGGUCACAGTTTCTGTTTUC
269280346	51768	CAGCTUGGGCCCCATTUC	51769	GTCCTGTUAGCGACTCGAAUCT
328361867	51770	AGAAAAUGAUCGCACCGCAGA	51771	CAAACCUCAGCUGAAAAGCAACT
321510429	51772	CGACGTTGUTCTTGGCTGUCA	51773	GATTTCUAACCTGCUGGAGACCT
318341084	51774	TGGTAAAATCCCAUGGTCAATTGAUGT	51775	CGCTGATGCCUTTTCAACTAAACTUA
268446679	51776	GACCCAGUGCCTCATGTCAUT	51777	CTGAAATCUGAACAGACUGAGCCA
264683586	51778	AGACAGTGGUGGGCCUCT	51779	CCCACCCCGGUGTTTUCC
260047737	51780	CCCTUGACACAGCGGAAGUC	51781	GAGAGGCAAAUTTCAGGGCUCT
260994314	51782	CCCACCAAUACGCCTCTUCT	51783	GTGGGUAACGGGCGUAGT
262570290	51784	CGCAAATTTCCUTCCACTCGGAUA	51785	GGCCATCUACAAGCAGUCACAG
267654325	51786	CTGGAGGUGGGACCUGAG	51787	CCACCCUCACCUCCGAGAA
264059829	51788	CATCACAGTGUGACTTGCATTUCC	51789	ACATTTGTGAAAACACUTGCTGGUC
268031531	51790	TGTGGAAGAGAUCCAAAACATCAUGAAA	51791	CGTAGTATGUGCGCCTGAGUG
263886345	51792	GCACATGGUGTTCTGTCTCUCT	51793	CATGTCATCAGUCACAATCTUGGG
262443231	51794	GAUTCCTCUGAACCCCACCAT	51795	CTAAGTGGAGUAGCTTTGTGGTTCUT
268144835	51796	GGGCATAGUGTGAGAGAUGGG	51797	CTTCAGATGCUGAGTGAGGAUGA
267817859	51798	CGCTACAACUATACAACUCCCAAGT	51799	GATCCCUCCAGTTCACUGGAAA
318200263	51800	TGTGTCTUCCAATAAGCGTTUCCA	51801	CCCTGACTCAGGAUATCTATCTGATUCT
323702265	51802	GCAGCGGGUCCAGAATCTUC	51803	TGCTGATACTUGGCGAGGTTUT
325557596	51804	AGTGCUGCCCAAAGACCUC	51805	ACUCAGGGCCGUGAGAGAA
325558098	51806	CATGAUCCTTCGGUCACGCA	51807	GCTGCUGGAGACCTTGAAUGT
325568530	51808	TCCCCCACCCUCTUCAAGA	51809	CTGGGCGAGGUGATCTTCUG
240265478	51810	TGGAGCAAAAGUAATACGTAAAUGGAAAGT	51811	GGTTGTAACTUACCTTTTCCAGGCUAT
237229091	51812	GGGTAGGATGUGATATTCCTTCTAGUG	51813	AGAAAAAGUACAGAAGAAGCUGACCAT
239297691	51814	GGTTTGTTGTTUTTCCTGGCTTUG	51815	TTCCCAGGACAGUCTAUGAAAACAAG
332907122	51816	GGGAUGGAGGAGGACTCACUT	51817	CATACCACUCAGGTCTGAUGCC
332965814	51818	CTCACCAGUGCCCTCGUT	51819	CCTCACCCCUTTCCACCUCT
312924552	51820	CCTGTGGATTUCCTCTCCAAAGTUT	51821	CTGCACGTUGGGTGTGATTUC
226608355	51822	CAGAGGCAUCAAGCCUGGA	51823	CCATUCACCGCCCTGCUT
225861671	51824	AGGAGUGGGACUGAAGCCT	51825	CCCCTTUGCCACTTTCUAACCT
253773466	51826	CATCUGACCAGGAGCTCCAUT	51827	AGGTTCTTACCUTCTACCTCTTUCCT
253715048	51828	CCCAAATGUGGTGGAGUGGAA	51829	GTCTTCCTUACCTCTTCCCTUCAAT
333068269	51830	ACGGCGAGAGUCGGAGAUA	51831	GGAGACATGGUTAGTGCTTTAUGCT
328404591	51832	CACCCGCUCACAGUACGA	51833	CAAGGTCGAGUGAGCTGUGT
255070403	51834	CTGCUGGAGAAGAGUCACGA	51835	TCTAGATGCCUGGCCATGGUA
266622635	51836	GCTCCTTGTCUCCAGGAACAAAUG	51837	CTCAGGATGAGCUGGTTGAAGTATUT
316684242	51838	CCACCTCUACACACTGTUCCAC	51839	AGGCCCAAAUGTTGTCUCACT
320447532	51840	GCCCAGAAUCCUCAAAGCAACA	51841	TGUCCACACCCCCACCAUA
316596478	51842	CTCCACATTCUCTGCCTTTTCAUC	51843	CGATCCCUGTGCCACUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317469570	51844	GCTGAGAGCUTCGGCTUCAA	51845	GCTGCUCTGCCUCACAGG
315741623	51846	TCTCTGAGAGGUGCCTUCCAA	51847	TCTCGTGGUCTAGTTCATCAUCCT
330715219	51848	GCACCCGUCCAGTGGUAAAC	51849	GCTCCCTTTCUCCTGCAGAAAUAA
267710554	51850	TTCCCTTTTAGACAAUGAAGCCTCAUAG	51851	TGCCGCACUAAATGAGGATGTTUA
266305307	51852	GAGTTGGACTAUTCAGTGCTGCUAT	51853	CTAATCGACTTGUGAAAAGCTGCTTUA
265279817	51854	ACAATCAGGGUTTTAGTTGTCCUGAA	51855	AGCACAACAGAGUGGCTTTUAAAGA
262394532	51856	CAGTTACCAGATUCCCACTGAAAATUCT	51857	CACTGCTAATTAAACUCTGGGTCAGUT
327476785	51858	CCATGCCAUTTGTTTCCUCCAT	51859	CAAAACAACCCUCGAAGGTCTGTAUA
313950598	51860	GCTUAGCCAGAGCAGGACTUT	51861	ATAGTCTCTUGGGTTATCGAGGUAGAAT
267842940	51862	GTAAACCCUGGCTTGACTUGGA	51863	ACCTUCACCAGCTCAAAUGGG
332645936	51864	GAGGCCGUGTATGGGAUGAC	51865	AAATAAGCCCCCUCCCUGAGA
325330745	51866	AGGAGTTGUCAGGAGCAGGUA	51867	GAGCTTGAGCUGCTCCTUGA
323524607	51868	CAACAGTUCCCCAAAGCCCTUA	51869	GACTGCTUCAAACTCGAAGUACCA
325340178	51870	GTCTGACUCAGGCUCCGAAA	51871	CAGGAAGCCUGGUGGGA
324796243	51872	GCCTGAGGUCTTCACUGAGGA	51873	GCAGCCCACCUGTAACTUCAC
324113041	51874	CCTCCCCUCCATCTCTAGAUCC	51875	GGTTTCATTTUGACCCTCAAUGCT
324244699	51876	GCUTGTCTTGUGAGCGCAT	51877	TTTCACCCACCCCAUCTTCTUC
324969068	51878	CTGAGGUCCAGCAGGUAACAG	51879	CTTAACAAGAAGAGGUCCACUCGAA
324774571	51880	CTGGUGGAGGGAAGTGUAAAACT	51881	CCCCAAGGCCACUCACUC
256369596	51882	CGGCGGAGTTUATAGATAAGTTGGAAUT	51883	GTGGAGGCACAGAUAGACGUG
325602536	51884	GGGAGAGCGGUACCACUT	51885	TCCUGGACCCUCAGACAGG
267638555	51886	GATGACCUGAGGGTCCTGTUT	51887	GGCAGAUTGATCTUCAGAGCCA
319635440	51888	GGGATTAGGCUGGAGCUACA	51889	GTGCTUGGAGGCGTUCAG
327629406	51890	GGCATCCGGCUGAAGAAGUA	51891	CCCCCTTAUGCTTCTCCGTUT
316126334	51892	TTAAAGTTUCGGAAGAGCTUCCAGAT	51893	GGAGAAGGAUGGGCTGCUG
325596197	51894	TCTAGAGATTTCACUGTGTCTGCATUG	51895	GGCCACCUCCGTTGTGAAUAA
263072240	51896	GATCCTCAUCCAGCAGGTGUT	51897	ACAGGGAGACUTCAGTGCUCA
264470086	51898	CCCCACUGCCCTGUGAG	51899	CTGCCCUGACCACCTGUT
256867765	51900	CGGGTUCGGGTTCAGCUA	51901	GCCGACCACGCUCACUC
266886479	51902	GTAGGTCGUTCCCTTUCCACA	51903	CGGGCAAGCUTTGTGACTUAGA
324993310	51904	TTTAACATTCACUGCTGATCCUCACT	51905	TGTTTTGGCAGAUTTCGGCCUA
268174717	51906	AGGGTAAAUCCTGAAGCCUACAGT	51907	AAATGCACTAUCCCATGGUGGAAT
265624843	51908	ACAGGTATTGUAGGCCAGGCUAA	51909	TGAATTTGACCUCCTTGCCTTUCT
269336029	51910	CCATGGAGGGUACTGAAATAAATTCUACA	51911	CGCCTGUGGAAAGGGUGAAG
262706247	51912	CUTCAAAGTCCTUAGCACAGAGGT	51913	AGGAGGTTTCACUGTTAGGAAGCUA
260763712	51914	CCTTGAGAGCAUTATGTTTTGTCTGUAAC	51915	TCAGAATGAAGACAAUGAGGGTACTGUA
267914085	51916	ACTCTCTTGGGUTGTTTTCTTUGGAT	51917	GGCATGAGTUATTGTCATACTUGGAGAA
265851010	51918	AGTTTTCUCCAAACCTCCCTUCAAG	51919	AAATTGAGTGTAUCTGATCCCCAUGAG
259867182	51920	GCAGTAGTUGTCATCTGCUCCAAT	51921	TCATTTCTTTCAGUCTGTGGGTUCAG
266953752	51922	AAAATCCAACCAGUCTCCCTUGAAA	51923	GAAGTACAAGAGCAGAUGAATCTCCUAAA
324883931	51924	CAGGAGCUGATUGGGAAGACC	51925	ACGGUAAGACCAGCTTTTTGTUCAT
262401836	51926	CCCUCCACAGAGCCACUT	51927	CAGTGGUCCAGAACGUCCA
289311762	51928	TGCTTTCCCCAAUCTGGTCTUC	51929	GATTCUGCCACGCUCAGGAT
291343086	51930	GCTACAACCCACUCACCCUCT	51931	GGTCCCUCCAGCATTCCUAGT
304840692	51932	GGGCUTGGTGTTUAGAAGAACA	51933	GUTCTCCTCTAUCACAGAAAAGACACT
305878252	51934	TTTTGGTGTGUTTGTCTCAGATUGAAC	51935	GTCCATTTTCCUCACTATATTCUGCAAGA
305646670	51936	GGAGCACAUCGGGAAAGAUGAAA	51937	TGGCCGAUCTTTACTTTUCCAGAA
257399551	51938	GAAUGTTTTCTGAAGUAGCCCAGGA	51939	GGTACTUGGGCTGCTTTTUGAC
256225706	51940	CAGAGTGACUTGCCCTCAGUAAT	51941	CTGACACTCCAAAGUACTTACTGTCUT
263831731	51942	GAAGUATCUCCCGAACAGAAACGA	51943	TTGGTGGUACAGGTTTTAGTTCUGG
260188843	51944	GATCTTCTGGAUGTAGTGGCAAGTAUT	51945	ACAGGCTTCCAAUATGTTAGGTCTCUA
258704479	51946	CCATAATAACUTAAGCTGAUGCCCAGT	51947	GCTGCTGTATTCUCGAGGATTACTAAUT
264888396	51948	GGGCTCCUAAGCTTGGGATUT	51949	GGATTCTAGCCACUCTAACACTTTACUT
262648660	51950	CTGTCTGUGGAGATTATGAAGTAUCACC	51951	TCCATAGCAAGAUTTTCATTGACTUCCT
268755697	51952	TCCAAGCCAGGAAUAAAGCTUGT	51953	CTTCTCUGCCACCTTATGTTAUACCAA
315040647	51954	CATUGCACAGACTCUGAGGGA	51955	AGCAGCACCATUAAGTATCTAGACTTUG
320258380	51956	TCTCCAAGGGAGAUGAGCUAGAAG	51957	CTAACCACAGUGAGCAGUAGACA
229148238	51958	CAGTACCACAUTCTGGUGAGCA	51959	GCCTGAUTCAGCCTUGGACAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
227395314	51960	GAGTTTCUGGCACCCACTUGA	51961	TCTCCUAGCTCCCUGCGAA
317512183	51962	GGAGGACCGGGCAUTCUAAG	51963	CAGAGGGAAACTUTGAACCATGAGTAUT
333305161	51964	GGAGGGAACGAAUGATGGAUGAAAG	51965	CTGGTTCUGAGCTCCGTCUG
313602384	51966	CAACAGATCCUGCAGCTCTUAGT	51967	TGAACTCTTCCCUGAAGAAACTTTGUC
266772408	51968	CGCAAGGTTUCCAGTTGCCUA	51969	GGTAGACTUTGTGGGCUCCAT
312965181	51970	CCTTCTCCUTCTTGCCACUGT	51971	TGCTCTCACUCGCACCUG
314394185	51972	GCTCAAGCCUCTTACTCTCAAUGG	51973	TCTTGGTGGUGGGTAAGTCCUA
313640662	51974	GTTCTUGAGGAAGCCTGGAGUT	51975	ACCTCTACTTUGCCAATGTGCUC
333803255	51976	GAGCTGAATUGAACTGGAGGAUGT	51977	CCCAGATGCCAUCTCTCTGUC
333144239	51978	CGGAGAACAAGUCGGCTGUG	51979	AATGAAGTCCGUCAGGGCTUT
268068255	51980	TGGGCCACAUAGTGGTACUGA	51981	AGAAAGTAAGUTTGCACAGUGCCT
268124711	51982	TCCAGCGUCAGTATTTTGAUGGT	51983	ACAUTCCAAACUGAGGACAGCA
235410093	51984	TCACGCTUCCCCAAATTTCTTAUAGG	51985	ACTATGAAAACAAACUGACAAACCTCUCT
269119277	51986	GTTATTGTTUGGGAGGGAAGAGCUA	51987	AAGTGAGAACUGACTGCTTTCAUAGAAA
328078763	51988	GCAGGCTCUCTAGCATCUCAA	51989	ACACTTCACCUCTGAGCATAUCAAAC
328267528	51990	GGGCUAACCCCACCCTCAUA	51991	ACCATGCTAUCACCAAGCACUC
327183513	51992	ACCTCCAAUCCAGCACCUCT	51993	GCAGCCTCAGUACTCTCATTUCC
327635592	51994	GTATCCTCUGCAGGAAAGTTCTACUC	51995	GTGAAUAGGCGTTCTCAUCCCT
315407654	51996	CTGACGCUGCTGAAGACGUA	51997	ACCCCTGAAUCAAAGCTGUGT
261773039	51998	TCAACTCACTUGAGTCAGAATTTUGGT	51999	CCACAATCCAUAACTTCTCATUACCCT
257817812	52000	GGAGGATUCACTTAATCTCUACAAAGCA	52001	GATGAGAUAAGGCTGAGGAGUGG
259342413	52002	CATGCATAAGUGCCAATCCTTUGA	52003	ACCTAGTAACUTTGCTTTGTGAUGAACAT
268809625	52004	GGCTCUCCAGGTTCACCUT	52005	GGCTGTTTTGAAAGAUCTCATCAGAGUA
260469542	52006	GTTCTAGTTTUCCTTACTGTTCUCAGACT	52007	TCTTTCTGGTAACUGTCCTTCTGTTUT
260215631	52008	AATTCCATTCUGAGTGCTCCTGTUT	52009	AUTGGTTCACGUGGACCAGAG
268103489	52010	GGCAAGUACCCAGUACGGAAC	52011	GGTACTATTCUGCCGGTTAUCCA
268549983	52012	GGAATGGGUCAGGGAGAGGUT	52013	GGCATAGAGUGAGTTCTGGAACAUT
269352973	52014	GGCAAGUGAGTGACGCUCAA	52015	CGGGCCAAGUACTCACCTUC
236455510	52016	GAAGCTAGAAGAUCCTTACTAGTCUGAAGA	52017	AGCTTGCAUGACTGCCTTAUGAA
234600799	52018	CCUGGGAAAGCACUGGAGAAAT	52019	GTACCGAAATGCUTAGTATCTGCTUGA
324412591	52020	CCTAAGTCUGCTACCCGTCUGT	52021	GGAATCCCUGGACCTTTACCUC
258658571	52022	CACTCAGGCACUGGTTTTCUCA	52023	ATCUGTCCAGGUGAAGGCAAG
317835595	52024	CAGACACTTGAUGGCTTGGCUA	52025	TGGTACTTTCUTCAATTGCACUGACAT
316726124	52026	GGATCCCAGTGUATCCAATCATAATUCA	52027	GTAGCAGTGCUCCTAAACCATTAUGT
317745918	52028	GCGGGCUGCCTGTCUAAG	52029	CGGGCCUCGGCTACTUG
254326193	52030	CTTAGGTUAGGAAATGCCCAUGGA	52031	GAACAGAUACAGACUGAAAGACACACA
332078517	52032	GTGGAGGCAGUTCATGATGCUA	52033	CTTTTCTCTCCUCCCCCTTTCAUT
332060787	52034	GTTCUCCACCAGCAGTGTGUAG	52035	CAGCTGCAUCCTTCAGGAAGUA
332058255	52036	GTCUCCACGCGCCTCUT	52037	AGCCCCTTTUCCTCCTGCUA
332099627	52038	GCTCCCGCCCUTTGGTTAUT	52039	CAGACCTGACUCATCAACTCTTTTUCT
263105387	52040	CCACTAGATAAAAUGTGTTGGGTCGUT	52041	CTTCACTAGUAGGCAGCCCTUC
324979717	52042	TTTCCCUGCAGATGCTGUACC	52043	GCTGAGCAACCUCTATCATTTUAAGCA
229021837	52044	TGCTCCCACUCGGGUCAT	52045	CCTCCAAUGCGGTGCUC
320280678	52046	GUGAGGCTAAAUGAAAGCCAACT	52047	GCTTTGAGTCUGGAAAGATGGTATUGAT
319961499	52048	CCAAAAATAUAAAGCATCGCGGUACA	52049	TGCTCTTTCTTCUCTCTGCCTTTUC
318236687	52050	GCAACTTATAGUGGAGCTGGCUAT	52051	GGAGGGATGCAUGTCCTCAGUA
333327823	52052	CATTATTGCCUGCAATGUGCCA	52053	AGGAATGCTTUGTGACTAGCUAAAACA
333072157	52054	TACTAGUAAGAAGAAAGAGTGCUGGA	52055	ACAATCAACGUAGATGGGTTTTCCUT
332979125	52056	TGATTCTUGGAGTGAAATUCGGGAAG	52057	CCACTTCGGGUCATTTCAAACAAUT
332325208	52058	GCAGGAGGUGAAATGCAAAUGT	52059	CGGGTUCTTGTATGAUGGGAGAG
315367999	52060	CCCAGGTGCUTCTTCAGAAAGTAUT	52061	CCATTCGATUGCAAACTATTTAGACTTUT
323480265	52062	ACAGUTGACTGCUGGAGGAAG	52063	CACACAATGGAUCTGTGAACTTGUAGAT
316084246	52064	AGGAATCUGGTGGACAGUAACAAAC	52065	ACACTTGUGGCAGCCTCTUC
316026710	52066	GGACTTGTUGTTGGGCGTUC	52067	TGAGATCTCTTUAAGGCTCTATGTTCUT
268224658	52068	TCTATAAGGUGCGACATGTTGCAUT	52069	CATGGACAUGGTGTTCTTUGCAG
267929955	52070	CTTCACCAAACUCCTCCTCUACC	52071	ACGGCATAACAGGAAUTACTAACACAUT
269083997	52072	CATATTCCACAAUAGGGCCCTCTAUC	52073	TTTGTTCAGAAUGGTCCAATGGCUA
292085560	52074	CACTAGGCATCUCAATTTTTCTGACUCT	52075	TGTGATTTTTGGAAAUGTTGGTTGTUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318084297	52076	TGAAGCTCATCAUCAAATATGGCAUGA	52077	CACTTTAUTTACAACAGCUCCAAGACAG
289465955	52078	TTCATGAACACTUTAATGTGTTTTCCUC	52079	ACCTAGACCAAUGATAGCTTTTGTTUGT
223558752	52080	ATTGCTTCTUGCTGATCTUGACAAAG	52081	TGTACTGCCAAGUTACTTACATTTUCAGT
224525490	52082	AGTCAGTAATGCAUGTGGAACTTUGT	52083	CAAGCTUGAGCCAGGAGACAUAA
222756111	52084	GCCTACCAATTAUAGTGAACGTTACUCT	52085	GCTTTGTCCAGAUGAACTCTTUGAGAA
222815524	52086	TTGATGATGAUGATGTTGACCTTUCCA	52087	GGGAAAAGTGGAUTGTTTCTGAAGUA
327385898	52088	CACTCACATTCUCCTTCTGGACUC	52089	GATGACTCCUCACTACTGCTCUCT
327714086	52090	CCAGCCAGACAGCAUCUGA	52091	ACTTGAAGGCUGGGTCCUG
324994415	52092	CTTTTTGTAGUCAAAGCGAUGAGACT	52093	TCTTTCAGCTCCUACTACCACTTCATUA
332036992	52094	AGGGUCCTTGGCUGGGT	52095	CCCTCCUCCTGCAUGCT
236182186	52096	AACAATTTTGGCCUGTGGACTCUA	52097	AAGUTCTGACUGAGCCAAGGG
238549363	52098	GCTGGGUCAAAGATCCTUGCAT	52099	AGAAATGATTUCTTACCTTCUGAGCACA
269283317	52100	GGGTTGCUTGCCTUACAGAAA	52101	CGTGGCTUTGGGAACTUGGAT
268996568	52102	TCAGGACAAAAAUAAGGAGAUCGAGAGA	52103	CCGGUAGCCACTGGTAUCCT
331906760	52104	GTCCCTGUCCTTGTACUGCAC	52105	TCACCTTCTCUGTCCCCTCUT
331648140	52106	CCCCTGTGCAUCCTTGTACUG	52107	ACCTGGCUGGATCTCCTUGT
331829649	52108	GTCCATCCCUGTCCCTGUACT	52109	TTCCTATGUGGGATTTGGCTUCC
331559281	52110	GCAGATUCCCTCTCTAGUCCAGAT	52111	AGCCTAUGACCAGAGAGGACUG
261160974	52112	AGCCCTCUGAGTCCACGUAA	52113	CTGTCCTGGUGCCGTAGAUG
260241824	52114	AGGACACGGUAAAGCTGCUG	52115	CCCTCTTATGAGUTCCCCCATUT
323617314	52116	TCTTTCCTGGUCATTTTGTCATCAUCA	52117	CTGTGTTCACAGUGTGGTTTGATTUA
324164040	52118	GGGAGGAAGAUCCATCCCAUCT	52119	GCTCTTGACAAUCGTCTCCTUCT
314101438	52120	ACTTATAGCAUGACACCAGGCCUA	52121	TTCAGGTGCUTGATGATATUGAGAAGT
314884362	52122	TCTATTTCCUGCTTGUGCCACAT	52123	TCTGGGCTCACUTAATAGAGAAAATGTUT
314750130	52124	AGGTTTAATTTACUCACCTTGGUGCAA	52125	TGGAUACCATAUGCAGGAAGCAG
314378674	52126	GGATGGTTCUGGAGGAAAAATGTATGUA	52127	GAGCAGTTATUCCAGTTCTTGCAAAUT
271272952	52128	CATCCACAGUGGGTCTCUCC	52129	TGGTCCCACUTACAACUGAACAAAAA
270767888	52130	CAAAAUCUCAAGCAGAAGCAACCT	52131	CTTACCTGGCUTTCATTCCTCUGA
271354238	52132	CTATUGAAGAACCAGUCACAGCCT	52133	GGGTTCCTTACUAAATGAGCACTATUGT
271373443	52134	CATGTCTTUAACCTCTAACTUCCAAGGG	52135	TCTCCACAGAAUTTCCGTCTCTAUCA
317921097	52136	AGTCUTGCTTGACAUACAGCAGAA	52137	TCCACAGATTUCAGTTGTGTTCGTUAT
317862576	52138	GTAGACCGTUCTTGTTCGTCUGA	52139	CCAGCCAAAAUGGTGAAACTGAUG
317626313	52140	GGTTGTGGAUGCCATTCTUCCA	52141	TGTAAAATACAGCUACCCGAAAAUGACT
267101951	52142	TTGTCAAAGAGAUCAGCATAAUCAGCA	52143	TTTGGTGACGUGGATGATACTTTCUAAT
258797559	52144	CAGGAGAGAAAAAGGUGCAAAGUT	52145	CGCTCATAGACUGCTCTCTCTUT
269059371	52146	TCAATTGGGCCUCTTGGCTUT	52147	GAAGGAGCAAGUTGGCATAAAGAUT
256934683	52148	CCGCGACUGUCGAGGAT	52149	AGGTUCCAGAGAGUCAGGAAGT
323755191	52150	AACGCUAAACAGAAAGAGCUGAGA	52151	CCTCTTGCTTUGCCAAACATTTATCUT
325149951	52152	CTTGAGAGAAATGUCAAAGAAGTGGUG	52153	AAACCAACUCCAGCTTGTTCAAAAUAAA
320691598	52154	GGGAAATAUGGACAGAAGAAAAUCAGA	52155	CAACCGTCAAACAACUTTACACATGUAT
267960533	52156	ACTCTCCCTTUGAAGAATTACCTTGGUA	52157	ACTTTGTTGAUGACATTCACCACUCT
262222801	52158	AGCTTTTCUGTGTTCCTTTUCAGGT	52159	ATCAGAACTAGAACGUTAAATGGCGUAA
267985095	52160	ACAAAATTTGTGCUTGATGGGTATAUGG	52161	CCTGCGACGGAAAUTTCACUG
267879903	52162	ACAAGAACTTUCGCCTTATCCTUCA	52163	GTGTTGGTGGUGACGTAAACATTTTUA
257372861	52164	CTGTTUGAGAAGGACAAGCUCAC	52165	AAAUTCCCCTCAUGCCACCAA
265812066	52166	GTATCGTTCACACCAUTCCTACTTGUT	52167	GTAATTTTTCTTUTTCTGGACACUCGGA
267651746	52168	CGAAGTATGUGGAGAGGACCAGAUT	52169	AGAUCACTGTGAACUGAAAAGAAGGG
313043904	52170	CCTGAAGTCAUGCTTCATCTTGAAUG	52171	TTGAGAAGATGUGTTACTCGCTUGA
313439476	52172	CCTTAGGTTTAUGATGCTGCAGUCAG	52173	CTGGCTACAUGATCAGGTTATAAAUGGT
327464073	52174	ACTTGTTUTACATGTGAUCCCACGA	52175	GGCCACTGUATTTAAACACAUAGAGGAT
327076304	52176	AACCAGUTGTAUGGCAGCGA	52177	TGTTTCCTGTTUTGCTTTTCTGATUGT
258849605	52178	TCUCCCACAGGGAACGUGAT	52179	CGCTUCCGCACCUCCAG
260642574	52180	ACTCCCTGUCCTCCAGCTUAG	52181	GAAGCTGGGCUGAAGGACUAAA
231235909	52182	TGGGCAGGACACCUCCTUA	52183	CTCCGCCUAACTCCCTCAUC
224486019	52184	GCTTGCCTTCUCAAAGTAAAAGATGAUT	52185	CCATGAGTTCUGTTGTATCCTTTUCAAC
223488432	52186	TGAGTGAUCAAGAATGTGUGAAGAGAAAT	52187	TTCTTCATUAGCGGTTTCTACTUGCT
332386087	52188	ATTACAAAGAUGCAACUGCAAAGAGAAG	52189	TCTGGCTGAGUTTCAAGTGUGAAAA
223789797	52190	GAAGAAAGCAUGGGATAUAAGGGAGAA	52191	CTGGCCAGTUAATTTCTGTAGTTGUAAAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
223655430	52192	CAAGTACTTCUTGTGGCTCATUGAC	52193	GCAGAAATGAUAAGCATGCACTAATUCT
318212758	52194	TCTCUGCAAAACCCATATUCCAACT	52195	GCCCAATUGGAGGCCTUACAT
266332278	52196	CCTACTTGCACAUAGAAAGGTCUGA	52197	AAGTTAGCAAUACGTAAGACACCTUACC
267290512	52198	CAGATATGCTGUTTCATTATTTGCUGGT	52199	TCCCCATACUCCACCTTTGTTTUC
324498891	52200	CATCTGCAAUAAAGACAGAGUCCAAAAC	52201	TCCAGCAAATGUCTCACAAAGGUA
263124388	52202	CAATTTTGGAUGACCTTCUGCCT	52203	ACAGGACTUCAACCCTCAATCAAAUAAA
262760168	52204	TCTTGCTGUGCAGCATCUGAAT	52205	GGGTCCTGCACAGUATTTTGTCTTTUA
257387351	52206	GGGTCCCUCGCCAAUACAG	52207	CGACCUCACGGGCTATTUAAAGG
268092868	52208	GCAGGAGUGCTATTTAGCAUCGAG	52209	CACCCCATUCCCAGCTTTTCTAUT
263161412	52210	TGGAACCUGCCUGAGGACA	52211	TCTTCCAGCCCUGGACUCT
315266090	52212	GTCCGAGCCGUGTCUGT	52213	CCATGGCCUCTTCGCCUG
313952758	52214	GCCGTCGUTGCAGTAGAUGA	52215	GCTGTGTGAGUGGAGAATGUGG
321442983	52216	CGCTAAAAACUACTTACAAAAAGCUGGA	52217	TTTTCTCGAAAGCCUCCTAACAACUT
332319486	52218	CUTGACCUGCGAGGGAGA	52219	CCGCCCUGGAGGUAGGA
332421760	52220	CACCTTTTACTUGGACATGAAGCAUT	52221	CTGAGAGAUGGGCAUCAGAAGG
317389730	52222	GCTAAAGUCCCCGGAGACTUC	52223	GGTTUAACAGAAGGAAUCAACACAGAAA
317391455	52224	AGCCGCGUGGACATUCA	52225	GCTGCUGTTCATCCUACCCA
317153615	52226	CACAGGGUCACTCTTGAGAUGG	52227	CCAAGGACAUGCTCCCACTUG
330151403	52228	AGTTCCAGGTTUGTGCATTTATGTAUGA	52229	CCATGACAGCAACAUTATCTCTTCTTUCT
262566121	52230	TGAAGATTUGCGCCCTUACGA	52231	TCTTTGGACACAAUTCTTCATTAGCTUGA
266423713	52232	AAATCCTTTTAUTGCCACCUCAGGA	52233	GTCTGGCUCCGAGAACUAAAGT
263776241	52234	GCCTGGAUAAAGCTGTGCUACA	52235	AGGTCGAAAAATAAUCAAAGGCTGAGUA
254141710	52236	GCTGTUCCCAAACAACTAGACATUG	52237	TCCGGGAGAAGGAAUGTTTCTUG
316632653	52238	CCAAAAUGAACAAGCACGAGCAUT	52239	TCAGGAAGTAGTUCATCATGTGCTTTUA
313920221	52240	ATTCCAAACACACCAGUATTTCCTCUT	52241	CTGCCTAGTCUGGATTTTTCTCTUAAGT
316445667	52242	AAGACCACAGUGTTGCATAAUGT	52243	GGCAGATCAAUTTTCGGCTTTTUGA
259429420	52244	TCTTTTCACAGGGCUCGCTTUA	52245	CAGGATTTTGATUCTCCTTGCCTUAAAA
263543861	52246	CTTCTCCACAUCATCTACCAAUCACA	52247	GAAAGAGAUCAGGCAACAGTGATTCUA
266833813	52248	AGCTGTCUGGGTAAAGATUGCAC	52249	GGCAGAGCUGTAGGAACUAACAC
264532244	52250	CTGGGCTAUGGCACTGUGA	52251	GTAGGGACUCAGTGAAGUCAGGA
317502144	52252	GGAGCAGCAUGTGGACUCT	52253	CCCGGCGCGGAUACTUA
319835505	52254	CACAGGCAAGAAUAATTAACTCAGCUC	52255	GAAACAGAGGUAGUCCAGCACAT
298439996	52256	TAGGACCAGAUGTCTGAGUCGAT	52257	GAGUACCTAUCCAGCCACCAC
316417175	52258	ACACAGGACAAAAUAACGUGAGCAT	52259	GAAAAAGCCAUTGGCCACCUC
240572887	52260	ACAAGGACUGGGAGTGAAGAUACT	52261	CCAGGUTCUCAGCGGAAGAC
266962722	52262	CGTCCAUACCCGCUGGAAA	52263	GUGCATUCCACAGGCCAAG
267314616	52264	CTGGGATTTCUGCCCGAGUT	52265	GGTCUCAAAGGCCGAGAUGG
267449544	52266	GACACGAAUGAACCTCCTTUCCT	52267	CTTTCUGAGGCCAACCTGUCT
269257630	52268	GCCACGTTUGACCTGAGATCUT	52269	CCUGTCCTTTAAATUCACCACCCT
269334746	52270	TCCATGGUCAATGACCTUCGAAAA	52271	GUGAGAACCCCACAGTUACCT
267111778	52272	CCGTACUAGCGGCTCATGUT	52273	CAAACAACCGCAAAUCUGCCA
257536378	52274	GGTCTCAGUCAGGTTGCUGAT	52275	TGGGAGUTCAUCACAAAGAACCA
268461921	52276	CGGCAUGGAAGAGATCTUCGG	52277	CTGAACUGTCCTUGCCACACT
333370253	52278	AGGGACAGTGUTGTTTTGCTCUT	52279	TCAAGGTGAAACAUCATGCTGTUAGA
332552332	52280	GCATACACTTCUATCCCCTTTGATUAGA	52281	CGGGAGAGGAGAGUTTAAAAAGCTUAA
333366118	52282	AGCTAGGTTAGACUTCATTTCAGCTTUT	52283	CTTGACTGGTUCCACACTAGGTUC
264857009	52284	GCCTTGGCUTGGTCCCUAAAC	52285	TCACUGAGACGGCGGAAAUT
321157382	52286	GTGAATTTTCTUGCAGACTTCAGTTUGT	52287	CTGTGTCACAACUTGTTTCCTTACATUT
318328749	52288	TCTTGAAGAATAUCCAGCACAGTCATUT	52289	GUGGAAGAAGAAGCCAAUGCC
318636198	52290	CACACCAAGGAACAUACCTGTAGATTUAA	52291	CGTAACCATCTUCTTTTCCTCTCTTUCT
318694875	52292	CATACTCCCUGAAAATAGTTUCGGACAT	52293	TGATTGCCGUCCACTCACTTAUC
265278632	52294	CAAACTCAAGUCCCTCCTCTCUT	52295	TCAGAGCCUGAGATGCCUACT
260977353	52296	CTCCTGCAACCUGTCTGTGUT	52297	TGGACCUCCCACAATTTGTGUG
254585098	52298	GGAATTCATUCCCTACTTGGTCUGG	52299	TCGTTGUCCGTGCAGTUCA
259153727	52300	GCCTACAACGUGCCCCAUT	52301	AGGCAUAAGGGAGGTCCUCAG
266706191	52302	GUAATGCCACCAUCGACAGAGAG	52303	CGTGGTCAAUGGCCGUGAT
324145309	52304	GGGTCAGUTTCCCUACCAGAGT	52305	ACUATACCTTTTUGCCAGCACCA
312812365	52306	AGCGCCUCTCCCGTCUA	52307	CCTCAGCAUCTCCCTCCUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
313347138	52308	TGACAGAUGATAGCTTCUCCCAGAA	52309	GCTGGACCAUACCGGAUGAC
254259110	52310	CACATAGGUAACGAGTCAGAGCUT	52311	CAGAUGTGGAUCAGCAAACAGG
320119938	52312	CCCTCCCAUAAGACCAGGAGAUT	52313	CTCCTCAUACTCCTGCAUGCT
332465779	52314	AATGTGTCTUCCAGCACTGAUGT	52315	TTCCAAGATGUCTTCTTCCATGUCC
314224846	52316	TGGCAAGGUGAGCATGTUCT	52317	CAGACCCCUCTCTGACCTCUC
312688273	52318	CTCTGCCCGUCCTTCTUGAA	52319	GTTTGAGUGTGAAGTAUCGGAGGAG
313350498	52320	CTGATGGUCAGGGTACGCUT	52321	AGCAAGTAAGUTCCCCTCUGGAT
324143967	52322	GCTGTTCTUCTCGCCTAUGGA	52323	ACTTTGTTCTCAUCCCCCACUG
326415145	52324	CTCAUGGCCCGGTACTUCAG	52325	CCCTACCTGCUGTTAGAGAAACCUA
324793672	52326	GTTGAACCCAUCCUGGAGGT	52327	AGTAACAGGUCCUGGGCAGAA
265446477	52328	CTGCAGUCCCATGAUCACCAT	52329	AGACTUGAAGGCGUCCACAG
268004438	52330	CCAUCGGCGGATGTGUAGG	52331	CCTGGTGGGCUACTACATCUT
313236816	52332	ACTCUCAGCCTCUGGACACA	52333	CCTGCTUGAGCGGTUCCC
312810287	52334	TGCCCCUGCTGCCTTUT	52335	CAGACCUAGAAGCCGGUGAC
327698456	52336	TGCAGACCUTGTGAGGACUAGA	52337	CAAGUGGTGCATUGGACAGAAG
328752297	52338	TTCTCAGACUGACGGATTAAATUCCAAAT	52339	AGTGTTGGACUTGGTTGTCTCTUT
329461826	52340	AGGATTTCGUAATATTGCCGUCAAAGAA	52341	TTCTGATAGTTUGAAAGGAATAGTUGCAT
222802821	52342	GCTTTTGGTCTUCTAAGTGAAGCTUT	52343	GCAGCTACUACCCAGCTAAAATTAUCAT
328553750	52344	CTGGCTTTTUCCTGCGATTGTUA	52345	CCTGGCCTTAAUTTCCACATTTGUAAAA
329146211	52346	TGCTTTUAAAGGAGCTTCCUGGAG	52347	TTTACAAACATCTUGGTCACGACGAUA
222424844	52348	GCTTCAGCAAACAGCUTTTGAAAAUG	52349	CAGTTGTTTUAGAGCAGCTTTATACUGT
223202554	52350	ACGTTTAGAAGACUTTATGGCATCUCAT	52351	GTATGTGUGTTGCTGGUGAGG
224477897	52352	TGCTCAGUGTTGGUGGACAAG	52353	CCCTACTTAAAGUATGTTGGCAGGTUAA
333180443	52354	GACCACGGCUTCCUCGAAT	52355	GGTCCAGCCUTACCTTGGUG
333168775	52356	GTTCCCTCCUACACTGTTCCCUA	52357	CCUCACAGCUCCAGGAAGGA
333650700	52358	GCTCCUGGCATCTCCUGAAG	52359	CCTTCCCCAGGAAUGCTGAUG
333112449	52360	CTCCTTCUCCTCCTCTCUCAGG	52361	CAGTACUGGCCCTTGAATGUCA
333431169	52362	GTUCGGCAACCACGUCAG	52363	CCCAGGGCGGUGTTGUT
319798464	52364	CCCACCGCGGUAGTACUC	52365	TCGTGCCGUCATCAGTTCUC
264890294	52366	CAGGCTCUCAGCAGGTGTUT	52367	GGCTGCAUACGCCAUCAC
314511384	52368	GTCCGAGCCAUGCGUCT	52369	CCCTGUTCGCTCUGCAC
313554698	52370	GAGAGGGTGCUGGGAAAGAAUC	52371	GAGTACTGCUCAATGACGTCCUT
264610153	52372	GTTTGTGAGAGACUCAGGAGAUACC	52373	AAACAUCACCCAGCTGTUCCA
254228995	52374	CCAGTGTUCTCTTTGCUCCCAT	52375	TGTCAGTCAUCCCATCCATCUGT
253948540	52376	CACAGGAGGUCAGACAGGAUG	52377	AGCTGCCTTAAAAUAACCTGAAGACTUT
267014510	52378	CTGGCACAGCUAGGGTTUACAT	52379	ACAGAGTTATTGAUGGTGCTACAATGUC
268886885	52380	CAGTTTTCAUCCACAGAAGCGTUA	52381	TTCTCTCTCTCCCUCCTTTTATACCUC
285945847	52382	ACCACCAGAUGTGAAATTACAGUAAACT	52383	CATCTAATGCATUCAACAATGATGTCAAUGA
285945377	52384	GCTTCTAATAAACAAUTGGAATCACTUGCT	52385	GGTCCUCAAGGTATCUCAGGGAAA
265725259	52386	CACTTACAGUCTCCCCACGUT	52387	CAACAGAAGAGCAAAGUAAAATAGCTAAUGG
266956643	52388	TTACTTTTUCACCAGGAGGACCAAUT	52389	AGCAGCTTGUGTAAAACTCCUCAT
268583898	52390	CATACCATGTUCCCTTTTGGUCCT	52391	GTATAGGTCTTGUCTCTTCTTCGTTUCC
269266422	52392	AAAGTAAGTUGCTTACAGCTUCACCT	52393	GGTGATGATGGAAUGAGGGTATGTUAAT
263904662	52394	AAAGAACTTACACUGATACCACATGUGT	52395	GGGTCUGCCAGGUGACAA
266363885	52396	CACCAGCUCCTCTGAACAAAUG	52397	GGGTTATATTTCCCUGGTAGAGATGUT
314804406	52398	GACTCCGAGCAGUCTCTGUC	52399	GUAGACCGCCAAGCGAUCAT
325202046	52400	AACTGAGAAUGGCTTTTCAUACCCT	52401	GAGGGCTCCUGAAAGCACUAA
318157466	52402	CCTCAGGUCCCAATGGTTCUG	52403	AGCAACTATCUGAGTCCCTTCAUCT
315827422	52404	CAGAGACCUCGGCCATTTTUGA	52405	TGGACAAAGCCAAUCACTGCUAT
326948126	52406	GTGTTAAUGACCACAGACTCUCCAC	52407	GTTTTGAAGUGTGCAGCTGUCA
328121409	52408	TCACTTCUCGGCTCGGTGUA	52409	TGGAAGGAAAUCCTGTATTTTGUGAAGA
326460882	52410	CAACTGCCAAAUTCCTAATUGCACAA	52411	ACACAGCUTGCCCATUACAGT
326494470	52412	GGACCCCUGGTTTTGTCTTGUAA	52413	GATAGGAAAGCAGUTAGCAATGATTCTUC
327864450	52414	CACCAGCACUGAACCAGAGUT	52415	GTCACAGGCCAGUGTTTCTGUA
333461704	52416	TGCTTGTUACACATTTGCTUCCC	52417	TTTCAAAAATCCAAUCTGACTCCTGUCT
323574558	52418	CCAAAUCAGCAACGTTAAGTTUGCAT	52419	GGCCCTCTAAUTGAAGTGGAGUT
323590711	52420	GAGAATTCAAATTUCTTCCTCCACCUG	52421	AGTGATUGCCATTCGAGUGGAT
325373506	52422	CTCAGTGAGAAUCTTTCCUGGACAA	52423	GGAAAAGGAATAGCUAGGTTCACCAAUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324065689	52424	TUCACUCACACCCGAAACCA	52425	GTAACCCAGATGUGGCTATTACTGUT
323682244	52426	ACCTTCTAGAUGCTTCTTCCUGCT	52427	AATTTCCGUGCCACTTCCTTTUC
326502962	52428	TGCTACTTTCCUCCTTTTGCTAAAGUT	52429	CTTGGTTCTTTUGTTTTGGCAACUG
327595942	52430	TTTAATCTACTACUGAAAAGACAAAUGAGACAT	52431	ACCUGTTTACAGACUAGACCACACA
332876097	52432	CACTCCTATTAACUCACACTCCTUGT	52433	GGATGGGAAGCUGCTGTUGAG
321394286	52434	CACTAGAAAACCCUGTGCACCUT	52435	AAAAAUGGGACAGAAAAGAGACUGGT
332335364	52436	TGCTTTTGATTUCTGCAGGATUAGGT	52437	TCTTCTCTTTGAGUGACAGCTGTTUT
333197793	52438	TTTTCTGAGCCUCTGCCAACUT	52439	CCATTCATCTTCUCTTTTCCATGTGTTUT
332833536	52440	GTTGTTACCACAAAAUGAAAGGCUCA	52441	CTTTGGCACAGAGUTTCTTATTUCCT
329967168	52442	GTCTACTGTTCUAGAAGGCAAAUCACAT	52443	GGAAAATTTGGUGTAGTGGAAACUAGGA
318986715	52444	AGATTCCUCAGCAGCGAGAUG	52445	TCTTCATCAACCUCTGGTAATCUACAGA
312671677	52446	TGTTTTGGCUGGAAGCCTGTUA	52447	CATAAGGAGAUTATTTAGUGCCCAGCAT
313243210	52448	CTAGAAAAATUCCAGATTGCTTUGCCAA	52449	CAGTAGGAGGUTTACACUAGAAGCAAAA
279511781	52450	TGTGAATTCAGTUCCAAGGTATTTGUGT	52451	AGTATTTTTCCGGUTGTAGCCCAAUA
261376128	52452	GCAATGCTGUTCTTGCAGUGG	52453	AGGTCCTUGAACCATGAACTCTUG
267336843	52454	CTTGAAATCCTUGAGGCCCCUA	52455	TGTGTAGTAAACCCCUCATTTTCTGTUC
317462027	52456	CATATGCAUGTATACACUCACCCACA	52457	TCCCCATACCUTCCCAATTUGAAC
320423263	52458	CCATTCCACUTACCAGGTUGGG	52459	AGTCATTACTUACAATGCGCAUAACAGA
319557445	52460	GGAGTAGGAAAGUTTCAAAGACCUGA	52461	CAAGTACTAGGUTGGTTCTGTGGUT
319678362	52462	AGAACAUGGAAGTTTGCUACGACAT	52463	CAGGAATGAAUTGCTAAACTGUGGAAAA
313803347	52464	AGAAAGGAAAGCAGGUGTUGGT	52465	CATGUAAGCCCTGTGTUCCGT
265648399	52466	CCCCGAACUGGATTCTGUACT	52467	GGTACCTTGAUGAGCTAAAGAATTCCUAA
326751580	52468	TGAAACTCTUAGGCTGCAGCUT	52469	CTTTCCTGAGACUGCGTTTAUAGCA
262539419	52470	TCTTGGACTTGUAACATCTAATGGACTUC	52471	TGGCTAGAUTCTTCTUGGGCAAAA
332732494	52472	GATTCTGUCCGTCTCAGCUGAA	52473	CCTGTCAGACUGCTTTCTTTAUGGT
332468608	52474	CTGGGTCUCCTTTGTCACCUT	52475	TGTGGAUCACAAGGCTTTGTUCT
332459977	52476	AGCUCAGGAGAGTCUCGGAAA	52477	GUCGGAGAGAAAGGUGAACCC
333222687	52478	GATCTGAGTTUGTGGGTTACTUGT	52479	CACCAGGCUTACCAGGGAUG
320550392	52480	GTGTATAAACTCUCCAGGTTGCCUT	52481	GCCCATCTAUCCTGACCTGUAGAC
313462483	52482	CCGCCGCAUCTTCUGGAA	52483	CUTTGTGTCUGACCCAGGCA
314356280	52484	AGCAUACCCAAGGCAACUGT	52485	ACTGCAGCUGGAAGAAAAGCTUAA
312861903	52486	CCAGTCCCUGGTTGUGAGAT	52487	CCACCAUGAAGGAAGAGTUCGG
312847569	52488	ACGACTACGUAGCCCTAGCUT	52489	CCTGTTGATUATTTCTCCTCUCGCT
315459531	52490	TGTTCACUCCAGCTGGCTCUA	52491	GGTGCUTTTCAACCUCAAGGAG
313723167	52492	CCTCCAAGGAGGAUGGCUCT	52493	TCCUCGCUGGAGAAGACCAA
315275331	52494	ATCAGTTCCUGTAATGCTGUGAACA	52495	CTTACCTCACCAUCCCTCCTUC
313541814	52496	GGAGCGAGUGAGTGATTGTUCT	52497	CAATATGGGUCTCTCCUCCACCT
327171849	52498	AGCTGCAAGGUCTGGAACAUT	52499	ACTTTATGCTGGUACTCACGCUT
328080766	52500	GGAUATGTTATTGUCGGCACCAAAG	52501	ACTATCACCUTCAATGACATUCACAGAA
318217950	52502	CCUTCUCGGAGGAGGCAGAT	52503	TCACACAGUCAGAACUCAGAGGA
317720180	52504	GAACTAGGGUAGTCACCTGUACCT	52505	GTGAACTGGGUGATAATCTGAAGAUGAA
317715191	52506	ATTCGATCAAGUATCTGTTGTGATUCGT	52507	GAGAGCTAAGUGGCATATGTACATTGUA
317405737	52508	CTCTGCUAGGACAGGTAATTTUGAGT	52509	AACAGTTCAGUGGAGGAUGCC
317130385	52510	AGACTTGTAAUCAACCAATTGTUCCCA	52511	TGTTTTGGACACAUTCCTGGTTUCT
316003221	52512	AGGTACAGACAAAACUTCCAGGAGUA	52513	GCAAAGTAGAUACAGGCAAAGTTUGG
315857658	52514	CCAGUCCAGGGAAGCATUCAC	52515	CCTATCTTCCCCAUTTTCAAGGGTUA
316354258	52516	CCCTGGTUGTTAATACACUCACCAC	52517	AATGGCTAAUGACATATTGTAGUGGAAA
326789697	52518	CCCGTGTGUTGTGTGTGTCUA	52519	GCTGTCCUCCGCCTTGUG
333725575	52520	CCACTTTGAUAGCGGTGUCCA	52521	GTCACGGACACCUGCAUGA
321197685	52522	GGACACAGGGCACCUTAUAAACT	52523	TGUAAAACCCCTUCCAACCCAAC
319137988	52524	CCAGGUAGCGAACCTCGUC	52525	GCTTCTACCCUGGAGTTAATUGGT
321589186	52526	GTAGGGCAGGCUCTGCTUC	52527	GGCUGCACGAGCAAATCTUC
240819712	52528	ATGUCCGAACGAGGTGGUG	52529	CCCAAGGUACCATCTTCUGAGT
321561028	52530	AGCUGGCUGGAGGAGGT	52531	GCAGCCGGACUGACUGA
319900999	52532	GTGACAGGUGCCAGGACUC	52533	GGCCATCCUGGTAGGUGACT
320082882	52534	CUCTGUCCGCCACACCAT	52535	ACCGGGUATGGGCTCUGA
318387781	52536	ACCAAAGAAAUGGATGACTTCCUACAAA	52537	GCCTATGATACUTGGCAACAATAUCCT
257621923	52538	GCTACCCUCCAGACUCAAGGT	52539	CTTATTGACCCUGACCTGTCTUCC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
239276738	52540	AGCAGTUCCACTTACGUGCAT	52541	AGCATGGAGAAGCUTTAGAAUGGG
266199553	52542	GGGACACACCUGCUGGAA	52543	CUCCACCGAGCTCUCCAC
262477371	52544	GGCCTTCUCCCTGACACATAUT	52545	ACAGGAAAGAUGGGUGGCAAG
261728381	52546	CAGCCGTTCTUGAGATTTCCTTATUC	52547	CTGGCTGCUGATGGATUACCT
262804669	52548	GGCACAUAAGAACCTGGUAGCC	52549	GTGGUTCCAGCTTAUGAAGAAGAGA
327101725	52550	ACGATTTTTAGUCTGCATTGCTTUGG	52551	TGCTCAGCTGCUTCTTTAAACAGAUA
318250571	52552	GTTGTTGCCCUTGTCTGTGTUC	52553	TGGCGAGAAGACCAUTATCAUCAC
320271054	52554	CTACAUGCCCACCTAGTUGGA	52555	TGAAGGACACACCCCUCTAUACAG
268124648	52556	CACTCCGAACUGGCCAUCAAT	52557	GGTATAGAAACCCUGCGAGUCC
265254729	52558	AGTGGTGGCUGTAGCCTCTAAUA	52559	CTCCAUCAAAGAACACCTCUGCT
263767242	52560	CCAGACGGAAACCGUAGCUG	52561	CCCGGACGAUATTGAACAATGGUT
264814045	52562	CCTAAACUGGCCCCACAUGA	52563	CTCCCATATCUCAGAGGCCCAUAT
266502612	52564	CCCACCTACUCTACCACTCUCT	52565	CAGTAAGGCUGTCAGTGGTUGA
265764716	52566	CAGCACAAGGUTGTGTGTUGA	52567	CCACCACGUATTTGCTTCCUAACT
323699035	52568	GCGGCGUCTACCTGGUG	52569	CCCGAGACUGCAGACACAUT
235101719	52570	TGGACAGTCUACGAAAAGCTCTUG	52571	GGACTGAACAAGUAGGAAAAUGACAGA
236390839	52572	GCAGATACACCUGTCAGCAAAUT	52573	GAGAACACTTUACCTGTCCTUGGG
239102154	52574	GGTGTGUGTGTGGCTUCAAAAAC	52575	AGACATTTTACAUCATCATCTGCUGCT
332841014	52576	GTTTTCTGCCCCAUGCAATAGUC	52577	TGAGUGGCAGCAGACAUACAC
312731535	52578	CCCAGUTCCTCCUGAGAACAA	52579	GGCUCAAAGCACGGCUAAG
313156360	52580	GUATGTTAAGUCCACAGAACCACAGA	52581	CAGCAUCCAACCCACCCUAC
226706669	52582	GCCTTCTUGAGGTTGCCAGUC	52583	AGGACTAGAGGUTCCCGCAUA
226423407	52584	TGTCAGGCGGAAGUTCCATUG	52585	GCCAAGAGCUCATGCTTTCCUT
253781331	52586	GCTUAGGCAAGGCCACAAUG	52587	CCTATCTCTGGCCUGACTCTTTCUT
226129532	52588	TCTGGACUCTGAGGUCCCAAA	52589	CCTCACTCUGACTTCTCTTGTTUGT
329246933	52590	AGAGTGCAACGCUTACCCUT	52591	GCTCUAACGCGCGTCTCTUC
254012826	52592	ACTCUCAGCCCACCTTCTCUC	52593	GGACAGTCCACGUTTGCTTCTUA
266205722	52594	CCAUACCAGGCCAAACAGTUG	52595	GACCTAUGAAGGGCCTGGACUA
327151160	52596	CGGAGGAAGUCGGUGAAGAAC	52597	CGGGACGGAGAUAGCTTGUC
258611089	52598	GGGCCAGUTAAUCAGACACACA	52599	CGGAAGAGGCUACGTTCTTCUC
262778540	52600	ATGCTGAGAAGGGUATAAATGCAGUT	52601	TTCAATTGCAGCUTCCGCTUG
262898015	52602	GGGTGGCGUCAACTTGTAUCAA	52603	GGCCAAGUACTGAGCCUCAA
256801008	52604	GAUGGTCAAGGUGACACAGGA	52605	GCTTTUAAGGCTGCGUGCAA
262731891	52606	TCTTCCCTGUCCGCCAAGUA	52607	GCTGCTCACATUTCTTTGTGTTTCTUC
262137042	52608	TCCAAGCAGUCCCTAGUGCT	52609	GACAAACACAATUCCGGATCTCTUC
317469829	52610	CGACGGUACTGCCUCAAGT	52611	CAGTCCTUGAAGGCCAGCUT
316609309	52612	GUAGCACUCAAAGCCAGCAAC	52613	TGACTAGCAAGUATGACTCCAUGACA
331113069	52614	GATATACUGCCCTGTGCUCAGAA	52615	GACTTAUAGCCAGTAATGUCACCGA
331394083	52616	CATGCAGGUACTGACTGAUGGA	52617	ACCTCCUGGCACCCTCTTAUT
330270456	52618	GAGAAAAACCACAGAUAAGCGCAUAC	52619	GGTATAACCTTUGTTTCCCTCTGUCC
269338995	52620	CCACAAACUCCCUGAGCAGAA	52621	AAAAGGCATTAUCCGCTTGATGTUG
269378440	52622	GCTGTGCTCAUGGCTGATCUT	52623	TCCCAACAUGACACTTAACATATTUCCA
257676222	52624	GAAUGAATTAGCAGTUCAAAACCAGCAT	52625	GCGTGAUCACCACAACATCAUC
268674906	52626	CAGAGGGCUCCGTUCCA	52627	GAUGAGAGGCAGGCGCUT
268767340	52628	CTTGAAAGAGCTGUAGATGTTAGAGGUT	52629	CTTTACAGTGUATGTGCCATTTUGAACA
313918070	52630	TGATTGCTTUCAGGTGCAGCUA	52631	ACACACGUCACTGCTCCUAGA
268959677	52632	GGCACUGACCTGGACTTUGA	52633	GGCAGCCUTCGGCTUCT
268087477	52634	CCTCCAGACAUCGAGUACCAGAT	52635	TGACTUGGAACCAAGGATGCUG
266588928	52636	CCTGATTUACCCACAACCCUAACT	52637	GGGTTTCCAGGUTAGCTCGATTTTUA
320908469	52638	AAAGACUGAGGAAATCAUGAAGGAAGG	52639	CAAGTAGGCCAUTTTACAAACAAGCTUA
323735240	52640	GGTCATGAUGGAGGAGGGUAGAG	52641	CCUGGCACCGCAAGTCUA
323338038	52642	GCTGGCUGCCAUCGAAGAG	52643	GGTGCACCCGGUTTTCTUCA
325127543	52644	GAGCAGAGCAGUCACUGAGT	52645	CACTCCTUCGCCAAGTUCCAT
323360728	52646	CACUGCAGGAACCACTUCAGT	52647	CTTGTAACCGCGUAGCCATUC
326281703	52648	CAGCAUCCTTCCCAUCAGAACA	52649	GGGAGAUAAAGGGTCCAAUGAGG
325004829	52650	ACTGTCCUCTGTCCTCTUAGCC	52651	TCAGCUCTGGAAUCGGAGAGT
323682310	52652	CCAGTTGGUCCTGCACTUCA	52653	GCCTGACCAGCAAAGUGATATTUAAAGA
324123774	52654	GTGTCTUGGCGCATCUGAC	52655	GGGCGGAAACUAATTCAGUCAAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326121562	52656	CCAGGAATCCAUCAGCGACUT	52657	GAAGGGAUCAGGGATCACGAUG
324237764	52658	AGAGAATUGAGGCTCUCCAGGT	52659	CGCAGTTGAUCATTTCGTTCTCAUC
324248769	52660	CCGCAUCGAGCGCATCUA	52661	GCTGGACGAAAUGTGUACAAAAGG
323996229	52662	TGGCAGACCCACAGAUGAAUC	52663	GTGCTTTCCUCCAGGAAGUAGT
325455778	52664	CTGACCUGGCCCCAUCC	52665	GGGCUCACCGTCATCAUGT
323678203	52666	CCTGGAGGUAGGTAGCUGGAG	52667	TGACCCCCUGAATCCCGUAAT
324570399	52668	GCACAGCAUAGTTGTGTUGAGG	52669	ACTCUCCAGCCAAAGACCUAAGT
269370787	52670	GUCCCCAAGACCCUCCAC	52671	GGGCGTAGGUCATGGCAUA
327647478	52672	GTTTCAGCUTCGCCAUCAGG	52673	CGACAACGCUGAACUCACAGT
327322132	52674	GGGTCTCTUGTCACTTACAUCGAA	52675	GGGAGGUGGCUCAGGGA
317424093	52676	TGAGAUGCGGCACTCGAUT	52677	CAGAGCTUAAACCGAATGGAGUACA
316256503	52678	TACAGAAAAATUAGACAAAGGGCTCUCA	52679	GTCTCTTAGTGACUCCAGGATCTTUT
332992865	52680	AAGAGGCUTATUACCAGAGGGACA	52681	CCTACGAUGCAGAGCTCTCTTUT
333239591	52682	ACGUCCUCCGCCAGACT	52683	GGCUCGGAGGCGAAGAUG
324477316	52684	CCAGGATAUCTGGGCTUCGG	52685	CTTAGAUGCCCCAGGGAAAGUG
254247057	52686	CACAAGCAUAAGAAGCCTTTUGGAAA	52687	AGAGTCTGUGGAAGAGGUGGT
256204367	52688	GCTCACCUAAGCAGCGGUA	52689	CCCCTGCCUCAAGTAACAATTGAUT
256531256	52690	CCACCCUCTAGTCATGAUGGAGAT	52691	CATAGCGCUCCAGGTTGTAGUC
318765799	52692	GGGTGGGACGUTCACTGUA	52693	TGTGGATGUGTCGCTCTGUC
315764002	52694	TGAGGGAATTTGGUTCATGCTTATCTUT	52695	AGAGGCGAGAGAGUTTCUGAAGA
315545468	52696	TGAACCTACCAGAUGTATTTGGGTUG	52697	AGAGCCCTTTCUTGTGAATATGTCAUT
258972504	52698	GGGCAAAGACUGGAGTUAGCA	52699	GCCAACCUGTCCGUGGAG
316418701	52700	GGCTCAUGTATTCCCUGCAAGA	52701	GTTGTGCUTGTCCCCUAGCA
324260803	52702	CCCUGCTUACCCAAAGCC	52703	TGCTTGTTGAGUATTGAGATATGTGUGA
324818887	52704	GCAAAGCCAAAAUCACAAATTCGAAUAG	52705	TGCATTGCTUGACAGTTTGTGAAUAAAG
267724882	52706	TTCTCTGTTATCAUGTGGACTTTTCUGG	52707	CTGAGGATUCAGAAGCTGTTUACGA
258882969	52708	TGTCCTAAGACCUGCTCAGCUT	52709	GTCTCCTCCAGACUAGCATTTACTACUA
269207404	52710	TCGGUAAGTTCTGUCCAAGCC	52711	TGAAATTGGCTCUTTAGCTTGTGTTUC
269244915	52712	GCAAAAAGTTCCCUACCTTAACGUC	52713	GCTTGAAGACCUTGAAGAGCAGTUA
267644080	52714	GTTGUGAGAAAAACACTTUAGCAAGGA	52715	CTAGTATCCCACUTGAACCUGGAAAAG
265608736	52716	ACATGTGCCAATUTTTGTTCTCAATCUT	52717	CTGCATUGGAAACAAAGAGTGUGG
265995913	52718	TCTTCTTTTTCUGAAAGCCATGCACUA	52719	ATGTGTGAGAAACUAGCTGUAAAAGACA
268425214	52720	AGAAATCTCUCCTTGTGCTUGCAAT	52721	GCAAAGACAUTAATTGTGUAACACCCAA
325056252	52722	CTGACAUTTGGCTTTUAGGAAACAAGT	52723	CAATCACTTCATUCCTACTTTGTGCUC
323366966	52724	AGACCCTAACAUATAAAAGCAGTTCUGA	52725	GGATCAAAGUCAGCCAUCAGCAA
242193485	52726	ACACCCCTCUCAGATCCCTUG	52727	CTGGTCCTCAAUGAAGTCGTAGAUAAG
290748951	52728	AGATCGGUGCTGGAGTCUGAT	52729	GGAGATCTGUTTAAGGAGCCUCAAA
290271180	52730	AGCCCAUCCCCCATATTCCUAA	52731	GTCCAGCAGUCGATGTGGAUAG
302844782	52732	ACTGTGTACATUGGCTTGTCCUT	52733	AGAACGAGCCUGTTCTGTUGAC
262374184	52734	GATACCTCAAGGAAUTCTCCTAAACUGG	52735	ACAAGTTAAACUGGCAGCACUCT
315779335	52736	CCTGGUCCAGCAACAUCAAC	52737	CCTCCTTTAAACUGTTTTCATCUCACAA
269297309	52738	GTGCAAGCTUCCTGAGAGGUA	52739	TCCUGGAGAACACCCAUAGCA
262453311	52740	GCCCTGAUGGCTTCTTTCTTUG	52741	ACTTCTAACCUACTCTGCCTGCUA
266295062	52742	TTGAAAGCACCAAUAGCCCUGT	52743	CCAGAGCUCAAGATAUCAAGAAAAGGAA
314103744	52744	GTACTCAUGCCCAAGTTAGCUAGG	52745	CTTGGGCTTCCUTATAATTGTTGTCTUT
315381388	52746	CAATCAGGTUGCAGATTCTAAAATUGCT	52747	TGTTCTCAAUTGTCCTTTCUCCACA
321424353	52748	GCTUCCGAAGGAGACCCTUG	52749	CTCTGTGGGAAUCAGGTGGTUA
318369081	52750	TTTTAGAGGACACUTTTCTGTTGGTUCT	52751	CAGGUGAAGGACGAGAATATCTUCAAT
228105755	52752	GGCUGGAGGAGGTAUACAGGAT	52753	CCATCTCGGUGGTGTGCTUC
228432856	52754	CATCAGGAAACCUGGCCUACC	52755	GCCCTACAAUAACATACTCCATUCAGAA
333091863	52756	CTGTGCAAAUCCCTCCCUCAA	52757	CAAGCCATACAGUTGTTGGAAAAGAUG
312880030	52758	ACACTTACCCUGCTCTTTTGGUG	52759	CCATTCTTATGGACUAAAAGGTGCTCUT
315094959	52760	CAATGCUGAGAGGTGUGGACAT	52761	CCAACACGUCCACCTUCGT
312755216	52762	AGAGGTCUGGACTTCCAGCUT	52763	AGATGCAACUCAGATCACUCAGG
314513877	52764	CCATGACAGUGGGCAUCACAG	52765	CGAGGAGGAUGATGGCGAGUA
317577241	52766	CTGCTAGGATUTAGCACAAAGGUAGA	52767	ACTCTCUAGACCCACCGTTACUG
317103269	52768	CCACATTGCTACUCACTATTGCTGUA	52769	GCATAAACCAATGUATCTCATGCTCAUT
317716731	52770	TTCTCTACAATTUGCTTGGTTTGATTUCC	52771	TGACTGGCACUAAGAATTTCAUGAAGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317664678	52772	GGTCCATGAGCUCTTTTCCCTTUAA	52773	TGGCAAAAAGUCATCTCCCCTUAC
317567875	52774	ACCTTAAACAUGGCTTCAGGATTUGT	52775	CTCTCCTTCCUTTATCCAAATUCGCT
317107308	52776	CCACCATUACAAAGCACACACAUC	52777	CCTTTGGCGGACAUCTCATUCT
326792555	52778	GCTGCCCCAGGCUTTGAUAA	52779	GTGCCCCATAAUTAAATCTTTCTGUGT
239694744	52780	TGAAATTGGAUATTGCAGCAGUCAGA	52781	GCTCCTTTATAAGCUTCTTCAGTATATGUCA
318236073	52782	GGGAGGACUTTTCTCTUGGCAAAT	52783	GCAUAUCACCAGCCCGGAAA
267410060	52784	GGTGCAGUAGGTTGGTTUCCT	52785	AGACAGTUACAGGGAGGGTCUG
259442217	52786	TTTATGUGGCGAAGCUGGAACT	52787	AAGACCTUCAGGCAGAAGUGG
262152075	52788	TGGTTCCUCAGAACAUCAAGCC	52789	GAGATGTUGGCCAGCTGGUA
268185465	52790	TCCTTGAAGCAUCTCATCTATGTCTUG	52791	CGAGAGCCCACCAUGGTTUG
268843784	52792	CATGTATGTCUAGTTGGATGATUGGCT	52793	TGGTCAGGUCAGGCTAACTTUAGAA
327167423	52794	CACACAGGCCGAGUTTGTUG	52795	TGGTTTTAGCTTCUCTCACATTTCCTUT
314307122	52796	TGUACCTAATATAUACCAGGACACCACAA	52797	GAACACATACCUGAAGGAAGCGATUA
323671082	52798	GCTTCTUGGACCCCAGCTTUT	52799	TGTAGACAATGAUTCTGGTTTTAACUACAT
324730801	52800	GTGCAATUGGCACTGUCACT	52801	GGAGAUAAGACAAGCAGAAGATCUGAAT
324558130	52802	GGAGAGCAATUCCAGATCAAGAATTUG	52803	ATGCCTGACTGAUTTGTATCTGGTUAG
253978663	52804	AGCAAAAGCUCGTGGGTGUA	52805	AUCTTCGAGAUCGGGAGGGA
267849948	52806	CCTCCUGGTATTCCUGGGAGAAAT	52807	ACCGTAAUTGTTATACCUGAGGACCA
265784438	52808	TGTTACTGGUGATGATTTGTTAGUCGAA	52809	TCAAGAAAUAACCAGATCTGTUGCAGT
257973195	52810	GGACTTAGAGGUGGAGCUGGT	52811	CCTCCTCTTUCTCCAGGCATUC
268096471	52812	AGAGAAAAGCAUAGCATTCAAGCCAUA	52813	AAGGGUTACCTTATCUCCAGGCT
261828988	52814	AAGTGAAATGGCUCTTACACGTUCT	52815	CACAGGTGUAAAACATGCTGTCATTUT
267409789	52816	AAGCCTGCUCAAGAAATCATTTCATTUT	52817	TTGGTATGGUCACTTAATGTTGGTUCAT
267760053	52818	CCCATACATTCTUATTCACTTTCCCUGA	52819	CATAGACTCACCUCACAAATATCTGUGT
266985518	52820	TTCTCTTGAGUTGCTGAATGCUGA	52821	GGAGCCATTCUCTGTGACAAGAUA
316720962	52822	GCTGTGGATAAAUCTGCCGAATCATAUT	52823	GATATGTATGTTTUGATGTTGGCTTGUGA
267781313	52824	TCGTTTCCACUGCCAGCTTUA	52825	CAAGCGAGAAGGACAUGGUCA
236712630	52826	CUTCCUGGAAGCACCAAAGG	52827	TGGATATAATTUCCGAGCGAAGCUG
235587751	52828	CTGCGGCACAGUCCACUAA	52829	TGATTGCACUGACTGCCAACUAAT
333175151	52830	CAACAAGCACAGUCATGCUGAG	52831	CGTAAGGCGCCAAUGATGUG
272489774	52832	AACTCATGGUGCCCTTUGGAT	52833	TGTTUAGGGAGCCGTCTUCAG
333179443	52834	CTCCCGCCCAAGUGAGTTUA	52835	TCTTCAAAGACCCACAUCTTGACUG
233127617	52836	AATGCCUCAACCGTGGACAAUAT	52837	TCTTGAAAGGTUCCAAAATAATGTGAUGGA
325335866	52838	GCTCCACUGCTGAGTAGGAUCA	52839	GCCATTAGAUGTGGGCATUCACA
324915915	52840	CAUGGCATGGAAUGGAAAGGAAG	52841	TGCTGCUCAGCTTTCCTUGA
312983533	52842	GTCCTCATAGGUGCCTGTGUC	52843	GGTGTAGACUGTTGTAGAACTGUGT
262043514	52844	AGGAGUCTTCTGGUAACAGCACT	52845	GGCCGATGCUATGGGAAGAUG
316258502	52846	CTCCAGUAAGAAAAACTCCTTCUGCT	52847	ACATTGGAGAAAAUGAAGGTGGTATUGA
257496214	52848	AATCCTATCATCUCCTTAGTGACAGATUT	52849	GGGATAAAGTGGAUTACCTGGATGATUT
256371414	52850	CAATGCTUAACCAGTTTTGCUCAGA	52851	AGGCUGAAGACACACAGTATTTUGT
332085943	52852	GAAAGTGGCTUGAACAACACAAATAUGA	52853	CCTGCTCAAAAAUCTCCTGATCUCT
332133101	52854	GCACATTTGTUTCAAGCCACUGAT	52855	GACUCAGCCAACAAGACGUG
332179189	52856	GCCAGUGTCTTUGCAGAGG	52857	AGCTCTGCCCUTTGCCAAUT
332157135	52858	TTTTGGCAAUCGGTGACCCUAA	52859	GGGAGCCAAGAUGTTGUGAG
262508879	52860	TCATCTTGTTGUGCATACTTCUGGAG	52861	TGTAATCTCCCCUTTTCTCTCTCTCTUT
329017035	52862	GGUTCCGGTUGGCACACA	52863	GCTGACUGCCGGUGGAG
227845110	52864	GCCTCAUGGTTGCCCAUCT	52865	GGGAGGCAUTCAGCACCUG
227442268	52866	GCCCCUGAGCGTCAUCT	52867	TGCTTGAGCCACUGGATGUG
227917304	52868	CAUGAGCUCCAACACACCACT	52869	CCTCTGACUGGTGGCTGTUT
329306679	52870	GGTGTCTGAGAUGGAGATGAUGAAGA	52871	GCAGAAACUCCCGCAGGTUAC
227995002	52872	GGAGAGGUGGAGAGGCTUCA	52873	GCGTCCUACTGGCAUGACC
318022765	52874	GATCTAGATTUCCCACTTAATGUGGCA	52875	GAAACCACCCACAGCUTTGUT
319855306	52876	TCCCACUCCCACAUGACAGA	52877	CATGTATACUAACACTGTGCTUGCCT
320803977	52878	ACAATCUGATGCTGTUGCAGGT	52879	GACTTGGCAUGTGTGTTCUGAAG
319847665	52880	GTGATGGUAAAAACAGAAAUGAAACGGA	52881	AATTCCTCACCUGCGTTGACUT
333396912	52882	GCCAUATTUGAAGCCCACCAAA	52883	ACTATAGGGCUGAAGGTAGCTTUGT
333632867	52884	AGAGTATGTUGACTGTATGCTUGCC	52885	AGCCGAUAACAAGTGACACUGT
333689156	52886	CAGAATCUACAGAAACATCTGTCCUGAA	52887	CCTTCACCAGCUCCTTCACTTUAAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
333763754	52888	CAAAGAAAAGUGAGGAGCAAACUGG	52889	CCTAGAGUGGCCTCTTTCUGAAAA
333725714	52890	CTCAAGACTCAUCCATTACTACUCAAACA	52891	GGATGTGATGGUAACAGAATACACTUCA
268101358	52892	GTGACCCAAATUGCTATGACTTAAAGAUG	52893	CTACGAATTUAACCAAGCGGACTUT
261078291	52894	GCCTAACUCCTTGAGTGTTUCCA	52895	CGGGAAAGAAGAUGACTGTTTTTATUGA
264403341	52896	GGCTCGAAAAUGATCTTGCAGTUT	52897	ACTTATGTGTACAUGCACTGCAUGA
263570996	52898	TGTATCTGCCUGTGTATCCCTCUT	52899	GGAAGACCACCUGCAUCCAC
268716401	52900	CGTTGCCCUGTGAAGCATATUAC	52901	GGCATTTCCAGUTTATCTGCATATUGAT
260274989	52902	GGTAAATUGGGCCCCGAGAUT	52903	CCATTTGCUGAATGTGTTUGACAACAT
267506076	52904	ATTCCAGAGCUAGCCAAGAAUGG	52905	AGAGTGCAUGGCCCAGAUG
265978752	52906	GACCTTGGCCAUCCTGTTGUA	52907	GGGCTGACAUTGATATGATTUCAAAG
292200777	52908	GATATGCCCCAUGTCCCCAUT	52909	GGGCAGTTTCAGUTGCTATTTCTGUA
292834591	52910	TTCATATTGTUGGCCATACCAGUGT	52911	GGGTCATCACUGCCAAGGTUA
291675384	52912	TCACTGAATTUCCTAGACCCTAUGGAAT	52913	TCCTATGAUCCCCAGAGCTTCTUC
290303826	52914	TCAGGAACTGCUCTTAGGAAAACAUC	52915	ACTCTCAGAAGUCAACAATGAGTTTUCT
222872619	52916	CCATGCGACAGUCTGGAUGT	52917	CTTGTCAUCAGGCTGTGAGUGAA
224540010	52918	AGGAAGCTTAGAUAGTTCTCGTTCUGAA	52919	CCCAGAACTUCTGTCTTCCUGAG
224538936	52920	CTGCCCAGCAACCAUTAAGUAGA	52921	CCTGAGGACUTAGTUGAAGCAGT
326926125	52922	TCCTTUGGACTCCUGGAGACA	52923	TCCTCACTGCUCTCAGAGTCTUC
323739178	52924	CCTGTCATAAACUTGACCAGGTTGUA	52925	GCTTCTGCAUTGATTTCCACUCC
325969284	52926	AGATGCUGCGAAAAUCAGGCT	52927	TGCCAACAAUGTCCACTAUGGAT
237660713	52928	AGCAAAACAGAAGCCUCTCATUAGT	52929	GCCCCACCCUTTATTAACGAGTUC
239795618	52930	CCTTTTGUAAGCAGCAUCGAGAAG	52931	TCTGACATTTUGGGTGCCUGAG
239764859	52932	GCATAUGCCGAGAGCTGTUG	52933	CCTGCAGAAGCUCTTCCUGAG
266403520	52934	AGCCTGTGAUGAGTGTTGCTUT	52935	GGTAATGTAACUCAAGGTCGGCTAUC
268525883	52936	GGTCTTGTUGACCCGGAAGUG	52937	ATGGAGCGATTUATGGCATCCTTAUAG
256788296	52938	TGCTTTGTGUAAACCTATTCCCTGUT	52939	AGCAACGAAUGCCUGCCT
332028111	52940	GCCGACCAUCCTTATCCTUGT	52941	CACTCTCCAUGCACCTCACUG
331876278	52942	ACUCACCAGTUAAACCAACAGCA	52943	GAGGGCCAGUTTGACCATTUC
331858935	52944	GTACTGGACTAUGAAGGAGTCAAACUG	52945	TCTTTACUAACAGCCCCCUACCAT
331551700	52946	AGGATATTGAUCTGAGCAGAGUCCAA	52947	GCCTACUTCCAACUGCGCAT
257466277	52948	TCAGGATGCUTGGTGCTUGT	52949	TCTGTTTAATUTGGGAGCAUGGCT
269327248	52950	CTGTCTCCUCACGATAATCAUCCC	52951	AAGCCTCCUCTCAGCCCUAA
326710700	52952	CGCACTCAUGCCAGGAAUGAT	52953	GCACTAATGUGGCAAGCCTUC
326984840	52954	TGCTTCCCUGTGAGCTCUCT	52955	GCTCAAACCCCCAUTATGAAGAGTUT
324294029	52956	GCCCAGCGUGATCTGUGT	52957	CCAAGCGGGUCTCTTCCTUG
313101642	52958	TTGCTTTCTUCCACAGTACUAAAACCA	52959	GCUAAAAAGCAGCUGAAAGGCAAAA
272269557	52960	GAGGCCACUGATTTGGTTCUGA	52961	CTGCUCCACAAAATTCCGUCAAAAA
270619807	52962	ACTTAAGAGACCUAACATTTTGCCAUCA	52963	AGCATCTCTTGTUTTCCTAAGTGACAUAA
269980447	52964	CAGCCAGGAACUTGACUCCAT	52965	TCCCAGGGACUGACAATTTUCC
271944854	52966	CCTTGCAUGGCAGTGACUACT	52967	CAATCGGTCCUGTGACATTGUG
270751504	52968	GTACTCAGCAUCAAAATCAAAAGTTUCCA	52969	ATGACCTGCTTUGCCATATTGAGUAT
316064010	52970	TCTACCATATUCAAAGCCCCCUAGAT	52971	TCTGTGCCTAUGAGCTATAACAAUGG
316435204	52972	GTCTAGAAUGCAGCCCCUGAA	52973	TCTUTTCCACATAATCUGACAACAACCT
317539099	52974	GGGTTTUCCGAGTACATGATUGA	52975	TGCTTCTGGCUTTGTTTTATTGUGAAAT
317138785	52976	CTTCCATGUAGACAAGGATTUGAAAGG	52977	TGGTTTCATGTUTTGCCTTGTCUG
316393781	52978	GCAGTCAUCAATGTCCTGTUCACA	52979	CCTGTACTAAGGUTAAAGGAATGTUAAGAGT
317541854	52980	CCCCTTAAATGUGTACTAGTTGTUCCAT	52981	TGACTATTGCTUAGGGAACCACAGUA
317370540	52982	CCAGAAAGAAAUAGGCATCAAUAACCC	52983	AACTTATTTTGUGGCAGATGTTGUCAAA
266784645	52984	TCAGTAATATTUGGTGAAGATGTUGCCT	52985	GTGGCGTUGGAAATGAAAAGGAAUT
263925859	52986	CATGCCCCGUCTTTCTTTCUG	52987	ACATACCTTGAUTCCTGGGCAAUG
325371428	52988	CACAGAGTTACACUTCATCCTGAUCAA	52989	CTTCAGAGAUTGGTGUCAAAAGAGGA
265359853	52990	TCUCGGGUGAGGAGCCA	52991	GCGUCTUGGGCGAAACT
268719726	52992	TCTTCAAACCCCAUTAGCATGAATUACT	52993	AGTGAACTTCGUAAGAAAACTTCAUGGT
266688009	52994	CTGAAGCACCTUTAAATCCTCCTATUGA	52995	CGACACAGUTTGCGAUCCCA
314473435	52996	GCTCTATAGTTTAUGTCTTGGCTGGUT	52997	TCTCTGATGAGUCTGAAGTCCACUC
328257664	52998	ACUTCAAAATACUGGAGCAAAGACAAGT	52999	TGGCAGCTTAAAUAGAAACCAGACTUAA
255619151	53000	GACACTAUGAGTGCCGUGCT	53001	GCAGCAGTUTCTGTCCTTUCC
224098698	53002	ACTCTACATAGUGGAGAAATAACCAGUCA	53003	AAAUCATGATCAAATUGCGCACAGT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
224460601	53004	CCCTAGGAAUAAAAGACATACACGUGAA	53005	AATTTGTAGGCTUTCCTGTTCTCAUCA
222536443	53006	ACAAACUCTTGGTACTUCAAACACGA	53007	TTCCCAATCTCCUTTTTCATGTTCTCUT
222164949	53008	TGCTTTATGGGAUAAGGAATAGAATTGCUT	53009	CTGTCTCATATCUTCCAACTGTTCTUCA
224124924	53010	CCAAGAAGAAAGAGAAUTACTGUCCAGA	53011	CCACCTUAAGCCTTTGAAGAAUACAAAT
223211599	53012	GACCGAAAACACUTTGGAGCUG	53013	ACAGCCTCAACUTTGGTTTTAGATCAUA
224052762	53014	TGCATGTTUGAGCCACTTCCUAT	53015	GCATGTAGTTCTUGCATCTTCTCAATTUT
222613086	53016	GGTACTACAGAUGCAGTTGGTTTACUAA	53017	CATAGTGGCTCCUATTAAAATCTTAACCTUCA
332928697	53018	GGAGAGTTGUCTCTTTCTCAUCCC	53019	AAGCUGAGAACATGCUAAAGAACCA
318701824	53020	GCTTUGAGCAAACAGTGGCUAA	53021	GCTTAGGCCUGGTCGACUAGAT
321598717	53022	CACUTGTTGACUCACACGGAGAT	53023	CAACCTGCAUAAACCTAGAGACCUG
319464000	53024	CTCCTGTGAGUAAAAGAGCUCCA	53025	CTGGGAAGGCAAAAUTCAGCATUT
318457844	53026	CCTCTGATATUACCAAAGGAAGCAUGG	53027	TTTGGTCAGGCUTACACTTTATUAGGAA
319146607	53028	GATGATGAGUCAACTGGAATCTCUGAC	53029	GGCUGGAAACUGACACCAAACT
321110893	53030	CCCCCATTUGAGAGTCCAAGTUT	53031	CAAGCTATAGAAGUGGTCTGGAGUC
260507999	53032	CAGGUTGGAAACUGAACAAAGCA	53033	GGATGAAACUGAACAAAAAUGGAAGCA
264476951	53034	AACTATTCTGUTTCATCCGUGGCA	53035	CTGAGGGUAAGAAAGTTGTGGTGAUT
268418940	53036	GACTCAAGGGUGAACCTGGUG	53037	CCAGACCACCUGCCAAGAAUT
268583761	53038	AGGGTTCGTUACTGAGCACUG	53039	CATCAATCTGGGUTGCATTTTAAUCACT
324144145	53040	AAGCTGTTTTTAUACATGAGTTCUCCCA	53041	GTCTTGTCCTUGACTTTAACTACCTUCT
323324994	53042	GTTAAAGGGCAGAGUTCCCTCUT	53043	AAGCCAAACUGAAGGCTATACTGAAAUA
324504100	53044	GGAGAAACTAACUTGATGGGATGUGG	53045	AGTTGCAGTTGCUTCTAAAAATCATUT
324358145	53046	CGGCTCAGCUTCTTTCGUGAA	53047	CTCAGAACAACAGAUCCCACCATUAA
323425717	53048	GAAGUGTGTCTGUGAACAGGCT	53049	GAAATTAUGCAATCGGTAUGCAGAGAA
325381086	53050	GAATTAAUAGAAACAGAGCUGACGGAAGA	53051	TTCCCTGCTAUGAAGCCATCTTUT
263751057	53052	ATTACAGTGUCCGAAGTTCGCUT	53053	CCCTGTAACCAAGUTCAAATATCAUCAC
255286312	53054	CTAATCAAAGGAAUCATCCUCCGGAAA	53055	TCGCACATTTTUGCAAAGTTCATUAGAA
256018109	53056	GAGGGTAAAAUTAAGCACAGUGGAAGA	53057	GGTAGTGTGAAGGGUTCATATGCAUAAT
260068498	53058	TCAGTAAGUAACTTTGGCUGCCAAAT	53059	CGGCTACUCCCACGTAAATGUAAA
266680926	53060	AACATCTTCCTUGAGGCTGAATUGT	53061	CCCATCAGCUCTTGTTTTTGCAUT
268710443	53062	TUTTTAGTCTUCCACAAGGCAGACA	53063	CTGTACCTGTTTCUACTCCAGATTTCUT
267592437	53064	GAGGCTCUGTGATTTTCGUGACT	53065	ACAGGTCAGUGCATGTTCCTUG
314022452	53066	ACCTCCUCGTTGGCATUGAC	53067	CGTGTGGGACUGGCTCAUC
314902365	53068	TGCCACGUGGTTGUCCAT	53069	ACGACCACGUGCCTCUC
333301485	53070	GCTCCTACUCCAGCCCCUA	53071	CCCUCGACAGGGCUCAAG
315875615	53072	AATCAGACGGGAAGCUGGUC	53073	TGATTTCTGGACCUGCAGCTTUT
229660052	53074	AGGTCCAGGUACTCCTGTGAUG	53075	CTTCAAGCAGCUGGUGGAAGA
232833813	53076	GCCCCGUCTCTCCAATAUCAG	53077	GGATCAGUACTCCAGUGAGAAGACA
266874849	53078	AGTTTCAGAAACAUCAGCCACUAACT	53079	GCTGAGCATUCGGTCCACUAAC
255793184	53080	GAAGTTGAGCUAACAAACATUCAGAAGAA	53081	TTCTGGTGCTUCAATCGTCACTUAA
256803310	53082	TGTTTTTAACUCTTGCACCCUGGA	53083	TGCTCAGUGAGTTGGCGTTUA
255114864	53084	GCTCACTGCAACUCTGTTCTGUT	53085	CTCTCTTGAGGCCUTTGATAAATCUACA
320358777	53086	CTGCTGUGAACTATTAAAUCCAGAGGAA	53087	CCACATTATUCCACAAGCCTGGUA
228297369	53088	GGGCAGCAAUAATCTGCTGAUG	53089	TCACATTCACGAAGUCCCCTTUT
315129537	53090	CAGAGUTTCATGGTUCCCAGAGA	53091	GTTTATTCCTGCUGTGTTCAGGTUAAAA
317536230	53092	GCAATTTCCUGCCGAATGCUG	53093	AAGGGAUACGAACTTTTCTUCCAAACT
316076997	53094	CCCTTTGUTGCTCTUGGAGCAT	53095	GCCCCTAATUCTGTGTTTTGUGT
316287720	53096	CAAGGAGUCAGGAAGGAGAGTTUT	53097	CTTUACGGAACTCGUGGAGAGAG
326679579	53098	CGGTGGAGUTGTTGTTCTTCUGT	53099	ACAAAGCTGAAUGCCCACTATGUA
257292450	53100	GGCCUAAGCUGGAGAACAGAT	53101	GAATAGUCAGATCACTUACAAGAGCCA
268974256	53102	CCCACCATUCCTCCCTCATGUA	53103	AUTCAAGCGAUGGGACAGAGAC
295521631	53104	CCGACACCCCCAUACACATUT	53105	CCGCCAGGAGUACACCAUC
281283711	53106	AGAAATCTGGUTACTGGCATCUAGAAC	53107	TCCCTAGGTCTAAUCCTCTTCTTTCTTUT
279316717	53108	ACACAGACUCCTGAUCCAGCA	53109	GACTGGGTTAATUTGCTTGTGTTTACUT
261870077	53110	CCCGAUGCTGTGGTUGGT	53111	CCAGUGAAGCCTCUGAGGGA
265489025	53112	GGTTAGCACGUGACTGUCCA	53113	AGACAAGCTUGGCCATTGGUT
269206076	53114	GTGAGCUCAGGAUACAGGAAGG	53115	CTGCCACUGGACACAGGAUAAG
263267750	53116	GTAGAATTCCTCUCGGTCATGCUG	53117	CCTGTGTUGGAAGACAGCTAAAAUGAT
265003575	53118	TGGATATCCCAGAAUTTCCTTGTTUCC	53119	ATGTGCAACAUTTTTCGTCTTGUGAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
261944952	53120	CAACCACAUACTAAATCUGACCCAAAG	53121	CCCCTGUGTTCTTCTCTUCCAT
241045502	53122	CCCAAATATACCUCAACAGGGATUACC	53123	GTTCCACAAACATUCAGCCCTTTATAAUT
239640371	53124	CAGGGCCCAACAGGUATAUGAG	53125	ACAGACGTTUCCTGTTTGACCTUT
265193388	53126	CCCUACUACGAAGACCCCGAA	53127	CAACCCUCTACCCUGACACAAC
268066147	53128	GGCCTGAUGGATCTGGGAUCT	53129	CGGATCGTTUCCTCAGTGAACUC
268773411	53130	CATAGCGGGUGGGATGACUT	53131	GGATCAAGAGCUTGTTGAGTTUGAGA
263145809	53132	CTUAACCACCGGCCATCUGT	53133	GAGGUCACGAGGTTGCUCT
332867131	53134	CCCCAGAGAAAGGAGUCAATAAUGT	53135	TCTGATCTCTGUAACTGGATTATGCTGUA
333409552	53136	CAGCGCAGCCGUCATAAAUC	53137	GCAGTGUAGACCCCAAAGACTUT
321182585	53138	GAGAGAGATTUCAACTGTTCTGTUCCT	53139	GGAAAGTTCCAAAUAGACCAGAGAUCA
318902721	53140	AAGGCCCCTUCTGTGTATCCUA	53141	GCTCTTTCTCTGCUAGCATCATTAATTUT
318045340	53142	TCTGUTTACTGGCUCCAGGAGA	53143	AGCTGAUGAAGGGAAAUAGAAAAAGCA
318980098	53144	CTGACCUCATTCACTGUGGCA	53145	ACATUGCAGCCACCGAUGAA
267003137	53146	GCACCCCTUTTCTGTGTGTTUC	53147	CTAAAGGUGGGCCGGTUGT
257665455	53148	CCUGGGAAGGGCAGATTTUAGG	53149	CAATGAGAGAUGTCUGCAGGGAA
327999272	53150	AAGAAAGAGAUGACATTCTACGTUCCC	53151	GGAAGAGCAUCATAAGTGCATTUAACCT
327245809	53152	GTGATCUGGGAAAACCCCUAGT	53153	TCACAGACUGCATGAGGTTCUG
314872169	53154	CACCTTTAGCCCUGCCTTCUC	53155	GGTACATCUGAGCCATCUCCCT
313325445	53156	CTGGCAGAUGTGTGCTTTGUG	53157	GAGACATGGGUCAGAGGAAAUGG
333535178	53158	GCCAGAUAAACAGTGUGGACAGG	53159	CTTTGCTGGGUGACCTCUGAT
316500873	53160	CTTCACCTUAGGGTTGCCCAUAA	53161	CTCTGCCTAUTGGTCTATTTUCCCA
327117373	53162	CCTCTGAGCUCCTCTGTCUCA	53163	GGAGCTGTGATUCTGCTATTGGATUT
332436734	53164	ATCCUGTGACATCUGCAACACT	53165	GCAAGGAGCTUGGTACTAAGATGUA
333424067	53166	GTGTTTTCCCUCCATGGATGATGUA	53167	TGATGGACAAGUTTTCTTCTTUGGACA
313350658	53168	GUGCTUGGCCGAGGACA	53169	GCAAGCAGGGAGUGTUGACT
313859597	53170	CCTGAGACAUCAGTCCACUGGAT	53171	CCTCACTTAGCUACCCACTCTAUACC
313863444	53172	GGAAAGUGAGCAGAACCAAGACUC	53173	GTCAGCCAAGCUCCACTUCAT
324525034	53174	AGAGTCCUAAGCAACAACAGUGAC	53175	AAGGACCCAGAAUGGGAAGACUA
266805161	53176	GCUCGCAGCAGAAAGCUG	53177	CCACGGCAGGUTCTCGUA
264865610	53178	CTGGGAUGATCTTTCTGUGGGA	53179	CTGGCCACACCUGATGTUGA
332314809	53180	TCATACCAGGUCTCCGTUCCA	53181	GGTCATTUGAGCTGCAGGUGA
312663544	53182	GTTTCCATGGCUAGGGAGGAUT	53183	GCTAGUCAGGCAGCTCAUCA
315135328	53184	ACAAGTTCAUCAAGCAGATCTUCCAG	53185	ACAGCAAAGCUCCATACCCATUAT
313659010	53186	CCTTAUCCGGCAGGTCUCAC	53187	TGGCAUGGAGGACUGAAGGAT
315057820	53188	GGCTUCATTCCTGUCCCCAAAT	53189	GUCTGTGGTUCAGGCAGAGAAG
224735732	53190	TTCACAGGCUTAACCAATACGUGT	53191	AACAGGTAGAAAUAGCCCATGTCATUT
222602923	53192	CTAGAAGTUGCCAAGGTAGCUCAG	53193	ACCCTTATTGAGACAAUGCCAACATUAA
316133056	53194	GGCCAGGTUCTGAAGTTCCTUT	53195	TGTTCUGACAAACCTCCUCCAC
332663389	53196	GCATCTCUGGACTTACGCGUT	53197	GCTGGATTTGCAUATTCTGAACCUCAT
333588414	53198	AAAGGCCAGAGUCAGCAGUC	53199	TGTTCCTTCCCUGTCCATCUGT
333703368	53200	TTTGGTUCAAGGAAGGTCTUGCT	53201	CAGTGAAGAGCAUGTTGAGGAUGT
332423203	53202	GGGTCAUGCGTCTGGUGAAG	53203	TCCTTGTGUCAGCTGTGTTCUG
332697842	53204	GAGACCGUGGCTCTCTGAUG	53205	CCTCCCAUGAACCCCGTUAT
332391804	53206	GGGAACCUAGAACAAGCCAAUGAG	53207	CGCATUCTAAGGGUGCCACA
319814535	53208	GACTGGACACUGCTGGACUC	53209	GCCCUGGATCUAAGCCACAT
320312817	53210	AAGGCCACUGATGCTTTCUGT	53211	GAAGAAAGGUCCAAGAGGGUCAG
313272458	53212	CACGTGGUGACCCATTTUCAA	53213	CCUCCUAGCCAGGAAGAAAGAAA
313471617	53214	CCAGTGCTTCUCCCTCAACTAUG	53215	GCCCTTGAGGUGAGGAACTTUG
319318090	53216	ATGAAGCCACCAUGCCTACAUT	53217	CCCACTAAGAUGGGCATTTUGAG
318529612	53218	CATCTGGTUCAACAGGGCAUC	53219	TGTGUGCGGAGCTAAAUAAAGACA
325736282	53220	TGTCTGTAATGUGTGAGTCTTGUCC	53221	ATTCCACCACTUCACTTGAGATAAAUCA
318140068	53222	CCTGGGAGAAUCCCATAGCAUT	53223	CCTCTCACTTCUCTCTGGCTTCUT
314254953	53224	CTGAAAATAATGUTCTCCTCTCTUGGCT	53225	CCGGACUCCCAGCACTUA
313692561	53226	GGTAGGCUGGCTGTGATCUC	53227	ACCTTGCUATGCGCGUAGAC
254321630	53228	GTTTTCTGGAGAAGUGTAGGCTTUC	53229	GCCAACCAAGAACUGTTUAAAAAGCAA
261392701	53230	CCCCCTTACUCTGATCATGTUCAT	53231	TCTCTGTCTUGATCTCTGTCUGGT
262156604	53232	CCCTGCAUGGTAGGGATCUCA	53233	CCCGTCTTGUCCTCATTTTCTGTUT
257288140	53234	TCAGGGAACAAAUGCCAAGUGA	53235	CTCTATATTUGACATCGCCACUGAAC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
265677225	53236	TTTGCAACTACUAGATGACATGTGAAUCA	53237	CUACACUGCAGGGACCACAA
268611523	53238	AATGAGTAAAGACTUAGGTAGTACAAACATUT	53239	TCAAAGGUGACATGGGTCUAAAAGG
286190411	53240	TTACCTTTTCACCUTTAGATCCCTUGA	53241	GTCCACAAGGUCCTATTGGAUACC
285264859	53242	TGTCTGGTAACUTTCCATTGTUCCAT	53243	TTAACCCAACUAGATAAATACTCACTUGGC
332280930	53244	CTGACATACCTTGUTTGGAATCTAGCUT	53245	GGAAATCTCTTGUTTGAACATGTGUGT
313285533	53246	CUCACTCAUCCCAGACACAGG	53247	TCTCTCCCUGATGCAGCTGUA
324526574	53248	CTCCCTGGUGACAGTCTGUG	53249	CTCTCTATTGCUATCCCCACACUT
316795325	53250	CTGTAATGGTTUGTTCCGGACAUC	53251	ATAGATGCAGUCACAATAATGTGCTAUT
328440982	53252	GTGCAAGCTUTCAGCTGATAUGAAT	53253	GCATTTCTUCCGAACACTAAGATTUGT
327047938	53254	TGUGGACTCCATUGAAGACAGAGA	53255	CATTCACCATGUCCTGCATTTATTGUT
327902559	53256	CCGATATTCATATTUTGTCCATGGGCUA	53257	CCCAAGUCCAGAGCTGTTCUC
328405844	53258	GGGAGAAGAAGUGGAAGGAAUGG	53259	GTGGGATTCUGGAACGCTATGTATUAT
327994420	53260	ACCCCAAUTAAGTGTAAUGCCAACA	53261	TGGTGGAATGAACUTTGAGATTTCCTUT
328233132	53262	GATCCTTCUCCACGCCATUGAT	53263	CCAGCUGAACAAAGUAAAGAAGAAAGAA
323884687	53264	CCUCAAAUACGGAGCGAAGCA	53265	GCTGCAGGUACAGUGACCAA
325321514	53266	GTTGTGACUGGAGAATGAGAATTUGG	53267	CTCATTTCTCUCCTGGGCAGUT
326255301	53268	TGACTGTTCATTGUCCGACATATGTUT	53269	GGAATGGCTGUCCCCATCTTAUG
324206803	53270	GGGAGGAUCAGCTGAAAGTAATTUCT	53271	GTCAGGTGACAUTGTCTGTCUGAA
326272051	53272	CACTTTCUACCACACAGTTGAATUCC	53273	GAAGGCAGGTUGGAAAATAGAAAAAGUT
324728411	53274	CTGTCACACGUCCTGUGGAG	53275	CCAAGCGUCCCAATCAGAAUG
326294465	53276	GTACATTGUCCCCAUGACGGA	53277	TCTGTCAGCAUCTGTATGGTTTUGG
324960132	53278	CCTCCTTCTTCCUCTTTCTTGTTTTUCA	53279	CGCATATACACUTAATTTCGTCUCAGGA
323930202	53280	TTCCGGCTCAUATATCAGCTGTTTUT	53281	CCAAGTGAUGGCCATGCTTGUAT
326385259	53282	TCAGCAAAAGAUACUAAGAAGGGAAGAGA	53283	GCTTCATTTTCUTCCTTTCCTGAUCAGA
326227518	53284	GGGTGGCUGGTAATGTTUGAT	53285	GGCTCTTGTUATTACTGGCTUGAAAAC
325672966	53286	CCCAACGAUACCCGACTUCAG	53287	CCTTCGTUGACCACGUCAAAT
325796899	53288	TCACGTTUACCATGTTCUGAGCA	53289	AAGAAGCUGAGTCATGAAUGGAGAAG
332334688	53290	GGTGTCCTUGAAGAACTAGAATGTTUCA	53291	CCTGGGAACACAUTTTCUGCAAAAG
332865245	53292	ACAAAACTGAAGCUACCGCTATTCUT	53293	GGCTTCCUACTATGTAACCAUAGAGACT
332358829	53294	TGTTCAUCCACCAGTATGTUGCT	53295	GGTCACCUGAAATGAAAATGUAGAAAAGG
318610792	53296	CTCTTGAATUACCTTGTCATCUGGCT	53297	GTTGGATACACAGCCUAGACTTACTTUT
278603846	53298	GGGTCUACAAACCATTCACAGUCT	53299	AAGTTTCUGGACTTCATCATUGGCT
269274009	53300	CATCTCCUCCCTTGCTGCUA	53301	AGCAUGACGCCGAGGUG
265555507	53302	CTGGTCUGGACATGATGGTUCT	53303	CCCTTCTCUCACAGGGUGAAC
269346910	53304	CGCCTTUGGCAGGAGAUAAGAA	53305	CCCTCACCUCTACCTGCTCUC
259667412	53306	GGCUACCACGAAGACCCCUA	53307	GGTTGATCACUTCTTGGTGTCUCT
316788299	53308	GCACATTTCAAGUAGCCTTAGTTCUGA	53309	CAAAAATACUGGGAGGCAACUAAAAGA
320612528	53310	CTTTGGAGTGACUGTAAAAATCATCUGG	53311	CCAAACAGCTCUCATTCACTCTCTTUT
318989511	53312	GCACATGCUTTCATACTUGCCT	53313	CATGCTTGCTAUGAGTACAATCACATUT
315430808	53314	GAAAGGTCCCUGCTGGGAAUAT	53315	CCTCTCACTCTUTTAATCGATGCTTTUT
266817680	53316	AGATGTCATTTGTUTGGACTAGCTGUT	53317	GCATGUAAACAAGAGAAAGACGAUAAGGA
266915030	53318	AGTTATACAACAAACCUGCTGCTCUAAA	53319	CTCACAGCCAAUGAGGAACTUGA
267026918	53320	GGGCTUCAGCGACAUGGT	53321	GGCGGCUCCTTGGTCUC
236445412	53322	GTGTTGTTGUGGAAAGTAGTGCUG	53323	CTCAGGATCCUCTCTTTTCATUCCAA
316488015	53324	ACACACTTUCAGCAGCAGGUAG	53325	CTTTGAAGCAGCCUTTATGTATGTGTUT
264234192	53326	TCACAGTAGTGTUATGTGCAAACTATUGA	53327	TCTCTCTCTGACAUGATCTGGTATCTUT
242180110	53328	GAAAAGAGTGGUAGAAAAGAGGTTTCUG	53329	ACAAAGTGTATTUAGCCGGAGAUAGG
333523759	53330	TTTGATTTCTTAGAUTCCCCAAGUCCAA	53331	CATGCCCAUGGACAAATGTAAAGTUAAT
333632510	53332	GAATTTCCCAAGUGGCAUCGAG	53333	CAGCATUCAGAGCAAGAAAATGTUCA
333212579	53334	CTCAUCCCCCATGCTUCAGAAAA	53335	GCTCCTGUACAGCTTACTCUCAAT
333281335	53336	ACTTCATGCUGCATCACGAGUT	53337	CTTCTTCTCACAUCAGGGTTCUGT
332475552	53338	GCUCUCACAGACCCAGGGA	53339	GTTTAATCTGCTUTCTGCAAGACAAUCT
333833401	53340	GGGCTCGUATTTTATGGACUGAACA	53341	CCAGGACAAGCUCAAGTUCAAGAA
321616064	53342	ATCAGCAAAGGCUCTGGGTUT	53343	AGCCAUGAAAGTGAGCTUCCAG
266748523	53344	TCCTTTTAACTCGAAUTGGAGAGGGAUA	53345	CCTCTCCAUGAAAAACCAGTCAAUG
325004254	53346	AGGAGAAAGGACGGCUTCCUA	53347	GGAGUGGUACGCGCACAAT
323316524	53348	TGTGAAATCAUAGCAAAGAGUGACCA	53349	AGTTTTGACAUTAAGAGCTCUGACACAT
330255003	53350	CTCACCGCAGUCCTUGAACT	53351	CCCGACAGGUTTGTCTTGUGA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
321423536	53352	GCAAAAACAUGGACGUGGCAT	53353	GCGGTAATTUCCTGTGCTTCUT
320089779	53354	GAGGAAGCCUGCGCTUG	53355	CCTATUGTACGGACUCCCAAGGT
264240190	53356	GACAATTUCACGTTCAGCUACAGAA	53357	CATGAAGAUCCTCACUGAGCGT
254787445	53358	CTAGTAUGAACTTTGCCUCCAAGCA	53359	GACUTCATGAGGTUAACCCAGGAG
266477808	53360	CACGTCCACCUCTAACAUGGT	53361	AGATTATCAGGUGAGATGCCTGTUG
316489051	53362	TGCAUGGCCCAGAGAGAAAUG	53363	GAAAGCAACUGAAGGGTGTCATAAAUT
317842974	53364	TGGAGAAACTAAAACUCACCTGTACTUG	53365	ATCACCAACCCUCCAATCCTTTUT
316630172	53366	AATGGAATGTTUGGTGCTGTTTUCA	53367	ACTCCACUACTCACTGTUCGGT
317001078	53368	ACTCAGGAGUATTTCTCAUGGGACA	53369	GGCTCTATTUAACCTCCCTTGATUCC
317039528	53370	TCATGGAAAATUAGGCTTCCTTTUGAGA	53371	GTGTAATGCGGGCUTTCATGTUAC
317421291	53372	CCCGTTTGUCAGAGCTGTGUA	53373	CCCAGTGUGAAGTATGGAGCUG
317155392	53374	CATTCTAAGGCUCCCCAUGCAA	53375	TGGCCATCUCTTCCTCTTCTUCT
317650743	53376	GGTAAAUCCCAGGGCGAUCT	53377	CGCCUGAAGUGGGAGCA
272703644	53378	CATGTCGTCCAUCCTGCCTUT	53379	GAGTTTCTUGACCAGGCTCTUGA
315739828	53380	GGGTTCCACUATGTAGAAATCCTUC	53381	TGTCCTTACUGCCATTTGACCTTTUAT
316880198	53382	CUAATGCAGCUCGAGGAGGAAG	53383	CTTTTCGGTUCCGGGTCTUG
332654515	53384	GCACCCACGAUCATGCUGAG	53385	CAGGGCCTUTTCTTGCTAGUGA
318310811	53386	AAGUAGCCCCAGCCAUGAC	53387	AACTGCCCUTACCATCGUGAC
319538716	53388	GGGUCCCAAGCACTATGCUC	53389	GGTTCCCGCAUGCGTUT
241511459	53390	CTAGTCUGGAAAATGCAGUGGGA	53391	CCTCTCTCTAGUAGCTCAACTGGAUAA
263003709	53392	GGGAGGTGAGUGGGAGATGUA	53393	GGACCATTAUCAGAACAGGATCTCAATUC
263178907	53394	CCCTGACCACCCUCTCCAUT	53395	TTTCUGCCGCAAGGCCUA
321558308	53396	GGAACCTACGUGCAGCCAUT	53397	TGTGGACCUGGCCACUG
318148914	53398	CCTGCTGGAUCAGGTCTTCATCUA	53399	CGTCCATTGUGGGTAGCAAUCT
321329675	53400	GCGGAAGGUGACAGCUGA	53401	CGGATGCUGGCACCTUCT
319646083	53402	TAGGAGACGUTGGTGCCAUC	53403	GGGTCCTACCAUCTCTTACACCUT
319665578	53404	GCGGCUTGCATUGACGAC	53405	GCTUACAACAGCACAGGUGACT
321344666	53406	ACGCAGAUGCTGGTGAAGUAAT	53407	GGCCCACUACCTCTUCGAC
318215092	53408	CACTGUGGAGACCUGCAGAC	53409	TGCCTTCUGCTCTGCTUCAT
236539858	53410	TGCTTTTCUCTGGCCUGAGAG	53411	CAGGGUCAAGCAGCUCAAGA
235718920	53412	TGGTTTACCTUCCAGTTCTGAAAUCAT	53413	TUCTCTTUCCCCAAAAAGGAACGA
269183297	53414	CCCAGGCUTAAUCCAAAAGCAAC	53415	GCGTCTTTGCUTTCTCTGTGAUGA
264481292	53416	GGGAGTCUCACCTGTACACGUA	53417	TGAATGCUCACCGTCCTGTUC
258969497	53418	CUCCCACCCACACAUACAGAC	53419	GCTGACTGCCUTTCTGTATTTTCUGA
263606258	53420	ACCCACTGUCTGAACCUGAGT	53421	CCAGAACCGAAUCCUGAGGAG
327187703	53422	GCGGCUCCTAGTUCAGAAGGA	53423	CAAAATGTCAGCUCGGTTCGUG
327678005	53424	CCCAGUCCAGCACCTTTUACT	53425	GCCCCACAUACACATCAGCUC
320994062	53426	TTAGCAUGGCCUACACAACACA	53427	CTGAGCCTUATTTGTCTTCUCAGAACT
319867433	53428	TCCCTTAGGGCCUGAGCAAUA	53429	ACACGTATCAAGAUTGGACTCAACUC
319134033	53430	GTCAAGGUTAACATGUCCGAGGAA	53431	CTAAGUGCCGCACCAGCUAT
318078023	53432	GUGGAAAGCATUCCCAAAACGA	53433	CTACAACTUCAACCTCAAGCCUGT
319480291	53434	CAACCUAAACAGCAGCCTTCUC	53435	AGTCTGCTTAUTCTTGATGTTGUACCC
320003570	53436	AGCTAGACAAACCCAUACCACCUA	53437	CCTTGGACTAUGCTGACAACAUCC
318753060	53438	AATTAACTGGAAAUAACAAGGGAGCUGA	53439	CTTAUCGAGGGCCGGGUAAC
319526003	53440	GGGCTAAAAGUTCTGGAGGCTUT	53441	AGCCATTUGAACGAAGATAATCUGCT
268203191	53442	CTCAGGAGCUGCCAACCUAA	53443	TGGGUACACTGGGUCCCT
268898230	53444	CGTTGAUGGAGACCGUGCAT	53445	GAAGCCGCUCTTCTACGTCATUA
259869390	53446	GGGCCUGATCCCTGAUGAGAT	53447	AGAGCTCCTUCAGCTTCCAAUG
261189785	53448	GAGTCTAGCCAUCCCAGAGCUA	53449	GGCAGGAAGUTCGAGATUCGG
262550795	53450	CGCGAGAACAGCUGATGAGAAUA	53451	ATCTGAACCAUGCTCTGCTCUG
260055075	53452	GCACCATUGCTTCTCCTUGAAAT	53453	CCTCAGGCAUGTTCATGTCAUCAA
264881581	53454	TTTCTAGGACTCUGGCTACAAGCUA	53455	TGAGAGAUGAGAGCTTGGCTTTUT
261267734	53456	CCAGGGAUGGAATCGCTCAUAC	53457	CCCTCTGATUCACCCCTCAAAATUAA
325586707	53458	CAAAACCGAGGCCUTCACAUC	53459	TCCACCAGAGUTGTCCUCACT
236361235	53460	GTCATGGAAGAAAUGTTGGAUAAAGCAT	53461	GAGTCTGTGUCAGACAAATCTAUGGA
235389989	53462	CATACTCAGUAGACAACATAAAGCCUCAT	53463	GAAGTCCCAGCUTGGTAGAAAAUACT
235988966	53464	GGAGTTATATUTCCTTTCCTUGCAGAGT	53465	CACAATTTCUGTGTTTGTUAACCAGAGT
241777431	53466	AGTGTCTGAAUCAAATGTTCTCTUGGAT	53467	GGCCTCCUAAAAGTAGACTGGAAUAAAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
333693994	53468	CCACACCAGGGCAUCUAGACT	53469	CCCCTCCATGUTTCTCTCTCCUT
269436192	53470	GGGTGAAACUGGTTGATCCUGT	53471	AGCCTAGGUCCCTCCTUACC
262882764	53472	GGUCCACCAGAAUCCAGAGAAAG	53473	TCCCAAGUTCCTCACAUAGGGT
331203591	53474	AGGATCCAGACUCTTCAGUCACT	53475	AGCCATCCUAAAGGAAGTGCTUT
264127330	53476	AGCTCTCCAGUTAGCAGTATUCACT	53477	GAGTAGGATTTACUTCACATCGTGTUCA
268257852	53478	GTTTTCATTTUAGAAAGCGGCCTCTUA	53479	CAGCTAGTGUCTTGAATTTAAGUCCCA
268408220	53480	TGTCCGCGAUGGAGGUG	53481	AGGCUACACGGGACUGAGA
266011911	53482	GCTGAAAGCCCUGAACCUGT	53483	CCACACGUCCGTGCTUCT
266564837	53484	CGTGUGACCGAAACGTGUCT	53485	GAAATGAACAGCGAGGUCTTTGUG
266032291	53486	GCTACATUGGCGTGGUGAAC	53487	GCACACUACGUGCAAACCCT
263131618	53488	CCCCACACAUGACACAACCUT	53489	TTCAGCTUGACGACCTGCUT
325096537	53490	CCACAGCACCAAUGGCCUAT	53491	GAGGUAGAGAUGAAAGAGGCCAAG
324670052	53492	AGAGGAGAGCAAUGGGACUGA	53493	GGTGTAGACATUTAGGCGGTCTAUG
323466270	53494	AGAAUGAGAAGGAUGCCACCAC	53495	GGGTTCATUGGAGACATGATAGAAUCT
323619319	53496	ACCCAUTGAGTCCUCCCAAAAAC	53497	GTAGUAGAGCACGGCUGACA
324985108	53498	TGTCTCAAGGGUTTGAAGATGUGAC	53499	GCTTGCTGUGAGAATAAGGCACUT
326535274	53500	AGAGACCAGCUGCATCUCAAC	53501	GGCCCCUTTTTCCTGAUACCA
320474322	53502	GACACATGCACUTAAAAGCAUCCC	53503	GAAAGGAAAGACCUGCCACUCA
333237526	53504	GTGCCCUCCGTTACCTGUT	53505	GAGGCGCUACTGCUCCAG
316079072	53506	CATGGAGTUCATCAGGGTCUGG	53507	AGGCACUGCATGTCAACTUCA
266787245	53508	AGCCTCUCCATTCCTTCUCACA	53509	CTGGGAGGUCTCTCCAUGGT
324657805	53510	TCATCACGGCUTGTGCCAAUAA	53511	CCAAGCAACAUGGCUGCAC
263476312	53512	GTCTGTGCUGTGACCUGAAGT	53513	CAGCATTUCCAGGAGAAAGUGGA
257751478	53514	GTUCAAGAAACACAAAACCAUGCAAAG	53515	CCATCATTCCCAUGTTTCTCTTTTTGUT
264850810	53516	CCCACCUTTGACTUAGAGGGAA	53517	CTCTCTCAUCAGAGCTGCATGUC
320206574	53518	GAGATGATGGCUGCTGAGTUG	53519	CAGGGACCUGGTAATACUGAAGGA
315688282	53520	TCCACAGATUCAGAGCATTCTUCAC	53521	GGAACAGAATUCAACTGAGGTGTUCAA
325584775	53522	AACAGAAAACAUTGCTGGUAGGAAGA	53523	GTATUAGGGCAGGGATCATTUGGAA
269448034	53524	GCCTGAUCCCAGCAAATCUGA	53525	GGTGTTAAAAATGUAATCATGGCCCTUT
267930726	53526	TTCAATCAATATUTGCCTGGCAUACAAC	53527	TGTATAACATAACUGTGTGGTGGGTTUT
267554089	53528	CAATGATUGGACACTCTTUGCAGAT	53529	CATCCTTTUGCCCTCCTTCTCUC
267955973	53530	TCTGCTGTCAAAUAAGAACAGTCTGUC	53531	GGGTCAGTAATUGTTTTCTGCTTTGAUT
269411430	53532	CTTGTCCAAAUACCGAAATACAUCAGG	53533	ACAGGAUGCTACCCGUAAGGA
261098978	53534	CAACACACAAUACAAGGAAATGCAUCA	53535	CCTGAAATGCUTGGATGACATUGAAAAA
265929880	53536	CAAGCATTTCUCCAACTGTUGCT	53537	TCTGCCCUAGACAGTTTTTATTCACUCT
268660765	53538	CACCTTTTTGUAAGACAGATTUCGCA	53539	GAACAUTCGACCUGAGAAAGACAGA
258878704	53540	GTGGAGCTUGAGCTATGACACTATUT	53541	CATTCTAACUGGGATGTTGUGAGAAAGA
259414039	53542	CTTACCTTAGAAAATUGTGCATTTACCCAUT	53543	CCAGCATCACUCATGTTTAATTCCATUT
323603975	53544	GAACATCGUGGAAAGACTGAATUGG	53545	AGTGTTGGCATACUTTGAACTTTCTCTUA
324641253	53546	GGAATTCCATTTTUCTCAGCCATTAAUT	53547	GAAACTUCAGAACCCAAAGTCATUGAG
291688986	53548	AAACAACUAAACGCCGCTTUCC	53549	CTTAGATTCTUCCAGCCTTTTCCTUCA
313626710	53550	CCACUCACGCAACUAGCCAAA	53551	ACCTCTTCCUTCTTACTGAAAAUGGG
290781760	53552	CATCACCAAGUACTTAUGGGAGCA	53553	AGTACAAGUTCAAGCUCAACCCAAT
305593159	53554	GCAAGGAAGCUTAAGGCGGUT	53555	CTCCTCAGACAAAAGUAGACAATCUCT
303987357	53556	GTGGTATGATAUGCTGGGTGUCC	53557	GGACCTGAGUACATTGATTCCTTTCUT
327588995	53558	TAGTGAGCCCCAAUCTGACUT	53559	TGCAAGATCACCAUCTCCATCTUC
255883354	53560	GACGGTCTTTUCTTGTGAGTCUGT	53561	GGUACACACAAUAAAAAGGACAGCAAAT
261266070	53562	GTCATTGCAAUTGAATGCAUGACA	53563	CTATGTCCTTUGTGAGGTCTGUGAA
269245809	53564	GATATGGTUCCCAAGGACTAGUGAC	53565	TGAGTGCTACAAAAUGCACATTTACUCT
266628086	53566	CACTTGAGUAGCTTGCTTUGCC	53567	GCAATTGCUACAAATGGCCTAUCAC
258413741	53568	ACCTTCUGGAGTTCCUGGACAA	53569	CTCAAGTATGUGCCTAAAACTATAUGCC
269200362	53570	GTGAAUTCAGTGTCUCGAGAACCT	53571	CCACCAACAGCAUGTTTTACTUGT
267495439	53572	CATTACUCAGTGCCUGCAAGGT	53573	CCCTTTTTGTTUTTGCCTCTCTUCA
313984161	53574	AGACATGAAGTUTCCATGCTAGTUAGG	53575	TTTACCAAGGCAGCAUCTACTTATUCAA
317792115	53576	TGGCAGAAUCAATTCAUGGAAGCA	53577	CCTGGTATTCACAUGAAGGTCATTUCAA
316918140	53578	GCCTGCTUCTCAGAAGUGACA	53579	CCAAAATGGTTUCAGCTTCAGTAGAAUT
332756489	53580	GCCGTCCTUCCAGGAACAUAG	53581	CCTCTGGTTTUTACAACAGGAAAUGAAA
314796672	53582	GATGGCTTCUGCATCAACTTCUAAAT	53583	CCAGCCCAAAAUGACCTAATATUCAAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
313879543	53584	CATATGTCCTTUCAATGGCCCCATUA	53585	ACAGTCAAUCTTGCAAAGUAGAAGAGAA
263654285	53586	GCGGATCAUGTCGTCGUACA	53587	CCTGAGCGUCCTCTAGCUC
255670846	53588	AGGTGATCUACCCGGACUCAG	53589	CACTTTAGACTCUGGATGTTGAGGUAAT
315367362	53590	GCGTGUAGGAGCTCTGGTUG	53591	CTTGTTCAAAGCCUTGGGAGGUA
313122836	53592	CAGAACCGAGUGGCAGGUA	53593	AGTGTCATCCUCAGTGGCTUG
313745458	53594	CCUGGAAATTUGGAAGCAGAGGAA	53595	TCAAGCTGUCGCCCTATGUC
312915925	53596	GGGCTTCUGGGCTTAGAAGUT	53597	CACCCTGUCTTCAGTGAUGGA
267905502	53598	GACAACUACGCAGATCTTUCGGAT	53599	CGTAAAGCCUACGAGTTGAUCCT
316116860	53600	AGCTTACCTTUACTTTGCCATTCUGA	53601	GGCTACTAGUCCAACTCTATUGCC
317341497	53602	CUCCTTGAAUACAAAGGACGGACAT	53603	ACAGTTTTCTTGTUGATCCTAGTCGTUT
327119937	53604	TGTAAACAGAAACCUGGTGGTCAATUT	53605	ACAATTAAAUGTTGTTGGUAAGCACAGG
239502259	53606	TGAGCTGATTTAGUTGAGACTTACGUG	53607	AACTTCTUGGCAAGTCGGTUAAGA
266633794	53608	CCUTTTTAATACTTUCCCCAAGAAGCCA	53609	TGACCACAGGCUTGATGTUCAC
267329214	53610	GCTGGGAGUATAGCAUCACCAT	53611	AGGTCTGCAUCTGTGCCUAC
267940853	53612	GGGACCAGACGCUCATCTUC	53613	GGAGTUAGGAGAGCACCCAUCT
324505753	53614	CATTTCAGCUGCAAAGATTCCAGUA	53615	CUGATAUGGGAGCCAGGGAAG
323813376	53616	AACCACAGCCAGGAUCAAGTUT	53617	TCAGATTTGCUCATGCCTGUCA
265612886	53618	GACACACAUGCAATTATCTGGCUAA	53619	CCTGCAGCUGATACAGCTCAUC
260865767	53620	CCTTCTTAUGAGGCAGGATUCGAT	53621	GAAGTATGGCUCTTATAATUGCCCGAA
253819444	53622	AGAGGGAGAAGGGUCAGTTTAAUGA	53623	AGTTTTGCCTTCUTTGCTTGATTTGTAUT
260297021	53624	GCCCTTUGAGGATTAGTAAAUACCGA	53625	AGAGAAGUCAGAAGGTTGGAGAUGAA
268916899	53626	AGTGGCGACUGAATGUGCAT	53627	GGTGTTGATTTUGAAATCCATTGGTUCA
258982148	53628	ATTACCTGAGACCCUCTGTTCATAUCA	53629	CUGCAACAUGGAAACAGGAGAAAC
266096782	53630	AGACACCUTTTAAAACUGAAGCCAGT	53631	CCTAAACTCAAAGCUCTTGTTCCATUAA
267861113	53632	AGCCCTCTCUCCTGCTGAATUA	53633	GGTTCTTAUGCCTTTGAGGATUGAAAAA
258625200	53634	GAAACTACTTACUGCCGGTCCUG	53635	ATGGTCATCAATUGACAACATCCATTUG
316827018	53636	GGCTATGUCACCACCAAUGGA	53637	CTTACACATTGGUGAAATCACATTUCCT
317122186	53638	AACTATAATATUCACCAACTGCCAGTUT	53639	CTTTAGTTGGCCAUGTTAGAGGAAGAUT
317407157	53640	TGTGTAGCAAUTCCTGCTCUGT	53641	TTGTGTGATCUACGGCAAAAAGGTTAUA
268903974	53642	GGGCTAGUGACAAGGAUGAGA	53643	TGGGCAAUCGGGCTCTCUA
267661364	53644	GAGCTGCUGGACTTCUCACT	53645	GAAGCGCACCUTCTCGAUG
267771047	53646	GGAGGGTTCTUAACTCTTAGGAGGUT	53647	CCTTTTTCTUCCCCAGACUCCAG
234923091	53648	CCAGAGAAAUCGCCTGGAAGTUA	53649	CAACCGCCGUGCAAGAUG
263306606	53650	AGGTTGUCCGGAGCCUAGT	53651	CAAAAGCTGAGAUGAAACAGTGTAAGUT
236239648	53652	GCCAUCTTUACGAACCAACCCA	53653	CCCCATTAGCUCAGCTGTTTTCTUT
234934226	53654	GGTGCTGACCAUGTGGACAUT	53655	TGCCAATCAUGGAATTTTCTTTCUCCT
235612037	53656	TCTAGAAUCCAGACCTGTCAGUCAA	53657	CACCAAAGTACCUACTATGTGTGUGG
266570607	53658	CTGACCAUCACGAGGCUGAAT	53659	GAGAAACUCAGGTUCCGAGGAG
272362046	53660	CUCCACGTGUGCCAACAAC	53661	AAAGATCTTGACUGCCACTGTCUC
333688929	53662	CCCCACCAGUTCATTCACAGAAUC	53663	GCAGATGAAAGUGTGAGGAAATGAAAUT
333640576	53664	CACCTCGATUGGAAACGGGAUA	53665	GAGAAGGCCGUTCTCCATTACUT
332816475	53666	GCCTGGGACUCATGGAAAUGAT	53667	CAGGAGUCTCAAGUGAGGAAGG
323888893	53668	CAGCAAAGAUGAACACGATGAUGG	53669	TTUCAGGCAGGAGCUAGAGAGA
324434167	53670	CCACCCUCAAAAGATCCTTCUGT	53671	CACCATCACUATGTGCATCGUACT
324459827	53672	CAGGTUCACCAGGUAGAAGGAC	53673	TCTACCCTCCUCCCTAGGCUAT
261780504	53674	GACTGUCCCGGTACUGCAC	53675	GCCTTGTGUCGTCCACTTAGUT
326896156	53676	TTCATGAACUCCAGGAACTCTGUG	53677	CATCGACCUGGATGAGCUGAAG
260755651	53678	TTTAGCTTATCAAAUGCTGAGTAGCCUT	53679	CTCGGCTAAUAACACATCAAATCGUT
261918436	53680	TCAGAGTGAUTGCTTTGATGUGGAT	53681	CCAGATAGCUGACTCCACATUGT
332076288	53682	CUTCCAGGGATUCAGGCAAGA	53683	CCTGTTTCAUTCCAGATGCUCCAG
332032359	53684	CATUCAGGGTCUCGGCACT	53685	CCCCCAGCAGGUCGATTTUC
332160390	53686	CCGTCCACUGGTCGAUACCT	53687	ACCAAGTUACCCCATTGCCAUC
324641359	53688	CCATGGCAGUTCTCCAUGCT	53689	GAAGACGAAGUATCCAUGCAGAGA
261982492	53690	AGGAGATCUAGAGCTCUGACGAC	53691	ATACTTTCAACAGGUAATACAGCACCUT
254179374	53692	ACTGTTTCATTUCACGAAGTTTGATGUC	53693	ACATTTTTGAAGUCCCAAATCCTCCUT
260826892	53694	GTTTACGAUCAGCCACAGAAATTCTTUT	53695	CCTAGGAAUTAGCAAGGAUAAAGCAGG
266799779	53696	ACTATGAGAUGTTCCATGACUACACGA	53697	TTACAGTTGUCAAAGCTGAAGGAUGA
323547167	53698	CTTAGATGTTTGCUCTGAGTAACTTTUGG	53699	CGGGCGUAAACACCTTCAATUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328674656	53700	GACTACAUCTCCCUCCACAGGA	53701	GGGTGUCCGCGAACTUG
227640662	53702	CAACGCCCAUGTCTTUGCAG	53703	ACTTTCTGTUACCTGTCGCTUGAG
228971278	53704	CGCCTTUCGAGCAGTACUCC	53705	GCTAGGGACCCCUCACATUGT
323309072	53706	CTCCCTGCUCTTCCATTUGGT	53707	TGAAGTAGUAGACGCAGCGTTUG
325536675	53708	CCGAAGGAUGAGCGAUCCC	53709	GACAGGUGGAAGGACTTGAGTUT
320178736	53710	TCCCTTTTGCCAUTCATGAGATTUCT	53711	TCAAAACTTUCCCATTAGUGCAAGGA
326882904	53712	GGCAGGUACAGATACTTCAAUCACT	53713	AGTGTGTGCUGTCTTTTTGATTTTUCT
332948560	53714	GGGTUCCTAGAGATUCCAAGAAGA	53715	CATATGTTGUAGAAGCAGCUGGACA
332408000	53716	CTGTTGAGTGUGGCCTCCUA	53717	GAACATGACAGGUGTCATAGAAGATUGA
332947719	53718	CCCTUCAGAAGCGAGUGGAA	53719	TUTCAGTTTTUGCGGAAGAGGAAAG
332932500	53720	TGTGCAGAGGAGGAUGATUCAGA	53721	CCTGTATGUTTTGGTTCAUCCACAT
333547171	53722	AGACACTCCAAAUGAGTTCTTCACAUT	53723	GCTGTGCUATATTAATGCUACGAAGGAT
314531612	53724	AGTAAAATGGTCUGGTTCTTCCCTTUT	53725	GCTCTAACACACUTTCCTGAAUGAGA
266573751	53726	AGTGCACAGAUATAGAATTCAGCTUGG	53727	CACATGCAACCUTGCTCTTUGT
266897915	53728	GACATTAAAGCAAUGCAGAAUGGGA	53729	GTTGGATGGCUTTAGACTCTACATUACC
263528046	53730	GCCTUCAAGCATCCCUGAAAGA	53731	TGAGUCGGGUCCGACAGAA
267902842	53732	GCTTCATGTCUCCCCTTAAAATAUGCT	53733	AGATGGAAAUGTCCTCTGCUCAC
257317130	53734	ACGTCTATCAAUGTATTGAGTAGCUCCA	53735	TCACAGCTGTUGATCACATTGTATTUCT
259120059	53736	ACTGGCCAUGTATUCCAGCAG	53737	CGTCTTGGUCCAGTGATGTCUA
267842440	53738	GACAAACATTUGCTGAGCACAUACAA	53739	CTTAGCACAAUTATCAACUCCACCAAAA
259050464	53740	AGTTCATTTTCUCCCATTTCAACAUCAGA	53741	GGAGCAGUGAACTGTTGUCCAA
262953073	53742	GTACUGTGCTTGTUGACCACCT	53743	AGACGUTTGCTGUCGGACAT
293544600	53744	ACTTTCUCAGAATTCCAUGCACAGT	53745	ACCAGCAUATTCACCAUACAAGACAAT
292651550	53746	CUAGGGTUCGAAGACCAGAAACAT	53747	AGGTCUTGATTTTTGTUCCCCAGAA
291067092	53748	ATTTGCCTTUGAACAGATGTGGTAGUA	53749	CATCTGTGAAUCAGAGTACATCCTCAUT
292325885	53750	AAATGTCAAUGTTTGCTUGGCAGAT	53751	GCTCTTTACCCUTGCTAGAATACUGG
289607975	53752	AACATGTTUCAGGCTAAAGCAUAACA	53753	GGTTATCAGGAGUCAAAAGAACACUCA
292824856	53754	GGCGUCAAGGGATUAAAAGCAAT	53755	GCAATTTGTGGUCGATCTTTGTACUT
223193687	53756	CUTACAAACAGATAUGACCAGAAGGCA	53757	GCTCTTCGCUGTTTTATCACTUAGAAAC
329085597	53758	CGGCAGAAUGAAGGUCAAGGAG	53759	ACATTGGTACUGAATGCTTCUGGAAAT
222832849	53760	CCGCAAAAGGAACAUGGAGAAAAAUAAA	53761	GTATTACCTGUGGGAGATCTUCCAGA
328316775	53762	CTCCCCATCUGTGCCATTGUAA	53763	GGGACTTCUGAGGTGTGGUG
332087631	53764	CGCCGUAACCCGGAUAGG	53765	CGGCGCUACAAGUGCAAG
242674594	53766	TTAGGTGAGGAUGTCAGTGACUCT	53767	CAGGTTTUGAGCAGTCAUCAACC
240578276	53768	GAATGAGGCUCAGAGAGGGTAGTUA	53769	TCCCCACAACUAAAACACTCATCTUC
268594903	53770	CTTCACAGACUAATTATGTCACUGGCA	53771	TGGGCCACUGTTATAAGCTTUCAA
267799145	53772	CAGGTTAUGGGACCUGGAGAAA	53773	ACCCAATTAATCUCAAAACAGCTAUGGA
267606854	53774	AACTGTGGAACUGTAGCTGTTAGUG	53775	GGGCAGGTTTUAAGAGATATGTGAUGA
265548304	53776	TCCCTAAAUGCAGGCCACTTUT	53777	GTTCCUCACCCGTACGAGUC
316048125	53778	CTCCCCUCCTACTACACAUGGT	53779	GCCACATCUGGCTTGAAATTCUACT
316169219	53780	ACATCACCAUGAAGTGGCUGAA	53781	GCTCCTGGCUCTCATCAGUCA
331698191	53782	GTTCAGUGCACGCAACUGT	53783	CCAGAAACUCCAGGUGGGA
331887722	53784	CCATGGCUCCTGTUCACAGAAT	53785	GTGTGTGTGUAGAGGGCTUCC
265297255	53786	GGAGATGTTUGTGCACCCUGA	53787	ATGCAGGAAGAUGAGGCCAUAC
267731627	53788	CACATTTAGAGCAUGGAGCUGAGT	53789	CTGCUCACACCCATCTTGUGT
267792033	53790	GGGAATCUGGGAAGCGTUGAT	53791	CGCCTCTGATUTTTAACCTTTGACUC
265825975	53792	GGGTCTCAAGGGUTTCACAGUT	53793	GCUTCCTGTAUGAAGACCAGACT
328430545	53794	ACCCTCUAGGCTCCCAAGUC	53795	AGGAGTUCACAGCCTTGTTUCC
325024465	53796	CCACGTTTCTUGGAGTGCACUAT	53797	CCGAGGAAUCUGAGAGCGAGA
325258883	53798	GGCCAAAAUCCCAAGGAAGAGUT	53799	ACAAGAUGCGGAGTCGTUGG
313275399	53800	GCTACAGCUTTGGCCATUCC	53801	ACACACAAATTCTAAUTAATGACTTTGATGTUT
270380019	53802	GTTTAGGGUTTGAAGAATUGCCAAGT	53803	GGAATTAUGCACCCAAUAACAGCAG
272657385	53804	ACAAACAGTCUCCCCCTACAUGA	53805	GGTCCCCAGCUAGTGATTTTUGAAA
269691508	53806	GCACTTAGGGUGGCCCAUT	53807	GTTCCATGACAGAAUTTACCAGAAAUGT
269580192	53808	GGGAATGTGAGUGAGAATATGUGAGT	53809	AACCCAGACGUTAATACTTTGTTTCUGA
271086981	53810	GAGTAAGCCAGUCAAATAGAUGAGAAAGA	53811	TTTAATTCGCTTUAGGCATTCCATGUG
315723559	53812	ACAGCTGTTTCUTGTTTGTGCTAGUA	53813	TGTCATTCCAAUGTGACTGUCCA
315584640	53814	CAGCCCCUGGAATGCTTCUA	53815	AGCAGCCACACUAGGTTTCTTUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317509849	53816	TGCTTTUACCACACAACTTTTUCAAACT	53817	GGAGAATTACCTGUTTAACTCCCATCUT
320581301	53818	CATAAATCCAGGUGTGCATAAACATGUC	53819	GCTTTGTAATTTUGTTGAACAGGAUGGT
317916934	53820	AAGTTAGAUAGTCCCCUACCCACAAT	53821	CAGAAACAACUCAACATGCTTAGCUT
266362181	53822	AAAGTCACTCTUGTTTACCCTTGUGT	53823	ATGGTTTCATGCAUAAACTGCCTTTUT
265618725	53824	GCACTACTUGCCTGATCAUCCA	53825	TCTGTCTGTCTUTCTTTCTCTTTGTUCC
268866598	53826	CTGGAATGAAATUCATCTGCCATGTUT	53827	CTTGGCCGUGTAGGACCUG
321289888	53828	GCACCTACTUGGAGATGGTAAGATUCT	53829	AAGAAGTCAGAAAAGUCAAAGAAAAAUGC
268269781	53830	GACAACATTUAAGTGTGGCCAUGT	53831	CGATTAATAUGCGTGTCTGUGGGA
263166771	53832	CTTGAACTTCCGUAGAATGCTGCUA	53833	TCTGTCAAATUCCAGAGTTTTGGACUT
257637861	53834	GGGTTTTCTTUGCTCAGTACATUG	53835	GCTGTCAGCUGCTCGTCAAUAG
267611600	53836	ACTGTGTTATAUCTTGGGAGCUAGGT	53837	GACCAAGGAUACTGACCCCAAUAG
262282412	53838	CTTGGCATGAUGGTCTATGTATUCAAC	53839	AAGTGAGGCACUCAGAATTUAACAGAA
265045629	53840	CTCCCAGACAGUTCTCGTUCA	53841	GTGTCACCUACAAAGACTGTTTTUCC
268017996	53842	TAAACACCATCTAUGGCCAAATCTTUAG	53843	CAAGAGGCAUAACATAGAGCAGUCAA
266395956	53844	AGTCTGTTTAACAAAUTCCTCACCTGUT	53845	TTCTGGAACACUTCAGTCTGAAUGG
268724389	53846	GGGAAGAGGUTTGTCCATTUACC	53847	GACTTTCTCAGCUGTTGCTTTTUCAA
268496741	53848	GTAATCATUTTAGAAAAGCUCGAGCACA	53849	GGGCCTCGTUGATTTTTCTTTCAUT
259376917	53850	GAAGCCACAGAGAUTACAGGGUT	53851	GTGAGATGACUCTGACTTCATTGUCT
267244955	53852	TTTGCTUCCAAGAATGUGAGAGGAT	53853	TGTCATAACTCAAUGCAAACTGCUG
327049001	53854	CCAGTTTAAGTGUTAGTTCTTGGTGUGT	53855	GCTTGTCTUCAAACTGTTGTTAAUCCAA
326639133	53856	TGTTGGCAUGGTTATAAACCUCAGT	53857	GGTCGAAGTAAUGCCAATGTCTTTTCUA
256930703	53858	TTGTCTGCCCAGUTAGAATGATCUG	53859	CCAAAGGUGCCGGTCGUAG
254085295	53860	GCAGGGCUGAUGAGGAAAACT	53861	TCCUCAAGGTUGGGACAACAC
224037450	53862	GGCTCTCUAGGCCGUGGA	53863	CCUCCCACCCCGTGCUA
223420540	53864	CCAGCUCACTGCTAATTUACAACAA	53865	GCATTAGTAATACTUACTTGCTGAAATTGAAUC
222713662	53866	GGGACAGUCGAAGAACTUCAG	53867	CATTTCTCCCUTATGCCGTGTTUT
222660691	53868	CAGTCATGTGAUACTCAAGTAAGCTCUT	53869	AGATGGTAAGTGAUCCAAAATCAACUGT
223043846	53870	CAGAGAACAATGUACCCTGGAAGUT	53871	AAGGCATTATCCUCATATTTATTATGCTUACT
222892884	53872	TCTTTGTTUAGCTTGAACAUGCGAAAG	53873	TCTACCCTTAGTUGTCAATGGCAAAUT
223524897	53874	GGGTCAGATATAUCAGCATTAACCTUGA	53875	TCTGTAGTTCUAGCAGCTTCTTTTCTTUT
222336971	53876	CTGTCATTCAGACAACUACTGAGCTAUT	53877	CTCTTCTTGAAGUTTTTCAGCCTTTUCT
222167343	53878	GGGTCAGGGAAUTTATCTUACACAC	53879	TCTCTCTTCAGAAAUGATCCCACCAUAT
224244809	53880	GTCGAAACTUAGAGCTTCAGGUACT	53881	CGACTGTGTTUTTCCTCTAGCUGT
321093564	53882	GGCATTGTTCAAUTCTTCAAGTCCAUT	53883	GCCCAGCTTUACTGTGACATAUGG
263407974	53884	GCAGGAGGUTTCGGCUAAGT	53885	TCUCCCCCAAACAAGCUGAAG
266940559	53886	CTCCCCTTTTGUAAAAACCAAGATUCC	53887	GCCTATGATGUTTGTGCTATCUACCAAT
268318980	53888	GGGTTGGGUGAAGTGTTTUGG	53889	CCCCTTTCUAGGAAGTAAGTGAUAGACA
265931310	53890	GCCATGGATGUCTCTCACTGUAA	53891	CTTCAGAGTAGCAUCAACTTCATAGUCC
325458727	53892	TGACTUCCTGGTCATUAGAGCAAAAG	53893	CAAGCATUGAGAAAAACGGTGAATTUT
323757613	53894	GCTGCAGCUACATGGUGT	53895	CCCGCUCCGCTTCTCTCUA
325923054	53896	TCTTGCTGAUTTCACTGCUGGAT	53897	TTGTTTGUCAACCAAATAATGCUGAACT
269044788	53898	ACGTTTGCCCAAAAUTGTTCTGUT	53899	AAAGGAACTGUCAGCTAATGTGAUGA
267919096	53900	TTGCTGCUAACAGCAGAGCUAA	53901	CTCAGACUAACACCAGGTGGTTTAUAAT
262275112	53902	GGGAATUGGAAGCAAATGACAUCA	53903	TCTTTCCGAAGCUCGGTUGG
266983730	53904	AAAATAAAACCACAAUGGTGGCAUGAA	53905	CTGCCAGAAAAAUTACUAAGCACCAAAT
266822086	53906	GAAGAACTCUAAAACAAGCATTTGCUGA	53907	GTTGCAATTUGCAGGAACTAUCACAT
268598630	53908	GCTCAGCCAUGTTCTGCCUAA	53909	GGAGAGAUGAGGUGGCAGAAGA
316815343	53910	AACTTTGGCAUTGAGCCAGTTUT	53911	GGGCGCUAAGGTGAGGAAUG
239174003	53912	ACGATACGTCCUATGTAATTGAGAGUGA	53913	TGTTACATAATTAGUAGCAATTTCATTGTGGUA
262290449	53914	CCAGGGACTUAAGTTAACGAACAAAUT	53915	CCAGCTCTACCAAUCTCCTGATAATAUGA
242598542	53916	TTCGAAAACUGTATCTUCGGGCA	53917	CTGGCCGAAUTTTATGCTTTGUT
264785472	53918	CAATAAAATGGATGUTCCCCCAGCUA	53919	GACAGTGGAAGCUATGGTCATATTAUCA
240518556	53920	ACAGTCTAUGGCCATCACATACUCT	53921	GAGGAAATUGATCCCAAGUCAGAACT
227958207	53922	GCGAGGCCAAAGUCTGCUAT	53923	AGTTCTATGAGACAAGUCGGCTAGUT
229692679	53924	GCCAGAAAAUAAGGCCCAAAGCUA	53925	GTCTACAAGAUGAAGAGTGGUACCAAG
228278945	53926	CCTCCCCTGUTCCCATTACTCUAA	53927	GGACAUCCCCAGAAAAGAUGGA
266541284	53928	CCCATGUCACCCAUGAAAGCA	53929	GTGCCGAGGACAUGCCTAUAA
266946463	53930	CCCUAAGATUCCCAAAGAGCCAA	53931	CCTCCCACCCCUCATTTCAUAG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
266720818	53932	ATTTATTTAAATCUGGTCCAGCCTGUGA	53933	AGACCACACCACUATGCTATTTUCAAAT
263145003	53934	CCCTTUCCTCCTGUCCACAAT	53935	CAGTCTTAUCCAGGCTCTCCUC
327696773	53936	GACATAACTTCUCATTGAATGCTCUCAGA	53937	GGTTTCCTTCUAAAGTGTTTTGGCUAT
327932377	53938	GCCCAAATTCCUAAAGATGAATGCATUG	53939	CCACUGGCAGCAAAGTTCTTATUT
230794256	53940	GGGCTTCUCTGTCAACTUCCC	53941	GCTTCATTAGGCUCTACTCTCCTTTTUA
317083878	53942	CCTGCACACCUGCACAUACT	53943	CCCAATCAUCCCGTCATTTCACUA
317843534	53944	TCAGGTCGUGGGTCTGAGUT	53945	CATCAACAUGGAGGACAGGUCT
327889062	53946	CGATCTCTATUTCTGCTCCGUGAT	53947	TCAUAGAAAGCATCAUGGGAAGAAAAGAA
316841361	53948	ATGAAGTCCAUGCCACCATTCUT	53949	GCTTAATUCAGCAAGACTGTUGAAAACA
315816607	53950	AGCAUGGGCAACCAACTGUA	53951	GCTATACTTGCCAAUGAAAATGGTTUCT
316360799	53952	TCTGACAAAAACAGCCAUTAGACUGA	53953	CATGCCAUAACAAAACTGGCUCAT
316142075	53954	GAAGCATTTGGUAATCATGTTTUGGGT	53955	GCTTGTCUGCAAGGTCTUCAAA
315782298	53956	CCTTCTTTGAGGCUGTGCTTCUT	53957	TGGAGATCTGUGAAGTTGTGUGG
264233117	53958	GCUTGTTUGCAGAGAGCCAT	53959	AGCCCAAUCTGCTGGAUACC
263815748	53960	CCGAACTCUGGAGTTTCCUGAT	53961	CAGAGAAUTCCCUAAAACCAGCCA
333208875	53962	CGCUCCGAGCCGACTUT	53963	GCGCTCUCGCTACCTGUG
332847259	53964	CAGTTGCUATGCTGTUCAGCAAA	53965	CTTUAAACCGCACCGUGCAT
333760947	53966	ACTTCTAATCCACUAGGTGCAAAATCUG	53967	AAGGCAAGAACAUCGGGAGAATATTUAT
319462880	53968	GCCGTTGATATUACTGTGGATACUAGGA	53969	GTTTTGGATTUCACAGGCAATGTAAUCA
321137555	53970	CCAUATTTGTTACTTCUGAAGGGCACAT	53971	CCTGCCGAGAAAAUTAAGTCCUCT
319506268	53972	CGGGTAAUGCGGCCUGAAT	53973	ACCCCATTATUAAAAGGTGGCTTATUGA
320012399	53974	GGTGCTGTUCAGGAAAAGCAUT	53975	CGCGGTTUAAGAGCATGATCTTUG
256979565	53976	TCTGCTCTCUCCCTTGGCUA	53977	CTGUCCCCAGGAGAGAATUGG
266640988	53978	CAGCCTGUACGAGAACGUCA	53979	CCCCTUCCTGAAGAGUCCAAAA
254013268	53980	CACCCATCTUACCCTGTCCUT	53981	GGCTGGUAGGAATGAGATGAUAGAG
259927399	53982	TGCACAACAUCTGTCGCTCUT	53983	GGGCTGTUCTCGCTGAUGG
261824085	53984	GGCCAAGAAGCUGGGTTCTTUAA	53985	GGCCCCUCACGAATGATCUG
328110604	53986	CCACAUCGCACCACAGAAUG	53987	GCGAGAAGAUCTTGCCGAUAAGG
326827641	53988	CCCAGCUGAAAGTGAGGATGUC	53989	CCTGCTCAATUCTCTGCATATCUGAA
324738087	53990	TTCGCTACAUGACTAATGGCUACAAAT	53991	CAATTAAGCAAAGAUTGATGTGCCCUT
323629843	53992	ACAATTGCAAAGAACAAAAUGGTCAUCT	53993	CCAAGGAGTCUAGTGATCTACAUGACT
260310754	53994	CTCUCCCCCTTATCUCCCACA	53995	TGACTTAUCACGCCCAATTGUCT
333608318	53996	CAAGAGUGTGGCUACAGAAGAGAG	53997	TGGTCAAATACTCUTCGATCATCAGGUA
333462665	53998	GAGGCCAUGAAGAGCAGUGAA	53999	GCTTCUGGTTATAGAGUGGAAGACAAG
333412753	54000	GGTACCCAAGUGTTGATAUCCACAT	54001	TTCACAAACAGUCAAACAUCAACAGAAG
312886343	54002	CTCCACCUGTCCCAUCCAC	54003	GGACCAGGCGGUGTUCAAAT
313422313	54004	CCTATGCCCUCTCCTCTCCUG	54005	AGGCACCCCCAUCTGAGUA
324154910	54006	CTTCUCCAGCACCTTTGUCCA	54007	GCTGCTTTTGUTCCCACGTTUC
264132004	54008	CAAAGGAGTGCUGAGGTTCCUA	54009	CCCGGAUTCGACCUCCAAG
265567607	54010	GGGTGAAGUTTGCACTTTCUACA	54011	GGTTCUCGCCCACCATCAUC
313719834	54012	GGTGGTCUTGGCAAGTUGGA	54013	GTCAGCTGCUTGCTGATCUG
314326256	54014	CACTTTGGGUTTTGGCACGUA	54015	GTACACACCCGUCCAGTUGA
224417294	54016	CCAAGAUCAAAGTACACTGUAAAAAGCAA	54017	CUGCATCATATTTCUCAAGGAACCAAT
223705993	54018	TTTTCAGTGGAGGUTAACATTCAUCAAGA	54019	GTCCAGTCTTTGUGGCTAAAATGTTUT
223561270	54020	GAAGCACAAGUATTCUGGGCAAAA	54021	TTAAATAACAGTAAAACACUAATCCAGCCAAUA
223800280	54022	TGAAGTCTUCATGGATGTTUGCCA	54023	AAGTAGCTACACUGCGCGTAUAAG
316362771	54024	GGGACAAGAUTCTTGATACUGCAC	54025	GGGCACCACACUCTCCTATCTTUA
317261642	54026	AGGCCTGAUGTCCTAGGAUGT	54027	AGAAATCTTCCCUGCCACCTTUC
332745996	54028	TCCTAGGAACGAGUGGAATATCUC	54029	CGCAACACUGGTAAGAUAAAGGGAAA
332304660	54030	CTGCCUCTTTGCTGUAACCCA	54031	GCGTTGUGGAGAGGACAUAGAAAC
332545429	54032	TTGACTGCUTCGTCGTGUGT	54033	CCTTGCCCUCTGGAAGAACUT
332479183	54034	TTGTTTTGTCCTTUCTTGTTGGTTCTUC	54035	GTUAGGGACAGACGCCAUGT
318603316	54036	ACGCCATGUGCGTCTTCUAA	54037	ACCAGTGAAAGGGUGCTGAAUG
319348565	54038	GCCTAAACATUCACCTCGGUCA	54039	TCCCCGCAUCCTGGCUAT
314485266	54040	CCTGCUCCACCGAGGTCTUA	54041	CAUTCCCCAAACUGCCAAACAG
320889198	54042	TCTGATGCUGGCCTCATATGTTUG	54043	TUCTTCAUAACGAGGAACAGCGT
318370646	54044	GGAGCCAUCGCCTATGAAATCTUC	54045	GAGAACAGAGGUTTCUACCCACA
262132513	54046	CCCGAUCTGTGGAUAAAGCCA	54047	CTCACGTCAAUGTCCCTGAUGT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314477155	54048	GGACUGAGAGGCCTCACUGA	54049	CACTTGTCCUCAAAGGGCATUG
258536143	54050	AATGGCAACAUCATGCCAACUG	54051	CCCAATCCUGACCCCTTTTCUT
260031094	54052	GCCAUAGACAGCAGCAUCAAGG	54053	CATTGGAUAAAAGGCACTGCTCUT
261752611	54054	GCTATTTCATCAUGGGATAGTTGGCUAA	54055	TGTTGTTGAAACUCCTGCAGUGT
268814516	54056	AGAAATCATUGGCAGCTUCCAGA	54057	GGCTCTACTGUAAGTACTTTTCCCTUT
257915763	54058	TTCAGAGTTCTUACATCAGCTCCATUG	54059	ATGAAGGATGACUTATAACCCTGATGUG
259414300	54060	GCATGAAAACAUACCCTATTGUCACCAA	54061	GTGCTCTUCCAGGAGAATATTACUGAAT
267357916	54062	TGTTTCTGTAATAUCAGTTTCTGCUGGT	54063	GACGGCAGGGAUTCTGATCUT
268283839	54064	CAUAAGGAACCACAGGAUGACGA	54065	GCCACTAACACAAUTGCCTGATATTTUT
268929249	54066	TTGAAAAGTCTUCTGGGAAAGTUCCA	54067	AGAAACCTTAAUGGAGGACCCCUAT
332592878	54068	CACCTTGUGCTGTCTGTAUGGT	54069	CTGGAGGACUGGATTGAGGAUG
332732847	54070	TCAGAAGTAATAACAUCCCTGCTAGUCA	54071	GGAGCTGGUGGAGTTTGUGAAG
317100535	54072	ACCTACTAAAAGUCTACCACCAGCTUA	54073	CAGGAATGUCCCAAGCCTTUGA
313433055	54074	CGTCCCTCCUTCCCCATACTUA	54075	CAGAAGCTCCUGGTACTCGUC
325647178	54076	CTCAGTCCCUAAGCCCATCUG	54077	CTCCCTATTGGUTCTCCTCCAGTUA
324590176	54078	GGAAGTUGGGAAGGGATCTGUG	54079	CCACUGGAAGGCCATTTGAUG
319825472	54080	CAGACTUGGGATGATACUCAAAGCA	54081	ACTCCTAAAUGACGCTGGCTTUT
327558349	54082	CTCATCACTCUGATCCTGCACUA	54083	TGCCACTTTTUACTTAAGACTGAUAGCA
326499211	54084	AATAAGGGAGGCUCATTTCTTUGCT	54085	GCATCGTTAAGCUATGAAGTGAGUGA
327027961	54086	AGCTGTGCUGTGTACAGUAGG	54087	TGAGATAGGACUATAGTGGAGGAGUGAA
327146935	54088	GGAAATGGGUCTACAGAGATGTUGT	54089	CTTCTGGUGAAAGGCCTAACATAUCAAT
326605171	54090	TGAAATCUGGCTTGCTCUGACA	54091	CCCCATCUCTTCAAGAGTUCGT
333418107	54092	ACTGACUGCAAACACGTGTGUA	54093	TCTGATGGGAUGAGTGATUACAGAA
325080064	54094	AGATGATGCUGCTGACTGCUC	54095	TGACACCTGUGAAAGAAATTGTTCCUAT
323728973	54096	CGAAGGCUTCCACAGUCGAT	54097	CAACCAAGAAGCUGTTTTUACAAGAGAA
325026780	54098	TCTCTTTCACCUCCCCAUCCAA	54099	CTCATGTCUCCAGCAGUGACC
324277351	54100	CACAUCAATCGATAUGCAAGAAAGGA	54101	ACTCAAACUGGAAAACATUGGGACT
326131598	54102	GGAAAATGCAAAUGTCGTGGUGA	54103	ATCACTCGUGAGGGTGTGTATATUAGA
324857841	54104	GUGCTGCCUCAGAAGAAGAAC	54105	GCCATACGUGTCTTGGTUAGCAAA
324941701	54106	AAGTGAAGGCAGUCTATTTUAGAGCAAA	54107	AGAAATACGACGAGUCCGGTUG
323832105	54108	CAGAGTTGTCAUGATGAGGAAGAUGA	54109	TTCAGCAAATGTUAGGACTCAGGTUT
325709609	54110	CCGTGCGATAUAGGTAACAGAATUGA	54111	GTTTTGGTTTUTAGAGGTGATUGGGT
327591588	54112	ACATTTCTGAAAAGGAUCTTAGCTCAAUCT	54113	CCCAATTTTGTUCGGACATTTCTUACA
333190474	54114	ACTGTTTTACCTTAUTGGTCCAAGGAUT	54115	TGTGCTTTTTGUGTTGGTTGCUT
326888191	54116	TACUCATGAAAATGGUCAGAGAAACC	54117	GCCTTGACGAUACAGCTAATUCAGAA
280776917	54118	CGAAATGACAUTGGACCCUCAGT	54119	CATCAGCATATTUAGGCAACCCTTTTAUT
278503027	54120	GAACTAAGATCCUTTCCCAATGAAAUGG	54121	TGTCCATCAAAGUCACAGAGAGUAGA
278630632	54122	GAATGTATUGGCGACAAGGCATUT	54123	TCATACTGUCGCAAAGCTTTAAGGUA
278966678	54124	TGCTGATAGUAGAATATTGTGCTUAGCC	54125	GTCTCTTTTTCCCAUCTTCGGTATUGAT
264524305	54126	GGGAGCUACTTCUCAGAAGGGA	54127	CTCTCTTCTCAUCCGCCTACUCT
317197320	54128	TTTCTTATGUCATCCAACUGGCCAA	54129	GGATGTTGAGUCCACTACGGTTTUAA
316372292	54130	TATGATTTTTAGGATUACTTGAATCAACAGUCA	54131	AGGAAAUAGCAGACAGACAGTAUGGA
261096698	54132	GCTGAACGUGAGAAGGAUGGA	54133	CCTCTCAAUTCTTTCCTGUCGCT
266256511	54134	GTTACTCAATUCATGCAGCAUGCAA	54135	TCTCATGCCUAGCTCTCTAGCAAUAT
265170506	54136	ATTATAAACUCACATAGGAGTUAAACAAAGACA	54137	CCCCTCTGCUCATGGTTCUC
326443437	54138	CTGCTGUAGGAAGGCAUGCT	54139	CATCCCTAUAAGAAGCCCTACAUGG
260627787	54140	GTTCCCAGGGAGGUTATATUCAAAAGAA	54141	TCCAGAATUCGTTTCCTTTTAUGGCA
242362921	54142	CATGTATGGCAUATGCAAAGUGAAGAAT	54143	AGATCAAATGAATUACCTATGTTATGTTAUGGA
241676359	54144	TCTATAACUCGGTCTTCAUGCAGAGA	54145	GGAATGUGAGGTATTGGUGACAAGG
333261100	54146	GCTAAATGGCAAUGGATTCAACGTUT	54147	TGCAACTTUGCATCACGAAAUGAC
333756017	54148	CCCCTTTGAUGATGTCGUAAGGA	54149	TGTGCAGATUGGACATGTTTTGUG
332261985	54150	TCAAAACAGTAAUAAGGCTTTCACCUGA	54151	CCCTCGCTTUGAAAGTGTTCTTCTAUT
314235992	54152	CTTGATGTUGCGTGGCTTCUG	54153	CAGATTCCUTTTCCTGUCAGGGT
313633111	54154	TTGAACATCTTCUCATACACTGCCUT	54155	TGCTCACTTAUCCTTTCCCTCUCA
314922110	54156	GACCAAAAGCCUGGAGCUCA	54157	CCTCAACCGAGUTACCGTGTUC
325013498	54158	TCTCCAGGAUCTTGTAGAGCUCAC	54159	TCGATGCUGCCGTCGTUT
325618738	54160	TGUTGAACAGTCTUAAGGCAGCAT	54161	CCTTTGAGCUTCCGGGUCT
325823198	54162	GTTACCUGGAGCCCACAUACA	54163	CCAAGTCUCCCCTCTTCAUGG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
319934182	54164	GCACCTTTTCUTCTTCAAACAGUGG	54165	TCAGATGCCAUAACTCATTTCTCTTUGT
321046025	54166	GCCCUGCAGAAGCAACCTTUA	54167	TTTCCCCAUAGATGATCTTAGUAGCCAT
319072146	54168	GGGCCGAAAUCAGTGTCCUA	54169	AAGCCTCACCAUAACTTATGCTUT
265645493	54170	TCCTTTCCTUGAAGGTAGCTGTAUCT	54171	GGAAAATUGCGGCTGATGAUGG
315645433	54172	AGCATTCTTUCCAGGTCTTTCTAAGUC	54173	TTGCTGGGAUTATGACATCTTUGGAAT
317027027	54174	AGCGTTTTTGUGCAGACAAUCC	54175	ACAGGGACAGUGATGCATGAUT
326553909	54176	CTGAAGCUACCACCCTCACUT	54177	CAAAAGATGGCUGATGAGGCAUT
319717318	54178	GGCAAAAAUGUCCAAGCCCAT	54179	CGCTGCCCAUTTCTTGUCA
332493138	54180	GGTACTCCUCCAGCACCUCA	54181	TGCCTCAUCCTGAGTCCUGAT
262026071	54182	TGTCCCUCTGGUCAGGAGAA	54183	CTCACCCUGCTGTAGGCAUC
262611399	54184	TCTGTGGACCUCTCCTUCCA	54185	AGCACTTUCCCCGUCCAG
318030018	54186	CTCAGGTTCCUCAGACAGGUAGT	54187	GAGGCTCCUATGGCCTTUCAG
320595115	54188	CCCUGGGCCACGATCUC	54189	TGCACUGACCUCACGCA
318741691	54190	GGGTGAUGGCCAAAGACCUA	54191	CAAGGGCAGCCUCUCCA
321337923	54192	TCGAAGGUCCACGTGATGTUG	54193	GCUGCCAACCACACCTAUG
320145887	54194	GGCAGGGCAGACAUTCUCAAA	54195	CGTGUCCAGGCACAACCUC
235094211	54196	ACTTTCCTTAUGAGGCCAGGAGUA	54197	TGGAGAAUGGCAAGAAGGUCAC
317425940	54198	GGGTTACTCAGUGTCATCTTGAUCAG	54199	CAAGATTGAGGCGCUCAGAAATTTATUT
328299450	54200	CCTCTTAGUCCCACACCTUCCT	54201	GTTGAAGGACAGUGCTUCCGA
318562222	54202	CCTGGCCTTCUTGAGAAACTTCUA	54203	GTGCAGCUCAAGGATCTGAUCT
318692467	54204	CAAGAGAAGCAGGUGAGGUGAT	54205	ACACTCTTUAAGGGCACTTACTUCC
318320195	54206	GGGAAAATCTGCUCCCTCTACAUAC	54207	TCATATGAGAUCACGTTTTGACTUGAAT
320895759	54208	GGUAGAACCAAAGGCAACUGCT	54209	CATTCACCCTUCCCATTGCTTUT
318234482	54210	AGCCCAAGAAAUAGAATACTAGGUCAGA	54211	ATGCGTGGCAUTACCCCTTUA
261988694	54212	GCTTCGUGGCCTACAGTGUAT	54213	GCTGAAGAAGACGUCGTUGCT
259220732	54214	GUCGTTGTCUACGGCAAAAGT	54215	GAGGUACAGAUGGGAACAGAGG
255570672	54216	GACAGTGAGUCCTGACUGCT	54217	AGAATGACTGGUTAGTTGCCAUACAC
258245343	54218	AGCAAGAGCUCUACCGCAAC	54219	GCTUGAGGGAAGGCACAUAACT
268685036	54220	GGGCAATGATUCAGTTCAGAGTUG	54221	CTTCTGTCCUGAAACTCTTGCTUGA
267376054	54222	GGAGAGGACUGAGGTGCTCUA	54223	AGCCUGTCTTUCAGGAACACAAT
267168002	54224	TTGTCCAGUCTTTGACCAAUGCT	54225	CATCAACTCTAAAUTAGCCACAAGCUG
264754404	54226	ATGTATGTGTAUCCATGGGTCUAGACA	54227	CCTAGACCTTUCTGCAGATGCUC
325578662	54228	GTTTCCAUGGCAAACAACAGAACUA	54229	CTGCCTCGGUGGTACTTGUC
325578363	54230	GAUCCCGCAGAGCCUGAA	54231	GCTUGGGCGCATCUCCA
323652176	54232	CCTACTACCCUGAACACUGCCT	54233	TGCACACUCGGGACCTTUG
236474471	54234	CAACCAAAGGACACAAUGAGATTAGAUG	54235	AGCUGAGAGAAAAUAAAACCCCAGAG
237436422	54236	TGTTGCCCTUGGGTTTTTACAUAGT	54237	TGCTTTACGUTTGGTGCTTUCAG
237408995	54238	GCTGGTTCTTCAUCAGTTAGATAGCAUT	54239	CAAAACCATAAAACCUTTGGAAGTGUAAGT
238335871	54240	AACAGGUGGCTTGGGAUCAAT	54241	ACATGGGACUCAAAGTTTUAGCACAA
238972679	54242	CTGTTATCATTGUGCCAAGATCCAAAUT	54243	CATCAACCATCCUTCTCCAGATACATTUA
332515512	54244	CAGAGCCUCTCCUCGCA	54245	CCCATGUGGCAGAUGGACAAA
333306636	54246	AGGGTGUAACTGTCCUCGGT	54247	GCCUACCCCATTCCUCACAAG
332770768	54248	AGTGCCATAGGUTTGTTAGAGCUAC	54249	TCTTGCCGUGAAAGGGAACUT
253699979	54250	CAGTTTGGGUTGCTTGTCTGUT	54251	CAGUGATTGAAUACAAAACCACCAAGAC
226187372	54252	GACCAACAUAACCTGCTCCCAUT	54253	GCCAGTGCUCAGTGGACTUAAC
315991710	54254	TGCTCTCUGGGTGCTCUCA	54255	TGATCCUGGTCCAGCUGGT
315987330	54256	ACTCTGGGCAGAGUCACCUA	54257	TCAGAGAUGAGGGTGCTAAGUCT
316425916	54258	TGAGGACCAGCCUGACUCT	54259	CCACCCUACCAGACUGAGCA
331413397	54260	GTCCTAAGATGUCCACAGCAAGUC	54261	TGGCUGTTGGAGUGGACAAC
330432418	54262	CGAAGGGTAUGGCTGGTAAAUGT	54263	TCATTTTCTTCUCGCTGGTCTUCAT
331254345	54264	CCTGCGCUGGACACAGUA	54265	CTGCTCCUCCGCTCCUC
314604190	54266	CUGGCCACACCCACUAAACT	54267	AGCAAGGAGTCAUGCAACGTAATTTAUAT
257241741	54268	CCCCTUCACCTCCGTCUAGAA	54269	GAGTTGUGACGGGAGTTGUAGT
333670829	54270	GCTCGUGGCAGAGATGATTUAC	54271	TTCCTCTCUGGCAAGTGUGAC
323783226	54272	CCUATGAGTAGGATUAGGGACCAGAT	54273	CAAGACCTUTTCTGTCCUCCCA
323459942	54274	TGUGACCAGGTGUAGGACCAA	54275	AGTGCUGGTGGAACUGGAC
324881683	54276	GGGATTCTACAUCTTGTGCATUGT	54277	GATGCUAAAGAGCGCTUGCC
325133311	54278	GAGGTGTCGUCGGCAGUT	54279	TUCTTCAGTGUGGCCACGAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326220829	54280	GCCUGACGCCCACCTUT	54281	AAACCCAGGUCCCCUCCT
259250376	54282	CAGGTGAUGGAGGCCTTUGAG	54283	CTGAGCAGGUCTCACTTAUCGAA
326302357	54284	CTTCTUGAGAAGCCTGGCUCA	54285	TGACGAAGUATGGGCTTUGGAAAT
319127177	54286	CCAAGGCCAGGAUCUCCAA	54287	GGGAGGUACCTGGAGUGG
316516869	54288	AAACTTGGCCAUCTGAGGTTUT	54289	TCTCCTCTTCUAGGATTTGGTTAAUGGT
316972465	54290	GGTCTCUGGCCCAAGUCA	54291	GCTGCTTTUGAAAGTCCACUCC
256491194	54292	CCCTCTTUGGCCTTCATCTCUAC	54293	TGGGTTTAATCUGCCAAGGGUT
326028187	54294	CGTGAGGTCCUTGGGATTAGUC	54295	CACTCTCTGUACCTGACCCCAUA
226429377	54296	CCTACCAGUCTGUGCAGCAA	54297	CCTTATGUGGAACCCCCACCUA
328640719	54298	GATGCCCCAAAAUTTTCCATGTUCT	54299	TGCUATTGGTUCAGCAAGAGAGG
267010858	54300	TCACTTUGCAGGCACAUACCAA	54301	GGAUGCAAATCCUGGAAGACCA
263061549	54302	ACGTAGACATGUGAGATACCAGTUACT	54303	GTCCTGTUACAAAGACGTTTGGAUAAC
267989019	54304	CTCCAGTGGTUCAAGCAATTTTTGUA	54305	TGATTAGTTUAGCAACAGGAGGTUGAAT
267657785	54306	GGACAAAGATGATUGAAGTAACTGGTGUA	54307	GGATCATTCAGGCUGACACACTUT
258594401	54308	AGTATAGGCCACUTTGTTGCTCTUG	54309	AGATCATCTACTTUGTTTACATGTTTGAAUCAT
268787517	54310	GTACCUTCTGGATTUCCCCACAA	54311	AATTCAAAGCAUAGCCCUGAAAGAGA
267435079	54312	GCAGTTGCGUGATCTCCACUA	54313	GAGCAAATCATTUCAACACACATGUAAGA
324515582	54314	CATAGCTTGTTAUGAGGATCATGUGACA	54315	ACCUAGAGGAACGGGCCAUT
323456772	54316	CTCTCCTCAUCTTGCCAGUGT	54317	ACAGAGATCCUATCAGATGACCTUACAG
323695142	54318	GAGAAAGACGCUTTCATGCATAUAAGAG	54319	TTCAACTGUAGAAAGCCTUGGAGAAA
321470476	54320	TGACTTTTCAGUTGAGATGAUGCCAAT	54321	TTCUGAAATCAGCTTUGGAGAGAAGAAA
320178500	54322	CGCCTGGAUTTCATCTCCTUCA	54323	CTGGGTAATTGCAUCTGAGGATGATTUA
242465971	54324	CCTAAGCCCUCTGTGCUGAT	54325	GTGACTGCUGGGATTGTTTUGAG
315938364	54326	CTCCCTUCCCATCATGAUCCC	54327	AGGAGAUCCACCTCUACCAAACAT
290529982	54328	GTGTGAGCAGUCACTCATCUCA	54329	CTTCTCAGGCUATCTCTCAATGCUT
290663714	54330	CTGCCUCCGTGGATTCUACT	54331	CCTAUACACACTTCUGGCACCAC
292955758	54332	CAAATGCTTGCAGUCTTCTGTTTTCUA	54333	TGUGTGGUAGAGCAGCAACC
289543418	54334	GTGACACGAGGAAUGAATGAAAUAACC	54335	GTAGGAUGGCTGTUGAACGGA
300780414	54336	TTTACTGCCAUACATCTCCTTTCCUG	54337	TCTGAGCUGACTGGTTCCUCAT
327600008	54338	CTGCAAAUGGAGGGCTGACUA	54339	GATGTTGTTCAUCAAAAAGGGCAAAUT
254033845	54340	GCAGAAGTAAGGUATAATCCTGCTGTUA	54341	CTTACAACAAGTUCCAAAACACCAUCT
263929249	54342	CTCAGCAGTAUAAAGTCCTCATUGGT	54343	CCCTCATAGTUCAGAGGTCTCUCAAAA
315757969	54344	TGGAATGAAACAUTACCATCUGCCAA	54345	GGTGACTCTTUTCCTCCCTCUCAT
267718007	54346	GCCTTACGUCCAACCCTCAAUA	54347	GTCUGGCAGCAAACCTTGAUT
314363586	54348	GGUAGCCAGCAGACAAGTAUCAT	54349	GTCCGCTTUGGTTTCTTTTGUCC
318467709	54350	AGTGTTATCCTGCUTATTTGATGCTTCUT	54351	GATCAAGCCTUAACCTTCTCTGUGA
315663811	54352	GGCTCTUCCGAAAGCCUGAA	54353	GCATTGGGATTUGAAGGTCTTTGAUAT
316517249	54354	CTGTCCCCAAUTTTAGTGTTCTCUACT	54355	TGCTAAGTTCCUCAAAGGTAATGUGAAA
228185131	54356	GTCAGCACUAATCAGTTACCUGCAA	54357	CTGATGCATUCCTGGTTGTTTUCT
332688340	54358	AAGAGAACCCAGACUCUGGACA	54359	CCCGCCUGTACGACTUCAAC
312982713	54360	TTTGAGACTUGTTGTTGGCUAGGAA	54361	AAAAGTTCGGCGUTATGATATGCAUC
257067606	54362	GGCCAUAGGGUACGGGAAG	54363	CCTTACCTCUGCGGGATGUAGAA
313533937	54364	GAAGTAGCGUCCGGTGTCAUT	54365	TGAGTGTCUCGTCCTGGUAGT
313806252	54366	GTCTCCUGCACAGAUCGGAT	54367	ACCCAGGUCATGGTGAUCAAAC
261598032	54368	GGGCAAACAGUTCTGTCUCCT	54369	GACGAAGUCGGGUGAAGGT
316070604	54370	TTCATAGAAUCCTTTGAGCTUGCAAGA	54371	GGACTAACCCAGCUGAATTTAATCTCUG
316765654	54372	CTTGCCTCUGATCTTCCTCAUAAGAA	54373	GGGATGTAAACCCUAAGGACCTUAAGA
317700985	54374	TTTATTGCTGCTAUTGCATGATTGCUT	54375	CTGGAAAAGUTCCCTTTCUGAGAGT
315923042	54376	AGTAGTATAAATTTGUGCAAGGTCTGUGT	54377	GATGAAGAACTGUCTCCTCCTAGUGA
317084416	54378	CCGAUCAGACCCUACAGGAC	54379	GCTTCTCCAGUTGAACATTTGUAGCA
326459959	54380	CAGAGTCAGGCUCTGCAAAUCT	54381	TGCCAAGUCAGCUGAAGAGAAAA
242484850	54382	TGCACAGTTTGGAUATTACTTTCGTGUA	54383	CGACTUGCAAACCTGTUGGT
236815587	54384	ACAGGCTAUGTAGAACCAAUGCAG	54385	TTTCTCCAAAAUGGCTGGTCGUA
241364791	54386	GCCTTTATATGCUATGTCAGTGUAAACC	54387	GACUCACAUGGCACAAAACACC
257674686	54388	CCCCAUGGAGCTTGAUCAACT	54389	CCGAGCUGAAGTCTGGGAUAC
262294780	54390	ACAGUGAACAGAAGGUGGAGGA	54391	CTCGGCCAUGACACCUCAA
263315200	54392	GGACTGTGGGUTTCTGTCCUT	54393	CAAGGCAGCUCCAGGTAGUG
258397144	54394	CAGAGGCAAGGCACUCAUGAA	54395	GGGTTATCCUGTCTGGCUCCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267579922	54396	CCTTGGACCAGCUGGATGAUG	54397	GGAGGAACAGUAAGCATGTATTTTCUGA
328399616	54398	GAAGAGCUGAGTGCCACAAUG	54399	GAACCAAACACAUGAGAGCTCCUA
328453742	54400	GAAACAAGCACUTAGGCTGUGAAAA	54401	TTAATGGTGGUGTTACCTGCTCUC
327756644	54402	GAAGAAGCACUAACACCCAGAAGUA	54403	TCCAGATCAUGGTTGAGTUGGG
326638244	54404	TGGATTTCCTTAUCTCCACCATAGUCT	54405	TCAATATTGGTUGGTTGTTTCTUGCC
326606272	54406	CGGTCAAUGAGAGAACGGUCAG	54407	CGCTTCUGCACAGCGTTATACUAT
313674349	54408	CAGTGTTTTCATUTCCTCTCTTCCUCT	54409	CATCCTATCAGCCCUTACTGGGTAUA
323964401	54410	TCAACTGAACTUCCAGGATGAACTTUT	54411	TGGAATGTCCAACUTTGCCTATGTUA
324727999	54412	ACAGAATCCACUGCTGCATACAUAAT	54413	TGGACATGTTGAAUACAGCAAAACTUACT
323853033	54414	ACCTCTGGUAAGTATTAGGCGTUAAGA	54415	GGGTGGUGAATTCCTTTCUAGAGA
324514451	54416	AACAGCTGUAGTCCAATTAGUGCAA	54417	TCAGAGGCUTTATGTCATUACAAACACT
266990061	54418	AGAAGTTTATUGGCTACTCUGCACA	54419	CTGGGCTAUGGGACATGTATGTAUAAAT
266476175	54420	TGGCTTACTTUACACAAAACAAACUGG	54421	AGGTTGCTGUCTAACATACTUGGAAAA
264844134	54422	GAATGUGCCCAGCATAATATTUAAGCA	54423	TGUGGGAGAUCGAGGACCAG
265628329	54424	TTGTCTCACUAAGTTGACTUACAGCAG	54425	CTAAAGGCTUCAGTCTTCCTGUGA
257451366	54426	CAAGAGTGAUGTGGTAAGUAGAGACA	54427	GCTGGACATCUGTATACTAGCACATUT
269170997	54428	GACUCAGCACUCGACCCA	54429	GCTCCGGUGGCCTTGUC
267675837	54430	GGTCTTGGTUTTCAGCCCAUCT	54431	TGTACATGGCAAUCCTGTGGUC
259395990	54432	CTCGGATCUCCTCCTGUGGAT	54433	TCTCGCAAACCUGACACTCUC
326808049	54434	CTGCGCUCGGTGAACUC	54435	GGGCTUCAGACCGTGCUA
332337870	54436	CCTGGTCCCCUGGGTTTCUAA	54437	CCCTGACCCUCCTATTUGGAGAG
270338714	54438	GCTGCCUGGCAGTTGGAUAAT	54439	CTCATGCAGGAUTTCTGGTTGUC
271958165	54440	AGGAGAAAGAAUGACGAGAACAUAACAC	54441	GUCCCACACCCTUAAGAGAAGAAAA
272311872	54442	AGGGACCUCAAGAGCUCCAAT	54443	AGATATGGAUCAAGAGGTAGGGUGAG
232109369	54444	TGTCTTTCCUGAGGTGATTTCAUGAC	54445	TGGTTGAGGAGUTTGGTGCUAC
234245975	54446	ACAGCUCTGUAGAACCAGCAC	54447	TCTTCCACCATUTCCACATCAGAAUC
323749503	54448	CAGGCTGTTCUCCTCATCTTCUT	54449	GCATUGCCACCCCCTACUC
323618335	54450	ACAACACCCAAAACUACCCUGT	54451	CTCCCCAAGUCTGACUCAGAAG
264769376	54452	GUTTCTAAUGGGCAAAGGCACAG	54453	TCTGCCTGTAUGGGAATGACATUG
315641475	54454	TGTGTTTAACUCACACTTACCCAUGAAA	54455	GGGATAAGUCGCTGGCATTTUG
316726062	54456	TGAAGCAACACAGUATUCACAGAAACA	54457	GTTTGATCATTAUGAACCGACGTTCTUT
261165028	54458	ATTTCGAAUGAGTAAAAACGAUGCACAT	54459	AGCGAACTGAAGAAAUCAAGGTTCAUA
265573086	54460	CCTCCTCCUTTAGCATATCTUCCAAAT	54461	TATGAAATGCTTTUTAGGCACGTTTUCT
318354462	54462	CCTCAUCAGAACTCATCTTUAGCAACT	54463	GGTTTGGCAUAGGAAAAGCTACUGT
320738020	54464	GGGCCUGGAGAUCGAGAT	54465	GGGCGCCACUCTACGUC
320963416	54466	AGGGCTUAACACTTTCCATTUGAGT	54467	CACCTCCACATUTGATGTTCTGTATAUG
332484014	54468	CTGTCTGTTCTCUGGGTTATATGCUT	54469	ACATAAATGTTACCUTAGTGGCAGAAUCC
332884664	54470	CCGUTACATATTGCUGCCAAGAAG	54471	CCAAAACACUCTTGATTGAUGCAAGAAA
332867593	54472	CAGUATCGCCUGGGAGAACAG	54473	CCUTCATCAGCUCCCGAACA
314410583	54474	AAGTGTTCTUGCTTCAGCAGUCT	54475	ACAGAAUACACACACTGACAUGGG
324023169	54476	GTCTCTGUCCAAGGCATCATTAUCT	54477	AGGTCCTTTGUGAGTTATAGATCCCAUA
268704671	54478	ACAAACTCAGACAUTGGTCACTAAUGAT	54479	TTGCCCTTCUGTGTGATGUCAA
267708595	54480	AAAGAGCACTUTTGGCTTTGATUCAA	54481	ACCGCTCCAUTCATCTTTUGCT
269062833	54482	TCTGTAAAAAGTUCCCTGCAGTCAUC	54483	GTTGGGTGAUCGTTCCTTTCAUC
265310518	54484	GTGAACTGAGAAUTCAAAAGGAATGUGG	54485	ACACATTTTAACATUGCTTGCTTGGAUT
263431208	54486	AACAAGCCCAGUCTAGAATTTCUCAA	54487	CAGGAAGTTUTTCACGCTCUACAAA
263847738	54488	GAGGAATACCUCCACAGCACUAAT	54489	CATCTGACUGGCCAAAATTAAGTTTTUC
264023711	54490	ACAAGACCCTUTCATTACCCCAUC	54491	AGGCAGTCAAUGAGCTTGTAAATAUGT
320259656	54492	GATTGGAATCUGGCAGAGTGTUAAGA	54493	GTATGTTTCUCAAACCACCUGCAAC
290142525	54494	AUCAAGGCCUGAAACCCCAAA	54495	TCCCTCCTAUTGTCATGCCUGT
292477909	54496	TGAAGTCCGAAGAGGAUTCCTCAUAT	54497	GAAGUAATCATUAGACAAGCAGAGCCA
222797864	54498	CCTCGATTGAAUCCTATTCTGAAGAUGA	54499	GGTCTTGCCCAUCTTTCATTCUG
328147900	54500	GCTTTGAUGAGCAGCTGGTTUG	54501	AGAGGGCAACUCCTAGGGAUG
328086852	54502	AGCTGAACAUCTGTTTGCCUCT	54503	GGAATGATUGGGAAGCGUACCT
323884495	54504	GCGGAAACGAUGCCTGTATTUC	54505	GGAAGAAAGCUAAACAAACCTAGAUGGT
235405510	54506	CAATGATTUAGACCCTGGATTTAUGCC	54507	ACTGCUGACACACACACTAATTUCT
235281148	54508	GGUCCCAACCACUGGAAAGAC	54509	GTTTGTCAGUAGGCCTGTCUGAA
266287457	54510	CUGTACGACUGGAGCGACAA	54511	GACCAAUCATUCCCCGAGACC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
265335562	54512	GACAAGCAAGAAACAUGGAUGCT	54513	GGTAACCAGGCAAAAUACTAGCAGAUA
268464265	54514	CUCACAGTGTAUCCAGGGACAAT	54515	CCAGAAGGCUCTCTCTTTCCUG
265551545	54516	GCGGAGAACUGGAAATGUGGA	54517	GCCAACAUGGGCAGTCUGA
316592926	54518	GGCAGGACCACCUTGAATUCT	54519	CAGAAGTGTGTUTCCACCATACCUT
331569015	54520	CGAGCGCCUGGGAUCAG	54521	TGCTCAUCGCCTCGCATUT
331742469	54522	CCTGTACUGGACCAGGAAGUG	54523	CGTGTCUGTCCAGCUCCAA
331683853	54524	ACUCACCTGUCACCCCGAT	54525	GGTUCCCGAGGGACAGTTUG
331572326	54526	GCAGCUCCGCGUACCAC	54527	GGTGACGACUGTGGCAUGA
266127553	54528	TGGGAATTCUGAGAACATAGGUGGA	54529	CCATCCCCTGAUCAGTCTACTTCUAT
257438107	54530	AAGGGAAGUGUCAGAACAAGCA	54531	CATATCTGTUCACCAGCTCAGUCT
268544860	54532	AAGCCCCAAAUCTCCTTGTUAGAC	54533	CCGGCGUTTCGGCTUCT
326947881	54534	CACAGTGUCAGTGCCTAUGGA	54535	GGCCTCAGUCAAGAACTUCCAG
324848408	54536	CGTCTGGUGGTCGTAACUGT	54537	CCCATCUCCAGCTGTCTGTTUC
315309951	54538	CCTTCTTAAGTTTUTCAATCTGCCTGUT	54539	CTTTGGGAAATUACCAGGTTCTGAAGUA
319029122	54540	CCATTTCTACATGUGCTCTTTCTTCUCA	54541	TCTGGGTCAAACUGGCACTTTAUT
270536070	54542	GTCTCUCTGATCCUGCCACAAC	54543	TGCCAGTCAUGGAGTACTTTTAAAUGA
272127084	54544	TGCTCAGAGUCACAATAACTGGATUT	54545	TTCTCTTCCCTUAAGTCAGTCCTACTUT
271957249	54546	TGAGACCCUCCCCAGATUACC	54547	CAGTGAACAAAACGAGUTGCAAAGTUA
320167961	54548	GGCCAGTGGUGTCCATTCAUA	54549	AAGGGCTAUCGGCTAGAUCAGT
271468275	54550	GCTATCCCAUGATGCTCUGCT	54551	GATGCCTGGAAGCUGCATAGTAUT
270170044	54552	GTAACCUGGGCAGAATTGUCAAAA	54553	ACTGTTGCUGGACTTAGAAAGTUAAAGT
316819358	54554	AAGGGCTAACTUATGTTGCCATGUA	54555	AAAACTGUGAGAAAGCAATUGACCAC
268812968	54556	CUAGAAAATTCUCCACAGGGCCAA	54557	TTCAGTGTUGCAGTGACAGUAACT
261182394	54558	GTGAUCAAAACAGGGCGACUG	54559	TTGGCAUGTGGAATUGCACAAG
328433017	54560	TGCCGGUCTGGCTCTUC	54561	TCCGTCCUCCTGCTCUCT
268933581	54562	GTTCTGCAACTUAGTATTTGAATGTUCCT	54563	CACCACAATGUCGTCAATGAATTCUAC
264924999	54564	GGAGACAGAUTCCGGACTUCAG	54565	GAGGGTGATCGUTTCTTTTAGAGGUT
266639514	54566	CAGCTGAGUTTGCTCTTCUAAAACC	54567	TTCTTGCATCUGCAACATTTCTTCTUC
269308070	54568	TCAGAAATTCTUGAGAAACCCCUAGAGA	54569	TGGGAGAGAGUAAACTACAGAGACTUG
268316667	54570	AATGGCTGUGAATCCAGAAUACACT	54571	CCCTCTAUCAGCAAAGUGGCA
264387160	54572	TCUGTGTAATCTAGUGGAAGGGAACT	54573	AGAUGACAUCACCAAAGGCCAA
331900319	54574	CGCCAGGAGGAUGGACUT	54575	GCAGCUCAAGCACCUGGA
333488196	54576	GATCGACCCUGAGCAUCACA	54577	GGATATCTTUCTTGGGTGUCAGCA
230677765	54578	CAGTGGUGATGTCUGCACAGAT	54579	TGGAAGTGACGUGAGGCTTUC
228163177	54580	AGAUGGCCCAACACACAGAUG	54581	GGGTCCTTTAGUTCTGGCAAGUAA
224477058	54582	GAAAAGAAAACCCUTGAAGACATGTUGA	54583	GTGTTCCTTTGCUTTTCAATCTCTTCAUT
222262253	54584	AGAATGATTUAAGGCTACAGAUGGAAGC	54585	TCCTTGATCUTTTCCTCTUGAGCAAA
222164940	54586	TCATAAGUAGAACCAGGGCCUGT	54587	ACAGCTTCTCUCTTCCAGCUAAAG
224425371	54588	TGTTCCUAGGATGACAUGGAGAAACT	54589	TTGGTCAATTTCUACCTCTTTTTCCUGT
223501147	54590	ACGTGGCUATAGATCATCUGAGCA	54591	GGGTAAGTTCUAAGTCCTTTGCACUA
319202713	54592	GCTGTACTUCCAAAACAGAATCTGTUAC	54593	TTTACTUAAGGAGGACGAATCCAUGAAC
320122315	54594	ACTGATATCUGCCCTCAGTTGAUCT	54595	CCTCTTCCTUCCATCTTTCATTACUACA
320172954	54596	GTCCAGCAAUGAGGUCAAGGT	54597	TCAATATCGAGCUTTTCTAGTGCTTUCA
265391241	54598	TGCCAGGTTUATTTCACTCTTUCCA	54599	GGCTTUAAGGAGAAAGCACTACUACT
263630779	54600	TCTAAGAGAUGCGGGAATGAUCCA	54601	GCGGCGAGAGUCCATTGTAAAUA
266806714	54602	CAAGGUCCAGTUGGCCGAA	54603	ACTCATCAACAAAUAGATGCCACTUGAA
268876211	54604	ACGAATTAAGCAGUATTTGTGGUGAAGT	54605	TTTATGTGCGAGAUGGCTACAGTTUA
269312050	54606	CATTCTTAUAGCCACGGGTUCAGA	54607	TCCCAAAGCTGAAUGACCATCAAAATAUA
266684436	54608	CATGCTATCAGAAUTCACAAGGUACCA	54609	TCCTAGTTTTGTUAGCCATCAGTTUACAG
313672201	54610	GAGACTUGTTTGCTGUGCCAA	54611	CGCUACCACACACAGAUGCT
318781225	54612	CCAGCACCCACCUGAAACAAUA	54613	CAAAACCGTGUTCCCGTTCUC
316947802	54614	TGGAUCTTCCGTUCCACCAC	54615	GGGCCAUGAGCGAAUACACAT
240007153	54616	TGAAGATGACCUCCCCTTCTUAGAA	54617	CACACCTCACCUGTAAAACTCAGTAUAT
264611149	54618	GATCATTGCTATUCCATGGATGACUCA	54619	ACTGCAAACCUCTGAAGAAAAGTGUAAT
229180966	54620	ACAGTGGTCUCCTTCCCAGUA	54621	GTAGCAACGUGGAGTTCATGUG
266323371	54622	CAACCAGAACACCGUTCAAAGAUG	54623	CAAAUTCCTUGAAAGCAAAGCAAGAA
257258525	54624	AATGCTTCCAUGAGCACTGCUA	54625	TUTGGUCAGCAAAACAACAGCAA
261854525	54626	GCGCCTCCAAUGAAGGATCUAC	54627	GGCCAACAGAAAAUAAGAAAGACUAAGGA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267089049	54628	GAAUGGACCUGACGAGCCT	54629	GTTTCCAGUAGCAGCUGACAGA
326981222	54630	GGCCAGGUCCAGATCGAAAUC	54631	GCAGCUCAACGCGCUAC
315920684	54632	TGTGGGCACAGACAUGACTUT	54633	TTGTGTTTTGCTUGGATTATTGTGCATUA
315904501	54634	CUTAAAATGTTTUACAAGCACACACACA	54635	AGGUGCAAACATCUCAAGCCA
313761707	54636	GTTATTACACTCTUGCTCCACGTTGUA	54637	ACTCCAGTGUAAGAGCTTTATGTTUCC
312663961	54638	ACCUGTGGGTUAAAGGCCAAA	54639	TTGAGCCUTCCATCCTUCACAC
312869843	54640	GGCACCTGGUTGGCTAGAAUA	54641	GATGGACCUGTGATCATATCUGAAACT
316686056	54642	GGTTTTTGAACCUGTTGAGTTTTUCAGT	54643	CCAATGCAUCCCTGCUGGAT
326721486	54644	ACCAGAACTGUAAGATTGCTCCUG	54645	CACGTCTCAGAUACAAGGAGUACAAA
317944763	54646	CAUTCTAGCTCCUGAACCAACCT	54647	GCATCTCCCUGTGTGGGUAGA
317413768	54648	AAAACCAAAGCUTTCCTCTTCCUCT	54649	TGCTTCGGGAUGGAAACCTAUG
298436137	54650	GCTTTGTCCTUCAGCGTTTTGAUG	54651	GCTGCGGUGACAGTGATGUT
327475805	54652	ACATAUTGCTGCAAUCAGGACCA	54653	GGCAGGATCTUGGTTACTCTTATAAGUC
327957333	54654	AGATGTGGAUGAGATAGAGAAAGCUGT	54655	CTCATTTCTUCAACTGATGGGUCAGA
278228582	54656	GTTAAATCTGUGGTGTGGCAAUGAC	54657	CCTTTCTCATTCUGGTGTTCTTCACTUA
280822163	54658	CCATCUCAGAAGAAGCTGCAGUC	54659	GGAACGTCTCAGUGGTTTTTAAGTTUT
279976003	54660	GATGAAGGAAAUCCCATACCTGTCUAC	54661	ATCCATAACUGAAAGCCAAUGACAGAT
279781491	54662	GGCTATTAGUGCACAAGGAAAUGG	54663	AGGTACTTAGGAAUGGCAAATTTGTUACA
267260703	54664	GATCCAGAGGUTGGGAGTTUGG	54665	TGTCCGCUTCAGTGTUCCAT
259313251	54666	CTGGAGAUGCAGGAAGACACUG	54667	AAATCTGACUGGACTGTGTGUGT
241494343	54668	TGTCTGGGUCTGAAACGCTUT	54669	TCGGATTTTTCACUTTGCTCATGTTTUT
267449326	54670	CCTGGTUGCACTCTGACTUG	54671	CCACCTCCGACUGATAAGGGUA
260444534	54672	CAGGTTCCUCCTATCCTGCUCT	54673	CAAACAUGCCCACAAGCUGAAA
332436229	54674	TGTTTTTGGTCUTTGACATTTTCUGCAA	54675	TGGCGAACAAAACUATTTGAGGTAGUAT
265572299	54676	CCAGAACAAGCAGCUCCUGAC	54677	AAGAAGTCTCUTTGCAGCTGUGA
321193691	54678	GACGTUGAAACGGAAAGUGGAAAAA	54679	AATTTTGCCCAUCCACCAAACAUC
319828875	54680	TUTCCACTAGAGUAGGAGGCACAT	54681	GAATTTGAAAAUCAGAAACCACTGTGUCT
254965183	54682	CCGGGUCAGGATCAATGTGUT	54683	GCTAAGATAAAUGGCAGGAGUGCAG
256254262	54684	CCACACCCUACAATACCCCUT	54685	GTCTGTGTCUCCTTTGGTGUGT
326988697	54686	GAGAUCCAUCAAGGCCAGGAT	54687	CAAGCTTTCCUGAATGGTTTUCAAAGT
327102210	54688	GGCTTTGGTUACTAAACCAGCUGAA	54689	ATTAACAGCAGCUCAGGTUCGT
327110264	54690	TCATTCAGTGUGCCAAGGACAUC	54691	ACCTAGTTTTTCUCTCCTGCTTTTCUC
314961597	54692	GUAACAGCCCACGTTTUGCC	54693	AGCAGAGTTAUACATTGTCAAGCAUCA
262401357	54694	GAGAACACAGGGAUTATGCAUCCT	54695	GATGCTGACUCATAATGTGTUGAACC
313956327	54696	GCUGTGGCGAUCACGAAAAG	54697	TTGCATCUGAGCAAGGUGGAT
314619154	54698	GCTCCAGUCCCAUCCGT	54699	ACCCCAGCUGUCCAAGGA
319939087	54700	CCTGCCCAGAAUTTTACUCACACA	54701	AGCTCTCTACAGUAAGTTCTCATACCAUT
238600226	54702	GGGAGAAGGACUCCACTUGGT	54703	CGCTGACACUGTGCTTCTCUC
262314456	54704	GCUCCCCGGCCTACTUAC	54705	TGAGCGCCUTCACTGUCC
333451876	54706	ACACCUGAAGAAGCUCAAAAGGAA	54707	GGCAGAGAUGTCGAAGGTUGG
333468470	54708	GCAATGAGGAGGUCAGTTUGGAAAA	54709	GTCAUGCACACGGACTUCAC
333415508	54710	TGAGTCAGGAUTGCACUGGAGA	54711	GTGTGCTACAUCATACATTCTUCCAGAA
324825940	54712	CTGAAGCTCUACCACGCCUT	54713	AAATGACCUGGAGAGAATUCAAGCA
312941121	54714	GGCTGTTCGUGTGGATTGUG	54715	GCAAGGGAGAGACGUGATATTTCUT
314982983	54716	GGAAGCUCCUGAAGAAGAGACA	54717	GTAGACGAUGCCTGCAAAAUGG
314588051	54718	GCAGGUGGTCCUAGAGGAGAC	54719	AAACACCACACGUACACCTGUAT
313234671	54720	GCCAUGAGCCTGTCAAUCACT	54721	AGGAUCAACACAAGCGGUGT
313373280	54722	GTTCGGGTTCUCCCTCTACATUG	54723	GGAGUCAGGCAGAGCCAATUA
222453945	54724	GAGCTGATTGUAGCAACATACTACUCAA	54725	AGACAGAUACAGACAGAGTGCTTUCT
223782500	54726	TTGTGGTGGAGUTATTGATGACGUT	54727	AGACATTGAAGGUGTCAACCAAUAAACT
224716834	54728	TTCCTTCTTCAATUTTTGTTGTTTCCAUGT	54729	GGGTTTTACACACACAUAACTCCTUCAT
332273515	54730	CAACACGGUCCATTTTGCCAUT	54731	ACATTTCCAUTGTGCUGAGGGA
315948027	54732	CTTGTTCUCACCAAAUCCCACCT	54733	ACAAACCAGUTAATGGGCAUCGT
332445867	54734	CAAUGCGACCATCUCCACAGT	54735	GGUCCCAGGAGCAUGCC
332767751	54736	CCTGCTTGUGCTGTTTGUCAT	54737	CTCTGCTGGUCATGTTGGTGUA
321495290	54738	ACTAAATCTUGGCGTTCAGACUC	54739	GCAGAGAAUGUGGACAGGAAAAGAAAT
315056599	54740	GCTCATUGCCCTCTCCTTUGG	54741	CTGACCCUGCCUAAAGGAAGT
260591757	54742	ACCCACGUCGATTGCATCUC	54743	ACCTTTTTAUGCCTCCACCUGT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
319858249	54744	CCCAGCAUTCAGTGTTTTUCGG	54745	TCTCTGCGCUTTATTTTCAUGAGGAAT
315494339	54746	CTCTAGCCAAGCUCCACCTTUC	54747	GGTCCAGCUTGTGCUCGAT
254223135	54748	CGAAGCCGGGCAUAAAGGUAA	54749	TCCACTCCTUGAAGGATACTCAGUAAT
257257252	54750	TCTCATTCATGGUAGTTAAGCAAGUCAAA	54751	TGGTCTGAGGAUTTCCTGTTUCC
266724180	54752	ACCCACAGAGGAGAAUGGUGA	54753	CCACAGTCATGTUTATTCCACGTCTAUT
259023602	54754	CAGGAGGCTUTAGCTGGAACTUA	54755	CAATCTGGGAUCTGCTCCUGAAG
267664076	54756	CCCCACAAAGGCAUCGGTATUT	54757	AATGACTTTGGUGATCAGAAUCAGAAGT
264566488	54758	CATCAUACCAGGCTGCUGACT	54759	GTCTGCAGUGATTTAATTCTTTGUAGCA
260581473	54760	ACCTATCAGTUAGGATTACTTTCCTCUAAGAC	54761	GCUGCAGGCCAAGAUGGA
260151355	54762	GTTGACCAGGAUCTCCATCTUCA	54763	GAGAGTGAGAGGUACCACAATCTTTTUA
264502914	54764	CAGAAAACCUGGTGAGAAGUAGGT	54765	TCTTCTCUAGGGAGGTGATGGUG
267061252	54766	TTGAATTCTTTCUCATAGCATCUGCCT	54767	GCATTAGTTTGGGUTCATCTTTTGTUCT
266372753	54768	ACTTCTTCAUCCAAAATCCTTGTUCCA	54769	ACCACTGTTUCTTTGAAGCTUACAAAAG
239846069	54770	CCAAGAAACCAUATGCTCACCTUG	54771	TTTGGATTGTGUCCGTTGAGCUA
316968986	54772	GCCCUCACCGGTTUAGCA	54773	GGGTGACTTCUTAGATGAGGGTTUC
314606917	54774	CAAGCAGAUGCAAACCAACCUA	54775	CCGAGCCUGAGCAGCTAUC
314376618	54776	AGTGTCCTUTTCTCCTCUCCAGAT	54777	GCTCCGAUGTTGGCCAUCAG
327491650	54778	TGATCTTCATUCAGGTGGTCAAUGG	54779	AATCTGGCCAGUTTACTCTGCUT
326488359	54780	CCGTGTCCACUGCACCAUAC	54781	ATGGCTGTGUGCTTCTATCUCC
327936002	54782	GTAAACCGGUTGTTACTACCUCACT	54783	TCATGGACATUCAAGACAAGAAAGUCT
327803099	54784	TCAATTTTTGTUGAGAGGGAGGTGUT	54785	CCGTTTGTTCUGAATTCTACTGGAGUT
326771643	54786	AAAGAACCAGAAAUACAATTGAGCCUCT	54787	AAGGCAGCTTGAUAACTGATCCTAUAAC
326597329	54788	CTTTTGTUCGAAAGCTGGCCUT	54789	GACCATGCGAGUATATTGCTGTGUAT
328253266	54790	CCTGTGAAAACGCCAUGGGAAUA	54791	GGGACGACATUCATTGTTTTGATGUT
324177899	54792	GGTAACACUCTGACCAGCUGT	54793	CCAGUCAAGGGAGGCUCAAAG
333656301	54794	CAGATGCUGGCTGCTTCTTUC	54795	GGCTAGTGCUGATGTGCTCATUT
333832134	54796	CGACAGAGCCGUCCTGTTUAC	54797	ATGGACAGAACUGCAGGUCAC
325278675	54798	GTCTCTGATTTGUAGTTACCAGCUGA	54799	AGTAAGTCUCAGACCAAATGCTAATUCC
324228440	54800	TGUATAGTTGATTCAUGCCGGGAAG	54801	TTGGGAUGTTGAGUACGGAAAACA
324388188	54802	CCTGTAAATTCTGUGAAAATCAAGCTCTUT	54803	ACCTTGTCCAUTGACCATTTGUCAT
323344384	54804	GAAGUACGAGATATAAUCCGCAGCA	54805	AAAGGCTTUGCAAGTAGGATAAUGACT
324663254	54806	CTTAGGTGAAACUGGACCAATGGUAG	54807	TGCTCTCTCTUCAGTACTGTGGUAAA
324536657	54808	GGTTATGGTTUGACACATGGUCACA	54809	AGAUGTAATGACAAACUGAAACGAAGGA
323315041	54810	TGATGUTACTTAATGGTUGAAGCCAACA	54811	CUAAGTCTGTAGGAUAGAGCCGAAGT
327759137	54812	GGGAGGTUGGAGATGTAGUGGT	54813	GACAGUCCCCCAGCCAUT
327577734	54814	ATTGATAGTCACCGUGTTGGTACTTUT	54815	CCCATGTAATUCAATTCTGTGTTAAUGCC
319556922	54816	GCTGGAGAUGCTGTGGATGUA	54817	GGAAGGGTAUAGAATTCTGTCCCAUAGA
333641816	54818	CTGGCAAGGCAAAAUAGCUGT	54819	CACCAGCACUAAGTGATATCCAUCAT
233359144	54820	AGACATCTGCTTUCTGCCAAAATTAAUG	54821	CCAATGCAACAGACUTTAAAGAAGTUGT
318712518	54822	GCGATTTCTUCCCAGGGUCAA	54823	TCCCTGATCUCAGAATGTCCTTTUCT
319924933	54824	GCGGGAUAGGAGGAGGUGA	54825	CUCCGAGGCCAAGCUGAA
278712027	54826	TTCTAGAAAGUAACAGTCTGTTCAACUC	54827	GCTGCTAGGACCAGUTTGTGAATAUC
279419619	54828	ACTGTTTATTCATTTUGCCTGTAATTGCUT	54829	AATGAUGCACCAGCAGCTUAGA
278700684	54830	GTTTCTAAACCTCUGTTGCAAGTGTUT	54831	CAAAGACAAAAGUGAGGCCTTGAAUA
313265128	54832	CCAGAATAGTTCUCTAAACATGGTCUGT	54833	TGAGGTCAUAGACAGCAAGGUACAA
279093783	54834	CTACAGGAGUCCTTCTTCATTTUCAAGA	54835	CCCCGUGCCACAAAAAUAAAAGAC
314482759	54836	CTTUAAGGGACAAAGUGAGCACAGA	54837	GGGAUACAGTGUGAAAAGCAGCA
279465625	54838	ATGCATAATGGUGGTGGTGUCA	54839	GTTCTTCUGAAGGCAGAGGGUT
267663074	54840	GGTAUGGCAAAGGACUGCACA	54841	GCTCAGCUCACCTTTTCTTTUCCA
258258179	54842	GGGCTACUGGCGTTTCAUC	54843	GAGGAAGCUGGGATATCTCTCUCT
268371291	54844	GCAGUGTTTCUCCAAGAGCCAT	54845	TGCTGTCATCUTACCATGTTCTUCAC
324191260	54846	GAATATTTGAGTAAAGUGAGTTGCCGUT	54847	GGCTCTCACUTCCCCACAAUC
320502015	54848	AGCAAGGCUGACTUGGACAAAT	54849	TTCCCGAAGTTUAAGAGACATGATGUT
317837506	54850	CAGTTUAACACATCCTUACCAGAGCA	54851	GACAUGGCCTGUGCCAAAC
316209083	54852	AGTACTGUCAAAAACAACAACUGAGACA	54853	CCAGCCAACAUCACCCUGAAG
326872652	54854	TCTTCATGATGTUTCCTTCGTAGGUG	54855	AGGCCUAGCAAGAGAAUGAGAAT
317908458	54856	TCTTCTTCTCAUGTCTCCGGUAGG	54857	CATTTTTCGCATUATGATCCTCGTUGT
316462638	54858	CCGGGAAAAAGUGGTCAUAGCA	54859	GAAGGTGTGGAUCACAGTCAUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
242580836	54860	TGGATATACTCUACCCTGCGATTTUCT	54861	TGGTTCTTUGAGCAACAUGGGA
239932898	54862	AACTTGAGGUTGCTAACTAUGAAACACT	54863	CCTTCAGCACUTCTTTUGAGCAC
332369305	54864	GAGCAAAGAGUACCCGTGGUAA	54865	GGAGCGTGTTUGTAATTAGGGAAACUAA
313742065	54866	GCCAGAGAAGAAACUTCCACAUCT	54867	CGAGCAGAUCGCCCUCAA
315095293	54868	GAGAGUGGGTGUGAGCAGAA	54869	GCAAGUCAAGAGCCUCCAGA
315081800	54870	GGGTTCUCAGACTCCUGGCT	54871	CCTTCTATGACUGTGCCATCTUCAC
314038761	54872	CGCTGCTUCAGCTTGAACTUC	54873	GGATCTCACTUACCCATCATACTTCTUT
312804562	54874	GAGAGGUCAAGACCAGATGGTCUA	54875	CTCATCACCACUCTCTTCCATCUC
313881820	54876	GGCTGGGAUCAGGGAGATUCT	54877	TCCTGAAGGGAACUGGGAUAGG
328032802	54878	ATGCTGTAACUCAGACTTCCTGTTUT	54879	GUGGACCATATCUGGGAAGGAC
324441121	54880	TGGTTGAGCAACCUTACCTTUAAAGA	54881	GCTAGTGGAUAAGTTTTTGGAGGAUGT
261817414	54882	CATACGATCAGCAAUACCAGGGUA	54883	CCTTGACCUGAATGCACTGUGAT
320394718	54884	ACAAAAUGGGTCUCGCCAAGA	54885	GGGAAAACAUGACTGTACUGAAAAACAA
315984924	54886	CCUAATCTCAUCAAGCCCAGCA	54887	CGAGGAAGAGUAACGTGTGTTUCT
317518671	54888	AAAAATGTTAACTUGAACAATGCAAGAAAAAUA	54889	GCTTTCCTCCUGGACCTCAAATUC
327874343	54890	CTGGAAGAUGAGCTGGTGUCA	54891	GAAAAGGTAAACTUCCTTCATTGCTCUC
271277460	54892	CCACAGCCCUGTTTCTGTGUT	54893	CTGATGUAGGCAGCACCCAUA
319374393	54894	AAGCAGGCGCUAAGAUCACAA	54895	GGTAGGUACCTGAUCCCGGAAG
320242989	54896	CTCAGAAGCUGGTCGTAAAACUGA	54897	TCCACCCCCACUAGTTTTUGAAC
239196326	54898	GATCTCTCCAUCCTGACCCUGT	54899	GCTGCAGAGCUCTCCTTGAAUT
242281956	54900	CCUGCACGCAAATGUGAGT	54901	GCUGAGGGAGCCCCATATUC
320074095	54902	CUCCCAGCCGAGGAAUGAG	54903	CCTCTCACAGGUCTGTCTCUG
240643159	54904	TGACTTCACTAUGACTCCTGCUGT	54905	GGAGCAAGCUCCACGAGAUG
238394426	54906	GGGAUACAUGGACACACAGCA	54907	TTTTGCAGUGCGGCUAAAGAAG
235085723	54908	CAAUTCTCCAGCUCAAAGCAGAAC	54909	GCCTTGGTTTCUAAGTTTCTAGTTUCC
268744903	54910	AAGCCCAAGAGAAGCAUAAAAGGUAA	54911	GTGGAAGATACUGATGCTGATAGCUG
327382209	54912	GGCAGCAUTTCCUGGAACGA	54913	CUCATUCACAGGAGCCCACA
321452339	54914	CTGTCGCAUCAGCTTGTATTTGTAUC	54915	TGCCTTCCAGGUAAGGTTAGGTAUT
253876923	54916	GTCAGATCACUTGCCTGCAUCT	54917	TCGTCTTCCCAUCAAGAGTUAAAAACAT
263349177	54918	TCACTCCAAUCAGACCGGGUA	54919	GATCCAGCCAAUCACCTGGUT
257909751	54920	TGTTTGGAGAUGTTAAGCUCAAAAGGA	54921	CATACTGGGAUGTGGCGAUAGG
264495351	54922	GGGACTTUGAAGCTCAUCAGAAC	54923	AAAGCTTGCTUCCATTGAGGGTAUA
239556324	54924	GCATCTGTAUCAGGCAAAGTCAUAGA	54925	GTAGCTAACTAACUTCAGAACACCAACUT
258201049	54926	TGTCATTTGGUGAGTAACTGCATUCA	54927	CGCTCACAGUTGATGAGAAUGG
325572880	54928	AACUGCAAGCCCCTUCAGAA	54929	CTGGCTTTUATGCTGCTCUGG
323714975	54930	CTCTCCUGACGACATGUCCAC	54931	GCTUCAGCCCAAGCTTTGUC
325564111	54932	GACCCCACUACAGCAGCTTUT	54933	CCTCATGGGUGTCCCCTTUG
237186614	54934	GTATAGGTATCTGUGGTTGATGCAGUT	54935	CAGTACTGACTUTGGTATGTGTGTUC
257923164	54936	GAAAAACCUACAGACCUGGAGACA	54937	GGCGTTTCAGCUAAACCCAAUT
236743239	54938	GTGTGTATGTGUGTGCTGAGGUA	54939	CACTTCAAAGCUAACATGTUGCCA
235374615	54940	CTGCCATTGUCTCACCGTAUGAA	54941	TAAAACAAAAGCACAUAACUGAAAACCA
235093821	54942	TGGGTGTATCUGGTGTTGAAAATTCUAA	54943	TCACTAUCCCCATGACUGGGAAAT
239206598	54944	TATTTTCTGTCTTTACUTGTTCCTTTATTCUCT	54945	GCAGCTGACUTGACTTTGCTAAUG
239663032	54946	TGAGAGATATUCCAACGTGCAAGUG	54947	TCCACAGAACTUATAAAAACCTTTGUGT
239688556	54948	GCCACCGTUTTCCTTTTAGCUT	54949	TTGCCTCCAUTAGTTGGAAAATUGAAAC
235934655	54950	TATTAGAGCTTUCTTTGAGTCCUCAGT	54951	GTTGTGATCCCUGATTCCATTTCTUG
333053153	54952	CCACACUCAGCTGATUCACCA	54953	CTCCCCUTGGACATATUCGAGAAG
312937973	54954	CGCCACCACUGCGTAUCT	54955	CCCGAAGGUTGGCGUGT
313525070	54956	GTCCGTACUCCACCCAAGUC	54957	GCCCUACCCTUCCAGGCA
329536618	54958	CAATCCAGTACUCTCCTGTGGUAG	54959	CTGCCGUGACCTCAAGAUGT
333069911	54960	GTCCATGAAATAGAUGAAGACAGTCCUT	54961	CCTGGAATAGUCCACTTTGTAGTAGUG
327622743	54962	GGGCAGCUACGGCAUCAG	54963	CTCAGCGUGGUCAGCGT
316893857	54964	CGTCTUCCACCTGAGCTUCA	54965	GGAACUCGAAGACGAAGTCCUC
260012382	54966	TCATTGGTGUTTCCCACAUGGT	54967	CGGAGATUGTTGCGGTUGAT
268825367	54968	CATTTTTGATGGUCTCTGCCTCUCT	54969	CAGTGGCATAAGGUACTTACCATTCUAT
267895025	54970	TGATATCAAUGACAACGAACCAGUGT	54971	ACTGCTTTCTTAUCATTTGTTCTGUAGGT
266663015	54972	TTTTTCTAACUGGCCTCAGUGGAAA	54973	TTCCTTGGCCAUACCTCCUACT
268950790	54974	GTCTAGAGGGUGGTGGACTUCA	54975	GTTACCCCCUCAGGGTCUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268201139	54976	GCCCCGAGGUTCGGATCUA	54977	GCAAGCTUGAAGAGCCCUCAT
257457271	54978	GAGGTCTGUCGCTGACTCUT	54979	CUCAGACCCCGCACUCAC
262387186	54980	GGGCCAGGUCGTUGAGG	54981	TGGCCGAUGGAGCUGAAG
257603185	54982	TGGGCCCCCUCATATCTCAUT	54983	AGGCCAGUACCTGGTCCUT
261776694	54984	ACCTGGGCUTTGTTGTCTTUAGT	54985	GATTTAATTGTUACGCTTTTCCCCCUAA
326166543	54986	TCCCAUGGAGCCCUACCA	54987	TCCTGCACUGCGCTGUAG
326411812	54988	CCUGACTACCAUCAGCACGAC	54989	TCCCGCUCCAGAAAGTTCCUA
325391912	54990	GCCTCAGCCCUGCCAUC	54991	GGAGTTTUGGGAATGUGGGAGAA
323877630	54992	TCATGAGCCUGTTGGAGAAAGUG	54993	CCCTCTCACUCCTGCCTATCUA
324106178	54994	CGAGACAAGCAGGAGUGAGAUG	54995	GGCCCGAUTTCCTCCCTUAG
324720460	54996	ACAGTCGCUCAAGACAGGUG	54997	CGGTACACGGUATGCAGCAUAG
323817799	54998	GUGCCCGCUACACAGAGAT	54999	GTTGTTGACGAUGATTCTCAGGATATUC
323314946	55000	GGAGGTGACUGGAGTCUGACA	55001	GACGTUGGGAACCCTCCUAA
325764356	55002	GCGGUGAGGATGATCTUGCC	55003	GCTGCACAGUCTCCACTTCUC
323677497	55004	TCTCCAGGUCCTCAGGACTUC	55005	GCGTCAUAACCCCTGGAAUGAT
319435806	55006	GACAACCTCCUGTCCCGTTUA	55007	CCTTGACCGUGCGGATGUAAT
318626197	55008	CUGGAUGGACAGCGGAAGAA	55009	GGGAGTCUGACCTCUCCGAA
326980262	55010	GGACTAGAAACCUCGCATCCUT	55011	GCCTGGUCTTTATCCUGAAGCC
317417455	55012	GTTGGCCCCAUGTTTCTCAAUG	55013	TCTTAACTGTGGCUTGGATCTGTUG
317417682	55014	GGACCAGCAAGUCGGCUAC	55015	ATTTCTCATGCUCATCCCCATCUC
320493853	55016	GUCCTGUACAGCGAGAGCAT	55017	CUACAGCCCGGACTGUGAC
266972287	55018	ACTAGATTUGGCCGCATTGAUGT	55019	ACAAATUAAGAACACGACCTCAUGGT
326044496	55020	CATGTGCAUCCGAATATGTUGCT	55021	CTGTCAGAGCUCCCTCAAGAUG
314128308	55022	AGCCAAAGUTGATGCUGAGAACT	55023	GTGGCCTTCGAUTCTTCTAGATUCAA
320077084	55024	TTGGCAGAAUTTCACGUGCAG	55025	TTTACAGAGGUCGCAGAGGGAUA
226242301	55026	CCACGGUCCCTCGATTTCUG	55027	CAGGAAUGAACCCCTTGCCUT
253752693	55028	GCCCAGCAACUTACTCATCTTUACT	55029	GTAAAUACAGAGCTTGUAGGGAAAGGAA
226152245	55030	AAAGGGTCUTACCAAGATUGGCA	55031	AGGGCATAUCCAGCTCCTCUAC
256007365	55032	GGTCACAGCUGCGTCTAACUG	55033	AGUGATACCACUGCAGACCCT
315832179	55034	GGGCCUCTCGTCCUCACT	55035	CCTCGGUCCGCATCCUG
324872997	55036	GTTCAGCCAAGUAGAATTTGACATCTUC	55037	AGTGATTGGTTGACUGATTAGATAATTTUGCT
324620555	55038	GGGATTTUGAGGGATGAGGUCAA	55039	TTAACAUGGGCACCAAAAAGAATTUGT
267975754	55040	TCTCCCCTCUCTAAGTAAAAATGUACCC	55041	TGGGTTGTCUGTTATTTCTGAUGGAAT
268721203	55042	AAAGGACAACAAUGTTTACAATGUGCT	55043	GGAGAAATUGCGCCTCUGAAAGA
258509808	55044	GGAGGTGACAGCUATCCAGTUACT	55045	ATTACTTGAAGGUCAATGCTCTCCTUT
267482188	55046	CCCTTTTCTUCCTACCTACCUCCA	55047	TGACAAGCAGUTGGCAGCTUA
266579266	55048	TCTGCACTGUTTCAGCTGCUT	55049	CCAGTAATGCCUTATAACGGGTCUC
260476433	55050	GCCAAAGCCCUCACUCAAAC	55051	TGCTGGTCAGUGAACACTCTTUT
326068714	55052	GCGGCTCAUTGTTATTCTUGACAA	55053	CTCTAACAGAUGCTAAGAAUGCACCA
325386461	55054	AACACGTAAUGAGTGCCCGTUAT	55055	GCCAGTCCAGUCAAAACGACTTTUA
319554819	55056	AGTCAAAAAGTGGUCTTATCCCCAUC	55057	ACCACACAAAGAACUTATCCTCCATUC
239707767	55058	ACGAGAACCAGCGACUCTTUG	55059	GGAGAUGAUGGAGAGGGAAAGGA
314007323	55060	ACAGGCAGUTGAAGTUCGCT	55061	CCAAAGTATGAAGUACCCGTCCAAUG
290851747	55062	CTTTCCTCTCUCCACTCCCAUCT	55063	CACCCTCAUCTCCCCAACTUC
292301886	55064	CCCGCAUACCATCTGCUGAC	55065	TCGCUACCCCTTACCTUCCA
300514363	55066	GCTCAGCUGAAGATAGTGACTTUGA	55067	TGCAGTTACGUAGGCTCCTTTUT
305743957	55068	GAGTCCAAGUTAAAGCUGAGGCA	55069	GGCTTAGGACCUCCATCTTUACCA
254553901	55070	CAGTGCCUGGAGGTATGGATUG	55071	CACTTAGATGAATUCTTTCCTTCCTCCUT
260715804	55072	CCTGGCCATUAACATGAAGTTTGUT	55073	CCATACCAAGAGGGUGGCAAUG
256880939	55074	AACAAACAATTTCUGCACAACTGATUCT	55075	TGTTGUAACCACCATGACTUGCT
265688557	55076	GACTCCAGGUATTCCATGGCUT	55077	GGAGAAGACTAGUTCCTTGCCTTUC
257231228	55078	CACCGTTTUTGAGCTGGUGAAT	55079	CTGAATCCTAACUGCTGAAGTCUGT
265226415	55080	TTCAGGAGAACAAGGCUTTTCTTCUT	55081	GAACAAGGCCAUAAATGCAATCUCA
257506456	55082	GGAAATTGGAAAACUGGGTGUAACCT	55083	TCACUGTGGGTAAUAAAAAGGCAAGT
260584038	55084	CCTTATAAGCAAGCUTGTAACTCGGUAT	55085	GTTGCCTUTAGGTCCTUCCAGAG
263727466	55086	CCCATGGAAAUCCTAAAGGAUAGAAGG	55087	CACAGGACCAUCATATACAATCAGTGUT
315275113	55088	GTTGCACAATTUGGTCAAGGCUAT	55089	TTTCAGTGTCUGGAGCATTTCAGAUAAA
320308769	55090	ACCUTTGTAUGGAAGCGAAAAGAAAGA	55091	GCCAAAAGGAAAUTCCAGAAGTGUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
319556599	55092	AGTGTCGAUACATTCGTGATATUGCT	55093	TGACAAUGCAAAAGGTGGTGTUG
316292245	55094	CTGGCCAUGGGTGACCTTAUT	55095	TCTCAGTCAUAAAGCAGACCTGTTUAC
329656896	55096	CCAGAAUTTCTCACUGGGAGGT	55097	AATTATTCAGAAUGCTGCGGTTTUCC
319785723	55098	AGTACTGUGGGAACAUCACAGAT	55099	ACCTCTTUGGCCGATTCAGAAUT
333612120	55100	CACCAGGGAAUTTCAAAATGCTUACC	55101	CATTATCTCTGTAUGCCTTGGCAATTUA
315221711	55102	GCACATTGCUGAATTGTATTGUCACA	55103	TGAGTTGAATGUATTTTCATCCCUCAT
313211366	55104	ATCAATCGAGUTTTATATCCAGTUGCCA	55105	GCAGTTGACAUTGCTATCTTTUAACAGT
266769747	55106	GGCCAAAGCUGGCAUGAA	55107	TCCTUGCGGACGAUGCAG
312742730	55108	CTTGCCCTCTTUCTCTTCTTTCTTATCUT	55109	CTGGCATGTUCTCTGTGATACTUACA
268652620	55110	ACAAGGTCAAACUGCCGCUT	55111	CAAAGGGTGUCCTCCCTACAAUT
317654653	55112	TGTCATCATCUGGTAAAGTCAAATGUCA	55113	ACTATTTTATUGCTGCAGUGGAGAGG
317686621	55114	TGTGGCCUGAAGTGTGTCATUT	55115	CATAGAGAAGACUGACCCTTGGTTUG
320548186	55116	GCTGCTTTACUCACTGTGCAUGA	55117	AACATCAGTAGCAUTTCTTTACCCCUT
264660095	55118	CCTGGACCAGUACCTGUACCA	55119	CTTGTCCCUGCCAGTTCUGAT
267932553	55120	GAGGGAGGGUTTCCAACTCUG	55121	ACCGACUGTCAGACUGAAGAGA
267637419	55122	CCAGTGGGAUCACCAUGGG	55123	ACCCUGGCAGGACAAUCAG
326943221	55124	ACTGAGGAAAUGACCCTGCAAAUT	55125	GCAGCGGGAAGACUATTTGUG
326785535	55126	GTCUGGATGGGATUGAAGAAAGGAAA	55127	GAGCAGTGCUTATATCCTTCCUGT
328093668	55128	CTGCCAGGUAGGAAUGAGAGAA	55129	TCGTGACTGUAGCAAACTGUGG
327819667	55130	ATCAGGAAGCUGACAGCGUT	55131	CCTTGATGGAUGGAAAACTCACTUG
323506845	55132	ACATCAACAAUTAGGAAAUCCAGCCA	55133	TGAAGCTTAAGUTGTGCATGATUGAAAC
253786883	55134	ACAGGUTTAAAGCAUGGCCACA	55135	GCATTGGCATTGUGTACCATACTTAUT
265413432	55136	CGAGTGUCATTGCTTUGAAGCAT	55137	GCTGGAATGGCUGAATTATAGCAGAAUA
262027668	55138	CTAGGCTCTATAAACUTTTCCATAATATTCUGT	55139	GGGTCCAGGAGCUCCATTTUC
268456856	55140	CAAGAAGCTUGCTCCCCCAUA	55141	GAGACCGTUAGCTCCTGGTUT
269256968	55142	AACTCACCATUGGTCCAGGTTUT	55143	CTGAGTGAGGGUTATTGTCAGTTAACUT
268417448	55144	ACCAGCCAAAAGCAGUCAUGT	55145	TTTGCAACGTTUCTCCTCATTTGUT
237358806	55146	GCTTACCUCGCTCGCUCAG	55147	CCTGCTTGUCTCAACCATGUG
267236161	55148	GCCTGGCCUGACCCUAAGAT	55149	TTGACCAUGAAGGAGAUGAGCAC
333134564	55150	GAUGGGCAGAAGGACTUAGCC	55151	TCTTCATGGAGUTGCTCCTTAGTUC
263373697	55152	CTCTGGAGUCCTTTTGGUACCAT	55153	AGCATTCACGUTCCACTUGGT
231118321	55154	TTCACTACTAGUAAACTGCAGTCCTTUG	55155	ACAGACAATGTCAUCACAGGAGGAUA
234336842	55156	CATGTTTCAGGGAUTACTTCTCCCAUT	55157	GGAGAGCTACUATTTTCAGAAACGAUCA
325234871	55158	CCAGCCUCCCACTTGACAUAA	55159	GACGCTCTUCCGAGTCAUCC
325696998	55160	GAGCTGGTGCUCTACGTATCTTUT	55161	TCTCCCTGUGTGATTTCUCCCT
324728742	55162	ACTCACACUGGCTCTTGTTGTUC	55163	GAACTGAGCCACUTCTCTGUCC
325052525	55164	GCAATGGGTTUCTCCTTCCTGUT	55165	AGTAUGCCGACAAGATGTUCACA
325131456	55166	CCCTCUGCAGACTGGTCUT	55167	GUGCATCUCAGGCCGACT
324311970	55168	AGAGATCUGGCAGCTTTTUGGAG	55169	AAGCAGGAUGAGAAGAUGGCAAA
266735109	55170	CCAGCGTUGGACACCACAUA	55171	GAAGCCAAAACGCUCCACTUT
316569015	55172	TGTTAACCCUAAAAGGTTACACGATGUT	55173	GCTTACTAUGCCAGCTTTGGTUAC
332138003	55174	GCACAAAAUCCTGGCCCUCAA	55175	AGTGGGCAAGCUGTGATCUG
326408371	55176	CGGTACGUGGTGGTGTGUAAG	55177	TGGAACCAGACACUACUGGGT
255446399	55178	CTGCTTCAAGGUTTCAAAATCCAGTUT	55179	TGCTGTTTAAGAAAGCUCAGGAGTUAC
227391156	55180	GCCTATCGCUCTGCTCTCUCT	55181	ACGCAGAGUGAUGAGAAAACCC
323517385	55182	CAACAACGUTTTCCCCTUCAAGAT	55183	CCCAGCCACACCUTCTCTTUG
325034502	55184	GTTTCUCAGGGAGCCGUCAG	55185	CCTATGCCUCATCAGGGAGAUT
332964764	55186	CCAGTAGAAUGCATTTTGCCAUGT	55187	AGCAUTTATTCCAATUGGGCAAAAACT
333376707	55188	GCATTTCTGTGACUACACTGAAGAUGAA	55189	CACCCCTAGGUCATAAGAAAGAAAUGAA
332942356	55190	CAGCUGGAGGAAAGGAGAAAGUT	55191	GCGGAATTGTUGGTATTTGTCATTGUC
315296115	55192	CGAACTGGCUAACATGTTTTTCTTUCT	55193	GAGTACTTGAGUGAAAGATGAAGTGGUA
314301158	55194	AGTCGGAGUTTGCTGTUGCT	55195	CCTTTGAUTCAGGTATTTUAGCCAACAT
258803406	55196	GGAGGACAAGCUTTAAGGTCTAAUGA	55197	TGTTTCTCACTATGAUTTATATTTCTGTGCTUA
258018609	55198	CAGCATGGCUAAGTTGAUAAGAGAGAAT	55199	CTTGTAUCGCTTCTGTAUCCAGAACT
267714549	55200	GACTTTTTGTGCUCCTTTTTACATGUCA	55201	ATCTGGCTCATUTTAGCAGCTACAUAAT
269034844	55202	GGTCUGTGTCAGUCACAAACCT	55203	GCTGCACUGACAGGCTTGTAAUA
268895797	55204	GATGGCTTUGGAAGGGUCAGT	55205	GGACTGCAAAAAGCAUTTGTGAAACUA
290464475	55206	CGATACUGAAGAAGAAGAAAGGTTAUGGA	55207	AATGTACACAGCUTTTGGCATGTUAG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
289406381	55208	AGCAGCTTACCTUAGATACTGAAAACAUT	55209	GTTCCTTAAACUCCTCTTGCTGGUT
292193542	55210	GCCAAATTAUGCATCGAGCUGAA	55211	GCAAGCATCATCAUAGTCCACAGTAUC
290304877	55212	CAGATGAAAGCAGUGGCTGGUAT	55213	CTGTGTCAUCAAAGAGGTTGAGUAAAG
291057339	55214	CCAGAAAATUCAGCTCCTTTAAUCGAAT	55215	TCTCTCACTGCUTATGTAACCTUACCT
224043938	55216	GATTGTCTTTTUCCTCTTGCCCTTUT	55217	CCATTCCAGCAUATCGTCTTAGTGUAAT
224532731	55218	CTTTACAAGTAAUAAAGGCCCACGAAUT	55219	TCATTGUCCTGCCUCGAGAGAT
326599028	55220	CGGGAGCUACTTCCCCUGAT	55221	GCCGCTGAUCTCCACATCTUG
326701016	55222	AGAGCAAGCUGCCCTTTCTUT	55223	GCGTCTCCUCCTCACTGUCA
332117288	55224	GGCAGAGAGACGCUTGGUAA	55225	GCCTGACTTUCTACAAATGCUGAGT
237834154	55226	AGAAGAAATTGUCTGCTGCCCUT	55227	CAGTGGAATGUAACAAGATGGAGAAUC
238371345	55228	GATTCTTATTGAUGCCCCATGTTTUGT	55229	GCAACTGCCUTTAACATGTATAAUCACT
240318875	55230	TTACAGTGGGUTCAGACGAUGT	55231	TGGUAAAACTTUCCACACAAGGGT
262181786	55232	TTGATGCAACUGCAGTGATACUCA	55233	TGCTTCTGUAGTCTGGGTUACGA
258934940	55234	AAGTACTGCTTCUTTCTTGGAATGUGA	55235	GCAAGCTUCGCTTTGAACUGG
268533959	55236	CTTAUGACGAGGTTGGUGAGAGAAT	55237	TGTAGGCTUCCTCCACUGGT
268534101	55238	CAGTGGTGUCAGCGATGAUG	55239	CCCGCTCTAUACCTTCTGTAAUGG
267353701	55240	GCTGCAGAGGAUTGAGGCTTAAUT	55241	GCUCUACGGGAGCACAGT
331782916	55242	CAGTGGUCAACCUCACAGGAA	55243	GCATGGGCCCUGTGTCUG
257303733	55244	CCTGAGAAUGGGUAGCCAGGA	55245	TGCTTTCCAGCUGAGAGTUCAC
267473214	55246	CUCCCTGTUAACCCCAAACCAA	55247	ACCTGGACCUTCTCTCCTUGAC
267374697	55248	GATGGGAAUAGGGAGAUGAGGGT	55249	CAGCAGCAACCAUCAAGACTUC
327519936	55250	TGAGCUGCAGGGAGAAAUCAG	55251	CGAACCCCGGGAGUTTGUG
327381268	55252	CCCUCAAGCCCCTCCCUT	55253	TCCTTCCUCGACCTCCTCTUG
324628790	55254	CGCTATGAUCGGGTTCTCTTCUG	55255	CCCCTTUCAATTGCUGCGA
314055821	55256	GGCCGUCCAAGGGAGTUAAG	55257	ACTTTCTGACUGTTTAGACTCCUCGT
318725640	55258	GCTGTGAAGUGGAAGGAAAAUGT	55259	GCAGCCACAAUTGGTATTTTUGGAT
271103854	55260	GGATGAAATCATUCCAGTGCTCCUT	55261	CCTACTGTGACUTGCACTAGTCAUT
319267128	55262	GCAACTTTACUGGTGCACUCACT	55263	TGTGGACAGAAGCAAUGTTCUGA
271108217	55264	TCATAGCUCCCACCAGAGUGA	55265	CTTTAGGTTCUCTGGACTTTATTTUGCAT
269732805	55266	GCCCAAUGATCUGGCACAAAG	55267	TGGTTCTTTCCUAATGGTGACTGTUT
271881009	55268	TCCAGAAGUGAAAGGAGCUACCA	55269	ACACCGUTCTTCAGUGCGT
271936438	55270	GGCAGGTCUGCTGGTCAAUAT	55271	GACCCCACUACCTGTCAGTTTUT
269601864	55272	GGCTTGUGGAGGAGAGAGAAUT	55273	TTTTTCAGCUGGCAGTTCGATUG
269656496	55274	CGGACAGCACCUCGTUCAAAT	55275	CATCTGGUGGGAGACTTCTUCAAAAA
272542877	55276	CTCATCCTGTCUGGTCTTCCTATUC	55277	TCTATGCAGCCUGAGATTTCTTUCC
270222529	55278	CATTCTACTGACCUGCCAAAAGUAGT	55279	TGCTCCAAUCAAAACTGAAAATGCTUT
316674213	55280	GTTTGCCAGCUGAAACTUCAGG	55281	TCAGCAAAACGUAACCCTCACTTUA
316472466	55282	GAGTGAAGUAGAACGTAGGAATGUGAA	55283	TCCAAGGCAGUGAAAAACTATCACATUA
315534926	55284	GGTCCCATAGTUATGCCATATTGTCTUA	55285	CTTGGAAGAAUCCATTACCCTAUCAAGT
317638948	55286	ACCAUGACCAGAGCAAAATTCUGA	55287	GUGCAAAAUACCACAACGGAAGA
268371968	55288	AAAGUGAGAAAAGCACCCCUCA	55289	CGAAGUGCCACCTATGCUAGT
263218672	55290	AGCTTTGCUACAGTGAGCTTCUT	55291	AGGTTTTAACAGTUGGGATCAATGCUA
320981925	55292	AGACAATATGGCUGAGTTCTTUCGAC	55293	TGCTAGTGAAGAAGUTGTTGGTTUAACA
327661528	55294	GCGGTCCTUACCTAGGTCUCC	55295	GCCAGGTACAUCGACTTCCTCUA
267640663	55296	GGTGGCTGTUAACATCTTAAAGACTTUC	55297	GCTTTTUGCACCCACCTUCAA
267869595	55298	CACGGCCCCGUATTGTACTUT	55299	GGTTGCACCUCCATAACACAGTATUAAAT
267822206	55300	AGATGAAGCTTUTCAAGATGGTAAUGG	55301	ACATATGTTCGGUTCAGTGTTCUCAAA
259737630	55302	GCTGTCCACUCTCTAGGGCTTUA	55303	GTGCAGTUAACTATGGCUGGGAA
268657103	55304	AGTCAAACAGUAGGATAAATGCAGCUT	55305	AGTGTTCATUCACCACTTTTAGACAGUT
262979102	55306	CCTACCTAGAUTATGCAGGCUACCA	55307	AAGGAAGGAAAGACCCUCTACCUT
312668319	55308	CTTCAAAAGAAAUTCTGCGCUGGAA	55309	GTATCTTTCTTUCCTGGACCAUGAGG
324831220	55310	TGAAGTACCAUGTTTACUGCACCAT	55311	CCTAACCAAACCUTAACCTTCTCUGA
332287035	55312	GCCATCAGCAUTATTCTTGTTUCCAT	55313	CTGGGTGTGUGGAAGTTTCATGUA
224473658	55314	GAAGACCTTGTUGAAGAATTGAGCTTUT	55315	TGCAGAAACAAUCTCAGCTTTCAAAUC
223556064	55316	CCAAGGAGAAGUTGAAGAACAAACATUT	55317	AGGACAAAGUCTATTACATUGAAACAACCA
258586616	55318	CTCTGTGAGAUGTGCGUCAGT	55319	GTGAGTATACAAAAUGACCCAGGTTCUT
326345688	55320	CCTCUGCAGCTTGGGUAGAAC	55321	GGAGAAAUCACCACTGGTCCUC
323492972	55322	GGACCGAACCAUCTTTGTGCAUA	55323	TGTGCAATTTATGAUTACTCCAATAGACUGAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
266705493	55324	TCCTAACUGAGACCTUACACCGT	55325	AGAATCCTCTUCGATGCCATTCATUT
259433108	55326	CTGTCAAGGTUGTAAATAGACTTTUGCT	55327	CAAGCTUCCCAGGAAACTGTUCT
314698994	55328	GTCTGTTTGUGGCGGAUCCT	55329	GAGGUGCGAGCCTTCUGAA
313408456	55330	AAGGACCGGGUGTCACCUA	55331	GGUGCAGGUGAGGCAGT
321177698	55332	TGCTTACCCCUCCATGTTTCAATTTUA	55333	CCGCCUCATTTTCTAATUGCGAAT
320712099	55334	GTTGAATUCCAAACCGGCATCUAT	55335	GTTTTGTTTCUCCTCTTTTTCTUCAGGT
332814716	55336	GAGGAGAUGCGTCCCAUCAAG	55337	TCTTCCUAGCGCAGAGGGUA
317532158	55338	AGACAGGCAUGGGAGUAGAGAC	55339	AGTCTGCCACUTCCGGAGUA
317393466	55340	TCCCATCTCUCCATCCCTCUG	55341	AGTCAGCUGAAGCGTAACACTUT
240004984	55342	GTTAAAAAGCTUCACAGTTTGTCCTUGT	55343	CCCCAGTAGTUGAATCTTCAAAGGAUAA
264507191	55344	TGTAATGUGTACATGGUGCCAGAAT	55345	ACATAAATTACUCACAACTTCCUCAGCA
266353615	55346	AGCCGAACAGAAUGAUGAGCAA	55347	CACAAAGGAUTGCCCAUGCC
257123957	55348	CCTCTGTTTTCAUGCCTGATTCCUA	55349	CCAAGAAAUGAAGCAAGCUGAAGAG
257395145	55350	GTTGTCTTTCAGUGAAGCCGAUG	55351	AGACCAAGCCAUACAGTTGAGAUG
258234182	55352	CCTCCAGTCAUCTCATCTGCUCA	55353	GCCGACCUCAACACCTTUCAG
317527466	55354	CCTUGCCAAAAGCUGCCAAAAT	55355	CAACGACACCAUCCACCAAUG
333286106	55356	TAATTATCCCUGCACCAATCAUACAC	55357	AAUCAAAGUGACCCAGAAGAAGCA
316619172	55358	GGGAGAGGCAUCAAATCAGUC	55359	GAACATCTCACAGCAUTTCCATCTTUT
259590919	55360	CAAUCACCTTTUCCCCCACAGT	55361	TCTGTTTCCTTCUCTTGTATCCCUCT
261533809	55362	GGGCTTTCUGTATGCTTGUCCA	55363	TCTCCGAAACUGGAAGAGGUACAA
265809866	55364	GCTGAGCTCCUCTGCTGAGUA	55365	CAGGTCUAAGCGGCCTTCUAAG
316486844	55366	CTCGGTTATCUTTTCTCCCGUCA	55367	CCCAGAACCAAAGCUTCAUCAC
315840825	55368	GGCTGGGCCAUATGATATCUGA	55369	GTGACTGCTTUTCCTTCTCACUCT
281194809	55370	GTTCTCAAUAGCCAGCCCUCAAA	55371	TCACAATTTCCCUTCCTTTCTUGCT
278171601	55372	GCCATCAGUCCCTGGGTAACUA	55373	GCATCAGCTATTUGTGAACTAGATCUGT
267271946	55374	CCTACTGTGACCUCAGCCACUA	55375	CCACATACTGCUCTCTCTTTCUCC
268008819	55376	GGGAGAUGCCCAGCTACGAUA	55377	GCAGGGAGGGAAUGAGAAAATGUC
262135869	55378	CCCTTCCTGUGTTCTCGAGUC	55379	AATTTCCTTGAAAACAUGCAGCAGUT
262261485	55380	CTCTCAGAAUGGTGGUGGAGAA	55381	CCAAGAAAGUGGCTGAACGUC
253804655	55382	TGGAAAUGCUCCCCGGAAAT	55383	CTUGGGAGCTAGUAGGCAAGG
321388708	55384	CGATTCCTCTTTUATCAGCTAATCCUCT	55385	CCAAGCUGACACTTCAATUGCAT
320217912	55386	TCAAGTATTATACUAGTGAGATCGACAUGA	55387	CTGGCCAGGAAUATGGACAAGATUAT
319889945	55388	CTTTTTGAAGGAACUCGGAGATUGG	55389	CTTATAGCGUAAAGACAATGACCAGGUA
320336820	55390	CCTGTCCAGUGCTTTCCCUAA	55391	TTTGACAGCCUTAAAAGCTGTTTUCAAT
320090606	55392	ACTTACATCTUCTATGTCCTTGUCCAGA	55393	CGGTCTACACAUTGAAATACTGGAUGAA
261833522	55394	CCCTTGTACUTGCTTTGCTCUCAT	55395	CGTTGACCGUGAGCTGGUAG
265235156	55396	CCCAGGACCAACGUCUGAG	55397	CTGTTGAGGCUGTAGAACTTGTUG
265818352	55398	TGCTTAAAACACUGCACUCCCAA	55399	AACACTUCGCCAATGGAGUCAT
255954549	55400	TGAGAAUGAUAACGCGCCCAT	55401	CCTTGTCTUGATCCTGCCAUCA
254482130	55402	CGGGACUGGGAGTTCTTCAUC	55403	AGTTCCCCUAGGGACTTUCCA
264171790	55404	CCTCUGCACCAAAGGCAAUC	55405	CCTGGCCAUATAGTGCCTTUCA
254094374	55406	CTGCGGCUCAAAAAGCTCTUT	55407	CCACCCAUTGCTGTCTTUGGT
263906427	55408	AAAUCCACACCCCUGCACAA	55409	AGCCAAGGUTGUCCCCAAG
327185468	55410	TATATTGTGAAGGCAUATTATGTGAGTAAUCCT	55411	CAGTGGTTUGAACAGTCTCTTTUCC
328250076	55412	GCAGGCCAUCAGACAGATCUT	55413	CCCACTACUGCTCTGUAAGGACA
313342676	55414	CAGTGCCUGCATCTACCUACA	55415	GGGTGCAGGGUTATAGTUGGG
314530245	55416	GGTCTTCACUCTGCTTTTCATTUCAG	55417	CCTCCUGCCTCTTCUCAGAAAG
314381911	55418	GGGCCUGGCCAAGAAGUG	55419	CGCGUGCTGTAGAUGGAGA
327561651	55420	CACTCCAAGUGGTCACCTGUT	55421	TCCCTAAGGCCUGTTTTCCTCUA
326985972	55422	CCATGGACCUGACCAGGUACT	55423	GCCAAGACCUATTGGTAACAUCCAA
326855910	55424	CACAGUGGGTCATTCUGAAGACA	55425	TCAAATGTGCCCUTTGTCCTCUC
328210245	55426	GATGGAGTUAGCCTTCCAAGUGA	55427	AGCTGAACTGTGUCTCATCATTTTGTUA
327982334	55428	GGGAUGAGAGAACCAGGUAAACT	55429	AAACATGCCAAUCTGCATTTGUGT
327787735	55430	GCAAGGTTUCCTCGGAAGUGG	55431	TCCGTGATTCUGCTTCTATCTCUCT
318509514	55432	GCAGAGCGCUGTAGGTGTUT	55433	TGTCUACCAACCAATUCCACAACC
333450699	55434	CUGGACAAGCATCUCCGGAA	55435	GATCGCCATACUGGTTTCATCTUCA
315401008	55436	CTGTTGGUGACAGGACTUGGT	55437	GCCAGAGCUCATCATUGGCAAT
312955911	55438	TCGGCACCACGUAGGUAGAA	55439	GTCAGCTCCUCTGCTCCCUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314327791	55440	ACATAATGTCUGCAGAGCCCTUT	55441	GGGATTCUGGACTTCAGCUCAC
312902042	55442	CAGCAAAGGCUTTTGAGACCUG	55443	CACCACGACUCCCATCUGAT
314207076	55444	TGAGACTCTCUCTCGCCCAUAG	55445	CCTTTCGAUCATCTCCCUGCAT
314531267	55446	CTTTGCCAGUGACACCCUACT	55447	TGGGTCTAUTCCTGCAUCCCT
315492628	55448	CTTTCUGAGCCTTTGTCUGGGT	55449	CGGATUCGGATGGTCUCCAT
313532772	55450	GCCAGGTCAUTTTGACAGCTUT	55451	CAGGGATCTUCTCACTGCCAUC
313343920	55452	AGCTGGUGCATTTGACTCUGAA	55453	AACCCACTCAUGTTGTCCTGUC
315384735	55454	CTACGCCCCGUACTGUGAG	55455	CCACAGAAUCUCAAAGCAGGGAAT
313623648	55456	GAATCAGUGAGAAGCCUGGGT	55457	CAGGATCATCUCAGAGCCATAGUC
312686439	55458	CTGTTCUCCGTGTTGGUCCT	55459	GGGCCACAACAUACTTAGATCTCTUC
314651728	55460	GCAUCAAUGAGAGGACCAAGCAG	55461	TGTGTGUCCCATAAGAUCCCAAGA
314977521	55462	GAGGCATATGUGCAGATCCUGAA	55463	TGTGUGAGGAAGGACTGCAUC
313283616	55464	GCCTTAGGUGGGAAGGUCAGA	55465	GCCUCAGATGAUCCCAGGAC
222998755	55466	CTGCAAATTUATATCCATCAUCCGAAAGG	55467	ACCAGAGAAAUCCAGAGGAAAGTCAUAT
223647854	55468	ACTATATATGGCUGTTGTGCCCTUC	55469	GGTCUGAGCAGTAGTUACACACAAA
223039345	55470	CCAGCTGTCUTCGACACTTCUC	55471	ATCCTGTAAAGUGCTTTTAGTGGGAUT
222347510	55472	TTAAATTGGTUGTGTTTTCTUGAAGGCA	55473	CCTACTTCCUCTTTGGCTCTTTUCAG
222587273	55474	ACGCTCUACCCACTGCAGUA	55475	GCTACCTCTGGUTTAGTCAGAAATUCAT
223621257	55476	GGACTTGGUGATAGACATGUACAGAAT	55477	GCAAACAACATUCCATGATGACCAAAUA
328931865	55478	CTCAAGGAAACAUGAAGTGUGCAT	55479	CCTCTGCTGUAAATACAAAGCTTUCAA
332851426	55480	GGTTTTGGGUTTGCTGTTGGUC	55481	GCAGCAGCAAAGGAUACAGUT
332754072	55482	GTCGCUAACACACATGCUCCT	55483	AGAAAGCGACAGAGGAUGCAUT
332772831	55484	GTACAAGAACUGTGAGCUGGACA	55485	TTGAGGAAUAGAGAGACGATCUCAGT
319379396	55486	AAGACACCGUGGATGUAAAACCA	55487	AGGAGCUGCAGGCUGAC
318183714	55488	CCCTCATCCUCCATTCCCATUC	55489	GACACTAGCUCCTAGATCCUCCT
315313733	55490	ACTATGUCCACACUGGAGCCT	55491	GCACCTCGUAGTCAGCAAUGAT
263837235	55492	GGAGGUGAGCAGGAGAGGAUT	55493	CAGTAAUCAGAAGGGCCAGCUC
269193733	55494	GCTGACUGAAGTTGAACTTUCCC	55495	GCCAAAAGACAUGACTGTTCCTATACUA
267636607	55496	CGACTAGTGAUGGTAACAGAAGCTTUA	55497	TGACTGTTTCCAUAAAAGTGTCTCATTUCT
263154089	55498	CCATCTATGUTCCAGAGTCUCAGGAT	55499	GGGAAGCUGGUCCACCT
258136770	55500	AAACTAATGAUCATGGCAGAUGCCT	55501	GTTTCTGAAACCAUCTCTCTTGATGCUA
261449980	55502	CATACCGGUAACATCAACATAGUACCA	55503	GGUGGAAAGGGCAAAUGCAA
268813538	55504	CCCTCTGGAGAAUTGTGAAAATCTAGUG	55505	AGGGAAGCAUGGCAAGTGATAAAUAG
333757349	55506	CTGCCTATUTCACCTCCUCAGAT	55507	GGTTACTCAACUCTCTTGAATCCUGT
324367833	55508	GACCACAGACAAUGTTCCCUCT	55509	GTATGTGTAGACUGTGCTCAGUGT
313147120	55510	GTGAAGGAGAUGTCATCUGAGACC	55511	TGCATCTGAUTCCCCACTTUGT
315793012	55512	CTCGUCACTCGATTUGGAACC	55513	TGAACUAAAAGCCAGCAGGCAUAT
327558657	55514	GAAGGAAACCUGTGGGCUGAA	55515	GCTCTTTGTCCUTCCCACTTTUCT
326525765	55516	CTCCGTCGGUTAACACGTACUC	55517	CCTGCACTCCUTCAAAGAGGTUA
328463489	55518	CAACTTTCAGUGGGACATGCATUT	55519	CAATGGCCUCGTTTCTCAATAUCAAT
328420650	55520	GGGTGAGUGGTAACATAGGUAGG	55521	CTGACCCUCACATCACTTUAACCAA
327245340	55522	CCGUCGGGCAGTAGCTUAT	55523	TGGACTCTUAACACACTCAGTCCUT
328148212	55524	TGCCGUAGGTAGAAGTTUCCCT	55525	GGGCAGUGTGAGUGCAAAAA
327294373	55526	CAGCCAUCAGGATCCAACUCT	55527	CCCTGTCTTGUACCTAATGAGCAAATUA
328450326	55528	CTTGGAAAGCUGAAGACAGTUGAC	55529	ATCATUCAGTTCTTTAGUCCACAACCAA
324264567	55530	GCATGAAGUAGCCTAAUGAAGAGCAT	55531	GGACCCTGCUGCTTATCTGUC
324399568	55532	GTTATCCGACUGGTCCUCGAA	55533	AGGTTGTCCGUGGAGAAGUAAAAG
326080097	55534	ACGGTGACUCAGTATGCTATAUACAACA	55535	ATCAGCCAATTATUTTTGACTTGTGCUT
323307261	55536	TCTTCTTTUGCAGCGGCTCUAA	55537	ACGAAGCAAAGAAAAAUAGGAGTGAUCT
324903793	55538	TGTGGACCGCAUTTGGGAUT	55539	CTGAGAACCAAAAGACUTCTGAGUGA
323352541	55540	GTGTCATTCUACCTCAGGUGGAAC	55541	AAGTAATTCCGACCUTGGCAGAUT
325666242	55542	AGAGCCUGAAGAAGCAGAUGAAAAA	55543	GTCTGGCAUGTTGGCUAACAG
324808397	55544	CCTTCTCGACAUTGCTATGGGATUC	55545	GUTTAGAACAGGUGCAGACCCT
324983994	55546	CCTGTGCTTUCCGATGGCUT	55547	AAACCCUCTCACCUGGGAGAT
332280914	55548	GCTTCACTGUGCTGCTCTUC	55549	TGCAUGCAGCCCTCTUGAAAT
333641714	55550	GGUGGCAATUCCCCAAACC	55551	TCCUCCTCUGGGAGCGT
319733970	55552	GGTCCTCTUGGGCATGGTUG	55553	AGTGGGACUGGAAAGTGACAAUG
332384463	55554	TCTTACTGGGACAACAUACAACTCCUA	55555	TCTCCCAAAGGUACAAAGCTGUC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
321397670	55556	CAAACACACACUCTCTCTCATTCUCT	55557	CGGAGAATTGUGTGTGCATTCUT
319751979	55558	CGGCCAGCCAUTCCTACTUC	55559	GCCACATAGUTCAGCCAAGUCT
280333064	55560	GGTTGGUCACTTCTGUGCAAA	55561	AGGGAAGGTTGUCATGTGTACAAAUAAA
278446570	55562	ACAAAAGGGTCAUCAAAACTTCAAUCC	55563	GCTCCAAAUGAACACTTATACAGCAUT
265315350	55564	AGAGUCACACACACUGGAAGAGA	55565	GCTCTATTTGCAGUGTTAATGTGCTUT
257730690	55566	CCCCTCACGUTCACTGGAAUT	55567	GACTCATTTTGCUTTTCTTTTCCTCAUGT
241315625	55568	TCCTAUGAACCCTCTGUCCGT	55569	AGCAGCATTTAUACGAGTCGTGUT
328108510	55570	ACTTTTTGGGAGAAGGUTCCACTUT	55571	CCAAAACGAAGUACATTCTTCTCAUGGA
326993127	55572	TCTCTCUACACAACAAACCATCUCAC	55573	GGGAAGGAAUGCCCACUACT
262072283	55574	CCTGAGCGCCAUCAGTTUGA	55575	CCAGAGGUGTACACAGTGUCC
332590026	55576	TCUATGGUGGCGAGCCAAAAG	55577	GGATCGATCTCUTTCCTGGTGTTUG
333155273	55578	CTGGCCAGAAAAGACUCCTTUAA	55579	CAAATGTGTGGCUTTCTTCTCTUCC
333276585	55580	CTGAAGACACUGCCCCTTGUT	55581	AACGTGGCAUTTTACCCTCAUCT
332268348	55582	CCAGGAATUCCCTGCAAUGAAGAA	55583	GCTCTTCACUGACACGCTTTUACT
315240928	55584	GCCTTUGGCCTCTCACUGAA	55585	GCACCGGCUACAGAATGAGAUA
312781879	55586	CCTCTGTCUCCTCCTCGTACUG	55587	TCAAACAGUGAGGUGCCACAT
313988875	55588	GUCAAAGGCACTCUGGGACA	55589	TGGTCACCAACAAUCCCUACGA
313583384	55590	GCTCUGGGCACAGAUAGACAT	55591	GATCATUGCCAAGCUGACCAAG
313963632	55592	GGAGATGTCCUAGGAGGTCCUG	55593	TTCCTGCATCUCTTTCTGGCAUT
257541841	55594	CCACAGCAACAUCCUCAGAGT	55595	GGCTGCAGAAGUTCTCATTTGCUA
330848026	55596	CTGCAUGAGAAGGGTGUCCAA	55597	GTCTTACAGCGUCAATGUCACCT
326524325	55598	TTTCTAGGGCAAUGTGTCAGTATUCC	55599	TGGTTTCTTTGATUCTTAATCCTTGATUCCA
326167778	55600	CTTCTTGGUCACCCTCAGGUT	55601	AGGCAUGTTTAACAUCCAGCACT
319702317	55602	GGAGGTGUGCGTTTACUGGAA	55603	GTGGGACTACUTTCATTTTCCUCCAT
320914379	55604	TTCGAGTGGUAATGGCCTGUG	55605	ACCTCTGTCATUCAACGTTTCTGAUT
316710320	55606	GTTCTUACAGGCAAAGGAAUGCAG	55607	CACAGTCACGCUGTATTTCTTUGA
317770215	55608	GTGTAATCTAUGCAGTCCTTGAUAAGCA	55609	TGTGCTGAGCCUTTTTCTAAAUCACT
317082841	55610	CCCCAACUGCAAAGCATAAGAUT	55611	TGGATGAAUGCCAGGCCAUC
317903292	55612	CTACAGTGUACTTACGTTGUCCACA	55613	GAGCTGTTGCAAUCTATGCATTTAAGUT
328451225	55614	GTGCTTCATTTUCATCCTCTAGTTTUCC	55615	TTGTTTTGCCAGGUTGGTATUCAAC
326811682	55616	CTGTCCTGCUTGAGGTCTCUT	55617	GCCTAGAATUCAGCCCAAGTTTUT
333561970	55618	ATTCCAUCCCCGAAAACACTAACUT	55619	CAACAGGGAUGCGGTTCUGA
272480187	55620	GGACACCCAAUGACCCAGUAG	55621	ATTCCUGTTGACATUGGAGAGCA
315814968	55622	CCAACCTUCCCACATCATCCUT	55623	CAGATACCCUGACCATAAATGAUGACC
319272110	55624	CCCCTTAAGACCUAGGGAACUCT	55625	TTCACTACTTUGGTCCTTGGACUG
319914155	55626	GGTTCCTTCTUCACCTTCTTAGCUT	55627	GCTGCTCUCAGGAGAGAGGUA
318948868	55628	GCTCGGUCAAAGGAAACATTGUG	55629	AGTTTAATGTCUCCATGGTGAACCUG
240171476	55630	CCCCUGACACGCATTGUGT	55631	AGGACTCTCUAAGCCAGTGUGT
241054930	55632	GUACTGGCCUCAGGCCAAA	55633	GTCCCGGUGCTCCTUGAA
321339346	55634	AAAGCAGUAGUGCCCCACA	55635	GGCGAUCACAGCGCAACUA
318747592	55636	CTTTCCTCUCTGCACTCUGGAT	55637	CUGACGCCTCUGGCACA
318730842	55638	GGAGCAGGUTGUGGGAGA	55639	TTCATTTGGGUCTTCCAUCAGAAAGT
320800879	55640	GGAGCCTUCATCTGTACTUCGT	55641	AATGCCCTAUGCTGGCTUGT
235964651	55642	ATGTCACTCUTATGTGTCAUCACCAAA	55643	ACTGCCATUCACTGTGTTCCUC
241165400	55644	TGTGAAGGCUCCAGAGUGAAGA	55645	AGGGTGUGGCTTCAUGACC
267431370	55646	GGCTTCTCUCATGGACCUCAAC	55647	GGACAGAGAAAGUGAAGGAGAAACUC
260655214	55648	TCCTCCGUGATGCTGUGAAC	55649	GTAGGUACTTTCCAAUAACCACACCA
327919818	55650	CCAGCTCCUTGCACTTTGUT	55651	CCCUTCUGGGAGAGGAGGAC
318549845	55652	GGAAAGAGGCCAAACUGCUGAA	55653	AAATATGAGCUACAGCUGGCGAA
318902701	55654	TGGCCTAGCUGAGTCCACUT	55655	TGAGCGAUGCTGACACUCC
319982261	55656	GTACAGTACCCUCTCCCCUCA	55657	TCCAGATCUTCCGAGCUCACT
318239298	55658	ACTGGGAGAUGTAGACAGGTUCA	55659	TCGTCATTTCTGAUAGCCTTCTCTTTUT
318835170	55660	GAATTTACGUCAGGTGGACCTCUT	55661	CCTCCCGTUAAGTCTGCTTTUAACA
321368275	55662	CCATACCUAACTTCTTGTGUGGGAAA	55663	CAGTGAAGAUGCAAAAGAAATGGUAAGAT
265149930	55664	AAGATTTGGCGACUGGTTCTUT	55665	GGTGTTGTGAAGGUCAAAAATAATGUCA
256911404	55666	TGCUTCACGTTTUGCCAAACAT	55667	GATATCAGCTCUCAGAACCCCTUG
265091309	55668	GTCAGCGUTGGTCTCAUCCT	55669	GCCAGAGCUTGTCCATTGGUC
257636957	55670	TCCAGCAAAUGCATGAAGAATTUCAAG	55671	ATGCAAGTAAAUACCTAGACCCUACAGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258323046	55672	GTGGACAAAGCUGCAAAAGAGAUG	55673	CACCUCCUCCAAGAAGAAAGCAA
268343847	55674	CATTCAUGTTCCCCUAACCACCT	55675	TCCAGGAAGCCAUCCACTTUG
260495790	55676	CUGGTAGTTACAUGGGCCGAAA	55677	CTAATATAATUACAGCTCGGGCUGCT
268310788	55678	CCTAGACAUAGGAGGAATCCATCUGA	55679	AGGATTAGCCAGCUTGGTGUG
263994616	55680	TCCCCUGGAGGAGGGATACUA	55681	GGAAGAGCTUTTCTGAGGTTUGG
323682960	55682	GGTGGCCAAGUATGAUGAGAACT	55683	GCAATGTCGUTCTGCAGCTUC
324712293	55684	GGGCCUATGGACTGUGAAGT	55685	GATCAAGGAUCGGCTCUGGA
236499063	55686	TGGCTCAGAATUCACCTTCTACATUT	55687	AACCTTTTUGAAAACCAAGAGUGCAT
257902551	55688	AGATAATCATACUGAAGGCAGCTCUGA	55689	TGTGCAGUAAAGAAUGGCCAGT
242714582	55690	ACCAUCAGAGAGCCTUGAGGA	55691	CATCAGCAGCUAGATCCTTCTTTGAUAA
239800318	55692	CTTCGGAAAUTGAAGAAATCUGCCT	55693	AGGGACATCUTTTGGCCGAAUC
258359458	55694	GTCTTTTCUCCAGGCCTGATUC	55695	AUCATCATTATGCTUGCAAAAACGAACT
235197865	55696	CTGCCUGGAATTGAUGAAGAAACC	55697	TGGTGTCTTATAUTGTTGCTCAAAGUCA
332795208	55698	CCAGGAAGGCUGUCAGAGG	55699	CCCTGATCACUGCCCCTTTUT
332736635	55700	GTCCAGGUCGCTGGTATTCUG	55701	CCTCAGCTCUGTGGAAGGGUA
314004640	55702	CCAGACCCAACUAAACAAACAUGGA	55703	TGTAAACTUGACCAGCUGCAGAG
253968640	55704	CGGAGCUGCAGAGATCUGA	55705	TCTGACAGCCCCUCCTAUCC
225775851	55706	CTGCTGAGGAGGCUATGTGTUA	55707	ACTGGAAATCUCAAGCTTATCCATGUC
266393561	55708	CCTTCUCCCACCCTCACUGA	55709	CCTGTTCTCUGTGAAGCTGAAUGG
333126840	55710	GTTGATAGCUCTGCTCCAUGGG	55711	CTGCGCCAAUGAUGAAAGCA
262622786	55712	TGGCTTCCTAAUTTATTTCTCTGUGCAT	55713	CTTTTCTTCCTCCUTCATGATGGATTUCT
264140263	55714	GTTCTGCACCAGGAUGTAATTUCCA	55715	GGTTCAGCTUGTCCTGCATCUT
316254778	55716	CGGGTCUCACCCTTTCUACCT	55717	GCATCAGCCCAUAGGACTCAUT
331329371	55718	TGAGCCAGGAACAACAUGACAAUT	55719	CAATATCACUGACCAGTTCTGCAAUG
330358295	55720	GTGCCTGUCCATTGTCCTTATUG	55721	TCTTGTCTCCTUTTTCCTTTGGGUT
264231315	55722	GGACATAGUCTTGGGCAUGCT	55723	TGAAACAGACCAAUCATGTGCATTTUT
268659277	55724	GACTUACAAAAGAGCAATGCTAUGCC	55725	ACTGTGUGACTGCATUACCGAAAA
261634037	55726	CCTTTCTGATTUCATATCTTCCCUGGT	55727	GGAGGATGGUTCAGTCTAUACAACAAAT
268798278	55728	GAGATGGCAAUGGAGAAGTUACAGA	55729	AGCTGCAAAACAUGAACACATGATTUT
262205322	55730	CTTCCUGACCCAATGGCTUCT	55731	CATTAGCAUAAGGCTGATCUACCAAGG
315450023	55732	GGCCCCATUCCCAGTCAATUA	55733	CACAAUGGAAGTGUCAAGAGCAG
269303842	55734	AGGUCGCCCAAATUGCAAGA	55735	CACATCCACUTCCTGCUGAAC
269056446	55736	CATCCTGAGUTGTCACGUGGA	55737	TGTGAAUGAGGCCATTGGTCUT
259942415	55738	GTAAAGTUAAAACCAAATGACCUGCCA	55739	CGCTGCCCAUGTCATUGAGA
325929436	55740	CCTTGTCAGUGTCTCCUCCGA	55741	GGAAAUGATCAAGUCGGGCAAT
323995581	55742	GGCCGCTUCACCTCTCATUC	55743	GAGGCCAGCAUTCAGAGTUCA
323574149	55744	GTCCATCUCCTTCCGCAUCA	55745	AAGCTGTCUCAGGTCAGTCCUA
323692950	55746	GUGACCCCGCACACUCT	55747	CCUGAGCUCCCCAGCAC
323928929	55748	ACCTCCCAUCTTCCCCTUGT	55749	GGCTAGAUTCAGAGGAUGCCA
323393848	55750	AGTGTUCGCACAGCCCAUT	55751	GGATACAGGGCGUAGAGGUC
323841675	55752	TCCAAGGGCUCCUCCACA	55753	GTCAGCAGGGCUGGAACUAA
325916493	55754	GCTCCTUGAAGCAGTAGACUGT	55755	GCTCUACCGGCTACUCGAGA
315832851	55756	CAGGCAUGCTCATCCCUGAT	55757	CGATCCGGTUCACAGAAAAATAAACUG
326082035	55758	GGCTTCCCCUTCCCTTTCTUG	55759	CTGGCACCCUTCACTCUGAA
264024952	55760	CAGGATGAACCAGAGUTAATAGGTCAUT	55761	TGAGTAAAACTAAUTGGTTGTCCUGCAT
326598555	55762	GCATGTUGGAGACTUGGGCAA	55763	CGCGACTAACAAUCAAAGTGAAAAGAUA
318362480	55764	GCCCAGCTUTTGCCTCAGAUA	55765	GAGGTCGAAGAAUCGCTCTUCA
225636022	55766	GGGTAGAGCUGTGGATTCATTUT	55767	GACGGACATTTUTCCTCCCTCTUT
317048368	55768	GAGGACTGTGUGGAGTGATTATTUCAA	55769	CAGCTTAUACACCCCGCUCA
317162186	55770	TTGACCTACCAUAATAAACCATGTGGUC	55771	TTCTCTTTACCUGCTGCCATTTUCT
325045995	55772	TGATATGCCUTGAGCTTTUCGAAGT	55773	GACCAACUGCCACAATACCAACUA
324183703	55774	CCCAGCCTAUGATGAGTTCTTUGT	55775	TGAAATTCUTCTTCGTTAUGGACAGCA
323840795	55776	TTGCTCACUTGAAGTCAGUAGAAAAAGA	55777	GCTATGCAGACAGUTGGTGUACAT
266375956	55778	GAGAGAGAATCUGCAAATGGAGCUA	55779	CAGATCTTGATUTCCTTAGAGAGUGAGG
263348146	55780	CTCTTGAAGTUCCCGGAGTCTUT	55781	GCCTAAAACCUTGTCATATUGCCA
262352123	55782	TGTAAAGUAGGACATGATCUGGAACCA	55783	ACAATCAACTCGUAATTATCCACAGGUT
323492455	55784	CCACAUGAAAGATGUACAGGGACAT	55785	GGGCAAAGCUGTCAUGAGACA
242743578	55786	TGUGGAGAGGAGAUGGGAAAGT	55787	CAACTTCCTTUCCTCCCCTGUG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317061632	55788	GCTGTTCCAAGUGCAATTCAUGT	55789	CTTCTGACCAUCATTTCTCTTUCCCT
289986298	55790	CATTGAGGAGUGAAGAAGCAGGUA	55791	CAGAGGTAACUAGAGAGTGGUAGGG
289258300	55792	TTCACCTCTTTCUTCTTTGGTTTTCUCT	55793	GATTCCAGUAACCGCAAACCTUG
292010765	55794	GGTUGAAGAAGGAGAAAAGTUCGACT	55795	TGAAGCTATCGUTTCAGCTACTTUGG
259828876	55796	TGACCCUAAACTACAGACUCCAAAGA	55797	AGTCAGUGACGCCGUAACAG
257501403	55798	GCTGGTACTTCUACATTCAGGCTUA	55799	GCTCTCTCAUACATTGCAACUAGAAGAA
266821176	55800	GTGGAACTTGUACAACGTGGAGAUA	55801	GCTTCTACAAAAAGUGCTTCATCTTUCA
254926060	55802	TTCGCTUGCTAATGGGUGGA	55803	ATTGGTAGCCGAUTACATTTTCTCAAUT
255757818	55804	CTGAAGTTGAUGGCACACAAGUT	55805	TGCAGAAAAAUCATGCTCTTGUGAC
266705515	55806	CAGAACAGGCCCUCAGTUCAA	55807	CTTAUGACCAGGAGCCACUCAAG
265956596	55808	TCACCCATTTTUATCTCGTGCTCUC	55809	AAACCCTCCTACCUTTTCTCCTAACUA
316754734	55810	ACUGATAGTAACAUCAAGAGCAAGGGA	55811	CCGACACAUCAGCCCUCAAG
317553417	55812	CAACTGTUCCCGTTGAGACUCT	55813	GGGCTAGAGCACUGGACAAUG
267525456	55814	AAATGCTTCTTCCUTGGGTGTATAAGUT	55815	ACTACTTACTCUGATTCCTTTTGGUCCT
267634229	55816	AGATCATTTTTCUGGTTTTGCTGGTTUT	55817	TTGAGGGATTGTUGTAATCTTCTGGTUT
262170131	55818	ATTCTTATGCCCUCAATCACCTUCC	55819	GCTATCTTGUCCCAGAGGAGTTTAAUAT
257329044	55820	GGCCTGTTCCUTCACTAGATTUGA	55821	CGAUGAAGGGAGCUGAACGAAA
318483094	55822	TGTTACCCTGGAUATGTTGGATGTUAGAT	55823	TCTCCUACAAGGCAAATATGTTTUCACA
316980980	55824	TTGTTTTCACAGGUTGTTTTGAAUGGT	55825	GCTAGTGGTGCUGCAGATTATTATTCUT
316636683	55826	AGGGAGATCAGCUTTAGTTCTTCAGUA	55827	ACCCCAGCUAATAATTCCAGTUAAGAAAC
315468224	55828	ACATGACTTTCTUTGAAGACTGAACUGT	55829	AGAGGAGGCACUGAGAACCUT
266776507	55830	CCTCTGUGGCCCACCTCUA	55831	CTCCTCUGCCACCAGCUC
313965371	55832	CCATGCGCCUGTCATCTUGT	55833	TGCTCATCCUCTGCTTCAUCAAG
268755138	55834	GCTGCTTTUCCTGGTCTTTGUG	55835	CCAGGACTUCCCCAAAGACCUA
265757724	55836	CTAAAATCCATTUCCTACCTGCCCUA	55837	AAACACATTACTACUCACGGCTACAUC
268823981	55838	AGGACTGAAGAGGCUGAAGACAUA	55839	AAGCACAUCATGCATTGUCACC
315967956	55840	GGATTCCACUCCCACAGATATACUCT	55841	ACCAAAAGCUGGTACTTCACUGAAAA
316753628	55842	AAACTAGAUCCCTGTACCUCAAGGAA	55843	GGTCTAUGAAGACACACUCACCCT
326577220	55844	AAACACACTAAUGTGCAGGGUACT	55845	CGAAGGTTUCAAAGAAGCTGTTCAAUAT
258191801	55846	AAAACACCAGAAAUTATTGTTGGCAGUT	55847	CTGTCCACAAAGGUGCTACAATTAGAUA
320163697	55848	TACAACCGCCUCCGTGUAG	55849	CATCCAATACAGCCCUGAAACTGTUA
267332243	55850	GCCTTTUCTCTTTTTCTUCCAGGGAT	55851	CACAATCCUACCTGCACCTUCAA
267943998	55852	GGCACTCTUAGCACCCCAUC	55853	TGCAGCTTUGGGCAAGTTTUC
268901709	55854	GAGCAGCAGAGACUCUGACC	55855	GTGCCUCCAGAGACCAAAUGT
268038610	55856	CAGGCTATUTGGGCCAUGGA	55857	GGUATTCCAGATAAUACAACGCAGGAAA
327412461	55858	CTCUGACAAGTGGUCCGACAA	55859	GAGAACAAGCAGGAUGCTGUG
326841953	55860	CCACCTCAAGUTATGGGAAAAGCUA	55861	ATGCUGGACAAGAACAATCUGGT
326755922	55862	CTTGGCAGGGUCAACACGUA	55863	GCTAGAGGTAATTUCTGTCCTCCAATUC
314264974	55864	TGTCCAGATGUGTGTGTTAATGAATUCT	55865	GGAATAGCGGGUAAGGCTUGG
314938486	55866	CCGCAGGACUTCCTCACTTUA	55867	AGAGAATAAATCAAUAAGCCCACAGCUC
313930534	55868	TCCTGACCUGGGTTTUAGAGAACA	55869	CCACTCCUGCATTTCUCGGA
314359016	55870	CGCCCCACCUTTTCAGTATUG	55871	GGAGUGCAGGAGGCAATTAUAGAG
325819058	55872	GGACACTTUGGAAGGATTUGCAGA	55873	TGGATCCUCCTCTTCTCAUAGCAAAA
323841117	55874	TTCGTTCTCTTUCCTGTTCTTTCTUGT	55875	TGGTCATGGUCATTGGAAACCUG
323542366	55876	TCTTCTGATGCUGTCCTCTGATUCT	55877	GGCCTCUCAGAGAGTTCTTCUGAA
263759862	55878	GAACUTAGTTCCTAAAUAGCCCCAAGT	55879	TGTTCGTCATUGCCTCCATCAUC
255049220	55880	GGCTGAGTGAGUAGTTGTTTGCTUA	55881	CATTTAACAGCUCTGATGATGUGCAAG
269112202	55882	CATAGGAGCCUAAAAGGGAAUGAAAGT	55883	GCCTTGAGGUCCTTGACCAUT
269175633	55884	TGAAATCCTTUGGACTGAAATACTTGUCT	55885	CATTTGTGGUGCTAGCATTUAGGAA
267647068	55886	ACAAUTATTTGTAGGGUAACCCAGGAC	55887	GCGATCCCTUCTCTCCTGGUT
269086903	55888	GATTACAGCUTTGAAGUAGAGCAGGT	55889	ACAGCCTUGCGTGTTCGATAUT
267896791	55890	TCCTTAACGAAGUGCACATGTAUGA	55891	CTTGTTAGGGUGATCGUGGAGAC
263360063	55892	TGCTCAAUCTCACACUAAAGAACACC	55893	TTGGACAGTAACCAUCTAAAATCTGCUT
268855615	55894	AAAACATGACCUGTACGTGACAUCA	55895	AGTGGGTTCTAAUTTTAACTGGCTTGUT
316692928	55896	GCATATGCUCACAAATCCCATTUC	55897	GAAAAUAACCCAGAAUAAGGACACCCA
317832478	55898	GGGAAAGAGCACUCAGGUGAA	55899	GAATAGAAGUGGGAACAAGATCCUGAAA
264961977	55900	GGCTACCUGCACTTCTTACUGG	55901	AGGGATGAAGGUCGGGAUCA
236801214	55902	CGCTGAUAGCCAAACTGCUGA	55903	GTGTTCTTGGGUTGAATACTTTTGTUCT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
263378654	55904	GGGCAACTTCAGUACTTCCTATATCTUT	55905	GCAAGGCUGTCAACATGAUGG
234691924	55906	GCTGAAGGCACUTCCGTUGA	55907	CCCGTTAAGUCGTAGCCCTUA
233218426	55908	CTAGCTTCTTUCTTAGTACTGCUCCAT	55909	CAGAAGUAGAAGACGAGGUCAGACT
325214841	55910	TGGTGGCUCTAGTGACACUGT	55911	CTGCAACGCUCTTUGAAGCAT
323592784	55912	TTTTGGACTUGGCACTGGUGA	55913	GCCCUCCAUGGCAAAAAGAAC
264067451	55914	CCACTTCTUGACACACCUCCAC	55915	GGATGCUGGGACCTGGAUACT
326947322	55916	GGCTCACCGUCCTCGUC	55917	TGCTGAGCCCUGACTACUGT
264529884	55918	CAGGCCUCTGCCCAGUC	55919	ACCCAGCAAACGAUAGCATCUC
253987860	55920	GTAGCAAAUGTTACAUAAGCCCAAACA	55921	CCAGACTCUGAAAACTGCCUCA
262320402	55922	CCAGCCGUGAACAATGUCCA	55923	AAGACACCAUGAAGCTGAATATCTGTUT
316026891	55924	TGAATGTTTCUGTCATCAAGAUCAACCT	55925	TCCAUCCAAGCAAGAGCUACAC
316668223	55926	AATCACAGTTATTACUTACCAAGGCCTUT	55927	AAAGAAGCCACGGAGUCTAAGAATUT
332121800	55928	AGTGGCACAGGUTCGTTTUACA	55929	TTCATTTUGCCCCCUCGGAA
328779354	55930	GCTCUGGGCCGAAGUGT	55931	CUGGAACCCCGGCTUACC
324614909	55932	CCCCGTGUCTGACAGUGAAA	55933	CCACCACCUGTCCACCUACT
263906362	55934	GUGGAGGGCCAGGUCAAG	55935	CGGTAACCCGUGTCGCUA
261684542	55936	ACCCCUGUACCCCCACAA	55937	TCTAGGCCCCUCCTGUGAC
261790486	55938	GTACCAGGUGCCCACCUC	55939	GTCUGGCCGCCTGAGUC
333586457	55940	AGAACTCCAUCAGTGCCTCCUA	55941	AGTACCTTTUGCAACATGGUGGT
333326438	55942	GGAACTCCCUCTTTATGGTUGCAAT	55943	AGATTTCTUAGGACCCCATCTTACUCA
332948459	55944	ATTGTGGCCUGTCACTAUGGAAAT	55945	GCTGAACCTTTUTGCTTATAGGAATUGA
333702320	55946	TCCAAGAAGCAUTTGTTGACTACTTUGA	55947	TGCAAAAGUAACGGATTCCUGGAT
333197058	55948	ATTCGAATTGAAAAUCCCAACTCUCT	55949	AAGACATGTCCAACUTTAGCCCAAUAT
332312990	55950	AAGAAGAATACAUTGATGAGCAUGGACA	55951	CTCTTCTTTCUCTGTGCCTUCAGA
323961816	55952	TGTCCTCTUCCCTTCTCTCUACC	55953	TTGAAGGCGAAGUTGAGAGCUT
267914987	55954	GTTGGATGCCUAGGATGGTGUC	55955	TGCATACCCUCATAGAAGCATTTTUGT
268416167	55956	GCTTGCATCUGCTACTGCTCUA	55957	GCATCTCGTUACCCTTTGTTAATUGAT
263621165	55958	AAAATAAAAGTGAUTCCTTTGCCTUGCT	55959	TTACAAGGTTCUTTCCCTCTCAUGAAAA
264764251	55960	TTGCTATTACGGUTCTCAAATCUAAGGG	55961	TGAAGCAAGUGATTAATGAAUGGGACAA
269372669	55962	AAAATGTTTTCCAUCTCACTCCGGUAT	55963	GTTTGACTTTTCGUACTGATTCGAGTTUT
259110172	55964	ACAUACCCCAGCAACTAUGCC	55965	GGATGCTCUTCTGAAAGTUACAAGGAA
265969606	55966	GCGTCGGUGAAAAGTTTCGAATTUT	55967	AGGCTTACAATUCCATCCTAATTTUGCT
268484642	55968	GACTCTACATCAUGCACTTACCTTUACA	55969	AACTTTATTTTAATGCAGAUGGAATGGTTAGUC
261860084	55970	CCTCCAAAGUGATGUGAGGGA	55971	CAATUGAAAAGCCCGGATGUGAAG
289996078	55972	GCATATGAACCAAAACUAACACCUGAAG	55973	TATTGAGGCTGUGAATCTCTTAAAAGTUG
293229192	55974	AGATTTTTCCCCUCTCCCAUAGGAT	55975	ACTTACAGTCUCTATCTGCCUGCT
222561014	55976	GATGCTGTUCCCAGGTACTGUT	55977	GAGAACUGAGGGTGGUACAGAAG
329273555	55978	ATTTTAGACTGCTUAAAGCAATTGTTGTAUAA	55979	CUTCCAUAAGAACGGAGGGACAT
224581599	55980	GUCTTCTTCUGCACCCAACAAAA	55981	GGAGCTTATCATUGAAGACCTTGGAATUA
326927060	55982	GAGAAAAGCUCATCTGGCUCCT	55983	TTAAATCCCAUAGGCAATAGCTUGGAA
326700454	55984	GAUGACUCAGGGAGCAGCA	55985	GCCCTAUACCCCCGTTCUGA
327098252	55986	GCTACCAACAGGAUACTGUGCT	55987	CCTGAGGGAUCGGGUAGACA
328340290	55988	GCCUCTGTTUCCCCAGAAAAGAC	55989	ATCCCCTTCUGAAGCTCCUCT
261828513	55990	AGCCGCUCTCCCGATUG	55991	TCCGAGTUCTGGTCGGUGA
267768395	55992	CTTCCTGGTAGUATGTGTTTTCCTUCA	55993	CCGATCCAUGCTCTGUGGAC
268993935	55994	AGGAGAGCGUAAGATATAAGCAATCUCT	55995	GCTCCTGAACCUTCAGTTTGTTTATUG
266178816	55996	CTGGAGCAGGCAUCCATTGTUA	55997	CTTCTATCGCCUTCTGGAAAUGCT
263201183	55998	CGACACACCUGCTGTAACTCUA	55999	CCTTCTCTAATUCCTCAGGAGGTUAAG
265523436	56000	TTGGCCAACUGGATGAUGGA	56001	CCCCCAGUTTGCUGCAGT
332007848	56002	GCCCGUAGAGCAGAAACTTGTATUT	56003	GAGGAGACCUCCAGCTCUCT
331984550	56004	CCCATCCCCAUTCCTGUACT	56005	AGAACCCAGGGACCUCACUC
331761672	56006	GCTCTGCAGUGCACACUCA	56007	CCGCTUCGACTCCTUCACC
331785469	56008	GGACUGGACAGAGACAUGGAAA	56009	GGAAUCCGACCACAGAUACCT
331775666	56010	CAGGGACCUGCAGGGAAUG	56011	AGTTCGACUCTTTTGTGGUCCAG
331668881	56012	CCGTCCCUGTCCTTGTACUGA	56013	CAACCATGUTCTTTGTCTUCCCAAAT
331889263	56014	CGGATGCUGCAGTCCUCAC	56015	GCGGCCAGUGCCUAGAT
331863230	56016	GGATCTCUAGACGGACCCUCA	56017	GAAGCCCCUCTTCTCAGCTUT
264964366	56018	CCTGGUTCCGAAUGGACAGG	56019	CTCCATCCUGCTCACACTTTCUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
264567485	56020	CACTTGGGUCCCACAGGTUT	56021	CCCTTAAGAGAAUGACTTCCCATCUC
268322332	56022	GGAACGCCUGTCCCCAUAAG	56023	CTCATGUGCTCTTCCTUCCCA
265658785	56024	GAAACAGAGUCAAGGAGUGGGAA	56025	GCATTTGGGTUTCTCTGACAACUC
259432061	56026	GTGCTTTCUGGAATCAGGGAUCA	56027	CTCACTCCUAACTGCTTCCTGUC
325482640	56028	CCACAAGGAAGAGGAUGATGTUGA	56029	CCGAAAGAGGAGCGAUGUGA
272221889	56030	GGAGGCUTTCTTCTCTUGGGAAA	56031	AGAGACUGGGAACUGGAAGGAG
271904592	56032	TGTTGTATCCUCCCCAGCCUT	56033	GAGGTGAAAAUACCACTAGCATCCUA
271878907	56034	TAACCUGGCAGAGAATGGUGT	56035	GCAGATGGGAUTTGCTAATATGTCUGT
317462071	56036	ACAAUACCTUCCCACCCAACC	56037	TGTGGGUACAACACAUGCAGAA
316718171	56038	ACATTGCAGAGUGCATTACTAGUGG	56039	TCTGTCTTAAUGGAGGGATCTGTGUT
316497916	56040	CCAAAGAATUACACAGAGGAAAGAUGAG	56041	TGAATATCCAUGTTCATGTGAUGCAGA
316471883	56042	TGGAAACAGACAUGTGGTUGACA	56043	TGCATCATCGTAUAACATGGTTTCAUAACT
264627686	56044	ATCTTCCCCAGAACUTATCAGATUAGGT	56045	AGCTCATACAGGUTCAATCATGUGAT
325636718	56046	CAGCAGCTUCTCCCCAATATUCT	56047	AGCAGGTGAUGATGTTTCTGGUC
325221161	56048	GCCCCACAGGCUAUACCAAAA	56049	GGGUAGCTTATGAUGGGAGCAT
268466543	56050	GAGATTCAGUGCAGCGTTTGUT	56051	CAGCTCAGGACACUTTGCTAATTTAATUT
268612758	56052	CAGGGTUGGAAACCATTCUGACT	56053	AATAACTTGCCAUGACCTAAGCTUAACT
257485279	56054	GCAAAUGAAGAAATUCCCGAACAACC	56055	AAAGGCTTCAUGTCCACCTUGA
268040455	56056	ACCTCCCTATUGATAGAATGCCAUCT	56057	TCGTCAGTCACUATTTTGGGCATAUT
268594847	56058	AGGTCTCTTCUCATCCATTCUACGAG	56059	ACATCGACAAGUGAATCGAACTCTUAAT
268112030	56060	GTGTTTUCAGCCAGUGCACAAA	56061	CTTTTGGAUGCCGTUCACCA
267927888	56062	GCCCAAGAACCUAAAACACCCUA	56063	GGGTGTCCATAAUCTTCCTTTGTTTUT
314063781	56064	TGACTGTATCTTUGCATTGTCCTTTUCA	56065	CTGAGAGCCUCCCAAAATGTATACUAC
258669404	56066	GCCUGAUGCCCCAGAAGAAAA	56067	TTTGTTGUAGGTGCUGGGAAGT
229294037	56068	GGAGGCAUCGCAGGTAACAUC	56069	GCTAGGGTCUCCGAGGTCUAT
232300771	56070	GAGATTACTCTCUCACCCCTTCUCT	56071	CCCCAGAAUGTGACAGCTUAAGT
230091786	56072	GGGAGGGAAUCTAACCAGUACA	56073	GTCTACAGUGCCTGGUCAGAAG
230460405	56074	CCCCTACCCCUGAAGATCTUGT	56075	GCTGAGGACUACGUAGCAGAG
224469905	56076	TGAGTCAAAAGAUAGAAACCAUGCAGT	56077	ACCCTTTTCTTUTTCTTCTTGTCUGAGT
223252646	56078	TTCTGTACACAGUGATTGTGCTATTUCA	56079	GCCTCATAGTTUTGTTCAGTTTCTTUCA
224494459	56080	CAGTAGGUTTATAGAGCUGGAACAAGAAA	56081	AGTATACUAGCAAAGAACATTCCACUGA
222469789	56082	GCCTCAACTTAUCAGTAGAAGCTGUT	56083	CCCACTGGAGCUCTCTTGATTTUT
320489080	56084	TCTCAATCCTGATCAUTACATAATTATAGCAUT	56085	AACAATGUTTCGACCUGGACAGA
320968536	56086	CCCTGTAAGCCUTCTACTCCAUC	56087	TGCCAACTAUGAAGCCTGATTCAAAUA
321487983	56088	CACTTCACAAUGCAAGGTGTUACAA	56089	TTTTTCTGTTGAGUCCCAATTTGCUG
261477450	56090	ACTTGAGCTUCTCTTTACCTUGACC	56091	GCTGGAGAAACUGGAAUGAGAAAAAC
263738274	56092	GGTTACTACUGGATTGACCCUAACCA	56093	GAAGGAGAGGUGTTTGTGGGAUT
325772016	56094	CCCCCAACGUGATCAGGATUC	56095	GGGAACAUACAACTGATGAGAAUGT
324497331	56096	CACTCCUCCAAAATCAATGUAGAACCAT	56097	GGACCAAAAGCUCTGUGGAAGG
325622737	56098	CCGGCCAUACCCTTTTAACTTTTUAAG	56099	CCTGTCTTTTCTCUTTTCAGAGGATGUT
325106475	56100	CTCAGCUGGATCTGCTCUCT	56101	GGGCAACAUGGTATTTAAGUACAAAAAT
323429259	56102	CCAAGGAACAGUGTGTAGGTCUT	56103	GAATCTCTATTTCCUTGGTTGGGATAUCA
324019268	56104	TCCTAGGAACUAACAAAACATTGTGUCT	56105	AGTATAGCAUCATGGACCGUCAAAAA
265425278	56106	GTGAAAACAUAGCCCGAATAGCTUG	56107	CAATCUCTGTGCTGUACAAAACACAT
267268882	56108	GGTGCAGAUGTGACAGCAGUT	56109	TTTTGCTUAAAGAGACAGGGATGAUACAT
264254203	56110	TTGTCATCTTCUTCATTGCTGTUACCT	56111	ACAATGGAAATUCAAAGAAATCACTTGUT
267707764	56112	GCTCCCAGGCUGAGACTTCTUA	56113	CAGGUCCTAGUGACCAGAGAGAA
314217515	56114	CCCUCTCCCTCUACCAGACAA	56115	GTACCAGGAGCUCCCUCGAT
314399198	56116	TGCAAGTGUCGCTGCTCUT	56117	GGAGAGCCCGUCCAGUG
315019241	56118	GGGACTTTTGUAGGCTGCTCUA	56119	GTGCTGGACAUGTACCCUGAG
314902096	56120	GCACCCAGGACGUAGUGAA	56121	CGCUCCCGAGAAAGCUG
319250236	56122	GGTGGAGAAAUGATGGTTTAAAUGCT	56123	TGTTAATTTTCACGUGTCCTGCTTTUC
239085638	56124	GACAGTACTACCUCTCAGTTTTCTTUCAG	56125	CACATCTTTTATUCTGCACATTCAUCCA
262051564	56126	GAAGGCTATCUGTGGGTTGTATUT	56127	AATTGCUACAGCGGATAGACTUGT
265754052	56128	GAGATTTTGGAUGATACTGUGCAAAGG	56129	CAGGACUGCTCAGACATUCAAGAA
264146212	56130	TTTACAGGTAUCACGCTCATUGCT	56131	TGTAATTTCGGGACAUCAGACTUGG
264527429	56132	CCTTCAGGAUCTGCAGCCAUT	56133	CCAAAACTAGGUGGAATTTGAAATATGUT
239377772	56134	GATTACCUGTGTGGTTUGCCAAA	56135	GATGCCAGTUCTTCAATAAACAGUGAAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
232244462	56136	ACGTATTTTGGCUTTGAAATGGAACUG	56137	CGAGAGTUGAGAGAAACACATTTTUGG
261269615	56138	CTGCCTAUCAGCGCAGCUAT	56139	AGCTGAGUGGAAACCTUGAAGAAA
264011624	56140	GATGATCUGACAGTTCTCTTUGGCA	56141	TCTGTTTCGGUTTCTGAAAUGAGGAA
315753077	56142	ACCAATCACCUATTTTCAGACAUGCAA	56143	GACACTCTCUTTCATGTAACCUGAAGT
313897591	56144	TCATTTGTGATGGUGGGAAGATCUAAG	56145	ACCTTGCUCCAAGGATATCTTTTCTUT
313881258	56146	GAAAAGATCUCATATCCGACAUAGGCA	56147	AGCGCTTACCCUATTTTCCAATTGUAA
312846449	56148	GGTAAGGAAGUGAAGGGTCCUG	56149	CAATCACAGGCAUGGTTGAGAATUAG
312896956	56150	GTACATTCGUAAAGGCTACAGTGUCA	56151	TCTTTGACCGUGCCTTCTTGUT
314387682	56152	CAGATGAGACUGCCTGCAGUA	56153	GTTTTCUAGATTCAAGATUGGCAAAGCA
313466372	56154	TUCCATCTTCATUGAGAAGCACAGT	56155	CTGGCATCCUGCCTTATCTTTUAAAAAT
315758027	56156	ATGTTCCCUCATCTGCTUCCAAG	56157	CTAACCGTGAUCCCTTTCTTCTUGT
320560561	56158	CCACACATUCCCAGTCCUGAG	56159	CTTTCCTCUGCCTTGCGTTTUAAT
326728944	56160	CTTTTGTGTTTTGUCTCTCTGTCTGAUG	56161	GGACUGACCGGGUGAGAAAT
328103731	56162	CGTCCCATUGTTCCGAATCUC	56163	GGUACGCCTUCGCGGAT
316649921	56164	CTTACCTACUCCCAAAATTCUGCAGT	56165	CCAGTAAGACGGAACUTGTTGTTTUCT
316833407	56166	CAGTGGCTCUTGAAGATCGAUAGAT	56167	CCACTTAACATGUATGGCAGAAGCAUA
320452334	56168	ACTGTTGCAAUGAAGAATAAGAAAAUGCT	56169	GCCCCGAUCATGTTTGGCATUA
295806128	56170	GGATTCGCAGUCGTGAACCAUA	56171	CTCTTTTGUGACCGCTCTCCUT
327879215	56172	GGCATTATATUGCAGTGTGTGACUCA	56173	GCAAGTTTTATCAUTCCTTCCACAGUAAC
278439149	56174	ACTGTCTCAGAGUATTCTGCCCUAA	56175	TCTGACAUGTGGCAACUGGAAG
279446848	56176	ATGCTTGGUACTTGGCTGAAUGA	56177	AGTGGCTTGTTGUGATAATTAAGGCTUA
264195864	56178	CACACUTTGTCTGGAUCAAGGACAT	56179	GCACACAGUGATCACACAGUGA
257557991	56180	AGCAGUATCAUGAGCCCAGAGA	56181	CAAGACCCAGAUCCTTGAGUGG
265682779	56182	CTCACCACCUGCTGTTCTCUT	56183	CAGCCTCCAUGGACATCTCUG
258800042	56184	AGAAGUGCGGCCAGCUT	56185	CCAGCCCAGCCCUTCUT
260554039	56186	GGCTCAGGCCUCCCTUCT	56187	CATAGGCAGACUGTGCUGGAA
318744058	56188	AUGCCTTCTACTUACAGGAGGGT	56189	CCTAACCTGGTUTCAACTGAAGTACUAA
319349113	56190	ATCTTTAAAGUAGGCTUGCCACAT	56191	AGCTGGGACUACCATCCTUCA
255279173	56192	GAGTTCAACAGCUCCGAGUACAG	56193	GGTGCCGCAAUGTTTGTTTCUA
264781125	56194	AAGGAAGUCACCCCTUGCAAA	56195	CGGTTGUCATTCACAUCCAGGAC
265706452	56196	CAGCTTCCUCTCCACTGUGAAT	56197	TCAGGAGCCCAUTGCUGAC
263064377	56198	GCAGCCCCACUCAGTTCUAT	56199	TCGTAGUCCAGGTAATUCACGGT
263174198	56200	CTCCAUCGACAACCUCAACCAA	56201	GCCATCUCAAGGACATTTTAUGACAAAG
261560933	56202	GGGCTAGAGAUGACCCACAUA	56203	AGGTGUCCAGCTGCGATUG
326455887	56204	GTAGGAAGAGUTTGAGCUGAAGAAGA	56205	TGAAGCAUCCAACAGAGATTUGGT
313135100	56206	CCAGAACAAGAUCAAGTCUGCCA	56207	TGTCCTTATCTUCCTGCACAGTTUT
313892711	56208	CCATGUAACCGCCACCTGUT	56209	CCTGGGAAUACATGCTGAUGGG
263781039	56210	CATAGTGGUGCCCCCTGAUAG	56211	CTGGGTTTUACTCTCCACTUAAGGA
333230022	56212	CACCCACUCGCCCAUGAT	56213	GCGGGUCGTTCCACGUA
332444179	56214	AGACCCACCAGCCUGTGUA	56215	CCATAACCAGUCTGCUGACGA
315496163	56216	GTCTGCCUCATCTUCAGCGT	56217	CUGTAUCAGGGCAGGACCAAT
327794668	56218	GCTTCCCACUGTGGTTCTTUG	56219	CTTCCCTTAUCTGGCCATGUGA
314460224	56220	CACCTTCCCUCGGATCTGUT	56221	GGCTGATGUGGGTCCAUCC
313281001	56222	CTCGUCAACCCCCUCAAGAA	56223	GGTCCCCAUATATAGUGGGAAGGA
323406402	56224	GTCTTGCAGUAGGAGATGGTCUT	56225	GCTGTGGUCCAGAUCGACAC
323538800	56226	GGUGATCCTGGUACCCCAGAA	56227	GAGTAACCCUAAGCUGCCAGAG
265754114	56228	AGGGCCUCTGATCCCUACAAA	56229	GAUGATGTAGUAGCAGAGCAGGAAG
268108133	56230	CCTCACCUGCAGCGTGUAAA	56231	GTGATTUCCCCGAGGUCCAT
261787430	56232	ATTCCTTTGGGUCCATACAATUCCA	56233	GGGATAATGUAAGCAAGGTTCTCTTUCT
328478416	56234	AGGGACCUATGGCCAAAUGAAAAA	56235	CCTGTCAGCUTCTGGATTTCTUGT
328149343	56236	TTCAACATCTTTCCAUGTCTCCAGATUT	56237	TGGCTTCUGGATAAACTTCTUGAAGAG
329548401	56238	AGCTATCCAGGAUATGCCACCUT	56239	GUAACAGUAGCAGCCAAGGACA
329186382	56240	CAGGCAUCUAACAAAGGAGAGGAAA	56241	GAATGGCCCAUTTTGAATAAGGAUCAG
224367400	56242	ACAGACTGCTTUCCAAAGATTCTTGUA	56243	GCCATACCTGTUTTCCCAATAAGTTTUC
223462800	56244	CTCTTGCTTACAUGAACTCTATGUCGT	56245	TGTGAGTTGUCCATTTCCTTTUCCAT
328878062	56246	CACCCGGCCUAAAGTTGTAGUT	56247	GCTAAGCGAAAUTCTGCTTTAAAUGACT
332790867	56248	CAGTUCACACACACACAAACCUT	56249	GATCUCAGGCCCGATGUCAT
318057940	56250	CCCTGAGCCUCCCTGUG	56251	AGAACAGGGUCCCCATUCCT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258995683	56252	GATGGGTGUCTCCACAGUGA	56253	AGACCTGAACUGGGCTUGG
319244094	56254	CGGCCAGCAGCCCUATTTUAA	56255	GATGGTAAUGACCTTAGGTGTUGCT
315020152	56256	CUGCCACCCAGAAAACCUCAT	56257	GAGGGAGAACUAGGCTTCTCUGA
260217273	56258	GTTATGCCUCCCTCTTAUGGCAAT	56259	GGAGAGGCACUACAACATGCUC
260628640	56260	GGAGGAAGAAAGUGGCACTCAUC	56261	GCAGTGCTATTACCUTCATCTTGGAATUA
264509396	56262	GCTCCTTGUGATCCCCTGTUC	56263	TGAGCTAUCCAAGCCCGTUC
267169440	56264	GAAGGGCCCGGCUAGAAAUA	56265	CCTTCATTCAAGUATAGTCATCCACAUCA
263436532	56266	GGAGGACCAGGUGGACCUAAG	56267	CACCATGGAAAAAUGTTTAAGCCATUCA
268784639	56268	GGGAGCACATUAGTGATGAGAAAAUACT	56269	AGGGTCCUCCTGGAGCUG
287545346	56270	CTTTTCTCCAGACUGGCCTUCT	56271	GATGCAAAAGUGTTCAATGTTTTUGAAA
257578871	56272	AAAAGCTCTATCTUCCCTAGTGTGGUA	56273	AGUACAGTGCCAUGAGAGACCA
333330228	56274	AGACAGCAUGCCCTTTGGUT	56275	GAAGGACCGAGUGGTAAGTCUT
317378287	56276	TTCTGTCAGTCTUTGGTGAAACTAGUAAG	56277	CACCATGCUCTTTGCCUCAGA
317987313	56278	CGAAAAGTTTCAAUGGCTCTATGUCAT	56279	TGATACCCTTAUTCCCTGTGGAUGT
325665109	56280	GGTCCAGCAAUTTGAGUCAGGT	56281	GAAAGTCGUGGGTAGATGUGAGAAG
324879397	56282	CTCCTTCCUCTTCCCACTTUCAG	56283	CCAAAAGTCTUCCAGAGCCTTUG
321519402	56284	GCATAAGAUCCAGCACCATCUCAA	56285	CATTGTTCACUTAATTCTTTUCCACCCA
314749361	56286	GACTCCCAGCUAAAACTGCCUT	56287	GACGUCAAAAACCCUCCAGACA
319860590	56288	ATTACTUGGAACCAGCCCUGAC	56289	GAAGTCUGGGAAACACATCATCUCT
315604631	56290	CACTGATATAAAGUTGCGAGCCATTTUC	56291	GCCAAAAUAAACTTCCAUGGCCAA
326922495	56292	CCGGCCAAUATTGTCTCTUGACT	56293	GGTGGGCTUTGCCTCTTCUC
327376580	56294	TGATGTUGACCACTGCTUGGG	56295	CTTGCTTTTGACAGUCTTGTTGATTUCT
326610820	56296	GGGTCTGTAUGAATGTCCAGUCA	56297	GGCCTGGTGUTTTAAAGATTCTUCC
328293814	56298	ACATTGTACUCCACAGGAATTUCGG	56299	ACAAACATTTGTUGCCCATTCTGUT
327544264	56300	TGGATAAGUGGGACCUGACCAT	56301	GCAGGTUGGGAAAGGTCTCAUC
327664856	56302	CAGAAAAGUAUGGCAACACCAACA	56303	GCAAACAATAUAGTGATGGAAAAUGGCA
328370853	56304	AAACTGTTGAGGUAAGAAGCAAUCAGA	56305	TCAGTTGGTUGTGTGACCAGUG
333259206	56306	CCCGGCGUGCAGUACAA	56307	TCCACAAAGCGCCCUCUC
332626306	56308	TCCCTUAGAGGGCACTUCACT	56309	AGCTTGTCGAUGTTGTTCTTATAGTUGA
324871355	56310	ACATTCTTTCCUACTAACGTTCCTTUGAG	56311	TGACCACAGGGAGAUGAAATCAAAUG
324933245	56312	GAAGGCCUGCTCCAAAUGAAAC	56313	GGAAUGCAAAGAAAUAAACACACACACA
324995463	56314	GGGTACAGGAUATGGACTTGAAAUG	56315	CCCCCAAUGCCGTCAUACT
323702684	56316	AGATGTTGCUCTGAGCTTUACCC	56317	AATAGCATCUCAGGAATCAAAGACGUT
325685142	56318	CATCTAATGAGTTTUCAGCCAAGGGAUA	56319	CTCTCCTUCAACTGGGTUCCAC
323632150	56320	CCAAACACAAAUGGCCTTCTACUC	56321	ACAGCCCTTAGAAAGUCTATACACAGUA
325044245	56322	GAACAUTAGCTTTGTUCCAACAGACA	56323	AGCGTCAAGCAUGATGTATCUAAGAAAT
324934052	56324	CCTTACAATTCTCUGGGATTCACATUCT	56325	GTTTTCAGCCAUCATTTCUGCCA
324270182	56326	TCACTTGGAAGACCUTAAAACAUAAGCA	56327	CTTCATATCUCAAAGCACUGCACA
325017782	56328	CTTTAAGGAGTAGCUGAGAAACCACUT	56329	CTACAAACAGUAGGCGTGATCTAUCAAT
324211142	56330	TGGGAAAGAUGTTATTGAUGAACAAGGA	56331	GCTACAGAUAGCAGCCATGTTTAAAUG
325026183	56332	AAGCCTGUTGATTCAGUGACCT	56333	GCAGTAGTAGAUACGTTCATCGUGAAAT
323782787	56334	CGTTTACTTUCTGAAGCAGTUAACACA	56335	GAAACGTGCUGCAACAGUAGAAC
332416109	56336	CCCAAUGGCGCCCTCTUAC	56337	CGAACCCAUTAGGAACATUGAAACAAAT
318948137	56338	CCACACACCGAACUGTUGAGA	56339	GGCGCCUAGCTTATUCCACAG
332527268	56340	CCCATTGTGCCUTCATAGTTCTCUG	56341	CCGGTGATUAACCACAACTTCTTACTUT
332895758	56342	GTTGATGATGTTATUGCCTAGTCAGCUA	56343	ATGAAGTTTATTTTUGCCCCTCTCUCT
332559581	56344	TCTTCTAAACUCTTACCCAGUCAGCA	56345	CGTCCATCTTUCCTCCATTTTACUGAT
333515883	56346	CTGTCCATTCUGCTGAGACUGT	56347	GTTGGTGGTGGUTTTATTGTTAACTCUT
321586104	56348	CGACCTTCAUAAGTGGCAGTUGT	56349	GGGCAAACTUCTCGTCATCUG
278213286	56350	CCTGGGATUCAGAAATGTGGATUAAAAG	56351	CAGTCACCAGCUAATGCCCUA
314443268	56352	AGATTTTACAAAGGGAAUGGACTGUGAA	56353	GCATCTCGGUAAAATTCTCCTACACUAA
279428723	56354	ACGCAAAGCCUGCATGAGUAA	56355	TGACATTTCUAGGCAGTTGAGAAUCAAT
312663140	56356	AGGATTGGTUAGAAAGGGAGGGAUT	56357	AGGTCAGCCAAAAUCAAGUCAGG
315285684	56358	GGAGAAGAAGUGGCTGTGAAGATTTTUA	56359	CACAAAACUTTCTACUCCACAACGAAA
280299321	56360	CATCAATCTUCCACATGAAGUGCAAAAT	56361	ACATTCCTTCAUACACACGAGCTATTUC
268242894	56362	GCTGAGGGAGGUAGAAGCCUT	56363	GGCCACTGUCAGTTCTCATCUC
268099147	56364	AGGGAGGUAGGUAGCACCAC	56365	AGTGTCTATGTTCUGAGAATGGTGTUC
268486366	56366	ACATTTTGCTTUTTGCTCACAAUCAGAT	56367	GACACTGACCUTGTGCATCATTUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
265230440	56368	CCGGCTUCCACACATCCTUA	56369	TCTGTCAAGTUGACTGCAACCUC
316853563	56370	GGCAGUGCAGGGUCGAG	56371	CTGTUCAAGCTCCUGCAGAGA
318663839	56372	CTAUGGCGATGGUAGGGAAAGA	56373	ACTCAAGCCUGTGGTTTUGGT
313605379	56374	GTCTGTCACTGUGAAAAGAGGGAUT	56375	GCAGTTCCCUCTGCTCCTUG
265814411	56376	GAGAUGCAGCTGGAAUAGGCAT	56377	CCTGAAGCCTCUTTTAGGAAGTAACAUT
316720103	56378	AGGTCAGAAUCTTTGTGTUGGGAAA	56379	GTGTTCATGAUTGCAGTGTCUGG
241627309	56380	CCTTTAGCAAACUTCTGAAUGACAACAT	56381	CCTTAACCUCACACTATCCCTCUCC
263342572	56382	TGCCACTGUCAATTGTGCCUAA	56383	TCUGGAGAGGAAGATUAAGAGGACAAG
315351995	56384	GCTCUGGCAGCTCTGAUACAG	56385	CCCCCTCACACCUCTTATTCTTUT
314913992	56386	ACTCCTCTCUGCTCCACUCAA	56387	GGTGACTCUGGACACTUCCCT
312832603	56388	TTCTTGCCACGGUCACCTAUG	56389	ATGAACCATGUCAGGCAAAUCCT
313869275	56390	CGGGACAAAAUCTTGGCTTUGA	56391	GTAACATAGCCCUCCTGTCTCUGA
312667567	56392	GCCTCGGUTCCCTTCACUAAA	56393	CAAGAGCCUCCAGAGCTUGT
314730711	56394	GCTTCTUGGCAGTGAGCUCAG	56395	TCTACCTGCAAGAAUGAGGACCTUA
314878018	56396	GCCAATGAUGTTGTAGUCCACGAT	56397	CAGTGATGCUCTCTCCTGCTUC
262768384	56398	GCACCTTAAAGUCCTCATATCAAUCCT	56399	CACCAAATGAUCCAACAGAAATAATUCCA
261169242	56400	TTTATTCTGTGGCAUGGAGGACUG	56401	CCACGAAUGCTCTAGAAAUGAGAGT
255859547	56402	GCAGGCTCCUGATTATTAACGTATTCUAA	56403	CATCTTCTUCACCCCTCGGAAUAG
323655327	56404	TCCATTCACUGGAAAGGUCCAC	56405	GGCATTCCTGUGACAAACAAATTAUCA
328048248	56406	TGGTCCUGAGAAGAACTCCAGUT	56407	GAGTGAAUGGCAATTGTTTGTUAGAAAAG
319094271	56408	CCACAGAAAUAAAAAGAGAAACGGCAUT	56409	GTGACCAGGGAAGUAATGAGUCT
258897396	56410	CTTACCTGGTCAUTTCCTTTTTGTTUCA	56411	AGGATCTGACCUGAGGCACUT
266800430	56412	GAACATCACAGCAUCCAAGAGGUA	56413	TCTGTGGTGUTCCCACCTTUC
262245463	56414	TTCAGACTGTAAUCCTCCCTTCCUT	56415	CGCAUAGGAAGCCCCTGUA
315886560	56416	CCCTGGGCUCAGATCTGCUAT	56417	TCUAAGGGCATTUGCCAGAACA
316940677	56418	GCATACTUACCCAAGCACAUGGT	56419	TCGTAATGAAUGTCAAGAAAUCCCCAA
316220194	56420	TCAAGTAGCTCAUCAGTTAGCTCTTTUC	56421	GTGCTGTCCUGTCACTCAUGAAT
316703497	56422	GCCACAAGAAAGCUCTCTTUGGA	56423	CATGGCAUCTGAAGACAUGAAGACT
316742277	56424	GCCATCAAAGCUTCATGGAAUCCT	56425	GAGACTCATTUGCTGCCACTUG
320525579	56426	GGAGUCAGGCCAGACTAGUG	56427	CTGTTCUGCAAACAAGGGAATCATUT
320430844	56428	GAAGGAGTCUCCAGGCAGAUG	56429	CCCACCGTGUTTCTAGGATTCUG
318473728	56430	GGCGTGGAGUGAACTCTTTCUC	56431	GCCTTCAUGCAGGCAAACUC
316083160	56432	CCTGAGCAAUGTGAGCCCAUA	56433	CCTATGAGTTCAUGAGCACATTCTTCUT
317907040	56434	TGGTTAGGAUGAGAGACCCTGTUC	56435	GGGTTCACAGUGTGCACTTUAAC
333258054	56436	CTCCTAAUCACAGTTAAACCUGAAGGAA	56437	GACATCCUCAGGTTCTTUGCCA
332609114	56438	GCCTTUCCCCCAAGAGGTTUG	56439	TCCATCCCCGUGGACUACAT
333719943	56440	CGCAAGGCAGGAAAGUTAACUC	56441	GTCAACAAATTCUCCCTAAGGATGTUC
319442294	56442	CCTCTGTGGGAAUCCAGGGTUA	56443	CCGTGCUCTGGAAAUCAACAAAAT
319158871	56444	CCAGCGCCACCUGATUACAG	56445	CTGAGAGCUGGTGGTGGTAAUG
239567295	56446	AGCTCTGUGCCCTGTGUG	56447	CACCTCAUAGAACTGCCTGTUGA
241965729	56448	CAGAACCAUGAGCCTGTGTGUA	56449	CTGGUGGACGCUAGCCAT
238413407	56450	GGCCTCAGCUGCTTCTCTUG	56451	CAACGUGGGACGGAUGGT
264924469	56452	GATGGCCAGGCUCTGTGUT	56453	ACACAGCUCCAGCGGAUG
262175904	56454	GGCAACGACUTTGTGUCCAT	56455	CTCCTCGUGACCGAAGCUC
318275733	56456	AAAGGCUGCAGAGCATUGAAC	56457	TTTGCACUCTTCCUGGCCAA
319532704	56458	GGUCCGCACAAACCTTTGUT	56459	CTTGCCUCCCAGGUACCAC
235711009	56460	CACCTGCUGTGTGGCTTUG	56461	GCAATACCCCUGAGGCAUGA
236507399	56462	CATGCCCCAAGCUCCTAGUG	56463	GGCAGCACACAUCTCTATUCCT
235593926	56464	GCUGCCCCTGUGACACC	56465	GAGAAGAACCUGCUACAGGAACA
239338678	56466	CTCUGCACGCAAACACTCUG	56467	AGGTTGCTTTCUCCAATAACTAGATGUG
265068064	56468	GCCTTCTTUCCCAGCCCTUG	56469	CAGAGGGACUTGTCACTTCTTUGT
317034022	56470	AATGTAAACAAAATUCATGGCATGGAUCA	56471	GCTTATTCTGTTUACTGGAGGGTTUAGT
326917212	56472	CATCGCCUACTCCATGGUGAAG	56473	ACCCUTGTGTGGUAGACCCA
318192843	56474	TCCCGAGGUTCATACCGTGUA	56475	TGTTTCTCATCTUGGACTTGATCTUGT
318133270	56476	AGGGTAGAUACTCATGTTGUCGGT	56477	TTTGGGATTTAAGUGGTTCTGGTUCT
321598982	56478	GCCCCAACAGCAGUTAAGUCAA	56479	CCTCAGAUGCCAAATGACTTTCUC
269246862	56480	CCTACAUCAAGCTCGCAGUCA	56481	GCTTTCCGUCCTGTTTCCUCAC
263327971	56482	CCAGAAGUGGGATTTTTGGCTUAA	56483	GCCAATGACCCUTCCTTCTUGAC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256165460	56484	CTCCCTTTCCUCTCCTTGAGACUA	56485	CAGGAAGCAGGAGAUGAAAATAAATCUG
261728171	56486	GGGATGUGATGAGAGGUGGAT	56487	TGTGTAACAGUTCCTGCAUGGG
261742834	56488	TCAGTCCCAUGGAATTTTCGCUT	56489	CTGGATCCCCACUTTTCCTCTUG
268392165	56490	CTCAGTTTAAAGUGCAAATCGACUCC	56491	GCTGGAAGAAAGUGAAAACAACUGT
268867629	56492	TGGAGGGCAGAUTGUAGGGAAT	56493	CTTCACAGTAAUGGCCACCTTTUT
265108451	56494	GGATGGAGAAUGGCTTCAACATGUA	56495	CACAAGGCUCCCACCAACUT
266665926	56496	CCGTCUGGACTGACCUCAAT	56497	AGGCUAGCAGAGACTTTCUCCT
269289570	56498	GCAAATGGUGGCTGACTGAGUT	56499	GCAGATCCTUGAGGGCAACUG
269283491	56500	GGATCTTATAAGGCUCTATCTGCAUGAA	56501	GGCCTTTCUCCATTAAACAGCUAGAT
267114788	56502	CTGCTCCCACUCAAGCCTTUA	56503	GCGCAGUGTGATCUGGAAGAC
268036451	56504	GCTGCCTAUCTGTGCTCCAUT	56505	CCATGAATCAUCTCGGGTCTCUG
265639084	56506	GCTAACAGAGCUAAGCAGAUGCC	56507	GTGATCTTAAUGGAGTTCUCCAGGAT
259195417	56508	GGUCAAGGCACTTCUGGAAGAA	56509	CCCTCCAUGCCTUACAAGACC
264803239	56510	CCCTGCAAUGTGACAUGACGA	56511	AGAAAGCUGCCCTTTGGTUCAT
320074088	56512	TCTGCTTTCTGUTTTCCCTTCCUC	56513	GTGGCATCUCAACTCGGATUACT
258513162	56514	AATCCAAGUAAGCCATTCUCAAGAGG	56515	AACCAATGCTCUCACCTTAAAGUGT
236073609	56516	GTGCATAACCUCTTGCCCAACTAUAA	56517	CAAAATCAGAUGCCATGTGCTTUGA
237111695	56518	GCACAGAATUTGACACACTUGCAG	56519	CTTTTCTTCCCCGCUTACTCTAAUCA
242447158	56520	AACTTCATTTGTGUTTTCTCCTAGGUCA	56521	GTGTTGTUGGCAGGGATACAUAAAC
237656672	56522	TGTCATGATTCAUCTTACTAGCCUCAAAC	56523	GAGTAATCUAGGAACCUCAAGGCAAA
332679607	56524	CAGGCCAUCAAGTGTGACTUCT	56525	CCCTTTCUGGCTCTGGAAGUG
226082590	56526	AGCGCAAGGCGCGAUAUA	56527	CCACAAAGAGUCTACATGTCUAGGGT
257443689	56528	AGTGAGCAUGAAGGACAATGUCA	56529	GGAAGCCUGGAACTUGGAGAG
328200390	56530	GCGAGCCCGAUCUGAAGAA	56531	GTTCAUGGGCCGCTUGAC
267991337	56532	CCAGGCCGAGCUGAACAUC	56533	GGCUTTCAGGUGGACAAGGAC
258377128	56534	GGCAATCUGAAAGGACCTCCAUT	56535	CAGACACCUGCCTGGCTAUG
268167968	56536	CAUGCCCGCTAAUCCCAGAAT	56537	GGAAGTUCTTCGGGUAGAAGGG
318902301	56538	CAATCCUGACCCCAGTGCTUT	56539	CTGAACACUGCCTGCTATCCUC
257473907	56540	CATGGCAGAGAGAGUGGAGUC	56541	GCAGUGAACAGGCGAGAUACAA
262663311	56542	TCATCAATTCAGAUGACACATCTTUCCA	56543	GGAAGTTGAUGAGCCCTUGCT
316869479	56544	CCAACAGCCGCUTCGATUG	56545	CGTGUAGCCCATTUCAGAGGAG
317490574	56546	CACCCTCACCUTGACAGGTUT	56547	CTGGAGGCCUCTGCTTTCUAAC
330921969	56548	AAACAAGCTTUTGCCCATGUACC	56549	AACTGCACCATTUTGAGTGTGTTAAAUT
330741971	56550	GCTCTTTTUGCCCTGGAUGAC	56551	GATGAGGUCACAGCACCATGUA
262993052	56552	GTATATGGTATAGUTTTGGGCCGUGT	56553	CATGCCTTGCUCTTGAAATTTCUCA
269326883	56554	CCATCACUGGCACAGTCCTTAUC	56555	GGUGGTTTGTCAAUGACGGAGAA
314144083	56556	TTTTATTGCAGGUAATTCCAGUGGAGAA	56557	TCGTGCCTCUACAGGATCAUACT
268951758	56558	GGCUGUGCCGACAGGAAG	56559	CCTCCTCGAUCTCCTTGTUGA
267410308	56560	GUGGAGACCATUCGCAACCT	56561	CCCAGCTACCUCCTTCTCATTTTUA
263327687	56562	TGTAGCUCACACCCTCTCCUT	56563	GCTGGGAAGAGGUCACTGTUG
259628303	56564	ACCCAGAAGCAUGAAACACUGT	56565	AGGCACGAACAUTACTTCAATCAATTUC
255857305	56566	GCGATTTTCCAUTCAGGTTCTTCUG	56567	CGTCATTCCTGAUCCTTCATGAGTAUAT
321058046	56568	CTACCTTAGGUACTGGTCTGACUGT	56569	GAGGCAAAGTUTGCAAGTCTTCUC
323775548	56570	GCCCAGAUGAGGACCTACAAAUT	56571	CCCATTAGUGCCCCCAUCAC
323885984	56572	GAGGAGCTGUTCAGGATGGUG	56573	CAGCAGUCAGGAAGGACATGUT
325698417	56574	AGAACGGUGAAGCUGAAGAGG	56575	TGTTAGTTUGGCGGGTGTATCUG
326287558	56576	CGAGGACACCAUCTUCGAGAT	56577	GTAGCUGAGGCCUCGCA
269372021	56578	CAGAGCTAUGGCGCCUACAG	56579	CGGGAUCTAAACUGCAGGGAAG
318633785	56580	CTGTCGGGCUTCTCGTCUA	56581	AGCTCCUGAGTGCUACCGT
326832868	56582	GCATCCTCTUTCCTGGCCTUA	56583	CAGATTGCAGAUCTGACUCAGAAGAT
327507705	56584	GACUCGCAAACCCACTUCCT	56585	CCCTCACUGACCCUCCAAAC
266863680	56586	CACCAGUGAGGTAGCUGGAC	56587	GGCTGUCCCAACTTCCTGUAT
326051928	56588	GACACAAGAUCTGCUCGAGGAC	56589	TGUGGTGTACCUAAAGACAGAGACA
326071530	56590	GCAATTTTTCTTAUGTTCCAGGAACUCA	56591	GGGCAGAGUCCTTAGCTTTTUCT
266887142	56592	GATGGGTAGUGAAGCAATGGTTUT	56593	TTCTCCATGTUCACCCTTAAAAGATUGA
262036395	56594	CTCCACGGUGGTTTTCGTTUC	56595	TGTTACUCACCAAAGAGATGGTTTUGT
255264810	56596	CCACCAGACAUCCGAGTCAUC	56597	CCACTCACTGTUTTCTCCTTACACUT
313879348	56598	CATGAUGCCCAGGGUGAAGAA	56599	GUGGAACCTTAAUGCCCAGGAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
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316207845	56602	GGUCCGGCTCCUGGAGA	56603	CCAAGCTCAUCATTTCCAACTUGAAA
317284048	56604	CTCCTGCCAUCGTCAACUCA	56605	AGTGGGCCAACUGGAUCAAAG
257944127	56606	CGGCCATUCCTGTGAGGUAG	56607	CUCTCTCUAGGGAAGGCCACAT
324618966	56608	AGCAAAACATTGAUGAACAAATGCUT	56609	AAGACAAGGCUATGATGCTGCUT
266379337	56610	GAGAAGTUGCCTTCCTUCCGA	56611	GTCAGGCAGGAGUCTCAGATUG
267055355	56612	CCCCAAAAUCUAACGCAGCAC	56613	GGCAUGATGGAGUGACAGGAAAAA
326132984	56614	AGCAATGCUCCCTTCGGTTUA	56615	CGAGCATAAGAUTAAGCAGCTGUC
316036682	56616	GGGCUTTAGUGACAGGGAAGT	56617	AGTGAAUGGAGCCACCCAAUC
289361657	56618	AGCCCTTCUTATCGCTGGUG	56619	AGTAACCCCTUAGGTGCATCCUT
303260558	56620	GAGGCGGCCCAUTTTCTTUAG	56621	GCACCTCCUTCCTCTGCTUAG
327807418	56622	TGTAGGTUCCTTTTCAGUGGACACA	56623	GAAAAATGGAGUACCAAGGTTTGUCA
304806866	56624	GACTAACAAATUCTGCCCCCUCT	56625	CATAGCACTUCCTGCCTGGTAUC
327517050	56626	GTTTAGUAGAGGAAACAGACGUGCT	56627	TGCATTGACUGGAGTGUGGAAA
300534542	56628	TCTATGGTGAUCACACCTUAGGGAAA	56629	CUCACAGTATTUGGCACAGAGACA
266846867	56630	TGAGGAAAGATUATTTGCATGGCUGAA	56631	CATACCCUCAACAGAAATGGUAACAGAA
265912573	56632	TGGTACTACUGAGAGATGCTTTTCUAGAC	56633	AGCAGGAGCUGTTATAATGATTUACCAT
259703450	56634	ACTTCCACATGUTGAATAGTTTTGUCCT	56635	CACTGCCCACUTTGATTAAAACTTCUT
264816293	56636	GTGGTTAAAATUAAACAACTCCGATCTTUCT	56637	GCAGCTGCAUGTTCAAGAAGUG
262464258	56638	CTGCUGCAGAACAGTGUACCT	56639	CAACAGCAUGACCTCTCTCTCUG
268454099	56640	TGTGTTAGGAUCTCTTGGTTUCCCT	56641	AGGAAGAGUCAAGGAAUCAAACAAAGT
268092023	56642	CCCAGTTGTATUCAGTACCAACCUA	56643	GGATTTCCUGCCACACCTUGT
267612587	56644	TTATTACCTAUGAAAGGCTGGCAAGUT	56645	TGCAGAACAUGAAAGGCAUGGT
319201703	56646	AGTTCCTCTUACTTTCATCTUCCACCT	56647	AACAAACGCCCCGUGTUG
316684228	56648	ATGAGAAATTGUGTGAGGTTGTUGAAAC	56649	CTCAATGCCAUGCTCTACCAATTUT
228922945	56650	AAAAAGATCACCUCTCCACGAGTUC	56651	GCCTCTTAUGCACAGATGTTTTGTTUT
261410348	56652	GGCTGUCCCCATCATCACUG	56653	CGAGCUCAACCTCUGAAAGCAT
315349364	56654	CCTCACATUGGGTCACCATUGT	56655	CTCAACGCAGCUCAAUGCC
313763388	56656	CTGAGTCTUAGCTGGCTCCUT	56657	CATCACCACCACUCAGAGUCC
269176627	56658	GGAAGUTTGGACUGAGGGACA	56659	CGUTCCCUGAGGCAAAAGAG
261246496	56660	CTCCATAUGCACATCCUGAGCAA	56661	CTTGATCTTGGCUACTATACCATGGUC
315874264	56662	CUACCCATGGTUGAGGGAAGAA	56663	TTTCCATGTATTUGTGCTAATCTCUCCA
317717157	56664	CCAAGGTTAGAAUGGCTAAAGAAAGGUT	56665	GAGTCAUAGCATCCCUCAAGCA
317692070	56666	GAGAGTTCTTUCCATGAGTCCTTUGT	56667	CACCTTTGATTCAUGACAGAATGCUT
316102166	56668	CTGUCCAAGGTCCAUCAAGAGT	56669	ACTTCATAGCCAUAGGTGTCTTATUCCT
327850624	56670	TTTCCCTCCCAACCAUCAATATTCTUC	56671	AGCTCTAGGTTTUCTGTCATCTATGUACT
327099904	56672	GTGTGCGCCGUCCTTUT	56673	CAGCAGCUGCCCUACGA
237760205	56674	GGGTATGUGGATTCCAUACAGAGGAA	56675	GGCCTGGAAUCTCCTCTATCACUA
240406328	56676	CATAGATGAATUGGGAAGAGGAACTUCT	56677	GTATCTGATUGGCCAAGGCAGUAA
265605809	56678	CGAAGGCGACAGCUCTCTUG	56679	ACCTCGGAAAGUCAGGCTUG
267488507	56680	CCATCCACAGCCUGTTCATGUAA	56681	CCCCUCUAGCCAAAACCCAAG
265329296	56682	GCTCCUCTTAGTGGUGGCAT	56683	CTGGCTUCACCTTCCCTCUAC
326959844	56684	TGTACCAAGCACCUAGCCAAUG	56685	TGTTGGGCACAGCAUAATAGUGT
327015684	56686	CCTACCTUGGCATTCUGGACA	56687	GCATTCTTGGUTCGCTGTCUCT
325773827	56688	TTTGGCAUAGACTTCCUCAAAAGAG	56689	CCACCACCUCTCCACCTTCAUA
324942385	56690	AAGAATTCAGCAUATACTTCCTUGAGCAT	56691	CTTTTCACUGGAGAATGTGTGCUAAA
326312239	56692	ACAACTCATAATTTCUACATACCCATTGUT	56693	TTCGGACACUGAGAGCTTUAAGAC
326373021	56694	CTGTGCAUTTTCCCGTUCACC	56695	GAAGCAGCAGAACAAGUCTTTTUAGT
324339837	56696	CTTTTCCTTCUCTTTCAGCCTTUAGACT	56697	CCAGGCCTGAAUTTGTAGATAAATGUCT
324310621	56698	ATTCCCCATCUTCATAAATGCAGUAACT	56699	TGTCGTCTCTTTUGTTCCTTGATTCUAA
325026777	56700	GCCAACAGAAACUGACCACUGA	56701	CATTGCUGAAAGAAAAUCAAAGGAACC
229746604	56702	CACGAGUTGTUGAGGAAGCC	56703	ACATGTUCGAGAAGGGCAACUAC
229731695	56704	GCCCAGAGGGUGUGAGGT	56705	GCCTGCAGUTCGCTUGT
229755698	56706	GGACAGCGUGAGCCTCUT	56707	CUGCUGGCCCCAGAGAC
314727212	56708	CTUAAAGGCGCTGUCACCCT	56709	TCGATGAUGGCATTGCAGAUGAT
313038759	56710	GCCTTGUCGGACCUGCT	56711	GCGCAGUGCGTAGAAGAUG
317402445	56712	AATGCCCUTACCTGTTUGGCT	56713	TTTCTTTCTTTUCAGCCTATCACAUGGA
326659382	56714	ATCCATGAGCUCCAAAAAGAACTGUA	56715	GCCAACUACGGCAGAUGAAAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316823660	56716	TGAGACAAACAUTGTAAAGGAUCCACAA	56717	GUTGATCTUGGCGGGACGA
295994388	56718	ACACAGTTCCAUGCGTACGUT	56719	CTATAACGGCUCAGGCAUGGAT
278835241	56720	AGGACAACUACACACTTCGGTTUT	56721	GATGACCATTCCAUACACACCTGUT
279460240	56722	AAGTCATAACATGCUTTCCTAACACCUT	56723	GTCTGTTTACACUCCCTTCTCCTTTUT
278208296	56724	GATTCCCCACUGTTCCAGUCAA	56725	GCTGGCATUACCTCGCCTAUG
317196780	56726	CUGGGCAAACAACACUCACAG	56727	CTGATTCUAGAGGCAGGCTTUCA
262406586	56728	CGGCTGCTGUGCTTTATAAGCUAT	56729	GCTTTTACUGCACAACCAGTTACUC
262563269	56730	AGAAAAGCCAAAUGCCUAGAAGGT	56731	AGCACCTCTTTUGCCTTCTTTACUAAAA
268069946	56732	GGGAAGGUGCGGATGACTUG	56733	GCACCCTCUCACCCCTTCAUA
262601645	56734	GGCCTCAUCTGTCAGCTUCAG	56735	GGAATTCGGCUCCGGACUAAG
267736792	56736	CTCAAAUGCCCCTTCCTGUCT	56737	GGGATCUAAAATGCCTCUCGACA
332434464	56738	GCTUGCCCAGAGCATGGAUAG	56739	ACCUCUCCCCACAAACGAAAG
333244907	56740	GGATTTGACCUTCTGTGCACUGAT	56741	GTTTTATGCAAACACUTGACATCTGUCT
263710523	56742	GGCTCCCAAUTAGCCCAGAUG	56743	CCCACTAGCUTCTCAAGGGUAAGA
254186843	56744	CTCCCATGAUCGCCCACUC	56745	GACGCTUTCCAGACUGACACA
319173951	56746	CATTACTAATCTGGUTCTGGAAGTTACUGAA	56747	TGGACCAAAUGGACAGATAGAGTAUGT
261848789	56748	CUGGACUACGAGACCACACAG	56749	CTCATTTCTATCAUGACTGTCACCACUA
256266088	56750	GCTCACGGCCCUTGTCUG	56751	CCACAAGGGAGGUGUGAGT
254712605	56752	CCUCCCCACCCTCAUGCT	56753	TGCAUCACUGGCCACCAC
264843440	56754	CUACAUCACCGAGGGCAACA	56755	TCTTGTUCCCCTCACUCGGA
265707346	56756	CTCTCAUCCATCGUCAGCCAT	56757	GTTGATGUCAAAGAGGCCACUCT
259538495	56758	CCTCAUGAACTGGTACUACAGGACT	56759	TTCTCACCTGUGTCCCCACUAT
328338645	56760	GCTCAGTGUGGGTGGTCTTAUG	56761	TTCATCCTTTUCCTCTGGTGGUG
327116031	56762	CCCCTGACAUGGAAGACGAUT	56763	ATGGCCGGAUGCATAUGGAG
324147784	56764	GGACUGCAAAGGCCAAUGT	56765	TGAGGTGTUAAGACACTATGCTACAUA
313353008	56766	TCTGCGGUCACUGCAACAAT	56767	GAAGGACCCGAGGCUTTCUC
258062628	56768	CGCCTTGAAAAUGTGGCACTUT	56769	GGGCAAGUGATCACCAUCGG
314127973	56770	GGGTGGCCACUCACAATCUC	56771	CCACUAUGGGCAGGAGAGAAC
327951096	56772	CATTCCUTCAGGCUGGGAGAAG	56773	TGCACCAUCCAACTGAGTGUG
326625185	56774	CACTCCACCCUTGTATGCCAUT	56775	GAAAUGCUGGAGAAGGAAAAGCAG
327331849	56776	GUGGAGAUGACAAGGGCCAA	56777	CGCAAACACACUAATCTTTCTCCATTUC
326630983	56778	CCTCCCCCGGACUCTGUT	56779	TCACCGACCUCTCCTGUGT
241419475	56780	AGAGAGACGAAAUAGAAGCUACGAAGA	56781	GGACGGACGUCUCGAGAGT
333374458	56782	CCATACACCUGAATCTGAAAGGCUT	56783	ATTACTGCAAUGAGCATGUGGAGAT
313358091	56784	GGCAGGGCUTTCTAATCUCCAG	56785	ATGGCTTCCCUCCCTCTCTTUA
313482333	56786	GTCAAUGGCGGGTCTTGUG	56787	CATCGATACUGGTGAAGGACCUG
312952546	56788	CCCUGACCAGTCTCUCCCA	56789	CGTCTGGACGUCCCTATCUCT
324794663	56790	TGGAGGTUTCCAGCTUGCC	56791	TCCAAGUCAGAGCAGAGAGUAACA
261441195	56792	GTCTTCACGUTCCTGCAGTUC	56793	TGAGACCUTCCTTTCCUGACACT
264886455	56794	CCTCCTUTATGGGCUCCACCT	56795	GCAACCTGTAUGCATTAACTAGTGCUAT
265463382	56796	ACAAGGCCUGGAAGCTUAAGG	56797	CACAGTCTTUAAGCTTTTGTCTTUGGT
314671686	56798	GCTTCUCCACAAGCCATTUGT	56799	CAGTAGAACACGUGGTAGTTCCUT
313545040	56800	CAAGUACCACACAGCCAUGAGT	56801	TUTTTCUGCAGAGGAGCCCAA
313281817	56802	TTCTGTCUGAACTGACCGTUGG	56803	AGGGCGUGAAGACCTCTTUG
313238505	56804	TGAGCCGUGTCATGGTGUC	56805	AAGGCAGUGUGCAGACGAA
313372832	56806	GGGCTCAGUATAGGAGGCAUA	56807	CTGCAATTTUGACAAAGAGGCUGA
313002431	56808	GGCATGTGUGGGCAAGUGA	56809	CACUAGGCCCAGCAGGAUG
224031286	56810	TTCTAACGCUGATGCAGCTUGA	56811	ACGGCAATAUTACGAAATCCUGAAGAAT
224419132	56812	GTGCAGGAGAAAGUATCACTCTGTTUA	56813	AAGAAAATCTTACCUTGGTACAGTUGCT
223657066	56814	CTTTTCTTAGACAUGCTCAAGTTCTTGUG	56815	AGCAACATCAGAUAAAATCCAAGAGCUT
223690725	56816	CGGCCTTAAGGUTAATTCTTGAAGUACA	56817	TCTAUAGGACCCACTTCUCCCAAG
224007776	56818	TGAAGGAGTUATGTGTGTGUAAAACCC	56819	ACTACACTAGTGAUGGCTTTACCAAAUC
329506452	56820	CCTCCAAGGAGCUTTGTCTTCUA	56821	TGUGCACCATUCAAGAACACCA
333504229	56822	ACCGCAUTGTCAAUGACACGA	56823	AUTGAACAATGATGUCAGCAACAGAAG
332607328	56824	CCTGCCATCAUCACCAGCTUT	56825	CTTCTGAGTGUCTCTCCCAGUG
333665912	56826	CTCTTGUACCCCAUGCAAAAACA	56827	AATTGCTCAGCUGAAGAATATGGUCA
332605628	56828	GCTTTTGAAAAUGAGTGGGAUGCT	56829	CCTGTCTGCCAUTGGGATGATUT
332344084	56830	AGTTCTTTCAUTCTTGTTTCCUCCACA	56831	GATGCAGCTGGUATTATTTTTCTTCCUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332868694	56832	GCUCCACGGAGGTTAAUGCC	56833	TGCAAACTGUACACCTGGTCTAUAAAAA
332972337	56834	GGTCGCCCAAAAGCUCTGUA	56835	GCTGAAAGGCACACAUTAACATCAATTUT
312730668	56836	TCCAGGGAGGAUACAGAATTTCATCAUA	56837	CACATGACTUCCTCCTATCAUAGCA
278128787	56838	GTTAGCACUGAATTUGCCAACCA	56839	TCCGGTCAAUTACGGGAAATUCAA
279614586	56840	GACAAGGTGTUGAGCTCTGTTTUG	56841	TCTGCTTTCTUCATCAAGTCAUCAAGT
280680180	56842	GGCTCACCATUCCAATATCTCAGAUT	56843	ACAAAAAGAATTACCUAGGAGAAACTCUGG
280782406	56844	GATCCAGTCAUACAGAGAAATCCATGUT	56845	CCTTGGAGGCUAACTCCAUCAC
257428720	56846	GCTCAAGUGGGCTCTGTGUG	56847	CTGACTCAAUCGGTGTCTGTCUT
265558472	56848	GGAUGGACAGAGATACUCACAGGA	56849	CTGCCTGCGUTCAGGACUAA
267513684	56850	GUGTATCAGCUCAGCCCACAT	56851	GCGTGTCATTGACUTTTCTTTTTCTCUT
317471584	56852	CGGTTTCGAUACTCTCTUGGCA	56853	TGTAACTAATAACCCUGGCTCTCTGUT
317112366	56854	AGAATAAGACAAUACAACACCUGCAAACT	56855	TTTCACAAAGUGCGCCATTCUG
265881487	56856	CACCUGAAGGGTGCGUCAT	56857	CTGTATGCGUAAAAGAGCTCTCUGT
235156587	56858	GATTTTGUTCTTTCTGUGCGCACT	56859	CATCTUGCCAGACCCATTTTUCAA
241322262	56860	CTGTACTCGAUCAGCCCCUT	56861	AAGAGCAACTUCTCCTCCACUAAAAAT
326463416	56862	GAATCTTCTTCACUGGGTGATGUCT	56863	TCCACTTTUAGCTGCCTGGUG
327444577	56864	ACTGGTATUGGGACCCCAAATUG	56865	CAGGGCACUGATAGGCGTUAT
328114021	56866	TGATCGUCGGCAGGTACAAUG	56867	AGGCTGCCTUAAAATACTGGCATUAA
326867722	56868	GGACCAACUGATCACCTTGAAUCT	56869	GCACTTATGCUTAAAATCTATTUGCAGT
238907536	56870	TTTTGTTTTTGCUCTAGCCCCCUA	56871	CCCCTCTCATTCUTTACTACTTCCCUAA
332518709	56872	TUAAGCAGCGAGAUGCAGAGAA	56873	CGCTGTGGAUCGGCTACUC
333453887	56874	CCTGGTTCUGCTCCTTCTAUCC	56875	AGCTTACTGCCAUACAGGATCATAAAUT
333301886	56876	ACGAGCTCUAGGCCTCUAAGAT	56877	GAGAACAUGGAGCGAUCGGA
333290729	56878	CCACGCUCTCCTTTCAAUCCT	56879	AGTGTGAGCCAGUTAACTCTAGTACTUAT
320577065	56880	TCGATTCUACAGTGGTTTUAACAGCA	56881	GCCTGCAACUACCTTCCUCAA
315129032	56882	CCUGAGACACGAAGGCGUAG	56883	CTCCTTGGUCCTTGCTGACUT
313604780	56884	GCCTCTUGCAGAGCTTTCTTCUC	56885	ACTGACCTUGACCCAGGCUA
315328300	56886	CAGGAAAAGCAUCAGAGGAGUCAA	56887	GGTGACTCUGGACACTUCCCT
254158169	56888	CTTGGCACTTUGAGATGATTAGCUG	56889	CCTCCGAGAGAAGGAUCCGATTUA
328034782	56890	TTCTTGTTAAAAGUCAGAGCAACCUCT	56891	CAGTAAAGGAAACACUCAGACAATCTUC
328060106	56892	GGGATCTTTUGGATAAACATTCUGAACT	56893	GATTTACTGTUGGTTGCTGATGUGT
319439923	56894	CAAAGCAAAAGAUAAGAAGAGCCAAUGA	56895	GGGAAGAGCACAUCGUGGT
266622534	56896	CGTCATCCUGACTGGAAGGUAGA	56897	CTTCAGAGTTCACUGGAAGTTTTTGTUT
264870979	56898	TCTCAGGATGUCCTATGAGGATTUCA	56899	CCTGGAACUTTTTCGGCTUAGAC
267004947	56900	GGGUTAAATAGUACAACAGGGCAGT	56901	ACTCCCACGCUTCATTTTCTCUT
315905983	56902	CACAGGUGAAGCTUCCAGGAG	56903	TTTGGCCTTTUCCGAGTTATCCUT
317119725	56904	TGACTTCCUTTGCTGAUGCACA	56905	CCACTGTAACCGUGTAACCACTTUT
315688875	56906	AATACTAGGCUTCCCCTTTTTAUGCAA	56907	ACTGTCATUGATGGGCGAUGT
317643286	56908	GGAGUCTUCCACAGGGAGAGT	56909	TGCTTTUAGCGTCCUACACGAG
319391181	56910	CCAAGAACCUGCCTGTGTTCUC	56911	GCCATCGCUGAATCAGAGGUA
333611626	56912	CCUCGGTATCUCCCCAAACCA	56913	GGACUACATCAUCCGGGAAGG
262033633	56914	CAGGGTUGGAGGACGTUGAG	56915	TGGAAGAACAUCUCCCCCAAGT
319902349	56916	GGCGUACAGCTGAGCUGA	56917	GGGCUGCAAGCAGACAGAUT
237725648	56918	TTTTCTUGCCGTGGUGCAAAA	56919	TCCCAACCAUGAAGATTTCTTTGCUAA
238362046	56920	TTCAGAGCCCUCTTCCUCCAT	56921	ACTTTCAAGGGUGGCTGAGTUG
238435747	56922	CTCCTGUCGGCTCTTCTCTUC	56923	GTGTTCATCUCCTCCGGGUAAAAT
238054094	56924	GATAGCCTUCCCCACAUGGAAA	56925	CTGAUGACCACGCUACGCA
239876856	56926	TCCCTUAACCCCGGATTCUGA	56927	CCAGAATCCCUAACTCCCUCCAA
235117895	56928	TTCTGGAUGTCATCTTUCCCAACC	56929	TGAGAAGTUCCTCTTTGUGGACAAAA
257545939	56930	CCTCCAGCUCAGTTCCTUGAA	56931	AAAGTTCCTUTCCCTTCCUCACC
269187440	56932	GCCCCGAUACCTGUCCGA	56933	GTGATGACCCAUGTTCCCTTUCT
262881844	56934	GGCATCTTCUCCACAGCTTUGT	56935	CATAAATGGCUCTTCCTGTGTUCC
318387000	56936	GCAGATCTGACUAAGGGTGTUGAC	56937	AGATATCCUGCTCTTTGCCUCCT
318727677	56938	GAAAAGCCCCUCCCAGGUAG	56939	CAAUAGGCACCCAGAAGCTUGA
262023493	56940	ACTTGGTGAAAUGACTTCTTGUCACA	56941	CGCCATTCTCUAGCCAATGCTUAA
256084342	56942	TGTGGACGAUGAGTCAGGGTUA	56943	CCACCGUCCCTCTTGUCAC
253807440	56944	GCTCAGCUCCCAAAACCAGUC	56945	ACAAATTATAUGCCCGTGCUGAGAT
268585224	56946	GCAATTGAGGAAUTTCTCGCUGAT	56947	GGGCAGAACUGACACUCAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
263911094	56948	CTCCTTGCGGGAUTTCAACAUC	56949	AGAGAUAGAGAAATCCUGGGAGGAAAA
268316261	56950	CAATCCCAAGUTCCGGCUCAT	56951	GGAGTACACUGCAGGCTCUAGT
325551562	56952	CCCAGGAAACCCUCCATUACC	56953	GAAAGTTCUCCAGGTTTGGCAUC
323722860	56954	AGGAAGCCAUCGGUGAGAAG	56955	GGGCTGAAGUCCTTGGCAUT
325560342	56956	GGCUCCCCAGGATGTGUACT	56957	GCCTTGGGUGAGGGCTUC
323653968	56958	CUGCCGCTUGAGAGAACACT	56959	ACTCATGTTUGCGACCCTUGT
235109655	56960	CCTGTGTCAAACUGTGTAAAGCAAGUA	56961	CAAGTCCUATGAACTTAUCAACGAAGAG
239127311	56962	CAGTCATCAUTTGCCTTAATTUAGCAA	56963	CCGAGAAUCAAACAGAGUAACCAGA
258376739	56964	CATGACTCCAUGGCTGTCAAAUCT	56965	AGCAAACUCAATACCUGCCCAA
332619575	56966	TTTGGCTGGCUAGAGTTGGUAG	56967	CACTCACAUCGCTCCTCTUCAG
333228405	56968	CCAAATCTGGGACUCCTAACCUT	56969	CTCCTCUCACACAGGATGGUG
313422808	56970	CTGCCACGUGAAGGACUCAT	56971	GCTCUAGAAACACAAGCCAGUGAA
253693046	56972	GGGCCACAUCGATGAUGGG	56973	TCCATCACUCCCACGTGGUA
333038350	56974	CAATCGUGGGCTGCATCAUC	56975	TGTGCUCGAACATGAGCTUCC
328202880	56976	GUCAACGGCUCCAGCAAGA	56977	GGCAAAUCAGCCCUGACCA
253799342	56978	GCAGGAGGGUAACCAGAAAGGUA	56979	GUAGCCACAACCUGGACCAAA
264133648	56980	AGTCUTACCCAAAAAUGGCAGGAA	56981	GUAGAAGAGAUGCAGGGCCAAG
262757257	56982	ACCAAAACCGUCCTGGAACUG	56983	TGTGTGAGUGGCATGTUCCAT
315995957	56984	GCCCUCGCAGTATAUCACAGG	56985	AGAAAGGGUGAGACCCGUAGAG
317473152	56986	GCTACACGCUGGAGTUCAAGG	56987	CAGAGACGUAGCGGTGGUT
315747868	56988	GGGTCAACGUCTCAGCCAAUC	56989	ATGAUGGAGGAGGAAGGGAUGT
331159939	56990	ACTTGAAAAGAAUGCCTCAGGATAGAAUT	56991	GGGAGCCACUCACGGATTAAUAT
331126238	56992	TGCCGTTAAUGCCCATGGUT	56993	CTCTCTUGACACCCAGGATTCTTUC
268829414	56994	ACCCACCCUGTTGGATCAGTUA	56995	GCAATGGAUATAAAGCATAUGACCCAGA
257681391	56996	TGTTTATGTTACCUCTCTGTCTAGCUGA	56997	ATGCACACACGCCUGAAGUA
266308808	56998	ATCTTGACTTCAGUGTTATTGTCGCUAA	56999	CCTTTGCTTGAUCTATCCATGCUC
260009852	57000	GTAATUCACCCAAAACAAGCTUGGT	57001	GGCACATCAGCAGUAAAAGTGGUA
266743397	57002	GGGCAGTCUAGTAGGAAGAAAUGG	57003	CTCUACCAGAAAGCAGGCTUCT
268239174	57004	TGTCTGCTGGUTACATGTGGAUT	57005	CCGTGCCCUGGAAGTATACAUAT
259658143	57006	GGGATCACTAAAGUTCATTCCTTCUGT	57007	TCTTTCTTTCUCCAGGGUCCAGA
263935021	57008	GGCATCCCUGGCATCAUACA	57009	CTTACATGTCUTTGAAGGACUGGGA
326173245	57010	CAGAAAAUGGGCACAACGUGT	57011	GGTCAGGAGGCUCGATGUT
325148773	57012	GGCTTCCUGCCCGTCUG	57013	ACTGGGCGCUGCATGUT
323315626	57014	AGGGUCCAGAGCTACUCACAT	57015	CTTTGCCATUGGCTGTAAAGGUC
324765917	57016	CTGTGGGAGGAAUCGGAUCA	57017	TCTTCAAGATCTGUTTCACATCCTCAUC
324359005	57018	GAUGGAACTUGGCGAAGGAGT	57019	GCAGCAAGAAGUCCTGGTTCUC
323828744	57020	TCTCAGACCUATGATCCUCGAGAAG	57021	CTTCCGUCCCCACGUGT
323445502	57022	TGGACCCUTTATCUCCCCCAA	57023	CCTCCAUGGGCAAAGGATUACAAT
323399556	57024	GGACGAGTUCTCTGTGCTCUG	57025	CCAGGAGGAAGAGUCAGAAGGUT
255046582	57026	CCCCGAATCUAGCCTACGUGA	57027	CTGAAGATAGCCUTTACATCCCTAAUCC
265765561	57028	TCTCCTCTCUGGTCCCAACUG	57029	CCTTUGGCCCAAACACAGGUA
320003837	57030	CATCAGCCUGTCCCTGGTTUA	57031	TTTTCGATCUCCACGGUCAGG
326657638	57032	AGATCTGGGUGTGAGCTCCTTUA	57033	GTGGCCCCCAGUTTACTGUT
327289738	57034	GAGGAGAAAUGTCGACTGCUGT	57035	CCCCTCTCCTCUAAACTCTTGCTAAUT
315871593	57036	GAACUTATUGCAGCCAAAGCCAT	57037	AGCCAAAAUGGUCAGGGAAGAAG
316130918	57038	GAGGGCUTCTUCCGCAAGAT	57039	AGGUGAAAGAAAGCTCTCUGGAC
320495756	57040	TCCGGGAAGCUGTCCTTTUG	57041	GGGCCACCAAUGCCAAUG
326078923	57042	CGGTGTGGGUGCGATAAUG	57043	ACTATAATUCCCCAAGGGCUGGT
326019651	57044	ACAUGACGTUCGGGAGCAC	57045	GCCGACACUCTGAAGACCUT
263511418	57046	GGCTGCUTCCTGTUCCAAAGAT	57047	TGTTGGAATGACUATGCAGTCTTUAGG
258450738	57048	GCCTCAAAAUACCCCTAAAAUGCC	57049	ACGGGAAGUGGTTTTCCTTUCT
313895285	57050	CGCUGTGGTGTUAGACAGGAT	57051	TGGGTTTUGGCCAATACGUACT
265590953	57052	GCACUCACCCCCACUGA	57053	TCTGACCCCUGACCCCUT
320228202	57054	TGGATCGGUGGCAAGAAGUC	57055	TCCGATCUGGAGGGCAATAGUA
319044033	57056	TGGCCTGCUCAGGTCTUAGAA	57057	GCCAGGAGACUCTTTTUGAAGGG
225923247	57058	TCGTGTUCAAACCACGGAGUT	57059	CCCCCACTTUACTGGAAGCAUAT
317157086	57060	TCTCTTCATCACUTAGTTCTTCUAGGGT	57061	GGGATCCTTGUAGTTCAATGTAATTGUA
317051202	57062	CAUGCCGGAGAAGUGGAAGT	57063	ACCAGCAACCAUGACTATGCTAUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317299413	57064	CAGTUTCCTCCACUGAGACCAC	57065	GCACCCCAAGGAGUTGACAUC
325037960	57066	AGGAAGGTCAGUAGGATAATTCAGCUA	57067	GTCCTGTTCACUATAACTAAAACCGTUGA
268182295	57068	CGTCAAACUTACCGGAGUGCAAT	57069	GTGTTCTTUGGGAATTTGATUCGAAGA
263137299	57070	CTCCGUCACCACTGATCCUT	57071	GCCAAATAAGCACUTCTTTTCATCTCAUT
269437132	57072	CCTTGGAGTCUTCTAGGAGCCUT	57073	TTCACTAGGUGCACCATTCTGATATUT
265163882	57074	GGGAGGAGUGGCGTTTAUCT	57075	GCCATTUCACACAGAATTAAGACUGGAA
269218594	57076	TGCTCAAUGGGCAAACUACCA	57077	CTCAACTTAGUGTCACCGACTAUGA
326257656	57078	ACAGAAUAGGCCACAATTGUACCC	57079	TGTGGCAAAAGAAAUTGAATTCGAUGAA
324721853	57080	GGGAAAUACTGTGACCUAAAACAGACC	57081	TGTCTCCTGGAUCTCTTGTGGATATUA
326148617	57082	GCAGCUGAAGTATTAGAUCCAGCA	57083	CTGCTATACACUGACCTGTCTCAUAAAA
263098226	57084	CGACAGUGGACAUCCAGAACC	57085	TCAGCTGUCCACTTGTTCAUGT
242231624	57086	CGACGCCGAGACCUCUAAA	57087	GAGCTGCUTGGGCUAGAGAAG
317255790	57088	GGCACCAGAUCTCTGUACGG	57089	AGACUACACCCAGGGAAUGAAGA
290297715	57090	CGCCTCAUGCAGCTCATTUG	57091	GGTTCCTATTGTUTCTCCCCAGATUG
292982255	57092	GAGCUATGGATGUCAAGGACACT	57093	TGCCGGUACACAGAGGTCTUAT
289558279	57094	CATGATAAGUACCATGACTCCAAUGAGT	57095	CAGGUCCCAGATGAAAUCCCA
327060657	57096	GATTTGGGTGCUTGGGCCTAUA	57097	TGAGTCAGAGGAACUACTGAAGUCC
301091682	57098	GGAGAACCCCAUGGCTTTGUT	57099	CTTTTTCAGAGGUGGGCGAUG
326446463	57100	CTTTTTGUAGAACCATAGTTTTGUGGCA	57101	TCACGGAAGCUGTGTCATCAUC
256231560	57102	GTCAGCAAGUCACTTAGATCAUAAACGA	57103	AGAAAAATCATGGUCATAAATAGCTAAUGGGT
257107914	57104	AGTGGCUCACTAAAUCAGAGCAAG	57105	TTCCAGAGCAGAUGTCTTTAAUAGCAAA
267618007	57106	GCTGCCTUCGTCGCTTUAGT	57107	GGGATTGGTAAAAGUCACAGCTAAAUCA
267457684	57108	CAAAGCAACCGAAGAAUGUAACCAT	57109	CTGACCUGACGCGATCTCUG
315056519	57110	AAAUCTGTTACUCACCACAGCAAAGA	57111	CTGTACCTTTUCCCTTTCTTCTTCUCC
313997788	57112	TTGTAGGAAAAUGAGACGCTGUCAA	57113	CCUGTTTGTTTCUCACCCCCAA
313407811	57114	CGGACCAGUCTTTCAGGTTGUA	57115	GTGTTGCAGCUGTTGTTGUACC
318279457	57116	TTTTAGGUGGCTGCAAAATUCGG	57117	CCACUCCCGTTGAAAUAGAAGAAAGAA
318195952	57118	GGAGGUAGCCAGAGATAATTAUGGGA	57119	GGTGAGCCCTAUTTAGTCATACACTUAA
318392298	57120	CATCCTGAACUCGGGAGAAGAUAAG	57121	TGTAAAAGAGGUTTATGTCTUGGGACAG
317514044	57122	ATTCCCAGUGAACAGAAAGUAAACGA	57123	CACTGTCTUACAAGCCAACTCTUG
227194202	57124	ATTCCACATACCUGGTTAATGTGCUT	57125	TGACAAACCTTTUCTTTACCTTCACCUT
227472558	57126	AGTTTCACTCTAGUGGTTTTTGACCUT	57127	GATTGGCAAGUTATGTGCCCATUC
229055814	57128	CTCCUCGGAGGCACTCATUG	57129	CCATGTUCAAGAACAACUACCCAAG
315007312	57130	TGTATGTGTCAAUGAGGCAGTAGTUAAG	57131	CTTTATGTATTCGUCGCGTAAGGCUA
313967663	57132	CCTGAGTATTUGCCGCCCUT	57133	GGGCCCCAACUTTAAGAGCAUA
314517429	57134	CGGTGACAUAGTACGCAUGCC	57135	TCCTTTCTCCCUTCTGCTCTCUT
312729176	57136	GCCCTGUAGAGATAGGAGTUGCT	57137	CAGAGACAUCAGAAGGGUCAGG
332264606	57138	GTCTGGCCUTCTGTCCACUG	57139	AAGTCCCTGUCTATGTTCCACUCT
317656642	57140	AGCTACTCAUCCCATAAUCCCAGAG	57141	TGAAACGCCAUCAACGGGAAAUA
315525030	57142	TTTTAAAAGAUCATGTCCATUGGAGACA	57143	GAATCAGGAAUCTTGGGACCTTUACT
319382399	57144	AAGGGUCGCCCACTGUC	57145	GGTCCACAUACCCATCCTCTUC
318592384	57146	GAGGATGATGAUGTGAGCCAUGT	57147	GCACACTAGAUGCCATCCUCAG
313266571	57148	TGGAAGGAUAGGAAAUGGGAAGT	57149	CCAGCTCUGTGGTGACAUCAA
320394068	57150	TTCTAGCUACAGCTTCCCTUCCT	57151	AGCATCTUCATTTTTGTTUCCACACAA
263018004	57152	GCCATCUCCTGACCCUCCT	57153	CGACUCACCAGCGTCCUT
256966336	57154	TCCAGTTCUGGATGCCCUGA	57155	GCTGAAGTGGACUCAATTCCTGUT
260697372	57156	TTATGCUCACCCGGTTATTCUCAAA	57157	CCATCACTCUGAGTTGTCTCATTUCA
255215397	57158	GAAAGAGUAGACAGCCGCUGAT	57159	GTCTGAACAUCACCTTCUACGAGA
261720017	57160	CUTTTTAACCTTAGGUCAAAGGCAAAGT	57161	GCAGCCTGUAGTGGTGTCAUC
263296299	57162	CAAGGTCUCCTTCAGUCGCAA	57163	TCCATCUGGGCTTTGTTCUCAAC
266371875	57164	TUCCTTAATGAGTUGGGAAGGGAAA	57165	GATCTTCTCTATAUAGGGTGAACCUGGA
266868808	57166	CAAACTAAUGCCAGACAAAUCCAAAGA	57167	GCACCAGGCTCAUAATTTACTGTGATAUA
267994606	57168	CCTTGAGACCUCTGACACCAUCT	57169	ACGTATAAGTGGUAATTCATCTATTUCAGGG
263904850	57170	GGAATAGATGUATCTTACCCTGUGACCT	57171	CACATCCTGUGTCAGTTCACUCT
237210293	57172	TGGATCACATCUCTACCAGAGTTAAUCA	57173	CTGGCCAAGAGUTACGGGAUT
318010922	57174	TCCCTCGUGGTGTAGAGUGAT	57175	CCAATTGGGUGCGTAACTTTGUC
325311918	57176	GTCCTCATCACUCTCTCTGTCTUACT	57177	CCACACTCTTUATCCCTGGACUC
320188415	57178	GAAUTCTGGTGTTTUCAGGCAACA	57179	CCCAAGAGAAGUTTTTCCAGGAACUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
319882132	57180	ACAAATCAGTCUTTTCCAACTCTUCCAA	57181	GACTTCTTCAGCAUTATGACAAGAGCUA
326518431	57182	CAGGGACCUGCAGCAGTATUA	57183	TTACTGGACCUCCCCATTCUCA
327936273	57184	ACUTTGGAAGUGCCACCAAGT	57185	GACCTTGATTGAUTTCTCGTGTTUCA
327787188	57186	GTGTGTTTCTUGAGGAAGATGAAUAGGT	57187	CCCTATTTGUAGGTGTTGAAUGAACAAG
328057130	57188	ACAATGGTUCCATCCCTCCUAAGT	57189	GCCTTACTCUCAGTATAACTTCUCCCT
327564140	57190	CCTGTCAGUGGTGTCAGTGUG	57191	AGTGCACTATUACAATAAATTGCTGCUT
327070226	57192	CAGAACCACCAAAAACUGTUAGCA	57193	GGCTCTTTCAUATCAGCAAGTGUGA
328301083	57194	GAGACCUAAAGGAAATTTTUGGCACAT	57195	CCCGCGAAGUTATACCAUCCT
327374976	57196	CCAAAUAAGTTTCUGGCAGACAGAGT	57197	GAAGTCATAATGCAUAACCTTTCCCUGA
326613137	57198	ATGAAACCTTATUTGCGTGGCTTUT	57199	TCTCAACATTTUGATTTCTGTTTUGCCA
325643792	57200	ACAGCGAGGAAGAAGUGTGUG	57201	CCGCAUCAGGGAATGAATGUCT
324375674	57202	ATGCTTTAGAATUGGAAGTAGATTGUGGT	57203	GAGAGCAAGCAUGCACTTTUAGAT
325058845	57204	ACACTGACAGUCCAGACCUGA	57205	AAAGAGTGCAAGUCTCAATGCAAUG
323716705	57206	TGTUTAGATCTGAGUGCCCCAAG	57207	TGGAGGUATGAGAAAUGAGAAAGGAAAG
325050983	57208	GGACGGUGGTATTTTGAATTUGAGAC	57209	GUACTGTGAAGCUACCAAGAGGAA
324069182	57210	GCAGTCAAUGGAGTTTTGCUCAGA	57211	CCCGCACAUACCATAUAGCAGT
324284305	57212	GCGGTTTTUGCACAAGCUACA	57213	ACCCTTGTGACCUGAAAGAGATTTUC
323649873	57214	CGCTTCTCTCAUTGACTCATTACTUCA	57215	AAGAAGCCGGAAUAGAATTTGTTAUCCA
324850745	57216	TGGGATUGGGCAATTTCACTUCA	57217	AGGCAGTAATATUTCCAGCATCTTUCA
323502101	57218	GCCCTGAUGATCATGCUGACAA	57219	CAGGTTGUGGGTTAAAGTUCCCT
324745521	57220	TGGTCTGTAGAAAUCTGTTGTGCTUAC	57221	AGCAACGAGGAAAUCUGAAGAACA
324986890	57222	CCAAGATCGUGAAGCCCAAUG	57223	CUCCAGAAGAGCCUAAGAAGCAA
324026125	57224	AGCCTTCUCGAACTTTGAACTUACC	57225	GGGTACACACAUTTCTGAAACTACUAA
326863295	57226	GGCTCGAATGAUCGGAATCAAAUAC	57227	GGTGUTCGTCCAUCAAACCCAA
327047268	57228	TCCCATCGGAUTCAAGTTTUCAAAGA	57229	TAAGTTTCTAAACTACUTAATAAAAGGCAGGUT
326685074	57230	GCTAGGAAUACTTACTTCUCAAACCACA	57231	CTGTACAGCCAUCAGAATTAGTUGGA
328117454	57232	TCAAGTAAAGUGAGTTGUCGAGCAA	57233	CAAGAGACAAUGGACCAGGTCATAAUAT
326471280	57234	TGTAAAGATAUCAATGCTGCCAUCCAAT	57235	GUAAATCAAATCAUGGGCAGCCAA
328260389	57236	AAAGGCAAGAAGGCAGUAGTUCA	57237	TTCCTATTTUCCAAGGAACGTGTUCA
266474737	57238	CTCACCUACCCCAAGTTTTCUGA	57239	CAAAAGGAGGGUGCAGUCCAT
267313394	57240	CCCCACUCCAAGCTGCAAATUA	57241	TGUAGTACATCTTCUCAGCAGGGA
269076218	57242	GCCAGCCUAGCATCCCTTCUA	57243	TTUGAAGAAGGAAAGGUCAGAGCAA
327796932	57244	GAAGCAACGCGUTCCGUT	57245	CTCTTTGCUGCCTGTGTCATTUG
327611050	57246	CTCACCAAUGGTGGTGTAGTUGA	57247	ACAGTCTTTGCUGGGCATCUT
327666104	57248	ATTAAAGAATCCAUTCTGAGGCUACGG	57249	TGTTGAGGUGGCTTTTCCTUCT
326631235	57250	ATCTAGGGATUCTGGTGTCCAUCA	57251	GTGAACCUGGGCAAAAAGAUCAC
314313811	57252	AGCTTTTGTTGUAGAAGAGCCCAUT	57253	GCCGACAGAAGGAUTTCTTTGCTAUAT
324723265	57254	AGGCTACTAUCAGGTGGATGTTCUT	57255	GCAACTTTUAAGGGATGGACGAUT
324114459	57256	CATGAGGACAAUGAAGCTTUCAAACC	57257	GAGTAUCACAGAAAGCAGTTUGCAT
326349768	57258	AGAGAGACUGACTGAUGCAGGA	57259	AGTAGGUCCCCACCAAUGCT
265609488	57260	CCCTGTTACCCAUATTGATTTCCTCUG	57261	CCTCTCTCCCCCAUAAAAATGATCCTUA
267583171	57262	GCCACAGAACUATTCTCCCCAGUA	57263	AGCAACCAUTCAAGATTTUACAAACCAG
269066917	57264	ACCTCATTGTUACCTAAAACTGGCUT	57265	GTTGTAATTGTGUGATGTTAGCAGCUAT
268302928	57266	CAGGTCCUCCCTTTTCTUCACA	57267	GACAGTCAGATAUGCCGTGACATTUA
260993887	57268	TGCATGGAUGAAATGGCATTUGG	57269	ACGATCACCCUGTGAACAAATTCAUAG
265562971	57270	CTCATTTCCTATCUGAAGTGTCTGTUGA	57271	CCTCGAUGTCCTTTGAUGCCA
268026633	57272	AACAGGCACUAATCCTGGTTCUC	57273	GTTTACATGGCAUATTCTAGGGUGACAT
267708096	57274	GCTCAAAGCUGTGCTUAAGGAG	57275	CTCTCCCATCUCATCCTTGTCACUA
268772456	57276	AUTGACCUGGAGCGCAGAAT	57277	GATCTCCTGUAGGGCATGACUG
268560938	57278	TGAGGCTCCAUTCTCTGGCUA	57279	TGGTGUCCTGGGAUGGAAGAA
267279549	57280	GGCTGAAGUGGAATGCUGAAGA	57281	GGACAAGAACCAUAGTGAGCTCUG
257992768	57282	GCTTCTGUGAGTTGAGGCTUCC	57283	ACAGACGGUAGCACCAGTACUT
272552166	57284	GGGCUCGGTCTAUGACGA	57285	CGGGCCCGACUGUCAAG
233194742	57286	GTGTCATCUGGCCTCAAATCTUCT	57287	TCGTGCAGGAAGUGAACTUCAT
324266860	57288	TGGGCUTTCAGAUGCAGACAC	57289	GCTCAAGCGAGGUACAGAATTAAAUGAT
326366317	57290	CACAGTCUCCACGGCCAUA	57291	CCTCUGAGAGCTCTGUCACGA
325068734	57292	GCATCUCCAGCACGAAGACAUA	57293	GCTTCATGUCCACCTTGTCUGG
325137978	57294	GACAAAGGCAUGCATTACCUCAC	57295	GGTGTGTGGACUCAGCTCAUA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256582055	57296	GGCGAUGACAAAGAAGAGTCUGT	57297	ACAUACGGGCAUGCCAAGAT
316029511	57298	GCTGTTCCAACUCGGTAGUCA	57299	AATGTAACATGUGTGCTAATTCTUGCAG
332037055	57300	GGCCCUCAGUGGGAACAA	57301	GGCACGUACACCUGCGA
332151484	57302	CAGGAAAGGUGCTTCUACCCA	57303	CCTGAGCCUTCCTGTGCUT
332043088	57304	CATCUGCAGAAGGUGAAGCAC	57305	GAAGGCAGCAUTGAGGTTTAUGAA
259457383	57306	TTTACTGCACCUGCTTAAAACCTTUG	57307	TCAAGAAGGCACAUAGTAAAAACAGUGA
324545151	57308	GCCUCACATGTCUGGGAGAT	57309	GGTTCTUCAGGTGCUAGACCAG
325530790	57310	ACCACUGCCAGCAGAGGAUA	57311	CTGGGAGGCCGUGCTUAG
318153174	57312	CAGCAGCTUCCCTAAGAAUGGT	57313	AGATGTTGTGTUAAGGCTTAAAGAUCCC
318025165	57314	ACATATATCAGGUCATGGCCTCCUT	57315	CCACAGAAAUTTACCTACATUGGAAGAGT
319202196	57316	GTAATAGCTAUCACCCTTCTUGGCAA	57317	CAGCTUCCACCCGUGGAT
319994420	57318	AGGGUGAGAGAAGACCTTGUGT	57319	CATTGGAGCUCATCATGCCGUA
320184783	57320	GCTGTAAATCUCCAGCCTUACCAAA	57321	TGGGAAGCUGCATCAUCGG
332498646	57322	CCTTCCATUTTACCAGGAUGGCT	57323	CGGCAGATTUGGTGTCGTCUT
333116494	57324	AAAATGTAGCAAAUTACTCTGACCTUCCT	57325	GTAGCCAGCTTUCAAACAAACTCAAUT
333713656	57326	GATGTGTCTGAUAAGGCAGGTUCT	57327	ACAATAACCCATUCCTCTTCAACTAAUCC
332891235	57328	CAGAGAGGATUGAGGAAACCATGUC	57329	GGTTAGTAUCGGCCCCTTTTCTTUT
332995582	57330	AACCCAUTTCTGTTUCAGGAAGGAA	57331	CCAGUAGCCCCTTCTTUCACA
265700447	57332	GCAGTCTTACAUAATGCAAGGCAAUT	57333	GAUTGACAUCCAGAGGAACCGA
261093291	57334	CCCACTCATUGATTATTGGCATATUCAC	57335	GGGATATTTUCACAGATGTTTCAGTUGA
260401779	57336	ACCTTTTCGUGGAACTTGACAGATTUA	57337	CCAGCTTTGTGUGGTTATAAAGGTUT
269357938	57338	GCCCAUGGAAGGCAATGCTAUA	57339	GAAAUAAGGGAGGAGCAAATCUCCA
264034163	57340	TTCAGATAAAACUTCCACAUCCAGCA	57341	TGTGCTCUCAAAAGCTAGAUAAACCAT
262103516	57342	CAACAGAUGTTAGGAACUCAGCCT	57343	ATTGTCCCUCACTUGGCCAAA
292839446	57344	TTTCTCAAUGCCAGAGAGTUGAAAGA	57345	AGCTTGTUAAAGAAGACACCTGGATUT
292086400	57346	CTGGTATCAGTGUCAGGAAAAGAGUAAT	57347	AAATTTAAAACAGUCAACACTACCTTAAUGCC
318870861	57348	ACTGGTTUGAGCAACTGCTUCA	57349	CCACAACCAGGCAACUGAATTAATTAUAG
292026713	57350	CTTTTAGGTAGUGCAACATTGTGUGAG	57351	CCTGCAGGACCUAGCAGAATAATTTUAA
289466104	57352	TTTAATGTGTTTTCCUCCCCTTAGGUT	57353	ATGCTCTATCCCUCTCAAATAGCUACA
289583846	57354	TGGATTTCUCCAAATACGTTGTTUCCA	57355	ACTATACTCCTTTUCACCTCTTCTGUGA
292841039	57356	TGTCATCGCUATTTGCTGUCCA	57357	GCTTATTAGCACUCGTTAGAGCAATTUT
326495748	57358	GGGATTAATTGUGGCTTTCTCTTUACC	57359	AGCTTATTCCAAGCUGAGTTGCUT
327249067	57360	CATACCAGATGUGTCTGTCACTCTUG	57361	CGTAGTATTTGCUGAGGGCTCUG
327391044	57362	GCCUGCAACCCCCUCAG	57363	TTGTAGACAGAGUCCCAGTGUGA
328317921	57364	GGGTCUCTTGGCUCCCAA	57365	CUGGGAGAAGCGGUCACT
332039213	57366	GTAGGCCUCTGGCTUGAAGG	57367	CCUGGCGCTGUGAGACT
236741594	57368	TGTCTAGTTCAGUGGGCATGUT	57369	AAGGATCUCCAAAAGCCUCCAC
236712556	57370	GAATGCCGUAAGATGGACTTTAAUGT	57371	CCCACATCATGUCTCATCTTATCAAUGT
267678893	57372	CAGACGCAGUGGAGTUGGAT	57373	TCTGCACTCAAAAUCAATGAAGAGGAUT
262208100	57374	TCTAAGAAGAUTGTACAGCUGAAGCC	57375	ACATTGACTGUGGTGATTATTGAACUCT
267436583	57376	CGCCCAAUTTGGTGACTUGT	57377	GAAGTCTGAGAGUGGATCTGCUG
268489637	57378	GGUCATAGTUGACCCAGAAACCAAT	57379	CTTGAATATCATACUGACTGCCTGTCUT
263573626	57380	GACCUGCCCCAAAACCAAATUAA	57381	AGCCGAAGACAUGTTGUAAGGG
263238079	57382	GACCGGCCUTCAAUGCAAAT	57383	CTCTGAGAAUGGCGAACUGAAGT
331878143	57384	GTCCCCAUTCTTAAACUGGACCAA	57385	TCCTUGCAGCAAGAGAAAAGATUCT
331826550	57386	GGUTTTGGGCUGAAGGGAAGT	57387	GACCCUGACCACAAGTACAGATUC
331864985	57388	CCTTCCACUGTGTGCUCGT	57389	TGAATGAUGCCAGCCCAGTAUG
261105121	57390	TCCATCCTTUCCACCTTCCUCA	57391	CGGAGACUAGCCCCTATGUCA
265313759	57392	GTGAGCCAAAGAUCTCCUCCAG	57393	CCTCACACCAACCUTGTCTCUT
257869172	57394	CCGGGAGUAAGGGCTTCTCUT	57395	TTCCTCATCTGUGGTGTATCTGTTUC
268889714	57396	CCCTCAAATCUCCAACTACCTGUT	57397	CCTGAGAGCAGGAACUCTCUCT
327522197	57398	GCCTCGAUCCATGCCCTTTUT	57399	TGTCUCAGCACUGGGACCT
326829498	57400	GGGCTATTTGACUACAGTTGTTTUCT	57401	GACGGTCUACGCCAGGTUC
314889577	57402	CAGATGTCUGACAGTGTGCTCTUAG	57403	ACGTTACTATTTUAGGTTGTCTTTCTTCUGG
271364675	57404	GGTTCCAGUCCACAGCATCTUC	57405	TGGGATTCTTUGGCTAAATAACAUCACA
318484912	57406	CAAGTCUCCCAGAGGTCAGUG	57407	CCATCTTGGGUGGGATGTTTGUAG
271186670	57408	GCAUAAAGACCACCCCCAGUT	57409	GCACCATCATTUAGTCTTGTCTGUCT
316922208	57410	TGAAATACUGAGGGCACAATTAGUGT	57411	CCAAAAACACATAUCATAATGGCCTCUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316850148	57412	AATAGTATTGGUGGAGTGGATTGUCAAA	57413	CAGACTGUGAAGATCACATCAAUGGA
316112138	57414	GCTTCAACUAATTGTAGCAUGGCA	57415	CCAGGATTATGGUGACTGTGAAGAUA
316363855	57416	TGTTACTCACCGAUAGCTTTTGUAAAGG	57417	CAGAGATATCAAAAUGGCCAGGAGUAAT
323810224	57418	ACAGAAGGGTCAGUTTTTCTGAGAAAUT	57419	CCTGCTCCUCCTCCACACUA
320678652	57420	TCATCATAACCCUGTGCTAATGTTUGA	57421	CCGACCATGTUGTTCAAGAAAAACUAAA
257540926	57422	TGGAGTAAATGACUTTTCTCAAGTGGUT	57423	CCTTCCCCUCCTAGCTCTTCTTUT
266524326	57424	TTGCCATGAACAAAUCAGAAGTATAUCAGT	57425	GAGCCCCACUCATGGTTAGAUG
262298686	57426	GCGTAAAAACCCCUTCTGTTAAATUCT	57427	CAAGAGAUAGCCTGCAUGCCA
266466898	57428	GTTAACTUAGACACCCAAGGTGGUAA	57429	GAAGGTACAUTTTCAGGAGUCAGCA
259847201	57430	GCTGAGAGUTAGAGCUCGGAAG	57431	CCTACTGAGGAUTTTCAGAGTGUGT
326783746	57432	AGCAAAATTACTUTCCCCTGACUCC	57433	GTTTGTCCUAGCCTCAGUCACT
265621950	57434	GGCTCCUGATGACCCUCAAG	57435	AGAACACUCAAUACCCCAACAAAGG
254373311	57436	GGGUAAGAGAGTATCUGCCCAAG	57437	CCTCCCCCUGGCTGCUA
229106641	57438	GTCTTGGTTAAUGATCAGCTCTTCUCAA	57439	CTCATTGACTCAUGAAACTCACCUG
224460722	57440	ACAUGGCACAGAUGGAGGAAAT	57441	GTCTCTGUAGAGCACACTTTTCTTCUAA
224478002	57442	CACATAAGUCCCTTAGTACAGUGGAA	57443	AGCTGTGTTCUCAGCCTCTCUA
223882959	57444	GCAGTGTACTUTTTAGTGGACAUAAGCA	57445	GGCAGATGACUGGCTTTTACUAGAT
319776597	57446	AGAGTGTTACCAUACTCATACCTCGUAAA	57447	TGCCACAAUGACAGGAACTATTUCT
318263604	57448	TGGTTTTCTTUACCAGTATCTCCCAAUC	57449	ACACCCCCAUCCAAAACAUACAC
263632698	57450	ACCTCCTGUAAGTAGCCACUGT	57451	AGCACATTTUAGCTACGCAGGUAT
269351526	57452	AACAAGCAGGAUTCAACATUGCAAA	57453	TGTGGTTCTTAGAUGAATGCTATGUGAA
268307652	57454	GTTTAUTCTCACAATCTUCAAGCCAACC	57455	GTTAATGGAGUCAGAATACTGUCAAGCA
268130882	57456	TTCAATTTTCUCAATCCGGAGUCCA	57457	CCTCTATTTCAGAGAUGAACTGTCTUCT
265946596	57458	AGCACCUTCTCUCAGACCCAA	57459	GGGTCAGUCTGGTCUGGACAT
325626749	57460	GTGGTCTGUCCAAAAACTTGCUT	57461	TGAGGGTTCTTTUATTTCTGCCATAGUT
254869759	57462	TCCAAATCTGTAUGGAGACCAAAUCAAG	57463	TCAGATAGATUGTCAGCAGAAUCAACAG
259606595	57464	TGTAGCACAATGAGAGUATAAAGTAGATGUAAT	57465	CCTCCCAGAAGGCUGTTACATUC
266986426	57466	TGACTACATGGAACACAUACCTTCGAUA	57467	TGTATACATCCCCAAACUATCTTAATTTAACUT
265835401	57468	AATGGCCAACTCUCGAAAGTTATGATUA	57469	GTCUAACAAAGCAAGCAGTGTUCAAAT
259465766	57470	GGTTGGGCUCAGATCTGUGAT	57471	TTCCCACTGUGCTATTAAGUAACAGAAC
265397991	57472	CAAAAGGACACAGCAGUTAAATGUGA	57473	TCGTTCAGCAGUTTCTGGAUGG
269335807	57474	CTTAGGCCTCUCATTCTGCCTTAUT	57475	CAGGCAAGCCGAUTGAUGG
268968223	57476	GAGAACCCACCCUTTCTGCUT	57477	AGGGTGTUGCTAGTGUCAGGA
313699188	57478	TCCAAGCUCCTCCAAGGUGA	57479	GCTACCGCACCAUTAGCAAGAUT
313117317	57480	CTGAGCCUGCCCUAAAGCAA	57481	GGGCTATGUCCTCCCACUC
318892240	57482	CTGGCATTGCUGGTTTTAAATTACUGT	57483	TTTTAGCAGUAGAAGACTCAGAAAGUGG
332389425	57484	CAGCAGGTGUGTGTCTTTCAAUG	57485	CTGAGGGCTCCUGATGTACTCATAUA
318002930	57486	GATAATGCTGUCCAGGATGTUGGT	57487	GGCTTCUACCGCGGUCAA
262312212	57488	GGTGCTCCUAAGGACAUGGAA	57489	GGATACUGGAAATAGCCUCAAACACT
241851549	57490	CACACTGAGCAUTTACTACCTGAAUGT	57491	GCCAAUTGTCAUGAGAGGCAGAA
266903266	57492	CCAGUGCCGGATATGACUCAG	57493	CCAGTGAGTTCCUATTTAGTTCTTGGUT
266323618	57494	TCTGTTTCTUGCTTTGCTTUCAAGG	57495	CCCTACCACGUGAACAAUGACT
256975436	57496	CCACCCCCAAAUAACTACCAUGT	57497	GCCTGGCAAAGGCUCTAAATUG
267053487	57498	GTTTTATCAUTGAGCTGTUAGGAGGGA	57499	CAGUGAGAAGGCGGUCAAAC
327933093	57500	GAGTTGTGTAUGACTTACCGATTCUGT	57501	TCATTACCATGUATGCCATTTGUAGACAA
316260122	57502	CGTCTAAAUCCAGTTTTGCAAATUGGT	57503	GCTGTATGGGUTAGGAATTGTATTUCCA
227708939	57504	CCTGTCCCAUCATTGTCTCCTTAUAC	57505	TGATAAUGGCCCCCTGUGAAAC
316167074	57506	GTTGTACATTUCCTTAACTGACUCAACA	57507	GTCCGAGAAAGCUTGGUGAGAA
326663638	57508	GTGTGGCAATAUCACATTCCTTGUC	57509	TGGAGATAAUGCTTCACGTUCCC
267633801	57510	ATGTCTGCUGATACTCUGAGGGA	57511	TCACTCCAAGGAGAUGGGTATAGAUG
316189197	57512	TCAGTGTUCAGCTGTCTTUGGAAT	57513	CTGAUTGTTCCTGUGGAAGCC
296693859	57514	GGGCUTCTAUCCCCGAACC	57515	GCAGCCCUGCTCUCAGA
295529197	57516	CTGAAGCCGCAUGAGGAUGA	57517	CACCATGAUCGGCACGTCUA
327961160	57518	CCAACTGCCUTATTATGATCTTGUACCT	57519	GCAGAAGCAGUTTAGAAAATTGCCUAAT
240418617	57520	CCTGTCUGAAGGAAGAATGTUAGCA	57521	TCAAACTTCATGUCCACGTCTCTUT
240613793	57522	AGTGTAAAGGCUCAGGGTUCAC	57523	ATACCGACUGCCATTTCTTTTGUT
239272325	57524	TCTCAAAGUGAGGCTUGCAAGT	57525	CAGTGTTCATATAUGTTCTGCCCTUGT
263695232	57526	CTCCGTGGCUAACTCTGCUC	57527	AGAAGGGUGCGGCACTUAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268788877	57528	CTCUGACCACACTTCUCAGCAA	57529	GGAGAGTAUGGAGGGAUGAGGT
267835332	57530	GCAATACCGUGCTGGCCATUA	57531	CAGAAGTTAUCGGCAGAACATCCUT
267190063	57532	ACAUCTCTTTAUGGGCCCAGCA	57533	CCTTGGTTAGGAUCGACCCAGUA
333386847	57534	TTCTGCTUCCCAAGCUGAAGAA	57535	TCCACGTGGUCATGGGAATAAUC
254945293	57536	GCCCCATUTTGCCTGAUCAAG	57537	CCAGCGTGUCCTGGGTAUG
265578912	57538	CCATCCTTTTCUGCATCTCTAGCUT	57539	GGTTTGGGAGGUGAAACCUAGT
321411143	57540	CTAGTATCGUAGCTACTTCCCTTUCC	57541	GCCTACAGACUCATAATACCACCAATUA
266161995	57542	CCCUGCCCCCACCTTTTUC	57543	GGTGUGGAGGACCAGGGUA
259971025	57544	TGAACCUGCCCATGAACAUCA	57545	GGTCCUCTTTTTCACUGGAAACC
255612856	57546	CCCATCCUGCTCCTTACCTUT	57547	CTCCATUGGGACCTTCATCCUG
327185611	57548	TCTTGTAGGTUGGAAAAGAGACTGTUC	57549	AAATCAGCTACUTTTTCTTCCUAACAAGAGT
328117793	57550	ATCGTCTGGCUAATGTTATGAUGGG	57551	CCCTCGUCTTTCAATAAUAGGAAGCA
314382869	57552	AACTTCCTCACCUGGTCTCATTUC	57553	CTGAUCCCACGGCCTCAUC
254329386	57554	GGCCCGGCUTCATCGTAUT	57555	ACTAACGACUGCACTAATGATGACAUT
314433179	57556	CGATGUCCAGGAACCGCUAAT	57557	GGGUCGCACGTGATAUGGG
314816548	57558	CCAGCACTUGGCCCTGATUT	57559	CUTCACGTUCACACGCAGAC
321097146	57560	GTAAGAAAUGAAGAGAGGGCGTUGA	57561	CTCCCTTUCCTCAGGUCACAG
239529153	57562	GGAGAGTCAGACUTGAAAGCAGUT	57563	AGTGTCTCUGACTGGCAATTGUG
242606698	57564	CAGGUATAAGTTACTGUGGAAAGGCA	57565	CCATTGCTTTUGAAGAAACAGTTGTGUA
313845146	57566	CAGGCAGGCUCACCGAUAG	57567	CAUCCUGGAGCGCAAGAAGAA
312695397	57568	GGGCAGAAAAACCUGTCCTGUT	57569	GAAGGAAGAUGAGGGCGTCUAC
313866989	57570	CUTGACCTCUGCAAGAGAAGGAA	57571	TGCAGGGUCCACAAACUGAC
323393006	57572	AGGAGGGCUGAATGAGGUAGT	57573	CCUGGAGAGCTUCGAGAAGG
267999045	57574	TGGCAGAACACGCUCTUGA	57575	CCACCTGCUGCCCTACTTCUA
265574317	57576	CAGTGGGAUCCAGTTGUCGAA	57577	CGCCTTCATUTCTGAATCCTUCAT
313722590	57578	CCCAGGGACGAGAUCTACUG	57579	CTTTGGAGCCCCUGGCTAUT
313359217	57580	GACACCUGUGACAGGGACAAG	57581	CTTGGTGGUCCCATCCAUGAAT
312998982	57582	AGTCCAGAAGGCUTCAGGGUAT	57583	GGCATCACCUGAAGTAGTCAUAGG
223260051	57584	GTCTTTGCCCCUCCAATAGCUT	57585	TGCTATTTTCTAAGUCACCCTCTAACUGA
223708537	57586	ATCAGCAGCUGTTACCTGTTUGA	57587	CCACAGCAAACAGAACUGTTTUAGA
223491844	57588	GCACAGTCATUTTGGAGATCCUG	57589	TCTTTTTCCCUCAGGCTTTCTGUT
222591174	57590	GGCCUTAGCAAAUGCAAACAGAG	57591	CCTTGAACCGATUTTAGATGGCATCTUA
333417972	57592	CCATCCAAGGCAUCTTCCTUCT	57593	GCTGTGCCCAGUATCCCAUC
316820848	57594	CCCTAGGCUCCACCACUGAA	57595	CAAGCCCCUTACTUGCAAGACT
332860700	57596	ACTTCATCATCCUCTTCATCTGUGGA	57597	TGAACCUCACCCAUGCCAAAG
333532359	57598	CGTGUCAGCCAAGACCUAGA	57599	CTCCCAGGGACUCTGGAGUT
333654826	57600	AGGAUGACGAAAAUCGGCAACT	57601	TGCUTTGGAAAUGCCCCACT
318413942	57602	GAGGGUCAGTTGAATAUGGGCAT	57603	GGGATUCGGAAAGAGGTATCUGAA
319406049	57604	GGGATGGGAAUAGAGACATTCAUCT	57605	GUTGAAAAGGACUCCCAAGCC
332938038	57606	ACCAAAGAGGUATACCAACUCCGT	57607	TCACAAGGGATUCAGTGGAATATTGAUT
333489365	57608	CCCCACACACUCTGATACTATTUACC	57609	GGGAAUCAAGGCACCUCCAC
332653218	57610	CACTTACGAGUCTGAAACAAUGCC	57611	AGCCTTCGGTTUATGTCTTTTTGTTTUT
326772204	57612	GTCAGCTUATTATATTCAATTUAAACCCACC	57613	GCAAUGAGGGACCAGTACAUGA
318464518	57614	CTCTAGCAUAACAATGAGCCCAUCA	57615	CAACAAATUGGAGGTGGCUGAAC
278457765	57616	AGAGATATUGATGCCCUAAGCCAGA	57617	CCAGTGACACAAAAGUAGAATGTTCTUT
279368663	57618	CAACAAGGTUGGGTGTTTTGUGA	57619	ATTAGATACTUACCTCTCCCUGAAAGCA
279471719	57620	ACAAAATGTCTTAUTCTGGGAGAGUGAA	57621	AAATTACACGTAUAAGTCGACGAGTUGAA
258227924	57622	TTTGGGTTUGCAACGGATUGT	57623	CTGAACAGAGCCUCCTCCTTTUT
267209816	57624	CTCUTTGTGAGGUGCAGGGT	57625	CCAAGAAAGCUGCATCTUCGAAAA
317038561	57626	CATCTGGCUTTCCAGUGGAACA	57627	GCATCTUGCCAAACAGCTUAGG
315509544	57628	GUAGGGACAGAGGCGGUACT	57629	CGTCCTUAGCACGTGTUGCT
263080990	57630	GGGAGGCUAAGTGAACAUCAAAT	57631	GTTGTTTTTGUAGCCAAAGCCTUCT
260083191	57632	TCTTTGGTCUGAACCAGAATUCGG	57633	TGTTTCATTGGCUTGGTACCTTTUAGAA
264127655	57634	ATCATAAATUAAGCTGATGAAAAUCAAAGACAA	57635	GGGATCCCAAUGATATGTTUCGAT
264913863	57636	CCTTGGCAUTTGGTCTGUGGT	57637	CAGATAGCCTCUCCTTTATTTGAAUGGA
235678543	57638	GCTCCAAAGAGUAGACATTGTTTCUGT	57639	GCTTCTUGCCCACCAGAUGA
237759649	57640	CCCCTTAAAAUAACCATTGTCCCUCA	57641	ACCATGACCAGGUAAAAAGAATTTCCUT
264236629	57642	TGAGTTUGAAGAAACAGAAGAACCUGAT	57643	GAAAATCCTUACCAATACTCCAUCCACA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
313744557	57644	AGCTTCUGCAGCTGCTTCUT	57645	CCATGTTCCUTGCCACCTCUC
312869871	57646	ACTTCTCCAGCGUCTCTTTGAUG	57647	TCUCTTTTATAGUGCCCCACCCT
312751362	57648	CTCCCCCUGTTCTATGAGCUCT	57649	GCTGGCAUCCACTTTACCCUAA
312920942	57650	CCCAAAGCCAGAUACAGTACAAUCA	57651	CCCATGCAGUTCTGCTCCTUT
313551804	57652	GGGAAGGGAAGUGATTTGAUGCAA	57653	AGTGCTGATCUAGAATGGTGCTUC
315438581	57654	CCGCCGCAUCTTCUGGAA	57655	GUCUGACCAGGCACGCAT
313172110	57656	AGGGUGGAAGAGCCAACAGUA	57657	GAGGAGTUCACACGCCUCAA
314256238	57658	CCAGCGTCUTAGCTCTGCTUT	57659	GTGTCCCACCCUAACCATGTUT
313499518	57660	CTCTCTGUCCACCCAGGTGUA	57661	CTACCUGCGCAAGUCAGAGAA
257474353	57662	TGCACACATUGAGGAGTTGAAAAUACT	57663	ACAGATGTCUGTGGGTTGCUG
326401633	57664	CCACTUAGGACCCCAAGUCCA	57665	GGAAUTCTCACCUCCCCAAAGT
320063024	57666	AGCCACCAGCAAUAAATTTTTAATGUGT	57667	GGATTGCAGAACAGCAUGGATAUG
316885563	57668	GCCCCACAGCCUCTTGUAAAA	57669	CAAACGAAACUGATGCCUCCAAT
317383437	57670	ACAGAGUTTCTUGAAAGCCACAGT	57671	GCTCTTAAAATTUCCTGACATCCCCUT
320453234	57672	CCAATGAGGUTCTTGCATUCCAT	57673	CAGAAGGAAAUACAGCCAGTAGUGAAA
316662549	57674	TCATCCUACCAGGACCATTUACCA	57675	CTTAAAGCACACACAACUTGAATTUCCT
315530577	57676	CACAGAGCUCTAGTGCCAAAUGA	57677	CAGACUGCAAGAATACCAUGGGAT
316229767	57678	ACAAACACACCUGUACAGCCA	57679	TCAATGAGTGUGACCTGAAUCCAAAT
326512150	57680	AATCTTGGGTTTUCTTGCTTGTCTTUC	57681	TGTACATTGCUCCCTGGCTUC
316887927	57682	TCCGACUCACCTGTGAGGUAA	57683	AACUTCCAAACCUCCGACCAG
333261943	57684	CUCTUGCCCCAAACAAAGACA	57685	CGCAGACUCUCCGCAGA
240579169	57686	CGGTTCCUGAGGAATUGGAAGT	57687	CTTTCGGACCUGGTGGTCUT
241388327	57688	GGAGCUCAGGCTUGCAGAG	57689	ACAGGACGGCGAUCTTGUG
319919866	57690	CGGACUTTGUGGCGGAACT	57691	CCTTGCGUGGAGAGCTGUA
321340389	57692	GCTGGCUCTGGGUCAGGA	57693	GCAUCTAATGCCTUCGAGAACCT
235190727	57694	TCATTACCTGTTCUTTTGTCTGAGCUT	57695	GCACTCACGAUGTTTCTTTTCUCCA
262513284	57696	AGCAAGTTUGCCGCCTTTUG	57697	CGTCTGTGAUGTCAATGGAUGCT
267440413	57698	GAGGTGACGUCAGGGUCAAT	57699	GCTCAGCTTUGGGTGATGTUC
327855147	57700	TCCTCTUAAGCCCTGAUAGCAGAA	57701	GGTUCAAGCCCTGCUAAGGAG
321626283	57702	CAGTGGCUATGTCCUGGAAACT	57703	GGGCATGGCUCACATTCTUAA
260633502	57704	GAGGAAUGAGAACCGCTTTTGTUT	57705	CACCGTTGUTGTAGGACUGGAG
268900932	57706	ACACAGGGCACGAUGAUGT	57707	CTCTUCAGCCCGCTGUCA
266823400	57708	GCCTCTGTUCCCATCTGUACCT	57709	CGATTGGCAGAACUGTTCGCTUA
269079316	57710	GGGAATGCUGACCATCUCCAAT	57711	AGCGGUAGGACTTGCATGUG
266793340	57712	GAAGAAATGGAAAAUAAGGTGTCAGUGG	57713	TGACTGGTTUCACAGGTGATTAGAAAUG
262627462	57714	GCAGGTTTAAGAAGAUCATTCCCAUCC	57715	GCTACAGACTUCAGTGTGGTTGUT
266789389	57716	ACAGTCCCUCCAGUCACAACT	57717	ATCTGCCAUGGCTTTCTCTCUG
268362473	57718	GAAGGCUGCTAAGGUCACCAT	57719	CACATCACAGAACACCUCATAAAATCUC
265784843	57720	TTCTGGCAGAGAUTTTGTUGAAGAGA	57721	CCCCAAGAAUGAAAGTGCAUGG
325569229	57722	GAAGGCCUCAGATGGCAUCA	57723	CACCTGCCUCCTCCTUCAC
236487854	57724	TGCAGCUGAACTTCGGAATUCT	57725	TCATATTACTTCAGUAGTCCCATGUGGA
236044556	57726	AGTTGCAAATATAUGTCTTCCACCCUT	57727	GCTTCAGUGTCAGGGTUCCA
236362724	57728	GCTGCUGAAAGCCTUCACAAGA	57729	CCATGGGUGGGCTATAGGUT
236397974	57730	TCCTGCTCTGUATCCAATGCTATTUAAC	57731	AGGCTTATTUCAAACAAGTCACTCTATUCA
236226704	57732	TGAACCTTTTGAAUGACTGCAGUGA	57733	CTCTTACATGCCAGUTCTCTAGGTUT
236762074	57734	CTCCTGGATCCUTTATTACGAATTGUGA	57735	GGAGAAGGUGCCTTGCTUCAT
236391839	57736	TGCTGTTTACAAAUCAGCTGACAGUA	57737	GACCCAGGUATGCAAGAAGUGT
235870627	57738	TGAGCCTTUAAAGAAAGCTACTGUGT	57739	CCAACCAAUGCAAAGTTAAAGTUAGAGT
235938675	57740	TCAGACACAAAGGCUCCUAAAAGG	57741	CATGTACTCUCCCACCTTATTTTCAAUGA
241696389	57742	CAGUCTTCTACTTCUCACCCAAACA	57743	GCACGAAGGUGAATTAAAAUCAAAAGGA
312964666	57744	GGCCCCUCTAAGGTGGAUCT	57745	AAAGCTCCCUCACTTCTGUCAC
225525720	57746	GGCTAGCCCAUCTCCUAACACT	57747	CAACCTGGAUGCCATCAAAGUC
253712235	57748	GCTCTGGUGCATCATUGGGT	57749	CCCTCTGACUGTTCCTATGTTCUCT
262170042	57750	CGCGGCUCCGCTAUAAAAC	57751	GGGAGCUCACCUGCACT
333087187	57752	CAAAGCAGAAGCACUGGAGUC	57753	TTCTCACCCACAUTGATGAACUGAA
265908185	57754	CCGAGGGUTTGGGAGTAUACC	57755	GTTAACGTAGUTCTCATCTTTCUCCACT
264411200	57756	CCCCTTCCACUCCTTCTTCAUCT	57757	CTTCCCTCCUCTCTCCAGUGT
258636120	57758	ATGTTGACAGCGUCGCCUA	57759	CCACCUGGAGCGGUGAAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
262814213	57760	GCATCCUGAGGAAGUCACAACC	57761	TGAGGAGGACUGAAATACGGGUAA
264153229	57762	GCCTCUGAGAGGGAGACCAUC	57763	GGCCTCCUACATGGTCTUCAAC
263131954	57764	GCGUGUCACCGGAGGAT	57765	GGUCTCTCUGCGGGCAAC
316874237	57766	GCTACAAGCUGGAGAACCUGA	57767	GGTGCGUGGGTGUCGAT
316798518	57768	CCATCCCATUCATCACCCGUAT	57769	TCTGCAGGUCGTACCATGUG
331431503	57770	GGCCUGCACCAGAAUGAAGAT	57771	CCTGTAACTAATUGGTGATTGTGTCUGT
330446161	57772	GCCUGACGAACACGCAGUA	57773	CTTGGCTCTUAACCTCCACCTUC
269321884	57774	AAAATAGATTTGUAGGCCACTUAGGAAAACT	57775	GGCUGGCCACCAUCACA
257886170	57776	CGCATTATAAGCGAAUTCATCCTTUGT	57777	CUGGGACGTCUAAACAACCAAAAG
264122906	57778	CATTGTATAUGAAGAACAGAGCATTUGCAT	57779	TTTTAAAAUTGTAACAGAUGCCAAAACCA
267139048	57780	GGCAGTGGAAGUTCTGGAGUAT	57781	CAGTCTCCAAGTUAAAGCCAAAATGAAUT
268256788	57782	CGTACGCCCUGCTGCUT	57783	GCCCCAGGUCGGATCUC
269338777	57784	CCAAACAGUGGCCCTTUCAGT	57785	TTCAGGACCTCAUTTCATAAACTCCTUT
266682354	57786	GCAGCCUCTGACCTCUGA	57787	AGUAATGAUAAGGACCCCACCCAT
267820329	57788	GGGTGAUACACAAGCCUGACC	57789	GGTGCTGAUGTCACCGAUGAT
255340014	57790	CTAAACTTAGTCUGGCAGGAGTUAACA	57791	TGGAAAGAAATUGAGAGCAGCTAATCUT
321490032	57792	CGCTGCCUGAGGACGUA	57793	GGGTGUGCAGTCGAGGUG
332989606	57794	GGTTGGGUCGGTCTGAUGAT	57795	CCAGCCCAUCCGCCTUAC
325336715	57796	GGTUCCGCAGGACGAUGAG	57797	CTCCCAGAACCCUCTTCTTUGG
324801285	57798	CCAGATGAAGUTGCCAGAGUCT	57799	GCTCACUGCCATATGCATTUCCA
324315447	57800	GCTCCAAGCCUTGCATTGUCT	57801	AGGCTCAUGGTGTCTUCCAC
324572657	57802	GGGTTUGGGAGGCTCTGTUAC	57803	AATCATGGCCUTCAGGGACUC
323623482	57804	GAAAATCGUGCGCAGAGUCC	57805	GATCCATTCUAAGCCTCGCCTUA
323417699	57806	TCGTGATCCCUGATCCCTUCT	57807	GCGAGCTUCATCATCATGUGG
324007061	57808	CGATGAGGAUGAGAACATGGUGT	57809	CCACCTTGAGACAAUTATAGCCAAUG
325754060	57810	AGCAGCCCCUCTGTUCCT	57811	GCTCUCCCAGAGGCUCAC
325600212	57812	GCCUGAGGGAGGGAGAUG	57813	ACTATTGAACCUGCCCCAGGUA
323670726	57814	CCGACUGAGCCTCCUCCA	57815	CCCAGCAGUGCTCCUCAAC
269372351	57816	CAGCCTCAGAGUCCCCTTUG	57817	GGCACCAUGGGAGAAAGGUA
319640980	57818	GGAGGCCUGCGACAUGG	57819	CCCCCATTCUACAGAAAAGGAUGT
318627342	57820	AGCAGGCCAACCGUAUGAG	57821	GGGCUGAATGGAUGGAAACGA
321180560	57822	TCCAGCGUGGCCTUCAC	57823	GCTGGGCUCTCGTCUCT
317436626	57824	CAGUAGAAGGCCGUCACCAAG	57825	TTTTGTTCCUGCGATGATGCTTTUT
316818203	57826	ACAGGAAUGTAAGCUAGGGAGAAGT	57827	CGAGTGTCGGUCTTCCAGUC
315605134	57828	GTGAAAAGUCAAATGGTGACUGCAA	57829	CAGTCCCTAAACUTGAACTCCATTUCT
333700445	57830	GAGTATTGACCUGGGCTUGGAT	57831	CCTGGTTUCTCCTGGTTUGGT
333239432	57832	CGCCCACCUTTGATGCUGAT	57833	GGACGUGCTGACCGUGAG
316047572	57834	AGAGAGCGAGCAAGCUTATUGG	57835	CCAACAACGUGGTGTAUAAGCAG
324695579	57836	GAGAAGUTCTUCCCACACCGT	57837	GGTTGGATGAUAAAGGTCTGGCTTUT
324491411	57838	CTGGCGCUGCAGGTUAAAAG	57839	CTATCTGCCAUGATGATGTCAUCGAA
326032331	57840	TGCCTTTGGCUAAATAGCTTATGUCC	57841	ACTTCUCCGGAGCTGTACUGA
254583300	57842	GCAGUAAGTACAATUGAGAGAGGCT	57843	TTGATTTGTCTUGTTTGCTTTCTGUGT
257296281	57844	GGUATGGTGAATCATUAGGAACCAAGA	57845	CAGGGACCAAAACCUGCATUG
262748851	57846	GTCCCAGCAGUCACTGACUC	57847	TTCCCCAGGUGGACCTCTUA
253754549	57848	GAATTGTTATUCAAAGGACGGCGUT	57849	GAGAGCTGGTAAUTTGGTCATTGTTUT
315946288	57850	CCUGGGACCCCGAAGTCUA	57851	TCCCAGGAAGGAGAUCCAGUG
323928176	57852	GGAAAGCGCAGAUGAUCCACT	57853	AGCGCCUGAACTGGATTTACUAC
324347691	57854	TGTACCACAAUCAACCTUAAAGGAAAGT	57855	TGGTGATCTGAUGCTTAAGGATGTAATUT
266085870	57856	GCTGCTTACUTACAGAGGTUCCA	57857	AGACAGTUGGGTGAAGTUGCAT
269250065	57858	GAGAUAACCACAGCAGCAGAUGAT	57859	TTGGCTTATGCCUTGAGAATTATTUACCT
267658590	57860	GGGTTTCTTTUTCTCTGATTCAUCCA	57861	CTAACCAATAAUGCCATGGTATGTCUCT
266987101	57862	CCTGAGGCAUTCCCATCTUGAA	57863	ACCACACCGATUTACCTAGAGTTCUAAT
268830022	57864	TTGTGTAGAAAUGACAAGTCTCAGAUGAAA	57865	CGCCAGATAUCAATTAGGCAUAGAGAAA
323695150	57866	GATATCAGTAGTTUCTCCAAGGCTTUCT	57867	CAGTTGCCTTUCACTTTTCTGTUGA
316706637	57868	CAGGCAGTUGGCAGTTGAUAGA	57869	GCTTTAACCUATGTGCTCCUGCT
314768712	57870	AATAGAGGTGTUGTTGATAGACTGUGG	57871	CAGCCTCAACUACACTCAGTTCAUT
300286979	57872	GATGAACATTUGACTCAACTUGAGAAGG	57873	CGGATTTGTTAACAUGCTCCCAATUT
255892050	57874	CAGATTCTTCCAGGAUTGTCTGTTAUGA	57875	CTTGCCTGCCAAAUTTTGCTTATTTUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256635386	57876	TCCTCTATAAGGAAAAUCCCCTTTUGGA	57877	CCAGAGGCUAACTCGGAGACUT
265914980	57878	CCAGAGCAGACAUAAACGTUGG	57879	CATGGCTTAAUCGGTAATAGGCUACA
264817582	57880	ACGAATCAACAUGCAGAACTCUCC	57881	GCAAGGAUGGGTCTCTTUGGT
317155746	57882	GGAGACCTUGGTTTCCTTTGTUGT	57883	CCCCAGCUGGAAATTCATTTCUT
315539833	57884	AGGGCTGTTUCTAAACAAGCTUCT	57885	GCAGGTTATGAGUACCTCTGCAUT
259736232	57886	GGGTTUGCCTGGTGAUCCT	57887	CATTTAUAACTCAAGCCUGGGAGAAGAA
262026705	57888	GTTAGAATUGCAGTTCTGTGTUGGAA	57889	GGTTTACCAGAAAGUCCTGGAAGUC
318493251	57890	CCACCUCCACCCTTTTCAGUG	57891	CTGCCCAGAUTGGGTATTTGGUA
332672775	57892	CCTGTTGUAAAAACCAGAGGAAGUAGA	57893	AGTCCTACGTUAGGTATATGTTGCUAGT
312985846	57894	CAACAGGAGGAGGAUATGAAAGUGAT	57895	TGCCTTGATATGUTCTAACCAATGAGUAG
266780488	57896	GGCCTTCUCGCCCAAGUT	57897	CACACGCUTCCCUCCGT
263681849	57898	AGCGCUGTCACTUCAAGAGG	57899	TGAGUGAGGGAGCGGGAAUA
313126759	57900	CTCCAGGUGGTAGGAGCTAUAGG	57901	CGAGGTCUCCTGTTCGCTUG
313765729	57902	GGGCTCAGGUGGAGGUG	57903	TCCACCCUCGGUGAGAAGA
313814965	57904	CGTTTCTUGGGAATGGCCUGA	57905	AGAGGGUGTGCAGGUGAAAAG
263887764	57906	GCACCTUCACCCGACTUCGT	57907	TGGTGAAGTAGCUCTCTTCATAGTAGUC
268839688	57908	GGCUGCTTTUCAGGACCACAT	57909	CTCATCTTUGGAGTACGTTCTTUCCA
316038176	57910	TTGGAATTAAGUTTGTGGAAGCUAAGAGT	57911	CCAGCCTCTACAUCTCTCAGTTTAUCA
315992566	57912	GAGCCCTGCAGUTTCTTTCCAUA	57913	ATAGGATTGAUGTCTTCCCUCCCT
316787247	57914	GGGACAUACACTGAGAAUGAAACC	57915	GACCCGCTATUACTCTAGTTTCGTUAAT
315689861	57916	CCUCTTTCAGGUGAAGGAACACA	57917	CACTGTGCCTUACCTACTCATATCUT
318415853	57918	GGAGGAGAAAUGGTCACTTUGCT	57919	GATGGCGCAUGACACACUC
315466772	57920	AAAAGTGUGAGGCCTGAAGGTUA	57921	GCTCUGCAAGAAGGGCTUGAG
266798459	57922	TGAGCUCAGCUAAACACCGA	57923	ACCCCAGGACUCCAATGUCT
265846516	57924	CTTTCTCAGGCUGGGTGCUT	57925	TTCAACACCCUGTTCTTTCTCTTATUCA
268004777	57926	CCACAGGGAAUCCTCATTUAGCA	57927	CACCTACTCACUAACTTTTCTGTTCCUT
266630393	57928	TCTACATACAUCTGGGAAGCUAAGGAT	57929	GTTATTATTTAGGGACCUCCTGGCTUAC
267830700	57930	TGCCTGCAGCUTACACACATUA	57931	GGTTGGTTUCCATCCAGATTTUGAAAA
261551842	57932	TGGATTTTCCUGCATTTGCAATTACTUT	57933	GTCATTCUAGGGTCCTGTUGGT
268158870	57934	ACGTAATCCUGCTGGTCCAUC	57935	GGCATTCCACCCAAUATTCTCATCATUA
267677208	57936	GGCTCTCTACUGAGGGCTTUT	57937	GGATTTCTTCATUGAAAGAGGCATGUT
266666016	57938	CTTGATACAGAGUCAGTCATCTTGUGG	57939	AGCACGTAAUTCAACATGTTUGACAAA
264825721	57940	CCATATCACTGAAAUACGAAGACCTUCT	57941	GCTAACTGAATCUGTGTCTGTTTGTUT
268922081	57942	GTTACTTACUTCCCGUCAGCGA	57943	CATGGTATUCAGCAAATTGGTGTUGAG
332746718	57944	TCTCAGGCACCUTTGGTGTUC	57945	TGGACAACACACUGCTATTCTAGACUA
317382145	57946	ACACTCTGCUCCCAGAACTUG	57947	CAAGGUCCAGGATCAGTUGCT
314619747	57948	GCAAUACCAAGAAGGAGGGUGAC	57949	AGGTAGAAGAGUGAGTGTACATGTGUT
312718145	57950	CGGACCCAUCTCCTCUGG	57951	CCTCGUCCTACCCCUCGAT
323981816	57952	CCTGAAAUGAGGACTGCCAUGAG	57953	CATCCATCAGGAAAUGGTCCTUCA
320100123	57954	GACTCUCCGCCCCCATTUAA	57955	CCTACGGCAAGUCGGAGGUA
314038850	57956	GGAGUAGTCUCCGCCCAGAT	57957	TTCTTTUCCCACCCCTCCUAGT
328020912	57958	ACCAAGGGCUCAGGCAAUAG	57959	CCTCCAGUGAGAACAAATGGTGAUA
326922409	57960	GTGGTTAGATGCAUAGGGCAATTAAAUG	57961	AAGCUGUGAGAGCCAGAACAAA
327141073	57962	CAAATTTCTCACUCTCTCTGCTTCUCA	57963	GAATGCCGUACTCCACCUCAG
327820506	57964	TGUATUCGGCCACCACAACA	57965	GTCTCAGATCUTCTATGCCTUACAAGAA
328406936	57966	GCATATGATCCUGGAAAAGTTCTGUACT	57967	AGTGTCACAAAUCCAAGTTCAAATGUG
327470601	57968	ACAATTCGCTGAUAACTCTAGAGGUCT	57969	CAAGAGGTUCAGCCACCAGUA
328423185	57970	CCTAGGTAGAUGCAGGCTUCCA	57971	GCCAGTGCUGAATTTGTCAAUACAAG
326945226	57972	AGATACTGCUGCAGATTTTGUGAGT	57973	CAGTAAATGGTTUGCAACCTCCAAUAAA
324573198	57974	CCCCTAGCAGGUCCAGAAUCA	57975	GCACCACCAAGAAGAUGGUCAT
324426887	57976	CCATCACGUTCGGGCUCAT	57977	CCAATGAAAATUCCCTGCAGCTUG
324938023	57978	CCATAGACAGUTCCCCATGTTUAAAGG	57979	AGCTGTCTUCATCAGAACCUCAAAG
323688646	57980	AGGTCCCAUTGGTTATTTTUAAGCGA	57981	CAGGAACUCCAACCAAATATTTTCAUGT
326331347	57982	TCCTACATTTCTAAUACCTGGTCCTUGT	57983	AGCAGGAGACAUTTTTGTTTATGUGAGA
325173321	57984	GAACCAAATAAUAGCTGCCCCUACA	57985	GGAAGAUTCUGAAACGGGCACA
239514182	57986	GAAGATTTACUTCGTCGATUCCCAGA	57987	GGACAGCACATUGCCAAGTATATATUG
262275499	57988	GTGCCUGAGAGATGAGCUACC	57989	GAGGAUGTCAUCCGCAGGAA
267816153	57990	GCCTCTCTTTUTGGCTGGAAGUT	57991	CAGCCCUGGGAAACCAAGAUAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268870324	57992	AGAGGGAGGCCAACAUCUAC	57993	AGAATGAGGAGAGUGGCUCAGAA
328218034	57994	CGTACUTGGCCTUGAGGAGAA	57995	CATTCCTTTUACCCTTGCTCCUGT
327007949	57996	CTAAGCGTCTUCTAAGATCTTGGUAACAA	57997	TCAATGCAGAAAUCGTGCUAGGAAA
326725229	57998	TCACUGCCCCAAGAGCAATATUC	57999	CCAACTATGAAGAUGTAGCCACCTTUC
327802232	58000	ACAAGGCTACAUTTTGGTCAAUGGT	58001	GGGAGCCACUTTATGGCCAAUA
268945734	58002	CCCTTCTCUGCTCTGGTAGGUT	58003	GGAGACTCTGUCTAACATTTTCCTCUCT
259305365	58004	GCAGTCAACAUTATGAATGCCTTUACA	58005	ACCAGUGTTTCCGUGGAACAT
261828979	58006	GGCTTUACAGAAACAGTTGTTATUCAGAA	58007	CGGGAUGGTGCTGTUGGA
268716349	58008	AATGTCATTCTUCACTTTGGGACUCA	58009	TGTCTAATACAAAAUGACGCCAAACTCUA
258061602	58010	CACGCTCTUCCTGAGGCTUAA	58011	CUTTTCACTCUCAGGAGAACCCA
239878384	58012	GCATCCCTAGUAAAGGGCCAUT	58013	CTTTTGAGAGAACUCATTACCCUGACAT
268638293	58014	GCTCAUCCCAACCTCATGGUC	58015	GCTCCTTGTUGTAGCCCTTCUC
264883903	58016	GACCCCTACUCCTACAACGUG	58017	CCTTGGACUCTTCCCCAGUCT
236155884	58018	CTAUAAGCCCAGGAGCACUCA	58019	GGCTCTTTUGGAACTGTTTAUAAGGGT
263574210	58020	CCTTGTUGACCGCTACCGUA	58021	ATCCAGGCAGUTGGGUACAC
272373477	58022	AGCAGAACACUTCAGAGCAGTUT	58023	GTACTCCTGUAGGTTGCCCTUG
232266922	58024	CACAAAGUTAGTTTAUGGGAAGGAACCT	58025	ACCATTCATTTUGAAGGCTAGGGTTTUA
234252676	58026	ATUGCAGAAAGAGACAUCGGGAA	58027	CTTGGCAGUTGAGGCCCUAT
325186083	58028	CCUGCUGACGGAAGAGGAAG	58029	TGAAGATCCAGAUGGAGGAGAAGUT
325244501	58030	GTCTGAGGAUGCGGCCTAUT	58031	CTCCTTGGCUCCTTGCCAUAT
325694022	58032	CATGUGGCACGAAAGCTUCC	58033	GAATGAGGTUGGTGCCTTCTCUT
323496961	58034	GGAGGAGGUGGGCAGATATCUAA	58035	CAGGAUGUCAAGGACCCAGAG
314382701	58036	CCACTCTGGGAUCCACTCACUT	58037	CTCCACATCCCUCTCTGTACTUACA
256522995	58038	GGCACACAAAUATCACACCTUCCA	58039	CCCAGATGCUCTTGTGTTTCUGT
264232568	58040	GTGAGTTTUGCACACTGTTGGUAA	58041	TCAGAGAAGCAGGCUTATTCATTUCAA
258999683	58042	ACTTGAAGGGTAUTTTCTAGAGCGUAGA	58043	GCCATTAGGCAUTTCTTCCCATAGUA
260884572	58044	GGGUAGTACUGCCAACCAGAA	58045	TTTGCTCTGTATCUTCTCTATCCGTTUG
229282611	58046	CCCTGUCCGCCCCTCUAA	58047	CGUCCCCAAGGACUCCGA
227627917	58048	GACGUGCACAACCTCGACUA	58049	GCCUGAGCTCUGCAGGAC
318304844	58050	AAGAAAGACACCUAGATTTGGUGAAGG	58051	TGCAACAGCTTTUCTAGGTCCTAATUT
319611118	58052	CCAGCUCUCAGGGAACAAGAA	58053	CCCTCACCAUCTTTGTGCTTATTUG
318526120	58054	TGTGAGACACUCTTCATCAGCCUAA	58055	GTATTTCTTTTGTAUGTGTCGTTGCTGUA
319028640	58056	AAAAGGAUAAACAAAAAGGCATGTGUCAT	58057	GCTGTGCCAAGUCAGATTUCACT
333430694	58058	TGAAGTTGAAAAAUGCCTGCACAUT	58059	ACATCAGGGAAAAUCTGAATGGAAUACC
332992835	58060	AGTCTGCTGTAUATTCTGATGTCAAAUGG	58061	TGCTGUAACAGGTGCTUCACA
332963013	58062	CCGCCUGGGUAAGACAGAAAT	58063	GGTCCATGTTCUCATGATGTCATTCUC
333114117	58064	CTTCAGGGCAGCUAACCCUA	58065	CACCCTATGCCUGTAAATCCTTTUCT
333702952	58066	TTCTGGCUGATAGATTGUCGACAG	58067	TTGTTGTTCAAGGGUCTTATCCACTTUA
333683550	58068	CCCAGATGCUGACTGTTCAGUAG	58069	ATGCUTGATGGAAGUGGAGAAGG
333020969	58070	TGCCTTTAGGGUTCTCGGUACT	58071	GCCATCCUGAAAAGTGGAAUAACCA
263033035	58072	CAATCCAAUGCATCUCGCAGA	58073	GTTAACATGUGCTTTGAATGTCUCCAT
261999071	58074	AAATCACTCAAGUGGATAGAGCTTUCAT	58075	CUGAAGAAAAACUGGAAGCAGCAAA
262342591	58076	AGCAGTAAAGAAUACCCATGCUGAAA	58077	ACACTACTUCAGAGGTCAUCAAGGA
268686664	58078	GGTCTTGGGUGAAGATTTUCAAAAAGG	58079	CAGCATCGUGGACATCCAGUT
264767138	58080	TCAAATTTCAAUACACTGACCUGAGCA	58081	GAGGGUGAGACGATTGAATUGGA
267692304	58082	GGTAATCGCUCTGAGAGCTTUCT	58083	AAATGGGUGCAGTACCTTUCCAA
267851182	58084	GCCAGACCCUCTTGACAUACCT	58085	CCTGAAAGTACAUTCTTGTGTGAGUAGT
265960351	58086	AACATATTAGCACCAUTACACAATTCUCA	58087	ACAATUGAAGGGCUGGAAGACA
261869051	58088	CGACCTUCAGCAGTTTCGACUT	58089	TGCAATGGCUCGTGTTTTUCC
262992709	58090	GGCTCUGAGAGCAGGAAUGAAG	58091	CTTAGTAGTTGTGUTGCATTTGAGGAUG
320045944	58092	GAAGTTTTGTAGGGUTGATTGAGGTUT	58093	GAGAAGGCUCTTTGTAGTTGUAGCA
319806304	58094	CACTTTAGGGTUAAGAGTATTATAGTTGTGTUT	58095	GGCATGGUGGACTCAATTTCUG
290465592	58096	CAGCGGATGCUTGTCTTACAACUA	58097	TCCATGAGGAUCTAATCTGUAAACAGGA
290410937	58098	GCCCCCAAAUACGTAAAGCTGUAT	58099	GCTTACAGTCAUGCCATATTTGATGAUG
290512899	58100	GAACATCUGGACCCTGAUGAAGAA	58101	GCGAAATACGUTGACTCCTCCUC
225051160	58102	CTGGAGUAAAACTGCGGUCAAAA	58103	AACTGGAGUACACAAGGCAATGTTUA
329251859	58104	CGCTCAACTUCAGAATCTCACUAAAAGAA	58105	TTCAGGCCUAAAGTTGGGUAAAACA
224557361	58106	TGCGAAGUACAAGGATGCCAAUA	58107	CATCATGUCGATTGGTGUCAAAAACAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328332408	58108	GGTGGAAAAGAGGCUGCTUCA	58109	CCTTCTTUCTTTCCTGTUCCAGCA
242556489	58110	GCAAAAGAAAACUGAATCAGCTUCCA	58111	AGGATCAGATTGCUTAACCTTGCTAUC
263433315	58112	TGATTCTUGAGGAAAACAGCGUGAT	58113	ACTTTCTTGTTUCAGCTTATTGAGCUCT
266156664	58114	CAAACAGUAGUGCGACGGAGA	58115	TCCTCTUGCAGGAGTCTTCUGA
268470117	58116	TGTAGTAGACCCUGTGAACAGUGT	58117	GCTTCTCUTCTGTACUGAAAGCA
267524436	58118	CCGAGAACUCGAAGCCCUT	58119	GGAGTTGAUTTATTGGCUGGAAAGGA
331719583	58120	GGTTTTCCUGGACCCAATAAAUCAGT	58121	CGCAAGUACAAGTTCCTGCUC
331743322	58122	GTGGTCUCGGCTTCATCCUT	58123	GGGCAGCAUCGTCCUGT
331562527	58124	CACCCGUCACCCCAAUGA	58125	GCCTGTCCUGGACGGUT
331761805	58126	CCCGTCCCUGTCCTTGUACT	58127	CTCACTCTCUCTTCCTCCTTCUCA
331789693	58128	GGAGGCACAGGUGTUCCA	58129	GTTTGACTCCTUTGTGGTCCAGUA
257852819	58130	GGAAAAGAAGAAAGAGCUAAGAAGUGGA	58131	TCCGAGTTUTCTGCAACTUCACA
267576981	58132	GAAGGCAGCUAGAAAGGUGGA	58133	ATGAGCACUAAAGGGACACAGTTTUAT
259630541	58134	GACACCGAACCUCTGCACTUA	58135	CCTCACTCUGGCTATCCTTCCUC
268657633	58136	GAGACUGAGCTGGUGAACAGAT	58137	CTTACGGCCAUCCTCTCTTCUC
267379955	58138	GGTTCCTGAUTTTGTGGCCUGT	58139	CGCTCCATCUCTCTCATGTCUT
327222376	58140	CCCAGATCUCCAGACAUGCAAC	58141	GACAGGCTGAUCCCTTTGCUA
314750284	58142	CCTTGGTGCAAAUTCATCAATTGUCA	58143	GUGGATACCATAUGCAGGAAGCA
269731439	58144	TGTTACCTGUGAAAAGTTACCTGCUC	58145	TTGCTACCAUAGGGATATGTGTAAUCCT
271111052	58146	GGAGTTTGATCCAUGAAGCAGACUT	58147	TTCTTGAUAGCGCTGAUGCCAT
271508805	58148	ACGAGATAACCUGCTCCTCTTUCA	58149	ACAACCACTGUCAATTATGTACGUGAT
271900199	58150	CATAGCCTCUGACGTGGTACUC	58151	GTTAUAACAAGGCCTTUACCCCAGAA
316190205	58152	GTGGACAGCAAAAUGATTTGAAATTCUG	58153	CACTGGGUGGAAAGGATCATUCT
315877280	58154	GATCAACGTTUGAGAAAGAAACAUGACA	58155	TTCTTTCCATCUTTCAATGGGAATUCCT
317608095	58156	GCCACCGCAUTTAAAATGTACTTUGAT	58157	ACCATGTAAAAATAAUGGCAGTTGCAUT
317656341	58158	AGTCUGCAGCCAAAAAGTAACUGA	58159	GCTGGTTUTTGGGTGUAAACACT
263016530	58160	TUGGTTCCACAUGGGCAAGAT	58161	CTTTTAGAACAUTTTGCTGAGAUGGCT
268872668	58162	AAAGTGCACUGTGGTACUCACAA	58163	TGTCATUGGAAACCAAAGCTAAUACAGA
269086259	58164	AAAATACAACAGATUGTGTTTGGCCAUT	58165	GGGUACAGGAAACAAGATGCAUGT
325640801	58166	TCUAGAGCCAAGACGCCUCT	58167	AGGATAAGGUGTCCCAGCTUCA
319380256	58168	GCCAGGUGACGAAGAAACAGUT	58169	CCCTTUCAAGCACGTTGUCA
268463531	58170	ACGUAACCCCACAACTCAAAUCA	58171	TGTGACCATTCAAUAACCACAGATUCAA
269352958	58172	GAAGGAAGUAAGCTACCTGTUAAACAGT	58173	CCAGGTATUCAGCGAGAGCTTUT
313387801	58174	CGCCGTGUTTGGTCGAUAGA	58175	GCAUGTTATTCAUGACGCCCAT
326640262	58176	ATGGATGCTTTCUTCCCCGATTTUA	58177	ATTTCTTAAGGUGCGTTTTCTTCAATGUT
328268305	58178	GCTACTGAGCUACACTTCTTATTACCUC	58179	GAAAACAGATAGUGACCCATGGTAUGAA
327996565	58180	GAGGAAAAGUGAAGCAATCTGCAAUA	58181	TGGATAAATTTTCTCUATTTGCTCAGGAGUT
266328864	58182	CCTGGTGACUGGGAACCTTUT	58183	CAGATGGAGGUGGCAGTUCAG
227982516	58184	GGCTGAGCUGCTGCTAGUAAC	58185	CTTTCTTCCTAUAGAGTCCCTGTTUCC
228482106	58186	CUACCAACCCACCAACCUGAAAT	58187	CTTCUGAGCAGGAGAUGGCA
332757193	58188	CTAGUCAGCCAAGGTAGCAUGT	58189	AGGATCTGTTGUTTGGCTTGTAGUAAG
222664072	58190	GACTGTUGGAGAAGAAAGUAAGCAAGA	58191	TGAAGGTGAAACCUTAGTGTGAAAUGT
223252989	58192	TCAUATCCTCTTUGCAGCAACAGT	58193	TCTCTTUCCAGCAACTTTGCTUAAGT
223931667	58194	AAACCACATTCCUTTATTCTTATGACUCA	58195	CCAGTTCTTCTCUAAACTGTTCTAATUGCT
223500523	58196	CTGAAAAGCUGGCCTUGGAAC	58197	TTCCACACTTUCACGTTCTCTCTUT
222474372	58198	CTTAATGACACAUTAGCAAGUGAACAGA	58199	TTGACATTTTAGAUGGAGGAAAGCCTUA
333329500	58200	GCGTAATGUCAATTGAGATUGGCT	58201	CAGAGGCAAUGATGGCTTCAAUG
223662377	58202	CAGAAAGTTTUCGAAAGGCTCUCA	58203	CCCTTUGGGCGATTGGUGAT
319651668	58204	GGGCTGGTUAGGAGAGAAAUCA	58205	CGAGATCCTUCCAGATGAATCAAAATUC
321489868	58206	ACTTGTATUGTAGTCTTCUGCAGCAAA	58207	CATCTCTGTTUCAGTACTAACTCUGCAT
321113959	58208	GCTTTGGAGAAAGUAGCTTAACTAGCUT	58209	CAGTCAAAGGTTGUTCCTCTAGACAAUA
321112524	58210	GCTCAAGAAUGCAGGCUGGT	58211	AGCATTGGGTGUTGGAAATGATTAUAGA
263048367	58212	CAATCGTGCUCATGTTGATATTUGGT	58213	ACTTGTTTTACUCACCCTTTCTCCUG
267616770	58214	GAATGGTAAGGAAUCGAGACATTGCUA	58215	CAAACAAAAUTCTACUCACACGAGCA
269226333	58216	CCTCCTACUCCTTGGTCTATUCCT	58217	TTGGCTAGAGUAAATGAAGACACGTUT
267975036	58218	CTCTTAGTATCTGAGUCCTTCTCCACUT	58219	GTTCTTGCAGUGGTAGGTGAUGT
323331968	58220	GGAAAGACUAGAGAAGACTTTGTCCUT	58221	CTGCTCTCUGATTCCTGUGCAT
325065061	58222	AGTTAAACCACTUCATTAGGGCAAGUT	58223	GGAGAGUCACAGCCAUCGAC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324366515	58224	GGACCTTTUCCAGTGGUGAGT	58225	TGTATAATUCCAACCAGCAGAGUCAG
260127814	58226	CCAGCACCAGUTCGTATTATGUGT	58227	GATCAGCAGTTUCATTTCTTAGACCUAGT
264629187	58228	GCCTCTCCUGTTCCTTCUCA	58229	GTCGUAAGGCAGCUCCGA
314035627	58230	GTGUGAAGACAGCCGTGUAGAT	58231	GCAGAGAUGTCATCGCUCCT
318791036	58232	ACTGAAGCUCATGCGUCGAG	58233	TGACTGCAUCCATTCGTCTGTUT
315535014	58234	GGAGGCUTGGGUAGCACAC	58235	TTGAGCCUCACTGTCCATGUC
231772097	58236	GCCTGCTGUTTGCTTGGAAUG	58237	CCCAACTTAUGCCACTCTCTGTUT
329648032	58238	CGGCACTGCAUGCAATTTCTUT	58239	ACGGTGCCUGTTCTGCUAAG
259072591	58240	CATGCAGCAGUCTCGUCCAT	58241	GCTGAAAAGAUGGCTGTUGACC
319750534	58242	ACTTGCTGAGGUACTGGTGGUA	58243	GCTAACTTTGGGCUTTTCTTGCAUAT
317549225	58244	CGGTTCTUGAAGCTGGTAAGUGG	58245	AGAUAAGCAGCAGTATTTUGACAGACAA
313214911	58246	AAGAAACUTTCGAGTAUCGGCAAGA	58247	GCACCATAGAGUCCATTCAGGATTTTUA
312680125	58248	CACTATCTCTCUCATTTTTGCTTGAUGG	58249	AGCATGTCUACGTGCAAATGTUG
316433244	58250	TAATCATGAGGCUAAGAGCGUACAC	58251	GTATTGCTCUGACCCCTCCUC
317864123	58252	CATTCATATTUGCCCCGTCUAGGT	58253	CATGTCCTTCTCUACCCCTTTTCTUT
316298791	58254	GGTATACCUACCCCACTCTGAUGAG	58255	CACGATTGTTCUTTGTTGTCTGTCUT
316687977	58256	GGCCTCUCACCTGUAGCAC	58257	GCAGTCAGTTUGGACAAGACCTUT
327902384	58258	AGAATGGAAAATAGAAUCAAAGGGCTGUT	58259	GACAGTACCAGCUGATGCAUCT
265337155	58260	GCTGCTACTUTATTGCCAATGUGAA	58261	CTGGGCCACUGGAGUCAA
267718983	58262	GCTCCAGTGUGCTAGCCATUA	58263	TTGCAGAUGGCCTCATACTUGT
316631876	58264	GATGAGCAAGAUAGGAAGGCAGTUA	58265	AUTGTTGCACUACAGCACCCT
319753231	58266	GCATGACUCCCTCTGCAGAUAAC	58267	GGAAUATGAGAAGAATUCAGAGCCACAT
327882446	58268	TGAGCATGGAUCCCTTTTTGATTACUT	58269	CCAGCCUCCACCTTCTATTTUCAT
279098870	58270	AAAACCAATCTATUTGCTTCCACTTUCC	58271	TTCATCGGCTUCTGGTTCTTCTUT
267334866	58272	CCCTCAATCCCUCAGAGGCUT	58273	ACCTTTGGUGCCTTCCTCAUC
257761098	58274	CAGGCTGGUCCTGATACCTUT	58275	CTGATGGUGCCCCTCTCTUC
268337503	58276	TCCCAGAGUGACCCTTGTCTUA	58277	CTCTGAGCCUGACTCACUCAC
268290866	58278	AGAAATGACACCUGCGTUCAGA	58279	AGCAAGGAAGCCAUTACTUACAGG
269320925	58280	ACAUAGGTCUCCAGGGACCAT	58281	CTTTCTGGGCUTCAAGGGCUA
332848309	58282	TGUGGAGAAACAGCCCTTUCC	58283	TTCTTGCAAGUTCAAAAATCCTTUCGAT
259299795	58284	CCTCUGACCACCAGATGCTTUG	58285	TCAAGUGCAGTGTTGUGAGGT
320219085	58286	GAAGATGTACCCAUGCTCATAACTGUA	58287	TGACCTGAAACGUGATAAGAATTCGUT
321212922	58288	CTTGCCACUGCTGCAGATCUA	58289	CACAGAGAACAGAUTTTGTAGACCCAUT
318985270	58290	CCTAGGTATTUCAGGTTCTTTGCTUACA	58291	CUATGCAATUGACCCCCAAACC
320948168	58292	GATTGACTCGUGTTATTACTCTUCCAGAA	58293	TCATTGCACTGUGTTTTAACTTGGUAAC
319541789	58294	TCCATGGATTUGGGTTGAAACUT	58295	CCCTGCAGTCAAUTATTACTTTTGGUT
261334792	58296	CTGCAGACCUACCACCCCUA	58297	CATCCTUCGCCAACCUCCAA
267020269	58298	CTCATCACCAUCCTGGAUGACAA	58299	GCAAACUCCGTGUCCAACCT
313936813	58300	CCCCTGACCAGCUCCTTTCUA	58301	GTCCCTTCCAUGAGTGATGUGA
312930443	58302	GCTCCCTUGACCTGTTGTCTTUT	58303	GUCGGCAGGACTUGAAGCA
333596218	58304	TTUGAAGGCAAGAAGACUGACAAAAAG	58305	CAATGGCTTTCUGTTCAAGTTTTUCCA
327986997	58306	TGAGGGUGCATCTCUAGAGCA	58307	CTAACCACCCUCCCATCTATTTUCC
333476593	58308	AGAGGCAAAGCGAUCCAUCAA	58309	GGATCGAGUCAACATCTGCCTUC
333476252	58310	GAGGGAGCUGATGGATCTTUACC	58311	CAATGGAGCCAUCCCTCUCAA
333379058	58312	GGGAGUGGAATCCCCUGGAT	58313	CAGACATUAAGCACAGCAAGATAUGG
312890904	58314	CCGAACAUTCTCATCUGAGACCT	58315	CACCCUCCCGAGCTCAAUG
313241268	58316	CTTCTGGAACUCACCATTTGACTUG	58317	CACGGAGCUCTTTGUGAAAGG
324910279	58318	CCCAGAUCCAGGACACAGAAUC	58319	CCUGCTGCCTUCACACACAA
324704078	58320	CCUACCTGCATUAGAGCAACCC	58321	AAGUAGGTTUCAAACAGGAGAAGGAAA
265525032	58322	AGCCUACCCTTCCUCCACAAT	58323	TTCTCCAGCAGCAUTCTGGUC
313767211	58324	GGAGAGCACGCUGACGUT	58325	GTAGATGAGGUGGTCCCGGUA
313095561	58326	TCCAGGGCAUACCTCTTGUCT	58327	GCCGCGAACUTGGCAAATTUAT
328149692	58328	CGAAGGCACCGUCCUCT	58329	GTAACACTAGATUCAGCAATTCCTCUGA
225122927	58330	TGAAGATACCAGAUCCTTGGAGATTUCT	58331	AGGTGATCTTTTATUACTTCCCAGCCUA
222171888	58332	GAGGTTTCTGAAAUGTGTATAGCTTGUC	58333	CGCAGAUAGGGCTACAGGAUAAAAC
224114330	58334	TCATTTTGGAAGUTCACTGGTCTAUGAA	58335	TCATCATGTATACUTACAGGGCTTTUGG
329002576	58336	CACTGCTATTTUGTATTCACTGTUGCT	58337	GGGATAGAGCGAAUACACAGACUC
224644666	58338	GTGAAGTTTTGTUAACCACTTGTGCUA	58339	TCATGAAAUCCTAGGCCUCCCA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
222974856	58340	ACAGGAGAATAUGGAAATCTGGTGACUA	58341	CACTAAAACUCTAAGGGCUAAGCCA
332434284	58342	ACCGCCUGCAATAGCTUGAAA	58343	GCATTGGCAUTCATGTUGGCAT
332347609	58344	CTGACUTCTTTCTCUGCCCACAT	58345	GCAUGGCGAAGGCAAAGUT
333562690	58346	GGCCTTGGUCCAGAGCUAAAG	58347	CCCTTGAUTCTGACACUGGCA
332878353	58348	GGGTCGAGUCCAGUGAGAAA	58349	CTGCCCAUCTGCGAGUCA
333082592	58350	GTCCTATGGCAUTTGGGATAUAAGCAT	58351	CTAAGCTTTUGAAGCATTCGGTCAUT
333508702	58352	GTTCATUCCCAAACACACGAGUC	58353	GTACCTTTGCAUAATCCTGGTGTTTUT
332677591	58354	TGCCAGACACUTCAGUGCAT	58355	CCAGCTTTCTCUAAAGAACTCCTTUCT
332628480	58356	GGGTCACACUGAGATTTCUGAAA	58357	GATGGCTGUGGAGATCAATGUCA
234764769	58358	CATTTAAGGUAAAAGCTAACAGTCUGCAT	58359	GAAGAAAAAGAAGUCAAAGACAAAGTGUGT
318852574	58360	CAAAGGCAGAAUATATCCTGACTUCCT	58361	GGAGACUACCCAAAAGCAAATGGUT
279439020	58362	CAGCTCAUAGGGAAGTGATGCUC	58363	TGAAAACAUGGCCCACTGCTUA
279065058	58364	GTAGGGCAUTAGCTGGUGACT	58365	AACCAGAATTTTUGCCAGCAGAUG
279544386	58366	TTGTTTCATTCCAAAUTGGAGATGUAGAGA	58367	TCCACTATUCAGTAAGAGTUCCACCAA
278709010	58368	CTTGCCTCCTUCTATGACAATCCUAAAA	58369	CATGTTTCTAAAGGUTCTGTTCCAGCUA
279692599	58370	CTTTGCAATGUCTGGACCTTTTAUAAACA	58371	AGGCCTTTCTUGAGGATTTTCTTUCA
279512880	58372	GTAAAGGAAGCCUTAAAAATGTCAUGCT	58373	CATCATTCACAUCATTGCCCTGUT
267033295	58374	CCCUGTGGGCAUGAGAAGAAG	58375	GGTTCATTCTUTGCTGCTTATTUGACAA
268572156	58376	CCAGTCTTGCUCCTCAAGAUACC	58377	GGTGTCTTCCCACUATAACCATCUC
324652050	58378	GCGCCGTTUTCCTAACAGTUT	58379	GCCTCCACUATGTTTCGAAUGAC
316215542	58380	AAAAGAAGGAUAAAGAGATGGCAGGUC	58381	AGTATGACAAGCUTCTCATTGCTGAUT
315675427	58382	TCAGTTTTACCUCATTGCTTTCUGCT	58383	ATTTAAGCTGGAGGAUTTGTTGGTTUG
321173910	58384	ATCAGCTUCCAACGAATUCAGACT	58385	CCUAAAAAGCCAGAGACCUCACT
313373451	58386	TCAGAGAUGGCCCTGCTGUA	58387	CUTTCAGUCGGGAGGCAAGAT
266847909	58388	CTCAGCTGCGUCTTTCTTCUCT	58389	ACCAAGTGCUAAGGATTCTTTCATUGA
235517465	58390	GCTTTGCTTTUCACAGTGTTTUCT	58391	GCAATGTAACUCTTTTTGGGCTTUGAAT
317871682	58392	CATCUCCCCACACCTCCTTUG	58393	AGAAGTCUCCCTGTTCTGUCCT
316473897	58394	CACGAGGATCAUGACTCGGAAAAAUAA	58395	TTCCACUAATAAACCTTUGCCCACT
241675134	58396	TATAATATGTGCUTCTTACCAGUCAAAAAGT	58397	CTCTGCAUGAAGACCGAGTTAUAGAAT
332430027	58398	GCTATTTCCTTUTGTGAATTCTGUCCCA	58399	CCUGGAUCCAAAGGAGAGCAA
332381982	58400	CTCCCTGTGUGTTATGGCTCAUT	58401	GTTCACCUGGCTTACCUGGAG
333393109	58402	AGCTTCTGUGGTGTTTTGATGUCT	58403	ACGCTGACUGTTGGTCTTTCUC
333820725	58404	CGCCTTTCUATTACACTCUGGCT	58405	GTGACCGAGGAUTTCCTGGUA
313737662	58406	GTCCTCGAUCTCATTCTGUAGCC	58407	GCTACACTTCUGAGGTTTCAAGGAUT
313073814	58408	GGGAAGGCUCATATCUGAGACCAT	58409	GUCCTGUACCGCAGAAAGGG
315394814	58410	CCCAGUTCCCTUCAGGAAGAC	58411	GCAAGTCACUGCTCCTTTTCTAUC
330861969	58412	ACTTTTACGCACUGCTGGUGA	58413	CTGGCTTATTTCUCCTCCTATTCTCCUA
328124724	58414	GAAAAATGTUCCATTTATTACTCUAACAAGACC	58415	GCTCGCATUGCAGTTTTAGTTAATTUGA
328085618	58416	TCAGACAGUTTAACAGAUCGGGAAAC	58417	GCCTTTGACACUGGAGAACUGAA
320944997	58418	CCATTCCACTCUGTGTAGAATTATCUCA	58419	AGGCAACCAGAGGUTAAAGAAAUGAA
320204494	58420	CGTGTCUCAAGTTCUCCAGCA	58421	TGATTCTGTTUCCTACCCTGTCUCT
257471946	58422	GATTCTCTGCCUGCACATCTTUG	58423	GGGAATGUGCTGTGCCTAUG
317412185	58424	CAGAGCCACAUTCATTGATGTCUT	58425	ACATGCCGCUTCTTATTTUGCC
316941441	58426	GCACTGCCCAUGACTGCATAUA	58427	GACTATGCCTGGUAAATGAGAGTAAGTUT
317166006	58428	CAACACAAAAUAGCCTAUCGGGAGT	58429	GCTTATGTTTGGGUGTTTGTTCTTCTUA
317041984	58430	CTTCACAGTUCTTCCCATCUCGT	58431	CCAAGATCAUGAGTTTGCAAAUGGA
271742204	58432	TGACTTGTGUAACCCCCUGGA	58433	GCCCTCCCCUACCATACTUGA
319186976	58434	GACTGGCGUGTCGUCCT	58435	TGTTATAAGGCUGGCCATGAAGUG
333257842	58436	CTATGGTGGUGGCGGCUA	58437	CGUCCCAGGUGGACACA
319460633	58438	GGCGTTCCUCCAGAAAGAAAUC	58439	TGCAGGTACUCACGTTGGTUC
316599924	58440	GAGAUGGCGCCTTCCUCT	58441	TCAGCACGGUGCUCACA
242470420	58442	CAGGGUTCTUGGAGAGCACAT	58443	CTGACGUCACCCAUCCCA
264508710	58444	CTGCTCACAUTCCGTCTCUCT	58445	CAGCUCACUGCACACAGAAAC
241060031	58446	GAGCTGTCUAACGCCCUCAT	58447	GGAGCCACAUTGCCGUCA
262616508	58448	GAGGTUAAGGCCCGGUCAC	58449	TTTAAGGCGUCCCTCTCTACUCT
321101293	58450	GGAAAGUGGCGGCCCUA	58451	GTGTCCAGCGUGGTTGTCUAT
319536438	58452	GTCCACCCCAUACAGCAUGAT	58453	GCUCCTTGAGUGCGCACA
320592366	58454	AACGGAGTUGGCGGAGUT	58455	TCGAUGGCATUCCAGACACAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
321033512	58456	GCGTAUCTGGGCUCGGT	58457	CCGCAUCACACAGCGTCUA
321331118	58458	AGGCATUGAGCCGGAUGG	58459	CTGTGAGUGGCCUCAGCAT
242141683	58460	CGAAGTTUCCACACCAACCAUGA	58461	CAACAUGCAGGCGCUCAAG
237072766	58462	CTCCUCCCCACAGAACUGG	58463	CAAGCAGGAGGUGGAACAUAAGAA
239091356	58464	ACTCTAGGGCCUACCCCATUT	58465	CGCTGACATTTGUTTTATACTGTGTTGUT
263640207	58466	GCTCTACCTCUCACCATGGACUC	58467	GGGCTAAGGACUCTGTCTCCUA
319463310	58468	TCAGCCCAGCACCUTAGGUA	58469	GAUCGCTGAGAUCGAGAAGCA
321036026	58470	GGTUGGAGAAGAGCUCACCAT	58471	TCTCGTCTTAACUTTTCTTGACCCTTUT
319164898	58472	GTCCTTGUGGGTGAACTCCUC	58473	GCTGTGACCAUGTGTTCTCUGT
318407716	58474	CCACGCAUCAAGAGAGUAAACCAA	58475	CTTACCUGGACCAGTACCTGUG
318030160	58476	GCCCAACAUGGGCAAATATATACUG	58477	TTTGACTAAGCUGGTGGTGGAUAG
318064126	58478	GGGAAACAGACUGCAAAAGUGG	58479	TCCGCCAUGACAAAAGGGTUT
265159334	58480	GGTCCAAAAGACAGUGAAGATTCCUA	58481	ACTGTTTTCTGAUTGTCTCACAUCCAT
259958080	58482	TCCTAAGCCUAACTGCTUGAGAGT	58483	CCTACCCAUCCGTTAAGATTGGTUA
268133781	58484	GCAGCCACACGAGUTCUGAA	58485	TCTGGATUGGAATCGTGAGUCAAAT
256170917	58486	AGCCGGCCCAGAUTTATTTUCA	58487	CGAGTCUCACCTCGAUACACCA
263994656	58488	GCTCTCUGAGCGAAGUCACT	58489	GAGAATAAGUGCAGCCCUGGT
242506164	58490	GTGTGATGAUGGTGAGGAUGGG	58491	CCTCATCTUGGGCCTGTGTUA
262610073	58492	CCTCACAACCUCCGTCATGUG	58493	ACTTTCAACTCTGUCTCCTTCCTCUT
258376698	58494	AGAACCTGGUGATGTCCAAGTAUG	58495	CCCTGGATCAGAGAAUAGAGAGATTCUA
260129370	58496	CCAGGGAACAAGAAACUCATCTATTUCA	58497	CCGTUCAGGCAGAAUAGAGACT
258760538	58498	GCTTCUCAAGAGAAGGGCAUGT	58499	CTCCCCAAUACCATTUGCAAAGT
258240571	58500	CATGTCCGUGGAGAAUGCCA	58501	AGTGGGAACUTCTGTGCUCAAC
264826262	58502	CTGGGCTCUGGGTCTGATCUA	58503	TCCCCGCUGACTAGTCTUGT
319368270	58504	CGTCTGAGACUTCCAACTGTCUG	58505	AAACUCCGCUGAGCAGAACT
323688664	58506	GCAUACCCCAAGCUCCAAAGG	58507	TGCTGTGCAACUCTTATAGGAGUG
324979544	58508	GCTCCAACUGGAGACUCACCT	58509	GCTCCAAUGCCCTCCTGTUC
257426404	58510	AGGGCCAGUTACTAGAGACAUCAG	58511	TTGCTAAAUCCAGAAATACACTCTUCCAA
333168608	58512	GTCCCUCCCCUGAGGACA	58513	CGTCCCAGCUGCTCAAGUC
312942565	58514	GCTCCCCUCCTGCCUGA	58515	ATCGACGUCGCGGTCUT
226042985	58516	GAGTCCGCUGGAGTCATCTCUA	58517	GCCTCAAGGUATTGCUGGACA
227086360	58518	GTTGATGGCUGTCTGATTAGCUAGG	58519	AGATTCTAAACCTUCCCTCCCTTCUT
225766511	58520	GGGACUCCCCCAGAAGACUA	58521	ACTCTCAGCUCATCCTCTTCUCC
226018350	58522	CACAGAGAAAGGAGUGUCAGCA	58523	CCAGGGTGGCUTCTGATATGUC
226504563	58524	GGAAGCCCCGUTAAGUCCA	58525	CTCATCTGACTUCTCTTGGTTTGGUT
327622945	58526	GCCACGUGTGGATGUCCAA	58527	CTCCGTCTUGATGTGCGTUC
268185726	58528	CATCUACGCCCUCCAGAGAAA	58529	ACATAUGGAGGCUCGGGACT
262914177	58530	CTGGAAGAAGACAUTGCCCUGT	58531	TCACUGGAGGGUCGAACACT
262688458	58532	GCACGAUCCTGAUCGAGAGGA	58533	CCTTCCAGGAGUTCATGTCUGA
330997353	58534	TGCCGCAAGUGTCTAGCTUC	58535	GCTTGTAATCUGCTTTTTGATGUCACAT
268408274	58536	GGCCTCUCAGTCCCGTGUA	58537	CCCGGCUCAGCACACUC
257459291	58538	CCUGCGUCCAGCGAGAG	58539	TCAGCAUGGAGACAACCAAGUG
263334051	58540	GACCCCAGAGCGUGTTUG	58541	CAGCAGCUGGGCACGUA
324701131	58542	TGCTCTCCAUGGTCCTGAATUG	58543	AAGAGGTGUCAGATCCAAUAGGACT
324277054	58544	CTGGTGCCUACACACCCTTUA	58545	GGGTTGAGAGGUTCTGAGTTCUG
326298995	58546	GACUGAGGGUGGCAGAACT	58547	CCCUGGGCCCTCACTUG
324724838	58548	GCUCTTUGCGGGCACAGAA	58549	CACCUGCAGAGCGACAUGA
323729237	58550	CACTGTTCAUCTCCCCUAGCA	58551	TCACACCUGAACCGTCUCAC
326287708	58552	CTGCGAGGCCUCAGCUA	58553	GAGCTCGGUCACCGUCA
325911350	58554	GGGCGCCUGAGATTGUGA	58555	CUCACGCAGGUCAGCAAC
319447212	58556	GGAGTCCTUGGTCCCCAAUG	58557	CTCCTCUCCATCGTCUCCAGA
326954561	58558	GGGAAAGAGGCCUGAGAGUC	58559	GCTGTCCCAGCAUCTGTCTUC
316449074	58560	GGACAAAAGGAGCAAGUCUGGA	58561	TGATATTTGCAGCUGGACATCGATUA
316543151	58562	CCAGGTGGACAGAUACAGCGAUA	58563	ACAGTCATGCUAAACCGCUGAA
332633812	58564	GAGGUAGAGAAGCAGUGGAACA	58565	GCCATCCUGTCTGTGAAUGGG
255669361	58566	GGACCTGUAGATACCATACUCCCA	58567	CTGATTCTCTCCUCCTCCCTCUT
256802977	58568	ACUGCUAGGCCAGGAGGT	58569	CTCAGGCCCAUCCCTACUC
325611736	58570	GCCAUCCATCTUGGAGACAGT	58571	CGGACGGAAAAAGAGUCUCAGAA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
260303302	58572	TCCTCAAACAGAUAACTCACTTCCUCA	58573	GTTGACCTGGAGUTGTCATCCTUT
264238081	58574	GGCAAGCUCAGGTTUCCCAAT	58575	GAGAATGAACAUGCCCATTUCCAG
256142007	58576	CCAAGAACCAGGAAAAUCAATCTGUT	58577	GATCTCCCGCUGGTACTTUGA
324733521	58578	TCAATGGTTGAAUAGCACATACCTUCAT	58579	GCCAGCTCUCCAGTTCAGUAAG
323840888	58580	ACATCCACUCACCTGAACAATUGA	58581	GTGTCAACAGUTTTTCCCTTAATTUCCT
323940311	58582	CCTAGCCUAGCAGGAAAAATUCACT	58583	GCTCTGATGCUAGGCAGCTTTAUG
268691834	58584	CCAAGCGAGCGAAUGTGTUG	58585	GTGTCTCCTUCACCACCTCATTUT
267638171	58586	CAGGATGATTTAUGCTTCTACTGCAUCT	58587	CCGUCGAGGACCGAGUCA
268371214	58588	AACAAATTTTCTCUCTCACCCAGUCAT	58589	GGAAGTTAGAAGAUCTGAGCTCUGAGT
268310868	58590	CAAAAACAUAGGAACAAAGCCTUAACCA	58591	AAAGAAUGAAGCAGAGCCAGAGUT
263893404	58592	AATCAACTCGUGTAATTACCATUCACCA	58593	GGCTUGAAAGGGCAAGUAGAAGT
326206620	58594	GGAGUATTTCTGAUCCCAAAGGCA	58595	GATGAAAGTGTUCCTACAGGTTAUCACA
325393983	58596	GAACCTGAUGGCCCGTTTUT	58597	GGCAGGAUGGAGAGGAGUACA
323467774	58598	CCTTCACUCACCTCTGCTTUGT	58599	CCCATAATAUCCAAATCCAUGGCAAAGT
319490800	58600	GCCGTGACCUTCTCACTCUAA	58601	TTCTTTGGGAAGGCUGCCTTUAA
262403303	58602	ACCACCCCCUCCAGCUAC	58603	GCTGAATTCCCUGCCGGAUT
290402164	58604	CCTCCACACUGAGTCAUGGT	58605	TCCAGTGTGTAUTGAAATTTGAGGUCT
291779886	58606	ACTTTCTGATAAACAUATTGGCTGCUGT	58607	GCCCTACCCUCTTCCTTCTTCUC
292970486	58608	GCTGGTTUGGAACAGUCCGA	58609	GCCCCCGGUTTGTCAGTTUT
305895735	58610	CTCACAGGCAAAGAUGGTGATCTUAT	58611	GCAGTTTGTCUCACTACAGCTAUGT
299810576	58612	GGGTGTGGUGAAGGATTCTCCUA	58613	ACTACATTCCAAGUCCTCCACUCA
302929735	58614	CCCTTGTUTGCAGACAUACCC	58615	GACCTTTGCAAUCACGGAACATUT
305583006	58616	TGTAACCCAACAAAGGUGGUGAA	58617	CACAGUCACTTGATUACAAAAAGGCAT
300066940	58618	GGAATGGUCAGGTAGAGGAUGGT	58619	TCCTCGTCCUCTGACAGGUG
257075441	58620	AAGTGGTAACUCATGTTTAATGGUGGAA	58621	CCTCTGTGTTTTGUGAGACTAGACTCUA
256710858	58622	AGTTCTTTTATTTUGTGCTGCCCCUA	58623	CCTGAGAAGCAAUAGATCTAGCTGTTUT
259081402	58624	CACUTAGGACUACCGCCAGT	58625	AAGGCTCCATGUCTGAAGATGAAUT
299078680	58626	CTCAACTTCUATTCACTGGGUCCT	58627	AGCAATGCAUCAACCAATAACCATTUT
317566616	58628	GGTAGGCGUCCTTGCCAAUC	58629	GGAAATTTAUGCTGTCCGGUCAC
268102116	58630	GCCCAGUAGGUGAAAAAGGCAT	58631	GGAAGCCATGAGUAGCCAAAACATAAUA
319968798	58632	TCCTTCTCTGCUGGTGTGAGUAT	58633	GCCGAAACUTCACATTTUCAAACACAA
319013656	58634	GCCCTGAGGUTTTGCTTAGGUT	58635	GTCUGCTTCTAGAATAUCAGAGAACAGT
316321114	58636	ACTCCTGCUCTGCAAACATAUCC	58637	CTAGCGGUAGGAGCAACAUCAA
333391365	58638	CCCAGCACUTTGCCTGAUAAC	58639	TGGTCCAATUCCTGTGGACTTUC
266767680	58640	CCUCGCGGCCTAUGGAG	58641	CCGGTTCAUGCCAGCTTUG
266773488	58642	ACCTTCCTGUCGGTGTATGUG	58643	CTGGGAGAAGUAGAGGCGGUA
315101848	58644	GCCTGGACUTTGATCTCAUAGGG	58645	CTTGGCCAACCAACUCCTCUT
313749001	58646	CAGTTAAUCGGGAAGCTTTGUCAGA	58647	TGTTTCAUCCTCCAUGCCAAGG
265765929	58648	GCGGAAGUCATUGCCAGAAGAA	58649	CCATTCCTUGGAAACCTTUAAAAACACT
265386341	58650	ACCAGTGACUGCACATGTACAUT	58651	ACCCACUCACAGGCCTAAUGA
317660501	58652	CTTTGCAGAGCUTTCTGTUGCT	58653	ACCAGACTUGCCCAAAACAUCT
317587909	58654	GTTTTAGGATGCUTCTTGGCAACUG	58655	ACTCTGACATUGTTTGGTTTGTCUGA
318930990	58656	GCTATGACGUGCTGTTUGCAT	58657	GCAGTAGAUGGACCCCTCUG
319141628	58658	GCTACAGUCCCTGGGUGGAA	58659	GAGAGUACTGUGGCCCACAA
320775030	58660	CCCACCCGCUTTCTGUCT	58661	TCCAGAGGGCGUCCUGT
314683298	58662	CCCAGCCTCUTATGACCTATTCUT	58663	CGTUGAGCACCTCCTUAGCAG
320895704	58664	GTCGACTACCCUGATGTGCUG	58665	CTTTCTTCUCCGGAAGGGUGAT
266339340	58666	GCTATCCTUACCCCGCCAAGUA	58667	CTAGCTAGGUGTCCTGTUCCAC
314511449	58668	GGAGCTAGUGGCGCUCA	58669	CCGCUCCAGCACGTUGT
313696070	58670	GAAGCUGCTGGGCUCAGT	58671	CCCACCCGCUTAGACCUC
264641433	58672	TGACCTGTGUCCATTTCTGCTUC	58673	AGCAACTTTGAGGCUGATTATGGAAUAT
267922098	58674	AAATGTCCTACUCAAGCCTTGTTUGA	58675	CCCTGAAGATACCUCATTTTGGTTATUG
267358940	58676	CATATTCGCCUAAATCTCCATCUACCAG	58677	CTTCATGTTCCUCAATTCCTTGCAATUT
267640154	58678	CAGUAGGACCGACGGCAAUC	58679	GGGTTGAGUTCACAGTTGUGAGT
332805051	58680	CAGGTTCUCCAGCTTGTCCTUT	58681	CTCTGTGGGCCUCTTTGTTUCT
333345380	58682	CCTGCTUGAAGTTCTTCUCGGA	58683	CAGCAUATTUGGGAACGAGAAACAA
315274090	58684	GAGGACCAGGUGGAGCAGTAUA	58685	CATAGCCCAGCGUGGGUAAG
313438206	58686	GCUGCUGGCGGAAAAGGA	58687	GGGUCTAGUCAAGGCCAGT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
312784348	58688	AGAUGGAAGGAGAGGCCUCAAT	58689	GGUGGGAACCGGTAAGUCAG
323504700	58690	GGGACAAGCGUGGCUGAG	58691	CAGCUGGGCCTUCAGGAA
314770829	58692	CCTGAGAGGUCTTGCCCACUA	58693	TCTCACATGCUTCCCCTCATUC
315625587	58694	GGCTGTTUCTCACAGAUCCCAAA	58695	CTGAAGTCUCCCGACCACUC
327491932	58696	CCUTCCTCCTCUCAGCCAGAAT	58697	GCAGGAAGAAGAGCAUAAGAACCUG
327791907	58698	AGCACCACAUATAAGCTGCCAUT	58699	CTCCTTTAATGUCTCCTGGACUGAG
327796382	58700	GTGTGTGUGCACATATGCATTUGA	58701	TGCCAGCCCCUCATTAATCTATAUGA
325332437	58702	GCCTCUGAGAATGCTGGUAGA	58703	GATCGCCCAGUCAACTCUGAAA
326182993	58704	GCTGCTGTCUTGGGTTATTCUGG	58705	TCCATCAAGAGTUATTTGGTTGCACUAA
325131247	58706	GTAACTTUGCAGCCUGGGAAGA	58707	GGTCAUCCAGAAGAGTGUAGGGAA
326265802	58708	TCTAATCTTACUACCACTCTCCUCCCT	58709	AGCAAACCAGGCAUGTACTUGT
325005792	58710	CATGTTTGUGTTGCTCCAUCGG	58711	TTCTTTGCCCAUTCTCACACUCA
324056773	58712	AGTGAAACCUCAGCTCTUGAAAACT	58713	GGCCAGTGUGGTGAACTCAUC
323394123	58714	CCCCTGTTATUGTACAGTTTGTTTUGG	58715	CCAGUTTGTCATTUAAGAGAGAGGAAGG
327115349	58716	GTTACTGGAGATAUTCCCCAACACAUA	58717	CAAGATATTAAAGUGGCAATGTGUGCT
236941969	58718	CGGGAAACAGCUTAGUGGGT	58719	CCGTGCGCCGUATAGAAGUC
242651479	58720	GTCACTTUGTTCTGTTUGCAGGT	58721	AATTATTCCAACCUCCAATGACCCAUT
320457042	58722	CCATTACTATUCTGTTGGACCUCCAAA	58723	GGTAAAAGATUGTTGCTGCTUGGAAA
264061688	58724	CCTGCAGTUCCTTTCCTGTGUT	58725	CTCTCAAAACUAGAAGTGTAAGCUGGAT
264652487	58726	CTCAUCAGGCGCATTCCAUCT	58727	CTCAGTGATTUGGCTCAGGUGAT
267195366	58728	CCCTAGTAAAGGAUGCCCAGUT	58729	CCACCACAGUGTCGUCAGG
327521445	58730	CTGAGGCUTTCCCAUCAGACC	58731	ACAGTGGGAAUGCTGCTTCTUT
313287347	58732	TTGGTAGCTGUAGCCTGTCATCUA	58733	CTTCCCUCTTCACCCUGGAAC
313674351	58734	CTTTGTGGTTCTUCATTCTTCTCTCCUT	58735	ACTAATCGTGCUCTTCTAGGGTTUAGA
323950467	58736	AGTACTTTCTUCAGTGGCAACACUAAAA	58737	GGATTGCTAGCACCUATTCTTAACAGUA
324555503	58738	GCAAGTACATTTUTGAATTCCTCAGUCA	58739	CCTTGGUGGTACAGATTUGCACA
255053265	58740	TGAGTTTTTACCUACCTTTCTUGCACAT	58741	CCCCUAACCAACGGAGAGATTTUG
264462988	58742	CCATATGTCACAGUGGTCTTCACTUAAA	58743	AGACATATTCUCTGTGAAACUGAAACGG
261175165	58744	CCAAATATGUGTCTGTGACUCAGGA	58745	CTTTCATTCCCUTTTAGGCTCCTAUGAT
261698498	58746	AGGAGCUAAAGGCGAAGAUGG	58747	TGACAGTGAUGCTGCTTTTCTTTUAGAT
269444877	58748	AAACACTGTCACAUAAAGATGAGCUAAGT	58749	GGAAGGAAGAGUGTAGTGGAAAAUGA
260175546	58750	GAAGATGAGCCAACUCCAGCUT	58751	GCACAATGCAGGAUCCAAATATTTUG
267880802	58752	GAGATAAAATATUGACCGATGCAGCUACT	58753	GTACAGTTTTACCCUGGATAGTTTCUGA
268804354	58754	CACCATUAGGACCCTGAAUAGAAACA	58755	TGACGGACAGCCUGGAGUAA
268011585	58756	AGCTCCAGUTGGCCCAUT	58757	GACCTTGGGAATUTTGTTCTATGACCUAT
261365124	58758	TGGAAGATGAAAUGGAAAACCGAATUAGT	58759	TGGUTCACGUAGAGAGGAAGCA
267284415	58760	TCAATTTGUCAAAAACATACCTCCUCCA	58761	ATGAAACTTACAUGGCTCCTGUCAA
265737498	58762	CATGTTATTACUCTTGGCCCUCGT	58763	ACTTACCACAUCACTCTTGCTGTUT
320367850	58764	GTTTATTTTGUCCATGTGTTCCUCAAGT	58765	TGTCTGAATTTTGAUCATACAGCGGUA
264908082	58766	CAGGCCTTTUCCCTCATGCUA	58767	GAGGACUGAGCTGTCCACUG
261433337	58768	CCTGTGGUACCATCCAUGGGA	58769	CGCAGGTGUAGGACTGGAUCT
235189691	58770	CATGTGTGGCUTAATCTTGCCTCUA	58771	CCAACATCUCAGTCCTACTGUCC
235602534	58772	CGAGTUGGGTCCTTUCGCA	58773	GGTGATAAAUGCACTTTTGTCATAUGGT
255942624	58774	AGCAGGUAAGAAGCCGAACUC	58775	CCCUCCCCAAGUCCAACT
270342389	58776	TTGTGATGTGAGAUTTTCCACCUGT	58777	CAGGUGTTTACATTUAGGAGACAGAGAT
232901699	58778	ACATTTATGGTTUCTCACCTGCCAUT	58779	ACTCAACAATGUATTCAGCAAGUCCT
234741715	58780	TACAGTTTUAACGCCTAAAGTAUCACAT	58781	CAAAACATTCCTTUTCTTCGTCCCAAUT
233393018	58782	TGGCTCCATUCCAAACTCCUG	58783	AGAACACAUCCCACAGTGCATAAAUAA
325217530	58784	TGGCCACGCUGAAGTUCT	58785	CCTACUGCGACCCCACUC
323598150	58786	CCAGTAAUGAGACCACCCCATUG	58787	CCTGGGTTCUGAAGCAGATTTUG
323630372	58788	GATTACCAUTGCTCUGGGACCAT	58789	AAACGTCCGUTCCTCCACUC
324053321	58790	CCACACTUGCTGTCCCTUGT	58791	GCATGGAACAAAGUCTCTGTGUGT
323525729	58792	GGTACUCAGCAGGTATTAACUGCAA	58793	GGGCCTAAUGCTACTGTCTGUC
262229167	58794	CTTCACTTGAGGGUATAGTAGTTTGUGG	58795	CTGATGCGUGGCTTATGCUT
263147793	58796	CCCTGAGAAGCUGTGTTUGACT	58797	GGCCTGAGGCUTTCAATCTCTUC
316669803	58798	GGGAAGAAATUCCCACATGAGATUCA	58799	TGAGTGTAGCUGGTGCCTTUT
332088737	58800	CCTCCGGGAUTTCATCTCUGG	58801	CTGAGGUGGGATTTTGACUGAGA
332044003	58802	GGTCTTGGAAGUCCCCTTCTUG	58803	ACAAAGACCCUAUCGGAAGACGA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
261983747	58804	CCACTCUGGAGGAATATTCAAUAGCAAT	58805	GAAAATACTGAGAUCCGTATTATCCTUCAA
253915732	58806	CCGTGACAUTCTCCGTUCCA	58807	GCCTAGTCCAAAGUCATAAGAAAGTATUCA
266364930	58808	TCTTACCTTGCUGTTTCTTCATGAAUGT	58809	GGGTGTGATGUAGGTTAGAACTUAAAGT
328675494	58810	GCAGAUCCGGCAGCTCTUC	58811	CCGUCUCGGGAGGAAGGT
328779965	58812	GCUGATCUACGCGAGCGA	58813	GCUGCAGAGCCCGTUGT
261688681	58814	AGAGCAAUCCTCGTCGUCAG	58815	ACGAGAGGCUGCTGGAGUAA
261790619	58816	CGGGTGUCCCTCUGGCT	58817	GTTTACCUTGAGTCCUCCACAGA
320737185	58818	GCCAGUGACCGCGAUGG	58819	ATGCGCUGCATCTCGAUCT
326920174	58820	GGAAUCTTGAATACUGGGCCACA	58821	GGCTAGCTUGAGACTTATGTCTUGAAT
333079736	58822	TTTCTCTCTGTTTUCACTCAGGTGTUAG	58823	ACTAAAGGAAGUCAAATTCTGCCTUGAT
333716648	58824	CTGAGGTCAUTAAGCAAGAGTUGGAA	58825	GGCTACCCCCUCATTCTTUAGG
333686316	58826	CTGCTCCTGUCTCTTCAGGTCUA	58827	CAAACAAUGAGGCAAAGAGGAUGAA
333758734	58828	GAACCAGCTGUACAAGTCCAGUT	58829	CTCATACTCUGCAGATGGAGGUG
332348662	58830	GAGGAGAAGCUGTACCUCCAGA	58831	GGCGAGAAAGUGGAGAGGAAUG
333698143	58832	TCTAACACTUGCAGACTGCTGUT	58833	ACAGCTGTGGUGTTGAATTTTUCAG
314533131	58834	GGTGATAAAACCCGAAUGACTGAGTUAT	58835	TCACACUCACCAACGGTTUCAA
314541490	58836	GCAACAGAAAGUTTGGATGUGGAA	58837	CAAGAAGTCUGCTGCTAGTCCUG
312835928	58838	AGGAUGAAGAACCCCATGCUG	58839	CAACACGGUTGTCTCCUAGGT
317521388	58840	TGAAGTAAAAACACAUAGCCAGAACCUT	58841	TCCTTTGTCTTCUTCTGGAATGTCAUC
267463422	58842	CAAACTCTUGGCTTTGCTCUGT	58843	AGCCAGTGGCUATGTTTATTTCAGUAAA
269038798	58844	CATCACCUGTCTGTAAGUGGAGT	58845	TGAGTGATTCUCATCAGAGCTCUAACAT
259151275	58846	GTTTGCGAAUGGCCTCTAGTGUA	58847	AGAGAAGAAGGAAAUTTTGACACCTUGA
267241986	58848	GGCCACACCCUACACACUAA	58849	GTCTCCGACACCUCATGTTTTACTAUC
258924889	58850	ATGTGTTTCUCGCAAATTCATCAGUG	58851	CCATUCCGGAAGAGCUGACT
290161568	58852	AAUGAAGGGCGACCUGAAACA	58853	TCTCTGCTTUAAGGCTTCAGCUC
292654591	58854	GGGACUCAAGGGAAAGACCAUC	58855	GTCAGGGTGUGCTTTATTAGTGTCUAC
290959075	58856	TGCTTTCTTAGTGUTTTCCAGTAAGCTUAT	58857	GCAGUGACTAACTTAAUGGCACACAA
289406398	58858	ACTTCACUTGCAAGATUACCAACCA	58859	GCTGTTCTGATGUAACTGCCTAGTTTUT
292446429	58860	ATGACTTTAUGGGACAATAUCACAGGAA	58861	GATGCCACTCUTAAAGCCATCUCT
292180921	58862	TGCTAATTTCAUCAAGCTCAAGTCUGT	58863	CTCGAUGCATAATTUGGCCAGT
224555236	58864	TTCCAAGGACAUCATCCCCUAGT	58865	TTCTACCTTTTUATTGGCTCCATUACCA
328174911	58866	GGAACCTTCUCCAGCCTTTCTUT	58867	GAATCCTCUGCTGGTCTCUGG
326937436	58868	CCAGGUGAAAGCUGAAAAGCAG	58869	CAACACUAGCCCCCAGUCAAG
326890108	58870	CAGCACAGGCCGGUAAATUG	58871	CCTCCTGTTUCTTGCCATCUGA
328212748	58872	GACCAGGTCUTACTTGCCCUAA	58873	TGAAGAACTGUCGCTGCTGUC
324571073	58874	ACAGCCTGAGGUGTTTTGAAATTTUG	58875	GAGCAACAATAAUGCCTCCTTCUCT
257512191	58876	GCAUGATAGUAAGACGAAGGAGCAG	58877	CCCACUAGGGCTAGGATUGG
259011022	58878	GTTGTAGGTUTTTGTGCAGUGGT	58879	GGACACCAGGCUCTTCATGUT
268467944	58880	TCAAAGAATCAGUGTACTCAGGTGGUA	58881	GCGGGAAUATTGAGTCTUCCACT
268492677	58882	TTGACACAGAAAACCUGGAGAAAAUCT	58883	GCCTAUGAAGGCTTTCUGAGCA
331701712	58884	AGGGUCCTGGTGUCCACA	58885	GCAGGGCAGGGUCTGUT
331741590	58886	CCAGCCACAAGCAGUTCUGT	58887	GGCCCTGUGTCTGCCAUT
331552461	58888	CTGGCAGCACUTCCTCAUGT	58889	GGACTACCGAUGAGCCUCCT
331560405	58890	AGTGACCUGGTACTCCTGUCC	58891	GGTCAAGTUCCACACAGUACCAT
269236806	58892	CAGGCACAGAACCCUCAUCC	58893	GCCTCACUGTTGCCCATTUCT
265837609	58894	ACTGGCUGAGAGGGAGGUT	58895	TTTGCCTCTCACUCTGTGTGTAUC
327920869	58896	CCAGCCUCCACTGAATCCTUT	58897	ACTATATCGUGCTGCAGTUCGG
272237046	58898	ACAAGAAGCUGAAAGGGTTTCCAUAG	58899	AATTTAGTTGCTAUTTGTGCCATTGUGT
269700141	58900	CCTACACAAGAAUGCAGAAATUCAACA	58901	GTCAACAGAATCUCAGGAGCCATAUC
271910033	58902	GCATCACUGCAAATTGCUGGAG	58903	CAACGUGAGCCTGTCUGGAT
270907385	58904	AGAAUTTCUCCAGGGCAGCAAA	58905	CACTGTGAAGGAGGAUCTATACACTUG
272734737	58906	CAAAGACTGCUACTCACGTGTGUAT	58907	GCCTGCCTTTCUATTTTATCTGAACUG
270485156	58908	AAAGAGAGAGAAUGTGTGTGTGTUGT	58909	GGGAGTATUGCACAATTATCTCTTGUCT
269773966	58910	TCCCACTCAUAAAAACCACUCACC	58911	ACATGCTCACTUGTGGTACTATTTUCT
317475423	58912	CTAGAAUGATAGTTCTGUCGCCAAGG	58913	ACUTATCCAACTUGGCCAGAAACAG
316910496	58914	CAATATTGTUAGGGATAGCCTTUGCT	58915	ATGCUGAAAAACTGTTUGAGGACAAAAT
317494190	58916	CAGAAATATGUTGCTGCACAUGGG	58917	ATGGCTATTCCUCATTTCTCCACTTUT
316999463	58918	GTTACCUGCAAATCCCAATUGCC	58919	GCATUCCAGGGUGCACAAAA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
262285176	58920	GCAUTGTGTTTCGUAGAAGGCAA	58921	GCCTAUGCCTTTAGCUGAAGGAA
267915050	58922	AGAAAACTCATCUGCAGGCTATAUGG	58923	TACTTTTGCCTGAUGAGCTTTCTAGUAT
267835224	58924	TACTAGCAATUAATGCCAGAUGGCT	58925	GTGGTTTGCCUAAGGATGTTATGAUAGT
261580786	58926	AGGTGGCAAGAUGGGAAAGUG	58927	AACCTTACCTGACUGTCTACTACCTUT
263933050	58928	TCATTCTCAGAGUCCTGAAGCATTTUT	58929	AGAACTGCUAACCTCCCCTUCT
265362411	58930	CGACCCTUCGCCTAACCUC	58931	GGTTGTCCUCGCTTTCCAAAUACT
268423964	58932	AAATATTTTGCUGCTCAATGTAGUGGA	58933	CTTGTCCATTUAAAATTGCTCCTTUGGT
257498314	58934	GAGGACTTTAGAGUGTTTGATAGTUGGT	58935	CATGAAACTGGCAACAUTAATACGCTUA
268178943	58936	GGCCCCUGACATTGAGCUAA	58937	ACAAGAAAACGUAACAAATGATCCCUCA
268046128	58938	GGTACTCAUGAGAGCATTAAGGGATTUC	58939	GCCAUGAAAAGCAAATGCUCCT
267990471	58940	GGTGGUGGCAGAAAGAGAUGAAA	58941	CTAATACAAUTGCTATGTUCCACACACC
268671327	58942	CAGTAGAACAGAUGTCAAGTGGAGUT	58943	CTCAGATGAGUGTGTTCAACTGUGA
313041454	58944	CTGGAUGCAGCAAACCAATAUCA	58945	GACAATGTCUTTAAGGTTAAAUGCGGAT
325787032	58946	TGAGAAGAGAAUGTTGAACAAGUCACAT	58947	CAGTTACUGGAGGATTCTACCUCAGA
325541882	58948	CCCUCATTCATCUGCAGGAAAAGAAA	58949	AACCTCCUCCTGGGCTTAUCA
326441540	58950	GGACCAUGGAGAGGGAAGATUT	58951	GTCAGTCTGUGGTTCGGTTTCUT
224091035	58952	AGAGACUCCCAAAGCTGCTTTUT	58953	CAATATTCAAAUCATGGTGTGCUGACA
224642519	58954	AGTGGTATTTTATGUGACTTTTCTATCATAUGT	58955	CAGTCATCTGCUGTGGTTGAAAUT
332398095	58956	GTTGATTUGGAAGCACCAATTTCUGT	58957	GAGCTGGGTUATAATGCCATCUCT
224481857	58958	GGACCTCAAACAACAAUGTATTCAGCUA	58959	TCAUCTTTTACTTUGAGAAGGCAAGCA
222266906	58960	TGGATCAGGUTCGTGAATATAUGGAAAAT	58961	AGAATGGTGGGCUCTATCCAAUACT
332564081	58962	CTTCTTGTGAGUGCAGATACTTTUCAA	58963	ACAGAAAUGGTTACAATGUCAACAGAGA
223234899	58964	AGTCTTTTGAGCAGUTACCTATTTTGUAGAAA	58965	GCCCACCAGAAGAAUGATAAAAUGAGT
319209283	58966	CTGGTTTTGATUGGTCCTGGTUG	58967	TTATGTGCTTCCUTGCTTTCAATGTUT
261646526	58968	GTCACTCTGTGCUTAGAGGTATACUAGA	58969	CUAATGCCTTUGAAGCCAGGAAG
261072967	58970	TGTGTGTCUGGCATAATUGAAAAACAAT	58971	ACTGTTTGACCUGGAGTTCCATTUT
260522635	58972	CTGGUGAGAGAGGACGTGTUG	58973	AACTCCTTUCAAACTCCCCAGUG
265510395	58974	CTGCCCTUCCTTGATATUGCAC	58975	AGAAGAAAUGGAAGGATTCAGCTTUCA
324507598	58976	ACACATTATTTCCAUACCACCAGCUC	58977	AGTGAGAATGUGACCAGACUGAGAT
323830510	58978	CTGCTGTTTCCUATAAGAATACCUGCT	58979	CCCCTCTGUAGAACTGTTGATTTGTTUA
324783843	58980	ACACCTAAGAUGAGTAGCAGUAAGCA	58981	CTCAUAGAGACCUCCCGAACC
269306990	58982	ACCATGGTGUAGCATTACTAAGUAAGG	58983	CAGTGACTTGATUTTTGCCAGTTATCUT
263006528	58984	GATACAATAGTGUCATCTACAGGTGCUT	58985	AGGAGGUAAUAAGAGGCAGAAAGACA
314400794	58986	CCCTCATCCUCACTGCTCUCA	58987	TCTCTGAGGCCCAUTCTCTGUT
315050033	58988	GACCAGAAGUGGUCGGAGAA	58989	AGCTCCCUGTCCTCUCCAT
314902141	58990	GCGCAUGGCCTCGAUGT	58991	AUGGACAACCACGUGGCA
332320426	58992	GCGTCCUCGCCAGTCUA	58993	GGTGUAAGCGGCUCCGT
317538128	58994	CCAGGTUGAGTTTTCCAUGGAG	58995	TGGTCCCTGGUACTCTCATGUT
241445317	58996	CTCACTTTAGCAUGAGTCTATCAGAUGG	58997	AGUAACATTTGCTCUCAGAAACACACA
262083925	58998	CCTCTTAGGUAAACAGCTCCUGAAAG	58999	AAATATTTTGGTAGAGUTTCTGCCACUA
239542949	59000	AAGGTATCTTGATTUTAAGTTGTAATTCCTUGA	59001	ACCTGAACAGTAUTCTGGAGTTACGUAT
256139322	59002	TGGGCATCUATAGAAGATCUGGAAAAAG	59003	CAAUATGCAAGTUGACAGCACCAA
261459434	59004	TTGCAAUGGGTTTUGAAAGCAAGT	59005	CTTCAGTTTUGGCAGCAGCUT
266523287	59006	GCAGCTAUCGACAGATTCUCCAA	59007	TTTTTAAAGGCAUCAGGACTTTCTTGUG
262396835	59008	CAGCCTTTGAUTATTTTTCGACCUCAA	59009	CCCCTTTTCGUAGAAGATCCTCTATTUC
256860797	59010	CATTCTTUCCCACGGACGCUA	59011	ACCCUGUAGCACAAACAGCAT
258055203	59012	CTCTCGAACUCTGTACCGCAUT	59013	AGGATAACUCAGGGTCATUGAGGAT
326707450	59014	ACAUTTACCGTAAGUACAGCAGCAA	59015	CCCAAAGTTTTUACAGCTTATGACGUAT
232644468	59016	CACAATCTGGCUCTGCTGAUGA	59017	AATACGTTUGCCAGCTGGTTUG
232756910	59018	CUCTTTAGCTAUCCCAGGAGAGGT	59019	TTCATTTGCTGTTUACTCCTCTTCTCUT
231408410	59020	GGAAATGUGCACGCTGGAAUC	59021	GTTTTATTUCGGAGGCTUGCAGT
314035362	59022	CCCAGCTCUGATCTACCCAGUA	59023	GGGAACCTTUGGTCTAAATGGCUT
315134295	59024	TCCATATTTCTGTUGATCAGCTCTGUC	59025	AGTGUCCAGGCACAGAGUAGT
316449600	59026	CTGAAAATTTGACUTACTGTGCCAUCC	59027	TGAGGAGCAGGUTTCTATATGAGAGTUT
327902573	59028	CCTGCTTCUGGATCGTTTACTTTUCA	59029	GATCTACAUCATTGTCATCUCCCAGAAA
263568896	59030	TCCTGAGCAGCAUCCCTTTCUA	59031	GGTTCTCCACAUGGTGAATGAACTTUAT
262449111	59032	CTGGGAUGCGATGTGGGTUA	59033	GGACAUGAAGACCTTGGTGUGG
316153752	59034	CGCTGGACUCTTTAGCAGAGTUT	59035	CTCTGCUGGAGGGAAATTCTTCAUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
297218079	59036	GGGAAACAACCCCUGAGGAUT	59037	CATCGCTUGCCTTTTCTTCTUGG
317112891	59038	AGCCAGGAACCUGACCTATTTCUA	59039	CTTGTTGTCTTCUTCCTGTTCCCUT
261890239	59040	CUTCCUGCAAACCACAGACCT	59041	TTCAGCTTCCUCCTCCACTTCUA
265627078	59042	CCCCTAGAAAUGCCACCTCTUA	59043	TGCCATCCTUGAAGTCCATGUC
241849253	59044	GTTCTGTGCCAACAAUATGCAAGUT	59045	CAGTAGCCTTUCTGAGAGCCUAAAG
265465871	59046	TGGCCAGAUGCCTCTTCATUG	59047	CAGTGTGAGUGAGTGTCAGTGUAAT
261800752	59048	CCTGCAGCUGTCCTCUGAAAG	59049	CTTGATACCUCCCAAAAACGGATTUT
267983153	59050	CCTGACUCCAGCTGTCTCUGT	59051	CTCGCCAUAGGTGAGGTCAUC
265170570	59052	GCACCAGAAUGGATTTGGGTUT	59053	GAATACACUGACACCUCCACCAG
267543452	59054	GGGCTTTGUTGCTGTGUGT	59055	CGGAGGGCCUTGTCGUAG
333577113	59056	GGTAACATUAACTTCCAAGCUCCCA	59057	GGCAGGAUAAACACAGCTTATGUCAA
321195711	59058	AGGCAGAAGGAGAGAUGTTUGG	59059	ACTGTGGAACUCAAATCAGAACCTAAUG
319871167	59060	CAGGCAACCAGAAGUCATCTCUA	59061	GAUTATGAGGCATTUCCAGACCAAGA
319359146	59062	TGCTTTTUCCCACACACCTCTAUT	59063	ACTACTATGAACUTGTTGTTGUGGCA
318957561	59064	ACAGCUGAAAGCCTCTGATUAGAAG	59065	TGAGUGGGCGCCATATCAAUT
262934793	59066	GGGTTTCCUGTGGACCUGAAG	59067	CTGAAAAGTUCCCAGATCTCAUGAGT
265237712	59068	AATGGCACCCUGGTGUACAG	59069	GGGTCCAUACAGTCAGUAACAGA
264821184	59070	GCCACCGUGTTCGUCACT	59071	CTCTGGUGCCACUGAGCAT
261571512	59072	GCCATCTTCUCCTTCATCGUCAAG	59073	CAGTGTACUCAGCCTTGGUGAA
328416170	59074	TCTTCTCTGTCUTACGTTCTATCAUGGT	59075	TCGUTGTATTGAUCAGAAAAGCAGAACT
313109786	59076	CCTGAGUGCCCTCUCACT	59077	CACACAUGCCCTCCUCCAA
313342915	59078	CAATTACAGUCCCACTCCCUACAC	59079	GAGAAGCUATCATCTGUCACCCA
312720394	59080	CCCTCTCUCCTTTCTGTCCUGAG	59081	CCCACATGCCAUCGAAGTGUT
314163258	59082	TGAAATCTGCUCATGCCCUGT	59083	AGCCTCCCGAAUCCTTTGTUG
333518147	59084	CCAGCCTGUGTTTCTCCACTUT	59085	CAGTTCGGAAUCGCTGCAUC
314383080	59086	CGCCGGUGAGCCUAGAC	59087	CACCAGCUCUCAGGAAGCA
314074787	59088	CTGTTCUCAGGGTGTCCTUCAG	59089	ACGUACTCCGUCCCGAAGAA
327797967	59090	TGCACCCAUGGAGAGGAUGA	59091	ACACCACUGACCUGGACGA
327329791	59092	CUCTATUGGCCCCCACACA	59093	TTCACCAGCTUCCTCCTCTTTUC
318503495	59094	CCTTTCUCCAGGGCCTCAAUT	59095	AGGCTCCAAGTUAATCCAAATTTCTCUT
333483800	59096	GCUGACAAAGAAGAAGGUGGAGAT	59097	TTTCACAGTCCUGTACATCTTGUGG
333500471	59098	CCGTCUGGAAGCCTCUCAAAAT	59099	GTGGAGUGCATCTAUGGAAGGG
315414333	59100	GAAGACGCGGAAGUAGUAGCC	59101	TGCTGATCTGAAUCCCTCCATAGUA
313854230	59102	GCAGGAGCAAAAGGAUGGGAAATUA	59103	CGCTGAGGUCAAATGGCUCAA
313427245	59104	CAGUGACGCCGTACUGGAA	59105	GTGGCTACAGCUCCTTGGUC
314061165	59106	TCAGGGAAGGCUGAUCAGGA	59107	GCGGAGGCAGUGACAUCA
323670108	59108	AGGAGGAGGGAAUTCGCUAAGA	59109	GUCCCCCAUCCCACAAGG
324656304	59110	CCCGACTCAUCCTGCAAGUA	59111	CTCTGCAGACACUGCCCAUT
313779405	59112	TCCAUCTACUCGCCAGAGCA	59113	ACAGTTGGAGCUCTAGGTCCUAAG
313381050	59114	GGGCCUGAACAACACCCTUAC	59115	GGGAGATGAUGTTCATGGGCUT
314986629	59116	ATGAGACCCAGUTTGGCAUCAA	59117	GGATATCTTAUTCCTGGGCUGGAG
315497374	59118	AGCTGCGGUACTCAGGAAUG	59119	TCCTGATAAGAAAAUTGGGACCCTUG
313629226	59120	GCCTCCCAGCAGUACTTTGUA	59121	CATCCCTTCUCTAGGACTCCUCT
313075487	59122	GGACGUGAGCACTCCUCT	59123	GCTGUGCACGAAGGCAACUA
327716940	59124	GGCAGAGGTUCCTGTCAGAATAUC	59125	TGGUCCCCAAAAGCCAAACUT
223221577	59126	CTGTTCCTCAGUTTGTCACTAAAATCUC	59127	GCAAATTACCUTAATTTCCATAGUAGGGACA
332760232	59128	GCAGTGGUGCCGTCCTUC	59129	GAGATCUCCACACGGTAGTTGUA
332713113	59130	CATGGGAGUCTCCTGCACTUC	59131	GAGAGGGACAGUCAGGAAUGAAA
319426816	59132	CGCCTGUGTGCCTUCCT	59133	GGGCCAGGCCUCAAUCC
318975984	59134	GCATCCCTAUCCCAGGACTATTUG	59135	CAGGGAGAAAAAGCUCATTCATTCATUT
333687653	59136	TCCATACCUACCGTAAGTGCAUACA	59137	TGGTTTAAGAACTUGGGAGTAACCTTUT
318080912	59138	GCAUAAGCUGAGACCGAAGCC	59139	GCAACUACACACAAGAAGCAUCCT
319917167	59140	CACATCCCTAGUTTTCCATGGTAUCC	59141	AAAATGATTTTGTUGGAGGCCGUT
319925799	59142	GCAGGCTCUTGACTGTCUGG	59143	CCAGCUGAGTACGGCUACA
278043070	59144	ACCTTTTTGACUTTTCTCCCCGUT	59145	AGGGAGAAUGAGTTGAAGUGAAAACAAT
277862074	59146	CCAGAAGCAUAGCAATACGUAAGAACT	59147	CCATTCATCAAATTUAGACAGCACATCUT
313225874	59148	CTTCUAGGCCACATGGTUGCT	59149	GCCCTUAGGGTGTTTUGGACAA
279935416	59150	CGAGACCUGAAACCCCACAAUG	59151	TCAGTGGTTAUCCATCCTGAAGAUAGAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267435826	59152	CAAGGCTGTUCTGAGGAGCUA	59153	CCCAGAAGTCUGATTGAACATTTTCUCT
317070428	59154	TGAAATTAUGGAAATCCCTGUACCACAC	59155	GATTCCATCCUGGCTGAACCUT
316372502	59156	ACATACCAAGUAGCCCCUCCA	59157	TGCCAGACACCAUAGTTGAGTATUC
312946979	59158	GTGTATGCCAUGAGTATTTCTTUGCAT	59159	CCCACTCACCAGAUACTGATGUT
264617377	59160	GATAAAGAAGCCACUCCAUGCAG	59161	TCGGTTGTGUACATGCTCCTTTUT
265178670	59162	CATGCGTTUAGGCATAGUAGAGACA	59163	CCACCTTCUCGCTACCAGUC
257775957	59164	GCCUCTCTGATUACACAAACCAGT	59165	AGGGCUCCAAATGTGAAGUACAAG
327831356	59166	CTCCGUGCACAGAGTGGUA	59167	AACCAUGGCUCCCCACAG
241902207	59168	ACTGCATTCTAUTATGCATTTAACUAAGGT	59169	AAGAAACTTTUAGCACCAATGCAGAAUT
261119271	59170	AGTAGAATGTTACCAAGAUTATTTTTGACCUA	59171	GCTATCCGUGCACTCCTGUT
240330971	59172	CTGTGTGCUGAGAGATGTAAUGACA	59173	AAGCAAATCAAUCAAATATACCATGUGCAA
241480691	59174	TCCTCGACATUGATTTCTGTTTTUACCT	59175	CGAACTGGAAAGAUGCTGCTTTTAAUAT
242181132	59176	TCTTATTCCCACAGUGTATCGGCUA	59177	CAGUTAACAAGTAAGUAGGGAGGAGAGA
239943702	59178	GAUGGTATGUAACAGCGACCGT	59179	GCTACTGGAAAACAUTCAAAACTGGUT
333027794	59180	CGGTTTTCATATUGGACAGTGAGGUA	59181	CAATGGTCUGTCTCTGTGUCGT
332462631	59182	CTTACTCTGGGUCCTGGTTTUCC	59183	GTCAGTACTCAGUTTCTGCCTATCATTUT
313236335	59184	CCAACTCATCUCTGGCCTCTUG	59185	AGTATGAGGAGUCGCAGTCUGA
314614812	59186	AGCAGGAAAAGCAUTGAGCATCUA	59187	GGAGCAGGAGCUGATUGAGAC
312682364	59188	CCCCTCUGGGTGAGTACCUT	59189	GGACTCGCUGCAGACCUC
313051581	59190	GGGCTGCUATTTTGTCTAUGGT	59191	GCAUCAACTUCACCAACGAGAAG
264177814	59192	GTAGGGAATGAUGAAGTAAGTGCTUAGG	59193	CCCCAAAGTTCUGCTATACATGTTUCAA
327851640	59194	TGCTGTGTTATATUCTGCTTTCGTAAUGT	59195	GCATCATCCTTAAUCTCATCCCATGTUG
328072276	59196	GGUGGGAGAAGUGAAAGGAAAAGT	59197	GCTTTACCGAGUTTTCCUCCGAT
324476988	59198	AAGGCTTCTGAGUGGTACAACTTTTUA	59199	CAAGGCUGACACTCACGAUGA
321506639	59200	GCACACCAAGCACAGUCUGA	59201	CCAAGCTUCGCCTTCCTTUCT
320053325	59202	CCACCTTTUCATGCACCUGAGAA	59203	CTCCTCTUCACGCCTGUGAC
319050987	59204	ACAGUCAGAGAAUCAGGCGAAG	59205	TTGCCACUAAGGCCCTACTTTUT
266841526	59206	TCCATGGTUCCTACGAAGCUCT	59207	GTAAAAGGCTUCCTGACACTUGGA
316557308	59208	AGACTTTGATGAUTGTCCTGTGCUT	59209	ACTCCAGATATAACUGGGACTTCCUG
315910562	59210	CCATCTTGGTACCUATATTCATGGCUAT	59211	CTTGCTTAAGAUATGGACGAAUGCAAAG
316710560	59212	AAATTCTGTCTUCTTTGCTTACCUACACA	59213	AACAGUGGAACCAATAUCAACAACCT
317338003	59214	TCTTTAAGAGGGCAGUCAACUGT	59215	GGTTTTTACACCUCTCCAGATGGUA
326553941	59216	CCCTTTTCTUGCTGCTGTGTUG	59217	GTGUAAGCAGGCAGAGUGGAT
272425910	59218	TCCUACAGCCACGGATGCUA	59219	GAATAAGAGCAUGACCCTGCAUGA
318476194	59220	CTGCAGGAAACUATCTCTCGGTUC	59221	AGGATAGAGGCCUACACACAUCT
315672576	59222	GCUCCGACCATUAAAGCCCAAT	59223	ACACTTACTAGACACUCCTCTCCUC
316103584	59224	TGGGAAGACAGAGCUGACTUCT	59225	GTGACTCGTGUCCTTACGTGUA
316533678	59226	GTCTGTCCGUTGCTCCAUCA	59227	GCTTCCTTUGAAACTGACATGTUCA
333254796	59228	GGCACUCGGGAAGGTUCT	59229	GGGAGTTGUCCCTAGGTCUGG
333434485	59230	GGTGCTCGUAGTAGTCGUGGA	59231	TAGACCUCAGATCUCAAGGAACCA
333601338	59232	GGTCCTACAUGCTGGAACUCA	59233	GTTCCTGGUACCCATGCUACAG
321540650	59234	CTGCCCAUGCTCCAAAGGUA	59235	GTCTGCCCUCTGTTTCTGGUC
241709768	59236	GTGTTATTGACGUCATAGAGTGACUAGA	59237	GCACUGACCTCTATGUCCACA
264637151	59238	TGCTGTCTUAGGACTGCGTUT	59239	GGAACUGGCUGCGCAAC
241099729	59240	GUTTCCCTGCUGCCAGGAT	59241	CUGGCCUACCGAGAGACAC
239505060	59242	GACATGATGGCUCGATACGUCT	59243	CGCTTGUCGTCACAGUGACA
239348263	59244	CTCCCAGACUTACUGCCCAA	59245	GCCUCACACAAACTCGGUGAA
321558950	59246	CUTGTTCTUGGCCCGAAGG	59247	CCAGTTUGACCGACUCAACCA
318179402	59248	TCACCCGUGCATUCGAAGT	59249	GGGATACACCUTCACGCUCA
319654006	59250	GTTCTCAGCCGUGACGATGATAUT	59251	CTCGUCGTCAAUGCAAGCC
320138881	59252	CCTCGGCCAUACTCACCACUA	59253	CCAACGAUACCCTGTTCUCAGT
319765516	59254	AAACACAGGTTTUGATTCTTTGCATUCT	59255	ATCTTCCUAGAGGCATTCATTGUGAAAT
318947269	59256	GATAATCCUACCTTTGUGGCCAGT	59257	TCCAAGTTUGGAACACAGGCAATAUA
240651582	59258	GGTGGACTUGAACTTGGACTUGA	59259	GGTCTCAGUGCGCTCTCTUG
239185226	59260	CAAGGTTCUGCCACTCUCAGAC	59261	AGGACAAGACUGAGTTCTCCAUCA
235266587	59262	CAAACUCCACATTCCUGGCAAG	59263	CTGCCCAUCTACUCGGAGAAG
268963268	59264	AGATCCUCACCGAGTGCTCUT	59265	CUCGCAAGACGUCAAGGGA
259573079	59266	GGCACCTCUCACACCAATGUT	59267	AGACCTGGUACGAGTACACCUG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
264638343	59268	CAGACACGAAGAUGCCAGUG	59269	CACCCTGGAGUCATCCGTTTUA
261759123	59270	CAGGAAGUAGATGAGGUCGCAT	59271	CTACCTGAUCCAACTGGUGAAGAG
268765807	59272	CCCCTGUAAGCAAAGUGGACAA	59273	ACCCTAACCCAGUCCTTTTAUCCT
328175871	59274	TTTGCTTTGGTTAUTTAGGAGTACACUGT	59275	GCAGCTACUGACTGAAGAACAUCA
327196640	59276	CACAGACCAUGTCATCGUCCT	59277	AGGCTUCACACCAAGAAGUGT
327651181	59278	CGTGTTCCCAGUCTGCCATUT	59279	GACACTGTGUGACGCCGUA
318258992	59280	CCCCACCAUACTTCCUCCCAA	59281	GATTCAGCTCUGTACTCCTCTTUACC
318248551	59282	TTGCCAAGCCAUCGCTCUAA	59283	TCTGCCCAGGUTTCTATTGTTGTTUAA
262007802	59284	CGGAGUGAACCCCGUGAAC	59285	GAATGAACACACACCCUTCCTTUC
263915787	59286	CCCAGCCCCUGTGGAAAAUAC	59287	GCCCCCAUTACTGUGGAAGAAT
268167175	59288	CACTGGCUGTCTTTGCGTUT	59289	CCTTGTUCCACCCCCGTUG
241053357	59290	CAAATGCCCCAAUTGCAGGUA	59291	ACTTTTATCACCTUTCCTTGCCTCTUT
268712801	59292	GGTCTCAGACACUTTGAGCTUCT	59293	CCCTGGACUGCTTCTTTCTGUC
268888446	59294	GCTGCCTGAGAAAUGGAACAACAUA	59295	ACUGCAGTGTUCACAGAAAGAGAG
267727189	59296	TATTCCTGUCCTCACAUCAGCAT	59297	GCATCTUGGCCATGTTGUCAA
267960681	59298	GCCCCCAAGAAUGATGACCUA	59299	CCTTGTAAUCCATCTGCUCCGA
325582458	59300	AGGACTATTAUAACCCGCAGCCTUA	59301	CTGAAGGCUCTCCUCACCAG
325561094	59302	TCCUCGACAACAGCCACTUG	59303	CCAGGTUCCGCTTCTUGGT
325569064	59304	TGAAGCUGGAAGCCATCGUG	59305	CAUAACGGAUCAGCCCCAGAAG
325571961	59306	CUCCTGACUCCCCGAGACA	59307	CCGAGUGAGGCGCTUCC
237780540	59308	GTTACTGCAGCUCACAAAUGCT	59309	TCACCATTACCAUTCCAAATATTCTUCCA
236222301	59310	GATTTGTTGCAGGUTTTGGTTTTAAUGG	59311	TGTGTGTTCTUAAAGCAGGCATACUAAT
332697158	59312	TGAUGGCCAGGAACTUGGG	59313	TCTGGGACCUCAGCGTACUAA
332852086	59314	GAGTGGAUACCCGAGTCGUAG	59315	CATGGUGATGATGUGGGAAGACA
226255020	59316	CAUCCCCAGGCCTCUAAGGA	59317	TGACCCATAUTCCCCTGCUCT
329550528	59318	GAAGAUGCTTGGGUGGGAAAC	59319	CATCTCTCCAAUCTGACTCCTTTUCT
226281609	59320	GCAGCAAUGGGAAGGAGGUAG	59321	TCCCTTAAAAAGUCCCACTCAGAGUAA
225659492	59322	CCTGAUCCAGAACGCCUCAT	59323	CCTAACTGTUCCTGTGACTUCCC
227017398	59324	TGGACACACAAGGCCUCUC	59325	AAGGGUAAGCGTTGCACUCT
253669462	59326	AGAGCCAAGGUTTGCTAAUGCT	59327	ATGACGUGATCTGUGACGAGAC
266447687	59328	GAAGGTCGUCTGGACTGTGUT	59329	GGCTTTTCTUGCCTGTCTUCAG
258635441	59330	GCUCTCTACCCUCCAGAGGAAT	59331	TCTATTTGTCUGACTAGCCTGCUCT
316429920	59332	CCCUTCAUGCGGAACCACAA	59333	GGGAGAGCUGCACTTCUCAG
316325585	59334	GGATGATGACAUCACGTGTCCUT	59335	CCAGGAAGAUGACCTGTGTGUAG
315882837	59336	CTGCTCCATTUGTGCTCTCTCUT	59337	CTCCAGGUGACACAUGCAAC
331345609	59338	GATTTGGUAAAGGAGAAGGTACCUGAAG	59339	CCCTGUGGAGCAGGTCAGUA
330761759	59340	ACAGAGGATCTUGTGATCAGCATTUT	59341	CCCTGGUAACACTGAAGTTTGUGT
268958422	59342	ACTGAGGTCUCAGAGCCAUCT	59343	AGCTCTUGGCTGCTGGUG
262389686	59344	GATCCCGCUGGUCAACAAAC	59345	CCGGCCCACGAAGUTCUC
324589668	59346	GGAGGCUGACCTCCCTCUAC	59347	ATTCATGUCCCCAGGGTAGUCT
323438384	59348	AGACUGTAATGTCCAUGGGAGAACT	59349	AGAAGGAGGUAGCCTTGGUGT
323699665	59350	GAGACGGUCATGGAGGUCAT	59351	TCAAACAUGGAGCGCTGGUT
323369502	59352	GGAGCTACUGAAATTCCUGCAGAT	59353	CTGGTTCCAUCTTTGCTCCUCA
323824208	59354	CACCTCUGACCACCTCAACUC	59355	CTACACTCUGACTCCUCCCAACT
323332797	59356	AGGCTTCAUCACATACCCCCUA	59357	GGAAUCCCAAAGGAAGATGTCUCA
256112718	59358	GGCCTCGUGCATGTTCCTUA	59359	CGTTGTAUACGGCAAACACATCATUAC
324222850	59360	GGCTGTCAGUTTCTGGGTGTUA	59361	GTTTCTCTGACGUCCCCCAUAG
324910858	59362	CCACCTGUGGTGGGTAGTUAG	59363	ACCAGGATTACGAAUGAGGCAATTTAUT
315784931	59364	CCACACGCUCGTCTTCTGUA	59365	TGTCAACCCCCUCCTTTTCTUG
316822810	59366	CACCCTGGGUCTCATCCCUAA	59367	AAAAGGCTAACCUGGAGGTGUG
332998152	59368	CTGAACAGGUGAGTGUCCACA	59369	CTGTCCTGUTAGGTGGUAAAGGAT
266208663	59370	CCCTGCTTTCUGCCTCTCTAUAC	59371	CCATACTTGGCUCTATTCTGCTTCUC
225434981	59372	CAGGAUGAGAAAGGCAAGCCUA	59373	CTCTTGGGAGUTTCTCACTACTTUCC
315790595	59374	CTTTGACTTUCAGCACTTAGTTCACTUT	59375	CACTACAGAGCAUGGGTTCUGAG
323667823	59376	AACTCTTTTUGGGTCTGATTCTUCCA	59377	GCTTTTCAAACUGAAGGGAAGTUGT
258709215	59378	CTAAAGGTCACCUGTCATTTAACTUGGA	59379	CGAATGGTUCAAAAGCAAAAATCATGUT
263099334	59380	CGAAGTTCACUCCACTTGAAGTUCAT	59381	CGCTTGTTTCTTUTGTTTGGTAATTCUG
264668639	59382	CTGGCATUGGATTGTCTCUGAAAC	59383	AGCTAATCAAUGAGGAACTTGAGACAUT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268512062	59384	CTAACCTGUGCTGTACTCTTTUCAAGT	59385	CAGGCTTATTCTGUGATCTTTCTTGTTUT
324650288	59386	AGCTGTGTGATTUTCTCCACAAGAAAUA	59387	GTAACAGTGTCUGCTTCCATAAUCCT
318434158	59388	ACCTGTAATGTUGGTAGGTTTTCAUGT	59389	CCAGGGTGUCCAAATCTGATTGTTUA
315511019	59390	CCCTGGGTUGGGAAGACTUAT	59391	GTGTCAGGAAGGGUATTACAACGTAAUT
290213833	59392	ACTCCCCAGUCATGUCCCAAT	59393	AATATGUACAGGGAGGTGCUAGGT
289756287	59394	CCTTCATCCCUCACTTTCTCCTUT	59395	TGTGAGCUGCAGGGTTCTCUA
327896849	59396	GGAAGAGGCAAAUATTCCTCCGTUA	59397	AGCTGUGTCACCAUCAGGAAG
304880539	59398	GTTTTGCAGCCACUCTTGAUGA	59399	GGAGAAGAAACACUGGCCTCUG
302867539	59400	GAUTGATGTGGUGCGCACAAT	59401	GGATTTTCUGCAGCACUAAAACGA
257419549	59402	AGCTATGGGCUTTCCAGCATUT	59403	GGTATATGATGGACUCCTTTGCTGUG
263776537	59404	AAAGAUCGGCAGAAAACGCUAGA	59405	TCTCACTGGUCTCTGTTUGCAC
269305032	59406	TTTCCCTCTTUCTCTTCCTTAUAGGCT	59407	ACTTAAGTACTGAGAUAGAAGCTCTGUT
267630140	59408	GCTCCTAGCUAGCTCTAGTGCUT	59409	CATGGGATACTGUGTACCAATACCAAUT
259463743	59410	AGGTCAACCUGGTTUGCCA	59411	TAGCUTCAGGTATUAGAAACAAGAGCAT
268707335	59412	CACTCTTAGGUCTGTTATCUACAGGGT	59413	GATCCCTGGACUGCCTCTTUC
261808994	59414	GTTTTCAGGGUGAGCCUGGT	59415	TUGGAGTAGAUAAGGAAGGAAAGAAGGA
257393811	59416	CCTGGUTCCTGCTUGGAAGAG	59417	TGAAGGAAGCTUTGGACCTGAATUAAA
259647316	59418	CCTTAATGTGCUGTTGAGTTAGAAUGG	59419	TCCCTTCCTUTTCTCTTGCTTUGG
313634317	59420	GGAAAAACCAAAGUCAGGCAACUAA	59421	TGGCAGAAGAAAAAGUTATGCTGGAUA
313077562	59422	GACTTCAATGAAAGCUACCTGGTAUACT	59423	TCCAACACTACUGGGATGTTCTUG
318637327	59424	CTTCCTGCUGCTCTTCTGAUCC	59425	GTTTGATCAAGTACUCATCCAGCTTCUT
229057169	59426	CTTCCCCACCUTCCAATTTTGUT	59427	TGTGAATGGCAUGTACAGAATCTAUGAC
316944969	59428	GACTGTTTTTCCUGATGTGGACTATGUA	59429	CTCCAGTTTUGACACACCATCAGTAUAA
316590633	59430	AGTGGTCCCAAGUAGTCACTUAGA	59431	CACTAAGGGUTCGTCCAGTUCC
314763393	59432	GCTCTGTCAUGTGTGATCTGTAUCA	59433	GTCGCGCCUCCCATTTUT
266570983	59434	TCCAGGAGCUCUGCCAGAT	59435	TGCATGGGUGGGTGCUG
312774806	59436	GAACCTTTCTUCTCGATTGTGCUG	59437	CCAAAACAATGTUACCATCATGGCUAA
312722746	59438	GGACACGACACUCACCACUA	59439	CCTGTCTCCUGAGGCTGTUC
314921322	59440	CCCTTCCUCACCCTCCTCTUC	59441	CCCGUACTGGCUGCACAA
332562165	59442	CGCCCCCGAGAAUGGTUAC	59443	TGTTCACTUTCCCTGGUGAGAGA
261281270	59444	CACAGCGGUCATCTCTACCUG	59445	CACGCAACCCAGUACCACTUA
316044342	59446	GGATTCATTAUCTGAGATTCUCCACCAG	59447	TTACTGTGTUCCACCCGTTUCAT
317666266	59448	CCTTTGCAATGGGUAATGGAGATCTAUT	59449	CTCCCACUAGAAGAAACAGAACTUGA
318129195	59450	GGTGGGACUGTGCTTTCUGA	59451	AGTGAGAATGAAAUTAGGGCTCUGG
314262552	59452	AGAGTCUGGCCCTTGGTTGUA	59453	TCCACCTAUCTGCAGTCTUGGA
319712797	59454	CTTCTUCCGCCAGUCGGT	59455	CTCCGCUCGGCTUAGGA
262159587	59456	CGCCTACCAGCUCATGCAUA	59457	CAACCGCAAAUCCCCTAAUGG
264892401	59458	GTCCACGAGCAGAACUACGUC	59459	GTGGGAAGUTGGCATCTGUCA
320776974	59460	GTCCTGCATUGTCCATTTCCTTUAG	59461	CTCAATTTTAATACUCAGGACAAACUGCAT
315283080	59462	CCCUCCGGAATCGUCAAGT	59463	GAUGTACUCCAAGCCGAAAACC
315037401	59464	GATTGGCCCUATTGGGCTUG	59465	CCAAAGCCAATUAAGTCCTAGCAAGUA
260269252	59466	GGAGGAGGAGACCUGGAACUG	59467	CTUAGGCCCAACCACUAACAGAG
257317529	59468	CCAATTTCUGGAGGCGGTUCA	59469	TGATCCTTTCTTUGCTGTTAGCTTATUCA
269204060	59470	CCTGTGAAUACCGGAGGTTTTGAUAC	59471	GCTCAGGAAAAGAUGGCAGAATACTUAA
257283083	59472	CTGGAAGACCACUGTCACCTUT	59473	ACAGAGACACAAAUGCTCCAGATTTTUA
264521869	59474	GCTGTCCTCUAGGACCTGGUT	59475	GGGCATTCAGTCUACTTTTTACTTGGUT
263208014	59476	CCATTATTUCAAAGGAGCUGCAGT	59477	GGGTAGAGGUATTTTCCAATUGAGAAGA
266476488	59478	CATGTAAGGTGAUCCCAAATGTAUGGA	59479	CAUCAGCAAAAGCCAAACUAGGG
314805437	59480	AGGACCUGCAGGAGCUCA	59481	CGCGCUCCTTGGCUACT
325289495	59482	TCCCTTTCCCUTCCTTCCUCAA	59483	TTGGGATGAAGUGGGAAACCUG
327099126	59484	ACAGACUGGGCCAUCAGAGAA	59485	TCTCCTCTGGACUCTTTGGAGUG
326700286	59486	GAGGAAACGACUGACCCACUC	59487	TGCTCCCAGACUAACCTGUCT
327765902	59488	GTTCTCAGUTCAGCTGUCGGT	59489	TCCATTTGUAGGAGGTGGGATCUT
326906096	59490	TCAGTTCAGTAUCTTATCCCCGUGA	59491	AGAGACCCGACGAUCCUACAT
324192191	59492	GAGCCUTCAUACCCCGAAGT	59493	AGAUGCCTCTGAUGGGAAAAGG
332364906	59494	CTGGTGTCTUCAGCAGTATTTTUGT	59495	TTGATCTCCAGCUGGCATTUCT
323956267	59496	AACAGACGAACAAAACCUCTACTUACA	59497	CCTGCAGGGUTCTCTCUGAAC
326265573	59498	CATUAGGTGGAGUGGAAGCCA	59499	ATCAAAGGAAAUATGACCGGGUAACAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324279228	59500	CATGTTGTACUGAATGCACCTATGUAGA	59501	CCTTGTGATTTCUTCCATGTTTGTCUAAA
325247175	59502	CCTAGGGUGACAGCTCUCACA	59503	AGGTGCUGACATCCTTUCCAAAG
325453947	59504	CCAGATUACAGCACAAGCCAUT	59505	AGAAAUAAACGACAAAAGCUGCAACC
324880551	59506	TCCCACUGGACATCCUCAAGT	59507	CTCAATCAACUGCAAGATGTGCTUC
325114070	59508	CTAGTAGUCCCTTTCCUCGGAGA	59509	CTGCUCCTGAACUCCCAGAAA
325024345	59510	TGCTTTCTAACCUTTGCATTATGGAUGA	59511	GCAACGATCTAAUGAGTAGGGTATGUAAA
323305162	59512	CTCAGGGCAAUTTATACAGCATTTUGT	59513	CAGACACTGGGUCCTTCTTAATATTCUT
325115544	59514	GCTTAAGCTTTCUCAGGACAATGUA	59515	GTTCCCAAAGCAUATAAGCTAGUCAGAAT
324560144	59516	TCTCTGTAAAAACUTGCAGGTTCUGT	59517	CCTTTGACATCUTTGACTTGGTAUCAGT
326415668	59518	TCTTTGTTCCAUAGGCAGCTGUT	59519	CATTACCGCUGGGAUGAAAAGGA
324603937	59520	TTTAGATTCCCAUCTTCCCATTGUAACC	59521	GGCTAAGGCAAAUATGATTGAATUGACA
323357127	59522	TCCGGAUGGCCCCCTTAUAT	59523	TCTTGGACTATUGTACCCCTATUAAGGT
325608884	59524	GATGGTGGATAUGCTTGTGGAAUCT	59525	GCACAAGACAAAAGAAAUTCCGTTUC
326608397	59526	GATCAAACAAGTAUTTTCTGCTGGCAUA	59527	AAGAAGCTCAUGAATTGAGTGAAGAUCA
327595952	59528	AAACACATGUAGAAACCTACCTCAAAUGT	59529	GCTGTGGTGAGUCGAATTATTGAGAUT
326579927	59530	CAGAAGCAGCCUGGGUAAAAC	59531	GGCAGCACTTTAUTTGCAGGTATAGUAA
235555845	59532	TTCATGGCGUAGTAAGGTTTUCACT	59533	CCACTGGTUAACAAGTCTTTGUCCT
320137099	59534	CACCTATTCTUCCAAGGCCAUCA	59535	GAACAAATCTACUGGGTGGAAGAUCAT
266019492	59536	GGGAUCACCAGAGGATGTTGUC	59537	TTTTTGTTTGUGGTTTGGUGCCT
267656162	59538	GAGACAAGCGUGTGGCAUAC	59539	AGAAGAGAUGGGAGAAAGGCCTUA
269191432	59540	CTGCCTCUGGAGAAGGACCUA	59541	GGUGGTGTGTTGUCAGAGAAGAC
327219980	59542	GTTTCCTUGAGCGTGCTGUC	59543	AAAGTGTCUGCCAGGAATTGAACUA
314046002	59544	TCCAUCCGUCCGGAGAGAA	59545	CAAACUTGUCCAGCAGCCA
312955485	59546	GTGAGTTGCUCTCATACCACAUGA	59547	ACCCTAGAAGAAUGGGATTCAUCACT
315238274	59548	GGCAGAAACUGCTTGCAAGUT	59549	CCAAACCCUTCCAGGAUAGCC
323506360	59550	TCCTCACAGAUATATTTCCACUGGCT	59551	GCCTGGUGTTGGCUGGAT
324513019	59552	TCTTCACTCTCUAGGGTATTCATTAUGCT	59553	GACTGTGTTCUGTCTGAGTGUGT
323642558	59554	CUTAGAGGACUGAAAGGAGAAAGCAT	59555	GCCATGTAGAAAGGUAAACTGCTGATAUT
268420839	59556	GGGTCGATCUGCCTGTTTGUT	59557	ACCTACCACUTCGTCAUGCAG
255191386	59558	TCATCCTCCTCCUCCTCTGGATTAUA	59559	GCGTTAGUAGCTAGAGAUAAACCAAGT
268784425	59560	AGAAAATGTCTCUCTCTTTTGGAUGCAA	59561	AGGGAACUGAGGGCAAAACUG
268189387	59562	CCCAGAACAUCACATATCACUGCAA	59563	GCTGACTGCUTTATGACCTATATUGAGAA
258621639	59564	CCTTATCUACCATTCATTGCUGCAAA	59565	ACAGGCAUACGTGGTCGUC
268084182	59566	CAGCTUGGCCCAGTTATUCAGT	59567	GCTCCTTCCAUAGCTCCATGUC
235298457	59568	ATCTTGUGGCGGATGTGGUT	59569	GCGTCGGUGCTGTAACAUGA
333183691	59570	CAAGAAACTUCAGAAATTTGCCUCCA	59571	GCACAACUTGCAGAAUGAACCAAT
332450939	59572	AAGTTGUGTAGCCAUGGGACAT	59573	TGTCAAUACCCATCTTCUCACGGA
333642304	59574	TCUAACCTTUCAACAGGCAGCA	59575	GCTAACATTUGCCTTGCTTGAUGAAC
233506067	59576	CCTTTCCCUTTGGTGAGGUGAC	59577	GGATTACUCTGAGACCUAGGCAAAAA
323756160	59578	AGGCACCUTCTCCGTCUCT	59579	ACAGCCCCUGAUGAGGACA
323863971	59580	TUGGCCAACTUACCACAAGGT	59581	GCTGGCACAUGATGGACTTCUT
314650481	59582	CCAGTCUCCCCGGTACUAACA	59583	CCTCTCCUGGCAGAGTUCAAG
327939946	59584	CTGGTCUCCCACATGTGUGAT	59585	TGGAATGGGUTGGTTTCCUCAG
264456900	59586	TTGAGATTCGCCUAAAACATGATGUCT	59587	GCGCUAAGAACACCTCCACUG
257497511	59588	CTTCCAACAAUAGGATTCAGCAUAGAGA	59589	AATAAACCAGCCAUAGTGGTUAGAAACA
257757269	59590	CTGCAAAAUGACCTAAAAAGCUGGAA	59591	GCCAGGGTTTAUCTTTGATGTTCTCUAA
332136240	59592	GGAGUAGGGAAGCAAAGACUGAA	59593	CCTGCTGUCCTGCTCTTGUC
332187944	59594	GTACUCCACTCCCUCCGAGA	59595	GGCTTTCCUGCCAATTTCTCCUA
332033087	59596	GGAAGCUGAGGCACTGAAUCT	59597	GGCAUCTGAGACUCACACCAA
332163219	59598	CGGCATGUGGCTAGTTCCTUC	59599	GTGGGTGATGUTGTGCTTCTTTAUC
332069291	59600	ACAGGCUGGATCAGGGUCA	59601	CTCTGCCAATTUCCTTACAGGGAUAG
328832557	59602	AGAGGCUAAGCCGCTCAUC	59603	GCCUCCCCAGUGAAGAAGT
328619261	59604	AUCTCCTGGCUGAAGAACGG	59605	CACGACGCAGGUGTAGTUG
328931069	59606	GCACAAGAUCTCCCGCTUCC	59607	AAAGTACCCUAGGCTCTACAUGGT
264379159	59608	GGGAUCGCCCCATTTTGUAT	59609	CCCTTGAUACGCTCCGACTUG
263999876	59610	AGATCAGCTUCCTGTTCGACUG	59611	CCTGGAAAGGUTCTGGTTCCTUAG
327878942	59612	TTGTCCACGUAATGAGCATGUAGAG	59613	CCCCACAGGAAGGAAUTCUGG
333577144	59614	GCACGGUTTGAUGGCAGAGAT	59615	CCATAGCCTTGCUGATATTACACACUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332331440	59616	GGGTTCTGUGGAAGACAAUACC	59617	GCAGCCAUCAATTTGTTTTAAGUCACT
332324907	59618	CTAGGAAAATCATUAGGCGGTATGTAUCC	59619	GAGCTCTATTTUGTTCCTCTCCAUCAA
312977335	59620	AAGTAATGGUGATTCTTGGCAUCCA	59621	GCACAATCAAGUCTCCATCAGATTUAG
324302644	59622	GGGCUGAGAGCGUCGAG	59623	TCACCUGCAGCAGCAGUT
268110520	59624	GATGAACUGCACAGTGGCAUT	59625	TGATACATTTTUCACCCAACUGACCA
263619062	59626	CTGTCAUGGCTCTCAUCAAGGT	59627	GCCATCATTGUTGTGTTTCAATGUG
264831451	59628	AGCTGCCGAAGGUGAATGTTTUA	59629	GCAATAACAUGAGAGCTTGCCATTUT
262669332	59630	TGGTTTTAAAGCUTGAGGCCCAUAA	59631	AGTCCCAGATTCUCTATTTCCAAAACCUA
259057501	59632	AGAATCACTGUCTTCATTACTCUGCAAA	59633	CTGAACAAAGCCGUGGAGUG
265983462	59634	TGAAATCATATCAAUGTCAGCCCCAUAG	59635	TCCATGTAAATATCUCATTCTTTTCCATUAGCA
267856241	59636	ACCATTACCUGTTTCAGTTTAAUCGCA	59637	TCCAGTTTACAAUCCATGGCTGTTTUAT
289972831	59638	AGAAAACCATCCUGAGACACCUAAAAA	59639	GCTCTCGTUTTGTTTGCATUCAGT
292328437	59640	GTTCGAACAAAAGCCAUGAAGUG	59641	TCGAATTATCCAUCAATCGTCCAUGAA
291781287	59642	CCAGTGTGUGCCATATTTAATUGCT	59643	TGUGGGCAGAGCATTTAUCAAAGAA
321459287	59644	CAACACAGACGAGCCUTTCTTATUT	59645	CCTTCACTTCUGACTGTGTACTTTGUA
329454935	59646	TGGGCTTACUAATGACCACUACAGT	59647	GAAGCACAGGTUTTTATCAGTCATTGUT
223605033	59648	GGAAGTGUGAAAGCATTGAUGGAAT	59649	ACTGAATAAUACACAGGTAAGAAATUAGGAAA
222774177	59650	TCCTTCAUCACAGAAACAGTCATTTUCA	59651	TTTTGAGGCUGACCACTTCTACUC
326756821	59652	AGCACCCUAGAACCAAAUCCAG	59653	AATCGAACGACUCTCAAAACTAUCAA
327580185	59654	GCTCTCCCCUCATCCTGTUT	59655	GGCTGCCAGUGCCTCUC
326566219	59656	CUCTGTTTTCTGTTUAGGACCAGGAG	59657	CCTCTGGAGUACAGGAAGAUAAGGT
325000666	59658	GAAAATTGCUCTTCTCUGCAGACAA	59659	CTTCTCCTCUAAAATGTACACAGUAGCA
237611217	59660	CCTGAGGGUGCTTTGATCUCAA	59661	GACTCTGAGCUGTGTTCTAUGGG
242566923	59662	GACAGAGCAAAAUCATGCTGACUG	59663	TCAGAAGGACAAUGTTTATCAGCACTUT
238549388	59664	CATGTTAATGTUAGCTGGTGCTTUGT	59665	CCAGTGGCAATAUGATGAAAAGTATTTTUGT
235819819	59666	CTGACTTGTTTUATGCGGTGTACUT	59667	GGGUGGCACTCAUAGAGCAG
239855743	59668	AGAGCAAUCAACAGGAAUGGCT	59669	GGAAACCAAGGAUTGGGATTUGG
268961285	59670	CAGCUCACCAUGCAGAAGGAA	59671	AGTGGCCUTTTGCTGTUGGAT
316083975	59672	CCCGAACUCCATGGGTTUCC	59673	AAAGATGAAAAGCUCTGACAACCUCA
331569084	59674	GGGAUCAGCCCCUGGAGT	59675	GGCGGACAGCUTCAAAGUC
332008894	59676	GCUACCGUCCAGGACAGG	59677	CTUAGGCAAAGGCAGCAUGT
331946855	59678	CCACACAGUCTCCATGAAUCCA	59679	CTGUACGGCCUCCACGAG
331711245	59680	ACAGAGGGCAGGGUGTUACT	59681	GCGAGTTUGACTCCTTCGUGAT
259425792	59682	GACCATUCACCTTAGCUCCAGAC	59683	GGGTAATGTTCUCTCTGCTTCATUCC
325925876	59684	ACAAUGACAACUCCCCAAACCA	59685	TGCTGATGUGATGTGCTTTCUCT
324299616	59686	CCTGTCUCCTCAGGUCCAGAT	59687	TTCTACTGTGCUTGGGAAAAGAUACC
314390827	59688	GGTACACCTTGTUCTTCTCCAGTTACUA	59689	TTTGATCUGGCGACACAUCGT
271522863	59690	AGAGAAGCUCACAAAAATTTGTCTTUGG	59691	AGGAAGGAGAAGUCGACCAUCAT
270895342	59692	GCACACAAUACACACACATGCAUT	59693	AGGAACAAAAGCUTCTGATTCTCCTUAG
271882226	59694	ATTACCAGAACAAGCAUACCCATTUCT	59695	GCCUTGUCCACAAACACCAGT
270073156	59696	ATGCTCGCCUCCGTTAAGUT	59697	CACAGGTGCUATGAATTCTTAGTUCAGA
271383849	59698	GTGAGUGAATGCUGACCCCAT	59699	GTCAGAGGCUATTGGATTCTTCUCAA
272501880	59700	GTTATATTAACAGUGGTCACUCACCCA	59701	GGTGATCCCATUTGAATATGCTGTTUT
271971206	59702	AGACTACATUGGTCTGGTTUGAGAAAA	59703	AGGAACATTTGAUGATAGTGAGAGGUCT
319473951	59704	ACACGTGTCTAAUATCACATGGAAUG	59705	ACATCUCCCGACTGCCUCT
269582037	59706	CTCATAGTCTTUAGGATTGTGGGUCAA	59707	GGTAGTGGTTUGAATCTGACCTUCA
317483957	59708	GCCATTTACUGTACATTCACCUCCAT	59709	GGCAATAGAAAAUGAACCTGTAGGTTUT
317097805	59710	ACTCUCTATGCATGUCCCACCAT	59711	ACACGAAGTGUTTTTGCATTTCTUCA
317748331	59712	GTGGAAGUGACGAAGGAAUGACT	59713	GCATTCCCCAUGTGTCTTCUCAT
315544373	59714	GTGAAGGGACAAUGGATAAACAAGTCTUA	59715	TGCACTAAUGGGAGCTCAAACTAUC
263235645	59716	CAAAGTATGCUTTCTGTAGCUAGGAAA	59717	CTGGAAUTCCTGGUGCAAAGG
265224530	59718	CACACAUAAACAATACUGCACACACA	59719	GCTTCCTTTAACAUACATGACTGATCUCA
262014505	59720	GCTGCTTTATCUACCTGGAACUGAG	59721	CAATGTACCCTAUTGAAAATGCATGCUT
254417419	59722	GCATTCAACUAGTTTTTGAGGCUAGAAC	59723	TTTCAGGGAAAUGACATTCTAUCACCAT
333211379	59724	GCTGATCTGUATCATCGTGAUGCT	59725	TCATGTTTACAAGAUCCAACAGAUGAA
318273153	59726	CGTAATCCAUTCTATTCCAGUCAGCA	59727	CTGCTCAACGAGAUTTCTGATTTCTTUT
321165432	59728	TGTAATGATTTTTCAGUCTTTCCAGTGUCA	59729	CCCAAGCTUTCTTCTTACCUGAACAA
269310884	59730	AACTGGAAACCAGAUATAACTTTGAGUGT	59731	AGGAUCTTAACCATTTUGAGGACAACAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268011970	59732	ACGCACATAATUTGGTCTTGACUGT	59733	CAAGCAAAGTGGUCATTTCAACATACUT
267968740	59734	GGUCAGGCAGGAGATCAUGAAC	59735	GAATTTCTTCATUTGCATGAGCAUCCAT
268869295	59736	TTTTAGGTAACAUGTCACCTUGCCA	59737	CCCCTAGCAUAGAAAACCTCATAAUCAA
264973316	59738	GCTCGTCUTCAACGTGTUGT	59739	AATTATCTTGUCCACATCTTCAUCGCT
267287321	59740	GTACTTAACCACCAUTTCCCACACUT	59741	GCCTCCAATCUCTCTACCAGTTUG
261114578	59742	GACCCUTGCTCTUGGAAACCA	59743	AAATGGTGAGGUCTCCAGGATUAAAAG
314275595	59744	CTTCCTGUAAACAAGCACACUAAAAACT	59745	AGGAAAGTGGAACAGUGAATTAACAUCA
230412109	59746	CATGTCAGUGGATTGGCTCUCT	59747	AGTAATGGGAAUGGAGAGGCUAGG
231730447	59748	TTCTACTUGGCTCCCTUCCCT	59749	CATGTCCCCAGGUGTGACUAA
224486247	59750	AGAAACATTGGAAAUGGGTGAGGUT	59751	TCACCATGTTUCTGTTTCAATTGTUCAG
222978904	59752	TGUGAAGTAAAUGCAGAAGACAAAGAGA	59753	ACAACTTGGCUGGGTGATTAAATCAUAA
222173926	59754	CATGGATGCTTCUAGACAACTAATGTUG	59755	ACCCTTACCUGGGCTAATTGTCTATUA
224492231	59756	TCTCAGCCTTUCATGAACGTAAAATTUG	59757	TCTAGAGCTUTCACTTGTTTTUGAAGGT
224068866	59758	GAGTGAATGTUCCTCAGAAGAAGTUACT	59759	CAGACACTGUATCACTGCCTUCA
222609455	59760	GAAGTACACAUGCTCCTAGGCTTUT	59761	AAAACUTGTUGAAGGGCAAGCAG
224695759	59762	AAAAGAAAATTTTAGUATGTGTGTTCCATUCAT	59763	GGCATTCCAUAGCTGCTTGATATUCA
224419705	59764	AGCAGTCTCAAAUGCTGGAGAUG	59765	TTGTGCAAGCUCACTCTUCAGT
320482786	59766	TTTTATGCTAAAGUTACTTTCTGUCCAGGT	59767	TGTTTGCCAACAAUCCATTATCTTTUGT
318217340	59768	CCACUCGAGAGCAGCATUCC	59769	GACTCTCTACCUCTGGCAGAUGAT
321628759	59770	CCCACCAAUCTTGUCCCAACC	59771	TCCAGCTAAGAUGATGGCATATTTUGAA
318392721	59772	CTAAAGCAACTAGAAAUCTTACAAAACGUGT	59773	CCAGATGACCUGAGGAAGAGACTAAAUA
265227354	59774	AAGTACTGAAAGCUTGTAATGCCTCUT	59775	GGAGACCCAUCATTTCACTAAGGTUAT
325930680	59776	CAAATTGGTTGUGACTGAGATUGGA	59777	CCAGAACUCTCAATCUGCCAACAT
325843828	59778	CAATCATCACAUGGAAAACCATUCCC	59779	GGCAGGAAGCAUATAAGAACCAAAUCT
261731291	59780	AAGCTTCCCCUCAACAATTGCUAT	59781	GTCAGAAGAAAAUTTAGGCAACCAUCAA
263590435	59782	AGAUGACACUCCAGAGACAGGAT	59783	TCACTGTCUCCTTGGGCUCA
263719124	59784	AGAAUCGCCCATCAGUGAAAAGT	59785	CATCGACTGUGCCCATGTGUA
259820389	59786	GGTATAGCACCCAAAGUAAAGTAGUGA	59787	AGAAAGATCCCGUCTTCCCCUAA
314711874	59788	CAGCCCCAGUGACTGCAUA	59789	GAAGTUCAAGACCACACAUGCAC
314008798	59790	CGATGGCGUACCAGAUGCAG	59791	CCUTGCCCCAUCAACGGAAT
319638117	59792	GAAAAUCACCAUCAGCACACCAT	59793	TCCAGGAATGCUAACAATTACAGATTUCA
317401565	59794	TGCAGGAAGGUTGTGGAGTUG	59795	TGGCATTUTGCTCCTAUAAACACGAT
317156409	59796	GTTGACCTTCCUCTCCCCATUC	59797	GAGAACGGCAUCGUGAGACA
330151527	59798	AGTTCAGTGGAAAGUGATTCATTCAGUAT	59799	CATCTGTTCTTUGTTCACTCTCTUCT
262964168	59800	CCAAACGGGUCTGAAGCAUGT	59801	CACCTGTAACTUGTTGTGTCATTTTUCT
238378845	59802	GTCTTGGGTAGAAUCATCTTGTCTCAUT	59803	GGAAGAGAAAGAAAGACUTTTAGAATGUCCA
262591353	59804	ACAGAATCUCAGAGCCTCAUCCT	59805	ACTTGTGAGAGGCCUATAAACTGGTAUA
230104831	59806	CACCTCCCUGGCAATTGCUAT	59807	TTTCATCUGAGAAGCAAGGAGUGG
227977219	59808	CGGAGAAGUAGGTGGTGUCACT	59809	GTGACCUGCTGCAGCTUC
254782445	59810	CTGTUGGCAAACAGTCCUGAAG	59811	ACCCAGATTAUCTCACTGAGGTUGA
265340451	59812	TCTTTTACTTTTUGTCCTCCAGTUGACT	59813	GAAATCAAACAUCTGGCGCCTAUT
254190152	59814	TUGAAGAAGATAUAGAGACCCCACCAA	59815	GGTACATAACTUGGCATATCAACAGUGT
267117026	59816	GGGCGGGCUGTTGAAUAAC	59817	GCATCTGTGCUTTTCTCAGAGTCUT
316644962	59818	AAAATGCTTGGUGTTGATGTGAAAAUCT	59819	TGTAGTUAAAACAGAGCCAAUGAGCA
314507664	59820	AACGCGTTUACCATTGCAAAUG	59821	ACAAAGACAAGCUGAGGGACTAUG
312859465	59822	TTTCTCACAUAGGATACCAACTCUCCA	59823	TGCCCTCUGTTGGGUAAAACC
315859435	59824	CGAAAUCAGCAGCAGCACUC	59825	GGCCCTATCAUCTCTGTGTTTCUC
326744122	59826	TCGTTTCCCUCCAGGCTTTUC	59827	AGGACTCTGUCCAGAGCTCAUT
259456795	59828	GAACACTGTTUACCTTGTGATTCUAGGA	59829	CTCTTTGTCATTTUGATTAAGCCATAGTUGT
261262640	59830	CGGTTTTCUACCACCTTCUCACA	59831	GCACAGUGAAGAGCUGCAAAG
268724089	59832	AGGAAUCCCACACTCUGACAGAT	59833	CTGCUGAACATGTACUCAGGGAA
317960508	59834	GCAGCACAGUTGCCATCATUG	59835	CATTATTTCCTUGTGTTTGTGGUGGA
317870760	59836	GGTTACAGGCACUCGAATGUAGAAG	59837	AATCTGGTUGAGGCCACGUT
315649746	59838	AGGCAGATATACACUAGCTCATTTTGUG	59839	CCCAGTCCAGUCATAACGCUT
327463360	59840	AGAGCAACAAACAGUGCATAGAAATUG	59841	CCCATCTGUCACACAAGTAAAATTGUCT
327905701	59842	GAAATGTCUGAAAGGAGGTTCAUCCA	59843	CCCAGAATACUAAGCCCATTGCAUAG
280564998	59844	AGGACAAAACAUCTTCGTTCAGAUCA	59845	CCATGGAGCUCAGTTTTTGTGAATAUCT
280099502	59846	GCATGCTGGCUGATTCTGTUC	59847	ACCATCCCCTUAGTATTAGGTGAAAUCT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
279036664	59848	TTCCCTCTATAGCUATGGAAAGTCCUC	59849	TTCGATATTGUAACACTCTGAGTTUGCT
260922213	59850	CCAGGATUACGTGGTTUCCCT	59851	GAGGAUGGGACAAAGGCTTUGA
264266665	59852	ACAGAAAAGGUCCAAACGGTUGT	59853	ACGTUGGAAGAGAACGUGCAT
332444318	59854	TCTGAUGGAAGCACGTCATCUG	59855	TTAAGGAAAAGAGUGAAACCCACCUT
318422602	59856	TTCCUCCAAAGACAAGGCAAUGA	59857	GGAATATGGUGAGGTGGTTGGUG
318039413	59858	GCATACCTUCACTCTGAGUACAGAA	59859	TCCCCCATGAAUAACCACCAAUAAAAA
318852192	59860	AGGGAAGGTUGGCGTGTTAUC	59861	TGCACCCTTUCAAATTGTAAGATUACCT
319026265	59862	AACCACAGCAAUTAACAAAAGAACAAUCA	59863	CTTCATATGTGCGGUTGTGATCATTUAC
320097618	59864	ACTGGGCATTGUAAAATATGGACTTUGA	59865	AGTGAAACUCCAAAAAGAUAGCACGA
255487045	59866	GAAGCTTCUCACCCTCTTCTCUT	59867	GAGGCUGCCCATGGGAUAG
254532634	59868	GTTGGTGGAGCUGGCAGAATUA	59869	GGTCATCUCCACCAGGTUGAT
254598616	59870	GTCTGTGUCCGAGGACGUG	59871	AACAGTAGAGCCCUGACCTCUT
261842911	59872	AGCCUGAGGGTCAGGUCAAT	59873	CCATGUAGTAGGTGAUCCCAAAGG
257421579	59874	GTUCGAGGAACCTTGUAAAACACAAA	59875	AAGATTCCGUAGCTGCTCCTUG
266901503	59876	ACACCCCAAGUCAGUGAAAGG	59877	TTCTCCGGUAGGTCATCCUCAT
261845800	59878	GAGTATGACAACAUTGCCAAGCUG	59879	AGGTCTCUACCACCCTGUGT
326473472	59880	TGGUGGACGAAGCCATUGAT	59881	TTTCACAGCCUCACGGAACUT
324623144	59882	AGAGGAAACAAAUGGUAAGGAAGGG	59883	TGGCTAGTTTTUCCCGAATTTCUGT
332432857	59884	CAGAAGGCGUGGUCAGGAT	59885	GGGTAACGUTCTGCTCGUGT
327758215	59886	ACCCAGGAGUGACCTUGAGAG	59887	CTCAAAGCTUCCCACTGTCTTUT
320148161	59888	CATUCACCGAAGGGCUGGT	59889	CGTGAAGGCAUCTTTAATGAUCAGACT
262325189	59890	AGUGAACUGGCCGGAAAAGT	59891	CGGCTUACGGGTCGTUGG
314349282	59892	CAGGACUCACCTCTTTTUCAGCA	59893	TCCTGCTCCUAATCCCTTUCCA
323944945	59894	AAGGCCTUGGCTATGGUGA	59895	AGUGGACAGGGCCCTTUG
264170219	59896	GGTTTGCCAACCUGTCAAUGAA	59897	GATTGCTGTUGGAAAAGATTCUGCAA
313229490	59898	GCCTCUGGACACTGCUCA	59899	GGGTUCAAAGGCCTGTTUGG
313398219	59900	CAGGTCTGCUGTCCTAGUCCT	59901	CCCTGCGUGCTTGTTGAAGUA
223697825	59902	GCTTATCUGCTGCCGUCAACT	59903	GGAATCTGAAUGCCGATCTAGAUGT
222989777	59904	TTCTTTCAGCAUACCACTTCATAACUGT	59905	AATTCGAAAGTUGACAGCCAAAGUC
222203805	59906	AATTCAGAAACUCTTGTCCGGUGT	59907	CCTACCTTGGCUTTCTGGAATAATUCT
223505899	59908	TTTACCACAGCAAUGTGTGTTCTTUG	59909	CATTCGUATCCACAGAUAGCAAAAGAAA
223779456	59910	ACCACAGTUCTTTTCCCGUAGG	59911	CCATCTGCAGCAUTCCAAATACUT
223037706	59912	ACTCATTTTTACUCAAACTATTGGGUGGAT	59913	CCCTGAACATGUGTAGAAAGCAGATUT
333266825	59914	ATGTCUGGCAGAUACGCACA	59915	GAATCTCTCUGTGTAGCCTUGGAA
333404929	59916	TGTTTCACTUGTACTTTCTGUGGCA	59917	AAAAAGCAGAGACUTGAGGAUGGT
332516113	59918	TGTTGCAAACUACTGCTCTTCUGT	59919	TCCACCCAUGCUCCAGAAAAAG
332916288	59920	GCGCCGCAGUCAAGTCUAA	59921	CUGAGTUACCAGGAGGAAACCA
333023534	59922	CCACTCACACUGGTGTTCCTUT	59923	TCTCUGGCACCCCTTGCUA
332929696	59924	TGGGCTAUGGAGATGCUCACT	59925	CTGTCCCUCCTTTCTGGUCAA
320047732	59926	CCTGGGTGAUGGCCTAGGAUAG	59927	CTCACCCACACCUTTCAGTGUA
333238076	59928	CCACTTUACAGAGGTCAAGCUGAT	59929	GCTCAGGAAAAUGGAGTATTTGCTTCUT
333167238	59930	ACTCTTCTGAAUTGGGCTCUGAAC	59931	CACATTTCTGGGAAUATCCGCTTUC
333369188	59932	CCUGAACAGGCAUAGCCCAT	59933	AAATCCTTAGGCUCTCTACGTCUAACT
231133876	59934	TGTTGGATCATAUTCGTCCACAAAAUGA	59935	AGGTACTGGUGGAGTATTTGATAGUGT
318545099	59936	GCUGACGGGCAGAACUGAA	59937	GTAGCCAAAGAAACUCTCCCUGA
313470288	59938	CACATGAGCTUCACTACAGGGAATUA	59939	GATCTAAGGTCTUCAGTCCAATCACUG
312676967	59940	CAAAGCATUAACGTGGCAUAGAAAGA	59941	CCATCTTCATCUCCAATCTTCTCATGUAA
278213074	59942	CAUTTTAUGACGCAGCGAGCA	59943	ACTGAAGCAATUGTTTGCCCAAAAUAA
313016979	59944	ATTCAATTCAGAAUGGTTAGGGAAGAAUAT	59945	ACCACCACTGUTATGATGTTGGAAUC
268872447	59946	AGACAGGAACAGAAGGUCCTTCUA	59947	CAGCTCTAAGUGCATTCTTGTTUCAC
268785526	59948	AGAGACACCAAGAAGUGAUCAACC	59949	GCCTTCACTCUCACACATCTTTCTUT
257319218	59950	GGACCACAAGGACUCCACTUC	59951	TGAAGGCTCACUCTGTTTCTCTTTUT
268219849	59952	TCTTTCCUCCCCCTTTCCAGUA	59953	CCTCTCATGGUCACTTCCTTCTUG
316338908	59954	GTGTATCATTTTCUAAAACATTCAGATGCUAGT	59955	AGGGCTTAUCGAGACAAATTGAAGTUT
316799452	59956	ACATATCTGAGGGAAUCTGCAAATGUA	59957	CTTGTGCACUAAACATAATGCTGAGUT
318406251	59958	GGGATCATAGAACUGTACCTGGTTUC	59959	CGAGCTCUCTGTGCTTTCUGT
314000329	59960	CCCCCGAAGAAACAUAGACACAUA	59961	GTCCCTGAGUGTGTGTTTCCUAC
266924528	59962	GTTACTTACUACGTCATTTUCCAAAGCC	59963	TGTGAGTGTAACUGATTGCCAGATUAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317861409	59964	GTGACATUCAGCAGGATGCAAAUT	59965	GUGGACCUACACAAGCAGCAT
333397680	59966	CAAACACCCCAAUTCTGUGCAT	59967	GCAAGACAGUGCTTTCCCTCUG
332497916	59968	GCAGAAGCCAUGCTUGCAAAT	59969	ATGAATGCTGUGTTGCTGTCTTTUT
333838283	59970	CTTGGUGGCGAAGTCTCCTUT	59971	TCTCTCTGCAATUTTTCATGTCTGCAUA
332746535	59972	GCCAUGTCCAAATUAAGAGCGA	59973	TCGCATCTGAACUCATTTCTTTCUCAT
333406469	59974	AAGGAAATGGAAUGAAAAGAGAGAAGUCA	59975	ACACAGTGCGUATGAATGAUGCT
332832483	59976	CCCACGCAUGGAATCATCGAUT	59977	GGTGATCAATGACAAUGGCATTTCTAUT
320109858	59978	CGGCGCAGCUCUCCAAT	59979	TCCTCAGGCUCCAGTUCCT
313593035	59980	GGGCAUGCTAATGUGGAAGT	59981	ATCTCCAGCUCATTCACCCAUC
313190045	59982	GGCTCTGCACUCAGTAGGTUT	59983	GUGCCAACGACGACCUGA
315101312	59984	CCCCCAUGTACCTUCAGCAA	59985	CAGCGGGUGGTGGACUC
314215343	59986	GTGCCUGCCTATGGAGUCAT	59987	CCTCUCAACGAGACTGTTGUGG
315471086	59988	CATATATCAUCCAGGCCGCGUAG	59989	TGGTCACTCAUCCTCCTGCTUA
312839867	59990	GGGTCTGCUTGTACTGTTAUGGG	59991	CTCCTTCTCUCTACCAGCUGGAA
325007354	59992	GCUTCUCACGCGGCGAT	59993	GTGGCUGAAGGCGCATUAC
326324485	59994	CCACTTGCUCCTGCGUAAAG	59995	GCAAAGCCUAAGGAGGAGGUT
325480146	59996	TGTGAATGTGUGTCTTTCCCAUCT	59997	AGAAGAAACAUCCATGGGATTCUAACC
266956318	59998	TTGAGCTGUGTGGGAAUCCAA	59999	AAGAGCTAUGAACTGCCTGAUGG
264282955	60000	CAGTGGUGACAAAGGAGUAGCC	60001	GTCCTCAGGAAUTTACCTTGTTCTUGT
255886149	60002	CTGCAGAGCAUGAGAGCTCUT	60003	ATCTTCAATACTCUCATGGCTCAGTUC
266733487	60004	GCTCCTCAUCCTCATTCACAUCT	60005	AGGCCCTCUCCTATCACAGUC
256230877	60006	GGGTTCTCUAGAGGCTGGTUCT	60007	GGACTTTUCGCACAGAAGATCUAAAC
317768826	60008	CCCCTTGCTUTTCTTGTCTTCUG	60009	CTCCCTUCCGAACATCTGUGT
317083967	60010	GTATTAATGCAAUTTCCTCCCUGACAGA	60011	TCACATTTTATTCUGCAATGAATTTCATAUGAG
318337847	60012	CCUGAGGACUGGGAAAGGGA	60013	CCGTACGCUCCTCTUGAAGAAG
317966156	60014	CTGGCUCCACTACCATUCACC	60015	GGCTTATCTUGCCATTTCTTCATGUC
316650631	60016	GAAAGAAGGGUACTAGUCCAGAGGT	60017	ACCAGACTGTUGTTGCTTGTTTUC
333270471	60018	GGATGATCTCATUCTCCTGGTAGTUGA	60019	AGGTCTGCACCUGATCTCCUT
318667906	60020	CCCCTTCCCUGGGTGGAAUA	60021	GCTGCTGCUGCTACTGTTCUC
319555963	60022	CATGTGCAUGCTCATGGTGUC	60023	AGCATGAGGATUCTGTATTTGGTGUT
321590973	60024	CCAGGCATCUCCCCTCCUT	60025	TGGGTCUCCAGCUCCGT
239210463	60026	TTGAATAACTCUCCACCCGUGAAAG	60027	CAGACGAUGAGGTCAUGCAAG
318251179	60028	GTCTGGCUGGACUAAAGGCAAA	60029	GTACATGCTTUTTCTGCTGGUGAC
321340424	60030	CCACAGGCUCCACGAAGUC	60031	ATGGCACCAACGUCTCCUAC
320685808	60032	AGCGTAGGUGTGCAUGACAT	60033	CCGGTUCACTCACUGCGT
235599692	60034	CCTCTGCAUACAGCTCTGTCUCT	60035	AGAATGAGCUTAAGGAGCUGGAAC
268042500	60036	CCCUGAACCCCGTCCUAGT	60037	CTTGCTAUGGCCCATGACCUT
265623669	60038	CAGGTUCAAAGCAGGGUCAGT	60039	CCCATGTCUGTCTGTCTGUCC
318561205	60040	CACCTCGUGGTAGAACTCTTUGG	60041	AGTAGGGAUAAGGUGAGGCCAT
320002099	60042	CTCTCAUGGATCTTCUGCCACA	60043	CGAGTCTCTUGATCTCTAATGUCACAT
320043137	60044	CCTCCAGUGGCTCAACATCUA	60045	GAAATGGTTGUGTGATGTCTUGCC
263380739	60046	AGCAGCGCCAUTAGCATCAUA	60047	GAGAGAGCCUGCACAUACGG
260092448	60048	CUGACGCTCUGACCAGGAAA	60049	CACCCAGCUCTGATTATCCCTUC
265303054	60050	GGGCAUCAAGGCTUCAAACAC	60051	TCTGTTUGGGTTACCUAGGGACT
267810877	60052	CCCTCATTTCUCTCCACCCTACUT	60053	GGATATUCAAGGAAATTGUCAAGGCAGA
262828421	60054	CCAGGGTTAUTTTCACGCCUCA	60055	CTGGACTTGGUAGCTCCATTUGAT
267218024	60056	TCTCCUCCAGGGATTTCTAUCGG	60057	CATGTTTTTGUCAGACTTCAGAUGGT
268161794	60058	CTCTUCCCGCTAUGAAGCGT	60059	AAGGTAGGAAAUGAAAGCCGTTAUAAGT
265649310	60060	CAGGGTCUTCATGAGUGCAGA	60061	AGTTTGCAUCAGCTGACTGUGA
325584270	60062	CACCATATGCACUGTTGTCAACUC	60063	GGTACUCAGGGCCTUGGAAA
237442947	60064	GCTATTTGACTUGGTGGATGGTTTUG	60065	CACCTTGAGUAAAATAAACTGCTUCACAT
257710522	60066	TGTTTTTGTUGCTGTATGTAGUCGGT	60067	TGAAGGTCAAAUAGGCTGAAGUGAAG
239322145	60068	TGGCCUCAAAGGUAGCAAAAGG	60069	TGAATCGTTUACAAAACACAGACUGGA
258078851	60070	AGAAGAAGTAACUGGCTGTTCTCTTTUT	60071	GTGAAGAGCCCAUGTTAAGTTGATTUT
332276267	60072	GCTTCTACCUGCAGAGCTCUT	60073	AGAACCCAGCAGAAGUCATTUCC
332341030	60074	CTTTGGCCTUGGGTCATTGUC	60075	CTGTACCCUGCACTGCUCAAT
332705854	60076	CCTCCCACAGUACCTCAGGUC	60077	GCTGAUGGCACCCCTAUCC
313190837	60078	GCTGGTCTTUCTCTGGCACUT	60079	CGAGTCTACCAUGTCGATGCUG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
329006000	60080	ACTCTCTGUCCCTTGGGACTUC	60081	GCCCTTCCTUGTCTTCTTCATCUC
268751366	60082	GAACCTCACAUCCAGCCTUCT	60083	CCCAGATGUATGAATCGCUGCT
265916962	60084	GCAGACGCCAUAAAGCUGAC	60085	GGAGACTUGGGATGCTTUGGAA
315780568	60086	CTACTCCUCCACCGCTAUCAC	60087	AGCCATCCUTGTTGAACGUGAA
316894209	60088	CGACGGAGGGUTCTGGUACA	60089	CGGCCUCAGTACUCCCAAAG
330993546	60090	CGTTGCAGUTCAAGTCCUAGGAT	60091	CAGACGAAAACAAAUGTGAAAGAGTUACA
268668519	60092	GATCTACACGAUGTGTGCAGUCA	60093	CCTCCATTTGGCUCATATGTAGTACCUA
267625298	60094	CAGGCCAGAGAUGTGCATATUAAAC	60095	GGTCTACAGACAACUTCAACTTGTAUCA
268033741	60096	GGTAAGAGAUGGAAACTATAGACUCCCA	60097	AAGAGAAGAUGGGCTCCAATUCC
262067788	60098	ATGCCAGATACUCTTGTGATGAAAAUCA	60099	GGATAGAGAGUTTAAAGAUGGGCAACAT
268477582	60100	CTCAAGTTCAGAUTCGTATTTTGGAUGT	60101	GCGTAACTTCUACGTTGACTTGATTTUC
268769926	60102	TCTGTGGATTCUGTCACATCTGAAAUT	60103	CCCGGCCGAGAUTAGGTTTTTAUA
315119712	60104	AGCGGTTTGUTCCCCTTCUC	60105	GCTTCCGGAAAGGAAUGATGGUC
315301196	60106	CCCTGTTGUTTCTCCCUCAGA	60107	GCCTTCAAGGGCAAGUTTTAATGAAUG
269283569	60108	CUCCUGCAGGCACAGAGAAG	60109	CCAGGUGCAUGAACCAACAG
269312004	60110	CTCATTTUCAGCATCTCTCTUCCCT	60111	CGACCAGAAACGGUCAGUGAT
267996543	60112	GAGCGAGGUTCCCTGCUAAG	60113	TCATCCTTGUACCAGGACAGUGA
321489236	60114	CCAGAAUCGGAUCCGGGAA	60115	CCGGCAUGAAGCCTUGGT
321081441	60116	ACCCCCACAGUTCUACGAAGT	60117	GAAUGTGAATACUAACAAAAGCACCGAT
332516827	60118	GGAGGCUGCTGGCCTUA	60119	CACAACTTCUGAAGCTGACTUGG
333810181	60120	TCUCUCCAGCCCACGGA	60121	TGCAGCUGCTCAATCCUCAT
325269072	60122	TCAGGACTGUGGCTCACCUAT	60123	CCTCAGUACCCTCCUGCAC
323490186	60124	CCAAGAGGUCTCCCUGGAAGT	60125	CCACCUGCAGGAAGTGGUT
323853243	60126	ACTCTCCGAUTCCAGAGCUGAT	60127	GCAGUGCCACAGTGGTGUAG
323791223	60128	CTGACCACUCCCCTGCTUAC	60129	AGUTAAGGGAUGAACAAAGCAGACC
325632787	60130	GCCCCAGAAGGGAGUGTUC	60131	GAAGAACTUGAGGATCATCUCCACAT
323543241	60132	GCACCTCCUGACCTCTCUCT	60133	GGGAGAAGAAGGUTCAGGUGAC
324326830	60134	GCCTCCACUCTGATGTCTCTUG	60135	AAAGCTAAGUACCCCACTGCUG
259261453	60136	GAGCACUACCCACTGGAUCAC	60137	GCTGAGTATTTUAGAGGGAGCUGACT
325917851	60138	CGCTCGGCCUCATGGUA	60139	GCTUGAGCCGCTTCCUG
317935422	60140	GTTTCCAUTGCAAGUCCCCAA	60141	GGTGGTCGUGTCTGCTCTUC
316083070	60142	GGTGCGAUGATCCAGUCGT	60143	CCAAGAAACGGGACCUGTUCT
263076287	60144	GCCAUGCCGAGGTATACGUG	60145	AGTTGCCTGAUCTTTTTGCTTCUCT
326047460	60146	TTTGCTGTCUAAAGAAAGACTCGGUT	60147	ACUGGAGAGAGACCCTUCGT
325454224	60148	CCTCGAGGAUCCCGCGUA	60149	CCGATGCUCGCACCAUGT
254291529	60150	GGTGGTTCUCTCTGTGGCUT	60151	TCCTTCCCUGAAATGTGTTTAATUGACT
313839339	60152	GTGTCATTAAUCCACCCCUCACC	60153	GTCGTGCUATGTCGTUGAAAACC
253998121	60154	TGTCTGTUGGAGACCAGAUGGAT	60155	TCCUCATTCTTCUGGCACAGG
264591548	60156	GAGGUGGCACTCCUGCT	60157	GCACCGGCAUGCAUGGA
225795695	60158	CAGCAGGGCUTCCCATGUA	60159	TGGCCTGTTAAUTCTGGCATACUC
226173874	60160	GAGAGGACUGGCTGGAGTTUG	60161	TCTTGTGCCUTGAAACUCACCT
317917221	60162	CTACCCCUCAGCTCCGGUA	60163	AGGUGCGAGCGCAAAUG
255632974	60164	GCCAAGGAUCTGGGAUCAGG	60165	CCTTGAUGGCGAACTGAGUGA
316428478	60166	GCCATGATGUGATACAGCAGGAUG	60167	CCTCTGTGTACAUTTTCCTGACCUT
324184504	60168	AGTGATAATGTUTGGATGCTGUCCAT	60169	GAGGTAATACCCAAGGUCTGTAGCTAUA
264260543	60170	AAAACCAUGCGGGAAUCAGGA	60171	TCTGCACCTTTUGTAAAGTCTGTCTUT
268744200	60172	TCATTGACGUGGCTCACGUT	60173	GGCACUGCACCCUAAAGAGAAT
267754806	60174	GTAATTTCCAUCACCCTUCAGAACCT	60175	GGCGGCGUTTTCATTATGATAUAAAGAT
260764550	60176	AGTTGTCTCCUCTTTGCAACAATUCT	60177	TGUAAAAGAAAGGCTAUGAGCACAGT
267502450	60178	GCGTCCACCUTGTCTGCAAUA	60179	GCAGGATUACAGAAAAGCTAUCAAGAGT
258561160	60180	AGCAAATCGCCAUCCTTTGUAAAAG	60181	CAGCTGGUTGAGCATTGUCAA
268793852	60182	GGAACATGGGUCCTTGTCCUT	60183	AGGGTATTAAGCUAAACTTGCCTTACUG
267795753	60184	CCCCGTGUCTTTTACAGCUAGT	60185	GATGCTGTGCUTGATTGTCTCTUC
264713780	60186	AAACTATGTTGUCAGTTTCTGGTCUGAA	60187	GGAAGTGTGCTUTGTTAAATTGAGTGUA
326060881	60188	ACATTACAATACACUTGGTGACTGUGAA	60189	CCAGAACCACAUGAGTCAGAATCAUC
324247152	60190	GGAGGTTATCUACATTGTATCCCTCUGT	60191	TTTATTUCAGACACACATCAUGAGCCT
325058228	60192	GAAATGTGAUGCCCTTACCAATTUAACT	60193	GGCCTTATGTAUACTTTTGGAGAUGGT
264807684	60194	GGAAACTCUAACTTGCCCUCCT	60195	CACAGGGCAGCAAGUAACUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316055833	60196	TTGAAGTATTGCUCCCCCAGUG	60197	TCATAGACACCCACUTTCCCUCAT
315973059	60198	GGTCCUGGAGCUGAACAACAA	60199	GTTCCTCTTCCUTCCAACCTTUCT
291963135	60200	GGGTAACCAUGGTGAATGAGTUG	60201	CTGAGAGUACCAGGCTAGUGGT
293381127	60202	GAGAGGAGGCAUTCCATUCCA	60203	GGAUTGGGAATUAAGAGGAAAGGGT
305043659	60204	TGGTGTGGGAGUCGTAGGTTUA	60205	AGTAGGTGGCUAGCCTCCUC
302165306	60206	GAGUGCUCGGAGAAAGAGGAA	60207	CTCATAGGCCTUAATCTCAGGTCTCUAT
305661224	60208	GGCAGGTTTTUATTTACCGCCUT	60209	AGGCAGACAAAUAACTAGUCACAACAG
254855545	60210	CCAGGCTGUGGTATTAGCUGT	60211	TGCCCCAUAATTGGTACUACAAAGAAAA
253990020	60212	ACTGTACTGAAUGGCGAAGACAAUAA	60213	CTTGCCTCUGAGAGATTTTTAATACTAUGA
255787543	60214	AGCTTCUGTGGAGTTUGCAGAT	60215	CATAAGCAAAACGUACACTGAACTUGA
267731020	60216	AATCTGGCATGUTTCAAAATGGCUT	60217	CTGCTTCTTTTGUTAATTCCTGTGTUCA
267401146	60218	GGGTAAACUGGAGAGAAGAAAATGUT	60219	GGAACCCAACUCTCCTTTGUCAC
268732936	60220	GTTGTGAUGATGAGATGUGGAGGAA	60221	CAGCCCACUCTTTUGAGCAAG
265917826	60222	GGGTTGGGAGUAAGAGAUAGAGAG	60223	ACTGTTAGTCAUGTGGGCATGUG
317900064	60224	GCAACATGAAUGCCCCCAAUG	60225	CAAACCACCTTGUTATCAGCACTATTUT
333103236	60226	AGAAAGGACUGGCTGACGTTUT	60227	CTTCATGGCTUCATTTCTTGCACTUA
333309169	60228	GGCACCTGUGGTCGAGTUG	60229	CUTCATGGGTUCCCGACGA
313794353	60230	CTAGTGGCTUGTATTCCTAGTUGCT	60231	GTTATGCAAATCTUATGTCAGCAGGUC
313934701	60232	AGTTTCAGUCCCAGTTTTTCAUGCT	60233	GACTACATACATTUTGGCAAGCCTAAUG
257080823	60234	TACGGTGGUGTGCTCUACAAG	60235	TCCTGAGGUGCTGACTCTUCA
315367965	60236	CGTGTAGGAGCUCTGGTTGUA	60237	TGCAACTTCAGGUTCCATATCTUGT
313760969	60238	GGCAGTAACCCUAAAGGTGTAGUG	60239	TCACTCCATTGUCGGTTCATTTCUT
313186748	60240	CAGCUTATTGCUGGCAAAGCA	60241	GUCCACTUCAAACCCAAGGAAGA
333619592	60242	GGTCGAGGUCGCAGACCUA	60243	CACUCACTGGUCCAGAAGCA
332500768	60244	GCTGTCCCUCATTCCCUGAGAT	60245	CAGGAGGAGGGCAAAUCUGG
318923451	60246	CTTUACCAAAAGCCCGTGTUAAGG	60247	ACCUACCTGTCUGCGAAGAGAAT
312932826	60248	CCAACTGGGUCCCTTCTCUCT	60249	CCTGGAGCCCUAACCTTUGG
254150424	60250	GGAAACAAGUAAAGGCCUCAGACT	60251	GCTCCGAGCCAUGCAUC
325257752	60252	GTCCAGAAAAGGAUGGGATUCAGA	60253	ACAGAATTGCACAUTTCACTGAAAACUT
316032937	60254	AGCTCATCUTCGTCACAUGCC	60255	AGCAGGUAGAGGAAGAGGAACUC
318430951	60256	GCTATGAAATCAGUCAGCAACCCUT	60257	CTCATGAGTTUCCATCATTGTGTTTUGT
314895765	60258	GCATCUGGCACCUCCAACAAT	60259	GCCCTCGAUCGGACUCAG
264094092	60260	CAAGAGACCCAGCACUTGGTTUA	60261	CTTCTCCAAAUGGCATTTCTTTCTCTUC
264417358	60262	CCTCTTGGUCTGGTCCTUCAG	60263	TGAACAAAUCCAAGCACCUCCA
254482339	60264	AATTACTACCAUCAGGCTACUCACCT	60265	AGACTGTGCCTAUGTGTGTATATACCUA
267028222	60266	GAUTTCCACAAATUGGAGAAGCGT	60267	TTGAGCTCUGAACAAGTGAAGGTTUA
260581810	60268	GAAAAGATCUTACTCACCAUAGGACCAG	60269	TGTAGATGTCCUCCATATGGUGGAA
267916351	60270	GTTTCATTTGAUGTACGAAAGCUGCAT	60271	TCCUTAGGGATTUCAAGGCAAGAC
268611531	60272	ACTGGTGTACATTTUCTCTATACTTACTCUGT	60273	CACAACTACCAUGCACATTTCUCAAAA
263920654	60274	TCGTGGCUCATAAGCAATTTUACCA	60275	TGGTCTTACAGACAUTTAGGCTGTTUT
268808660	60276	TTTGGUGACCACAAGGTATTUGGT	60277	ACAACUCAGUGCCCCAACA
257613650	60278	CCTTCGCCUGTCCTCATGUAT	60279	GCATTGCATTCCCUGTGGTTTTTAAUAA
317105229	60280	CCACTGCCUTGACTCACUCAC	60281	GGGCTTGCUTTTCAGTCATUCC
317663748	60282	TGACTCAAACUGCCATGTATTTCUCA	60283	ACGAGAGUCACCCGAGUACC
326591178	60284	GCTGACGGGUGCAAACAAUC	60285	TGCAGCCAAAUGGAAAAGTTTTGTATUA
328161654	60286	TCUGTTCATATTTAUCCAGGAGACCGA	60287	CAACACCAGAAGAAAUCTATCCUCCAT
328469448	60288	GAAAAGCAAGTUTCCATTACGACUCA	60289	GATGGTGTGACUTTTGATACACTGTUT
327666438	60290	AGCCTGATGCCUAATAGCAATTATTUCA	60291	ATGTATGCATGCUTGTATCAGGAUCAT
328126846	60292	AAAAGGAATGUCATTGTGCACUGAAA	60293	GTGTGAGCCUCACAGGUACAA
327097914	60294	AGTGAATTCAGCAUTTATCCTTUCGGT	60295	AGGTATTGCTTGGUAAACAGAGACTUC
333198645	60296	ACGCAGGUAATAATTCAGTTTUCAGACA	60297	CCGTCTCTCUAGTCATGAAGUCGAT
323730907	60298	CTTTCCTTACAUGTGATTCCCGUCT	60299	GTTGCUTCAGCTGUCACAAAGG
323454802	60300	TGTGATTGAGACCUCAACGTAUGAAC	60301	ATTTACTUACCAAGACCAACACUGCT
325693744	60302	GTCTAAGGGCUATCCAGACATUGG	60303	CTTCCTTCAUGAAAGTGCTGAGAUGA
325180848	60304	AGAAAGCCATTUCATTGAAAACTGUGT	60305	ATCCCAUAGACCCTGUCAAGGAA
324388193	60306	TCATTAACAAATAUGCAGAACACUCCCA	60307	CTGTCATGGUCAGAAATATTUGAACAGT
324364309	60308	TTCTAGAAUGGAAAGCCTGTTTUGGT	60309	CACUGAGUAGAACCCCCAAGAAG
326335480	60310	TTTGCCTTUGGAGTTCTTAGAAUGACT	60311	CGTATTGTTTCAACAUACCAACCCTTUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
325679520	60312	TCGTTTTTAGCCUTTGCTATTAGTCCUT	60313	GGCTTGTCACUTTGGCATTTUCA
323596230	60314	CCAAGTCTTGUCCCATTGAATGUG	60315	AACTCCCACAGUCTTATCTAAUCAGAGT
327763202	60316	TGTGGGUTGCCUAGGAGGAA	60317	TGTTTGAAAACCCCAACUTAATTCTTAUAGT
328248981	60318	TGAAGGCCUCACTTCTAGGAUGT	60319	TTTCTTGTTTCCUTTCACAGGCAAUG
328381294	60320	GCTTTTATGCAGACUTTTCGGGUAT	60321	GCCTCACUGAATTAATGTGTTTUCCC
239680547	60322	AACACCAAGGAAAAUGAGGGACUT	60323	AACTGTCCAAAGUTGGAATCATCUGAT
240387263	60324	TCCATTATGTTTGUGGCATATCCTUCC	60325	GCTAACCCAAAUCCATCGUAGGT
235399185	60326	TTGGCTAATGUATTTGAAGTAAUCCGA	60327	TGAAUCCCAAAACTTTGAUCACAGACA
237702442	60328	GGACATUCACATGTGTTUCAGCAA	60329	ACCTTCATTCCAUTACTGGGATTTTUCA
263477422	60330	CCAAGCATGCUGAGGGTCTUC	60331	TGTCTCTCAGCUCTAGGTGCUC
257540691	60332	CCAAGCUGAAGCACAGGTCUC	60333	ACUTGTCCCUGCAGACACAAC
267322330	60334	ACAGUCAGGGTTTUAGAGGAGAGA	60335	GAAAGUCCCCUCCCGAGAGA
268825151	60336	GTGGCTGGGAAGUTAGAATGTTTUC	60337	GTCTGTCTTTUGCTTGTGTTCTUCAA
328386826	60338	CAAGGTTAUCAGACCTGGGUCA	60339	CCAGATUGAGCGGCCCAUT
324723743	60340	GCATTCTTACCACUTTGCTGTATUCACT	60341	CATTTATTCACAAUCCCAGCCUCAC
324751539	60342	CACTGCAATCUGGAGGTTGTTUG	60343	TCTCCCTATTUCTCTACCCCCUCT
323851764	60344	CACCGUGGGAGCGUACAG	60345	TTTGCTTTTAGCUCCGAGTCTUCA
323516841	60346	CACTCACTATCCUCTCCCGAGUT	60347	GGAGATGCUGAGAAATTGTCGAAAUC
268202652	60348	CCTCCAGCACUTTAGCCUCAA	60349	AGTGAGCCGACUCGCTTUC
265931329	60350	CTTATTAGGGAAGUCAAGGAGAAAGUGG	60351	ATGCTTUGAAGAGGAGACTGAGTUT
257948705	60352	AACCTAGTGGCCUGATTCAAAAUGAT	60353	CTAGGTGAAUGGAATGCTGUGGA
266114059	60354	TCCCTACAAAUCCTGAGAGTTACUCC	60355	GCAGGACTGUCCCATATGACATAUAGAT
267656908	60356	AGAAAGATATTCUGGCATTGTGATGUCA	60357	GCTGTGTTTCUGAAAATTGGAAGATUGT
266373975	60358	GGCCAGGCACUTAAGACCAUA	60359	GGAATUCGGCGTTGAAATUGGG
316109965	60360	AGGTCTTUGAAGACCCCUCCAT	60361	CTTTGGCAGGAUTAAGCTAGGGTAUAA
317446882	60362	CTATTGCAGUTTCTGGCAUAGCAA	60363	GAAGCAAGTUCCTGTGGAGTAUAAAGAT
316196989	60364	CCATTUCCAAAGCTCUGAGCAGAA	60365	AGTACTCCCTUCCCCCAGTATTUAAT
267153725	60366	GCGCTCTAUACGGATGCTTUCA	60367	ACATATGGAAUCCAGGAGCCCUT
265502616	60368	CATTTGGCTCUGTGCCCTTUG	60369	GGTTGGGUGGATTGTGTGTTUG
235252282	60370	CAGACCGCGUCCTTGAGUA	60371	GGACCGUCCCAGAGGATUCA
261851066	60372	CACCGGUGTGGCTCTTUAAC	60373	CCTGTACTUACCACAACAACCTTATCUT
333184245	60374	GGAGAAUGAAGGAAGGCTGGUG	60375	TUCAAATCCUCAGCCAGACAACAT
272298050	60376	CATGAACCCACUTCCUGACAGT	60377	GCGGTAGCAGUAGAAGATGATGAUG
314956995	60378	CTGCUGAGCCCACCTTCAUA	60379	CCATCUAGAGGGATTCAGUGGGT
255025870	60380	CCTCCAAGAUCAGCACCCTCUA	60381	CAGAGGCCUGGACTACATCUC
315646672	60382	GTTTGTATACATUTCGGCATCCAUCAAC	60383	CACACCTCTTCUACGATGTTTCCUAAC
316569304	60384	AGCTGCAAAGAAGCUTGTGATTUG	60385	ACGACCAAAGCUTCTAGATTGTTTGUAA
316918325	60386	ACTCAAGACTUCCTCCTAAATTUCCCT	60387	GCTGTATAUCCCACCAAAGCAGAAUAAA
316258703	60388	AGTATAAACCACCAUCAGCACATCUG	60389	TCTTCAAAGGUATAAGCAGTTUAGCCAAA
332162496	60390	GGATTCTCCUGTTAGCAGCCUT	60391	CAGAAGACTUCCAGCTCCAUCAC
332042675	60392	CACCCAAAAUAAAACAACATCCUCCA	60393	AGGGAAATTTTGGUGTATACAGCATUCT
332144757	60394	GGCTCCUTCTTTGAUGCAGAGG	60395	CUGATGCCUGAAGGGAAGACA
267040918	60396	GCTACTACTAGCACUAGATGGCCUA	60397	CCTTTTGCCAAUAATGAGAGGGTCUAT
262013437	60398	GCUGAACATUACAAGGACCAAACAA	60399	AAGGTGATGTTUGCAAAACCACTUAAAT
228569220	60400	CTGTACGTGCUGGTGGAGUA	60401	ACAGGACACCAGGUCCTUGA
333207501	60402	TTTTCTTCTTCAACUGTATCCCTTUGGT	60403	ACCTGTCACAAUACTGAGAGTGATTUG
333404176	60404	AGCTGGTUAAGAAGATCCUAGGCA	60405	TCAGAACTCTCUACGAACACAGUCA
333685457	60406	AGGACUCAGAGACCTCTACUGAGA	60407	TGTGGGCUGAACUACCAAAGG
333517623	60408	TGCATATCTCUTTTGTCTGTUGGCT	60409	ATGAGATGAACAAUATCCATTCGGTUGA
332893125	60410	AATTUCCCACAGGGTUGCCA	60411	AAGGACCGUCUGCCAGAAAG
315325121	60412	CCTTTTAAGAGCACCUTTCCGAUGT	60413	TTTGCTCTTTAUCAGAAAGTCCTTCUGT
323984536	60414	GGCCAACGUGATCCGTTACUT	60415	CCAACCTGGUCCTAGCAAAGUC
267617723	60416	CTGCTAGUACCAAAAAGAGACAGUCA	60417	GGTTTTCAAUGGCCGACCUCA
268765441	60418	GACTTTTTACCUGGGCGAUGG	60419	AGATTGTUGGGTGGCAUGACA
268425768	60420	AGATCTTGCCUTGAGTCTGUGG	60421	AATGACUGGCGGAAGGAAAUGA
268520586	60422	GCCAUAGCTTTCGUCCAGGAA	60423	TGACTTTAUGGAAAGAAGTGTTUCGACT
265748464	60424	CUTACCTGTUGGCCAGGGT	60425	CTTCCTATGATAUTGACTGCAGTTUGGA
268240267	60426	CCTTGACUAAGTGAACCAUGGCAT	60427	GCAGGTATTUGCAGAAACTTAACTGAUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
268052084	60428	CCCCAUGGGTTCCGUCT	60429	GGCGGCUGTTCGTGTUC
257279184	60430	AGTGATGCTCUCCAGCACTTTAUC	60431	GTGTACTACGGGACAUGAATCTTTCUAA
267509464	60432	CAGUGGAGAGACTUCCAGACC	60433	TGAGCTAGATACUCTGCATGAATUGAAC
290321328	60434	AGAGAUCAGAGGACTTTGUGACAGT	60435	GGCTATTTTGCUGTGGCATAAAUCT
293499012	60436	CTAGATTGACCAGGAUGTTGTCATUACT	60437	TCAGATTAUGGCAGGAAATTGGATUCAT
291330162	60438	AGGCCTATACUGGACCTATTUAGGG	60439	ACCAATCTTCCAGAAUTCACACCTUT
291052209	60440	TTCAAGCTGTUGAATGGAGCAUACT	60441	CGAGGCCUGGAAACTTCTTCTUC
224544462	60442	GGACACCTATAAACUTTTCCACAGCUAC	60443	TCCTCTGCTTUATTGTCATCCAATUCA
224583560	60444	CCAACTTCACCAGUAAAACCTAUACCA	60445	ATGAGGTGAAUCAAAAGCAAAACTUCC
222829825	60446	TCGAGGUCAGCCUAAACCCA	60447	GCTCAGTCTCTUTGATAGGTTCATTTUC
325104581	60448	GCCCTGCCUTCTGGAAGTAAUC	60449	GCTTCGCUCCCGGGAATUA
332089059	60450	CCCACCAGCUCCAGAGUCT	60451	GCAGGCGCAGGUCTAUGA
332031468	60452	AGCCACCGACACGUCUC	60453	AGTUCACCCCAGAGCAUCAC
235724513	60454	CCATGGCAGCUGACAATUCAGA	60455	CAAAGCACTTCAAACUTACTACTGCAUT
259196001	60456	TCAGCTAAAUCAAAAGAGCTTTCCTUCA	60457	GCCATCTGUAACACCATTGATATTTUCC
268767760	60458	AAAAATGCTCAUCTCCTAAGCTGUAACT	60459	TCTGATTTGTCUCGTTTGCCAGATAUT
265972026	60460	TGTCAAACAAGCUCACTUGAGGAAT	60461	TTATCACTGUCCGCTTCGCUT
265482330	60462	CGAGAACCCUTAATCCUGCCT	60463	CAGAGUGCAGAGAUAAGCAACGA
316602850	60464	GGGAGAGGUGTTTUGGACCAAC	60465	GATTGAGAAAGUCCCTTCCCAGAAUT
331983550	60466	CCCAGGAAGAUCTGTCAGUCCT	60467	GATGAACCUGTACGGCTUCCA
331814080	60468	GCCATCUTCCTCACUCACAAAC	60469	GCCACTUCGACTCCTUCACC
331600281	60470	CCTCACAGUGACCTTGCUCT	60471	CCTGACTCGCUGAGCCTTUC
331638475	60472	CCCGTCCCUGTCCTTGUACT	60473	GCCATCCTCUCTGTGTCCCUT
331776293	60474	GGCCCGUCTTTGTCCTUGAA	60475	CAGTCAAGGAGUCGTTTUGGAAAAA
331572195	60476	GCCCGCGACCUCUACAG	60477	GAGGACGGCGAAUGCATUT
331572439	60478	GCCCCCUCTGACUGCAA	60479	CUTCUCAGGCCCCGACT
263893543	60480	CCCAUCCCACCTGCCAUT	60481	GCCACCCCAAUTCCTCTCUC
261045154	60482	AGAAGCGAGGUGGGUCAGA	60483	CGAAAGUCCCCTTCCCCUGA
264154798	60484	CAUCGATGGAAAUGAGGAAGAACC	60485	TGCTACTCTTCUCCTTCTCTCCUT
326966956	60486	CGGTCAUCAGCGUGGACAAT	60487	CTGTCCTCUCCCTGTCTACUCC
313119433	60488	TGTGCCATAUTAGGTCTTCUGGGT	60489	TCTTATTTCTATUGGGTGTTTCCAUGCT
272302150	60490	TGAATTCCUAAGCACAATCUGCACT	60491	AGAATCTCTGGCUTCTTGGCTTUC
319506337	60492	GAATAGAGAUAAGGCCACGUAGCA	60493	GATCTAUGAACGGCUCAAACACC
272539402	60494	CAATGACCAUGCAUGCCACAC	60495	GAGAACCCCAGAAUAAACACGTAATUC
315945518	60496	TGTTTGCTTTUCCTTATCCCTUGGT	60497	TTGATACATGCCUGTCTTGTTAACACTUA
317864436	60498	CTGACATGGTACUAATGAAAACTCACUGA	60499	GCTCATTTCTTCTUTCCTTCCTTCCTUT
267894651	60500	GAACTTACTGAAUAGCACCGTTCTUCT	60501	GUCAGCGAGCATTUAACAAAGGG
264403129	60502	CCCCCTTUCTCCTGCTUCAC	60503	GCTATTTTCUGATTGGGACUAACCAC
257511073	60504	GTGATTTAGUAATGGAAAUGCCACACT	60505	GGGAAAAAGAAUGTGACTGTGTGUAAGA
255513017	60506	CTTGAAGTTAAGCAUCCTGACTCUGT	60507	AGCTTTCTCAAGAUGCATACCTACCUA
323468034	60508	TGCTTCTTCAAAUGCTCTTGACATGUA	60509	CAACTCATTCTCAUTTTGTAGTGCAUCA
268178111	60510	TCCTTCTAGATUTCTCAGCTGAAUACACT	60511	GCAAUAAACACCACTTUCAGGAAACAAT
267377410	60512	GGGAAAGTACUTGTTGCTTCUGGAT	60513	CGGATUCCAGCCCAGATCUT
268345718	60514	TGCTUCAACAGCCCCTCATTUAT	60515	TGTGGAAAAGCAUCGTGACTAGTUAA
266438432	60516	GTGCTTTTCCUCTTTAATTAGGUGACAG	60517	CTTTGAGGAAACUCAGGGACCAAUAA
268728596	60518	GAGCAGACUCACGGCTUCAT	60519	CCCACAAGCTGAUCTGAACATTTTAGTUA
265829274	60520	GCAGUGGAGGAAGTGGGUAGAA	60521	CAGATCCTCCUAACTCTTCAGACUACAT
229946923	60522	CAGGATGGTTUCTGGATGCTGUA	60523	GCATCTUGAACCGTCCCTCUG
228166956	60524	CCTGACCACUCCCCAACTTTUC	60525	TUTTTCTATTGUGACCACCCCAGT
232262220	60526	CCTTTCUGACCAGCGGAGUC	60527	ACACACACUCACTGATTUCAGAACAA
332953054	60528	CTTTTGTGATTUGGGATGTTCCAUGAT	60529	TGGAATACATCTCUCTCATGTTCTCUGT
224430418	60530	GGAATCTGAUGCCATGTCTACUCA	60531	GAGCAACATTAUAACCATTTTGCCCTUT
222337094	60532	GTGGCUACCAAAGCAGAACTUG	60533	CATCAAATCCACAAAAUACTTTTTATCTAGCUT
224263135	60534	GACCTACUGAAAGAGCUGCAGAA	60535	CTGCAGUGTTTTCCTGUGAACC
223802796	60536	CAGTTTGAAACAGCAGAUGATGAAGAUT	60537	GCTGCAAGTTUCAAATTATCCAGTTUCT
318351722	60538	ATGTCTAACATGCUAGTTTGGCCAUA	60539	CTTGCAACTGUAGGTCCTTCUAGAT
265427958	60540	GGTGAGCCCGUAAGTAGCTCUAT	60541	GCAGATCCAGCUTCCCCATUA
264575487	60542	AAAAGTGATTAAAAUGCAACCCAGATUGA	60543	CACTGAGGGACUGGTATUCACAAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324867973	60544	CCATTTTGCUCCGCCUGT	60545	CGCCGGGACUAGAAGUGA
324624609	60546	GTCGTCTGUATGGCAGTUAAGGA	60547	TTTTCCAGGTUGGCTCCATAUGAAA
323443564	60548	TGAGGAUATTGAAGATCUGGAGGAACT	60549	GCCAAAGCUCCAAATGTATAATUCAGAAA
257686010	60550	TTGATGGTAAGUACATGGGTGTTTCUT	60551	TCTGCAACTTUCCATATTTCTTGAUCACT
264811166	60552	CAGCTCTTUGGAGGCAAATGUT	60553	CCCTGTAUCCCCAAACACATCUC
263170172	60554	GCAAGGUAGAGGGCGAGTUG	60555	GCCTCUCCACGGTCTTTAUGA
313677277	60556	TGGTGGAAGCGGAUGAACUC	60557	GCTGAGACUGAGACACUGACC
320668694	60558	CAAACACACAAACCUGACTCAUCC	60559	GGTCTAGAACGUTTGCGTTTATCTUC
320312448	60560	AGGCCCUGTTTGGAAUGAAGAA	60561	CAAACAGCAAAUGTGTTACTAACUGCAT
239088279	60562	AGCAGCGGAAAUGTCCUGAA	60563	AGTAACAACUGACTCTTUGCACAGT
264503242	60564	CTGTTGTCCUACCAGTCTCTTUGT	60565	GGATTGAAGAACUTGCAGUAGCAGT
230392874	60566	GTTACAGCUGACGGTGGAGUC	60567	ACCAGTACUCCCCCAGCTUT
229662222	60568	CCTTACCUGGTTGGAGGUCAA	60569	GGGCTAGACUAGAGAGTATCCAUC
229208392	60570	GCGGGTCACUGTACACCTUA	60571	CCTCTTTAGCCAUGGCAAGGUC
257156928	60572	CACUCCAGAACACTGUGGAAGAA	60573	TGCCATTTCAUGGGCTAATCTUCAAT
255144214	60574	GTGGUCTCAGAAAAUGGACAAGAAAA	60575	CATTAAGGAGAUGCCTTGUGGGT
230104383	60576	GGCACGGCUAAAAGAAGCAUT	60577	CCCACTGCCUACTTCTACTUCC
313998829	60578	CGTTAGCUAGGAGGTAAGGTCTUGT	60579	AAGCAGTUGCTGGAAGAUGGAA
313620616	60580	GCACTTGAGCAUGCACTCTUT	60581	ATCTTCGAGCCCUATAACTGTAATCCAUA
313335752	60582	TGTGTCCTTTUCCCTCTCCACUA	60583	CAGAATTAUGGGAAAGCAAACTGGAUG
319793277	60584	AGTTTACTGUGGTGCCUGCAT	60585	CTTGGGCUGAAACAACTTTCCUG
317091103	60586	CAGGCATCCUCATTCCGCUT	60587	CCCAGAACCTUCCCATTAGATTAAACUG
326735576	60588	TCACTGTCATTAUTTAGGTCGTCATUGG	60589	GAGCTGGATATUAATGTAGCCACUGT
258015223	60590	GGCTCUGCAGAATCACTGUGT	60591	GGGATTTGACUTTTCTTCCTUGCC
316544688	60592	GGATGGAGGUTGCTCCCAGUA	60593	AGGAGCCCAGAAAUGGTGTUG
315590055	60594	ACTTGATTCCACUCAGGAGCUCT	60595	GGCCAGTCACUATATCCACATTGUC
298417192	60596	GCCAGGUCCTTGUGAACCA	60597	AGCCCCUGAGCATGATCTUC
295876766	60598	GGCATTUGGAGGACAUGGAGA	60599	AGGCTCCUGAAAGGAAAACTTGTTUAAT
316988673	60600	GCGGTCTTAGAAUTGAGGAAGAATUGT	60601	TCTAGGTCCCAAUTCTACTGCAAAUAGT
316735071	60602	GCTTAGGAAUGTGGGCCCUAGA	60603	TCATGGUAGCTGAGAAGUCACAGA
257563603	60604	GUCATTCAGCUCAGCAGCAGA	60605	TCCACAAATTACTUCCTGACCTCCUA
240472077	60606	GTGGGAGTGUGAAGAATGATTCTUG	60607	AGGAGCUGTUAAAGAAAGCAAAAGGA
240217793	60608	TCCAGAGACAAAGUTGCAAAACAGAUA	60609	CAGAAGCCTCAUATGAAGATGGCTAUT
262099822	60610	CTGAGCTGAGUTGAGTGGGATTUT	60611	ACAGCGAUGGACCTCCCUA
320170811	60612	CTCGGGTTTCUCTTTTCCTATTACAUGA	60613	CCTTAGTTTTCTTAGUCTGTCATTAACTCUGT
318928238	60614	GGTTGATGGUGAGAACACAAACUAAAA	60615	CATCATCTUCTCTAAACCUGCAGACC
318995958	60616	CCTGCACCACAAUGGAGTGUAT	60617	GAAAAATGTACUGAATGAACGAGUGCT
265718574	60618	CTGGTCACACCUGAATGCTUC	60619	TGGAGGTUGGCATCCGAGUA
258039902	60620	CCTTCCTGACUGGCTTCTTCUG	60621	CCACTCCAAAAUGCCAGUGAGT
257126739	60622	GTTAACAAGGGUGCGATGTUGT	60623	GGACATGGGUTAGGAAGTGUCAT
265834224	60624	CCUTTGAGATCGUCACCACCA	60625	ACTTAGCCAGUGGTCTCUCAGT
266858170	60626	GTCTTTTCCTCUGACTGTGCTCUT	60627	AGGAGAGUGTGTGCTUGCAG
327006032	60628	AGGTATTTGAUGAGAGGGCAGCUA	60629	GAACACTGUATGAGGAAUGAGCAAAAC
327271585	60630	GGAGAAAUGGATTGTACUGACCCT	60631	GGATTTTGAGCUGGGTGCTTAUG
327263179	60632	GAGATGCUGGTTCACAAUGCC	60633	TGGGACTCAGAUCATTTTCCTTCTTTUT
314876134	60634	CAACCCCAUTGGCCTGUACT	60635	CACCTGUGGAGAGCTGTATGUC
333588647	60636	GCTACAAACAAUTTCTGTGACTTUCAGT	60637	GGGAAACAGGUTTAGAAUCCACCT
313624153	60638	CUCAGCCCCACACCAUCT	60639	CGTCCTGUCCCCAACCUG
316531462	60640	AGGAACCUTTAATAGAAATUGGACAGCA	60641	GCCCTTTTGCUAATCATGTTCAUACCT
328158355	60642	CCAACCAGAGCCAUCAGGUG	60643	AAGGAACGGGUCGUGCAA
319105812	60644	GTATTTCAAATUACCCGGTGTGGUG	60645	CTCGACGUAGACACAGTGCUAA
318206826	60646	TCTCTGTUCCCCCAGGUACAAA	60647	TTTGCUTGGGAAAUCCGAGACA
240690866	60648	TGAACCAUGTTUGCCCAAGACT	60649	GCCTCCCTUCCTCTTACTCTCUG
266347323	60650	GCUGCTGUAGGCACCCA	60651	GTCCGCUCCCCCACTUC
333385274	60652	GATCTTTUGGGCCAGCCTTUT	60653	CACATGTGAAGGAAUCTAAATACGAUGAT
313889238	60654	GCCAGCACUCATGTCUGGAT	60655	CAAGGACAAAUTTGACTGCUCCAAC
323497275	60656	GGGATGGAAUCAGGCTGTAUCA	60657	GGTGGUGGCAGAGGAGUAG
312668405	60658	GTGTTGCCUGTACCAGGUGAA	60659	CAUCAAGAGCCCAACTUCCCA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
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312683397	60662	TGGGAAUCCCUGCAACAACAG	60663	GCCAGCAAGUGGACACCUAAG
312741249	60664	GGGAACACCCCUAACTTUACCT	60665	GGATGCCAUTGCCGATGAUGA
314344339	60666	CCAAGAACGACGUCATCGUG	60667	CACTTCAUGCCTCTTCACTUCCT
328270233	60668	CACACTGGGUATCCAGAATGUAAAGA	60669	AGGCATCCGCUATCCCAGUA
222536404	60670	AGTGCAGTTTTAAAAUCCTTTTTCTGTAUGG	60671	ACAGCAUCCTTTGGUAACAGCAT
223528247	60672	GGCTACAGATUGCAACCCAATTAATAUC	60673	GACTTTTGTGAGCUTTCTAGGTTUGAC
223073665	60674	AAGGCAAAGCAUTAGGTACTUGGT	60675	GACAGAGAAGCCAAUACTGGACUG
223736495	60676	CCCAGCCUGATTAGGTAAATTTUGACT	60677	CCTCCACCTCCAUTAGATTTCCATTAGUA
328741172	60678	CTGCTACCAAGGUCTATGATATGCTUAAA	60679	GGGTTGGCTAUGCTAGATAATGATUACC
222211833	60680	CAAGAAGGAAGAAGGUGTGUAAGCA	60681	ATCCTAAACGUAAGAAGCAACACTCATUA
332303025	60682	TGTATTUGCCCGTGUCGCT	60683	CCTUGAGGACCCCGATTCTUT
316738148	60684	CGACACUGTGGTCCTUAGCAA	60685	GGCAGAAAGGAGAUGCAGAUGAG
332382194	60686	TGAGCTAAGUCACTGACTAAAAUGCAA	60687	CCAATCTCCCAAUCCCAGGTUAG
333717075	60688	GCCTGTUCAAAATCGCCAUGA	60689	CTGGGAAUCAAAGGTCTTTCUCAGA
333293604	60690	AGCAGACUCCCTCAGAGGTUT	60691	CTGTCTATTUCCCCATCCCAUCC
332384318	60692	CCCAGTTACUCACCTGATCAATGATAUT	60693	AATGCCCAGGTUCCAAATAGTTTAGUAT
313990072	60694	GAGGACAGCTCUCATTTCTTGACTUAAA	60695	GCTGTGATTCUAAAGCAAAACACATTUG
266106271	60696	GCCCAACAGAAAACUGGAGGAAAAUA	60697	TTCCCAAGAAGAACUGGUGGAG
269288466	60698	AGGGACTUGAGTGTGGCAUC	60699	ACAATCCTGGCUGATCTCTCUGT
265191821	60700	TGGATAACUAGCCCCTCTGCTUT	60701	CCTCTGCGACGACAUAATCTGUG
323361128	60702	TTTTCTATTCCTUAGCCTATGTGCTUCC	60703	ACCCTCCAGGAUGAAATTTUAACCAT
319021658	60704	GCCACAGTACUTTTCAAGAAGUGGAA	60705	TTGAGACACCUATTTTGTGCCTGUAT
313608585	60706	CTTGTAGTGGCUTCCTCTCCUC	60707	GCCTCACCUATGACUGCCAAAA
255945408	60708	GGGTCCCCAAGUCCTTAGCUAT	60709	ACGCAATATGUTGCCTACAGUCC
240092527	60710	TCTGATCTCTUCCAGAGTAAATGTGUCA	60711	GTTCCCAAAGUCTCTAGAAUACGACAAT
326774766	60712	CTTGTGGTTCUGGTAGGAAGUCAC	60713	GGTTTTATCUGGAGACAAAGGGAGUT
316439953	60714	AGGTGGTACCCAUTGTAAAGGAAGUA	60715	GGAGAGAAGAGGAAUGATTUCAAAGACA
326815367	60716	TCTTGATTCUGGAACAGATTTGTCTUT	60717	GGGATTCCAUGATTCGATGTUCACAT
333135140	60718	AGTCTGACAGGUTGACATCUACAGA	60719	CGGGTCATTGCUATTTTCTTCTCUGA
313467800	60720	GCAGCTUCTCCACCTUAGCC	60721	GAACCTAAGTUCCTGGTAGCTTTUCA
313100695	60722	GACAACACTCUAGTCTGGGAGUCT	60723	GATGAATGAGAGGCUGGAGGAUG
313977253	60724	AAGCCUCAGAGTCTCUGGGAT	60725	GGGCUTCACTUCAGAGGAGAAAG
314401894	60726	CCCTAGGCAUCAGCGTGTAUG	60727	TCTCCGACAACGCCUATCAGUA
266752333	60728	TGATTGGGTUGGAGACTACAAUGAAC	60729	TCAAAAGTGCAACUTCAAGGATCCUAAA
255992871	60730	TTGAATGGAATTGCUTGAACATGAATCTUT	60731	CGTGTCTTAAAACAUGCCTCCTCATUA
325942186	60732	CCACCAGTUCACCTGCCATTUA	60733	CCAGCATACGAAGUGGACCTTUC
324102386	60734	ACAGCCCAUGCTTTGTGGTTUA	60735	CCGCCAUCATCATTCTCUGCAA
318017518	60736	CAGCAAATATUCCTGTATGGTUCCCT	60737	CGTCTACGCGCUGATCATATTUGA
256873304	60738	CTGACCCCUGTGAACCAGUT	60739	AGCAGUTAAUCCAGGAGAGAAGGA
317580376	60740	CCACCACAAAUAAACATGCAGCAUT	60741	TGTTTTGACTTTGUTTGACTCATGTGAUT
317634013	60742	AGAAAGTTCUGACAATGCCGUCA	60743	CCTATCCTCCCAUCCCACCTUT
316840291	60744	GGAAGAGTCUCCTAACAAGACAGUGA	60745	CAACACCGUTGGCAACUACAC
315758743	60746	AGAGTTTUAAAGGACGTCCCCUCT	60747	GCTCATAAACTTAUTTTGCCCCACAUT
315771257	60748	GGAGTGTGUGTCTGTACCUGAAG	60749	ATGTGAAGTGUTCCCAGGAGUG
317726396	60750	AAGTATAAAGUGTCCATTUGCCCAGT	60751	CTGATATTUGCCCAAATGGAATCUGT
316412699	60752	CATTCAGGAAGUAGCCAUGCAGA	60753	GCGTCTCAGCUCTCTCCTTATUT
316078907	60754	TUCCAAGTATTTUGGGCAGAACAGA	60755	GTCAGATAGCUCCTTCCTGUGG
327092437	60756	GCUGCGACTUCCGGACT	60757	TGCAGGCUCCGGATCTUC
327225237	60758	CCATCCCTCUCCTTTTTCTCUCCT	60759	GGCCTCTTTUGAGCAGCTCTUAAA
272706670	60760	GGAGGAGAAAUGGUGCGAGAAG	60761	TCTCCCTCUTCCCATCUCCAG
272494146	60762	CCTCCAATUCGGAGCGCUT	60763	GCTAAGGAUGGACGCAAGGUT
315817744	60764	ACAGTCUCAGAGAGGAGUAAACACT	60765	GGGACATCTCCUCATTGAAAGATTTUT
333722763	60766	CGCUCCACGGCTTTCUG	60767	CTCGGUGGACACCGCUA
241056300	60768	CAAAGCAGAGCCUCAGATGCUA	60769	CTTTAUAGCGCAGGGACUCAGG
320503303	60770	CGGCACUCCTGGAGAACUACT	60771	CTGGGAGAGUCCTCACAAUGG
318279392	60772	ACCTUGCGGGCTTCTUCC	60773	AGGCUACAGGCCTCCAUCA
320216886	60774	AGACAGACCUGUGAGAGGCA	60775	GGATGAATUCACAGCCTACCAUGT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
321342301	60776	GTCAACGUGGGCCUCCAA	60777	AGGGCCGAGCACUCCUA
321335563	60778	GGCUGAGTCATUGGCAGCA	60779	CCTGGCUGGTGGCAUGT
321335934	60780	AAGGTCCAGUCGAAGAGGUAGT	60781	AGGCAACAGUGGAGCAUGT
321596469	60782	CACGUCAAAGCUGCAGGAG	60783	CGCCAACGCCUCGUCAT
236860074	60784	AGAGAAGTUGAGAGGACCCAUGA	60785	TCTTTGCAUCCCTTTUGCAGGA
235993401	60786	GGATAGCAGGAUGGTGGGATUG	60787	CTGAAGAAGAUCCGGGAGCUG
235719601	60788	CGTTAAGTCACUAATCCTCTCCUCAAG	60789	AACTCTAGTTGUATTTTGTTATAATGUGGGT
268136181	60790	GGCCAACCAUCCTCCTCCTUA	60791	CTCAGTTUACCCATGACCCTUCC
327592651	60792	CGGAATCCCCAAGUAGTTAGTGUT	60793	CCAACCACAGCACCUACCUC
328316074	60794	CTGTTUGAGCGGATGUGCAT	60795	AAATTCAAAGCTACGUCTACACCAGAUT
318580060	60796	TTTTCTUGCCGTAGUCAGCCA	60797	ACCTACCCCACUCTTCCAAATCUT
318058943	60798	CCTTCUCACCTCCAUACAACCAT	60799	CTTGUACCGCTACAUACAGCCA
320351029	60800	CAGCAGGAACCUATCTACCCUACT	60801	GGAGGCUAATTTCATGUCCACCT
318315422	60802	CCTTGGTGGUGAGCGTTTUC	60803	TGACTCTTACUCTCCATGTUCCCA
318761886	60804	CTCCGACAUGTAGTCCGGUAG	60805	CGGGCCTGUGGTTAGTGAATUT
319592558	60806	AGUGCAAATGUGAAACAAGAAAGGAG	60807	CTGATGCATUCAAAGCCCUGAAAA
320507702	60808	AGGTGGGUCATGATAACUGGGT	60809	GGCACUCCAAAATCTAATGTUCAGAGA
253913493	60810	ACTGGAAACCACUGCATCCUG	60811	CACCGTGUAAGATGTAAGCUGGAA
268209254	60812	CCTUGACACCGCCATCTCUT	60813	TGCTTGATCUCTGGGAAUGCAG
264688660	60814	CCCAGGCUCUGGCAGAA	60815	GTGGGCUTATTGCUCCGC
267866970	60816	CCAATTAUGCTGTGCCUGGGAA	60817	CCTGCCAGAGCUCAGAAUAACC
256584449	60818	TTTGCACACCCCACUTCTTTTCUA	60819	TCATGCAUGCCCACGATCUC
239777409	60820	CUGACGCACACCTATUGCAAG	60821	TCATCTCTCCUCCCTGCTTCUG
263780413	60822	ATCTGGACCUGGGTCTUCAGT	60823	GACTTCCUGAAAACAACGTTCUGG
266466791	60824	GGAAATCAAUACATCTGCCTTUCGAGAA	60825	CGTTCTTUAACAGCCATAAGGTGUC
258608470	60826	ACAGTTUGCCCGGCATAUCC	60827	GGTCCAUAGTGAAGCUCACACC
263763017	60828	CCTTGGCAGGCUTATTGUGCT	60829	GTGTAGTAGTTGAAUGGCACGTTTTUC
264997516	60830	GGTTCUCCCCACCCTTCUGA	60831	AGGACTTTTAGGAGUGTCTCCTTTUCT
323707775	60832	GTGTCAAGAACCUCGTGUCCA	60833	GCCTGGUTGCAGUAGAGGAA
325560557	60834	GGAGTCCGUCATCCUGCT	60835	GCAGGCTUGTTGGGCTUCT
258118639	60836	GAGCCUGCACUCCACAGA	60837	GUCGAAGCGGCUGACCA
239859185	60838	ACUCTAUCCCCCAACACACCAA	60839	AACCAACACUGCATACCTUCCAA
241493432	60840	GCATTCCAATAUAATCCATCCCUGCAA	60841	AGUGAGGGCGGAACAGGUA
333353601	60842	CACCCCTUGCCATTGTCAUCT	60843	GTTCAGCCUCTACUGGGAAACC
332875838	60844	CACAACCAACUACTGTGGUCCAA	60845	CCTGGCTTTUCCTTTCCTCTCUG
312929488	60846	CCCCCUGGAGTTCACGTUT	60847	CAGCAGGCUGCTTTUCAGA
314160066	60848	TGGCGTGUCACTCATCCTTUT	60849	CUTCCTAATAATUCAAGCCACAGCAC
225676299	60850	GCTGGGATUGAAGGGAAGAGGUA	60851	ACTTGTCTTCUAACCCATCTTTTTCCUT
256502507	60852	GGGTAGUCCAGGCCCTTCAUA	60853	TCTCTGAATCCUAAGAAGAAGCTCUCA
327267923	60854	CCCCGCGCCUTCCUAAG	60855	CTGCTCGUCGGTCATCTUCA
327619077	60856	CCCTTGTUGATTTTCTCGUGCT	60857	GAAGGTCTCGAUGTTGGAGAUGA
255740643	60858	GTGGCAATUAAGCCCTGTUGAC	60859	CCTGTGCAGGUGGCTCAUC
266632546	60860	ACAUGACCUCCAACAAGACCAC	60861	GGACGGCUTGCCCTCAUAT
259827660	60862	GGAGAGACAAAACCUGGCUCA	60863	CTGCACCGGUTTTTATTCAUCAACAT
320393998	60864	CTCAACTCUCCGCCTGTGAUT	60865	CACAACGUCCAGGTACUGCT
319897411	60866	CGTCCACUAAGAGUGAGGCT	60867	ACAATCCACAUGCCGUCGAA
317470262	60868	GCUACCTGUCGGCAGAAGAG	60869	CAGGUGCACGGUCCACA
330490272	60870	GGAGCUAGGGACAAACUGAGACT	60871	ACACTATCTUCAACCTCGGTGUG
330751961	60872	GCCACAGACAAUAGAGCAGTCUT	60873	CAGTTGTTTTATGUATTTCAGTGGGCUT
269127557	60874	GCCACTGGCUTTCAGAGACTUA	60875	GCCCAAGACTAUGTCCTGACATAUAAC
267349865	60876	GCAUTCTTGAUCGAGAAGAAACACCAT	60877	TCTACATTGTTUCCTCTTGCAUCCAA
268285542	60878	GCTAGATGACCGCUTCTTAGATGAUT	60879	ACTGCCAGAGGAGUAGGTATTCUC
313954493	60880	GGGAAUGGCGGTCAATGUGT	60881	ATCACATTCCACAUGACAGACTGUAAAT
267853769	60882	GCATCTUCCACGAGCGGUT	60883	GAGGTAGGAGCUTGAGACCTTATUG
263204557	60884	GCATUCGAGGCCATTGUGAAA	60885	GTTTCCACAAGGUCAGGAGUCA
325923676	60886	GTGACGTUGCGGCAGTUAG	60887	CTTCTCCUCGTGCUGCAAGT
324568762	60888	ACAGACTGUCCCCCAUAACCT	60889	CCCCTCCCGUCGATACUCC
324070619	60890	ATGGGTCUGGTCTCTGACUGA	60891	GTGACCAGUGACTCCATACTUCC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
323341206	60892	CCCCUCCTCAAUAGGGCAAC	60893	TCAGGGTCUCACATGCATCUCT
324697384	60894	CCTGUGGAGACCCTCAAGUG	60895	TTGAGGGUTTCTTGGAUAGGAGGA
324055466	60896	TGCATGGAUCCTGACUGAAGAC	60897	GCATTTCTAUACCCCTTGATGUGGA
323971438	60898	AAAGCCUGGACTTGCCTUCAT	60899	GGAGGAGUGAGGTTAGGAUGAGT
324855718	60900	CTCTGATCCCUCTGGCCCUAA	60901	GCCTGTGAUGGCCTGGUG
320974199	60902	CAAGTTTTUAGGGAACGCTGCUG	60903	CTTGGCGAUGGTCTTGACUGA
320186403	60904	ACCTCTGUCTGTCTGTCUCACA	60905	TCCCTGCUGAGGGTCUCC
327479124	60906	GACTUGGGTGAATUCGCGAAA	60907	GCTGCAGACACUCATCGATGUA
315824363	60908	GGAAGGGUCCCAGAGAUAGCA	60909	GCCGATTGUCTCCCCTTUGAT
264651872	60910	GACAGGCCUGGTCCTAGTCAUA	60911	GGTCCACCACUCACTGTTTTGUT
225437160	60912	GGTGATCAGCCUTTTATTGGTACTTACUG	60913	CCCAGGAGTGGUAGGTCTCATAATUAAA
315766653	60914	GGGAAAATGUAGCCAACATAUACAAAGA	60915	CAGTCAGATGTCAUACTCACCAAGAAUA
316234235	60916	CACTGTTTAAUGCAGGACGAAUGAA	60917	CTAGTCATTTCTGUGTTATGGACATTAGUCT
264642215	60918	TGTGCACTGUGTCTCCTGACUA	60919	CTTGAAGAGACGCUGGTCAUCT
265132142	60920	CCUGCAATCCATUGGGAGGAAA	60921	CCCAACATCGUGCTGATCTTUG
316901117	60922	GCATGCAACAUGGCAAGTUGT	60923	AACACCATACAUAGTTCCTTCTGTUC
315833403	60924	GGCAGCAGAAGGUCCCUA	60925	CCGAGCCUGGCTCTACUG
324595974	60926	GCUGAGUGGGAAAAAGGAAGAGAA	60927	GCCTTTGACCGUGACTTTTCUG
324622088	60928	AGTAGGACACCAAGACUCCATATAUCAC	60929	GGTAACCATGTTCUGTTGAAATTTTCCUT
324090561	60930	GGCGGATGAATTUCTCTTCTATACAGUT	60931	TAAAATTATCAGTGAAUCCATTTTTGATAGGUG
325589931	60932	AAAAGCACACACUCATGACTUACCT	60933	CCTGTTTGCTCCUCTTACGTTTATCUC
267047398	60934	TGTAACTGTGACUCCAGCTGTTTATUG	60935	AGAAUATGACCGTCUAAAGCAGCAG
265654405	60936	TTTTATTGAAACTUGTCATGCATCTUGCT	60937	CAACGCUGAAGAACCCTGATACUAA
265922075	60938	TTACCATTGGTTUTATCATGGTCCUGAA	60939	AGTTGAAGGAAUGCCTAGTAATTUGGAT
267919003	60940	TCTACTTCATTUAGCCACTTGTTUGCT	60941	GCTGCATTTUGAATTACCTGCUACAA
293369865	60942	ACTATTTGCAATGUCCATCCAGGUC	60943	GCAGTACACCUGGTGTTAGGAGTUA
289648372	60944	CCAGTTGTGGUTCTCTTCATCTTTUC	60945	CCCCACCAGUACCAAAATUCCAA
292729123	60946	CCACTTTTCCUCCTTAGGCTUCAC	60947	GACTTCCCTCUCAGACATATTATTGCUC
313252895	60948	GACATTGACCCUAGTTCCAGTGUT	60949	CTTCCCCUCACAGGGCAUAG
289306128	60950	TCTGTCCCAUAGGGCAGGATUT	60951	GGAAGTTCTTCUGTTCCTCCTGUC
290588157	60952	ACCCTGTGUCCTCTGTCTGUT	60953	CTTGGUCCACTCCCUAAGCC
290857425	60954	CCTGAGACTUCCCATCCCUGT	60955	GATGGAAUCGAAGCCAGCAAUC
290795186	60956	GCCTGGGAUTGTGAGACUAGG	60957	CGGGTAGGATCUACAAGAGTAGGATUG
300417938	60958	AGATGGAGAGCAAUAAGCTTGGTATTUC	60959	GGCCAACCACAAAAAUATCCACTAATUC
260717901	60960	CTCAGTGGCTAUTTTGTTCCTTTTATUGT	60961	CACTCCAAACCUTTAAAGATCCTGGUA
254096493	60962	TCTGGAAAGGUGATGUGGAGGAT	60963	TCACTGTTACUTTCAGCAGTUCCC
258710392	60964	ACTCGTCCUTCTCGAAAUGCAA	60965	AAATATTTTCTTTGUACAGCTGCTGTATUC
253937392	60966	GAATGTGTGCAGCUATCAGTCTTUG	60967	CCTCATCTGGCUTCAGAGAAGGTAUAT
316967283	60968	GGAGAAAAAGGUGGACAGGAAGUAG	60969	TGGGTAAAGGAGUGGCCTGUA
262494113	60970	GAACAATGAGUAGTAATAAATAGUGAGACACAA	60971	GACCTGGTGUCCCTGGAAAUC
265980917	60972	CTATTTTGAUGGGCTTTTUCACACCT	60973	ACAGUAAGAAAAGGAAUCCACACCAAAT
266267812	60974	AGTGCCTTUCCTTTGGTGGUT	60975	AGGTGGGAAAGAUAAGAAAAUGAGAAGG
267676814	60976	GCCAGTGGCCUACTCAACUA	60977	ATTTGGAUCCATTGGUCCAGGAG
267147755	60978	GGGTAAAGGTUGTAGCCCTGUT	60979	TCTGGCUGAAAGACAGAATGAAAACUT
265647213	60980	TCCATAAGAGTGGAUCAGAGCTTACUT	60981	GCTGTGGCGUGTAATAAGAAAUCC
315279194	60982	AGGCTGAACCCUTAGATCAAAGGUA	60983	GCCAACTTUCCCATTTTTGATGTUGA
317666114	60984	CTTGTGAGGCCAGAAUATATGCUCA	60985	GCGGAUCCCACATTGCUACAT
228118044	60986	CAGUCAGUGCACCAGGAAGAA	60987	GGTAGACTTGCAUTTCAAATCCTTCUCT
316179608	60988	CACTTGUCCCAAGAGGCCAUT	60989	TGAGTAGATATCCUAAAAGGCAGAUGGT
316693546	60990	TGUTACTGAAGUGGAAGGGACCA	60991	GAGGCCCUGTTAATTTTCAATUCCAAT
313939431	60992	GTAGACTGTUCCTTCACGCUGA	60993	GTTCATCACAUACCAGACAATAGCAUCT
312914119	60994	TCAGGTTGTGUGTCCGAAGUT	60995	GGCTACGUGCTCTCCUACCA
313245100	60996	GGAGGGUCGGTGCTUGAAAG	60997	CGCAGGTACUTCATAGAGGAUGG
313658010	60998	TCTGAGUGGTTGUCGGAGGT	60999	TCTCCGGAUCTACTGGAUGAACAG
312927049	61000	GACTGUTCCGTGAUGACAGGT	61001	TCTCCCUCTTTTCATGUCCCACAA
314887625	61002	TGGCACAGTUTGGCACAGTUA	61003	CTGUAGACCAGCUCCAACAGG
267740199	61004	GGCAUGCCAGAATAGCTTUGT	61005	GCUACCACCTCAUGGGAAGAG
317587194	61006	GGTGAAUTCGAAGGUAGCGAGT	61007	CCTGTCAGACAACCAAUAAATGCTAUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316532899	61008	AAGAGCACAAACAAGCUCAUACCT	61009	GCAUGGGCAGCAAUGAAAACAT
317242614	61010	TTGTAATTCCACUGTCCTTAACUCACC	61011	TGTCCCTCAGUTCAAGAAAGTUGT
317652120	61012	GCCTAGUGCTCAGUAAGAAAAGGT	61013	GACGTAGGACUCAAAGAGATGGUT
317653060	61014	GATTTAGCCUCAAAGCTGTAGCATTUT	61015	ACTCACATUGATGGCCCAUCAT
318672195	61016	GGAACTTUAACCCCCUCAACGA	61017	GTTCTGCUGGGAGTGCAUCA
318173480	61018	AGGTGCAGCAGUGAGAUGAC	61019	TTCTAACGUGCTCTGUGCCAA
319288430	61020	GCAACCAGGAGAGCAUTCCUAA	61021	GTGGGCAGCUCTAGGAAGUC
313080043	61022	GGCCUGAAGGGAATTTTGAUGGA	61023	GCCTCCGCAUCTGATCTTUGG
325627518	61024	GGAGAUGGTGTTCUGGGAAAGA	61025	GTGCTGATCAAUATCACTCCATUAGGG
317493206	61026	GGAUCCAGACCCAGGCAAUAAC	61027	GCCCAGTUCCCAGTGUCAAAA
261392641	61028	GCTGTGGUGGCTTACACTGUA	61029	GTTAGTGCAGCGUCTCAGAUGT
266632807	61030	TCUGCAAATGGUCCCAGAACAA	61031	CTGAAGAACUGCTTUGGCACA
256406432	61032	GAGGGTGCGAUCAGTGATGUT	61033	GCAGAGCAGUGACTGTATTTCTTCTUC
262985410	61034	ACTCCCACCCCAAGAUCTTUCT	61035	GCACCACTGAACUTTCTCTCTTTTUG
267668071	61036	AACAGGACCAACUTCAAAUCCGA	61037	CUCCACUCAGAAGCCCAAGAAAA
264452778	61038	AACCAATUGGGCCAGCTGUA	61039	GTGGATTCAACUGTTTCTCTTUGGG
285850381	61040	TGTAAAGAAATTTTAAUGACCAGGTAGCUGT	61041	GCCAGTGACUCAGGATAAGAATTUCAT
332790540	61042	GGGTGCCCAAUATCTTGCAGUT	61043	CCAGCTGGAAGUGTAACTTTTGTUACT
315807488	61044	CUGAGGACAUCCACAGGGAAT	61045	GCTATGAGAGUACACGCAGUGG
315107214	61046	CTCCTGCTUGTTCTTTCTTUGGT	61047	TTTCUCAACCCCACAGATGCUC
315814376	61048	TCCCATCAATTTUGTTCTTCAGCCAUA	61049	GAGCTCATCGUTAAATACAGGCUCT
327155762	61050	GGCTTTTCAGCAUTTATGATGTGUGA	61051	CATCAAGGATUTCAGCTCAGUGAC
327953130	61052	CCCACAGUGAGTTGTCCAUCA	61053	TGTGAAATACUCACAGCAACTTCCUT
328057086	61054	AAGTCACAGGAUCAAAGCTAAAAGGAUAG	61055	AATTCAGCUGGGCATACCTGUAG
328063312	61056	GTAGGAGCCAGCUGAGAGUCT	61057	AAGTTATCCCTTUTGCTTCTGTCCUT
327967650	61058	TTGGAGCAGUACGCATTCTTAAATAACUA	61059	TTTCAAGGAAGUTGTGGAGTUAGCA
326846604	61060	ATTGATGCCTUCCCTGTGGAAUT	61061	TCACAAAAGCCUACCCTATGTATGTCUA
326716319	61062	ATTAAATGCCAUTGGATGUCCAGT	61063	TGATAUACCAACACCCACAATUCGT
328115533	61064	TGGCCCTTCUAAAGTTTTCAAUGACA	61065	CTUAACCACACAGCCAUCGAC
328425708	61066	ACTTAACACUGCGGAAGUCACA	61067	CCTGTATCGUCACACTGATTCTAAGTUT
327250811	61068	TGGGTCTACAUAGAATATCCCAGUGAA	61069	GCTCAAAGCGAAGCAUGTACTTATTTUA
328373974	61070	AGTTUGTCCTGCUCCCGAAG	61071	ACTGCCAAGGUTATATTTTCACACUGAT
327869260	61072	CACTTTGAGCCAGUGACAAATTGUT	61073	CCGTCTTACTCUACAATGCTATTGGUA
327199910	61074	GGGCGTUAGGATGCAGAUCA	61075	GAAAGUTTCCATCGUGCCAACC
323386818	61076	CTAGGCTGTAAUGCCTCCACUG	61077	TTGATGAACACUAGGGCCAUGAG
333261819	61078	GGAAGGTGUCCGGCCUAAAG	61079	CCTGTAACUCAGCAAACACAATTTUCAT
326220542	61080	GTCTCTTAGAUGTGCCTACUGCT	61081	GTTGTATCGGAAACGUTGATTGTCTUG
324947939	61082	GGAGACAGCAUGGCCCTTUA	61083	TCTCCCTTCTAAAUTTTGTGACTCTUCAG
323924887	61084	GCCTAGCCUTCTGCTUAAACACT	61085	CGGAGATTCAUGCTACAAACAAAAAGUT
327760808	61086	GGGCUAGGAAAATATACAUCCCAGT	61087	CCAUCACCACCATUGACACAAG
237657546	61088	CTGGTTCGTCAGUATAGAGTTGAAGTUT	61089	TTGCTATTAAAGUGTCTCAAACCATUCT
263905997	61090	TGTCCCCCACGUCTCAUCT	61091	CAGGCCAACGUGGGCUA
257338612	61092	CGGGAUCAAAAGAAAGCGAAGUG	61093	AACUACAGATUCCCCCACAGGA
262753101	61094	GAACTGTGCCCAAUCCACATTUT	61095	GGAGAACACUTTGACTGCUGAGA
326833773	61096	AGATGTTUAGAGCACCACUGACC	61097	TCATCACCAGCUATTTTTCTTCCACUT
326769030	61098	CAAAGGCUTCUGACAAAGGAAAAAGT	61099	TGCCTTTGAGAGUCTTTACCAAGAUAAA
314291900	61100	ACAGGAAACGUAGCCATUCCC	61101	AATTCCTUCCCATCTTUCCACCAA
314341314	61102	CAAAGGCAUGGATUGCACAAAGA	61103	CTAAGAGUTTTTCTAGCUGCAGCCT
314389211	61104	GCTGCAGUCACAGCUGAAAAG	61105	CAGAAGAATTGGCUTGATTTTTGGAAUG
325783872	61106	GGACAUCAUCAAAGCAAAGAGCAG	61107	CTGTTTAGAGUCATCATTTCAGGUAGCA
323670865	61108	AAGGCTTGATUTGTCACTAGGUCAAA	61109	CCACAAAAGCCAAUTCCUCGAC
323802044	61110	CCTCTGTTGUAACCGTTTGCATUT	61111	GTGATTTTCCUGGGCTCCTTTTATCUAAT
324022723	61112	CCTGTTGGUAAAGGTTTUCCCAGT	61113	CCTGAAGACACUCTCACCTATAATGTUC
267849444	61114	AATCTGATAAUGATTGTGAAUCACCAGGA	61115	TGAGGACCAGUAGGGCAUGAT
257666052	61116	GGACCAGCCGGUGCTAAUG	61117	CACAGGGAGGAUTCGACUAACAA
267646992	61118	GTATAGGATGAGAAACUTACACATTGCUACT	61119	CCCAUCCTTGCCUGGAGAAC
265627457	61120	CTGAAATACCAGCAUGCATTATUGGAAT	61121	TGCTACAGGAUTTCCTGGTTCUG
259750862	61122	GTTCTCCTCTTUCCCCAGGATTUC	61123	AATTTTTCCGCAGUAGAAGCCATTUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267853430	61124	GAAAUCCGGCACCUCAAGGAT	61125	TGAGGTAAUCAGTAATCUCGAGCCT
262983084	61126	CCAAGGUCACAGCTAAGTCUGG	61127	AACCTGUGGGCAAACACUCA
269362952	61128	GGAGTACTUCCTGCTCAAGUCC	61129	ACAGAUGGGCUGAAAACCAAGA
235042201	61130	ATCGCTTAAUGGACTAGAAGGCTUT	61131	GGAGACCAAGUTTCAGATGTUCCAG
235212165	61132	GGCTGAAGGUGAGGCTTAAUAG	61133	AGTTGACCAGCUTTCCTTTTCUGT
332602491	61134	CTGGAGUCCACGCGGAUT	61135	GGCGAAAUGGACCUAGAGGAC
333138999	61136	CCTGCAGGAGGUGTTTCAUAGA	61137	GCTGGAAGGGCUGAGATGAUG
332990382	61138	TTTAAGACCAUTGAAGAGTUGGAGAAGG	61139	AGTCCTGAGAAUAGGAATGAUGGACAT
233218701	61140	GGGAGAUGGTTAAAUCCACAACA	61141	CCCTGCCACUAGAAATATCTGTCUT
324432916	61142	CAAGTUCGCACCTGGAUCACT	61143	TCTGTGAAGAAGCUGGCTGAUG
266896014	61144	CCCCTCCUCCTGTGTGTGTAUA	61145	CCAGTGAACUGTCAATGAAACTUCC
260797179	61146	GGGCTGUCCAGGGUAGAAGAA	61147	ACAAAAGGCUTTGATUCGGAAGGA
262119871	61148	CTCCCTACCCCUCAACGGUA	61149	GGGAGTUGACAGGCAGTUCA
317428410	61150	TTTCCTTTTCTUGGGAAGTCTAACCAUT	61151	GGACACAGGTCUAGTAAATGATAGCCUA
267109484	61152	TGTTATCAGAUCAGATCCAGACTGUGA	61153	CAGAGTCCATAAAUGCAAGCAGAAAATUA
332056767	61154	ACUGGAGCAGCAGCTTCUT	61155	GGGCAAUGCCAAGCCUGA
325717688	61156	ATGCAGACGTUTATGATCCCCTUT	61157	GAACATGTAGAUGACAAAAGACTCGTUG
261194463	61158	ATCTTATTTGUGACGCAAGCATTGTUT	61159	GTTAAGCGTACUCGAGAAATGCTUC
255751778	61160	AGTCAATGCUCATTTGGTGAUGGAA	61161	GCAAGGGAGCGUGAGACUG
328760104	61162	GCGCGCUTCCAGGUCAA	61163	CGCGGCUGGAGGAAGUG
227874749	61164	CGAGTTUGCACACTCAUGGT	61165	CTCCTCACCUTTCAGCATCTUCA
325539928	61166	GCCACCUCCAGAAACTGUGA	61167	ACAAAGAGUCCGGGCAUGG
262494870	61168	CCCGCAGUGCATAGGTUC	61169	GGAGGUCAGACAGCTUCCA
320227876	61170	ACTGCTTATAAGUTTGCACTGCUCT	61171	TGTGGAAAAACUGATCTGUGAACCT
318277281	61172	TGGCTGTATTCAUGTGTTGTTGTUG	61173	CGAATTTCCAATAUCTCTTCCACCACAUA
319958557	61174	ACCTGTTTGGCUTTGCTATTATGTUCT	61175	TGAGAAGCAGUGACAACTCTGATUAAAT
320105349	61176	ATGTCTCTGUGTTGAGGGUGAAC	61177	GTACCAAATCAAAUCCGGTTCTCCUAA
332503337	61178	GTGAAGCGCUATACTGACTGUCAT	61179	TTTAAGAAAGCCAUTGGTGTTCCTTTUT
333364528	61180	AAATAATCCTGCUTCTTCCTCTGATUGT	61181	GCACATACTTCUGGCTGACATCAATUA
332580379	61182	GTTTTGCTGGCACUTCTGTTCAUT	61183	CCAATCAGATUGCTGTCCTGTUT
332889625	61184	GCCAAGTCCUCTGAAAGAAUCCC	61185	GAGCTCTCCAUGAGCGATGUC
332936631	61186	GGCCGAGGAACUTGAGTUAGA	61187	GTGTCAGCCUATCCACTAATTUGGA
333083353	61188	TTGGAGAAGUGACTTCCTTTCTTUGAA	61189	TGTTGAAAACCUGGGTCACATUCT
323789503	61190	CTTCATAGCCGUTCGGCTUCT	61191	CCAAACAAGUTTAGATGAGUAGAGCACA
317009085	61192	CCCGACUCACATACTCGUCCA	61193	GGAGUGCGUCCGAAAAGAAC
268714858	61194	GGGACACUCCCCACATGTUAC	61195	GCTCTAAAGTGGAAAUTTCACCAAGTUC
263617206	61196	GAGAAGCAGAGCACAAUAUGAAGG	61197	CTGAATTTGCAUGCCTGTACTTCUT
266315246	61198	TGGCCTCUGAGCACCTTTTAUC	61199	TGTTCCATATUACAGATCTCTCGTGUCAT
263461125	61200	AGAAAGCUGCTCCUCACACAG	61201	TGCATCATTCAUCCTTGGGCTTTAUT
291147755	61202	CTCTCTTGCAGAAAUGATGGACTCUT	61203	GTAGGACACAUCACTAGAGTAACUGAGT
289853661	61204	CATTGAGCCAGAACACUAGCTGUA	61205	CTACTCATCCCUGAGGAAACAUCAC
223303241	61206	GGTAATATATAUAAGGTGCGTGCTTUGA	61207	CGCTCTAAUAAATCAATCTGUCCAGAAGA
222941406	61208	AGAATGATTTGACAUAACCCTGAGCUT	61209	AAGAAAGGCAAUTTACTAACCTCUGCT
222414448	61210	CTGTAGATGGUGCACTTGCATTTUT	61211	CCTGTGGTCCUCATTTGTAGCUAT
224566238	61212	GAAGAAGTGUCAGCCATTCAUACCT	61213	GAACATGTCCTATUTGAATTTTCCGACUT
222813651	61214	CTCUGGAAGGCAAAGTCCTUCA	61215	GAAACACATUCCTGCTGUCCAAAAT
224539791	61216	CCAGGTTCUTCCAGATGCUGAT	61217	GCCTCTTTCTCUTGGTTTTCATTTGAUT
224535592	61218	CCTTCAAGCAAACAUGCCTUCA	61219	CTGTTTGACCUTCACTAGGGCUT
326705869	61220	GCAGCAGCGAGGAGUCAUC	61221	AGTGGGAGAACAAGUCCUGAGAA
323774690	61222	CUAGTGAUGGAGGCCCCAAAA	61223	TTTGTTGATACACUGTAGGATCCAACUC
332081297	61224	CTGTTGAGGUGGGAUCGGT	61225	GCCAACAACAACUTCGTGAACUT
257523308	61226	AGUGTTGGACTUGCAGAACAGT	61227	TCGAGATTUAGCGCAAGGCUT
235232485	61228	GCAGAGGTCUCAGGAAGTCUGA	61229	TCAGCTGCAGAAUCCTGAAATGAUT
240627522	61230	GGGUGAAAUCACAAAGGAGCGA	61231	CCTGAGTATGAUGGAGAGAACGAGUAG
268888935	61232	TCTTTCTTTCTAUGGAGGGATCUGAGG	61233	CAGAAAGTCGAUGCACTTGAGAAAUAAA
268972287	61234	ACGAAGACCACCAUCAAGGAGAUAT	61235	TUCTGCATTATCUCAGAGCCACAG
265528530	61236	GGTGGUGACGAACGTGUGA	61237	CTTCUACGCAGGGACUCAACC
256792428	61238	GGGATCUCGCGCTTCTUGG	61239	AAGAGCCUGGATCCCCUACA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317950271	61240	CAGTGAGAUGAGGATCTGCTCUT	61241	AGAGACTUCCCCCTTGTUCCT
331783328	61242	ACCUGUCACCCCGACGA	61243	GGGACAGUTTGACCACTUCCT
331857530	61244	GGGTAACCAGAGAUGAGGACUGA	61245	AGCGAGAGGUCACAGTCUACA
331755677	61246	CAGTGACATGCUCTTTCTAGGTCUT	61247	GCACAAGTACAAGAUGCACCTGUA
331646492	61248	GTGGAGGCUTTGGCAAAAUGA	61249	TGGAUCCCGACCGGAAGTAUA
258830596	61250	ACACCCATATUCCCAGGTCUGT	61251	CAAGATTCCCUGGGCCAUCT
326714780	61252	CTCACATAGAUCACAGCUGCCA	61253	ACCCTTGUAGGAAGCTCTCUAAACT
324148827	61254	CCTCACCTCCUGCCTGTCTUA	61255	GCTCCCAUTCTATAGCAUGAAGGG
312919126	61256	TTCTGAAAACAAAGUTGCAAAGUGGAA	61257	AAGCTTTGGGUTTGCCAACUG
271127300	61258	GCCTACGTUGACCAACTCTTCUAT	61259	TCACTGTGAUGGTTTCAGTCTUAGAAAA
269791332	61260	CAGCACATGUAATTTTGTTGTGATUGAC	61261	AGACCTTTGCUGTAACATGCTGTAUT
270527593	61262	GACAGCCAAAACAUAGATGAATTUCCC	61263	TCTTTCTTUCCAGCAACCTTATCAUACA
269482626	61264	CCAGAAAGTTUCCCTCCTCCAUC	61265	ACTCACAGCUGGTTTCCUGAAA
316069507	61266	ATGGTGCCATTUATTACAACAGAATGUG	61267	AAAUTTCAGTACCACUAAAACAGAAGGT
319858442	61268	TCCTCTTCACCUCTTTCTGTCUGT	61269	GAAAATCTGTUTTGTGAGTGUCCAAGG
316476109	61270	TCACTACTGCTAUTTTACCTGCAATUGT	61271	CCCTGACCAGTUTGAAGCAAGAATAAUA
317211807	61272	GGTCCTUGCTCTCCTAUCAGGAA	61273	GCTTUCAGCAAAACACAGTCTUCT
316725186	61274	TCAAAAGTATGUCCAGGCCCAUC	61275	AGTCAGCACAUGGATTTACTUGCAT
317550652	61276	GCAGAGGCCAUGCACTGAUA	61277	TGCACCCCACAACUATCTTCATUAAAT
316819834	61278	AGTTGATGCUGAGCAGTTUACAGT	61279	GCTTTTTGGCUAAGATCACAGGTATGUA
268336740	61280	GGGAUGGAGTCUCCAAAGGGA	61281	CTGGTTTGAUAGTGTGCAATTGUGT
264611319	61282	GAGACCCUGGTCCTCTCUGAA	61283	TGCTCCACUAACCTATGTCTGCUAT
268656936	61284	TCTCACCTUGAGGCTCACCUA	61285	ACTGTUGGCAAACAAAGAAAAUCAACT
264158992	61286	CAGCAATTTGCAUAATATCTTTCTTTGUACCT	61287	AGGCACTUGTTACAGACUGGAAAA
327665046	61288	TGCAGCTUGCCATCTUGGA	61289	CGCUGCGGAAGATCAUCCC
257660413	61290	ACCCTCTGATUGAAGATGAGCUGA	61291	GTGCTCTCUCCTGGGAGGUA
268942908	61292	TCCCTCTCTGGAUACCTGGAAAATTUAT	61293	GCCTCTCTGUCTAGGGAAGGTTUAA
264943400	61294	CCGACAGAGAGCUACTGAUGAACT	61295	GATTATTTCACCUCTGCACTTACCUCT
265309361	61296	TTGTTTGACGUAAGCTAGTUACCAAGT	61297	CGCTGTGTAUGGATTTTCTGCATUAA
266692895	61298	GCAAATGAAGAGCUTGAGGCCTUA	61299	CTCCACAAACUGCATATGUAAAAGAACT
267620063	61300	CATUGGCACCAGCTGAUGAAAG	61301	GCATAACACAGCAAGUAGAGGCUAT
258352153	61302	TTTGCCTTTATUTTAGGTTCAGTUGCAG	61303	CCAAGTUCGCTGGACTUCCAT
268666206	61304	ACTAUGACAAAGAGCACATUCCAGAG	61305	CCCTTTGUGGAGAACATCTGUAAACA
268506484	61306	ACCAUAGGTGATUGAAGCCAAAGAA	61307	CAATGTUCCAGAAACAAATTGAACUCCT
267059287	61308	TCCTCTCACCCUCCTTCAUAGAC	61309	CCCAGTGTCTUCCCTGAAACTTAAUA
266717197	61310	GGAGGCCACAUCACAGAUGAC	61311	AAGGCCAAGCAUCCTCAATAACATUA
327217417	61312	AACTGTGTTATCTUTGCATTGCATTTCUT	61313	CCACGUACAGAAAACCCTUGGA
224460718	61314	ACAGGTAAATGGUTGCAGTTTTGUG	61315	CAGAAAGAAGTACAUGCAGGAAAAAGUT
224470710	61316	AGCAGTCTCTUGTAAATTCAAAGUCAGA	61317	CTGCTTCAAGTUGTGCAAATTTTTCTUG
332446425	61318	GAAGAGAACAGGGAAUAACTUAGAAGGG	61319	TGGAAGGTTTUCTTCTCCAAATUCAAGT
224115273	61320	GGTTGGAAUGATGGAAAGTTTUGCT	61321	TCCTGCUCAAGACGATCTATTATAUCAGT
223510881	61322	TTGCTACAACUTGAGAGCACUGT	61323	TTTGCATATTCCUGAACTGCCUCA
332299276	61324	TCAATTCCUGAGCTAGCACATUC	61325	ACCCCAGTCTGAUCCAGAATCTAAAAUA
222701945	61326	GCACTCCAGCUGATTTCAAUCC	61327	TGCTGCCAAGAUGTGGTUAAACT
318283880	61328	AGAGAATCCACGUCCTCTAGCUT	61329	GGGCCAGAGUTACUCAGCA
321180668	61330	AGTGTATTACCUGATTAGGAGGCUGAA	61331	CTTTTCCTAAGCUTTTGCACTATATUGCT
318814857	61332	GCGTGTCUTTGGCTGAAUAAGG	61333	AGCCATTTTUCCTGTTTGGGTUG
266335107	61334	CTGGTCCACCUGGTCCUC	61335	GAGAATGGGUAAAGCAGAATCTUGAGT
269101048	61336	CTGGTGGUGGGTGTGTCATUA	61337	GTGTGATTTGCUCAGAATCAGTTUGAAA
326192282	61338	CATCAGTTGUATGTTCCCCTUGGA	61339	CGATGGTTCUACATTGATTTUGGAGGA
323733372	61340	TGATTGCUGCCCTCCTCCUA	61341	TGGCTATTTCTTCUTGAATCTTTCCCUT
256851407	61342	ATTTACAGAGAUCAGAGAGCUGGGA	61343	TGAGGTGGAAGUCTACCATGAUAAACA
263693016	61344	AGGAAGATGUGCCTTTCAAATUCAGA	61345	GCAAATGCTTGCUAGACCAATAATUAGT
266684983	61346	TCTTAAAGCTGUGTCTGTAAACTGAUGG	61347	AATCACATCCCAUGAGTTTTGAGCUAA
263206634	61348	GACACACTUTGTCCACTTUGCAAT	61349	GTTGCAACAAAGAUGTAGGGTTGUAA
263707074	61350	AGCAGAGGCUTAAGGAGCUACA	61351	TTCTCAGAGGGCAGUCCGUA
319584973	61352	GCTTCCAGAGGCAUCATTCACUA	61353	AGTGCAATAAGCUGGAAATACUGGAG
315602156	61354	GTGGGACUGGACGAGCUT	61355	TGCCUGAGCGCTCTTUCC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316944416	61356	AGGCAAGGGCGUGTUGT	61357	GCGTGGCUTCCACCTCTUC
317831668	61358	CCAACGAAUGACCACAGGCUT	61359	GTTGCCACCAUGGACTCTUCA
317384500	61360	CACTGGTTGUGGTCCACUCA	61361	CTTTUCCAGGCACUGCAGAAC
317145414	61362	GCTGCCTUCTCTTTTCAUCACAGT	61363	TGCCACCCUACCTAGTGTCUG
239960609	61364	AGGTCTTTTTGUTGGAATTCATTUAAGG	61365	CTTCCTCAGAGAUTGAAGTCAACUGT
240019202	61366	ACTGAGGCCCAGCAAUAATTTAAACTUA	61367	GTTGTCTTCTACUCCATCTTCAAAUCCA
240546347	61368	TCCAAAGAATCAAUAGACAAGTCTGTGTUT	61369	CCAAATAAACTGUGCCTGCGAUAT
239407043	61370	AAACATTGACACGUACCTTAUCCACA	61371	GGATATGCAAAUTGAACAAACUGACACT
266452254	61372	AGGAUTATAGGCTTUGAGGGCAAAC	61373	GGCATTTGCUGACCCATAGGAUT
262957060	61374	GTGUGTTTTCTGUGCACGGAT	61375	CCTGCCAATAGAUGTGAAACTGACAUAA
326981277	61376	CUGCAGCAACGGAGAGUG	61377	CCAGGCUGGAGAGTGGUT
317483006	61378	ATTAAAAACTGAUGCCTCTTGGTACUCA	61379	GGCAAAGACACAUTGATTTGGTUCT
228005291	61380	TGTATGACAUCTTCAGGGUAAACAAGG	61381	TCATCCTCACTGUGTGCTATGTTTTAUT
231393147	61382	CCTGTCCUGGGATGATCCTUAGAA	61383	GAGATCCAAAGUGCAGAGTCUCC
314394886	61384	TGAGTGGACUGGTACATGCTTUG	61385	AAAACAACCTTTAUTGTCACTCTTTAUGCAAT
313253246	61386	CTATCTCAACAGCUCAAATCTGUACCT	61387	CGGTACAAUCCCAGGATCCUC
313026994	61388	TGCTGTTCACAGUATAAGGAATAUGGG	61389	AGTGATTTTGGCUTTTGTCCTCTUCT
328104188	61390	CCAGAAAGCUAGGTCGGUGT	61391	CCATTGGTGAUGAGCCCTTUG
255417905	61392	TGGGAGGGCAGAAUCAGGAAUA	61393	CAGAGACCAAGAUCACTGATAAGAAAUGT
263347778	61394	CAACGACGGCUGTCCCUAAA	61395	CATCAGAAGGAAGGUGTGCGUA
315638346	61396	CCUGCAGATTTUCCAGCGGAT	61397	GGGATGAGCGUTCCAACCUT
317441061	61398	TCCCTTGUAGCCTGUCCAGT	61399	GCAGAAGTCCCUCAAGAGGTCUA
316565936	61400	ACATTTCTGTTUCCACAGGGUGT	61401	GCUCAGACUCAGCCAAGAAACC
320468199	61402	AGTTCAAAGAACUCAGGTTCGGTUT	61403	GAACCUCUCAAAACGAAACAAGCA
298408190	61404	GCTUGGGCCCCACGUAG	61405	CCTGGGUGTATGCCCUCAT
296605170	61406	GCCCAGCCAACUTCUAGCAAA	61407	AAGAAGGTTGUATTCCAAATCAUGGAGT
327779218	61408	GGGTTGCCACCUACAGTGUT	61409	GCGATCTAAUGAAGGGTCCTCUT
327522542	61410	TGTGTUACAAGAAAGCATUGGCAAAG	61411	CAGGATGTTTUCATGACGTAACATUACA
278441734	61412	CCAGCTGGUCTTTGGTAAAGTUAAG	61413	TGATTGTCATATTUCCTCCTCAGTCCUA
278612512	61414	GTCATCAAGACUCCAAAAGACATUGG	61415	AGCTCCGAGUAATCTAGCTAGCTUT
278209117	61416	AAGCCTGTAAGACAUCTGGAATAATGUT	61417	TTGTTTTGATTGAAGUTGCAGTCAGTUT
279023073	61418	CAAGGGTCAUACCCACAUGCT	61419	GTACTTGTCUCGTGGGAAUCACT
261863016	61420	ACAGAGGUGCTUCACCAACA	61421	AGCATTGUGGCATCCTUCGT
264184718	61422	AAAGCGACUGTGCTCUCACA	61423	GGGCUGCCACTUGGAAGG
239690455	61424	CAAAATTTCCCUGTCTGCCGUT	61425	AGAAAACCUGGAGACTTTUGAAGAAGT
264271893	61426	GGUCTCCATCUACAACGAGCA	61427	CCACATCTGGUCAGTGGTAUGA
268914216	61428	CCTTTGCAGUCTGTGCUCGT	61429	CAAGTCACAGGAUAAAGCCGGAUA
267875911	61430	CACATGTUTGTGGCTUGGACA	61431	GCUGTCACUAAACCACACACACT
269338298	61432	GAAAGGUGATGAAGGUCCCAGAG	61433	CTACAGCACTUCCAGTTGGAAUG
332454542	61434	GGAAAGCCAGUGCCTCATATTAUGG	61435	TGCAAGTUAAGCTTCCTGUGGAA
260800401	61436	GCAGTGCAUGCGACACTUG	61437	CCCCTCTTCUATGGGTTCCTUGT
321234883	61438	ACTATGAAATUCCAAAGCCTCCTUGA	61439	ACACATGAGGAGAAUGTACCUCT
319630186	61440	TGATCAATTTCCUCCCTTTCAAGUGT	61441	GGCUATCAGGUACCAGCGT
318329566	61442	TCCACUTACTTTTACTUGACCCACAAA	61443	GCTCCTCTCACAUTTAATGCTTGUGT
258305147	61444	CCCTUGCAGATCTCAUGAGGAT	61445	CCTUCCGGACCCTUAGCAC
326701550	61446	CCAGACCCGGGAUTGTTUCA	61447	CCCCUATAAAATAAAGUACAGGCAGGA
324839755	61448	ATTGTTGTGCAUGAGTGTTACTACTTTUG	61449	AGTGGCCACAGCUAACATCAUT
313901334	61450	CATCCAUGCGCAGUACAACAC	61451	GGUCCAACGUGAGGGAAGAAA
256857155	61452	GTGTCCATUCTAACTCAACUCCAGT	61453	ACTAACTCAGCUCTTTGGATTGCUT
254262711	61454	GGATAAACAUGAACACAGAGGAACCUA	61455	TCTATAGAATCCUGTGAAGCAGCUC
314784484	61456	CCGGUAACCACGTCCUGAG	61457	ACAATAACAGUGACCAAAATGACAGUGA
316942689	61458	ACCCAAGAGUCTTCTCTGTCUCC	61459	GCTTACAUTTGCTTCUGACACAACT
314582625	61460	GCAGTGGACUGGAAAATGUGAG	61461	CGTGCATUCAGGCACTUACCA
314482635	61462	TGCTCAGGUCCACCCATTUG	61463	GTGACCGUGGGTGAGUGT
265768143	61464	AAGCTGCTATAUGGCGAGTTCTUAAT	61465	GTCTTGTAGUGAACTGGTACACUGG
266806574	61466	GTGACCCGCUGGUGGAA	61467	CAGGAUGAGCACGTUGCC
257860724	61468	ATTAAGGTCAUGGGAATACGCTCUG	61469	TTTGACTTCAAGCUGTTCTTCAAUGG
265300179	61470	GCGGCTTUCCTCGTTAUAGGT	61471	CCCCTTCATCGUCTACTACTTCAUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
313904219	61472	CCAGAAGCAUGACATGGTCUCT	61473	CCACGGGUAAGCATATGGAUGA
328485207	61474	CTCTTCTUGTTGCGGUGGGA	61475	CCCTACTCUGACATCGTATATCUAGCAT
224357617	61476	AATGCTGATGGUATTAAAACAGTTTTUAAGAA	61477	GCAATGGACTUCACCTCATCAAAAUG
223583332	61478	TGATTTATTCTGTTUTGTTTGCCACCUT	61479	GGCTTCCUTCTTCAAAUGCAAGAC
223533360	61480	GCTGTCAAACCUCCTAACTUCACT	61481	CCAGCCCAUGTAATTTTGACAUCAA
319769338	61482	CCTTCTCAUGCCCAGAUGGAAAT	61483	ATTAGCTUCCACTCCTTUCCAGAAAA
315970732	61484	GATGTUGCACGGCAGCTUA	61485	GTAATCACUCCCCAGATAGCAGUG
332313655	61486	ACTCTTUAAGGGCCTCACUCGT	61487	CTGTGCUCAACGTCACTCUGA
332538773	61488	TGAAACACCCUGTGGUAGCAG	61489	TGACCATGAGCUGCAGAGAUG
333734731	61490	AATTCCCCUGCTCCCCTCTUA	61491	CTCTTTGCGCUTCTTGAACTUCC
332795564	61492	TCACCATCCUCCCCTTGGAUT	61493	CCAACCTCTUGCTCCAAACUGA
333434672	61494	CUCCAACGCCAACAUCAACAA	61495	CTGTCTCCUGAGGGTUGCAG
321401034	61496	CTCCCAAGCCUATGGGTTCAUT	61497	TCTCCCCUCCCACTAGACUCT
333665053	61498	CGATTTCACAAGTUAAACCATCTTTCCUT	61499	TCTCTAGGGCAUCAACCUGAGT
333827216	61500	TGGCUCGCAAGCACAAUAGT	61501	GGTCACAAAUGGATACTTTTCAUGGG
321415391	61502	TCCAGCTGGUAGGAGAGGTTAUG	61503	GCTAAAGCCUGTGTCCTGTGAUAT
279479927	61504	GTGCTGCAUTGTTTACATUCCCT	61505	GGTTGAGCAUCCACAAGTTTCTAAAUAA
280882765	61506	ACTTCCATGGAUGAGAATTCAGCTAAUG	61507	AAATGCCTCTGUAAGAATCCCCTTTTUA
279420063	61508	GCAATCCTCAAAUTGTCAGCATCTTUT	61509	ACACTTGCAACAGAGGUTTAGAAACUA
278769489	61510	GTGAAGGCUCATTTCTTGUGAAAAAGA	61511	CATCAGGGAAAUCCCTACCAATUGT
278200195	61512	ATGAGTCCTCTUTGATGCTGTTCTUT	61513	GGGATGAAATGUGGTTCTTACTAAGGTUT
314030660	61514	GGTCTAGAGUAGAGAAACTGCATCTTUC	61515	TGGAAATCTGGATTUATAGTTGACAGGAATUT
267376888	61516	GTGAGCUCAGAAGCCACUCA	61517	CTGGTCCTUCTGGAAAAGAUGGT
262348842	61518	GGAUCCTAAUGCCCAGCAGT	61519	TGAGACCACAGCAAAUTCCTCTUG
319864631	61520	AAAAGCCAGACCUTTGTGATTACUCT	61521	GCCCTAGTTUCAGCTCTGATGUG
316561074	61522	AACTAGTTTGAAUGCAAGGCTGGUA	61523	CTCGCTGAUAAGTTCTGUGACCA
317843436	61524	GCCAUCCTTAAUCCAGGAACCT	61525	GGCAAACTUAAAGCACTTGUGAGT
317952047	61526	GATGGCGCUCAGATCCCATAAUAA	61527	ATCCTTGAGATUCAGTCTTTTCATGUGT
316854566	61528	TGGGACAGGCAGGUAUAGGT	61529	CGCCGGAGCUGCAAUGA
319474050	61530	CAGAGCTAGUGGCTCACCUT	61531	GGGAATACTGAUCCTGATTTAACAGUGA
319993348	61532	TGCTGTTATTTTAUGAAGACAGTGUGGA	61533	CCTGCTCUGACAAACATCAUCAAGAT
264207896	61534	AGCTAGGTGAUGTTTCATTGGGTTUAAT	61535	TGTTCAGTGTTTUCTTGTTTTGCTTTUCT
263006586	61536	CCGTUGCCGTTGCUACCA	61537	CCGAGTCUCGCCGCTUC
327448268	61538	GGATGATTATAGUCGTTGGGTUCGT	61539	CCTGCCCUGCGATUCGAAA
240121588	61540	TCCTTCCAAAGGAUATAGTAGTGATTUGA	61541	ACTTCTTCAACAGUCTTGACATAGCAUT
333279604	61542	GGTGGACAGCCAGUACGAGUA	61543	GAAACATCTCACAUTGTCTTCTTCCTUG
332682083	61544	GGCAAGAAAGCUACCTTTUGGG	61545	TGATCACCTTTUCCTTCTCGATUCAG
333222164	61546	TTCCCTTGAGUACAGAGTCCTTTATUCT	61547	GGTTACTGCUTCTCTCTUCGGT
333300987	61548	GCUGGCCGGGAACUCAC	61549	TGCGTAGCGCUGGAAGUC
315265595	61550	CAUAGGTGGUGAGGCCAAGG	61551	CCCCTGCAGUTCAACAGCUT
315155833	61552	CTACCCUGCCCACCCATUAT	61553	CAACTTTGCUACTTGCCTTTUCCT
324543160	61554	GTTAATCCCAGGUCTAACCGTUACC	61555	GCCATATTTCAAUGTCAGCTCCUCA
328115065	61556	GCCTUCCTTTTACAGUGAAGAAGAAC	61557	AATGTACTCCTGAAUTAACATAACACCATUA
326194668	61558	CCCAGCUGGACAGCTTCTUAC	61559	TGCTACACTCUTCCAAACCTUCAC
321051868	61560	CACAATAATCGAAAAAUCCCGTTTCUGA	61561	ACTATTCCAGGAAGUGACGGTCUT
254832354	61562	GCCAGATCTUCTCCATGTCGUC	61563	TGACATGGUGAGAGCATGATTTUCT
266541774	61564	CUTTTTCTUCCCAGGAGGAGCA	61565	GGCCCTCTUAACTACACTCTCATUAC
316163626	61566	CAGUACGAGGGCATCUCCAT	61567	ACAGTGTGAUGACAGATGCTTCTUC
316574448	61568	ACCAGTAGAGUCAAGGAACAGAATUACA	61569	GTTGGTCCGCUATCTCTGUCAAA
317524582	61570	CAGATATUCCACTGGTGGUCGAG	61571	CAGCTCAGCUGTTGTGTTTTGTUT
332478151	61572	AGCTGTGUGAGTTCGCCTUC	61573	GAGGTGGCUCAGTGUCGAT
321227027	61574	CCCGTATCUCCTTTCCAUCCCA	61575	GACTGTGAGAGUAGATTGGGTCUCT
320359122	61576	GCTGUCCTGAGAAUGGAGCAA	61577	CCTGCTCCUGATTGTCTUCCC
319919197	61578	GTACCUACAGAGCCAGTCCACUA	61579	CCAGCGGGAGAUGAAGAAGUC
319167269	61580	GGCACAGUACTGCAUCAGGT	61581	GGCACCAUGAAGGACATUCGT
321587869	61582	CCCCCAUGCCTGCTTAUGT	61583	CCGTACCCGUGGCCAUC
262859053	61584	GAGTGGAAGUCAGCCTGUGT	61585	GGGTCUCACAGGCCUCT
265783146	61586	GCTGGTGGTUTTGCATCAGGUA	61587	GCTGAGGCCUTCTCAGGTTUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318018128	61588	CAGGTTGGAUGTCGCAGUCT	61589	GCUCGGCUAGCAGGAGGAT
318285537	61590	CCCAGCUCCCACCTCCUT	61591	GCGCAGGAGCAGUGUCA
240404527	61592	CTTGGAGCUGACCAGGTCTUC	61593	AGTCACCTCUGGGTCTTGUGT
268756646	61594	GGGTGGAUTCTCTTCUGCCAT	61595	CCCATTGGGAAGUGAAGCTAUCAG
266412977	61596	CCCTAGCUGGGAGGGTAGUT	61597	CCCTAGATCUGAAGGATGAGAGATTCUT
318404636	61598	AGAAACAGCCUGAAGGTCUCAAG	61599	TTGATCTGGGAGGGUAGAGACTAAAUT
319898707	61600	GGAACCGACUTGGCATCTUG	61601	CCCCTGGCTCAUCTGTAATTTACTTTUT
318055494	61602	GGAGCCAGAUAGCCCCCUAA	61603	AGCTGTGAUGCATGATATTCUGGAC
320290333	61604	GCAATGCCAUTGGCTGTATUGT	61605	GGAGCTAAACCCUTAGAGGGATUC
319687694	61606	ACCTGGTGUAAACAGACTAATTUGGAA	61607	CCTTCTTTACGUCCAAGGCACUC
320293791	61608	ACTTCTGGGAAGUGTCCTGAUGA	61609	TCCTTTGTTGCUACGACCCAUAC
263984359	61610	TCTCUGGCAGCTCTAGUGACT	61611	AATGATAGAGCCCAUGGATGUAGGA
267547038	61612	AATGGCCUGGAAACATGGUCA	61613	GACCATGGTAAACAUGAGGTACTTGAUA
267654719	61614	CCTCUGGAGCACCUAGCC	61615	TGCCTATCACUCCGCCTCUT
268292919	61616	ACTGCAGUTTGTTCCUCGGAT	61617	CACAAACUCGGAGCUGCAAAAG
269357488	61618	CAGTTCTTTCAUGCTATTAAACGAGGUT	61619	CAATAAUAACCCACATCCAUAAGCCAGT
267354413	61620	GGCUCATGUCACCCACACAAT	61621	GGCCACTTGCUTCTTATAATAGUCCT
267688227	61622	CCAACACAAUGCAAATGACAGCUT	61623	ACTCCACAAACUTTTTCCAGCUCT
264018136	61624	CGCAGAGAUTGGCTTCCUGAC	61625	GAGAAAGGTGUGCATCTATGAUCCT
264710446	61626	GCCAGGTGUTTTCAGGGACUT	61627	CAAGCCTCUAGCTCCTTGATTCUG
237167296	61628	CCUTGCAGAAUCCAAGAAAACAGG	61629	CATTTTCCCCUTACCTCCATUGCT
236461306	61630	GGGAAGUGAAAGAACTTGAAAGATUCA	61631	GAAATAACTGTGAUTTGGCTTCCAUCAA
239213676	61632	GTCTGACAGAGTUCTCATTACCCAAAUT	61633	TCATTTTGGCTUCTATACCTCCAUGAT
235997238	61634	GCTATTGTUGCAAGAACAGUCAGAAT	61635	TCUGCTCUGCCACGCAA
237984418	61636	CACTUGGAAGGAGCAAACGAUG	61637	CTTAGTGTUGGCCTGAGAAGGUT
225558369	61638	CCCUTCUCCAGAGAGGCAAAG	61639	CTCAGGCUACATTTGACGCUCA
333034994	61640	GAGCCUGTGCTCTTUGAAGAGAA	61641	GTCCGTACUAGTGCTTTCUGGAA
318628566	61642	CTGTGGCCUTCTGCAGACUT	61643	GCCAUAGCCCGGTCAGTUT
316094017	61644	CTAAGTCCAGGUGTGGCGUT	61645	GUAGACGGAGCGGTUGGT
330284358	61646	ATCTUCAGCACCTCUGACACAG	61647	CGGGATUGGCAGTCTTCAUT
330946890	61648	CGGAAUGGCTGTTCUGGAAGT	61649	GACGTGTTTCUGGGTTTGCTTAUT
261641452	61650	GTAAAACTTCTCTUCTCCGAGGACAAUA	61651	CTCTCCCCACGUGCATACAUT
267712073	61652	CACAAGAAAUGAAAATAAGCTGCTUCC	61653	TCACACCACATUTTAGTCATATGCAUGT
262287053	61654	AGGGTGTATGCUCCAGCTTCUA	61655	CTTTCCCUCACCATGACGUAAGG
328001167	61656	GGTGGTCAGUCATGTGTGUCAT	61657	GTCCTUCAGGTCCACUGGAG
267422348	61658	CGAGAGCCAGGAGUCTGATUC	61659	AAGAGTGUACAGCGGCATUGT
262073382	61660	ATGGCAGGGUCAAGCTUGT	61661	GGAAAGCCAGCCCUGCUT
259078007	61662	GGAAATGTAACAUTAGGCTCAATTUGGT	61663	CCATTATCACCUCTAACCGGTGUT
333214446	61664	GGGACAGAAUCAGGGUCAGGT	61665	TTGTAGGTGACAUTGGTGATGAAGAUAG
324673749	61666	GCGATGACCUCTATTCCUACGG	61667	CAAGGTGTAUGGTCAGAGACTUAGAAAT
323463741	61668	CCTGGTGGAGAUGCTTTTCCUG	61669	CAGTCCCTUCTTTGCCGTUCT
325241886	61670	CTCATTTGTGUGTCCCCCUCT	61671	ACCCTCCACAUAGGCCATTTUG
323470921	61672	GACACGUGGCAGCUAAACAC	61673	GGAGAUTTGGACUCCCAGCAC
323894448	61674	CTGUCCGGTCUGCAACACT	61675	GTAGGAAGUCCTAGAGGGUGCT
326284789	61676	CGGTGACCCCUTGTAGCUG	61677	TCGTTCACCACGUCGAAGAUG
325318817	61678	GGAATGCCCUGATCCUCCAT	61679	GCAAAGAAGAAGUTGTTGTAGTGUCC
323863111	61680	TGTGCUCCCCTCCCUCAG	61681	TGATGUCGAAGACCACCCTGUA
267639453	61682	GACCCAGUACCCAGACGTCUAT	61683	GGCCUCCTGAGAUCACAGGAA
326601957	61684	GCGTGUCCCCATCCCAUAG	61685	GGCCTCTTCUCTCTGGTCCTUAG
326850537	61686	CTTAAACTUGCCTCGAAGGUCAAAG	61687	CGGTACUGGAAGACGAGAUAAGGA
328035709	61688	GAGCAGTACUCCCCGCUAAAG	61689	CCATGATCCUTCCTTGCUCCAT
317446257	61690	CCGCGGUCTGCTAUACGA	61691	CACAAUTCTGAAGUAGAAGAGGACGAC
316221108	61692	GTGACGCGGGACUGATACUC	61693	GGGTCAGUTCGAGTUGGAGAT
264222831	61694	CCCCGGCUTCTCTGCATUA	61695	GAUCCCACUCGCACAGCA
328436905	61696	GTGATGCAGGUCAGCACTTUC	61697	GCTATCGCCAUTATTACAAGAGTUAAGCA
326593555	61698	TGGGTATTGTUGGGAGGAGGUA	61699	GCCUCAGACTACAUCCAAGGG
314159925	61700	GCAGGAAAAGUACAAGAGCCAAAUC	61701	GCAAGGAACUCACTTTCTTCUAAGCAA
256544010	61702	TTCTGGAGGGUGCTGTUCAAG	61703	CAAACACCACUCCGGTUCCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256013029	61704	CTCATGAGCAGUCAGAGAGCUG	61705	CTCACTTCTUCACCCAGGGUAA
266427338	61706	GGATTCTCTCUAGCTCCCCTCTUT	61707	ACACTCCUGAGTCCCUAACCC
268938746	61708	CAGGAAGAGCAUTAGGUCCACA	61709	CTATTTAUGACCGCCUGGAGCAA
258868199	61710	GTCTACTGTTCAUTTCAGCTTTAACGUG	61711	AGGGTCCCUATACAGTAGAUGCAAT
269340667	61712	CTGGGAGAGAGCUTCCTGUAG	61713	ACACCATTTGCUACCTTTGGGAUT
265612924	61714	GCTGTGACTGUACTACTTCCTGUT	61715	AGGACCAGUTATTGTTUGAAAGGCA
265836702	61716	ACCUCTTCTCTUAGAACCAGGAAAGA	61717	TCAGAGAUGCACGAATGGAUGAC
262360855	61718	AGCTGGTGGUGAAGTTGATTACAUT	61719	CTTGCTCAAGGAAUGCATTTTCTTAUGA
263259812	61720	GAAAGGCATAUGGAACAGGAGUCA	61721	CTTTCCTAUGAAGGTGTGUAGCCA
323367417	61722	GATCCCAAACCUTTGACACATGTUG	61723	CTTTTTATTGCTUTGTGGTGACCUCAT
325097346	61724	GGTCCTCUGCCCTCAGUCAT	61725	GCAGGCUGCCCGTACUG
319267652	61726	AACTGTAACCCUGCAAAGCUGA	61727	AACCAACTCAUTCTGTTACUGAAGAACA
239105469	61728	CCCTGACCAGACUCCACUGA	61729	GTTGAGAACUGGCTUGCAAGT
239500287	61730	AGGAAUCAGAGGCAAAGUGGAG	61731	CCTTATTACCCCUACTTGCACUAGAG
301154193	61732	TGCTCACACUGTTCAGUCGAA	61733	CCGTTAGCTGTAAUCACACCACATTAUA
303062026	61734	CAACUGGTCTCATUCAGGAAGGT	61735	GGGTGCTGUAGTGAGTTAUAAAGGAAT
266851949	61736	AAAATGGATCCAAGUATGGGTGUGAA	61737	GCATTTGACTUCAGTTTCCAAAGAGUAA
254615933	61738	AAGGGAUGACACCAGTUCAAGAC	61739	AGCTCCCAAACUAGCACATAAAAUAACAA
255826748	61740	AAAGAATCAATCCUGTGTTACAGGUGAA	61741	GGCCAGTTTUAGCTTTTCAGGACUAT
256744738	61742	GAGAGAGAGAGUTCCTCCUGGAA	61743	GATGAACUGCCACATTGTTUCCT
316759553	61744	CCTTATCCUGAAGGAGAGCTTUGG	61745	TTTCTCCATAUGGGTCATCTAGGUAACT
263037080	61746	GGGUCAGAAAGGTGAUGAAGG	61747	TGAGGCCAACCUTTAGCTAGAGTUA
260594845	61748	CTTTCACGGUTTCCCTGGUG	61749	CTCCAAUGCACCGGAAAAATUCT
314129299	61750	CAGTACGACTTTUCCTTCTTCCAATCAUA	61751	CATTCTTTGCUAATTTCCTTTCCTUGCT
319582263	61752	GGGTAGCTGUGAGATTTGTATTUCA	61753	CAAAGGCUACAGGTGAGTUAACCA
318686705	61754	GGGTTGTUAGGGAAGGAGAAGUA	61755	AGCTGATTAACAUTTGTTCCTCUCCAA
229286319	61756	CATCTAAAATAAUCCCCAGAACTCACCUT	61757	CTGCTTACUGAAACATGAAAACCTUGT
333060052	61758	GGAGGUACGGATCCTCTUCCAA	61759	CATTCTGCUCTGTCGCTUCCT
332690211	61760	CGTGCACCCUCCAGUAGGA	61761	GCTACCAAGCUGTTTGCUAGGA
313613518	61762	GACAGGAGCCAUTCAAGUAGCA	61763	TTCTTTTTGUACCAGTATTUCGAACCCT
266440885	61764	GCACGGGCCUGTAGTAGGUA	61765	TCTGGGUCTCGTACUCGAAGAT
267541424	61766	ACCTTTCTUGTCCATTATUGCCCAA	61767	AAGGAACCUGAACGTGTTUCCA
317679718	61768	CTCAGAGGUCCACCAGACUCA	61769	GCAACAGAGTUGAAGAAACTTGATTUCA
316033628	61770	TTGTGAACTGAAGUACAGAACTCUGG	61771	AGCTGACTCTAUCTTTGCCTTCUCT
318579630	61772	GGAAGGGCUCCATCCTGUC	61773	GGGUGACGGTGACTUGACT
318846445	61774	GGCCTTTGTGUCCTCCTTAACUAA	61775	CCUCGTAAUCCACCCCGACT
313027932	61776	TCTTATCTCACCGUCCTTTGTTCUAGT	61777	CTCAGCCATGUGTCTCTTATTTTTCTUG
314318081	61778	CAGGCTGGUATCTGCGTUGT	61779	GCAGAACUTTGUCCCAGAGCAT
319078457	61780	TCTCGAAGGUCAGAGCCAATTCUA	61781	CTGTAAGTGACUGCTCCATACUCC
259653869	61782	TGGTCACUGCGGACCATUC	61783	GUTGTCATTGAGUCCCCACCAT
319678866	61784	GGACAGTTUGGGTAAACAGUCACT	61785	CCTGTAGCTTGAUCACCTCATTCTTUT
319933196	61786	GAAACAGGAUTTTGCAAGAAUGGCT	61787	CAGTCGGAGCUAAAACTCCCTTUT
313560070	61788	TGCGACCGUACGACGUG	61789	CAGGGACCUCCTCAGTCUAGAAA
315495662	61790	GTCCCCAGGUGCAGUCC	61791	GGAGATGCUGAGCGTCUGT
315355835	61792	CCTCCCAGAGCUGCAGAUAGAA	61793	CCTTTACCAGTCUATCTCAGCCTCUA
259079447	61794	GCAGCTGTUACCTGAGCGAUA	61795	CTTAACTCTCCCGUCCTTCTTGUG
255020306	61796	AGTCCAGTCUCAATCCCTTTCUCT	61797	CACGTGAAGUATAAGATCCGAAUGGA
260880134	61798	TGCCAAUGCACCUCAGAAACT	61799	TCGGATGGAAUGGAAGAAATATTUGGT
265677618	61800	TCUCCAACACCACCAACUGAAC	61801	TTGCTTTCCAACACAUTTGACAATUCT
284987101	61802	AGTGACTGCCAUGCATATAACACAUA	61803	TTTTCTATTATATTUTCTTAGGGTCUGCCAGG
262530519	61804	GTTAACTAAAATGUTGTGCAGCACUGA	61805	GGGTCCUCCAGGTCUACAAGG
332614601	61806	TCTTCAGUGTTTATCTTUCCAGAAAGCA	61807	CCACTCATUCATTTTGTCCCUCAC
325158714	61808	TCTCCATCCTUCACTTCTCCCTUA	61809	CAUCCTGCACTAUCAGCAAGAGG
319540480	61810	TTTTTAGGACAGACGUGAAGATCCAUC	61811	TGGGCTTTTCTCUATTTCATGTTCCAUT
327682308	61812	GGCTTATGGUAGCAGCCACTUA	61813	CCCTGTACUCCCAGCCAAAUAG
326571807	61814	CTTTGAACUATTCAACAUGCCCAGAAC	61815	TCCTGATGTUCCTGCTTGTCTTUT
327913828	61816	TTGCCAAGATAUAATCACAGATGTUGGA	61817	CCGTCTATACUTGAGAACTCCUGGAA
327996620	61818	GCAATCCATTTAAUTGGTCAGTTCUGAA	61819	GTGAGAUTTACTCAGUGGCAGACT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
327536863	61820	CATTTTGGAGCUTCGTGTCTCCUAA	61821	GAGAGTCATCUCTACCAGCTCUGA
326476254	61822	CATCTTAGGUGGACTTAGTCTTUGGG	61823	AATATATTTTGTCCUGTGCCCCTUT
327120629	61824	CACACTGAAGUCCTTTGGCTUCT	61825	TGAAATCATTTUCCCATCCTCACCUT
328451678	61826	CCTTCTTCCTUTGAATCCTTATTUCCGT	61827	GGGCTATGAAGUTTCTGGATGTCUAAT
333332488	61828	CGTCTGUGAGGAAGGGATCUGAA	61829	GATAACACAUGAAAGCATAGGAUGGGAT
332654447	61830	CAGAAATTGTUGATGGCAACGUGAA	61831	CTGTTGGACTTUAAAACATCTTGCUCAA
332622254	61832	CTCAGCAGGUAACAGCCUGAA	61833	GACGCCGACUCGTAAUCCT
332719411	61834	TCCATCAUGGCCAUCCAGAAC	61835	CCTTCGACGUCAGCTUCAAGAAT
332640927	61836	TGAAGCAGTAUGAGCACAACAUCA	61837	AUGAAGAAAGCACCCUGAGGAG
323664586	61838	CCTAACTCTAGTTUGGAAAAGAGACGUT	61839	AATGAAGTAUCAAACAACTACGCCUACA
326428917	61840	AGCAGAATGACAGUTTTGGATGUCT	61841	GTTGCTAUGAACCCAATCATGCUT
323367117	61842	CAGTGAATGTTATTUATGAGGGCTGGUA	61843	TGTTAAATCACUGTTTCCAUCCAGAGAC
324313275	61844	GCATGCCACGUCTTGCUAAA	61845	CATGAGTTTCUCCAAAGACGGTAUGT
325626001	61846	GTCAAGGAGUCCAAAAGACAGTUCAT	61847	TCCTTATTCGCUGACCTCUCGT
325615900	61848	GGTGCUAAAAAGATCAAAGTUGCAGAA	61849	GGTCACTTTCCUCTGTCAGCUC
327411283	61850	CTAATTTTATTGUCACCCCTCTCCTUGT	61851	CTTGAGTGCAGAACUGAAAAGATTUAGAA
327592995	61852	TGAGGTTUGCAAAAGGATCTGTAUGT	61853	CTTCTACTUGGCAAAACATTTUGGAACT
327656602	61854	ACAATTCTCTUGGCTTTGATGUCACT	61855	TGCTTAATGTUCAGAGTGGTAUGGAAAA
235692106	61856	TCTTGCACATTGUATAAACATTTAATGUAGGT	61857	CTGTGATCAGAAUTCCTCCTCTTUGAA
321525241	61858	AGGCTCTGAGAAUGAAGACCUCT	61859	TGGTATCTGAACCUGTTCCCTUACA
268959684	61860	GCAGGAUGTGGATGAUGCCAT	61861	CCCCTGCUCTATGATCCTGUGA
268853512	61862	CTTCCTTCTTUTCAGGGCCUCT	61863	TGTACCUGAGCCTGCTACUCT
261889990	61864	GGGAAGCUGCAGATGUGG	61865	CATGGCCCAAAUAGCCUGAAG
327963939	61866	AAGAGCAGGCAGAAAUCAAGAUGA	61867	ATGCTGAAATTCUTGGTTTTGGAUCAC
327780312	61868	GGAAAGTATGUCCCACTTCUCAGG	61869	CCTGGTAUGGCCTAGTGTTGUT
326972989	61870	CGCCCCAUCATGCTGCAUA	61871	GCACTGGATUGAGTCTACCTTCUC
327496820	61872	GGAGCAAACAUGGCACAAACUT	61873	CCTCATCCCCGGUTCTTTGTUC
327540452	61874	CTACGACUGCTCCCAACUCAC	61875	GCATTCCTGCCUGATGTAGTTTUC
326951826	61876	CTTCUAGCCACCGTTAGCUCAG	61877	TCACTTCCTTTGUTCCTTTTGTTGUG
327342051	61878	ACAACTATTGUCATCTTGGCCAUACC	61879	GGTGAGCTAAAUGCCTGGTTACTUT
314925760	61880	GAAATCTATUGCCAAGTTCTAGUCCAGT	61881	TTCATGCTCUCAGGCTGCTUAG
325788907	61882	TTTGCCTUAAGCGGTAACGUCT	61883	CGTTCACAGAUGGAAGAAAGGTUCAT
324800297	61884	CGTGACCCAUCTGTGGTGTUA	61885	ATGGCATTTCTTUCATGTTGCCTATUT
324504168	61886	AAAGAGCTCCACUAAACTTAAAGUCACA	61887	TCTTTACTGGAAUCTTTGCAGCUGA
324224846	61888	ACACTGTGCUGCCTGAGATUT	61889	ACATCTAGTAUCCCAATGGAATCTTGUG
267616927	61890	TCATGCTGCAGUTCTGTTCAUCA	61891	GGAGCCATUTTCCTCTTTTAUCCCAAT
263221028	61892	TGCCATAAUGCTGACATUCAAGAACT	61893	GCGCGTTATCUGTTTTATGTCTTTGTUT
263726078	61894	TCCATGAAGAGAAUGTGCCAAUACA	61895	TTTTTCATCTGAACAUTGAAGAATGACATCUAC
266771220	61896	TCTAACGTTUGCATGCCAGUGA	61897	ACTTGTCTGTGAUAGATTGAGGGAAGAUA
255490446	61898	GCTGGCUGCAGTAGGTTAUGAA	61899	GCTACCCAGGTUTATTATGAGAAGGTUG
268610822	61900	TCCTTCCAGGAAUACATACACTGTGUAA	61901	AGGACCAGAUGGACCTAUAGCAC
267829269	61902	GACCUGGAGAGCGAGGATUG	61903	AGGTATCCCAGCUGGACCTUT
263087242	61904	GAGAAGAGAAGAUAGAACACTTGCCTUA	61905	GGTTTCCCAUCACTTCCTGGUC
268590104	61906	GGAGGCCCUCCTGGAGUT	61907	ACCTCCAUGTTTTTCCATUAGAACACT
262495796	61908	AGGTTCAGGGAAACUCATATGATACUGT	61909	GTGTTTUCCCAGGGTGGCAUA
267425098	61910	CCCCCACGUAAGTATCAACATUGAC	61911	GGCTTGATGAUGGCTCCTAAAACTTUAT
267578188	61912	CTGTTTGTCUCCATTTACTTAGUGCCT	61913	TTGCCTTCCCAAUCTCCTACATTUT
268803709	61914	ATTATAATGGUGGACCCAAATGTAACUG	61915	AGCCAACTGTCUAAACAATTACACTGUA
269056619	61916	CAGAGCCAGGCAUTAGTCCUAC	61917	TCCAGGCTTUAAAGTCAAGCACUT
267660954	61918	AGUGGCCGAGCTCUACGA	61919	GGAGAAGGCAGGUGCUGAC
237580324	61920	ATTCCTAGTGUCCCTCTGGTCUT	61921	CACAGCAUCGACGGCAUC
261470555	61922	GCCCUCCCCACAAUGGT	61923	GGCUGTUCCCAGCACCT
264379746	61924	GAGCGCGUTCCATCCTCUA	61925	CCCCGCCGUCTTCTUCA
238438627	61926	AAGGGAUAGAAAAGAAGGCAACAUGAA	61927	GATATCAATGCUTGCACGCUGAC
236472540	61928	GGAGAAGUCTGAACACUGCACA	61929	CGTGGGCCAUCACAAGCAAUA
332783221	61930	CCCCTTUGGCTGTGAGAUAGG	61931	TGTAGACAAAGCUGCACUCAGG
333344055	61932	CCAGCTACUCCGTTCCUCAC	61933	GGTGTCTGTGUCCAGGAAAGUC
263469851	61934	CTCAGGAAGUCCACTGTGAUGA	61935	CTGTGUGAAGCCCAUCAAAGAC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
269565559	61936	CTGGAATTAAAUGATGGGCCUCACT	61937	ACACAATGAUGCTGGUCCACA
233154267	61938	TGGAGTTTGUTATCATTGCTUGGCT	61939	ACAAACATCCUGCTACTTTGAGGUT
325818729	61940	GACAGAUCAAAGTAGGGAUGACCAA	61941	ACATCTUCGACAGCATCATCGUC
264819778	61942	CTCCACAGGUGTAGTGTGTUCAT	61943	GTACAGGGAGCUTCCCATCUG
258712625	61944	CCCCUCAAUACCAAAGCCAAC	61945	TCCCCACGAAUGCCCATTTAAUAT
261968668	61946	GACAAACTCUGTGCCGACAUC	61947	GGGAUGAGGAUGAAGAGGACACT
254149116	61948	CTGCCTGUTACTGACCUCACC	61949	GCTGGCATTUGAGTTAAGTTCUGAAGA
316313016	61950	GGGTCAGAAGGUAAGACTUCACT	61951	TGTGCAGAGTUAAGACTTGCTTGTUA
262652832	61952	CCATAACTTAAGGUGCCTTTGGGUAA	61953	GTCGTTTUGCCACTATTATCUAGCC
332064994	61954	AGCUGCAGGACACAAACAAUCT	61955	GGCCTCTTGAUCTTTATTGATCTTUGGA
332109008	61956	GGGTGTGTTTUCTCTTGTCAGUT	61957	GCCTTGTGAUTCATGCTGUCC
324665360	61958	CTUCACCAGCACCCTCUACAC	61959	GGGCTTUGGATAACATUGACAGGA
255448141	61960	ACAGCTTTTTCTUTCATTGTCTCAGUCT	61961	GGGCTAAAAUAGTGGAGGGTUCA
323557470	61962	GGGAGCACACAGCUCTTCTUA	61963	AAAACCCAAAACCUACCAGTGUCA
329269423	61964	TUCACTGACTTUGAGGACAAGCA	61965	CTATCCCTTGUCACCCCCAUC
323325797	61966	CCTGCGCUTTGTCATCAUCCA	61967	GCTTCGGGAAAGCACUTTCCUT
323633981	61968	GGTGGATCACUCCGACGTUG	61969	AAGCUAGUGAGAGGGACACAGA
325838886	61970	TGACGCUCCCCCTTCTCUT	61971	GCCCCTGUGACTGCCTUG
318361107	61972	CGCAAAAATUAGAGCCGGAAGUAAAAAT	61973	GGTCCACATGACAUTCTCAAATTGTTUT
320693421	61974	AATCTGUAACATTCAAGUGCCCACT	61975	CCTGATAACUGTGGCTGTGUCT
320739802	61976	TGGTGGUGGAGATGGACGUA	61977	GGGAGGUGGCGAUGCAG
333557642	61978	CTCGACCTATAUCTCATTTGGATTUCCAT	61979	GGAAUAGGCAACATGTUCAGAGAAAGAA
332942419	61980	AAATCACACCACAAGUTTTCACTCTUC	61981	GTACTTTCCTGTUGGGATTCCATTTUT
332482968	61982	TGTTTTACAGAUGTTGATGGCAUGGA	61983	GCATTCATTTGGAUACTACCTGTUCAAG
313652895	61984	CTGATCGTAGTUCTGATTTCATTTGTTUCAT	61985	GTGCCCTCTCUCAGTAAGCATTUT
315727047	61986	TCCAATAGTTGAUGAGGGCCCUA	61987	TCAAAATTACCCUGTGGGCTUAAGAC
265756823	61988	ACCCAAAACUCAAGTGGCUACAG	61989	TGCTAAGGTTTGGUTCAGTGAAAATAUGT
262355456	61990	TCCTGTGACAUTTGTCTTTCATUACCA	61991	GGATGAAGGAACUAGAAGATAACTUGCT
258049712	61992	TCCAGCACCUCCATCTTGTATTCUA	61993	CAAATGACCATTUTCCTAGTGTGCUAAT
318844082	61994	GATCUCCACAGCCAGTAUGCT	61995	CCATGAUCCAGACCTGCTUGT
291682201	61996	CTTGGGAATAUGAAGAGCGUGACA	61997	GGTTTATGTAAGAAAUCCGTTGACACUGA
291409220	61998	CTTTAAGAGGGUGACAATGCTATTUCCT	61999	AGTGGAAAGCUTTGACCCAUCC
293148558	62000	TGACTTTTTGTUGCAGGATGAACUCT	62001	CACAAGCAUCCAGAATCAGAAAAAUCAA
222565086	62002	CCCCTAUGTACGCCUCCCT	62003	CCGGGAGGAGACGUCAAUG
224555367	62004	CCTTCAAGACUCAAGGGTGATAAUGAAA	62005	AGCAGCAGCTUGATGTAAACTACTUA
222793015	62006	CCCACCTAATCUCAGTCCCACUAT	62007	GCAGAAAGAATUGAAGATGAACTUCCAG
224554830	62008	AGGACTGTCCCAUTAACAATCCUAGA	62009	GGGCAUCCACCTGAAUAAAGGA
326532605	62010	CCCCAGAACAGUACCGTCUT	62011	TGGATGUGGCAAAGGTGTUACA
240548045	62012	GAACAUCCCAAAATGCTTAUGGACAA	62013	GTTCCTGTTTCAUAGCAAGTGCUG
235816566	62014	GCUCCTCAGACUGAAACACAGA	62015	CCAGGTAATTCUAGCATGTTTCCTAAUGT
242577814	62016	CCTGTCAUCAAGCATATCCAGUGA	62017	CCACTTTUAGAAATGCUGGCCAAA
240344689	62018	GGGAAGATGTUAAAAGGTGCCTUCT	62019	GAGGTTTTACAAUTAGACTGGUCCACAT
265135622	62020	TTGCCCAGAACGGGUTTTCAUA	62021	CCCCAAACAUTCACTGGUGACAT
258976465	62022	GCAGAAAUACCAGGCAGAGTGTUC	62023	TGTCTTCCACAGAUTTTCTTCTTCTCTUT
265548852	62024	CUCGGGUGGACCACCAC	62025	GACUCCGGCAGCCACUT
331888575	62026	GCAUGTCTGGAUGGCACAGT	62027	TGUGCAAGGAGTGUGCCT
259710812	62028	GUACTGGTGGUGACAGGACAA	62029	CCCAGTUGAACCAGCCACUA
261604288	62030	GTTCUCTATCCACAAAUACCACACACA	62031	TTGGTGTCTCUGACTCTCTTCTCUT
263035537	62032	TGGAAGGACCAAGCUCCUAAGA	62033	ACACTCUGAGGCCCCTTTATAAAUG
323319846	62034	CAGAGCCCUCTAAAGCUGACA	62035	ACCTTACCAAUGAGGGTATCCAGTAUC
327168240	62036	CCAGGACCACCUCAAGATGUC	62037	TGACGCUTTCACAUCCACACA
325403774	62038	GCACAAAATGGCUCTCAGAATTATUCA	62039	GCAACCCGGACUACACTUGG
315124806	62040	TCCAAATTCCUGGCGATAUGCT	62041	GTTAATGGAACCACCAUTTCATGTTUCA
270533001	62042	TGGTATCUGAGCAACTGCTCTUG	62043	CAGTTGAUGAATGGAGTGUCCAGAA
270999842	62044	ACCTGGAGGAGAAGUGACAGUAAA	62045	AGAAGACAUGAAGACATTGTUCGAGAT
318776201	62046	TTGTGAGAUCACATAATGACUCAGCAT	62047	GCAGAATGGACUGCATCCTUCT
272693807	62048	AGCTTTAGGACUGATACCUGCCT	62049	GTATCACATGCAAGUTGTGGCTTUT
320253687	62050	ACAGGTGGCCUCAGATTCUAACT	62051	CTAATGCTACAGUGTCTGCCTUCA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
315731400	62052	AGAAGCGGCCAGUGAAATGUAG	62053	CTTTGTTGAUGCTTCTGATGUGACA
317277161	62054	GCAACATTGGUGGTGACTTCUGA	62055	TCAAGAGAGCUTATTGGACAUGGAAAAA
315568384	62056	ACCTUAGCAGGAAAAAUGGGAGAC	62057	TCCTGCTTAUAGCTGCCTCCAUA
316502518	62058	GATCTTACATUGTGTGCTAGUCCCA	62059	AACCCAGGAAUAAACTCTGCTTUGT
317932549	62060	ACAATGCTGAUTTGCGTCUACCA	62061	ATGAATGGAGGUCTTTGTCATGAAUCT
262538731	62062	GGCTAGCCAUACTCTTTATTTTCTGUT	62063	GCAATTCCGAUTCCAAAUCCAACAAT
321280697	62064	CAGATCTTGAAAAAUCTCAGCCAAAGUT	62065	CATCTCCAAGUAGGTGCTGAAUACT
319426569	62066	CTTTGCTAGGAUCTGTTGACAAUGGA	62067	TGAATCCCACUGTAGTTTTTCTUGAAGG
268284139	62068	AGUGTCUCCAGGAGACGGAAT	62069	AAACCTACCUCACAGCAACAATTCTUA
263205805	62070	GGAGTTTGAAAGUGATTATGTGGCATUT	62071	AATTCACCCCTTUCATTTAACAGCCTAUA
267270106	62072	AGATTCAGCUTTAGCCATCTUCAAGAA	62073	TCAAGATTUCCAATGTACUGAGCAAAGA
267827600	62074	CTCTTTCCUCCTTCCCCUCAGAT	62075	ACTGAAAAACGGCUTTCTGGAUAGAA
265096724	62076	AATGCTAGTAGGAAAUGCAGGAGUG	62077	CCTTGATGATTTUTGATCCCTTGTTUCT
261921738	62078	GATTTTGCTCTTTUGTCATCTCCAGUT	62079	GACCTACAGTTTUTGAGAGCAGTATUCA
268121718	62080	AGAAGCAAAAUGAGGTAUCCGAGAAAAA	62081	CAGTAGCAGUGTATTCTTGGTGUCA
264388087	62082	GTTTTTGAATGCCAUTGAAACTGCUT	62083	GAGATGCTGCUGCTGAAAATCAUT
314070505	62084	GCAUGCGTGTTTUGGGACAAT	62085	GCCCCAAACCAAAAUACTTAAGAAGUC
323677462	62086	GTCAAAGGGCUTCTGGGAATGUAT	62087	CGTTGCAAACGCUATGGUCAC
327987543	62088	GGCCAAAUGACGTAGGGCUT	62089	CTAAATGGCUGCAAAGTCACAATGUT
256963345	62090	GAGAAGTUCAACGCGTCCATUG	62091	GCACTGTTUGCTCAGGGATTUG
264005246	62092	CUCCUCAGGGAAGCAACACAT	62093	GCTTCCAUCACACCTCTGTCUG
253834359	62094	GTTCUCGGGCGACGUGAT	62095	CCTCUCGCGCCCACTTTATUA
230522602	62096	GCCUGGCAGAAGUACCGAT	62097	CTCAGGTCUGAGGATGCATGUG
230563775	62098	CCAGAGCGUAGGAGTCTUCAT	62099	CUTGTGGCATGUCCCAAAGAG
222488576	62100	ATGTAGTTTTCUGGTGAATTTGGAGUGA	62101	AAGGCUCAAAGGGAATAUAAACCAAGAT
222171412	62102	TGGAAGCACUAAAGCAGCUGT	62103	CTGAATTGGTGAUCCATTGCTCCUA
222677239	62104	GGAACAGAGCUGUCACAACGA	62105	CAGTCGAGAGAGUGGGATAGTATATUGT
223529696	62106	CAGGTTGTTGAAAUGCATACTAGTTUGA	62107	ACAAAACTAACCTUGAGAACTTCAACAUCT
318721613	62108	TCAGGAGGAGGACAGUATACACATUT	62109	TGGAGTAGAAGGCUTACAGGGTAAUAAT
267253099	62110	AATTATTGCTATTGAUCCATGAAGTGATACUA	62111	ACTGTAGCCAAGGGAAUCAAAGTATTUT
267713759	62112	GGGAAGCCCUGTAAGUAAGAACC	62113	TCTACTCCCCAACUTAGGATGTTTUCA
326350340	62114	CGACAGACAGAGCACUGACUC	62115	ACCTTACCATTTCUTTGCTTTGATCCUA
325466744	62116	TCAAGTATCGAGUGACAAAGTCATUGG	62117	TTTGAACTGTUGGGAGATAATGGUCAT
324824489	62118	CACTAGGTTUTTGCCTCCUGAACT	62119	CCTGTTUCCAGCCCTAUAAAACCA
323710419	62120	CTCCTCUGAGCAACTGTGACUT	62121	ACCATCGACAUTGCCATAGAAAAUAGG
324021685	62122	GACGACAACATUAGAAAGGACACATUC	62123	AGACTAGACTTGUGTAATGTTTGCCAUT
260451296	62124	AGTGCAGAAACUATGTAGAAAATGCUGA	62125	TCCAGGACCAGAACCUATAACTGUT
268116567	62126	GCCATTGGUGATGTAGTTGCUG	62127	CATTGGCTUAAAACCACCCATGUT
256885320	62128	ACTTTAAAGCUGTCAAGCCGUGT	62129	AACTCCGCCTTUCCAGTTGTATAATTUA
258176514	62130	GTGATGACAGCCUCTTCTTCAGUA	62131	GTGAAGAACAAAAGAACUACCTUGCC
264239055	62132	GCAGGAGUCCAATTTTCACTCAUC	62133	ACAAGAACCAGUTGGCAGTATGUAAAT
254254655	62134	GAAATCCCUACCAGCAUCAGACA	62135	GCACCACACAGACACUTTTCUC
268602374	62136	CCCACTAGUCCTCATCCTCTUCAG	62137	TCCAGAATAUGGGAATGGGAATUGG
268775415	62138	CCCTGCACAAGGUGAGTCTUT	62139	GCTGCTCAAAUGGGACACAUC
313906010	62140	GAACAAGCGGGUCACGGUA	62141	GCTGCUACAGAGGCAGAUGAC
333567413	62142	ATGTGAGAGCUGGGCAUAAACAA	62143	TGCCGTTCAUCTTGTGGUAGAG
333716193	62144	CCCUCAGGAGCGTCUCCAT	62145	GTGATTATGUCCCCGTGACUGT
316429830	62146	CACAGUCGGUCCCCCAAA	62147	CCAUTGCCCCUGGACACC
317397301	62148	CCAAGACCCCCACCUTTAGUG	62149	TCATACTCTUGGCAACGTCUGG
242324680	62150	CAGGTGATTAATUTGACAGCTTGATUAG	62151	CTCCCAGAAGAAAUCTTATCACATGGUT
264738144	62152	TGGAGTGATACUGTTTCAGTGGTTUC	62153	GCTTATTCTCUAAGAGCTCCUGCAAA
229713390	62154	CTGGCTGUGGAAGTCACTCUT	62155	CTAACACCCUGTTCGCACUGA
266369765	62156	GTCTACCCUGGCAUGCAGAAT	62157	CCCCACGUGCCATATAGCUG
261271166	62158	GGGCUAAGAAGGCTGAATUGGAT	62159	TCTGAGAACUCCATCAGCTCAUCT
264016701	62160	CAGAAGAAUGCAGATGTGCTGUT	62161	GCATAGTGAUCAATTCCCTTUCCCA
314205966	62162	GGCTTCACUCCTGATGAAUCCA	62163	GGCTTATGATGUGCAAAGCAGTUAA
314439946	62164	GGGTGCGUAGATAATAAACAAUCCA	62165	GCACTACCTGUTCTTTCTCTTGCUT
317184575	62166	GCAGCAGAGCUCAGGGUA	62167	CTCCUGGAGCGCCTUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
261482126	62168	GCCAGAGAGCUACTGCUGAAT	62169	AATAGTGGTUGCCAGAACTUCAACT
259115483	62170	CCACAGCCCUAACTCAACACUT	62171	AGTGTGACCCUCTCTGGGAAAUA
315988841	62172	GGTACTGAAGGUAGCTCCCCUT	62173	CAAATCCTTGTAAUGTGTCACTGGUT
316388606	62174	CGGGUGCAGCACACATGAUA	62175	GTGAAGCUGCCAGATGTCCUT
278859813	62176	GGGTAGCTGAAUTCTGCTGGUA	62177	CTGTCAATGGAGCUGGGAATATAACUT
259788665	62178	GGAGUCATGGUGGGAAGAAAGG	62179	CCCCAGAAAAAGGUGCACUG
241686109	62180	TCTAGTGGCTCUAAAGTCAATCTCTUCT	62181	GAACCTGUAGCACACGUCCT
267821332	62182	CTCTGTGAGCUGCTTTTTCAUGAG	62183	CCAAGAUCCCAGCCAGAGTUAA
263963101	62184	GAGCTTGGGAAUCTTACTGUCAGAA	62185	GCCCAAAUCACTGAGGAGUAGG
264121528	62186	GGAAACGGGAGCAUGGTTUAG	62187	TGTAGCCTUGCAACTTGGGUT
261248341	62188	GGCCTCTUACACAAAGTCUGGAA	62189	GTGACCCAUGGAATCUGGGAA
258484795	62190	GCAGGCAGGAUTTGGCAAAUG	62191	CACCCGCUCGGCCAUAT
260663775	62192	CCTAGAGCUCCGGACCTCAUT	62193	AGAGACGCUCTGCATGAGTUG
333209788	62194	AGATCCAGAUGGAACTGCUAGAGAA	62195	CTAGAGAUCCCTGCAGUGGAG
332688628	62196	TGAAAACUGGGCTGGCAUCAA	62197	AGACTTGAAGUGGCTAATGUACGG
264907981	62198	CAGTTCTTTGTCUTGGATGTTGTCAUT	62199	CATGAGAUGGGCATGGAGAUGT
267033688	62200	CGCACCTUCCAGAACGCUA	62201	GAGGGCCACCUGGAUGAAG
319758795	62202	CCTTCTTCTUGCAAGCACAATGTTUT	62203	AAGCACUGTAGAAUCAGAGGAGGA
321154978	62204	TGTCGTTGTUGATAGCTGTGUCAT	62205	TTTTCCACTTUCCGTTTCAACGUC
318457353	62206	AATAGTATUGGAAGAAAAGGGCAUCACA	62207	TGTTGTTTGGCCUTTGATGTTTTUAAGT
318208047	62208	GAATACTUGCCGCGCTTCTUAAA	62209	GGGAGACUTCATCATCAAUAAAACAACAG
320129169	62210	TCAGUCCAACAAATUGAGGAAGCAA	62211	CATCAGAUAGGCCAGGAATCCTCUAT
318699500	62212	CTCAACTCAGGUATGGCAGCUT	62213	CTCCTGGCTATUGTGCCTAATTTCTAUA
264057394	62214	ACCUCAGCACCGCCUAAC	62215	TGUGATCACCUGGCAAGAGAAA
265713923	62216	GGCAACAACUTCCGGAUCCAT	62217	TCTGTTCTAGCUGTGGGCTUG
263082470	62218	CGAGAGCACAGGGCUTATCAUC	62219	TGAGGCAUTGGAGAACUGCAC
266728853	62220	CAGGCACUGTCATUGCCAAT	62221	CAGGCCCTUGTACCTGTGUT
255417512	62222	CTGAGATCCCUGTCTACCUGGAA	62223	ACTCACTGAUGCAGGCAUCAAG
257248905	62224	CCACUGCAGTCCUACGAGAA	62225	AGCTGGAAGAAGGAAAUACTGGUG
266615060	62226	GCACTGAGTCUCTGAGCCGUA	62227	GGGATCTCGUTAATGACGATCTUGAC
263897028	62228	GCCCAAGGUTCAGCCACAUA	62229	ACCACAUGGATCCCAUCGG
327644156	62230	CCCGTGGAUCCTACTTCTCUGT	62231	CCTCCUCGTGCATTAUCACCAG
326454759	62232	TTTGAGGGUGTACAAUGACAGCAT	62233	CACCCCTCCUGAAAATCACUGT
327959790	62234	TGTTTATGTGUGACAGGAUGGCT	62235	CGGTCATCCACUGTGGGATUAT
315094128	62236	GCATCCGGCCUTCTGTCUAC	62237	AGACCAGAUGCAGGCTCCAUA
326507065	62238	TGGTCUGCTCCTCUAGAGACAAC	62239	TCACCTGGGUCCCTGTTAAACUAA
326776971	62240	CCACCAAACUCATCTGGTCUGA	62241	GCAGGAGCUTCTCAUGCAGAA
332456629	62242	GAAGAUCGCCAACTGCAGUAAGA	62243	CCCATGACTUTGAGGCATCUGAG
332491467	62244	TCAGCTTTGGUGTCTGCTTUGAT	62245	AGAGCTGUGGGCAATAGTAATTTUCA
333380863	62246	ACATGAAAAGAUAGCCCATCCUGAAG	62247	CTGAAGCCAGAUATGGTCATUCCA
323411274	62248	GGTAGCTCUCCAGGAGGAAGUC	62249	GCTCTGGGTCUGAAAAGAAGCTUT
325725465	62250	CATGCTGGCUTCTGACTCTGUT	62251	GCTGCUGCACTUCAAAGACC
268005886	62252	GAACAGGTCCUTCTGGTGGUT	62253	GCACCGCUTGACCCCUT
332281258	62254	CAATCCCCAGGUGTCTTGGUC	62255	GTGATGACAACUCCTACATGTACATUCT
313030842	62256	CCATGAAGGUGCTCATGTUCACT	62257	ACAGAAACUGAGCTGCCAAUACC
312697333	62258	CCTGGTGGUCACCTTCCUAGA	62259	ACAGTCTGCAUAACACCCUGAC
315072685	62260	AGGTCCUGTGACUCCCGAT	62261	CGCTGTACCUCAGGGCTTUC
225134000	62262	ACAGAAUGTCTGAGAAUAGCAAAACCA	62263	GCGACAGTAATCUGTTAAGCCATTTAUT
222320255	62264	AGATGCUGAACAAAAGGACTTCUGA	62265	CATGAAGATGGUTTTCTAGAGCAUCCT
329279178	62266	TGTAUGGCAAAAGCAGAUGAGGAA	62267	AGTUGCCACAAACCCUCAGAC
222358249	62268	CGGAATTUGAAAACAAGCAAGCTCUC	62269	GACCAAGUCACTCTTTCTAUGCAAAAAC
223808104	62270	GCTATTTGGTTUGAGAAGCGATUGG	62271	CCTGCAACUCAGAATGTAGAAAAAGUG
223017608	62272	CTCTTTGACUGGACCATGAAUCCT	62273	TGAAAAACUGACAACAGGACCTTCTUAA
332793434	62274	GGGCUCAAGCATCAGTTUCAT	62275	CCTACTCTUGCTCCTCTCCUCAC
315821349	62276	CCCACAGTUGCCTTTTCAGUGA	62277	AAGAAATGCCACAGUCCTCCTUT
333466182	62278	GCAAAAGAAAACCCAGUCCUGACA	62279	TGUACACAAGAACGGGCTUCA
333546598	62280	GTTGCTGAGUGTGCCTCACUA	62281	GAAUACAGCCAGGAAUAGCAGAAAGAAT
333771000	62282	CAGTGGGCAGUTGTGAGAAUGA	62283	TTCCUCCAAAGAGCTGCAUCC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332660172	62284	AGCGGCCAAUGATTTCUCAGA	62285	ACCACACTTUGTACTGGTGCUG
318956483	62286	GTTGGTGGUGGTTAGTGGGUAT	62287	GTGTCTGCUCCTGCACTATCUG
329963600	62288	GGATTAAGAAGCAAUGCCCTCUCA	62289	GGACTTAGCAAGAAGUTATGGAATUCCT
321575933	62290	GGAACAGAAUGTGCUGGCAAT	62291	GCAUCAGAGCTCCTUCCACAG
321604004	62292	GTACTGTCUGTGGTATGTGUCAAAGT	62293	CTGGAGAUTTCTCCUGACAGCA
314201151	62294	TTTTGATGCCAUGCACTCATTUCC	62295	CTTGACAGACAACUCCCACTTCTTAAUA
280376905	62296	TGGTTCTGCCCUCCTGTACUT	62297	TGGTAATGATGUCTCATGACGTTUCAT
279758255	62298	TTCAAATACUAGGTTTCTUCAACAGCGA	62299	CACTTTGCATUCCAAGATCTGATTTCUT
278971585	62300	ACAGTCTGGUACTCTCCTGGUC	62301	AACAATTATGCACACAAUTCAGTCGTUT
268889880	62302	CTACCATCUACCCCCTGUCACA	62303	CCACCCTCUTCTCTCTCCUGAA
268544586	62304	GAGGAGAGCCACUCUAAGCAA	62305	ACCTCCTAACGUTGTTGGGTTUC
265604382	62306	CAGGTCCCUGAAGGUGAAGAA	62307	CTCTCCTCTAACUTACCATCCTGUG
266936698	62308	GGGAGAAGGAUGCUGAGGGA	62309	CCGTGCUCCTGCCGTUT
320542156	62310	CTGGGCTCUCCTTGTTGAGUT	62311	CAAACGAUGAAGAGTTCAAAAUGCAGAT
315446662	62312	GGATCCCAGAUGGTGACCCUA	62313	CATCTCACAUAGATCTTGACTGUCACT
256737476	62314	GAGTTGTAGCUCAGCCCTCTUT	62315	GAAATCACAGAGUTTCTGCUGGGA
235863556	62316	TCGTTCCTUGGGTTTCTTCAACA	62317	GGTCATAGTAAUCACCAGTGTTCUGAAT
332575061	62318	TTCTGUGCCCAGCTTTATUCACT	62319	GGGTGTCTGAUGTGACTTTTCUCT
332418925	62320	AATAAGGUGAGGCCCATGTCTUC	62321	TGGAAUAAAAGGAGAGAAGGGTTUCC
318494077	62322	CCTCCATACCCUCCCCACTUA	62323	CTAACCCCACAUTCCCCAUCC
321634505	62324	ACUATGGUGCAACAGCAGAAGAG	62325	TGTTAACACCAAAUAACTTACTGCUCAA
315251151	62326	CTACGTCCACCAUCAAGTCCUC	62327	GTTGCCCAGUAGAGUCACACA
313468593	62328	GCTCCATTUCTGGCACUGAGAT	62329	CACAAGCCCCUCATTUCACC
314362115	62330	GCCACCACAGUCTCCTACTUC	62331	GGATTTCATGTTTUCCACACTTTGCTUAT
314675540	62332	TCCUCAGGGCAGUGAAGAAGA	62333	AGGACTGATUGGACTTTGTTTCCTUT
314324104	62334	GCTGGTTGUCACTGTGGCUAT	62335	CGAGCAGAUCGCCCUCAAG
313168062	62336	GGAACACGGUAACTCGGTUGA	62337	CTATGAGGAGUCCCTGGAACAUCT
313323038	62338	ATGGUCCCGAAUGCACCAA	62339	TGCTTCTTTTGUTGACTCTCCTUCC
266065273	62340	CTTCTTTCTTTAGUAGCAGCCCUGT	62341	GATGTGTTTTCUGACGTTCTGTAGTUC
255876328	62342	CTGCAACTUAAGGAAGAATCTGUGAAG	62343	CCAGUCACACCAGCAATCACAUA
324104216	62344	GTACTTTTUAAGGGTTGUGGGACCT	62345	GCUTTAAATGATAGCUACACAGCACAAA
330330120	62346	CCTCGGGCUTCTTCTTCAUCAT	62347	GCCTGATGGTUGTAAGAGTGGAATUA
326822151	62348	GACGTCACAAUAGCGACUCACT	62349	GACAGCUGCCCTTTACCTCUC
325844610	62350	TGGGTGGGAUTCACCACTTTUC	62351	TTACAACGTGUCTCTGCTTCTCUC
318399623	62352	TCATCCTCUGCTGCCTUAGGAA	62353	ACACTGCAGCUGCTATTGUCC
265611361	62354	GGAAACCCAAGUGGCATCTATUCA	62355	ACCGGAGGUCTCTUCCAGAC
317726796	62356	GGTGAATTAAUGAAGCAAAACCTGGAUT	62357	AAGGGAUCAGCTACCUCCACT
317039077	62358	TGAGCCAACCAGGAAUATTTTCUGA	62359	GTGAGATGUGTCCTGCTGUGA
316117931	62360	AATAAAAGAGCCUGGGCTGTTCUT	62361	CCCAGCTTUACTGTGTGGGAUT
326949898	62362	GCCCCCTUGGGAAAGTACAUA	62363	GCTTCAGCAUCTGCATCTTCTUCT
326789867	62364	GAAGTTGCUGCGGGTGUC	62365	GUGGGUGCACAGAACCAGAA
328245228	62366	ATCATCTCATCCUGTGTTTGTGATUGAT	62367	GAAAGAATGUGGTCGCAGCUAAG
332625723	62368	GCGTGUCTCCACAAUGAGGAAG	62369	TCTTCAAUGTGGTGUCAGACACA
332962615	62370	GCCGTUCGTGCUGGACT	62371	GGCCAAGGCGUGGAUCA
319682942	62372	TGTGAGCCGGUGGTTAAACUG	62373	TGCTTTTCUCACTCCTGCTUGT
320970723	62374	GCCCUCAGAGCCCAGTTTCUA	62375	TGCTAAGACCCAUTTCCTUCCC
240316907	62376	TTGCTAAGCCUCGGCTGUT	62377	TTGATGATGAUGTCAGGCATCUCC
242600421	62378	GCTCCTACAGGUACACGGAGUT	62379	GGTAGCAGGACUGGAUGGGA
262388192	62380	CAGGCAGUAGCCGAGAUCA	62381	GCUCTUGGCGCCACACT
318857151	62382	GCGUACCGAGGUGAGCA	62383	GCCACCCGCUCCTACUGA
318153238	62384	GGATTUGGCAGGCGAGUAGG	62385	TGTGTGACACAUCCCCTGGUA
319241012	62386	TCGTGCCAACGUGTCTTGUA	62387	CCTACCCUGGGTGGTCGAUAG
236543421	62388	CGTTGAUGCGCUGGGACT	62389	GCAAGAUGGCCGAGCAGUA
235677714	62390	GAGGUATTAGGAUGCAGGAAAGCA	62391	GGAGCTCTUCCTTTCCTTCCTUT
237044500	62392	GATGAACAUGGTGTGGTUGAAGAG	62393	GGCTCCTTGUCTTCTGACTTCAUA
316170471	62394	TGAAGTCACAAUCAGCTAAACTUGCT	62395	AGTTTGGTGCUTTGGAAAGTGUG
315722238	62396	CGCAGCCUAAACACTTTUAAAAAGGT	62397	GCTTTTCTGAAAUGTTGGTCTTCUGT
327416676	62398	TTTCTCATGGUCCCCTCTCCUT	62399	CAAGTTAGGTUTAGTTCAAGCAUCAACA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
327849976	62400	CATGUCCGGCTTCUCCAACA	62401	AACCTGTTCUGAAAGACAUCGGAA
319526073	62402	CGAGCTATAGCAGAUTATCTTCGTUCA	62403	ACAAATGACAAAATUGTGCGTAACTGUT
256915082	62404	GGTATAGAAGUTGGTCCUCAGCCT	62405	ATCTGACCCAGGUTCCAATTGTTATUT
267658374	62406	CCACCCAGCGUCCGAAUAA	62407	GTCTCCAUCAACGTCCTGCUC
254063741	62408	CAGGGTGGUGTATGGCAACUA	62409	CCCGTACUGCCTTAAGAGAUGG
267654238	62410	TCCCCGUCGCUAGGGAAA	62411	GCTCCGCCUCAGCACUC
268551549	62412	GGGTTGGCTUACAGAAAATTACGUT	62413	GGAGTAUCCAGGACCGAGUG
268348058	62414	CAGCCGAAUCTCGAACTUCCT	62415	CCGGUCCTCCACAUAGAGGT
268908398	62416	TCATCAGUCCGCTGGAGTUG	62417	CAAGTCUGCCGGGTTGATGUA
268161134	62418	GCCCTGUCCTCTATCUACAGCA	62419	GTGTCUCGGAGCCGAUGAA
267167133	62420	CAGCTTTCAUCAGCTCCAUGGAT	62421	TGATGGAACUGTGGCTGGTUG
267317736	62422	GGAAAACTATCACAUTCTTCGCAGGUAA	62423	GGTACACAGAGAAGGUTATGCUGT
267489746	62424	GCCTGTGUGGAGGTCTTTCUT	62425	TCTTCTGUCCCAGTCATCTGUGAT
320092947	62426	GGATGUAGGCGAAACCGUAGG	62427	AGCAGATTTCCUTCCAGAGGUAGAA
237193452	62428	GCUTCCAAUAAAAACAGGACAGCA	62429	AAGCAAATUCCCCAAAACACAGUAAC
240266483	62430	GCAGTTAGCAGUTATAAATAGCCUGGAA	62431	TCCTGAAAATGAAUGTGAAACTATCACUCA
258513834	62432	CGUATAAGCCCUCACAACAACCAA	62433	GTCTTGAAACGAACAUCAATACATAATAGUG
236050823	62434	GGTGTGTGTUTGCATGGTCTUA	62435	CATCAATCTUAGGCCACCAAUCCA
241781507	62436	CTACTCCTTTUGGGTGGAGCUT	62437	AAGAGGCUTCCAAATUGAGGGT
235501936	62438	TTTAGAATGCCTTCUCTTTTGTCTATATCUGAT	62439	CTCTCCTTGCCAUCATTACTTCAACUAA
237203098	62440	AGCAGAAATTATATCAAUGAGAAAATTCATGUT	62441	GCCGCATAUGTTCTTCTTTTGUGA
235390517	62442	AGGCAUCAGGTACAUGAAAAAGAAGAAT	62443	TCAATTCCTGUTAAGTCAACUGGGAAA
240003548	62444	TGTGCTAAAACTUTGAGTCCCATGUT	62445	CACAUCAAGGGAATTGTUGAAGGAC
332777909	62446	GGGACACCGUGTACACCATUG	62447	CAGACCAACCCUTCCCTCTUG
333179433	62448	TCCAACAGAAGGAGGUTCUAGAGAG	62449	CCCATGTACUCCAGCGATGUG
333022304	62450	GCTCCTUCCCCTCGCCUAA	62451	ATCCAUGCCATCCUGCGT
313354423	62452	CTGATCAGAAGGGAUATTAAGGGUACCT	62453	GGCUAAGGCAAGGCCTATTTTUCA
226580065	62454	CCTCACCACUCTTCCAGUCAGA	62455	CAAGAGAAGGCUCACGAUGGT
225532498	62456	GAGAGAAGGAGAGAUGCUGAGAGAT	62457	CACTCCAGUCTTCTTGGTTGUCA
254032137	62458	GCTTCTTCUTCTCTGGCUACGA	62459	TGGGATTTUCAGCCACCUCAC
328409032	62460	CACUGGGAACAACCCGTCUAC	62461	AAAGGGAATTCUGGTTGGTCCUC
262676061	62462	ACGGCGAGAUTGAGGCCTAUA	62463	CTGAGGGCAUCCTCTGTGUC
316862580	62464	CTGCUGAGCCCGCTTUC	62465	GAGGAGCCACUCAGCTCUC
317964108	62466	GGAGGAAGCUCCCUGGAAAC	62467	GCCCCAACCUTGUAGGACA
330602192	62468	GCAGGCACUTGCTUGAAACAC	62469	AGCAGTCTCTGUCTTATGATTCATTTGUT
260095660	62470	GCCATGGAUAGGCTCAUCAGG	62471	CAGTGCAUACTTTTGTGGUGAAAACT
328123565	62472	TCAGAAUCAGCAGGTTUGCAGT	62473	CTTAAATGUAGGAATGGGATGUCACAGA
314152804	62474	CTATGATGCUAACTACGAUGGGAAGG	62475	AACTCCCGCAAUCTCATTGUGA
268768834	62476	TGGAGTTTUACCTTGGAUGCAAACA	62477	GAAACTGUCCGTAGATGCUGACT
268961006	62478	CCGCCUCTGAUGGCGAAA	62479	CAGCTCAGGCUCCTTGUCC
268964329	62480	ATGCCAAGUATGACCGCUACC	62481	GTAATGCUCCCGCGTCTUCT
265454894	62482	TGTCTGCCACUCCCTGGUAT	62483	GAAAGTTCTTGUACTCCTCCACCUC
265055473	62484	GCAAGGCCAGGAAAUGCTCUT	62485	CGACCAGCCAGUCTCTAAAAGUA
323362558	62486	CCCTGCAAUCGTCTCUGACT	62487	AGGGCAACATUAAGGGTCTGTUT
323554948	62488	CGGGCAGAGAAAUCCTAUACAGT	62489	AGAGUAGACAAGCTGUGGGAGA
325658235	62490	GGCTTGAAAGCUGGCTCUCAT	62491	CCCCAAAATUGAGGGTTACTGGUC
325404126	62492	TCTGUGCAGCCACGUAGAC	62493	GTGACCATTTUCTGTGCTCCTUC
323816438	62494	CTCAGAGUTCCTGCTTUGGGAT	62495	AGAGGTCUCGAGAGAAAGTUAGCA
325138222	62496	GTACTCTGUGCAGACGUCACT	62497	CTCAGTGGCAUTGTGGTTGTUC
324241277	62498	AGAAATCCAGUTCCTGCTTUCGT	62499	GCACATGCUCCGACAGGUT
266957518	62500	GCCCACUCGGCTAACCAUT	62501	CAAGGUACAGGGCATGCAUC
257559254	62502	GCTCGGUGGATGAGGUCAAT	62503	CACAAATCCTUCCCAAGCTCUG
325912004	62504	GCUCCGCAGGCAAGGUA	62505	CCGAGUGGAGAGCTGGAUCT
332560050	62506	GAAGACUATGGTTTUGGGACACGA	62507	CCCTTCGAGAAGCUGCAGAUG
254472663	62508	AGAACAACTGUAACCCAAGCAUCA	62509	TCATAGCGACAGUGATCGTCAUC
261275145	62510	GGACCAGCCGGCAUCUC	62511	GCUCCCCAGGGAAGGUCA
318366309	62512	CTTGGACCCGGACUCGTUA	62513	CGCUCGCAGGTCUCCAG
226431231	62514	AAGAACTUCAGGCGCCAAGUA	62515	CCTACGTGUCTTCTTGGACUGG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258978440	62516	CATGUAGCGGGCCTCUAGT	62517	AAAGUCCCCCAGCCCTUG
325087480	62518	ATGTGGTGCAUCCTGTCTGUT	62519	AGAAGCAAAACAAAAGGUTTAAGCTUGT
268434596	62520	AGTGGCUCCCTGAUACCAAGA	62521	CAAAGUGAAUGGCACAACGGT
267646565	62522	CTCAAGCTTTUCTTTTAGTTGCUGCT	62523	GTGTCCCAGTTUGCATTAACAAATAGUT
269171924	62524	TGGCAAAATUAAGCACTAGTGTUACAGA	62525	TTGCTCAGUTTCGAAGACUCAACT
261110291	62526	GCTCAGGUAGGCTGGCTAATUT	62527	GCAGCCAGAAGUGCACTATACATAUA
261116945	62528	TGCCCGTUGCTTTACAATTTAUAAGGA	62529	AGTCTGAAGUGGAAATGGTGAUAAAGAC
267264180	62530	TGACAUTACAGGUACCCGAGGA	62531	AAAAGAAGAGGCAGAUTACTGTGGAUT
265555386	62532	GAAGCAGTUCTCTGGTTTGUACAAC	62533	TTTCCCCCUCCTCTCTAUCCAC
324712694	62534	TGCGACAUCACCTGAAATTCTUCA	62535	CTTGATGATGCAGAUAGCAGTTCATUAG
320223673	62536	CATGGUGGGACCACATCTUGA	62537	TGGGACAGUAAAAGGCAATAATAGCTUT
291170022	62538	ACCACACUTTGTCCCUCAACAA	62539	TGTGGGAGAAAACAUCATGUCGAA
299452347	62540	TCCCCCUGGGAACTAGAAAUAGG	62541	CCTAAUCAGAAGGAAGCAAUGCACAT
259922178	62542	CTGTTTTAACUGACACCTTGTTTCUGA	62543	ACTTTTTCTCCAGUGTCCCAGTATCUA
265853418	62544	AGTATCACAAGUGAAGTTGAGAGUACCT	62545	CGTATGGATTTUACACCTGGCTTTUT
257519270	62546	CCATTGCATTUGCCTACTCTTTGATUA	62547	AGGTCATTTAUCCACCCAACATTTUAACA
259096597	62548	GAAAGCAACTTUCACCTAGGCAUT	62549	AGATAAGCAGUGACCCGTTCUG
256038667	62550	GGTGTTTGCUGAAGTTCTACCTUCT	62551	CATACTCCUCAAAGGUCAAGCCAT
259080084	62552	TGGTTTUGCAGCCCUGGAT	62553	CCGGCCGCUAATAATAATTCTCATUAAG
263541303	62554	CACAACTGTAAUAACTGCCCCCUT	62555	GAAAATGAGATCUAACAGCTGTGTCUGA
263845256	62556	ACCTTGTCCUGCATTGCTTAUCC	62557	CCCAAGTTACUGACTAAGCAUCCA
264478250	62558	AGCAAGAAUACCAATTAACACUGCCA	62559	GCATTCCATAUCATCACTGGCTUCT
263868675	62560	CUATCCATTCCCAUGAAACCAGACA	62561	ATTGAACCACCUTTCATTAAUGGGACT
320899375	62562	CAGAUCCAGGGAACTAGAUGCAG	62563	AAAGCTAGTACCUTGAACACATCUGAAG
316810501	62564	GAAATGACCUTCATGTGAAUACCAGGAT	62565	CCTATTGGTTUATGGCTAGAACUAAGGA
317470168	62566	GCTCCTGUGCTTGGTTCTCUAC	62567	TCTTTCTCAAGAGAUTCTCCCCAATTUC
317276043	62568	AACCCTACAUACCTAGCUGCAAAC	62569	GTTAGGAATGCAAAUTGTGCTATCAUCT
319793495	62570	TUTCTTGATCAUGAAAACGCCAACAA	62571	TGCATCUGAAGGGTATTATGUGGAAAT
314332887	62572	TGATAACCGUCAGTGCTTTACUGT	62573	CAACGCACAAUGACCGTCTTATUT
264555907	62574	AGCGGCUCATTTTTGACTTUCC	62575	GUACCTCCTTGUACGACGACAT
313294264	62576	ACCAGGCGCACAUTGTCUAT	62577	GAGACCTUCGGCGAGUACAG
268737063	62578	TCTTCTGAAGAGGAGUGCAAGGAUA	62579	GAGGUGGAGGAGGAAGUAGGAT
333151698	62580	TCCTTUCCCTCAGGUGGAGAT	62581	GAACAAATCTGUCTAAAAGCCACGUT
315525728	62582	CTGTGTGGTUGTCTGCCCAUA	62583	CTTCAAAAGCUCGACTTCACCUC
317709163	62584	TTGTATTTTAGGCAUAGGTGTTCTGUGT	62585	AGTTGTGACAAGAACACUGGTGATTAUT
316783508	62586	GACAGTTTCUCCTGAGAAUGGGAAT	62587	TGTGTCTAAATCUCTTTTCCCCATTGUT
316354917	62588	AAAGACAGAAAAUGCAGTCAGUGT	62589	TGTTTGTAGAATUCACGGATCACCTUT
319829812	62590	CCAGCGGCGGUTGATUAGT	62591	CTCCCAGCCGUATGCUGAG
320538881	62592	GCGGCAGAAUTTGAGAGATUGT	62593	GGGTGACTTGAUGGAGTCATTAAUC
319988948	62594	ACTCAGTCUCTCCAGGATUGACA	62595	AAAGTGCUCCATCTCCUCCAC
315469198	62596	CCCCTCACCCCUCTCATGUT	62597	CTTCCCGAGCAGAACUGGUC
313687146	62598	GTGACCAGUCCTGCCTGUAA	62599	CCCAGGCAAAUGTGUGACAG
312863425	62600	CCACTGUCCACCCTGTCCUA	62601	GCCGUAGGCCCCCATUG
266135297	62602	GCAAGTCAGTUTCGGTTTCCTUCT	62603	GCGAGTCCAUGTGATCTCCTUC
256496985	62604	GGGTCTGAUGATCACCCTUCCT	62605	CCAGGCUAGCTCTGTGTTTUCT
266851761	62606	GGACGTGUCTTGTGACTUCCT	62607	GCTGTACTTGTGGUATTCATTGCATTAUT
263105983	62608	ACTUGACAGAAACCAGCUGGAAT	62609	GGTCAAGAACUTATCTTCCTTCTUCCAA
258653893	62610	GACUCATCAGGAAUCACACCGT	62611	ACTCCTTCGACUTTCTCTGTTTATTUGT
262836861	62612	GGGAGGUCCAGGGUACACAA	62613	TCTGTAAAATCUGTCCCTTGTCUCCT
261754833	62614	TCTTGGTGTGUATGTTCATCAUGAG	62615	CCACATCTTAGUGGCCTTACTTUACAT
263089376	62616	CACCACTATATCAUCAACACAAGGUAA	62617	CATTGGAGAAGGGAUTAGAGAAGTAACUG
267177370	62618	CTTACCAGCAGUTGTTTUCAGGAAG	62619	CTTAGAGATAAGCCGGUATGGTTGTTUA
268213011	62620	AAGACACTCTAAAUTCTTTCTTTGATCAUACT	62621	AAGGAUCUCCAGGAGCAAAAGG
269340143	62622	ACATTTTCTCCCUTGTCACCCTUG	62623	AGUGGGAACCCAAGATTTUCCAT
267475919	62624	GAAAGAGAAAGAGAAGCUCUGACACT	62625	GTCACTGTGAUGAAGAAGCTGTAUGAT
267438589	62626	ATCAAGCUGTTTTACCTTUGGACCT	62627	TCTGCAAATCTUCCTTTTGAGTGUACAA
264591745	62628	CCTCTTGGUCCAATTTCTCCAUCT	62629	TGATTTAACAGGGUGAACGAGGUC
268594158	62630	ATCTTGAAUCACCCAAATATCGTAAUCA	62631	GGGCCAAAGGUGAGAGUGG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316601934	62632	GGACACAGAUCAGCATGGCUAAAT	62633	ACTTGGCUCAAGACCAAUGGAG
314910422	62634	AGAAAAGTUGCAGGTGGUCACT	62635	TCATCTCCAUCCTCATCCTCGUC
326218480	62636	GGAAGGGACCUGACCAUCAAA	62637	CTCTCAUAGACACTACAGTUGGCT
325221920	62638	CTTTGTCACTGUCACTGTCCTCTUT	62639	CCACATCACUGGCAGAGGUC
315838839	62640	TCCTCCTCUACTTGAGAAGUCAACC	62641	TCGCAATCCAUGAGCCTCTTTAUT
326456921	62642	GTGAAGGGAGACAGGUCTCUCA	62643	AGCTGGAGTTTAUTCAGTTTCTTCCTUT
326507816	62644	ACATATACTCUGTGTACGGTUGGAGA	62645	TTAAAAGAGAUCTCATTTGAUGGCAGAA
326774488	62646	CCTCCUGGAGGCATTGCAAUT	62647	AAAGUCATGUACAGCGGAGAAGAG
327646398	62648	AATTTGAGGAAACAUTTGCATUCAGAGG	62649	AGAATCGGCCAAUGAAAATGCATUAAAA
326567401	62650	GAAACCACAACAGCAUTTATCCUCAA	62651	CAGGGATGGUTTTGAAATCUACACAAC
327786822	62652	TATTTTCATTTGTUAGGCCAAGATTAAGTUCAT	62653	TCCCAGGAGAGCUTCACUGAA
333131036	62654	GAGCATCGGGUAATCTTTTGUAGACA	62655	TCTTGGCAAACUCCAGGUGAAG
324637871	62656	GGCGAAGACGAGAUCCAGUT	62657	ACCUGCACACACTTGGUGAT
326380858	62658	AATGTCGTGAAAUAGATGGCTUAGAACT	62659	ATGGATATTCTCUGCCAGTTTTTCTCUT
324934233	62660	GGCTAUGGCAGAAATGAUGGCT	62661	CATACACTCAUGGAATTGAGCUCAGA
324483010	62662	GATGGCCTAAAAUATTTGTTCACTUGGG	62663	TCTGGTTCUCCGTATCTGTGUGT
238698772	62664	GGATATGTTUCACGTAGTACACATUGCT	62665	GCCAGGTGACAUTCAGAACATTATUAGT
236818141	62666	CAGGCAUGCTTGTGTUGAAGT	62667	TCCCTTTCUAATGTTAAGAACUGGGAA
267932442	62668	CACAUGGCTCUGGAGAAGACAT	62669	CGCCAAAGAUCTCGATCTCGUA
267433052	62670	TTCAGGCCAGUGCGTTCUT	62671	CTGCCCAUCATCTCCCCTUC
265697022	62672	CTGGUCAGAGAGCGCUACC	62673	AAGGAGCCCACAAAUAAGUAAACAGT
267557031	62674	CCATGGAUAGAAGCTGGUGACA	62675	CACAAACCAUTCTGGGUGGAAAG
326594820	62676	GGAAGAGACUTTGGATCUGAAGGAA	62677	AGAACTCGAAUCTTGTGCUCCAAG
267200652	62678	GGCTTTCCAGAAAUGTCAGAGATAUCAAT	62679	TTTATGCTUGCCTCCUGGACAA
253980985	62680	AUGCCCCGGAGCAGAAUC	62681	CCCTCCACCUCCTTCUCCAAA
269262344	62682	GGTTTTATACATUTCCTAGGGCTUCGAT	62683	CAGAAAACAAGTUAAGGCTCACAATAUGAA
264098045	62684	GTTTAAACAGGACUGAAGGGUGAA	62685	AACTATGCTTACUCCCTCTCAACTAUGAT
268094681	62686	CCCCTTUGAGAACCACAGCUT	62687	CCCTTCAGUCTTGTGTAUGACAAAGA
269235345	62688	GTTTTGCUCAAATGGGCUGCT	62689	CCAGATCCACUTCCTGAGTTUACT
268408644	62690	CGTTUCCCAGCUCGACCA	62691	CTACACATGGACAUTTGCCTGATTUC
268630007	62692	GGCTCAACUCTCCTGTGCUT	62693	GUGAAGCUGGCCCCACT
317405134	62694	TGTACCTTCCCAUGCACTATTTUGT	62695	GGATTCAGACUAAAAGGAAGAGATGUGT
316715899	62696	GGGAAGCACUGAAACCUCAAGAAT	62697	AAAGTTCCTCAAUGCACTGACTCUT
315904214	62698	CTCUGAGCGCGACUCGAA	62699	GCTGCTTUAGCTTCGGAGUGT
267659394	62700	CTGAGTUCGCCCGTGTUC	62701	GTGGTCAGAAACUCCTGGTUCA
236045805	62702	GGAGGCACAAAGCUGTCTGUA	62703	GCCTAAAAGAAAACAUGATGGTUGACAAT
237933606	62704	GGAGGGAAUGCGAAGAAACTCUT	62705	CGTCGTAUGCGAGAGTCUGT
235627741	62706	CAAGAGTTGUCTGATGTTACUCCAGT	62707	TCAGCATAATTUACACCTGTGTTCTUGT
257518398	62708	CGGTTCTTCCUGCCATCTGAUAA	62709	GGCAGGAAUCACCTCTGTGUC
272508592	62710	GCTGCUCGGAGGAGAAGATUC	62711	GGTTTUCCAGGAAGCATCAGTUCA
231631673	62712	GGCTCTGACAUCTAGTGTGUGT	62713	AAAACCAUCCCCCAUAAACCAAGAA
324475741	62714	GCGCCAUGAAGAGTGTGTUG	62715	ACAGAATCAAACUAACTCATTGGCUGT
326355654	62716	CAGAGAGAGAGUCACTTGTAGCUGA	62717	GCTTTGTAATUCCCAATAACTGTGGTUT
324323875	62718	GUGCCCCGAGGTAAUAGGAAG	62719	TCTGTCCCUGGGCATAGAAUCA
326903239	62720	GCCTGTAGCCUGCAGCATUAT	62721	GCAGTCTCAGAUTCCAGGCCUA
316518675	62722	CATTACATCUGGCCAAGCGUAGT	62723	CTGGACCACAGCACUGACTUT
319818652	62724	ACATTAAGTACCAGUGAGAGAGUACACA	62725	ATGGATTGAAUATGTTTGAUGGGACAGA
332062351	62726	GGACUCTACCAUCCAGCCACA	62727	ATGACCTGGUCTTCTTCTCTGUCT
332145815	62728	GGTCCAAAGGCUGTACGGAUT	62729	GCTCACTTTCUCCCTGTCCUC
323758976	62730	GCAUTCTACATCTUCACCCACCAG	62731	CCTGGGAAGUAGCTTGTCCUT
329258406	62732	GAGCCGCCCCUTTGTUG	62733	CTCCCATCUGTGCCTCTGUAAG
329282720	62734	GCAAGUGGCAGTCCCCUAA	62735	CAGGGACCUGCCUAGGAC
227846601	62736	CCACTGUCTGGGUCAAGGAT	62737	GCACTCGGCUCCTTTCTGUAG
227442769	62738	GTTCCACUGCAAGGTGUACAGT	62739	CUCCAACCCCUAGACCCAAAT
227392369	62740	GCCUGGCGGGCAATTCTAUT	62741	CGGCCGUAAGTCACAGGATUC
329689148	62742	GGAGGACCUGGACCGUGT	62743	CCACCGAGCCCCUCTUC
325140686	62744	GCCTCCUCTGACCTUGGGA	62745	ACCCTCACUGCCCGGUAT
320313515	62746	CATGCACTUCCAGACTTTGCTUT	62747	ATCTTAGAGATAACAUGGTGTTTTTGGTGUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318734378	62748	TCAATTTTGGATUCATATGCCTTCTGUAAGA	62749	GGCTTCTGGCUAGAGGTCATTAATTAUT
320718954	62750	ACTGAAGCUGACAACCGAAGUT	62751	CGAGUGGCAATGAGUCACAGAC
320968133	62752	AGCTGTCAGTGGUAGCTATAGGAATUAA	62753	GTTGAACTGUATCTGCCAATAUGCC
333373103	62754	TCATCTTCTGUCCTCTTCACUCAAGT	62755	GGGTTATTCUGACCCAAGCCAUA
333774879	62756	CTAATTTTCCUCTCCCTCUGCCAAT	62757	GAAAAAGAAGAAAGCGUGGUGAGG
332916303	62758	GGAAAGACAUACCCCCAGAUGAGA	62759	TTCACCTAATGACUCTTCTGAACUACCT
332840130	62760	TCCCCUAAAACAGAAAGACACTCUACT	62761	CCTTTCAGTTTUTGTCGAGGGUGAT
314640186	62762	ACAACUGCGAGCACTUCGT	62763	AGAGAAAAGGUCAGGGAUGGGA
267795323	62764	ACCTGTAATAUGAACAGCAUGGCA	62765	GTCTCCTGUCTATGGGCUCAGA
266929766	62766	GGCTGGGUTAGGCAATTUGGT	62767	GACGCCTCAUGACCATTTCTTTUT
267598978	62768	TTCTACTAATUCTGTATAGCCUCCAAGGA	62769	CACAAATGACUGGACTGATGGGATAUT
269188117	62770	GAGGAAGUAACATTTGGUCCACACA	62771	ACCAGAUGGATTUCCGAGGACT
261855192	62772	GTTCAATTGCUGGGCATGCUAA	62773	CTACACAGTATCCUCAGCTTCTTGAAAUA
269085640	62774	CCTGAAACAUGATAAGCCTGUCACT	62775	ATGAATCACTTUGTGAGGCCCUT
269251508	62776	AGATATTTGTGCGUCTGCGTGUAT	62777	TGTGACCCTUTGTACAGCAGUG
292884085	62778	CAGCATCGGUATCAAGTCCCAUT	62779	CACTACTUAGCCTGUGCACCA
290986824	62780	CGTGTAAGGUCTTCAGACAUGGAC	62781	GCAGCATTTAGUGGGCGGTTTAUAT
321290947	62782	CCTTTCAAAGTAUTGTGTCATTCAUGCT	62783	CCCAGCCUCCTGTGGGUA
222616452	62784	ACAGACACTTCAUTTGGAGTACCTUAAC	62785	GCATTAGUGACCAGGGTTTGTAAUC
222892108	62786	TGCAGCACUCCACAACAUCA	62787	ACATGCACUACGATGTACACTAUAGAGA
224538823	62788	CGAGAUTCCAAAACUGACAGCA	62789	TCCAGAACAAAAACCCUCUAACAAGAAT
327518127	62790	CUCAGUAAAACCAGCCCAGGT	62791	GGCCTCCUCCTCACTTUCAGA
327555510	62792	CTGATAGGGCAGGGUGATCCUA	62793	CTGGAGTCUAGCTTGGGAGUG
236199775	62794	TTGAAAGGGAGGCUCCGTTUT	62795	TCCTGCTTCCUCTAATCATATCUGCT
238156460	62796	CCAAGGAGACUGTUGAGGAAGG	62797	ATGAAAACACAAGUGGGCAAACAUT
235296279	62798	CTCAUTACTAGCAGUCCCAAACCC	62799	TTCTGGCGAGGAGUTAGGTCUA
239820611	62800	AGGCCUTTTTATAUGAGCCAACAACT	62801	GGTTACCAACUTCTTTTCTTCAGUGG
261833181	62802	GCACCAGCAGGAUGTACTATTCUC	62803	GGGAAGUTCTTUCGGGACCT
266520495	62804	CGGCAGGAAGAUTACAUGAAGAC	62805	GGTTGAUACAAAGAGAAAGATGUCCCAA
267735550	62806	TGGCCCTTUGTTTTGCTGUACT	62807	GTAAGTAGTTCAAUGTACCGAGCAUGAA
268475659	62808	TGUTTGATGGGCUGAGGAAGAAG	62809	TTCTTTCTCUTGGCCTCUACCAAAG
268495106	62810	GGATCCTGTUAGCAACTTGAGGUT	62811	CGGTTGCGAUCTGTGCTTCUA
265552678	62812	CTTGTGUCCCGGCGUCT	62813	CGCACACCUTCCAGTTCATUG
331698405	62814	CACCCAUGCCGTTTTCTUGA	62815	CATCGCCUCGCATTTCCUCT
331685849	62816	CATTCTTGTACUGGACCAGGAAGUG	62817	CATGCCCACCCAUTCTATTTTCUG
267656646	62818	GGGTCCCUGTGGAGAGAUGG	62819	CCTGUGGCCCCCUCAAAT
264363791	62820	CACAGACCCCUCCCCAGUA	62821	GTGGTCTGAGGUTCTCTGGTAUG
267952032	62822	AAAGAGGCUCAGGGTCACUAGA	62823	CCCTGTGACTUCTCTTTCCCTGUA
268579270	62824	TCCTCCAUATCTTTCCUGCCCAT	62825	TCACCCCATCUTTTGCATTCTCUT
268572053	62826	GGUTAAAAAUCAGAGGCGACAGGA	62827	TGAGAUGGAGAAAGGCCTAGUGT
325036814	62828	GCTTCUTCACACTCUCCAGAAAGG	62829	CCTGTGGTUTCCTAATGGUCCAG
325417354	62830	TGAGCCTCAGUGTCCCCAATAUA	62831	TGAAGAAGACCAUCGACATGCUG
326384993	62832	GTGAGAAGGGAGUTGGAAUCCAG	62833	CTCTTCACUCACCACTATTTCTTCTUCA
314105161	62834	ACAGATTGCUGCTTCTTTUCCAAAC	62835	CCGTGAAAATGGAAAUAGTGGCTCTUAT
314990847	62836	CCCCAACAGUTTTTAGTACCUGGAA	62837	CCTCGTCTTCUTGTAGCAAAAAUGG
315313770	62838	GCGTCTTCTTTTUCCAACTGGTACTUAT	62839	TCTCACACCCCCUTCTCAGAUT
270381671	62840	TCTTTTATCTTTAGCAUCCTGGTCCUCT	62841	CGATATTTGTGGCUGGTGGTTTATAUGA
270552425	62842	CCAGCTGUGCCAAACACAAUAT	62843	GAAAGTACCTGAUGACATGCATTUGT
269928230	62844	AACTACAGAAAAGUATGGGCAUCC	62845	GCAGGAGTATUACCATACAAGGAAAUCT
271401003	62846	GCCCCAGCGUTTCCGTAUC	62847	AGATTGAUGACACCCCATTTAACCUC
270363964	62848	GCAACAAGACAGGUAGCTTTUCC	62849	GAATCAGUCTCTGTGGUGGGAT
270978201	62850	GUATGGGACUGGCAACAGAGAA	62851	GTTACTCTTGCTUGACTCTATGTTCUACT
271383285	62852	CCAACAUTGAGUGAGGCACAA	62853	CTTUCAGGCAGCCGACUAAAAA
316063768	62854	TCCCCGUAAGCAATGTAUCAAAGAAAT	62855	AGAAGGATACAAUGTTTATGATGGAGAUGAAC
317924785	62856	TGAAGGTCTGAAAUTCTAGGGAGATGTUA	62857	GGCAGGAAAGAGACGUAUGAGT
317521238	62858	TGTGTGGAAAUGGGATCTGTTCTUT	62859	ATGTCTATGGAAAUGCAAATGGATCUCA
317368959	62860	TTTCTAAAAAUCAGACAATTACAAGCUAAAGAG	62861	CAACCTATGUGAACGATCCTGAAGAUAA
265045936	62862	TTGATGCATCUGCTTAGAACTTAUCAAT	62863	GAAAUTGGUGAACCAGGAAGACAAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
325168258	62864	TCTTCCAAATGUAATGGAGTCAGCUT	62865	TCACGAAATTCCACUTCAGCTACAAUAT
325155216	62866	AAGAAATTTTTCACUGGGCGATUGG	62867	TGCCTTCAAAAUCAGGGTTTUCCT
325376216	62868	GATTCTGACTACAUAGAACAGGAAGUGG	62869	TTCACUCCCTATCAUCCCAGAACA
320908342	62870	GCATTTCTTAGUGAGGGCAGUCA	62871	GTGTAGTGCTUAAACAGAAAATGCUGT
268095691	62872	CATGTGTTTACCUAGGGTTACTTTCUCA	62873	CACTGGGCAGUCCTTCGTUA
269212961	62874	CGTAGGCAUCCTTCACATGCAUT	62875	CTGCCATGUTGAACTCTTCUGGA
267257255	62876	ATTATCUCCTGCTGUGGAAGCC	62877	AAAGCTCCGUCTGCATAGTTCUT
267949416	62878	CGCTTGACUGCTGATGTUACCAA	62879	CTGAGTAAGAAAAGGUTCCCCACTUA
312684963	62880	GATTAGAAAACGUTGTGTGACGUGAT	62881	TGTGGCCTTAAGUTCTTAACTGCTTUAA
313058432	62882	AGCAACTGCAGAUGACTTTATTCAUCA	62883	CTCTTTCCCUTGTCATGTGUCCAA
327925235	62884	CACTAGTGCUTGAATACCTTTUACAGT	62885	GCAGGATTTCUTGGTCAAAGUGG
263423960	62886	GCACUGACCCGAGACTCUGA	62887	CGTCACCTUAGCGAGAGCUG
230003019	62888	TGCATUCAGGACCAACTGUCA	62889	GCACCUGGGACAACTGGAAUC
222551477	62890	CTGTGTGUCAGCAAGAACAACATTAUT	62891	TUTCTTCTGAAATAGUCAGCACACAGT
222333933	62892	ATTCAGTAATGTUGGGCTGGAGUT	62893	AATGGTCCTCUCCATCACTAUAGGG
225148020	62894	TGTTCCCTTAAGAUAGACTGTGATAUGCT	62895	GTTCCTCCTCCAUTCATTTCAATCAAUT
261939298	62896	CACTGAAAGUGATGAATGGUGCAA	62897	ACUGGGCCAAACCAGCAAUAT
326104575	62898	AGTTGATATTUGGTGGCTUGCAGAT	62899	GAATGAACAGUGACCCAUCCCT
267825756	62900	TTCCTTTAGGCTUTATTGAACAACTCUCA	62901	CCAAGTCAAGCAGUCTGGTAATATCAUT
261633344	62902	CACTTGAGAAAUTGCTGGCCUT	62903	CCAGCTCTTCUAGTCCCAAATTCTUAG
263043229	62904	AAGTCTTGUGTTGAAATTCUCAGGGT	62905	GATAAATCGCGAUAGAGCGTUCCT
266715297	62906	CCATTGUGCAAAAGACTCCCTUAC	62907	TGACCTTGGTUAACTGAGTGTGUC
254197381	62908	TGTGAUATGTGCCCUAGGAGAAGT	62909	CTTACCAAGCUATCCACATCTAUGCT
266957036	62910	TGAAAACUGCCCACCTCTGTUT	62911	CAATCUACAGCCTCACUCCACAC
268613228	62912	TTGACAAGUCATTATGAGTATUGGCACT	62913	GATGTGAGCAAUCTGACCCGTUA
314219003	62914	CAGCCTGCUCTCCACGUC	62915	AGCGGUGGTGCGTCUAC
312732660	62916	CCATTGACUCGCACTUGCC	62917	GAACACCUTCCUGGACACCAT
321163015	62918	GCCCAGACUTACGGCTTUGG	62919	CGAGCCUGAACGGTUAGAGAA
319490696	62920	CTCTTCTGGCUGGCATTTTTCUT	62921	GGTGGCTUCAGGGTGUAACAG
239082195	62922	TCCCCAGGGAUTAAAAATGTUGCT	62923	CATCTGTCAACUCCACAAAATTCTUCAA
262208262	62924	GACACTGTCAGUGGTTTTGCUT	62925	AGGTGAGTCAUTTCAAACATACTUCAGT
238709495	62926	ACAGTTCCUCACAGCCTGTTATTUC	62927	TGCTGGCAAAAUACAGAATTTUAAGCAT
228261140	62928	CTGTTCCCACCCUGGCATUA	62929	CATCGUGGAGTATGCCUCCAA
329436125	62930	GACCACAUCACCTGCAACCAUA	62931	TGUGGAGCCTTGUCACCAAC
266380871	62932	TGTUAGGCCGCAAACCCTUA	62933	ATGGGAAUCCTACAGCATUGGG
262458333	62934	CACATTAAAAGUGAACACTAAGCGAUCC	62935	AAATAACCAAGGCUCGGGAAUCA
263395354	62936	CATAGTGGUGTGGTCTTUGGGAAA	62937	CATGTTGUACCAATTGAAAAGUAGCCA
254555250	62938	TCAGAGTTGUTCTTATAGGGUCGAGT	62939	GACUACACAGCGCCAUGGAA
266144862	62940	AGGCCAGCUCTGTGAAAAAUGAA	62941	AAAGCAACGCAUCUCACAACC
263212525	62942	CCTTTAAAGAUGGAGAGACCCTUGAA	62943	GTGAGTGUAAACAGTAGGACUACCAC
327768532	62944	GGCUAATGATATAGAUGGGCAGGT	62945	GAACCAGTAATTTUCCATGCTGTCTTUT
317230030	62946	ACAGGGTUAAGGAAAATAGCAATGUGT	62947	ACCAGCTTTUGAAAATGGACAGAUAGAT
313884025	62948	GCAACUGAGCGATCAAAAAUAGAAAGT	62949	TGTGGTATTGUGCAATGTGATTUAACC
229747046	62950	CCGGAAGGGCCUCTUCAT	62951	AAAUAGCAUCCGCCACAACCT
314733993	62952	GCATCTTCAAGAACUTCAACCTCTTUCT	62953	CAGACCACACAAUATCACCACCUC
227673791	62954	CCTTCTGGCUCCTTGACTGUG	62955	CATCCGCAGUCTCCAGAAGUT
313047378	62956	CCGTGGACCGCUACATCUC	62957	GCATGUGGACGUACAGCAC
314720259	62958	CCTGGCAGCACCAUGAACUA	62959	CGTCAGAGAUGGACACCUCCA
229745253	62960	GCCUCCCAGGCCATUGT	62961	CCTATGCCUCCTGCCAGAUG
324501516	62962	CTGACTTCCUCTACATCGAUGCT	62963	GTTCACTAAUGCCGTGATGCUG
326037165	62964	AGCUGCAGAAACCTGCUGA	62965	GCCUGGUGCCAACAGCAT
254507244	62966	TTTCUTCTTCAGCAUCACCAAGGT	62967	ATCCAAATGUCCCCTGCATTUAAGA
254008281	62968	TCTGCAUGGGCGTCTCTUG	62969	CTTCCCTUCAGGGTCAGUGG
320054968	62970	AACCAATCATUGAGCACTGACTCUT	62971	TCCTCAGCCUCCGAUAAGCA
226111566	62972	ACAATGACCAAAUTACCAGCTCUCC	62973	ACATGAAATUCAACAGCCCTCUGAT
316898411	62974	AGGAGCUAGGAAAUGCAAGCC	62975	TCACAGAGTTUCACCCCAAAAGTUAA
264657462	62976	GCATACCCAUTGTCTGCAGUGA	62977	AGTGCTAACUCCAGTCTTUGCC
263743122	62978	CATCAAACAAGAGUGTGTTCTGCUT	62979	GTCCTAAATCTGAUCTCACCATGATCUC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267540981	62980	CACTTUGGAGACGGUACGAACT	62981	CCAAGCAUCAGGCCAAATGUAAC
266100059	62982	TCAAUGTTACUGCCCCCAAAGG	62983	TGTGTTTTGACUGTTGCAATTTTCTUCT
267566601	62984	ACATTTTTAGGCUTGACAGGUGGA	62985	TCTGGGTTTTCUCAGGATTGCTAUG
262675831	62986	CCATGTGAAAGUCAAAATGCCAUCAT	62987	TGGAACAACTUCTCAATGCTCCUG
261147548	62988	GCTTTTTCTGUACAATCTGACGUCCA	62989	CCGCTGCAAAAUGCTACTCTATUAAAAT
268451768	62990	GACUGGAGTATAAUGCCCAACGA	62991	TTGTTCTTTGUAGAGCATGCTGACTAAUA
258576289	62992	GGAGTTTATTCATTUGCTCCTCTAGCUT	62993	AGGCTTUACAAAGTTCTCUGCAAGA
267431315	62994	AGCACTTCAGCUGATTATGAGUGT	62995	ACATGGTGGUGGTAGTTGATGAAUC
268831040	62996	AAATTTACCAACCUTCAGGATCGAGUAG	62997	AAGCATGGAAGUAAATCTCAUGGAACA
324799479	62998	AATTTTACAAAGCCACGUTACTGGAAUG	62999	CCTGGACTACUGTTCATTTTCATUGCT
318441443	63000	GATGCAGTATUGGCTCGAGTGUA	63001	GCAAGTCAGGAAUTATTTGATTTUGCT
292121619	63002	CCTCTCCCCCUTCCCGUT	63003	CCUCCAGAGCCCCGATTTUC
289801314	63004	CACCTGAGTUCATGATCGACACUC	63005	GCCCTTCCUCACTCAGUACAC
303966711	63006	AGCCTTAGGACAUCTGGGAUCA	63007	TCAAACCCACUGCCATCTUCAG
302694084	63008	GCCTGGTGCCUGACACATTTUA	63009	CCACTGCCTTUCTCTCATTCTAACUG
257483443	63010	ACAAACACGATTGUTTTGGCTTAATCUC	63011	TGCTGTCTTAUGCTTCAGTGCTTUA
259124183	63012	CACAGTGATUGCTGGTTCCATUAA	63013	GTTTGTGTTTCUCCTAGGGAGTUAAGT
255728133	63014	GCCCAGAUACTGTTTTCAAUGCAAA	63015	GGGAAAAAGAAAACCAUTGTGATGAUAA
256020848	63016	TGACTCCGGACUACCTCACUT	63017	AGTAATAGTCACAUGACACGTTUCCC
267756432	63018	ACAGTATCCCAUGAACCATTGUGAA	63019	GGAAGAAAGAAUAAAAUCACACACACACA
267473235	63020	GAGGCAGGUTGATGTTGUCAGA	63021	ACUGTAGCTTCUACCGAACCAGA
265929310	63022	ACATTAAAACUGGCATCTGTTTCCUCA	63023	ATTAGAGUAGGAAAGAGGGCTUGGA
316330669	63024	GGGTCTTCCUCTTCTAGACCUACA	63025	CCCAGATGGUCCCCAATUAGAG
317239450	63026	CUGAAGGGCTUGAAAGGAAAGAG	63027	TCATTCTTGAGGCAUTTATTAGGCUCAT
316776520	63028	CAGAAGCACUTGCCCCCAAUA	63029	GTGTACCTAUAACTGTTGTGAUGGACAT
316816541	63030	AACATTGCTCUCTAATGGGCTGUT	63031	GAGUGAAATTCCUGGAGAAAGCAC
332459508	63032	CACACCCACAGCUAGAGGTUC	63033	AGGGAGGGUTCAGTGUCAGT
314767331	63034	CTGGGTGTGAUCTCGAGAATUGA	63035	AACGTGCCTUGTTCTTTGCAUAAG
315036406	63036	GCAGCGTUACATGGAGCUCT	63037	CCAAATGAAAGUCAGCTATCGCCTTUA
313197004	63038	GACTGGUACACGGUCACACC	63039	AGAAGCCCCAAACCUTGCUAAT
313824392	63040	CCCAGGACUTTTCUCCAGGAC	63041	ATCCCTGGACCCUAATGATTTUGAC
312731126	63042	CCCCGGUCACGGATGAUG	63043	AACCCCTCAAGUTTAAAAAGGUGAAGA
317706783	63044	TGAGGTGTCAUCCACAATTATCCTTTUT	63045	GAGGAAGAAAACUTGGAAGGCTUG
316083875	63046	TCTTGGCTGAGGUCTAATACAGUAACT	63047	GCCAATAACTUTCCTTACTGCUCAAAC
315707441	63048	GTCTTTUACCAGGTCCACAUGAGA	63049	TGAGTGUACAGTGGATAUAGAAAGGACAA
316370047	63050	GCCTTGGCUTAGCGATGTUGA	63051	ACCAAAATGAACGACUTTTTCCTTTCUT
318873190	63052	CCATCAACAUCGCCCUGAAC	63053	CTCCTCCUGCTAGACTGUGAAC
313065701	63054	CGATGCAACUCTATCGUCACAGT	63055	CCGCAAATCCCACUAGCTAAATATCUAA
313293684	63056	CCTGTCACCUTTAGCCCTGGUA	63057	AAGGGUAAGACCTCGGUGGA
320438365	63058	CCAACAGGCUCACAGAGAAGUG	63059	AGTAATUCACCAGCTCCAUGCAG
317478871	63060	AGCCTCATCTUCAAGCTCATCAUT	63061	GTAGCAGAGCUCACAGAUGGT
254285816	63062	GGGCCGGAAGCUAAACTUGT	63063	GGCATCTUCATCGGGTTUCAGAA
288659903	63064	TAAAGTGAATATACCUGGAAATAACTGTTTUGT	63065	AGCTGCTCCAGUTGATGTACUAAAAG
333092002	63066	GGGAGGAUGGTTAATGTTGCUAAAAGAA	63067	CATCTTGAAAATGUCTCTCCCTTCAUCT
320353838	63068	GTGATGTCTACAAUGATGGGACUGT	63069	CCTCTCCCACAUGTGACCCTUA
313058164	63070	CCCGCAAGACCCUTGACUC	63071	GGGAGGAGACUATGGCAAAGTTAUC
320488133	63072	CAATGTTGTTACUGGAAATGTTCTCUGG	63073	CACTTCCCAACCUATTTTCCTGTCTAUT
326679253	63074	ACACCTCATUCCTCAGGGCUA	63075	TCCAATCCTTUCCCCTAATTTGCUT
326605692	63076	GGCTGAGTTGCUATTTGTCTTCTGTAUAA	63077	CACCCUGGGATGTGCAUCAA
328119468	63078	CTTACTTGGTUTAGCCCACCUCA	63079	TCGTACACAACAGUGTGGGTUT
328414947	63080	AGCCTCCTUCATTTCCCTACTUCT	63081	TGGAGGGUGCACAGAGAGTTUA
327476478	63082	AGCAAAGAACUGGGAAGGGAUT	63083	ACACTGTTCCUAAAGCAATTACUGACA
328246168	63084	CAAAGAGGGAGGCUTGUACACAT	63085	CTTTCTGAACAAUCACCTCAACAGUC
324280057	63086	AGGCATTCUGGAAGTTTTACACUGT	63087	AGTTCATTTACCTUGTGATTTCTTCCAUGT
325270204	63088	GTCTGGTACTUCACCACTGGUT	63089	GGCAGGCUTGTATCCACTUG
324702041	63090	TTCTAGUCATTACTTTGUGAACCCCAAG	63091	TTCAAAAACTGGUTGGGCATTCUG
323626254	63092	TCAAATTACTAUGCTGTGTTCTTGUCCT	63093	GAAAAGAGTGTGUACTTAGGGTATGUGT
325722046	63094	GCUCCCCACGAGAAGTUCAAG	63095	ACAGGTACCTUGGTGCCTTACUAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326685386	63096	TCTTTGUCTTCTTTTGUCCACACACT	63097	CAGACCTTUCTGTTGGTAUAAGAGGAAA
235692136	63098	ATTCAAAGAGGAGGAAUTCTGAUCACAG	63099	TCCATTTCUGGCAATACAGCACUAT
263469205	63100	CCCGTUCCCCTTUAAGAGCA	63101	GACGTTCUCGGCAUAGAGGAT
265606363	63102	AACCUCCCCAGUGCGAAG	63103	CTUCAGACCCGCCAGUGA
259921108	63104	CAGGGTGCCUTAGGCTAGUT	63105	GCAATGCCUTGGACCTUAACCT
268938434	63106	CAGUCCAGCCAGGAGCTATUG	63107	CCGATGCUGACCTCAAACUGG
267836253	63108	AGGGAACACUGCCTCTCTCUAA	63109	CCCATGTGCAGAAUGGGATTCUA
328092151	63110	GCTCACCUTGTCTGUGCAAC	63111	TCCGCCCACUTTTATACTCCTTTUC
326956622	63112	TTCGCAGGAUGGCAAACUCT	63113	CACTCCAGAACUGCCTGACTUC
325779223	63114	TCTTTGTCTGGCUTTGTTACACTAUCA	63115	GCTACTGTCAUTCAGCGTGCTUAT
323921298	63116	CAATGAGCUGGACTTTGTUGGG	63117	TGGTGAACATGUACATTGCAGTCAUA
267597478	63118	TGAGAGCCUATGATTGUCCAAGGA	63119	CATCGUCACCCACTTTCCCUT
261112025	63120	CAGAGTAACAAAAAUCACCTTUCAGCAA	63121	CAUATTATGTCAUCGCAGAGAACGGA
268878120	63122	CTGGTACUCCTGGTCUGCAAG	63123	CGATTACTTUCCAGGAGTGTTGCTUT
265211627	63124	GGCUGCACAGACATTTCTUGGA	63125	ACAGTCUTTGTTTCTUGCAGGGT
267661332	63126	AGAGCCTGCUATTCAGGACUCA	63127	GCTAAGCATGAAGAUTTCTGTGCATTUT
265774180	63128	CCAGCAAUGTATAGTGTUGCCAT	63129	CACTGGUAGCCTGTTAAACTUACACA
263076240	63130	GCAGAUATACTUACAGGAGCACCCT	63131	TGGTGGCCAATUATCTTGAATCTCAAUT
268026085	63132	ACTAATCTGTTCUGGTTTGCTTGUGT	63133	TUGTTTTTAATGUCACAGGGACAAAAGG
267022975	63134	TCCAGCACAUCCTGGCATUC	63135	ACAAGATGGCUCACCTTTTATTTTCUCA
316107130	63136	TCTAAAACTAACUGGCCTGTTGTGUT	63137	GTCTTCAAAGACCUTGCAAGAAGTACUA
317124616	63138	TCTTTTGAAGGAGAUTTCAAGGCUAACA	63139	GTGATTCACCUGAAGAGACAGCUT
317435035	63140	CCTTTCATUGTTGCATCUCACACA	63141	CGAGTGGCUACAGAAAAGTGTCTUT
267689875	63142	TCCTAGAAAUCGCCCUCACCT	63143	CAUTCTGTCCUACCGCAGAGT
237541899	63144	CACAGGTUAAACCCCCUCACA	63145	GAGGGTACTUGAATCTTCAGAAGTUGAA
235247006	63146	ACCTCCCAAUAGCTGAGATCGAUAA	63147	AGCUGGGAAAUCCGAGACAAAT
269359408	63148	TTTCTTGUGGCCCCTUGACA	63149	GCTTCUCGAACATGAGGUCACT
258026832	63150	GCTACACCACCUTCACTGUCT	63151	GAGTAGAUGTGGCTGAUGCACT
333666070	63152	GCTCTGCACAUAGTAGGCAUCT	63153	ACTCTCCCAGUGATCTCAUCACA
332469047	63154	GGCTGAAGCUCATTTCTGACAUCA	63155	GGACAGGGAAGAGUCTATUACAGAAAAT
233202774	63156	GAUGTTAATGUGCACCCCACAAA	63157	GCCCCAGAGAAGUAGCUGGAT
323505894	63158	GCCATUACCTTCAGUGAAGCAGT	63159	CCCTAAGCUCCTGCAGACUCT
313144289	63160	CUTCCUGAGAGCAAAGGCAGT	63161	TGCCACTCACUCTCCTCTTCUT
312975923	63162	ACAGAGUGGTTTCUCCCAGGAT	63163	CUCCAGCACATTUCCAAGAACAAG
261453537	63164	GAGACAAGGGUTTCCCAGCUT	63165	TGTGGCTTATGUCTCATGTGTCATUC
262270788	63166	GGCCATTCAUTCACCAGUCCAA	63167	GGATGGUGCCTGTGTGTTUCA
332052854	63168	CCAGCCCUTTCTTTCUCACCA	63169	GAGTCCAACCCUCGTGTCTATUT
332104370	63170	GGGTGTCUCCTGGGAUCACAT	63171	CCTAGGAUCAGGAGCTTTGUGAAAAA
332120790	63172	ACTTTCCCCUGTCCTCCUCAT	63173	GGCTCTTACCCUTTCTTCTTTTTCTUG
325588969	63174	TGTCCCCGAACUCCTACAUGA	63175	CATTTACGUTCACGTCUAACACACAAAA
329107786	63176	CTTGAGUCAGACGCCCTUCAT	63177	GTCTGGCTCAUTCCACGTCUC
328779126	63178	GGGACUCCTUCACCAAGGG	63179	CCCACCGUGTGGTUGCT
325533232	63180	CCAAGTTCCUGAAGATAGCUGAAGAG	63181	CCAGGGUCCCTGTAGCUG
325237849	63182	AGGAGGACUCACCCGCUAA	63183	GGTTTAGGAACUGTGGAGTCCUG
264395624	63184	GCTGAUGCTGGTCUACAAGGA	63185	GCTGUCAAAGCCCAGCAUGAT
258312972	63186	CTCCUCCACCGAGTCTTCUCT	63187	GCTCTCCUGCTGGAGGCTUA
318537329	63188	GTGCATTTCUCCACCACATTUGT	63189	TGTGCTACAATAUGTGCTGTTTCTTTUG
332881524	63190	GGTTATTGTTGAAUGGAAACGTGAUGA	63191	AGTGTGGAAGCUATCTGCATTTGAUT
333365408	63192	CGAGGTGCTUGTCTTGCTGTUA	63193	CATCCATGCCGUTAAGAATTTCATUCAA
332916320	63194	CTGAGGAUGACAGTCTUGAGCA	63195	TGAACCTCTTTUTCTCCCCGTUT
333725677	63196	GAACCAGUGATTCGAGUACAACCT	63197	TGTCTUCAGCCTCAGUGGAAAC
332888381	63198	TGTAAGGACUATGCCCACTUCCA	63199	CCTGAGGAGCCACUGTCTUCT
333191860	63200	ACAAAGCAAAAUGTAGAGACUGAAACCT	63201	CAGTGCAUGACTCTGGTCTUGA
323999787	63202	ACCTCCCTUTGCTTTGTCUACC	63203	ACTCCGAAGUAGGCAGCTCUAT
323471876	63204	GGAGATGUCCAGTGGGATGTUG	63205	TGGCTCCUTCGTCTTTUGCAAT
269299954	63206	AGGAAACUCCTGTAGACUCGCA	63207	GATTTCATGGAUGAGCTGATGGACAUA
264079402	63208	TGGAGAGAGAAGCCGUGUAGA	63209	CTCTTCACTCUGTGTGTGTCCUG
268052362	63210	CGTCCGUCCAGCUCCAG	63211	CCTTGTTCTUGGAGGGCAACUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267926049	63212	CTTGUGACCCAAATUGCCAAGA	63213	TCTGTTTUAGAACGAGTUGCGGAA
320278301	63214	GACTACCUACACATGGUGCACA	63215	AGGCTACUGGTCACACTUGA
289949500	63216	AGAAAACAAGAUTCTUACCCACAGGAG	63217	AATCCTGAGUTATAGAAGCCUGAGAGT
290375708	63218	CAGGTTCTGTAGCUAGAAAATTGTGTUC	63219	GATAAGCTGCUAACAATGTCACAAACUT
289949692	63220	AGCTTTGTGUTGGGCCTAAUGA	63221	AACAGUGACCACACCCTTGUT
320155732	63222	TTGCCACTATUGAGGAAGATCTAAUGAAG	63223	ACAGCTCACACAAUGTTGCACUA
224519463	63224	ACACAAGCAAAGUCTCTATGGTGAUT	63225	GCGTTCTCTCUCCAAACTTCTATCTUT
224568908	63226	TGAAACAGAAUCAGAGCAGCCUAAAG	63227	CTTGCCACAGGUGGAGGUAAT
222817672	63228	CTCGAGUAAGCACTUGGAGAAGAA	63229	CGGTCTGAGAAGUACTATTTGUGGGA
327073920	63230	TCTGTCACCCAGUTGGTAUAGACA	63231	TCAATATTCCAUAGCCTGTUCCCAAAG
326689926	63232	ACCTTCTCCCUCCTTAATTCCCTUT	63233	CTCTCUACCCCAACCCUCCA
324248731	63234	GGGTTGUGTAATGGATUCGCT	63235	CCATTAATCAAUGCAAACCAAAGUCAGA
332093136	63236	GGTACCGCUGCTGCTUGAA	63237	CGTAGGUCAAGCCGCTCTUA
237633876	63238	GATGGAAGCAGUGACCUGGAT	63239	CCCATTAAGTGGUCTGTATGTGAGUT
238539831	63240	TCTTTTGCTTGUCCCTGATTTUCCT	63241	GGGTAAAGTGATUAGGGCAGATGATACUA
266278778	63242	AATGCTGCCUTTGAACCUCCT	63243	GTTTCTGAGCGAUGTTGGTGTUC
259206149	63244	GCTTGCCAACUTCAGAGGTUCT	63245	CAGAGAAACTGUAAGGCAAGCATCUA
268767880	63246	CACTTTTTGTAUAGAACTTGCACAGUGA	63247	CAACAAATCAGCAAGUCATGCAGTUAAT
268499339	63248	GCATCTGCTTCUCCTAAGGAAAAAUACT	63249	CAGTGATAGCTUTTTCTGCTGCAUAT
268527094	63250	GGGCCACGGUATTCGCTUAT	63251	TGCATCTTTCTUTTAGTTGCAGAUAGGT
317169623	63252	TTGAAAUCCAATAGUGCCCAGGT	63253	CTAGTUTTGTCTCCTUCCCACAGT
331947764	63254	CCCCACUCACCCGTGAUG	63255	GACTCCTUCACCGTGCAGUA
331563423	63256	GGACCAGGAAGUGGTCAAACUG	63257	CCCACACGUGTCTGUCCAA
266407806	63258	CCCUAGGGAGAGAGGAATUGG	63259	CACCTCTGACCUTGCTTCACUT
326830507	63260	CACGGGCUACCAGAAAGGTUT	63261	CCTGTCUGAACCCCGCAUC
324157291	63262	TGGCGAGAAGAACAUGGACTUG	63263	GUGGAGTTAAGAAGAUAGGACAGAACAG
314051780	63264	GCTATCATTACUCAAGATTCCCAUCACA	63265	CCCTAGTUCCTGAACTCAUCAAAGAA
312816834	63266	ACTCTGAAAAGCUAAACTGGTCAACUT	63267	TCATGTAAATTGUCCCTTTCCTTGACUT
312932682	63268	CTGGCAATUCGAGCACTTTUCA	63269	AGTTGCTGTTTAAUCATGTTGCTGTTUAT
272335301	63270	ACATGGCACCAUAGTCAAAGTTCUT	63271	GACAUCAACCTCCAUGGCAAC
271907968	63272	CAAACCAAAGCCUTACCAATAUGCC	63273	TGCACTGTTAGUATATCCAATGCCAUT
271900712	63274	CTAAUCAGCACAGTGGUCAGAGA	63275	GTGUGATTTTGAGTTUGGGAGACC
271832752	63276	CTTTTGAUGTGGGCUCCCACT	63277	GCCCTGTAAUGTTTATGCGATCUAC
317955022	63278	CGAAAGAACUACCGTGGAGUACA	63279	GGAATAATTGUGGAAAGCAGTTTCTUCA
316852244	63280	CCTGGTTGGCAUTTGCAAACAUA	63281	CCAAGATGAAAAGUGATAGTGCTCAUGT
263032419	63282	CCTGAGTCUGGACGCTUAAGAC	63283	AAAGCCCACAGAGAAAUTAUCCAACT
325619256	63284	AGACCGCGGCAAAGUAACTUAA	63285	CAAGGGCUCAGACGACUCAG
323711616	63286	CCTGATTTTGTUAAGTTGCTGCTGUT	63287	TTGAGGAUAACCGTGTTGUCCAG
320664297	63288	TGGGCTTGCUTTTCTGCAGTUA	63289	TTTAAGGATGTGCUGTCACACAGAAUAT
321173401	63290	AGTTTGCAGUGAAACACCTAGTCAUT	63291	CCTCTCAGCAGAGAAUGTAACTTTAUGT
257673332	63292	GGTGAUCCAGCAGACCAUGAG	63293	TTGCTCTTCUCTGAACTCAAUGAAAAGA
268462568	63294	TGCAGAGACUTGCTTUCACCAA	63295	GTGGTGCUGAGAAAGATAAATTGTUGT
267764718	63296	CAAAAGGAACCGUTCATATATGUGGAA	63297	CCAAAATUAGCCAAGTAGAAAUGACCCA
269354577	63298	TTCATTCATGUAGGCTTTCTCTTTGUGA	63299	CCTCAGCUAACACAGTATAAUACGAGAC
265195269	63300	GTATTTTCCCCAUTCTTGCCTTGUAG	63301	GGAGTAAGTAGUGACCTCTGACATUCAT
267853976	63302	GCTTCUGGCCAAGGTCCAUT	63303	GCTTATAGTGAGGAUTTGCCAATTTTGUG
269217310	63304	TGTCTTGGAUGACATTTUGGAGAAACT	63305	TGCTGAAGTCTACUATAGCCTCACTTUA
313422189	63306	AGAGCAGTAUGTAAGCTGTTTUGAAGAA	63307	CGATTAGGUTCATCGTATTUCAACCAC
326469389	63308	GGAAGTAAACACAAUCCTCCCTCUG	63309	CAAGTAACACAAUTCCTGGTCTUGAG
232082958	63310	CCCTGATGUGGGAGGTCUCAA	63311	CCCACAGTCUAGAAGGGTCUCA
230013035	63312	GAGUAGTTGGTGUCCCAGGAG	63313	TATGGGCAGAUGGTTATGGTGTUAG
332257145	63314	CATTGGCCCUGGTGGAGUT	63315	CCCTAACCAGCUCTGAGAUCGT
230661476	63316	GCATTCCUGAGCCGTCAUGT	63317	GGAATGUCCCAGACAAGATCTUCA
222233508	63318	GGGAGCUTCCAGTUGAAACAT	63319	AAATAAGAACATUCTTCAGACACUGCCT
222533459	63320	CTGAGGUTTACTTCUAGCAGGCAA	63321	TTTCCATCUCACAGACCTTGCTUAG
223544861	63322	CAGTATCAATTTUGTGCACAGAGGUT	63323	ACATCTTCAGGTTUTCTGTCTAATTCCUT
333800077	63324	CATGTCTCCUCTGATTTCTCCUACCT	63325	CGCATCAACUCTGTCTGTGUCA
222612254	63326	TCAGACUGGCGAGGTGAACUA	63327	TGTTCTTGUATTCTCTGTUCCAAACAGT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318454139	63328	CATACTGTTCACAGGUATGACAGGUT	63329	TGGCUACAGCAGTCTACUACCA
321088780	63330	GCCTTTAGGCACUGTGTTTCTUT	63331	CCTGTGTGCUACAAGTAGTCUGG
321121259	63332	GGAGGTTGAGAUTTGCATACTCUGAAAA	63333	TGGGAATCACUGAATCTAAUGAAAACGA
258133019	63334	GGGAAAAGGUGCCTTTGTUAGAC	63335	AGGGTGCAATAAGUGTCCTTGAAAAUAT
325069488	63336	GGTGACCAUGATGTCUCGGAA	63337	GGGCTTGTTAGAUCAAGATGTAAACUCT
324628239	63338	TTTCAGACGAUAATTGCTACUGCCA	63339	AAGGAGTATCAGUGAAATGAAGCTUGT
266711528	63340	GCAGTCTGUCCTGAACCUGAT	63341	GTGAAAUACCCCCAAGCGATGUA
258624818	63342	GATGTGGGCAUGGGAGGAAUA	63343	AAACACAATCUACACAATAGGACAUGGAA
267792121	63344	CCAAGAGAUGAGGATTTCATGTCUGT	63345	GGAACTCTUGGAGAAACCAGAAAGUAAA
312881912	63346	GAGGCCUGGGUAAAGCAGA	63347	GGGCCCUGATACTGATTTUGGT
314006299	63348	CACTACCUCCCACCACATUCC	63349	TCAACTUCCGCACCACCUAC
321173344	63350	GAAGACGAGGCAUAGAUGCGA	63351	CTGACCGTCCUTGGTGTTTCUT
316671913	63352	GAGGGCAAACAUGAGAGUACCA	63353	GCCAAUGGCCGTTCTGUCT
239084035	63354	CAGTGGAAACTTCUACGTGACTTTGAUA	63355	AAATCTAACATTCAGAUAGAAAGTACATTCUGT
239543300	63356	TGTTTTTACAGAGGUAAATACCGGATUGT	63357	CCAGTGTCCAUCCATAGGTTTAACUT
262978349	63358	GTCCAACAATCAUCTACTGTCCTUCT	63359	CGGAGAGCAAUGATGATTGAUCCT
238916569	63360	GATGTTTTTAAUCGACAGGCACCUT	63361	GCCAAATTGTTGUCTTAAAAGAGCAUCA
264777716	63362	CATTCTAAGGAAAAAUGTGGTATCUGAAGC	63363	ACCAGTAUCTTGTTTGTUGCCAGAA
230738248	63364	CACATCCCAGUTCTGCAGTUAGAG	63365	CCCTACCUAGACCCTCCTAACTTUT
256908810	63366	CAGCAGTGTGUCATATCCATACUCA	63367	GGTTCGGAAUTCCCTTUCCCA
256987892	63368	TGTGAAACAGCAAUTTGACUGGAAC	63369	AAGGGCATTCUACATTGTACACTTUCT
327692981	63370	ACACCTGTGUTGCTCATGUCA	63371	GAAGTCTGAAGATUATCTCAGCAGCAUT
327774331	63372	TCAGTCAGGAAUGGTTTGATCAUGG	63373	CATAAGCTUAGCAAGTGTUCAAAGAAGA
313884449	63374	CTACTTCAUAAACTAGGCCUGCAGT	63375	TGCCTTGAAGUGAGTAGGAATTUAACAA
313464851	63376	ACTCAGATAUGGACCTGCCAGTUA	63377	TCAGCAAACCTUAGAAACTGTGCUT
320406287	63378	CACAGTCAUCCTGTTCCUGAACT	63379	GCTCTTTTCUGAGACATCTGTCTGUAAC
326754230	63380	TTCTGGACTUGAAGACTGTCUAGAAT	63381	TCGTAGCAGUGATCATGGUAAAAGAAG
268808740	63382	GCCTUGCTCATCUAGCCCAA	63383	CCTCACUGGGCCTGAAUGAC
267728148	63384	GCCCACATATUTGACTTAGCCAUCA	63385	CTTTACGTCTUGCAGCAGCUC
316203546	63386	CGUATGCTTCAAUGCACCCAT	63387	TAAAGCACCCUCAGTGATTTCTAUCC
320472369	63388	GTTATTTCCATTCUTCTCCATGATTUGCT	63389	TCACACAUAAGTGGAGGUGCAAAA
315658510	63390	TTTGTTTTGUCTTCCAGUGGACCT	63391	TTGGCCTGAUAGCTTTTAATGTCCTUAA
326648955	63392	GTATTGTAGGUCATGTGGGCUGA	63393	CTGCCAGUCCTAAGTCUGCAA
278236801	63394	GTCAGUCGTCCAGUGCCAAT	63395	CTCTAACGGCCUTCTTTTCATTTUCC
264173889	63396	GAGGAACCAGAUGTCCATGUCA	63397	CTCCCAAGGACACUTGUAGCC
266374592	63398	TAGATCTAAAAGAGAGCUCCTCCUG	63399	TTGCCACTGCUGATGTACTTTATUAACT
267319199	63400	CCCATGCAGCAUGACTCATUC	63401	GGCUGGAGAACCAACTTGCUA
260671943	63402	AGCAACUCAUGCAGAGCGT	63403	GAAGTCAUCCCACCCGCTAUG
267548200	63404	CCTACCACUGCTACCAGUCAGT	63405	ACAGGUAAACCCGTGCUGAG
262613924	63406	TGCCCCCUTCTAGAGCCUAAA	63407	CGACUGGAGAAAGCAAGCUG
319492634	63408	CCACACAGAATUCAGTAAAACCCAACUA	63409	CTGAGTGUACAAAGACUGCACGA
319884877	63410	CCCTGCCTTGUCATATATTAGCTGUT	63411	GATTCCCUGGAAGTGGTCCTUG
318737966	63412	AAATATGCTCTGUACCTGTGGAUGAAAT	63413	CACAACAGTTUATGCTGAAGAUGCAG
320129797	63414	GTTATCAGAUACAAACCAACAAGGAUGGA	63415	GCGGCTGAAUGAAACTCTCTTAATTUT
320721143	63416	GAGTGCCCUGATGAAGAAGUGA	63417	GGAAGAGGCUCAACTATGAAGAUAAGAC
263128703	63418	TCTGCUCAACGAGCUGGAC	63419	GCGTUGAAGCGGTACGUGAT
266679991	63420	TGCGCAGCUACTCCCTTTUC	63421	TTAGCCTGUAGGACTCCUGCT
255634797	63422	TCACCATGAUGGCCACUGAC	63423	AGTAGCTCTGGUTGAGACATCCUT
257757036	63424	CACCCCUACCCCTGGCUAT	63425	CTGGGAGACUGCAGCUCT
263903339	63426	CACCAGUGGAGCUCAAGGG	63427	CCAUGATCACGUCGCGAAGT
313126531	63428	TTCCUCAGGACCACCTTCCTUA	63429	CAGGGTGAGGCUCAAGTTGUAG
312797232	63430	TGCCCATAUCTCAGGTTCUCAGA	63431	GTTCUGGCTCTTAAUCACAGCCT
312934488	63432	GCUGCCCACACUGCCAT	63433	CCCTUCACACTCUGCACCAA
313338426	63434	TCAAATCTGGGCCAUCAAGAAGUT	63435	GTAGGGAGUGGGACTGTAATUGG
264946248	63436	GTGCTGCAUAGCCTCCTTCUA	63437	ACATCATTGTGUTTCTCCTCTGUCC
312897655	63438	GGGAGGAGAAGUGAUGCGT	63439	CCGGCACCGCUGAUCAT
316480986	63440	GAAAGAAAACAUCAAGCGTCCCAUA	63441	GATCTGTCCACUCCTGATGCUG
327393407	63442	TGAAAGAGGGCCAUGUGGAAAG	63443	CCTGAAUCCCGAGCACACATUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328003793	63444	CCCAGGGUGATCTCUCCAC	63445	AGGCATUCCCGGCATCUC
240947991	63446	CAGGGCCAAAGAGUCCAUCAG	63447	TGAGCCTTTTUCCCTTCTTTGUGT
333440704	63448	TCTTTTGCCGGGUCTGCAUT	63449	CCTTGTGACTUGAGATGTGGTGATTAUAT
333508729	63450	CCTGGCCCAUGTTCCTGAAATUA	63451	ATAAACTTCTGGAGGUATTTGGAGGUG
315414608	63452	CCTGCAACACAGGUTATCTUACGA	63453	ATGGGCAAUAGCTUCCAGAAGG
312964350	63454	CCTTCUGCCAGATCACAGUGG	63455	CTCTCCCGUTTCTCTGAACUACA
264409284	63456	TGTGGAAAUAGCAGCAGCUGA	63457	GGAAGGTCCAUGGTATGGTTUCT
268089883	63458	CTGGCTAAUACACGAGGCCUT	63459	ACTGTGTCUGGCTGCCTTAUC
257887021	63460	GACAGGTUGATGAGGGUCCAG	63461	CTCGCTAAGUAAGGTGGCTUCA
315128252	63462	GGTGAGAGGUGACTGCTGTTUG	63463	CTTACCAUGGCGACAUCGG
313294319	63464	CCCCCUGGAGGCTCTTCUT	63465	CACUCAGCCCAAACGUGGA
313012870	63466	CCTACACGCUGGAGGAGTTUT	63467	TCAUCCUGGCAGACAGAAACAG
328270927	63468	TTTAATGAACAGGAUTTGCTAGUCCACT	63469	CCCTCTATTTAAAUCCAATGAGCACGUT
223273229	63470	ATGGGAAUAGAGCAAAATATGTGUGAAGT	63471	CATCTGGCAUCAAATAAGUGGAGAGA
222325241	63472	CCAGACAGCCGUGACTUACT	63473	AACATAAAACACUCAAATCCTTCTAACAAUACT
223676930	63474	CCCAGCCUAAAACTTACAUACACAGAAT	63475	CTAAGTAACTATCUTAAGGGTTGCUCCA
329887079	63476	CAACAUGGCCGGTTAUGCAC	63477	TTCTGCTGACUGCTCATTTAUCAAGAT
332538899	63478	GCCCTGCUCGGATCTCAUC	63479	GGGACATGAUCTTGGTCUCCAC
332970686	63480	GGAGTGCUGGAGTTATTTAGAAUGGT	63481	GCUGGTACUAGAGAGAGCAGGA
333227945	63482	GGAAGGTUGGCAGTTTCTGAUGT	63483	ATTTGTUCCCACACTTGGGUCA
332409110	63484	TTTGGTTCUTCATGGCUCCCA	63485	GTCCCUGCAGTUCACAAAGG
319435431	63486	CCTUCGGCAGGAGGGAUT	63487	CUCCACCUCAGACCACCAC
332611390	63488	CCAGGAACACAGGAGUAGCAUAAG	63489	CAGCCAATATTUCACTGGGCTAATCAUA
333185287	63490	AGAAGCTCCCUATTCATTTGCUCAA	63491	TCTTCACCACAACCUTCTCAAUAAGAT
333369798	63492	CAGAGTCATCUCCCCCATGGAUA	63493	GTAGTGGCTGAUTTAAGAAGATGAUCCT
332346346	63494	GCCAACAGGACCAUTCTCUGT	63495	TCAACCATTTGUGAATTTGCTGUCAAA
332632401	63496	ATTAGCTACCUACCCTGACUCGAA	63497	GTCTTTTTCTTTUCAGCCCTGTUCC
333490847	63498	CATCACGGCUGGCAUAAAGAG	63499	TCCGCAGAACGAUGTCTTTCAAUAT
234764991	63500	CACACTTTGTCTUTGACTTCTTTTTCTUCT	63501	CCTGTACACAUGAAGCCATCGTAUAT
318960929	63502	GCCGGTTTAUCACCTACTCCTUA	63503	GUGACCCAAGTGUGAAAAAGACAG
278211317	63504	ACTTGATTTATATTTUGTCAGTCTATAACUGGT	63505	GGGATAACAUCTCTAATGCAUCAGGAAA
278139024	63506	CGGAGCGUAAAAATGUGCCAA	63507	GCUGAGCTTTGAAAAUAAGGAACGAAAA
280297283	63508	AGTCAACTAAAAAUACATGAGCCAAACUGA	63509	CTCTTACTCAACAGAUGTTCGTCTCAUT
261795216	63510	CCUAAAAGAGGCCCUGAGCAA	63511	CTCTTTCCUCACGACCTCTCUCT
267865639	63512	GCCCUTCCTUGAGGGAACAAT	63513	AAGAGCUCCAGGGTTTUAGCC
262245630	63514	CUCAGCCACAGAGAUCAACACT	63515	CCCAAACCAUCCGCCUCAT
259085428	63516	GCTGCGGUCCTAGTGGTCUAT	63517	GGATTGACCTGGUATCCTCATTTTACUT
315895795	63518	TGCAAAATTTCCUGTCTAATAGATGUACCT	63519	AAAAACACAACGGAACCUACUAAGAAGA
319281563	63520	AGCACAATAAUGGTTTTCTGUACCCA	63521	GTGTGCTCUCAGATTGACTTUCCAT
265183192	63522	GGUGGAAGAGAGTUGGGACCT	63523	TGTCCUCAAAGGGTTAAAATGUACAAGA
264127876	63524	TGCTATCATACGUAGACACTACACCAUA	63525	GATGTTGGUTATAACTGAAUGAAAGGGAAC
257777330	63526	ACCTCCATTTUTCACTTGTACTUCACA	63527	GTAGAGCCUCCTGAAGAATTUCAAGA
238240105	63528	ACTAAATTAGCAUTGTCTCTGAGUCCAC	63529	GGGAACGUCAATATCGCAGUCAA
316464145	63530	AGAAGTCTCCTUATGACGCAGCUA	63531	GCTTAACGUGGCAGAGTTGUG
331017229	63532	CAGAACAGGAGUGCACGGAUA	63533	TGCTACTGCAAAAGAGUTAGCACTAAUT
240874670	63534	AGCATAAAGTAAGUCATCGAAAGCAUCA	63535	CGAAAAGACTTCTUGCAGTGTAAACAAUT
333744376	63536	ACATGGGUGAGGAGGAACUCT	63537	CCTTCCCTAUTCCCACAGGUCT
333820349	63538	GAAGAGAGAAGCAGUAACCGUCA	63539	CCGCGCGCAGUCTATTATTTATUAAA
333626195	63540	CCTGGCAUCCCCTUAAAGGAAT	63541	GTGCTGATCUGTCTCTCGAATUCT
332840430	63542	ACCCUGGAACAGAATAGAAAUGCC	63543	TTTTGCCTGACUGATGTTCCTCUT
313244797	63544	CCTCCTTCUGTGAGGACUCCA	63545	ACCAGGGACAGAUCTUGGACAT
313985222	63546	GCTCCCGUCAGCTTGUAGAC	63547	GCCTCCAUTGATGACUCCGA
313510273	63548	CTTGAGGUCAAAAGGCCUGGT	63549	CCTCTTGACUCTTGAGCAUGGT
265659447	63550	CATTTCTTGCACAUGATGCTCUGA	63551	GTTGCATGAAGGAUACTGGTTTTGTTUAA
257475281	63552	GTACAAGCUTTACAGUGCAGCAG	63553	ACAATTGGTCAUGCACCTGTATTTCTUA
254782913	63554	GCACTACTGTUAACTCTTTCTCTUAGCA	63555	CCTTCAATGUCCCTGCCATGUA
265624404	63556	CCAGAAGTUCCCCATCCAGTUC	63557	CTCCCTGCUTCACACTUAAAGACA
261381088	63558	AATTTGAGTAUGTGACTCTGUGCGT	63559	CCCCACCUCACATTCTAAAGTGUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
264545504	63560	TCACAGCAGCUGCAACTCTUT	63561	CTTACCCTTCUGGGTCTTCCUG
316182255	63562	AGAGAAGAAGCAGAUTGAGAATACUGAGA	63563	TGTGGAGAAGCUTGTAATGAATTGCUAT
317020529	63564	GAGAAUGGCTCUCCAGAGCAAAT	63565	AGATGUGCCAGGGACAACUC
315721574	63566	CCTCUCAACCACCTUCCCAAT	63567	CGTATATCCTAUGGCCCTGACUG
319741581	63568	TTUGCAAAAAGCACAGCUGAAA	63569	GTGGCAUCCTAACCAATTUGCAC
319119617	63570	GGGATGAAAAGUCAAAACUGACCA	63571	CGCTTCUGCATCAGCAUCCAT
320361836	63572	CCCATAGAGGCCUTCCTCAUCA	63573	TGAGCCUCACGTTGTCTGUC
320508000	63574	AGAUCCGGCGCTGAAUAGG	63575	AACACTCCTGUTGGGTTTTGAUGA
318255154	63576	GGCATGAGGCAUCCCCAUA	63577	CTGGCCAGGUAGAGTCTUGG
319216006	63578	TTTTTCAGTGACAUATCATTAGCCCCUT	63579	AACAATGAAGGUGCACAAACACUT
236982469	63580	CAAGUCCTGTUCCCCAGCAA	63581	TGATGGGCUAACCGTGTGUG
235288000	63582	GCCCUTGTACATGUCGACGAT	63583	GAGGAGGTCUGGAAGTAAGCUG
259597269	63584	CCATCTUACCCAGCATGCCUT	63585	GGCTTCCTUGACCTCCCAUAAC
260869098	63586	GGAGTCTCUGTGCTGCGAAUT	63587	GTTCATGCGCUGTGTTCCUT
269276371	63588	GGCGCUGCATUGAGGGT	63589	TGCTTUCCCCGCTGCTUAG
319231566	63590	GCAAGAAGCAGCAACUGTCUT	63591	GATATCACCUCACCTGCTTCTCUT
321286193	63592	GGGUGTGAAAUGAGCAGAGGA	63593	CGGACATGTUAACCTTGACTTTGUG
321484757	63594	CTCCTCAGCAAAUTCTGAGUCAGT	63595	GACCACAACAUAGCCGACUACA
259472003	63596	TGTACGUGGCATCGGATUGAA	63597	GGCTTCUGAAGGAGACUCCCA
256085522	63598	CGGAAGGUCTGTGTGUGACAA	63599	CAAGGCUGCGGTGACTUAC
264669300	63600	CACATCUCAGCACGGGCAUAT	63601	CTACCCCCACCCAAUTCTCUG
268302995	63602	TTCCTGGGCUTCCTTUGGAAAT	63603	CTCCCGGGCUTTGGAAGUT
267578164	63604	CTGAGACCTCACUATCAGTACCCATUAT	63605	GGGTUGGAGGAGGAGATCTUT
267369899	63606	GAAGGCTAUGAGAGTGCCAUGA	63607	CTGTACACAAAAGUGGGCAUCC
268923351	63608	CTCTGTGCUCACAGGGATCTUG	63609	CCATGGGCTTUTTATTGCTGCTTUAA
263775540	63610	CCTUGACCCCGAGGCAUAC	63611	GAACUCAAGUCAGGCAGGCA
265335330	63612	AAAGAATGGGTUGGAGTTCTCTTUCAA	63613	TGACACCAAGUGCAAGGAAUCT
261165271	63614	AGCCAGCCCCGUAUAAGAGAA	63615	GTGAGGTCUCCAGTGTUAAAGGG
264754214	63616	CTGGTTUCCAGACCTCCUCAA	63617	GGACTCCTAAACUCTTCTCTGTTCTUCT
325561425	63618	GCCCGTCUGAATCGCUCAT	63619	TGATGTTTCCUGCGAGGTCUG
236066944	63620	GGTCTTTGUTTTTCTCTAGUCCGCAT	63621	AGGAGGTGAGAUTCAAAATTCGTGAUT
237283484	63622	GCTCTAGACUAAGTTGCTTTCAAGUGAT	63623	GAGCGACTCTUGAAAGATTATCAAAGUG
236382711	63624	CCUCCAGCAGAGAAGCAATUCT	63625	CAGATCCTTAACAUTGGTCCGTATTUGA
236401270	63626	AAGACGACCUTTTGATAAGAUGGCA	63627	TGGTGGCAAACUCTCCTTCUC
242446520	63628	AAATAGTTGATCAUACTTTGTAACAGAAUCACA	63629	GGTACAAGTUAAGGCACACAGAAGATUA
240026382	63630	GCACGCUACATGCTGAUGCT	63631	GAACTGGUAAACACAAATTCCTTUCCT
239676973	63632	TGCACATTTAACAGGUACTATGCTCTUT	63633	CTTCGAACTTCTUCAGACACTGTAAGUA
241766339	63634	GTTAGGTGAAGUGATTATCCAGGUGT	63635	GGATCTTCGGAUCAGTAAGTACTTCTUC
333237853	63636	TCCACAATCUCCTCCATCCUCA	63637	GCCAATUCCAAGAACCTGUGAAGT
312943826	63638	GAGCAAGGAGGAGGUGGAUG	63639	TCTGAGGCUGGGATCTCUGT
314010204	63640	CTGCTTCTCATUGAGTTACACCCTUA	63641	CCAACCCUCACCTUCCACAG
313204485	63642	CATCTCAGCAAUGTCTCCUCCAC	63643	GGGCCGGGUCATTATTCTTUT
328623261	63644	CACCCUGGAGAGAGAUGAAGAAG	63645	GGCAGAGGCAUGATGGTCTUT
268755742	63646	GGCATACTCCUGCTTGGATTTUCA	63647	GAAGAGTGUGTTCCTCCUCGAC
265909561	63648	CCCTGGGUACAGACCTCUACA	63649	CTCCGCCUTACCCTTCUCC
263575014	63650	GGGUGGCAGAGAAGUAACAAGT	63651	CGGAATAACUGCCCAUAGGGAAT
315783984	63652	GCAGACGGUCCCGTGTUG	63653	CTUCCCAAAGACCCACAGUGT
316681542	63654	AGCACCCAAGUGCTTCCTUT	63655	CTAGGUCACTCACUCCAGGAAGA
330715430	63656	GGCUCAGCAGACUACAGGACT	63657	GCAAGAAAUGGCGTTGTTATUGAGAAAT
331006229	63658	GCAAAACTCTGUCCGACGTAGUAT	63659	CCCTATTATGUGTGAGATCAUGCAGAA
260067958	63660	GTGTTCAATTTTGUGTCTGTACAGUGG	63661	ACACTTCCCUAGGCCCCTTUAA
266774490	63662	GGAUGGAAGGUGGGAAGAACAC	63663	CCCACCACCAAUACATAAAACTCAUC
263345379	63664	AGAGATTTTAAAGUGTTGTTCCCCTUGT	63665	AGCGATCTCACUCTTCCGGAUA
264177937	63666	GGAGAGAACGUTCCCCAGAUG	63667	CAGTGGTGACUCTCCTCGUG
267822532	63668	CCUCAAGGAGGCGCUCAAC	63669	GGCCGAAUGCTTGAGGGUA
323443077	63670	AGTACCUAGCGCUCACCGA	63671	CCTCCTCUGCCTGTGTGTTUAG
326175397	63672	CTCCTGGGCUACGGCUAC	63673	GGCTGAGUCAGGTCAGAGAUCA
325328629	63674	CTCCCCACACCAUGTCTTCUC	63675	CACCGTCCCCAAUCTCAATCUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326401120	63676	CCAACAGUCCAGGGAAACCAAUT	63677	CTTGCTGAGGUCGAAGCUCAT
325117755	63678	CCTGATGGUCTCACCTCCAUCT	63679	GGGTACGUCTTGCAGTCUCT
324726906	63680	CGTGACGUCATCGAGGACUG	63681	CGGGACAAUGCACAAGATGUAG
324103423	63682	CCAGCCTUCCCTAAGACCCUT	63683	TTCTCTCCAUAGGACCAGTTGTUCT
326337790	63684	GGGATGTGACUGTCCTGCUA	63685	CCTCCATTCUCCAGACTCUCCAG
323679501	63686	CTCUAGAAACCCTCUCCCCAAGT	63687	TCTTCACCUCTTTTCCGUCAGG
323739574	63688	TCCAGAACUACCUACGGACACA	63689	CTTGCCCGAGUAGTACCAGUAG
325642688	63690	GCTCGUGGAATCCTCAUCCA	63691	GCCCACACGAUGUCCCA
325332277	63692	CTGGTATATGGUGATGTCCCTCTUG	63693	CTTATCCCTUCACCACCCACUG
324108396	63694	AAATAAGGTAAGGGUGGTTCTGACTUG	63695	CTACTGACUGGCCTTATGTUAAAGGG
259136056	63696	AGTGTGAAUGAGTGTGAGUGCAT	63697	CCAUTGTUCCGGCAGAAGAAGA
259219568	63698	GGGTTTTCATUACACTTCTGCUAGGAT	63699	CGTCUGAGAAGAGTAGGTUGGG
325083100	63700	GCCTGTGUTCACATGCTUGAC	63701	CCUCCACCCGTTTUGAACCT
327483196	63702	CTTCTTCCGCUGCTCGAAAUG	63703	AAACGGTUCAGTTCACCAUCCT
327409402	63704	CCACUCCCAGGGTCTUGGAT	63705	GGGTGCGGUACGGUAAGG
316842534	63706	CTTTGTCTUCACCGGCUGGA	63707	CTGTGTTCUGGAATCAGGGAUGAG
253803467	63708	CCACUCAAAUCCCAGGGAGAG	63709	CTGAAAGGTCCUTCGTGAACTCAUAG
264271763	63710	GGATTGTCAAAGCUGCAGAAGAUG	63711	AGCAGTGTTUTGCACAAACTUGAAA
256170148	63712	GCACACTUCCCTTCAGUCACA	63713	CCTTTTCATGCUAAATGTGGTUCCC
255227014	63714	AGATTTTTGCAUAACAGCAGACTCUGA	63715	AUTCTGCTGAUGCGGAGGAG
313861100	63716	GTTGGGUTGTTCTAUGGCCAGAT	63717	CTCATGGTACUGGGATTCTUCGG
254507263	63718	CATTGCUGACGCCCCUCT	63719	GGGCCTCUCCTGTGGTCUA
319063598	63720	CGGTGAGCCACUTCTTTTCTCUG	63721	CTCCCCAGUAGGACTCUGACAA
329659848	63722	GGTGCUGGAGCGAATCAAGTUA	63723	AGAAAGTTTCAAGAUCTTCTGTCUGAGG
317917436	63724	CGGGUGCGGCTTCUGAA	63725	CCUGCAGCCCACAGAUGA
315662471	63726	TTTCTTGGCAGUTCTAATACCCGAUT	63727	CAAAGAGGGTUGCTCATTATTCUGGA
317271043	63728	GAACTAAAGGGAAACAUCCAGATCACUT	63729	GGGTTGGGAUAGAATGGAATGGUG
265145962	63730	CCCAUAGCCGAGGTCGUC	63731	GGGTCUGCGGTAUCGGAAA
316217286	63732	GGTGTCUGCAACACTGCAAAAUA	63733	GAUGCAGGCTCTUCCCGAT
325247391	63734	TGGTAAAGTTAAUGTGAAAGGAUCGACA	63735	GTTTTGGTAACUTCCTGCTUGCT
263299065	63736	GGGCCCUGAAGCAAAGAAGUA	63737	GGCAGAGAAAAAUAGATGAGACCCTUG
263144004	63738	GTCCACGUCAATGGCAAAUGT	63739	CTGTGAAGTTAAUCTGCACTATAUGGGT
258866001	63740	CACTATGCCUCACATATGACCATGUAT	63741	GAAAGTGAAACUCCTTACTGAGTCUGT
266358909	63742	TCACAGAUAACAAAGCACGGAGUT	63743	TGCAGAGTCCUGAATTTGCAATCUT
265989904	63744	ACTGGGTTTTTAUAAGACCATTGAAAGCUA	63745	AATTCTTTAATGTCUTGCAGTGCCTTUT
264347373	63746	CATTTGTUTCACACGUCAAGGGT	63747	CTAGGCATTUGGTCTCTTACCTUCAAA
325399829	63748	CATTTCCCTGUGTGTTAGTAACUGACT	63749	GAAGUAUCAGGAGACAGGCGAA
323590558	63750	CACAUTTATCCUGAGAGCAGACAGA	63751	GGCCTTTCUGCTTGTTTTCUCC
242072470	63752	TCCCUGCCCAGCUAACAAAAG	63753	ACTTTCCCAUCTCCTCUCCACA
239902735	63754	CTCATTCATTAAUTCTGGCCCCUCA	63755	TGGAAGTUTAGTGGAGUCCAAGAGA
290774660	63756	CAGCCAGUAGAAGGATATTCUAAGCA	63757	CGGTAGTATUCAGCCATCTTCTGUAAC
290246616	63758	ATTCAATGTUGCAGGAGAUCAGGAA	63759	ACACATGGAGCUGAACGUGAG
293001527	63760	TCATGGGTTUAGAACCCTCCTCUT	63761	CCCTGAGUGTCCTTGUGAAGAT
327221449	63762	CTGTUAAGGGCCCCATGTCUT	63763	CATGTTCTCAAUGTTCTTTCCCATTUCT
265876667	63764	TGCAGTCTATUGAGGGTGTCATAUCA	63765	AAGCAGCAAAAUGGAAGUAAAAGAACAT
254019737	63766	CTTGUGGCCCTGAUGGCT	63767	CCATCTCCTTCAUCAGCATTTTCTAUCA
256720720	63768	GUTCTGATGACUGGAGACAACAGT	63769	GGAACCAGAUAGGACTACTCAGTGAUAA
265671886	63770	GCAGAGGCACGCCUAACTUA	63771	AGAGATGUGCAAGGATGTCTGUG
254470396	63772	CCCTUGGGAGAGTGAUGGAAAC	63773	TCAGATGTGAUCTCTCTCTTCTTUCCT
266888261	63774	ACCATTGATTUACTCTTGCTTUCAGGT	63775	CCATCGGTGTUGAAGTTACTTTGAAAUA
267685891	63776	GAGAAAAAGGUAGUAAAGGAGAGCCT	63777	GATGCATTTAAGUGCCTTTGTUGGT
262037268	63778	GGUCAACCAGGCTTUGGAAAC	63779	TAACGTTAACACUAGGTTTGAGTTTUCT
267270676	63780	GTCCTCCAUAAATGAAGUCAGCGT	63781	TCTACTAAGCTGUCTGTGTCCTTTUG
268750104	63782	TGGCTTCUGTGATATCAGUGAGGA	63783	CCCAACTGGUCTGTCAACGUAAAA
319423358	63784	TGCTAATCGCTACUTCTGTTCATACATUT	63785	CAATCTCATCUCCCATCTAGGAAAGTUC
317695928	63786	AAGAGGAACUGCTTTGGGACUG	63787	TCCTTCTTUCACCAATGTGTCCAUT
312989223	63788	GAAGAATCTCATUGGTTGTCCAGTTUG	63789	AGGTAAGCAAATTAUAAAGCAACATAAAACUGT
315343504	63790	GACAGACUGGGAGTTAGGAGGUAA	63791	TGATCCUGAGCAACGUGCAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314118657	63792	CAGGUGAGAGAAGCACAUGGT	63793	AGTATTTCTCTCCAUTCCCTCCCUT
268748201	63794	GCTCCCUGGACCTGTCCTAUT	63795	GAAGUGGTAAAUGAAGAAGAGGACGAT
333549607	63796	CGTCGUCATGGGCTUGGT	63797	CTCGUACAGCACCUCCCT
262237613	63798	GGTGGGUGGGTCCUAGCA	63799	CGAGUCGCCCGGAGTUAG
318678325	63800	ACCUTGCTGCUGCACCA	63801	GGCACTUCACAAGGACCTGUA
319371252	63802	GGUTCCTGCCTUGACACAGAT	63803	CCTCCAGCGGCUACATGTUG
313658757	63804	GGGTAGTCCTAAUACTGCCTATCAUCA	63805	GGAGCCCACAUGGCACTUAG
258982444	63806	GGCTGCUCACTGACATTUACAGA	63807	GGAGCUGACCCTTGAGGAUG
318547694	63808	GGAGTACCTAGUGCTCTGAGGUG	63809	TCTGAGCTTCTUTCCTTTGCTTCUT
318136926	63810	TTCCAUAAAGCTTCTUACACAGGAACA	63811	GATCCTAAATUGCAGCAAGGCUAC
315287383	63812	CCACAGGAAUTCGTGATGAUCGT	63813	GAGTCGGGAUTGGGAGUAAAGG
314940124	63814	CTATTGGACACUCTACTGGTGGTUT	63815	CTCGCCUCAGGCCUCAG
264463960	63816	GGGCTCTCUCTAAAGACAUGGA	63817	GCCTATCUGCAGGACATGGUT
255685555	63818	GCCUGGAGCTTTUGCAAGGAT	63819	GTGGAUAGAAGACACTCTGTAUGCC
260975454	63820	TCAAUATTGCAAAACAUGGCAGGAAC	63821	GGTTGCUCAGGAGATTCCTUCAA
260147361	63822	GCTATGTTTTUCAAAGGCTGATTACTUCT	63823	GTGACAAGGGUGAAGAUGGAGAT
257321149	63824	TCACAGCAUGAGAGTAAUGAAAGAAGAG	63825	TCAGATATCTCCUCCTATTGGTATTCAATUCA
269193904	63826	AGCAATATCTUGGAGTACAAUAAACGCA	63827	CTCCTGGUGAGCAAGGTCTUC
267389279	63828	TTTCCAGAGUGAACUGACACAGG	63829	CGCTTAATCAUGCTGTTGGCAUT
261443928	63830	CCCTGAATTUCCAAATGCTGCUT	63831	CTGATGGTCUACCTGGTCCUC
237229810	63832	CTTGGCTGAGGUTTCAATGAAUGG	63833	ACCCAGCCTAAUCTTGTTTTTCTTAUGT
317113500	63834	GGAATGGUGCTCTAGGAAUCCA	63835	AGGTCCUACCCUCGCCAA
323989970	63836	TCTGATAAGGCCCUGACCTUCA	63837	GGGATGUCCCGGAACTCTTUA
313132054	63838	AGACTGUCATTTACCTUGCCAAAGT	63839	CTCCTTCTGGUCCAGTGAGUG
316790144	63840	ACTGTATCUGCCAAAACCATTTGCUA	63841	CTCTTTTGGUAGGTTGGGAUACACAT
327630659	63842	CGAGGAGCAGAUCTTTGGUGA	63843	CTCAGGCUGCTGTCCTATUCT
326657558	63844	CCCCAUCCCACCTATGCTCUA	63845	CTGATGCTGACUATTCCTCTCUCC
326513356	63846	CCAAGACATTTTAAUGGTGAGCATCUG	63847	TCCUGAACGGCCAACUGAAG
327040244	63848	CTCCCACACCGGAAAUTTTATAAUGG	63849	AAGCCAAACACAGAGUATTGGATCTTUA
327888073	63850	TCCUAAGTCUGCAAAGGAGAGAGAAT	63851	GAGGTTTATUGACAAGACTTCTGCUCT
327793880	63852	AGTTCACTUACCATTCGGATATUCAGG	63853	ACTTTUGGGACCAAGAGTGAAAUGAG
327286869	63854	AGAGATGTGACUGTAAACTTTTGCGTUA	63855	GTGCCAGAAUGGATTCTACAATCUACA
323407119	63856	CAGGCCUACCTCATCATGAUCAG	63857	CCTCUGCAGAAAGGGAUGCAA
332548322	63858	GCATCAAGAGGUCACTGTCTCUA	63859	GCTATTAGGUCAGTGUGGCAGA
332894145	63860	GCTGGCCUCTAACCCTTGTUG	63861	TTAUCGCAAGGCTTGUGAACAG
326075581	63862	TCAGAGGGCUGAATTTTUCAAGGAA	63863	AGCCAUAGGCCTGTGTCUACA
323714169	63864	GGAGCAGGAGGACCUTTCUGA	63865	AGGCTUACGGACTCTAUAGGCAA
323578188	63866	GGGAAAATGUGGCTTCTGATAAAAUAC	63867	ACAGCTTCAUAACAAGGAGCAUACC
326144412	63868	CTCCTACUGTTGTGTTGAUAGAAGGG	63869	TCAGTGTGAACAUCATGGTGUGT
325362834	63870	GTAGTGTTAGUCCTTTGTGCCUACA	63871	CCACCCAGACAUTAGCAGGTUC
324090186	63872	AAAUTCAGCAUCAAACGCAGCA	63873	CTCCCTAGAAGACUGATATCATCACUGA
324912814	63874	GGCATCTTUCACAACGAGGACUT	63875	TGCAATTUAACTGGCTCUGGCA
325041013	63876	AATAAAGTAACUAAGTGGTTAATCTTUGGACAA	63877	GCTGCATCAUAGAAGGTCUCAGT
323517471	63878	TGGAAAAACAGUCATCAATGGATTCUGA	63879	GGGCATGTATUAGAGAAAGTTCACTTUA
324338153	63880	CAACTAATGUGGAAGATGTTTGUCCAA	63881	CCACCAACGAGACAUGTAGCUG
324493297	63882	AACAAAAGTUGAGGCAGCTUCAC	63883	TGAGCCTAAAUTATTACGGTATUGCACT
328253885	63884	GCAGAGTAACTUGGATAAAGACGGUAT	63885	TTACAGCATTCUTTAAAACGACAAUGACAA
235559334	63886	TTGCTGAATAAGUGTAAAACCCCUCA	63887	GTATAATCATGTGGGUAACTGCAGGTUA
241383357	63888	GGTGATAGTACUCATGGCCCAAATUG	63889	CCTTCUCACAGGACAGAGACAUACAT
240418863	63890	CATGTTUGCAACCCATTTTCAUGAAC	63891	GGTAGTAAGTTUCCCATTACCAAGTUCT
267234648	63892	CCCCAGCUCCTGCAACTTUT	63893	CUGGGACCCAAGGGUCAAG
327425123	63894	AGAAAGGTCCAGGUGAGGTAGUC	63895	ATTCTTTATTACUCCTTCTCCCTCUCCAA
328280450	63896	AGACAAUGACAGGCTTCTUGGG	63897	CATCCAGGUAGGACCCACUCT
328205962	63898	CGGGACAAAGUGCAAGACAUT	63899	GAGGTGATTCUGCACCATGAGTAUT
326863627	63900	GCCCGTCTUCTTGTCGTACTUG	63901	GCTAAGAACCAUGAGCTGTGUCT
328188628	63902	TTGGTGAATCAAACAUTCGAAAGAAUGG	63903	AGCCTCATTUGTCTAACTGTUGAACT
326585576	63904	GGAAACUCCACACCATATTCUACAAGA	63905	CCAACATGATATUGATGGCACTTCTTUT
328050634	63906	CATCCAUCAAGGCCUGGGAAAT	63907	CCTGTGACUCAAGTATTAGCUAAGCAG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314375962	63908	GCTTTGUGGAAAGGCTUGCAT	63909	CAGAGUAUGGAAGGGAGACAGAG
324945265	63910	GTAGTAGTGUCTGAGGGAGAUCAGT	63911	CTTTGCAGAACAAAAUCCAAGGATGUAT
324389327	63912	TGGTTGAAAUTATCTATGAUGACACCAA	63913	CCTAGGAUAGCACTGTTTGAATUACCT
324500208	63914	GGCAACCTTAGUTTATGTTTACCAGUCT	63915	GGAATCTTTGCAGCUGAAATGGTATUAA
260674009	63916	ACCCATGCAGUTTGCTCACUT	63917	CATCAGGGCTCUTGATAACCTTAGATUT
269232777	63918	AGTGCTCTTGUCTCACCACAUT	63919	AGTGTTGGUGTCATCTGCUGT
256093790	63920	ATCTGTATTACATUGAGTTTTTACCTACCTUT	63921	GTTGTTAAGGCACUGGCAAAACUT
269043701	63922	TGTTGCTAUCTAGGTTAGUGAAGGCT	63923	TCATTTGTCTTGCCUTTCTTCTGTCUAA
268731378	63924	AGCATGACACAAUGGGAAGATUAAAGAA	63925	GTGGACCTGTAAUATCTTTCTGTGCUA
269096681	63926	GGGAAUGGAGCAAAACAGTCTTUG	63927	CUGGTTGACAAGATUAGAACAAGAGGAA
264855385	63928	TTACAGGTUGCCCATCTTCUCC	63929	TGCCCTCCUTGGTGTTTCTTUC
259718021	63930	CAAGACAAAUGCATTCUCACACCAT	63931	CAAUTTTGTGCUAGGGAGAACGAG
268931684	63932	ATCTTTUCCAGGAGCTCCCUAGT	63933	TGGAGGAGGTAUGTTTTTGACAAATUGA
320366170	63934	CAGAATTCAGUGCACTAUCAAACACAAT	63935	CAGTCTAAGATTGAUCGAGACAAGTCUT
316443059	63936	TGCCATGTCUTGACACTCAGUT	63937	CACATTACTGUTCTCATTGTTTUCCACAT
268563243	63938	CTTCGTCAGAUCCATCGGGUT	63939	GAGTCACCCCCAUCTCTCTUC
234927801	63940	CCCAGCUTGCTTCCUCCAT	63941	CAGTAAGAAGCCUCTAATCTGTTTUAGCA
260734496	63942	CCTCATUCCACAGCCCTGUA	63943	GGGAGUGGAGTGAGUGAGGAG
267256189	63944	CCTGAAUCCGCACTCTGUACC	63945	GCAGGACACUGATGTTUCCAAAT
326904257	63946	GTGAGATCCAUCAGTAGTACAGGUA	63947	CAGTCTCCTGUAATTCTCAGGCTUG
237668851	63948	GTTTGCACAUAAATCUCCAAGGCA	63949	TTGAAACCAGAGUCCTUAACAAGCA
332395205	63950	GTGGCACCUCATCACCTTUCT	63951	CGUGUCCGAGCAACAAGGAT
232047370	63952	CCTGGTGCUTTGGTCAAUGAA	63953	GTAGCUCTGCTTGTUCACACACT
323607070	63954	CGCTGTGCUGTTTTCATCATCUG	63955	AGAGCACATGUCATGGTCGUG
324451676	63956	CAGAAGACTGUGAGGACCAUCA	63957	CCCTTATTCUGTCCCCACCUCT
264523048	63958	CAAGUGGAAGCAACCGTTCTUC	63959	GTTTCATTUCCAGCAGGTAAGCTUT
260634237	63960	TCTAGAACCCUGACUGGGCAT	63961	GCUCCTCUCCCAAGAACAACAG
262655431	63962	GGAGGTTCAUGTTTTGTGCCTUG	63963	CTGAGGATACUTAAAGGTACUGAAAGGT
332107773	63964	CCGATAATCTAUCACACTAGGTGCTUT	63965	AGTACACCUGCAAGGCTGUC
332052504	63966	CCTGAGGCCCACGUATCTUG	63967	AGGUGGAGAACAGCGAGAAUG
332098042	63968	TCCACTGCUGGAGCUGAAAAT	63969	GCTTCTGACCTUAACTTAGTGCCTUT
323378341	63970	GGGCGAACCUCACTAACGUG	63971	CTATAGUCGGCCACAGAGTCCUA
254178805	63972	GGTGCTGTATUACCTGTTGAAAGTAUGT	63973	ACACAAAAGAUGAAACAAUGGAAGAACAA
262044193	63974	TCTTGTGCTGCUTTATCCAATTCUAACT	63975	CATCATAGGCACUGACTCUGCAA
329363604	63976	CCTGCTUCCTGACGCUGAC	63977	GCCAGCCCUGAATGGACAUC
323512216	63978	TGTGGGAAGGCCAUCCCTAUA	63979	CGGTGCTUCTTGCTGATAUGGAT
318037170	63980	GCAAAACAGAAAUACACATCUGACACT	63981	GGATTTTGCUGCTTGTGGAAUAGAC
321239138	63982	CAGGACAGCTUATCTCTGAAACAUGA	63983	ACCCTACTTACUAAATGAAGACUGGGA
320235247	63984	CCGGAATAATUCCTTGCTCGTGUA	63985	CCCCAGGGCUATTTTATAGAGTAUAGGT
326803474	63986	GATTATCCUAACCCATCACTCAUGAACA	63987	TTTCCAGTGUGGTGTAAAGGAATUCA
333275277	63988	GCTCATUGGCTCACAUCGCA	63989	GCTGAAGCTAGUCAGTCACTCAUA
332583042	63990	AGAATCTAGAGUCTGGAGTTTUGCCT	63991	GGTAACATATCAUAGTGGGCTTTTCUGT
332763460	63992	GCAAATCAAAUGTGGGUGAAGCA	63993	ACTCTACCUGAATTGCACTAUAGCAGAT
333524763	63994	CCTCGUTGAATGTCUCACCAAGA	63995	CCAGUGCCTCAATUAACCACACA
332553329	63996	TCCTCACATTAUAAGCACTTGGGAGUA	63997	GGAAGTTTGTAAUCAACCCTGTUAGGAT
313663237	63998	CCTGGTGCUGGAAAATCAACATTTAUAG	63999	CGAGACCAAACUTAGCTAGCAGUT
324304978	64000	CCCCCAUCGAGAGGGUCA	64001	GGCCUGGCGCAGATTTUC
267686680	64002	CCTGTGTUGATAATGTCAUCCAAACGA	64003	GGGACAAGAGGAACAUGAAACUCA
267806739	64004	CCCAAGGCAAUGATGGAATCUGT	64005	CAGGCCCGCAAGUACAUC
265721892	64006	AGAGTGAGAAACUCTTCATGCTUGAC	64007	GGCAGTGGGAUAAGCCTGATTTAAAUAT
264357422	64008	GCAGAAAAATUGGCACACACACUA	64009	GTGATCGGAUTCCCAUGGCT
267706719	64010	CAATCCCAAUTTCCATUCAGGAAAACA	64011	GCAGCCCAGCAAAUTTCCATTATUC
264796315	64012	CCCTCTGCCAUGACAGGTTUA	64013	ACTTTCTTUGGGAAGGACAAGUCAAT
263841286	64014	TCCCATTCCCUGGGAATTCCUA	64015	AGCCCAGTTUCAAGAAAGAGCUT
265960484	64016	CAATACCTGGUATTTAGTGGCCAUGT	64017	CAGCUCTGCTTUCACAAGACAAA
293544498	64018	AGCGTCTATATTUTGCTCTTTGAAAUGA	64019	TTGTTGAUAATTGGAAGAUGCAGGACT
290130494	64020	AGAAGAACUTAAACAGAAUGAGAGCAGAA	64021	AGGATGCCCAUCACTCTTTUGT
289993971	64022	AGTTGTCAGUCCTGCATTUCAGT	64023	ATTACAAGTAGACAUGTGAAGCUGAAGAA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318820643	64024	AGGAGAAAGUGGAGTTTGTGAAAUAGAC	64025	GGTCTGTAAUCTTCTTCACCTUGCT
292446611	64026	GGTTCATCAGUTCAGTAACAAGUCAAC	64027	GCAAAACTAAUGTAAGGACAUGCAAAGA
290520387	64028	GGAUAGAGGAGGAGGCACTUCAG	64029	TACATTACTTGGUGTACATTTAATAGACUGACA
329133468	64030	ACAAGGAAGTATUGAAGATGAAGCTAUGG	64031	ACATCCUGAGGGTAAGGCUAACA
223556481	64032	AGCACTTTAGGUAGAGAAGTTUGCAAT	64033	AGCGTAATACCAGUCTTTTTCCTTTUCT
326939934	64034	TAGCAGATGUACTTCTGTCAGTUCAC	64035	TGTTTTACTUCTGCTTGGUGGCA
224533540	64036	CAGUGACATUGACCAAGAAAACAACAAT	64037	CAACAGGTCAUCTTCAGAGTCAAUACT
327866619	64038	GTACGTGGUGTCCTGTGUCT	64039	GCTGCUCTGCGAGUCCT
332085869	64040	GGCTCUGAACCGCATUCAAGT	64041	CCTACGGUTATAACGCCUACCC
257563826	64042	GGTGACCATTTTUCTGATGTGCATTUC	64043	TGTTCATGCGCUTACGAGGUT
237703933	64044	ATGACTTGCAGUCTTGTGATCUGAAT	64045	TTTCCTTCAGGGAUATCAATGTUCAGG
235847659	64046	ACUCTGAATGCAUCAACCGCAT	64047	AAGCAACUGCAAAGAGGAGAAAGUA
239727885	64048	TCATCCACACCUTCGGACTGUA	64049	ATCCAGTTUGGAAATGAAAAGCAUCC
265294920	64050	AGGCCTAGCACCUTGATACCUA	64051	CGAATCTTCUGCAGCTCCAUC
332005487	64052	AGTCAUCTTTGTCTUCAGCCCAAA	64053	GTCACCGUAGAGGACCUGGA
332026111	64054	GAAAAGGUGGAGGCUGGACT	64055	GGCGAATUCGACTCCTUCGT
331905893	64056	CACCUCGCCTCACUCACA	64057	CCGCTUCGACTCCTUCACT
331756060	64058	GCCCCUCACTCACCTGUCA	64059	GCAGCTUCGACTCTTUCACC
331827649	64060	CUTGTTCGCAATUCCAAACAGAGT	64061	CCAGTTUGACACCTTCATGGUC
331862460	64062	CCACCCUCTTCTGTGAUCACCT	64063	CAGTCCTUGCTTCAGAGGUACA
267078121	64064	GCCCUGGGUAAGAGAAGAGAGT	64065	TTCTCTAATATCTUGTCTGCCTTCUCCT
267485463	64066	GGGAACTCAGCUTCCTTCCUG	64067	CTTCCCACUCCTTGACTCTGTUT
265267240	64068	GGAAGCCUGGAGAACTAGGUCA	64069	GCTTGTTCUGACACTTCCCTUGT
257683131	64070	AGCACAACCAUCCCCTCATUC	64071	CACCTGACCCCUACTCTTTTGTUC
323340017	64072	GGCAGAUGAAGGTAAUCACGGA	64073	CAAGCTTCTACTUAACGCCTTAACAGUA
327506679	64074	AGGGUACAUCAGCCCCAGA	64075	TCCCCAGAGCCUCCTAACUT
326401420	64076	AGAAGGTGAAUGAAGGTGAAAAAGTCUT	64077	TGCCATAATTTCTAUTAGGCTGGGTTUT
314377134	64078	GCATGTTGUAAAAATTCCTACATUCAAGGA	64079	AAGCTTACTGGUACCATCCAAAAUGA
271069298	64080	TCTTTCGAGUATTACTATTUCCCAGCCT	64081	ACTCTGGTTCAGUCAGCTTCCTUA
271139524	64082	AACTGGATAUAACTTCTGAATUGCCCAA	64083	GATGGCAAGAGUGATGGATTACAAAUAA
271896987	64084	CATAATCAGATCUGGCTGGGTUCA	64085	CTGAAACAUGGCAAGGTGTUGAAG
271087417	64086	TCCCTCAAAUCCCACATATCATCTAUCA	64087	CCTTCCAUAAGCATCTGAGCUCAC
269947043	64088	GCAGCTTCUCCCTCTCATTAGUG	64089	AGATTTGGAGTGAUGTCCTCAGTTCUAT
270924784	64090	AAGGTCCACACGUGTTCGUAG	64091	TGAGGATGAAACUCTGTAAGGTGGATUA
271455878	64092	GCTCCAUGGGACUGGAAAGAG	64093	TGGAGCCAUGTACTACCUGGA
318780644	64094	CCAGCTCAUGAGGGACCAUAA	64095	TGTATATGGCUGGATTATCACUGGAAGAT
317462242	64096	TGATAACTTGUCGGATACAGCCTUG	64097	ATGTAACAGAAAAGGCCUCCACUAAAA
315877290	64098	TTCCTTCUCCAGGACAAACTUCAAAA	64099	ACTAGTGTTACCUTTTCAAATGAATGCUAACT
317919907	64100	AGAGACAUCCTGGTGGUGAGT	64101	TCAGCTCCUATGGACTTCUGCT
315527248	64102	GTGAAGTTUGAACAGTGTATGAGAUCCT	64103	CCTTCACAAACUATCTCTTCAGACTUGA
317099821	64104	AGCTGCCUTAGTTACATAAUGAGCA	64105	CTCTGAACCUTGCAAAAATAAUGGAACA
316113333	64106	AGTTTTCTGUACCTGAAATTGTUGACCA	64107	GATTGCTCATCCAUACTCATCTCAUACT
315985942	64108	ACATTGTTACCAUGAAACAGTTCGAUGA	64109	GCTGGCAACAUGTATCTGGAAAAUAC
317623507	64110	GCTTGCTCAUCCCAATTTTCTCTTTTAUT	64111	AGTTCUGCCAGGAATCTCUGAGT
261207416	64112	GCCTTCATGGTUTTATTAACCCCCAUA	64113	CCACCCAAUAAGGTTCACTTGAAAUT
266065748	64114	AGTATTAAGGUACTGAAGAUAGGCAGGT	64115	CATTGCAGGUGGCTTACAAGUT
323715581	64116	ACAGGACCACGAGUGTGATUC	64117	AGTCTTCCUCCTGAAAAACGUCAAA
267632534	64118	GAGACGGTUACAGGGAAAAACUGT	64119	CTTCCCATAAAGUAGCTTGCCAATTUT
264923175	64120	GCGTATTAATGUTGCCAGTTTCAUGAT	64121	TCTCTCTGAAGUCCGGAATCUGT
265311408	64122	AGACACTAUGCCCCTCTUGGAT	64123	CAAAACAAAGACAAAAUGTGGCAGTAUT
267880551	64124	GGTTTGCATTUGTCAATGTGCATUC	64125	GCACCAGAUGCUAAGCCACAA
267596048	64126	GCCATAAUGGGCGCTUCCT	64127	GGTCAGAAGAACUGCCTGUCC
268109133	64128	ATGCTTTATTGUAATCTCCCAAAUCCT	64129	TGTGCCAUGAAAAGGCTAATAGAGUC
267642839	64130	GTTACTTCTAUCGTGTGCCTGUGT	64131	GCTTTCTTCGAAUGCTTTAACTAAGUCC
313392967	64132	AAGCTAAATTGUTGGCGGGTTUC	64133	CCCTCUACCAACUGCGGAAT
313913509	64134	CCCCCGCACACACUAAAGTUA	64135	GTTTCCTAAACTUCCACCACAAACAUAG
327992376	64136	CTTTTUCCAGGCAGAAGCUGAC	64137	TGTTCTTAACUGCAAACTGGAATCUGAT
328255836	64138	AGAATAAAGTGCAUTGTATGCCCUCAT	64139	GCTTGTGCTUCTTTTTCCGATAAUACT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
255615746	64140	GGTATTGAGUGTTCTTCCCAUGGA	64141	CTTGCCUGCAGCGUAGAGAT
223291853	64142	GGACAGCAGACAGAUGGTAUGAA	64143	GGTCACTACGUTAGCTCACATTTUAAAGT
222539784	64144	TTGUTTAGAACCGUGAGGCCAT	64145	CCCCAGATATTCUAGACAGTTCAGTUT
223483754	64146	GTGTGTGATCAUCTCTTTGAGGUACT	64147	CATTGAGCTGCUCTATTTCTTCTTCUCT
224701227	64148	TTTTTACCTTCCUTTGTTACAGGGUGT	64149	CTGTTTGTGUAACCATATGAGCTTGUC
224432233	64150	TCTGAGAAAAUGGTGGTTGCUGA	64151	ACTCCCACTCCUTGTTACATGTTTUT
224218976	64152	TTGATTTTCTCGUACCAGGATCUGAAG	64153	CCGAATTCGAACUTTCTCAGATUCAAGA
223235441	64154	GGTTACTTTAGGUGCAGAAAAGACUG	64155	ACAATTCCAGGCAGGUTTTCTCAUAT
224431156	64156	TGTGAACTCUGGTGGGTCUGAT	64157	GCACAAAAGAACCAUTGATTUACAAAAGG
318819838	64158	GTGCACATTCATUTCTACTTTGGACUC	64159	AGTGAATTGATCUTTTCGTCTGTUGGT
267866747	64160	CTTAGTGAAATGAUGGGTCTCCCAUT	64161	CTGTCAGGCAUATTCAGCTTTUGG
261779464	64162	TCCAACCAGAGUGCAGUGAAAG	64163	GGCGGGAAATTUTAGATATTGCTGTUG
325369510	64164	GAACAATACAGCUGAAGAGGATTCUGAA	64165	ACCTCATCCUGGACATCAAGTUCT
269307859	64166	AAGGTTGTTCAUGTCAATGGATAUGGA	64167	CGTGATUCCAGGAAAAGGAGUAACT
261643831	64168	CATUGGCCGACGACCCTTUA	64169	CCCCAAAGCCAAUACATATTTUAAGCAT
255257887	64170	GAACAGAACUGAAACTGACUCGGA	64171	AATGCAGAATGAGAUGGTGGTGAAUAT
258929852	64172	CACTAGAUGACCAGGAAAUAGAGAGGAA	64173	CAATCTATGAUGGGACAGTCTGUCT
265796082	64174	TTCATUGAAAAGCCCGACAAAUAACC	64175	CTTCTGTUGGCATGTCAAUGAACT
265471177	64176	ACAAAGUGCGGCAGTACGAUT	64177	TGAGCAAAUGTCCCATGUCAACA
263764600	64178	CCCCACCUCATTCTCATTCUGG	64179	CGTGGTCUGTCTTTGCUGAACA
268236336	64180	TGCAGAAAGGAGGAUAGUGGGAA	64181	TCCTAGATUGCAACTCTCAGUCAGA
264641018	64182	AAGAGAUGGCGCGGAAGUT	64183	CCAGACGACGCUTTTCCCUT
321173230	64184	CAGAGAGAAAAGGAUCTGCAAAAUGAA	64185	GCAGGUACAGATTTATGAATUAGAGGAACA
315710696	64186	GCGACAAACACUCACCTCUGT	64187	GGCTCTCTGATUCCATTTCTAACTGTUC
242598516	64188	CATCTTTCTGAGAAUGGAGTATCATGATUCA	64189	TGGTACTTGATTAUAACAATGCTCTTUGGT
230397695	64190	CCCCUGAGGAGCACGUAGA	64191	CTTGACCUCCAACCAGGUAAGG
229652415	64192	CAGGGACGUCTCCUGGAGAT	64193	CCCAGUAACUGCACCAACGA
227948825	64194	CCACTCCTUGCTTCTCAGAUGA	64195	GGTGACAGAGGACAAUGTGAUGAAG
329648453	64196	CAGGTACUCCCGCAGGUT	64197	GGGTAGUAGAATGGATTUCCCAGGT
254139219	64198	CATGCCTGAAAUTTTCTTTTGTUGCAG	64199	CCCAGGCCAUGATGACUAAAGAAAT
263706276	64200	CCATAATUAAAAGTAGCACUGGGCAGAT	64201	TCATCTTUGAACGGTGTTCUGGT
263089665	64202	AAAGGAAAUGAGAAUGAAGACGAGAACA	64203	GTAGAAACAUGGATGGGUAGAAGAGG
320430442	64204	CTATAAAAGGGAGAUGGTCACTUCACA	64205	GTTGAAAAATCCUCCAATTAAGGTGCUT
327891942	64206	TGUAAGGAGGAAGAGAGTTTUCACCA	64207	GCCCAGTAACAUTGTGTCTCTUCA
327907908	64208	TGTCTCCTCUTACAGATGAGTUCAGG	64209	AAAAUGGAGACAGUGAAGACACAAGAA
326667095	64210	TCTUGTTCTTGAATTTUCCGCAAAGAT	64211	TGTATTCACCUAGTGGTCCTGUGA
315956211	64212	CTCTCCCCACUGTCTCTCTTCUT	64213	GACGCCAGACUGTTCUGAGT
278339098	64214	AGAACTGTTCATUACTGGCATCTAAGUG	64215	GGCTTATTAGTTGUCTTGCCAATTGUT
262317843	64216	CTGAGTGTUGCAGCCTGTCUA	64217	GGAGAAAGAUGGCCTCCUGAAAAA
240502685	64218	GCACACCATCUTCCTCTGTGUT	64219	ATGCCAGACUTCTTUGGAGACC
240250121	64220	GGCUGAGATTTGGUGAGACACAG	64221	CGCTTGTTCTUTGCTATCAGAGUT
239713728	64222	AACAAGCAGTUTCAATTTACCTUGACC	64223	GCTCTTCUCAACGGGTTCCTUT
264744948	64224	CTCTGGUGGAACGCUCAAC	64225	CAACAUGACCCCAGGGAUGAC
263851749	64226	TGGUGCAAGGAACGACACAUT	64227	TTTCGAAGGUCATTGACCAUGGAT
332528706	64228	TGTCGAUGAGACTTTTCCAAUGCAA	64229	CAAAGAUCTUGGCAGGGAGGAA
333047459	64230	TGTTTGAGGAUGCGAAATAAGTGUCA	64231	GGGAAAGCATGAAAUGCAGTATGTATUA
332701987	64232	CCTCCCCAACCCUCTCCTUAG	64233	GGTGTCACCAUAGGCAACCTTUT
318875963	64234	TGCACCAUCAATATTTUACAACGCAAA	64235	ACCAGCATUAAAAAGAGAGGAGAAAGUC
319388006	64236	AGGGTGTACUGCTCCATCUGT	64237	GCCCGTCAAAACUTACGTGAATTTUT
318603209	64238	CTGTGGAAACCCUCCATCCAUAT	64239	CCATGAGGGUTGGTGCTGTTTUA
318223999	64240	TGGAGCGAUGGTGAUAAGCC	64241	GAGACCCAAGAGGAUTTATGTTGTGAUT
267043519	64242	TCACAGGATTUCTGGACCCCUA	64243	GGAGCAGCAGGUCTCTGAUAC
265244538	64244	TGATGCGCAAAAUCGTCGUC	64245	GCGTGGGTAUTACTCTACTCTUGGT
255602964	64246	CTGTAGGTCUCTGACCACGUT	64247	GTGGATCCUGGCTGTTUCACT
255919079	64248	CTTTCTTCTCCUTGCCCTTTCUG	64249	ATCCAGCAGCACCUCATAGUG
254075625	64250	ACCAGGATCAGAUGTCCGTGUA	64251	TTTTTGCACCAUCCGCTGUG
327790105	64252	ATTGTCAAACTUGTAGTGTTTGTTTUGT	64253	TTTTAAAGCTUCCTCTATGCCTUGGT
327283301	64254	AGGTATGUGAGCGAAUCCCAAC	64255	TUAAATTACUGCAAAACGGCACAGAA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
333595737	64256	CCCAAUTCAAGTGAUCCGCAAAG	64257	TGGTTTTGGAGGUGTAGCTTCUG
333609076	64258	TGTCAGGAAGGUTCAGACCAUCT	64259	CGGCACCCAUCTCCATGATUG
312972514	64260	ACTGACTCTCUCGTCTGCCUT	64261	GTAGGUGGGCAGGGTGTUG
313968792	64262	CTGGACCAGCGCCUAAAGUT	64263	TCTCGGUACCAAGTCCTGUCA
314586850	64264	GCCTTGTCCUCCATGTTCTCAAUG	64265	CCTTGGAGUGATCCAGGTUCAG
313850460	64266	GCATCCACCGGUAGCTCTUC	64267	AGAGGACUCCTGCACAGUACA
313861285	64268	CATCTGGATCUCCTGGCCATUC	64269	GCCACAGCCACAGUAGCUT
313896596	64270	CACCGUGGACAGTGAGATUGAA	64271	GGGUGCGGAGCCTTGUC
326404022	64272	GCTTCCAUGGGCTGATTUGGA	64273	AACAACTAUGGCAAAGGCUGGA
325738554	64274	GUGCTGGAACUGACAGAGACT	64275	GGTAGCGCUCGCCCUAAC
313100712	64276	CCTGGGCUGAGTTCCAGTUG	64277	CCACCCUCGGAACTCUGGT
312927719	64278	GGTTUCACACGGCACTTUGT	64279	TGTAAATTGCUGCGTTGATCTTGUC
314347826	64280	GAGAGGCTGUCCATTCCCTUG	64281	CCAGCCCACAUCATGGGAATUT
312744435	64282	CAACCUGGAGAAGCUGCACT	64283	GTUGACAGAGGCACCACUCA
315073379	64284	GCTTCCUGCAGUCCCGAAA	64285	GTCTAGCUGGCAGTTGAGGUA
313381720	64286	CTCCUCAAGTCCUCAGAGGGAT	64287	GCTGCAGGGAUGGAAGAAGAUG
222179771	64288	CTGTTTTACTGACGUTGATAGCTGUG	64289	AAGTGCCACUCAGAAAATCTAGCTTUAA
224359488	64290	GGTTTTGATUCCACATCTGGTGATUAGA	64291	GTACCCTCAUAGGCAAAAUAAGGAAGAAT
222737398	64292	GAAAATTCTTCUTGCCATATGUGAGCA	64293	GCTCCTCCUAAGCCACTTTTTATATCUT
326780255	64294	CTATATGTAGAGGCUGTTGGAAGCUG	64295	TACTCACCAAUCTTCTACCAGUGT
222602733	64296	TTTCTGTTAAGCAGUCACTACCATUGT	64297	GCUGTAAAGUGAGCAGCACAAGA
224447475	64298	AGAAGGTCCUGTTGTCAGTTTTUCA	64299	GCCTGCTGUATGAGCAAATUCA
332731929	64300	GGUAGAGCAGGTCGUGGAGT	64301	CGCTTCCACCGUAAAAATTAUGAGAAA
333013033	64302	ACCAAGGGTCAUTTTCTTTAAGAAUGGA	64303	CAGTGGGAAGACAUTCCACAAUG
333635827	64304	GAGGATUCAGAACCCAAUCAGGAA	64305	GGAGAAUTTTAGCGTUGGACAGAG
332589004	64306	GAGTCAAAGGCUAAATCCTAAGGCAUA	64307	CTATGTGTGTGUAACTTCTGTTTCTCCUT
332547732	64308	GTTCCTTCTCUTAGGACACTUCCAT	64309	ACTCACAAAUTACAGTATCUGACGCA
333667089	64310	CTCGUGCCACACAGATTCUCT	64311	ACTGTTGGCCAGUAGACAGUT
333249533	64312	CTGTTGGAAATAUGCTAGCACACTUT	64313	ATGAACATTGTTUGCTATACTTGCAGUG
332960723	64314	GCCTATTUGAACAACTCATAAAACUGCAT	64315	GCTGGACCUCTTTGTATTTCUGGAA
279474455	64316	TATTTAAGGAGATUACACTTGATGTATCUCACA	64317	GCACATGAAGCACAAUTTCCTCUT
277831338	64318	TGGACTTAGAGUTGGTCAAACTGTUAAG	64319	TTCTTTCTAUGCCACGTTAATGCTTUG
317018316	64320	CTCTTCCTGAGCAUGAGAAAGAAUGA	64321	GGAAGAAAGCUGCAGCATUACAC
320600558	64322	CTTGTGTCCACCUCCACTGUT	64323	CAAAAGAGGAGUTGAAGGTGCCUAT
316577762	64324	ACAGGACAAGACAUTGCAUGCT	64325	AGAATCCCUCTTCTTCCUCCGAT
317168731	64326	CTCAGAAAGACCCCUTAAACTGUCA	64327	AGTCTTTGAUGCGAAGAAAACGTTUC
312768346	64328	GATCCTCCAAGCUCCCACTUT	64329	ACCATTCTGTTUGCTTCTCTCTCUC
313383159	64330	CAGCCCTCUTACCGTCTCUC	64331	GCAGAACACUGCCCGGTUT
312950643	64332	TCCTGCTCCUCATGGATGUGA	64333	AGTCCTUGGCCCAATCTCTUG
239363589	64334	GGGCAGCUGCACAGUCT	64335	CCTCACCUCCGCGAUGT
237505086	64336	AAGAAGTAATGCUGATCCAGGCTUT	64337	CAAGAGTGACTAUTACTGAGCGGAAUAT
235527038	64338	CCTGAATTUGAAACCAAGUGCAACA	64339	GGCCAATCTGACAUGTCTGATACTTUAA
327835478	64340	GTGCTGGAACAUTCCCTCUCC	64341	AGAGGACAUCAGCUGCAACAC
327518261	64342	CTGCTGGCUTACCTGGGUAAT	64343	CAGCTTGTTCUCTCTTCCTCTTUCC
327450582	64344	CTCCTTACCUGCTGGGUGAAG	64345	TTGTCCUCAGAGCAGAACCTUG
241627128	64346	TUTTTAAATTATCTGTTUCAGGAAGAAGAACGA	64347	CGCACGCCAAUAAAGACATAUGAAAA
238045415	64348	CAAGATGTAUCTGGGTGUACAACCT	64349	GAAAGAGAGGUAGATTTCAATGGCTUCT
242362523	64350	TGAGCTCAGTAUGGAAAGAAATAACUCT	64351	TCACTTTGCAUATGCCATACAUGGA
332523387	64352	CCCCAGACACUTACCAUCACAAAA	64353	GAGGATGTUGAGTGTAGGUAACGG
332609892	64354	CGTCTGTGAUGGGAACTCCTUG	64355	CCAAACTTATGGAUGTTCTGGTGTTUT
314613482	64356	CATTGGTTCUCACAAATAGTAGGTGUGT	64357	GGGAAAGGUGATTGCATTTGCUC
312775582	64358	GCCCCUTCCTCTCUGAGAGT	64359	GCATGACUGCGACCUGCT
314326639	64360	GCTTCTGCAGCUGCTTCTUG	64361	TGUGAGGACTUGACCAGACCAT
313925255	64362	CCCTTUCTGCGGUACAGGAC	64363	GCTGGTCUCCAGTAGTATTGTUCAC
313316474	64364	GGACAUGGAUGGAGCAAGAACA	64365	GGCTCTUGCAGACAGUGACC
254194448	64366	CATTCCTTTGAGUTAGATGAAACUGCAT	64367	ACAUGAAGUGACAGAAGCACAGAAG
326742469	64368	ACAGTGATAUCAGATGAGTCUGCAGAT	64369	TTTTAGTCUCAGCTGUCCCCAAC
326512440	64370	GAAAGGATTAGUCTTCAGCTTUACAGA	64371	GGAAAGACAAACCUCCTCCAAATGUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
261755655	64372	GCTAACAGGUAAAGTTTGUAGGAGACAA	64373	GTCTTATCUGGAGGCACCACTAUG
256248221	64374	GCCATTTCCUAGATCGCUGGA	64375	CCUGCAGAACCCCCUGAAG
317901665	64376	TGGAGGCUGAGGTUAGGAAAGT	64377	TGACTCTTCTUGTTTTTGGTCCTUCAAT
316112930	64378	TTCATGAAGACAAACUCTTGGGUAG	64379	ACCAGATTCTGUTCTCCTTCAAATUCA
327655593	64380	CCCAUGCCCTTCTGTUACACA	64381	GTCATGCTGTUTAGTCACTGCUCT
272700216	64382	CCGAGAGTUGAGGCGAAGUT	64383	AGGCGCUTCACGAUCGG
270385364	64384	GGCTGTATTGUCCTTATCATCAGAAUCC	64385	ACAGAUCTCUGGCCAGCAAC
315798786	64386	GAGGGCTGACUATAAGCCTCTGUA	64387	ATTTGCCTAUGAACGTTTGUCACAC
317181755	64388	GGCCUGACTCGGTAUGGAAA	64389	GCATTAGGCUTTCAGGATGTUGAA
333259202	64390	TGGATGUGGAAGGAGGAUGAAGA	64391	CGCUGCCACCACTTCUGT
332489562	64392	GGAAGGAGAUCAGGUGCAGAC	64393	GCTGAGCGUGGACAACTUCAA
318097663	64394	TGAGAAAAGCAGCUCAGGAACAUT	64395	GAGTUGAAAGCCATGGUGCAG
319294092	64396	CTCAGGTGUGTCACTCUGAAGG	64397	CAGGGCCUGATATAGGTGUGT
242729062	64398	CCTGGGTGUCCTCTCCUGT	64399	AACCTUCCAGAGCAGTTUCAGAAA
240806165	64400	GCCCCUGATAAACGTGUGGT	64401	GATGGACAGGACGAUCTCAUAGGA
265942670	64402	TCTGGCTTUCACCATCCTCTUC	64403	ACATCCCUCAGACAUGCAAACA
240062671	64404	CTTTGGCCCUTGGTGAUAGGT	64405	CCATCATGUCCAGACAGGTTUCC
239514320	64406	AAAACCUGGCTGGTUGGGAA	64407	ACTTAGUCCCCAGGCTGGUA
241393036	64408	TCGACCAGAUCCCATCAUACGA	64409	CCCAGACUCCCTACCCACUG
262161704	64410	CCAGAGCCCCUGGAGTAAUCA	64411	CTCACCGGAGUCATTGUAGACA
319922384	64412	GAACAACUCCACCATCTCGUAGT	64413	GCTCTCUACCCTGTGTCCUG
318378972	64414	GTACTTGTGTUACCCTTAGAGTTTUGGT	64415	TCCGATTTTGAUCTTCTGCCTCAAUT
236868309	64416	GCCTGUCGCGGAGAGTUG	64417	ACCACCTGTUTTCCTTGCTGUT
237455671	64418	CCCAACCCCAAAGUCATUGGT	64419	CATTGACCTTUGTGTCTGCTCUG
262245596	64420	GCUCTGATAATGUGGCCCCAA	64421	CCGAGGCUGCCAGTUCAG
267802419	64422	CCCGGGAAGGUCTTCTCTUCA	64423	TGTCCCTUACCTTCCCCATUCA
269205569	64424	GCCTGGGCUTCAGCACUC	64425	TGGTCTCACCUAGGACTTACAUGAT
317422236	64426	ACTCTGCUGGCTTGCGTUAT	64427	TTGTCTTTTGGUTGCAGGTUGG
327596939	64428	CCAGAGTTCGUGGAGGTCATUG	64429	AGACCTCGCUTTCCTTCTCUACT
327674430	64430	GCTTGAGCCCGACUGTCTTUC	64431	GTACCACTGAAUCCTGGTGUCA
319487133	64432	GCTGCGATUGTTCCTTGGUC	64433	GGAUCCTTGTAATAUAACCCACACCAT
318429298	64434	GCCGGGAGACAUTCCACTUAT	64435	GCTTCCTTAACAAGUCTTAATCTCUCCA
318741462	64436	GGATCATGTCUGTACGGTAGTTGUT	64437	TGTCAGAACUGACTTTAAGCAGTAUCAG
318085370	64438	GAATCAAUGAACTCGCTCUCCCA	64439	ACCCTATTGCUCAGGCCCUAA
318457206	64440	GCGCTTGUCGGCTTCAUAC	64441	CAGTTGGUGGATTGGTGUGAAC
318086271	64442	CTTGATCCCCUCAGGCAUCAT	64443	GTAATCCCCTUGGGACACTCUACT
318060725	64444	CAGCCGAUACTGCACGUGA	64445	ATCAGTTGGGUCCATTGCTCAUT
319082608	64446	TCCCTCCACCUGAGCGTTUA	64447	AACTTTGGCUGACTCTTCCTTUCAT
319614117	64448	CTGCAGATAUGACCATTAAACTAUGGGA	64449	TGCTCTTCCACCAAUACTGACAATUAAG
269235463	64450	CTCTGTGUGGGTCCACATCUC	64451	GGTACCTGUGGAAAATACTUGACCA
266828308	64452	GUAGCTCTUCCCACCGGAAAA	64453	CCTGTGCAAAAAGCUCGGTTUC
265080639	64454	GCACCAGGGCUGCACTTAUT	64455	CCTCACCAGGCUGATGAGTUG
269089200	64456	ACGTGGTCUGTCTGATTUGGG	64457	ACACTTGTCTCUTCTCTCCTGUGA
258477665	64458	CATTTAAATATTUCAGCTGGTTGCUACCT	64459	AGCTGCTTATAGUCAGGGACATUG
267771204	64460	TTCAACGTCACCUTTCCAAACUCT	64461	GATGCTGAUCATATTTGAAUGAAGGCAT
267969759	64462	GCATCCTGGUCTATGTGTTCAACUG	64463	CTCCAGGGUTCAAACGUCCAA
268379754	64464	CTGCTCCUGGGTCATCAATATUGT	64465	GTATUGGAGGCGGACUAGCA
267511526	64466	GGAGAGAUCATGTAUGGAGGCCAT	64467	CUCACGACAUCAGAAGCACAGA
323696344	64468	CTCCACCUACTCCTCCTCUGT	64469	GCCCGACUGGUAGGCAT
323656023	64470	AGCTGCTACUGCTGTGAUGG	64471	CCUGCAGCCCAAAGAGCUT
237168971	64472	CATGCCAGAGAUTGCUCAGGA	64473	CCUGTTACUCACAGAAACCACACA
257885353	64474	CCTGTGGGUGCACTTACUCT	64475	CAATGCTAGCUTGCCCTAGAUGT
242686025	64476	CCAATGAAGUCTACACGTUGCAC	64477	GAAGGAGGTUCCGCTGGTUT
239696614	64478	TGGTTGGTTUCTGGAGCCTTUT	64479	GTTAAGGTGAACUGGTTCTCATCUACT
332678808	64480	CAUGTGGTATGTCUAGAGAGAGAACAG	64481	CCUAACACGCAUGGGAAGGT
332879041	64482	CTTCCGGTAGUCTGGGTTCUT	64483	ACTCAUGGAGTTGCUGCACT
332727422	64484	CUCATGCAGUGAGCAGGGT	64485	CGCTGUCGTGCGUACCAT
333173260	64486	CCTGGTAGUTGATGAGAUGCACAA	64487	ACTCAGUCCCTGUCCCCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
225531417	64488	CACCAGUCTCCATGTUGCAGAA	64489	GCCCATATGUGCCCCTACCAUA
328650207	64490	GAAACCAGUAGCACCCUGGAA	64491	GCTTGATGCCUCTGTGCTCUC
225946458	64492	AGAAGGGAGGGAAGGUTTAGAAUCT	64493	CCGTGACTGUAGTGTTCTCTCUG
333108074	64494	GTGAAGAAAGAUGGCCACTGTAAUG	64495	CAAGCTTUGCCCTCTTTGGAUG
333058123	64496	AGGAAGACGACAGUGAAAAUGGAG	64497	TCCAGAGAAGGAAUCAGTCAGUCA
327268429	64498	TGAATCTCCUGGACCCCTUCA	64499	GAACTTGTCCUCCTCGCTCUC
264171067	64500	CTCTGCAGACUGAGAUGGAGAA	64501	GGTGATCATTAAACAUGTGTCGAGTTUG
316803881	64502	GTGACTGGCUACTTCCCCTUG	64503	CCGGGACUCAACACATACGUT
316328166	64504	GTTCUGGGACGAUGGAGAGAG	64505	CTAGAGTGTCCUAGTGGCAGGUA
331431860	64506	GTTACACTGUGCACTGCTGUT	64507	AAATCGTGAAAGUGACAGTGATGUCT
330409011	64508	GATAUACCATGACATUCAGCCCCAA	64509	GGCCCCUCTCACUGACAAAC
330347502	64510	CCAGCCAGUTCCTTGGCTTUA	64511	CCACCAACUGGATTGAATACATGUT
269328734	64512	GTGTATCUGCAGTTGUCCACCT	64513	TGGCTUCACAACCCAAACUGT
264122952	64514	ACTACACAAAGAACUCCTTCATTGGUT	64515	ACGAGTTACTGTUGAGGATAAGGACUT
257701867	64516	GCACCUGCCCAATGAUGGAG	64517	TGAGGTGGGUGAAAAGGAATGAAAUAA
268480520	64518	GCAGCTUGAAGGGATGGTUGAA	64519	CCCACGCCAGUTTTGAATACTTAGUA
265250473	64520	TGTGGAATTTAAUGTTGCCTCAUCCT	64521	CTGTGAGTGUAAGGACCTGCUT
268299492	64522	ACTCTGTGAGCAAACUATGGTTAATUCA	64523	AGGAAGTTTCTGUTGCTATCACATTUCT
327232882	64524	CAATTTTGTTAACTUCTCACGTGTCTUCT	64525	GCAAACGGGAAGAUAAAACCAAGUC
268246578	64526	CCCCCAAUCTGATAACTGUGAAGAA	64527	TCTTCTAGAGAAUCAGGAAGGAGGTUAC
268958831	64528	CAGACGAGAGGGACAUCUGG	64529	CTCTCGCUGTCGCTGGAUAAG
268076884	64530	CGCGCAGGAACUTTGGUAGT	64531	TGAACTGCAGGAUCATGTCCTUG
268042098	64532	CACTGTCCCUGGGTGTCTTUC	64533	GACAAAUGCGGAGAUGAGAACAAAA
267404692	64534	GAGGTCAGUTATTGGUGGGACAA	64535	ATGGCCACGUATGAGUCCAC
325926226	64536	GCCTGCAGGACCUCATCATCUA	64537	ACTTCCCCAGGUCCCUCAG
323495295	64538	CTGATGCCAGUGTCCUGGAG	64539	CTGCCCACCCCUGCAUAG
324598428	64540	AGATTTACCGCUGGCCCAUC	64541	GCCAUGCCCCTTGTTCUAGAC
323839039	64542	GAACAACUGGCAGAAAATUACCACA	64543	TGCTGGTGCUCATCTCATUACC
325134860	64544	CTTCTCTGTCCCUGTCTCCTCUAA	64545	CTGGGAGCUATTTCTUCAGGGT
323867845	64546	GTTTCACATGUACGTGGGTGUC	64547	GAUGGCCAACAGGAUGACGAT
324235470	64548	GGUTGGCTCCAUGACCAAGAT	64549	TCAAGGCUACTCCATCAAUGCAG
325758102	64550	GGTGGCUGCTGUGCAGAA	64551	CCATCGUGACGGGTGUGG
269374260	64552	CTCCTATTUCAGCGGCCUAGAC	64553	GGTCCTTGAAUTCCAAGCTAUCCAC
316027750	64554	TGAAGUGGGATCCCUCCAACA	64555	GCTTCACAAGUCCTTCAGTTCTTTUT
315716933	64556	GCAAGAGGUGGCAGAAATGCUA	64557	GACCCTGTTTCUGAATTGCTAAATTGUT
332568150	64558	CTGGCACCGUCATCUGAAGA	64559	CCAGCTGUGCCTGTACCTAUG
326089428	64560	CAACTGCUGCAATTUCAGGGT	64561	CTCTGTAGGGCUACCTCAGAATCUT
326067361	64562	GGUGAAGCGAUGACCACAGA	64563	CACTGUGGCGCUAGACACAT
264264841	64564	CCTCAAGCCUCTCTTTGGCTUT	64565	GTGGATTATTCTGUTGTTGTTGGCTTUT
326583644	64566	CAGAGCATTAGUGTGTAGACGUGAA	64567	ACCATCTTUGTCAGCAGUCACA
226235955	64568	CAGAAAUGAGAAACCACCAAUCACAAA	64569	ATCAGTGAUCGCCTCTTGTGAAUAAAT
265276853	64570	CCAGUGAGGAGCCAUCACAT	64571	TGAAACAGCUTCAGCTGCUCAA
316779403	64572	GTACCCAGAGAGCUTCCCUAGT	64573	GCTTTTGAGAAGAAUGACTTTGGTTTUCC
324489070	64574	CTGAGTGAGAAUTTTCCGCUACCT	64575	GCCTTATGGAGCUTCATTTTGTTGATUT
324871822	64576	GGGAGTTTCAUGAAGCCACTUGAT	64577	TTAGGTGATGTUCACAGAAGAAGATGUC
267062875	64578	GGACAGGCCUTTATGTTCGUG	64579	TTCTTCGGUGGCAGTCAGAUG
268948234	64580	ACGTTGACCAAAUTGTTGTGCUC	64581	GGACACUGAAAGGAAGGTTTTACUCT
269102999	64582	CUTAACATGUGCAAGGCACGAG	64583	ACATGGTACGCUGCTGTTCTUT
263422452	64584	ACAUTTAACACATGUGACGGAAGAGAT	64585	CATTTTAAACGTUGTTGCATTTGTCUGT
257485980	64586	GTTAGTGCCUTTCACCCUGCT	64587	AAACAGAUGCCAGTATTCUACAGGAAAA
260763022	64588	GAGTTTCTGAUGACTAAGTCUGAAGCA	64589	GCGAGAGGAAAUAAAGAUAAAACAGCAG
269442115	64590	CTCTTGATAGCUTTTCTGTAATCCUGCT	64591	GATCCCTGAUCCTATAGTTTTGTTUGCT
269228807	64592	CCGAGTCTCUGCTCCATGAUT	64593	GGCAAAGTGUGAAACAATTAAGTGATUCT
267285698	64594	AGATGCTCUCACCTTTTCCTAATTUCAG	64595	GCAATGTCTGACCUCTGTTTCAATACUT
325059115	64596	CCAGTCCAAGUCCTAATTTUCCGT	64597	ACCACAGAGACCAUAGAGAGUGT
323490888	64598	TUCAACATGTTUAAAACACAGCAGCA	64599	CTGAAAATAAUCCCGGTAAATTCTGGUT
239690565	64600	CTGTTCCCTUGCTGCTCATUG	64601	CAAGCATTTUCGTCCAAGCAUCT
292913808	64602	ACTUCAGCAGCATTATUGCAGAGA	64603	GCCUGAAGGACAGGAAACAGUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
291791288	64604	GGCTCUGGCCTTTTATAUGCCT	64605	ACTATCCCCAUCCTTTCCTCAAACAUA
289833770	64606	CCCCACCCCUAGTCAACTAGTUA	64607	AGGCCAGAAUGUGGGAAAGG
290818304	64608	CAGAGCACCCACCCUTCUAC	64609	ATCTCTTCCTAGCUCACCACTACTUT
300777167	64610	GTAAAGTGCTAUGGTCATATTGTGUAGGA	64611	AATUGGCCAGGAUGGAGAGAAC
260061549	64612	GAGCTGGTUCCAGAACTCAGUT	64613	CCUTACAAAACAAUCAACACCAGACAC
263830251	64614	TGTAGGTAGCUAGGTAGGATATGUCACT	64615	AGAGGCTUGGAAAGCAAATCGTATUA
257994097	64616	GAGATGAGUTTTGAGTTUCAGAGACAGA	64617	CCTACAGACAGCUTCTTTTTCGTUGT
265950916	64618	GGAAGUACTUGGAGGGAGAGCAT	64619	GAGGAAAGCAACUTACCATGGUG
262792323	64620	TTCCAAUGAAGCAGGAUGGCT	64621	TGATGACAAAUGCAAGGAAGAGTGUAA
319533247	64622	CGCGGAGCUGTTCCUCA	64623	GCCTCCCCUCTCCCTTCUC
319365186	64624	TCTTTTGGTTGUAGTGAGTGGTTTUCT	64625	CAGGAGACUACAGGAAAAGATGGUAAAAT
318632361	64626	CTTTCTCCUGGAGCTCCTTUCC	64627	ACACAUCCCCAGGTCAGUAGAA
332773688	64628	CTTCACAGAACAUGCAGTAUACCCA	64629	GGGTGTTGAAAGACUCATCATGTTTUAA
266782178	64630	CAACAGUGCCATCCGTUACCT	64631	GGAGTGGCUTGGTCAGGTUG
255661510	64632	GCGATGUGAGCGTGUGGAT	64633	CCTTCCTTUGCATGTCCUCCA
315351902	64634	GGGACAGAAGGACAUGAATTGUG	64635	CTTTCGCCACAGUATGTCAGCUA
313622191	64636	CCTCACCAUCCTGTCGCTTUA	64637	CTCTATCCAAGUCACTGGTGGUT
314944170	64638	TGGTCTGAGCUCCCTGCUA	64639	CACCCACCCACUTTCUCCT
268385894	64640	CTTACAGGTCCUGAAAAAGGCTUG	64641	TTAGTTTCTCCUCCAGCTTCAAGUG
320537155	64642	GGGTTATATGAUCACGTGTGTTTGAGUA	64643	CAGAGTUCCAAGCCUCCAACA
315921138	64644	GAGGTTACGTTTUGTTTTCTTGGAATUCA	64645	GGGAGUCUGGCCAAGGAAAAG
320001269	64646	GATGTCTATTGGUTCCCCATCTUCA	64647	CCAGCACCCCUATGUCAAGA
314696583	64648	GGGACCGCAUCTTCTTTGUGT	64649	TCCUCAGCACGAGACAAAAUGT
313443411	64650	TGGUAGAGCCCTGTCUCCAAG	64651	ACACAGCTUGTCACAGTTUAGGT
255096802	64652	CAGCCUCTCAGCAUCCACAT	64653	CCAGGGCCGUGTTUCCAG
314511463	64654	GCCUGCAGAACTGGGUCT	64655	GGGAUCAGAAACCGGGCTUA
312865780	64656	TCTTGTTUGAGCACGUGCAAC	64657	AGAGAGGAUGAAGACAGAGAAUGGA
315503533	64658	TGUGGACCACGAGGACAUCT	64659	CCCACUCAGGCAGCTCAAUA
266937926	64660	GACTCTUCCAAGTGTCAAUGGAGAA	64661	GGAATCCUCTCCTGCUCACCT
261967053	64662	CCUAGTTAATATCTTCUACAGGGAGCCA	64663	AAGGTAATTAACGUGGGTGTCTCAUT
261744404	64664	TGTGGCAGGUAGAGGGTGAAAUA	64665	GTTACTGACGCAUGGCCTCUT
267923852	64666	CCAGTTCAGUAAGGTCAATCTCAUCA	64667	AGAGGAAGGGTUTAACTGAGAGAGUAAA
267638150	64668	ACTTATUACCCCACAAAATTGACUGGT	64669	GGCTCTTCTGGCUTCACTTTAAAAAUT
267993173	64670	GCATTGCGTAGUATGTAGTAATCACUCA	64671	GAGCAGATGGUGTCAGAGGUC
287545341	64672	GACCAAATUAAGGCATTTTCTCTUGGAA	64673	TGCTAAATAUAGGGTCATCCUGGGAA
266940616	64674	ACAUGAATGAAATCUCCCCACACT	64675	GTCTTCCTGGUCCACAAGGUC
268595288	64676	ACCUGAGGACCTGGAUCACC	64677	GCAATTGGCAGGAUAAAAGTAGTUAGGA
267355855	64678	AGGTGTCCTAGUGGTAATAGGCAUT	64679	CCTAATGAAGAAUTTGGTCCAGGUGT
313627461	64680	TCCCAGUCACCACAGTCCUAA	64681	GCAUCCGGCCCAGACTCUA
314783850	64682	GCTCACACCUCTCTCCTCUGT	64683	TCAAGCCCCCUCCCAUGA
323419489	64684	TCCACCCCAUCAGTTCTCTCUT	64685	AATTAGCAAGGUCACCAGGACUC
315816594	64686	GTTTTCCAUACAGAGTCCUGAGGAA	64687	GCCCTCAAAUATGGTCCCAUCC
326916172	64688	CATGCACGGUAGGGCTGTUAA	64689	GCCTGTAACUCCAAGGGTUCA
327886126	64690	GCATCACUGTGCAATTAGUGACAT	64691	GGACATTUCCAAGAGGTCTGACTTUC
327062782	64692	AGAAAAATCUCCCATCCTGCTUGAAA	64693	GGATTTGCTCCUTGGAGTTTACATUC
327546811	64694	GGATTCCTTUCATCATCGTGGUCA	64695	GTGTGTCUAGAGACAGAAACCAAATUCT
327786833	64696	ACATGAAGTCCUTCAGTGAAGCUC	64697	GGTGTTCCTUAGGAGTGTGUGAT
326549028	64698	GTACACCTTATCGUTTCTCATTACCUGA	64699	GCAGGAGACACAGCUGATAAUAGAGT
333615671	64700	CTGTTCTCCCUGGTTTCTCUCC	64701	ACUAAAACCAACAGAGAGUAACACAACA
332993605	64702	AGAGACTTAGAACUGATCTTTCCCCUT	64703	CCCAGTATUGCCCTTCAAATAAGUAGAG
324948674	64704	TCCTCTCTTTUCCTTATGCCCCUA	64705	ACCATACAGAAAACAUACAAAGUACCACAT
323905570	64706	GTTGGGAATCAUTGGCAAAGAAAAUAGA	64707	TCAGCAGATACAUGATCCTACTTUCCA
323305369	64708	TCTTGATCCAAUATTTTAGGGCUGCAT	64709	TGAGCACAGTTTUTACGATTTCCTCUAA
325009000	64710	CTGGCATCCCUTGGTCAGAUT	64711	AACATTUACGAGACAAAGGGTTGUAGT
323879372	64712	CGTTAAACAAGUTGCCTCGUGA	64713	TCTCTAGGCCAUTGAGCACTGUA
323913452	64714	CGTTAACATTUGCTTCATCTUCCAAGA	64715	GGAGACAGGUGATCCTTTTAATGUAAGT
327414092	64716	GCAGTTGCACAGGCUGTATATATTCUT	64717	GACTGGUGAAAACGTTTGTGGTUT
326580108	64718	AGAAGCAGCCUGGGUAAAACAT	64719	GGTTTTCATGAUCGTTTCCTTAGUCAG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
236947701	64720	CACAGUGCGCCTTTUCGAC	64721	TCUCUGAGGCGGGAAAGGA
318243446	64722	TGCTGCCGTAUCTGAAGAAGAAAUT	64723	TCCTCCAGATTUGGAAGCTCTAAATUG
267893206	64724	CATTGCTTGCCUGTTCGGTTUT	64725	CAUTCAGTCGUCCCCACCAG
268053187	64726	AGAGTGATACCUTTCCCCAGGUT	64727	TGTTTGTTCTUCCCTTCCCUGAG
314280444	64728	CUATCACUGAGGCAAGGGAAGAA	64729	GCTTTGATUCGACAGAGGUCAC
324770570	64730	AATACCAAGCACUCATGAAAUGGGA	64731	TTTGCTGGCAAGUTCTATGAGTGUAT
323556112	64732	GCACTTTTAGAGCUCAGTTTGGAUGT	64733	ATGTCCTGUCCTAGGGTTUCCT
324008426	64734	ACCTCCTAAUACAGGCTCTTAACAUACA	64735	CCTTGTTTAGGCUAATGACCCAAGAUT
324512769	64736	CCAAATTCACACUGTAGCAGCTUT	64737	AGCATAATGAAUACCCTAGAGAGUGAAGA
263785186	64738	TGTGTTGAUGACGATGACAGUGAT	64739	CCAGATGGGUAGTTGTGGGATTTUT
263724826	64740	CTAAGAGACAAAGAACCUGCCTTTUCT	64741	ATGTTTTAAAATTGCUTTGGCAGGAUCT
253979701	64742	GCUCAGCACCACGUCACAA	64743	GCAGGAACCGGGUGAGUG
263600503	64744	CAGTATGCCAACAUGACAAATGUGT	64745	TCTATAACCUGCTGAAGAAGGUAGAG
265145556	64746	AATGACTTTCAGGUACAATGCAGAUCA	64747	ACATACATGAAUGCTCTTTCTGAAGUGT
267728844	64748	TCTGATGTTACAAGAAAUGTCCAGCUT	64749	ACTTTGTACAAUGCCACTCTCGTATTUT
267046622	64750	GCCCUCCCCUCGGACAA	64751	TCACCTCUAGCCTCTCTGTUCC
267658825	64752	CGCCGCAUCCACTCUCC	64753	AGCUGGAGGAGCCCTUAGA
240912438	64754	AGGAAGAAAATCAAUCACTCTCCTTUGT	64755	CCTAAAAAGCUGCGTGTGTTUCC
267240056	64756	CTCTTCTACAUCATCAACATCCUGGT	64757	GCAGGGAGCUCCAGGAAUG
237940579	64758	AAAAATTACCUAACAGGCATCCUGGAA	64759	GTCTCTGTAAGAUTACTGCAAGCCUAAA
236823376	64760	AGAAATCTCUGTTATGCCUGGCAA	64761	AAAGCACGCTUAGATTGGAATACUGA
332264093	64762	TGGTCACCCCUCAGCTCUAA	64763	GTTCCUCCACCGTACGAGUAG
272340910	64764	CACTGGGAGUTGCCATATCUGT	64765	GCAGCTCUGTGTTGTGGTUGAT
231118245	64766	TCCTGGATTAAAUCAAGAAAATGGGAATUCA	64767	CCATAGGTAGAAAUACTGGCTAAAUCCT
326374658	64768	TCTCTTACCCUCATGCCCUCAAA	64769	CCTCCCCAUTTCTACTTUGCCT
323768230	64770	CAGCTGGAGGUTGTTCATCUCT	64771	CTTGGTGAGCCUGACCCAUT
323880478	64772	GGAAGATGAUGAGGAAGGCAUGA	64773	GGAACCUGACACTGGTGCUA
325090199	64774	GGTACCUGCAGCGGAAGUG	64775	GGCTGACGCAAAUCTCCUGAT
326201849	64776	GGTCAGGGCAUAAATAGAAAATACAGUCA	64777	ATGCAAGGCGGAAACUTTUGG
258838454	64778	AGAGAUGGCAGAACCAAAGCTUC	64779	GGTGGAGGCUGATTCTAATTGUCT
319872818	64780	CTCTAGGUCCAGAATGAAAAUAACAGGA	64781	TCGGCTGTTUCCTCTAAATGTGAUG
316923343	64782	TCCAUGAGGCACGAGUACAGA	64783	TCATGCTGTTGUTAACTGATCTTCTUCA
332071990	64784	GAGGTAAUGGGAGCCAGCAUC	64785	GCATAGGGAGCUCACGTTCTTUAC
326400261	64786	GGTTGCCUTCCTAGCUACCCT	64787	CCGAAGCGGAAGUTGCUCAT
255763678	64788	TCTCACGCUCCCTTGCTTUG	64789	ACACCAACTATATUGTAATCACAGTCTAAUG
328675749	64790	AGGGCGGACGUGACCUA	64791	GTTGGCCAGUAGCAGGTUCT
328630790	64792	CTCCCACCUTTGAGGACUGT	64793	GCCCUGAGGCCCAAGAAUG
227913054	64794	ATTCAATGCUGGTGGAAGUCAGA	64795	TGAGGACAGCCUTGCGAUG
228970654	64796	AGGUGGCTGUGCGAAGAG	64797	CGGAGUCGTCCCCUGAG
318984015	64798	AACAACCAAAGAUGATGGATTCATTGUG	64799	TCTCATTCCTUTGGGTTTTTGUGGAT
320233200	64800	AAGAGTUGGAACGCUGGGAAT	64801	CCACUTCCTCACTTATUAGAAACACACA
332509342	64802	CTCTGCAUATTGCCGCUAGGA	64803	CAAAGAGTTCCTUTCCACAAATGTGUT
332652512	64804	CATCCAGAGCGGUGGGTUAA	64805	GCTGCGAUAGAAGAGAACCUCAG
333721753	64806	AGGTGTTTCUGCATGACTGAUGA	64807	CAAAATGCGAACUTGTCTTTCACTTUT
332924504	64808	CAAGAGAAAGGUAAAGTTCGGGUAGA	64809	AGGTTCAGGUATTTTGTGGCUGAG
333753847	64810	GGTGCTTTAGAUGGCAGTTCUGAAA	64811	GTCTTGGTGCUTTCCTTTGTTUCC
333229829	64812	CATTCAAGUGCGCAACCAUCT	64813	CAAGTTACTUCCATCCACTTUCCCA
332905452	64814	CAGGTTTATGUCCTTTGTCAAUCCC	64815	AGTGGCTTUGCCAGTAGTTAAAAUAGT
258783308	64816	CCTAGTGATAAAUCAGAAAGCTGCUCAA	64817	TTTTAAAGGAGGUGCCTCATUAGACC
269221256	64818	TGTTCTGCACAUTGTCATCCAUAGG	64819	CCAATAGCAACCUTGTGATCCTGUT
265760077	64820	CATTGGACCACCUCCTTCTTGAUT	64821	GCTACAAAAAUGGTTTGCATTCCUAAGA
257313112	64822	ACTTCCATCUGTGAGTCTUACCAGT	64823	TCAGATTCATAUGGCTTCTGCAAGTAUT
269203607	64824	CCCATACCCUTAAAAATCCGUCCA	64825	GGGCTGGTTCUAGTGATGTTTCUAC
267698851	64826	AGCTCTCGAUGATGTCTGTUGAG	64827	GCATCACTTUAAAAGCCAGCAACAUAAT
262129542	64828	AGGTUGGAGAGCTTCAUCCAC	64829	AGAGCCCUACAGTTTGACCCUAA
266725631	64830	CACCTGAAATUGATGTTTGGTTTCUCAA	64831	CTGTGTGTTTUACAAAAGCATCATCUGA
268889140	64832	CAAUGATTGTCUCCACCAGAGGAAT	64833	GGGTATGUGTGTTCTTCAUCAGG
292658099	64834	CAAAAGGACAGAGGGUAACAAGAGUAAA	64835	TTTCGGCTCUCCTTTCATTUCCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
290959087	64836	TTGTGGAAAAUGTCAGTGAACUACAGT	64837	TGAATGTACUGAAAACCAGGTATCTUCAT
289609294	64838	GTGAGGTGAAAGUGCCCTGUA	64839	GGAAAACAGGCUAGATTGTCTGCTAUAT
222301696	64840	GGCTTCAAGTUGTCTTTTTAATGAUCCT	64841	GTACCTGCTGUAAGTCTTCACTTUCA
327254004	64842	GGGAAGTCUCCCAGGAAGUCA	64843	GGCTGTCCUGGAGACAAACTUT
327528223	64844	AGUCAGAGAGTAGUGAGGAGGGA	64845	TTGCTCTTCAACUTCACACCAUAGT
326695897	64846	GGCTCTCTCCUCTCATCCTGTUT	64847	GCCTCCCCAUCACTGTCUGAT
326896751	64848	AGCAAGGAGUCCAGTCGGAUA	64849	CATGTGGGUAAGTATGGAAGUAGGG
237768419	64850	GGAAGUGCAGCAGAAAGGCAUA	64851	GGGCATCTAAAUTCACTGGATUGGAA
257600958	64852	CTGAACAUTCTGCAGAUGAGAAGGAA	64853	GGCTATTTGCUATCCTGGAAAGTUCAT
235404750	64854	ACTTGTGCCCAGUTTCTAAATCAUCT	64855	GCCAAGGUCCCCCTTCTUG
235270946	64856	CCCCAGCCUTTAGATAAGGUCAGA	64857	GGATTTAUCCAGCCTTGGGUCAG
263473862	64858	GCATGAGUCAACTGGAAGTUAAAGAAAA	64859	TGGCACGGCUTTAAGTCATAUAAGAAT
259075329	64860	CTCTGUGGAACCAGCTCTACAUC	64861	AAGAAGGUTGAACTGTUGGACACA
268512859	64862	CAGGGTGGUCCTGGTAGAUAGA	64863	TCATGUCGGGAGCTGCUAAAAA
256783530	64864	AGGTUCCACTGTATUGGGAGGA	64865	CCTCGGUGGAGCTTGGTTUAC
267530692	64866	GAGGCTTAAUCCTGAGCUGGT	64867	CCAACCUCAACGGGCTCUA
331790827	64868	CTGCCCGUCCCTGTCTUT	64869	AACAGCUCAGCCGTTUCCT
331867630	64870	GGAGAACCAGGCUGGAGGTUA	64871	CGTGGGUATGTGCUGGAGAAG
268753555	64872	GCAGACAGACUAATGCUAGGGT	64873	TCACTGCATUCTCCTCTCTUCCT
327801779	64874	CCCTGCAUGTGTGGATGUGAA	64875	CCAGUAGACACCTTCTTUGCCT
272647951	64876	CCAAGCACAAAGGAACUATCTCATTUGA	64877	CCGAAATATACAAAUTCAGCCTGACGUA
271521218	64878	GCCACGAGGGUTAGACAAUGT	64879	AGGAATGTATUGGATTCAGAAUGAGCAA
271928257	64880	CCAGACTGUGAAGAGGGAUGGA	64881	CAUGTAUGAAGCGGCAGCAAC
319731311	64882	ATAATCCTTTATGUGGCAAGTGAGUT	64883	CCTTCCAGAGCUGCGGATAUT
270371161	64884	CAGGAGGUGACACTGUAGACC	64885	AGGAATCTATGCUTTAGGTGTGTACUGA
321443960	64886	CAAAATCCCACCUGGTCUCAAC	64887	AGAACAAACATCACAAUTACAGGAGACUT
272038156	64888	AGAAAGTAAGCAAGAUGAGAGAGAUAGGT	64889	TCCTGAGTTAAUGTGTGTTTCTTTGUGT
317458801	64890	TTCATTTTGAGCUATTCCCATCCAUACA	64891	TCATTTTCTTACAGUTGCCTGTGTACUT
316651555	64892	GGAGGCUGCATCUAGGCAAAG	64893	AGACATCAGCUTCCATTATGAATUCCA
317249941	64894	AAGAGGAAACAUCUGCGGAAGAA	64895	CCAAAGTGGUTCGTTTCTGATUCAT
316737786	64896	CAGTGTAUCCACGUGGGCAA	64897	ACAGAGGAAGGAAAUGUCAAACAAGT
267899241	64898	AGTAAGCCUTTCAAGGGUCAGG	64899	TCACATGTGCAAUCTTCTGTGUGT
265046045	64900	ACCCATTTTCCUTACCTTGTGUCC	64901	GCCTTCTGAUCACTTTCTGUACCAAA
268906480	64902	CCCACAAAACACACACUTACUCGT	64903	GGTCTCAACTTUGCACCTTTTTCUC
268573780	64904	GGCTCUGGACTTCGAUAGGACT	64905	TTCTCACTTTCUCCCCATCTTTTCTUC
261164349	64906	AAAAATCAGAUGACTGACCTGUCGAA	64907	GGGAGCCUCGTGACTGATUAG
320690799	64908	TCCTTTTCTTUGGGCCAATCTUACA	64909	AGCCTCCCTUTCCTGTATTTCUCT
264985202	64910	AAAATAAGGTGGAAUCTCTCCTGTUGG	64911	AAGACGAGCUGTCTCTGTTGUG
269301385	64912	AGACACAUCCCGGGTCTCUT	64913	CAGGACCATAGUTATGACCAGCTTTUT
262657984	64914	GTGAACAAGGCCAGUGACGUA	64915	CTCCGCACTCUAAATGTTGGAATUAG
268117071	64916	GCTACAATUGCCGCCUGGAA	64917	AGAAAGCCAGUCTCTTCAAACTUCA
325542805	64918	CCAAGAGUACAAACTTCACACUAACCT	64919	GTCTGCAAACCAGUGATAAAAGCTTAUT
327996834	64920	TGTTCCTAACUCCTGAGCAAAUAGAGA	64921	CCATGAATGTUAGCAGAATGTCTTTUCA
229329616	64922	CCTTCCTACACUCACTGCTTTGUC	64923	GGAUCCCACCCCATTUCACAC
224642543	64924	GAAATTUCAACCACAGCAGAUGAC	64925	GTGACAAGAAAUCAAGTAGCAACAAUCA
224413390	64926	CTCATAGUAGCACAGCUGCAGA	64927	GCTTCTACAAGTUAGCTGACTTCCTUA
224464905	64928	TGGCTGAAUCACAAGAAGCUGAAT	64929	TCAAATTGTCCUTTTCAAACTGCAUGG
224118293	64930	GTCATTGAUGGCTATGCAGAUGAAAAA	64931	CCTCTGCTTUCATAGCTTCCTTTUG
224044174	64932	AAGATTTTAACTGAAUGCCCTACTGTUCT	64933	GGATGCAATGCUCTTACTCAGTTUT
223671643	64934	CAGCTTTCACGGAUCTAGAGGUG	64935	CCAGCAGAGAAUAGAGGGAGAATUAAAA
318223008	64936	TGATGCTACAUGCTGAAGGUCAAC	64937	GGCTGTTGGTACAUTTCTCAACTTACUT
261653252	64938	TTCTAAGGGUGCTCGTGGTTUC	64939	CCTTTGGCAAACUCCAGGGAUT
268606928	64940	GCUTTCGUGGGAACCCACAAT	64941	GAAGAGCACAAGAGUGGGAGAAAUA
267980415	64942	TGGCCAACUATGCCTCUCAGA	64943	CCACTTCCCAAAGCUATTCCCATAUT
325758100	64944	ACUGCAGUACCCACAAAAAGAC	64945	GCCAGTTCCUAAATCCAGGAUCAA
326352937	64946	TGCCATTAAUAAGCTTTAGGUGCCA	64947	CTGCTCTCAUCAGGGAAAGGAAATAAUT
260458542	64948	TGCTTTTATCGUAGTTGATGCTGAUGT	64949	TTTACCATGUTTTTGCCUGCAAAGT
257656676	64950	ACATTCATCUCCCTTTTCACCTUCAC	64951	CCAGCTCUGGCTTCAGUCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
315264231	64952	AGGAGCTGUGCTTTCGAGUT	64953	ACACGACGCCUCTCCCUA
313406303	64954	CAGCCUGGGAGGGAAUGA	64955	CGCATCUCCAGCCTCGUG
313710589	64956	CCACAAAGTUGAGGGTGATTUGG	64957	CCTGGTCUCCACTCTCGATCUAT
319591782	64958	CTCTTACTATUCTGTCCACGAUGGT	64959	GCTCTCTTAAGCUCACTAATTTTGGUCAT
332320456	64960	GGAAGCUGCGGCCUACA	64961	CCCACGUCGGCCATGUAA
333741746	64962	CTCTTGGAACAGCCUGGTCUT	64963	CCGCTTCCCCUAACCAGATUG
318008997	64964	CUCAUGGCCCAAGCAGAGT	64965	CCCCACCAUCTTCCUCCCT
317146791	64966	CCCATGGUGCAGTCCATCUC	64967	GCTGUAAGGTGCTUGGGACAT
262075988	64968	AACTGTTTTCUCCCTCTATGTGGUG	64969	CAGGTTATTTGCCUTTTCCCTTGUT
264599258	64970	CTTCTGAAGCAGUTGGCACAUT	64971	CCAAAGUCCCAGGATGTATCCUC
240548524	64972	CTCAGCGUCTTGCCGAUCA	64973	GTCAAACAGGCAGACUCCUACA
232410604	64974	CAGGACAUCGAGAGGAGAAGUT	64975	TCCATTTTGCUTCCGTTGTCUCT
229762274	64976	CCTGGCUCTTCCCACUAAACT	64977	CCTCAATGTAUCCCTTTGGCATTUC
254572831	64978	GATTGTCCUGAGCTGCGGAAUA	64979	TCAGTGCAAUCACCAATATGGUCA
261546845	64980	GGCAAGCUAGTGCTGATUGAC	64981	GACCCCUGGGAAGGTAATTTTAGAUT
265362577	64982	GTTGAAAGGCAAAUGGCCAGUA	64983	TTTAAGCUGCAGAAACAAGCCATUC
227906815	64984	GCCCAAGAGCCAAGUGGUC	64985	GGGTTATTTTGAUCAAGTGCATCTCTUT
231410753	64986	AATGATTCCUACCATTGTUCCACAAGT	64987	GAGAAAAUCGCCGAAAGTUACCAAAA
314517880	64988	GTATCGUGGGCCTAGCUGAG	64989	ATTGCGTTTCCUGCTTTCCTTUT
312889381	64990	CTGGGTGGGUCATAAGGUGT	64991	GCTACAGGAAUTCGAGGATTUCAGT
327014053	64992	CGCCUGGGAGGTTACTGUAA	64993	CCCGGGACTUACCACTGAATAAAUC
262380334	64994	CTGCUGGCACTCAUGACAAC	64995	GCATACTGATUGGAGTCACGTTTUT
257942956	64996	CATTTTGACUCCAGCTCTTTUAGGGA	64997	TCAGGGCUGTAGCTUCAGGAT
264563000	64998	GTTTGCCAUAAAGCGGCAGUC	64999	TGGGATGUAGAGGGCACUCA
297236458	65000	GCTTATUCCGGCACAUGCAAA	65001	GGTTGGUAGAGAACTTAGAGUAGAAAAGG
327467470	65002	TGTTTCUGCCACCTCTGUACAAA	65003	CAATGGTCCUGATTGCAGCAAUA
327786149	65004	CATTCACCAUCGAGTGCCAAAUG	65005	CTATCTCACATTCUAGCAAGTTGGCTUA
279707578	65006	GCATGGGUGAAAGCTAGCUAGA	65007	GGTGGUAGAACTATGTGAUAGAAAAGGT
279308123	65008	GGCTACTGAUTTGAAAACTUCCACAA	65009	GCATTGUTGGTGTUCAGGACT
266962582	65010	GCCGAGGUCCCCAUGAC	65011	GCGCTTUCCAGCGGGUA
268016593	65012	CGACTTCTGGUGCTCTCAGUT	65013	CTGGATGCUGAAGGGUAGGAG
262056806	65014	CGGGTCCTCUTGCCTAGACUA	65015	GAGTTTACCTCCAUTCTGAGAAGCUG
265340635	65016	CGCAGTCUGAGAGCCTTUGAA	65017	TCCCCCAAUCCAAGGCAGUA
267901937	65018	TGGAGGTCGUGAAAGCTGUG	65019	CCCAAAACAUGAGCCGCTAGUA
267329272	65020	GGTTGGCUCTGAGGACTUGAC	65021	CCCCTGAGGUGTGTCTGGAAUA
267035884	65022	AGCAGAAAUGCAGCCCUGAT	65023	TTGTAACCCAGUTCAGTCTGCUC
321358122	65024	TGTATTCAGUATAGTCGCUGGAGGAT	65025	AGAGCCAGAATAUTCCCCATGATTTUT
318439218	65026	TCCTCCTCATAUTCTTCCTCAGCUT	65027	CATGGTAGATTCUACAGAAATCACAUGA
255251436	65028	TGTTGCTGUGATTAGCUGCCT	65029	GGAUGAAGAGUGGAAGGGCAAA
253813553	65030	TGAGGCCTUGGCTAAGCTTUT	65031	TCCATGAUGCTGTACUCCACCT
258320736	65032	GGAGTTTGTGAUCTCTCCTGUGG	65033	TGTTTACAAGAAUCTCTGUGGCAAGT
263562091	65034	GGCCCCAUGTGATGACAUCC	65035	GTAATCAGGGCACUAGCTCUGT
261588530	65036	GCUAGAGGACAUCAACGACCAG	65037	CTGTTGTUGCCAATGTCUGCAT
266635668	65038	GCAUCTACATCCUGAGGGACGA	65039	CACAATGCCCUGTCTCTCCUT
257430105	65040	GGTGATCCAGAUGATCGAUGAGAA	65041	GGAGGAUAGCCAGGACGAUGAT
327996487	65042	GTAGAAAGGAGUGTGTGAGTAGAUCAC	65043	GAAGUCAGAGCAGATATTUCCCCAA
326487839	65044	GTGGAGAAUTCCGAGGAUCCC	65045	GGTGAGACAUAGTGCCATGCAUT
327040782	65046	CCAGCATTTCUGACTAGTTCCCTUA	65047	GACTCCAGUAACAGGCAUGGG
326778981	65048	TGGAGGATCUTGTTGGACUCCAT	65049	CTGAGAAGACCACCUGCAUCT
333521673	65050	CTCAGCUAAACCTTTCATUGAGACAGT	65051	CTCATGATTGGTUTGAGGTTCATCTUC
314065294	65052	CCAGGCCGUACTTGTUGCT	65053	GGUGCACGCUCCAACCA
324507163	65054	GCCGTAUTCACTAAGUGAGCAGA	65055	AGGTGTTGAUGAGCTCCAAGUT
313769556	65056	CTTGCGCAACCUGCTTAUCC	65057	GCACAGCGGACAAAGUCUCA
314640556	65058	GATGTTCCAACUCAGCCTGUCT	65059	CATGACGUACACACTGUCGGT
313402171	65060	CTGTCCCCAUAGTCCATCGUC	65061	TGGCTCTTUCCCACAGTCCUA
328294643	65062	TCCUCAGGAGAAGTCUAACAACGA	65063	CCTCCAAUCGGCUACAGACAA
225125128	65064	GTCCCTUGCAAAAGGAAGAAAAUAGAAC	65065	GGTTGAGAUGAAAGGATTCCACUGAAA
223752611	65066	GTGGAGAAGUAGAATCAATGGAAGAUGA	65067	GAGGCCTCTTAUACTGCCAAATCAAUAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
222306847	65068	CTGAGAAGTTTAAAUGTTGGGTAGTUCCT	65069	CACTGAGTGGCAUCTAAGTTTGCTAAUA
332777874	65070	AGACAGUGACCUAAGGGACCAA	65071	GATTCCCTTUCCCTGTGTCCUC
332336451	65072	GGTGUAGAGGCCAGAGUCGT	65073	CCTACCCTCTUCTGCTCCTCTAUC
332758510	65074	GGTGATGCUTGGTTCAGUGAGT	65075	GCCGATGAUGGCGTAGATGAUG
333778219	65076	CTGAACTCUGTGCGCUCCAT	65077	CGAAUCCCAGCAGAGAAGAGUC
332271953	65078	TCACTCTTTTCUCCTTGTCCTCUCAT	65079	GGGAGCCACUCTCCTACTCUG
319975348	65080	GGGAGGGUGATGGCAGACUAA	65081	CAAGAUTCTTGCCTUCCAAAACCAG
318640981	65082	GGGTGGTCAUGATGGATCUCCT	65083	AAAGAAGGAAGUTCTGGAACCUGAAAA
318475162	65084	CTCACATGUGCCAGTGUCAGT	65085	CTUCAGCAGGTGUCACCAGAT
319331269	65086	CTGCTTCCTUCCATTGTTGTUCA	65087	CUAACATAGACAAUGCCAAACGCA
233467333	65088	CTGTCTTGTCTTUGCTGATGTTTCAAUA	65089	GAAGATGTACCUATGGTCCTAGUAGGAA
234355242	65090	GAAAGCCCUCCCCAGUCC	65091	TGCACTGTAATAAUCCAGACTGTGTUT
318103135	65092	TGAGGTTCUGCAGAGCTCCUA	65093	GCATTAATTCTGGAUTCCTTTTGTGUGT
279402333	65094	ACAGTTCATAAUGCCAGTGTAAACTUGT	65095	CAAGCTACCCUAATCCTGATCTUCAAAA
278043356	65096	TGCAGTCATTAUGCTGCCATCTATUT	65097	TGCUTTCATAGCTUCCACCACAAT
279421461	65098	GGAACAAAAGGAUCAACAGGUACAGT	65099	AAGTAATCATCCAUAGCTACTTTUGCA
277873146	65100	AGGCAGCGAUGGAAATTTTTCUG	65101	CTTGGGTCCUATTGTTCAATGUCAGT
315413595	65102	GAGGACUCATATCAGUAACAACCCAAT	65103	ACAATAAGCTUCAGGAGACCAATTUAAGT
279623712	65104	AGAAACTCTGTUGAAGAAATGGGCATUA	65105	GAAGGATCACTUAAAAGCATTTGTAAGTUGT
265097069	65106	GCCTGGAUAACCCUAGGGAACAA	65107	CTCTGAACACCUCCACTTUGGAT
316339016	65108	ATCAATGTTGCUAGTACACAAUGGGT	65109	ACTCGTGTTGGAAAUGTATATTGTGUGA
317053628	65110	AACCTCUGCAATCTTUCAGACACT	65111	CATGGAGACAUCACTTTGAAAGGAUACA
317808007	65112	AGAATGUGCCAGGCTAATUGCT	65113	CCAGCCTCAUGATGTGGAAAAUG
319065409	65114	TCCATCTTGUAAAGGATTTAAGGCTGUT	65115	GTGGCCCATUTTGATGGTGTTUT
314429145	65116	ACGATUCACGGCAGGUGT	65117	GGGTCAGGUCCCGUCAAG
261022545	65118	GCAUGACACACAGGGTTUCCT	65119	AGCACAACAGACUGTCTTUACGA
266729073	65120	AGAAAGAAGGUTGGTUCAGCACA	65121	GTCCATGTAGATTUCACTGGCCTTTAUA
256770982	65122	GGATACAAATTCUAGGCCACTGGATAUG	65123	ACCAAGGAAAAACUGTAGAGTGAGUG
326627708	65124	GGAAUCCAGGCCACGGUA	65125	TGAGCCAGGCCUCTAGUACA
239977367	65126	TGAGACAACAGAAGCAUTATACTGCTUT	65127	CTGGAGTGTGUGGAGGAATTACAUT
333312224	65128	GAAGTTACCUCTGATCCCCUGAAG	65129	ACTTTGCAAAUCAATTTGCTTCTCUGT
332688764	65130	TCCCAAAGGUCCTGTGCCTAUAA	65131	CGGCCTGUCCCATATGTTTUAGA
321357106	65132	GGGTCAGTUTTAGGACACTUGAAC	65133	TTTCCTCTCUCTCCTCCTAAUACACAC
313079635	65134	GTCAGCCTUAGGGTAAAGTGGAUG	65135	CCTAACUCCCCACCTTCATCUG
312820683	65136	TGTCTCCTGUCAGGAAGGTCUT	65137	CAGTACTTUGCCAGCATUGCAG
312818027	65138	CAGGCUCACCTGUCAGCAT	65139	CCTCAUGCCCAGCCTTGUC
314236080	65140	CTCCCCCUGTTCTATGAGCUCT	65141	ACAGACTCCUCCTACTTCCTTCTUG
323755345	65142	CTACAGAUACCAGGGUGCAACA	65143	GTGCCATGCCUTGAATTTCTTTUCT
320059855	65144	CAGAGGTGCUTTGCGTACCTUAT	65145	CACTAATGAAAGGCUGCCTCUGT
266999529	65146	CTCATTGCCAAUAGTGATGACTUGG	65147	CTCCCTATAATUGACTTCTTGCTUCAGA
254429271	65148	GGAGTCGGAAGUAGGGAGGUT	65149	CATGTTGATGUAGGTTTTGCTCCUG
316561950	65150	AGCCATCAGAAAUAGACACTTACCUACA	65151	GTGACCCCCUACATATTAATGTTGUCA
317784975	65152	GAGGTTGUGGCAAGTUCCAAAG	65153	CCAGATTGGTGTUAGATACTCTGCATUT
315559121	65154	CTUGCACAGACAGCGGUAAG	65155	GGTTGCTTAUCAAGGACTGCATAGAUT
315699054	65156	GTGGCTCCAUTGATGTTGATCUC	65157	ATGTCAGCTTTUCCTGCAAAAGAATUT
320391260	65158	ACATGATCUAGGGTTTTAUAGCACGAAC	65159	TTTTCATCCAGATUGGTTTCCTTCGUA
326951786	65160	CCACCAUGGACGCCAUCA	65161	GTGCCAGGCUCGAGUCC
270145662	65162	CCCTCAGUCCAGGGTTTTCUT	65163	CCAGTTGTGUGCACAAGGAGAUA
316893163	65164	AAGTTGTTCGGGUAAAGGACGUAG	65165	TCACGTGAUTCGCCGAUAAGT
333609805	65166	CAGCAGTCGUCAGGGAAGUC	65167	ACTCACCTAUCCCAGCCAATTUC
320161102	65168	GCCCUCCGAGGATAGCACUT	65169	CATGAGCCGCCUGCUCT
241952764	65170	CATTGCCACCCCUCACUGT	65171	GACTUGGAGGCACCGUCA
262623780	65172	CCCCGAGGUTACACCAUCT	65173	CAAGUGAGGCACCAGGTUC
239351939	65174	CCACACCUGGCTAUGAGGT	65175	TCAATAAAAGAGCUGTCTGACUGCAA
319908012	65176	CCUGCGGACGAGAAATCUGT	65177	CCAGUGGACCCGTTTCGUG
321313879	65178	GGGAUGAGCCCTCUGCAA	65179	CCGCUAGTGTGCUCCCA
321335555	65180	CACATTGGCCUGGATGCUCT	65181	AGTACCGCUGGGAGGTGUAT
319583375	65182	GCUCUGCAGGGCCACAT	65183	CTCGCUGCAGAAGGUCCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
321331286	65184	GGCATUGAGCCGGAUGGA	65185	GTGGAAGUGGATGUGCAGGT
319660137	65186	GCGGAAGGUGTAAGAGATGGUAG	65187	TGGCTCAAUGTGACGGUGAAG
318212534	65188	CTGGGACAAGAGCCUGGUG	65189	CGTCACCGUGAACTACAACGUA
319214786	65190	CAGCAAUCGTGGCUGAAGAC	65191	GTGACGCCUCTTTGTUAAAAGCAAA
258675034	65192	CATCTGAGGCUCTCCUAGCAA	65193	GGAGTAAGGACAUCTGAGCTTGUC
236012954	65194	CTCCTGGAGGUCTGAGATGUG	65195	GGGACATGGAUAGAAGGTGTTUG
235717531	65196	AAATCTCTTGGUAGCTGGTTTACCTUC	65197	GGAGAGGAUTAGTGACTUAACGACAAAT
235912395	65198	GCCATTUGGCCAGTGAUGACA	65199	GGAGGAATGGAUGCTGGAGGUA
236236349	65200	GCAATGATGTUCTGTTTGTATCUCGGT	65201	GCATAGATGAUGTTCCCGTGUCT
268964752	65202	CTTTGGGUGCGTGTGCUG	65203	TCCACCCCACCCACUAGAUT
266996756	65204	CATATACTCAACUCCCTGCCTCUC	65205	AGGGCACUCTGCTGAUCAC
328354219	65206	CACCUCCCCAGGACAUAGAGAT	65207	CAAGTCCTGUTTCTCCCTCUGG
259175293	65208	TGACUCTGTUGAAGCAAAGAGAACA	65209	TGAGTTATGACAGUGGGAACTAUGACT
257665792	65210	TGGCTTTTTCAGUATCAGCTCCUC	65211	TTCGTACTAACCUCGTCCCCUAA
256601569	65212	CCAGUACGCCCGTTUGGT	65213	CTAAGTGCCAACUGGCCTAAUCT
267252003	65214	AACCAGTGGUAGGAGGACUCAA	65215	CAGGAAGAUGACTAGGGUCCCA
264765877	65216	CACAGTGACCUGCAAAAGGTUG	65217	CCGCCTGACAUCCTCACAUA
262879486	65218	TCTATGCCATUGAGTCTGCAGUG	65219	AGCTCTAGCUTTAGTCTCTGUAAGACAT
263893649	65220	TTTCCTCTTTTUCCTCCACCTUCC	65221	AGTAACAGAATGUCCCCATCAAAAUCC
269279014	65222	TGTGTGGGCUTCTTGAGTTCUG	65223	CTTGGGAAGGAAACUTGACTGTTTUG
267789423	65224	TGAGCAGTUGCCTCCAATCUT	65225	GTAGAGUCTGATGAACUCCAGAAAGG
259125465	65226	CCUAGTTGACCUCGACAAGCA	65227	GTCTGUCACCCGCTCCAAUAT
318178248	65228	CCCGCTUCCACATGGACTTUA	65229	CTCTCCUAACCAAGTGTCTCTTUCC
323708806	65230	AGGAGGCCGACUACCUGAG	65231	CTCTGGAAGGAGUCGTCAGATTUG
325581402	65232	GGAAGAAGGCCUGGTAAATGUGG	65233	CCTTTCCGGCUCCTCTTCTUAG
258490074	65234	GCAGCTGGAUTTTACTGCCAUT	65235	GCAAGAAACAAGGCAGUCAATCAUT
242466922	65236	AGCCACACCUCACGTTAGAATUT	65237	AGTAAAAATGTAAGUGAAAGTCTTCACUGGA
235874055	65238	GCACUGCAAGCAAATGGAUCAT	65239	GCCTAGTTTGCAUTTAAAGTAAGACAUAAG
332630622	65240	CUTCAAAGTCCUACCCCAGGAAG	65241	CGAGGACAGUTACACCCUAGCA
226530247	65242	GCAGACAAGGCUGTGGUCAT	65243	GCTGACTCTCACUTCTCTCTCTCUC
328935844	65244	AGATTGGAGAGAUGCGCUGAC	65245	GAGCCTCUTGTCCCTUGCT
226591875	65246	ACTUGCCAGAGCCCCTUC	65247	GCGTCGTACUTGGCCCTAUC
263141949	65248	GATGATCCGUGCCATGGAGUT	65249	GCCTTCCUGGAGTGTTCCTUG
315977058	65250	CATGGTGGCUGAGTTCCAUGA	65251	GTGGGTTCUCCAGCTCATTGUT
316096256	65252	GGCUCCAACCAGCUGGAC	65253	GCUGCCCGTGUACCAGAAC
266314847	65254	AGCGTCATCUCAATTTATGTUAGCGA	65255	TGGATTTGAAGGAAUGAAGTGTUCAGA
262334130	65256	GGCACTCAGCAUCTTCAAGATGUA	65257	GTGGTGTUCCTAGCCGUCAT
315330421	65258	ACTCTCACUCCCTTGCAGGUA	65259	TTTAGAACACAGGAGUCACATGCUC
332644003	65260	GGGTCUGGCATTGCTUAGGG	65261	TGCAGGAGAUGCAAAGAATTTUGAAG
333233574	65262	CCAAAGACCUGCAGGATCUGT	65263	TCCCTCCAUCTGGCTCUCC
323496723	65264	GCGTGTACUCCTCGCAGTUC	65265	CAGGCCCCUAACCCAGAGAUA
326388399	65266	GGTCTTCUGACCCCTCACTUACA	65267	CCACCGUGCCCUAAACGA
324818329	65268	AGCCTCCCAUTGACCAACTUC	65269	GGAATCTGGTCCCUAATCCTACTCAUA
323382731	65270	AGTGTUCAGGGACTATAUCCAAGGT	65271	GATAGTTGGGAUGAAGTGGGACUG
326214327	65272	CATGGCCAGAUGACCCUAGAA	65273	GACTTGGACCAGUAGATGAAGATCUC
324244483	65274	ACGCGACAUCGGCTUCAA	65275	GGTTGGTCUCTGAGATCUCGAA
323840494	65276	GGTCTUCAGCAACCGCATUT	65277	GCUGAGGCCAAGGTTCUGAC
269369922	65278	ACCCCCAUCTCCGCTCTUAT	65279	AGAGGGTCUGGACACACAUCT
320024696	65280	GTCAUCGTGGAUGCCAACAA	65281	CTCGATCUGAGCTTGGGCTUA
318299565	65282	CAAGAGAGGUTCTCGAGCCUT	65283	CAGCCTAAUCCCCAATCCCAUT
326733169	65284	GCTCCUGCAGGCTGACUC	65285	GTCCATGAGGUTAACCCCTTACTUC
327002068	65286	CTCACCCUACCCCGAAGGUA	65287	CAACACACACCACGUTCCUC
316133650	65288	CTATCATCACACAAACUAGTCCCACUT	65289	TCTGACTCTCAAGUCTGACAATTGTTUT
256478283	65290	GTCAGGGATUCCCAGCAGTUC	65291	GCTATCAAAAGGAUCGCCTATGAGTUT
325457557	65292	GGTCCTCCUCCGAGTTGAUGT	65293	CAATCAGCUGTCAGGGCUCAT
262751263	65294	CUTAGGUCGGCGGGAGA	65295	AGGTCCUGGGCTCCTUGAA
318382506	65296	GGTGGUGCACCTGGACTUC	65297	GAAAGCGAGGUGTAAAGCUCCT
226541936	65298	ACCACAGCACAUACACATTTUAGCA	65299	GGTATCCACCUTTCTCUGAGCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
256014410	65300	GCAGGGTCUGCAGTGGTAUC	65301	GGACTGGAAAGUACAAGGCUCAC
324660013	65302	GCGAAATAUAGCCCTGTCCAUCT	65303	CCACGGUTCAGAACCUGCT
324902467	65304	GTACTATGCATGUACATTACAGCCTUCT	65305	GTGATGCTGTUGGATTTCTCTTTCAUT
326247314	65306	CTATCAGCTUACACCATGGUACCAA	65307	GTGTACGTGUGACTATCCATTGUCA
324808662	65308	ACTAATACUGCAAGCAAACTCTCUCAC	65309	GTGGATGAAUCTGGTAAUCCGGAAT
267991507	65310	CTGCAAGUGGAGAGGTGACUA	65311	GATATCTCTGCCUCTTCCTCTCTCTAUT
267714300	65312	GTATTTATCGUCTTGAACCCUCCCA	65313	TCTCCGGGATUATTCTGCAGATGAUA
269197121	65314	TGGGAAATGGUCTAGGAGAGUAAAGT	65315	CTGCTCUGGCAGATTUCAACC
269180858	65316	CCAGTAACAACUCACAATTTGUGCAA	65317	GGGCCCUGTATTGGTTTUGCT
267988509	65318	TTTCCACTCCTAGUTCATTCACACTTUT	65319	GAAGGAATTGGAGCAGUTTAACTCAGAUA
265847985	65320	TCTCTCAAGATACUCTTCTTCAGCTUGT	65321	TTTTGUGGAAGGTCTAUGCCAGAA
268324540	65322	GTTCTGUCTCAAGTCUCGAAGCA	65323	GCCATCAGUCCCAATTTTACATTTUCT
326064778	65324	CTCTCTGTATTTGUTGGTGGGATATUCT	65325	TGTTCAAAAGAGUCCCCTCAATAAAUCA
324721468	65326	GGTGTTGTTTCACUGTTTTCTAGGATUT	65327	AGCATCAGGTCUTGTCTTTTTCCTAUT
262397860	65328	CTTATGGGAGCACCUATACTGCUT	65329	CTGGTTCCCUCCTCGAGAUG
291355444	65330	TTTGTCCCCACCCCUACCTUA	65331	TTGGCCAATCTUGTTCTCTTATCTCUG
291202266	65332	CTTAGTACTGCUGTTCTGTGAACUGA	65333	ACGAUCTAGUGCAAGGAAAAGCC
290674952	65334	CTGCTCCTTCUGAAGTATCTTTTGUGT	65335	CCAACCUGGGCAGCUGT
301334729	65336	TGGGAATTAUCTGAGGGAGUGAGG	65337	TGGAATGTUCAAGCCAAUACACCAA
301108376	65338	CCATCAAACUCCGGCAGTUC	65339	ACCAGAATTCAATUATACCTTGGCCUT
304783742	65340	GCTTATCTCUGATATGTGTTUCAGCCT	65341	GAAGGTGGCGCAUTTGTTTGAUAAT
304409966	65342	TTTTTGGTCUGAGGAAGCATTCUGA	65343	GCCTTGACAUCCCTACTATAGATAUCCA
299944276	65344	CATACGTAAGGUGAGTGAGTGATTUGA	65345	AGATGGACGGAUTCATGGAAAGAAAAUAA
301385793	65346	TCCCTTTCCTAGAUAGAAGCTAAGTUGT	65347	CACTTGCAGGCACAAUAACAATCTTAUA
300094167	65348	CGAGCGTACUAAGCCAGGUC	65349	GAACCACCUAGGCUGGAGAAC
259808855	65350	ATTGAGTTGTCUCACTCTTCTTGAAUGT	65351	CATGTCATCAAUAGCTTCCTGUAGGG
261232120	65352	AGAAGGGACAAGAAAAUCAAUGGCA	65353	TCAAAAATUAACCCCCAACCUCCAAT
259162471	65354	CACATCATGACTUTGGCTTCTTCAAUG	65355	CCCCAAAGAAUCACACCAAGACTTTAUT
315763166	65356	CCCATAUGGAGAAACCACTTUCCA	65357	CTGGACATCTTTUAACCAGGAGAGAAUT
268256189	65358	AATCTCAACCAUGCCTGUGCT	65359	GCATTACTGGUTGGCAACATGAUA
265265860	65360	CTTTTTCTGGCUTGTCAGGCTTUC	65361	TTTGGAGATCAAACCUTTCACTCCUT
268924779	65362	TGTAGCTCTUAAAGCAATGCAGTTTTUC	65363	GCTGAACAUGATTTGACTTUCCCAA
265657475	65364	GGAACCUCCTCTGTUGCACAT	65365	AGAACCCAACAGGAUTTCUGAAACAA
312677994	65366	CCCAGAGTTUCAGCATTAAGTCAGUC	65367	AATGCCACUTGCCTTTAUGCAAAA
228922143	65368	CTGGTGCAAUTAATGGAGAUAGAAGACA	65369	ACCCTTUGCTGGAAUGGACAA
316197315	65370	GCAGAAUCACCAGGCCTCAUC	65371	GCTGTTAGACTCUTCAATATTGCTGUCAA
316508662	65372	AGATAGGAAATCAAUACCAAAACACTTTAGAUA	65373	ACTGATCTTTCUGAGTCCTTTUGACAAA
316963583	65374	ACACTAATTCAUCTGCAAAGCUCACA	65375	CCTCCACAGAAUGCATCAACTUT
316605530	65376	ACAACCAUGACATTGCCCTUCT	65377	CGGTCAACAAGUGGAACTCUAAGG
313879459	65378	TGCCATTTGTTGUGTATCTTGGTATCUA	65379	ACGATAATTTGUGATGTAAACTCTUCCCT
314341782	65380	GTGCTGUCATGGATTCAUCCAGA	65381	GCTAAGTGUCCAGCACATCATUAAGT
312956891	65382	GGAUCCGAGGCAGCAAGTUC	65383	TGGUTCGTTCATUGGCCAGT
314333197	65384	GCTTACCUCCCAAGGCTTUGA	65385	GGAGGGCCUTAGACTTCCUG
313801236	65386	CTTACAGGTCUTCAGTCCTTUCCC	65387	GAAAGCCGUGAAGGAGTCTUCT
267904497	65388	CGUGACGCGACAACGAUT	65389	CAAGGUGGTCAGCUCGGT
267491306	65390	GTTTAAAAGGCAUACATTTCCAUGGCA	65391	ACGTAAAAGCAGGCAUTCATCUGA
260311421	65392	TCTCAACCAGUGATGTATTTACAGUAGGT	65393	CTCTAAAACTUCTAGCCCCGUAACA
264962479	65394	GCTTCCAGCAUTGACACCATUC	65395	AGCAAGTGUGCCGTCTCUAC
317097921	65396	TATTTCCUGACACAAGCAACCAUT	65397	GGATGAGCACACUTTTTCTGGUG
318507325	65398	AAAAACGTATUGGGAGTCGUCGAT	65399	TTGTCGGATTUCAGGTCTCTGUG
312670060	65400	GACACCCTUGCAGCCTCTUA	65401	CTGCTCCUAGGGCTTCTUCC
315303966	65402	GGCCCTCUGATGGTTCCCTUA	65403	GCTTCTTGGUATGGCCAGCUC
314995455	65404	GGAAGUGAACAGGCCTAGCUT	65405	GTCAGCTCTTGUAGGTACACAGUC
257820961	65406	GCAGGCACAAGAGCUGAUGT	65407	TCTCAGTCCGGUTTCTTCGTAUCT
264464740	65408	GGGCTCACUCCACTGAUAAAC	65409	TCCCAAAGCCUGACTTTGTATCTUC
263165604	65410	GCATATGCTCTGUGCTTGAAGTTCTUAT	65411	ACAGAGCUGGCATCAGTCTTTUT
255056279	65412	TGGTTTTCUCCACCACGTCTAUG	65413	CACACTCTCUCAACTTTGTGACUCT
269207200	65414	GCTCCTGTCUGCTTTTCCAAATAGUT	65415	TGTCAGTTGATCAAAUTCCATTTTGAAACUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267635768	65416	ACCTTTTAAAGCUTCCGTTTCTATGUCT	65417	GTGTCTCAGTTUGATAGCATCTGUGA
333547711	65418	ATCTAGACAUCCACCUCAGCCA	65419	TGATCCCTACUCAAGGAAGCTCTUT
325190135	65420	GAAGCCTCUTCCACTGTCUACAAT	65421	TGTCCACCCAGUAGGAGAUCAC
325152553	65422	CCAGTCUCCCAAGGAAUGCAG	65423	TTTTGTGCUGCTGTCATCCUAGT
321494908	65424	CUTCTGAGAGAGAUCACAAGAGAGGA	65425	TGAAACCACUCAAAAGGCTCGUT
327489580	65426	CACCAAACUTGCCAUGGGAAAA	65427	GAUTCTGGCUGAGAGGAGGAAG
327157939	65428	TGTGAATGTGGUGCGTTCCTUA	65429	GGUCTGTTTUAGACCCCACCAT
327372344	65430	CAACCAGTCCUGGATTTTTAGCUCT	65431	CCACGTTCCAUGTGATCTCTTCUA
328032968	65432	CACGGAUGAAGAGGGTATAATTGAUGA	65433	CCCAGGTGUGGAGTATAGCUAC
328163685	65434	CTGGTGGTAUCCAAGCTACAAATAUAGA	65435	AAGTCTCTTGUGCATGGCCTUA
328395149	65436	GTTATGAAGGAGUTTACAGATUCCACCT	65437	GTGCACTTTATTUCTTGCTTGCTTUT
327299330	65438	TGTGATACTAGGUTCATATGAGGUCAAGT	65439	CTGGATUGGCAGAGTTCUGAAGA
326592393	65440	GAAAATAAAGACGUCCCTTCTTCAACUG	65441	ATCACACTTGUCTTACCAGGCAUT
327652758	65442	GTGATGGTUGTCATTGTTUGAGGAG	65443	CTAAAGTAACCCCUTTGTCTGAUGAGT
327142229	65444	GCCTCCAAACCAACUCAGGAATTUA	65445	GCCATUCCAAAAGCTGCCAUT
328445985	65446	GAAGUTGGTGGUGAAGGGAAGT	65447	CAATGGAGATTUGGAAAAACCTGATUCT
332371517	65448	CTGGAGGACUTCCGGGATUAC	65449	GACCCAGGUCAAACGCCTTUA
323748894	65450	AUTGATGGUGGACCACACAGAG	65451	AAAAGATCTTCUGGAACACGGUGAA
325145344	65452	AGAACAGAAGAAAUCCTCGCCTUG	65453	CUACTACATCATCTUGCAACCGAAGAA
323381034	65454	CTAGGAATTGAGCUGGATGAAGAUGG	65455	TGCCAGUGCACTCTCATACUG
323486047	65456	ACACCCTTTTTCUGAAATTGTGCTUAC	65457	AAGCCTAGACCCUCTTTCATCTUAGA
325230427	65458	GTTGCTAGGUTGCTTACCTTTUAAACT	65459	GGCTGAACCTTUCCATGATAAAATGTUG
327747089	65460	AGCAATGGAAUGAAGGTCCACUT	65461	GACACCTGAUGTTTTCTCAAGCUC
326444458	65462	ACCCAUGCAGGAAAGAAAAUCAGT	65463	GGCTGCCUAGTGCTGATGTTUAT
327663718	65464	ACCTCAGUCTTCGTTTUGCAAGA	65465	CTGGTTCAGAUTTGTCATTTUGGCT
327704910	65466	TTTGAAGTGGUCATGCAAATTUCACAA	65467	TCCACCUCAGGAGAACAAACTTACUAT
242478548	65468	TACATTGAAAAATGGUAGTAGGTATTTAUGGAA	65469	CGACTUGCAAACCTGTTGGUAAA
236818060	65470	TCAGCTTUGCTCACGTGUCAA	65471	TGCAATTTCAUCTTGAACTUCAACACAA
237702371	65472	GATGGAAATGAAACAAUTTGTCACTGUCT	65473	TGTTTCACCTUGGACAGGAACUC
259465360	65474	GGACATUGAAAGCAACCTGCUC	65475	GTTTTCCUAGACGCCTCTCCUT
268186624	65476	CATCCUGCCAGTAUCCCAGAC	65477	GCCCTAAAGACUCCAAGACUCAGAA
265875985	65478	CCTGGGUAAGGGATGCTGAUT	65479	CCTCCTGGAUCTGGATAUAGACCA
262053937	65480	CTCCCTGTTUGTCCACTTCUGT	65481	GGCUTGATGTTCUGAGGAACCAT
327764358	65482	CCGTCCUCAGACCCAAACAUT	65483	GCAAAGGGAACAUTATCAUCAGCAC
328423245	65484	GGAACAGGAAGACUACAUAGGCAAAC	65485	ACCAACAGCUTTGCCTCCUT
327501185	65486	CUAGGAGAACUGAGCAGGAAACC	65487	CCCTTGACCUTTTCCTCCTUGT
326585640	65488	AAUGCCCAAGTCUGAAACCCAT	65489	TGCCCTCTTTTUCTAATCCTTCATUGT
313034065	65490	GGAAGCTGAUCCGCTGAGUAA	65491	GCAAUATACATTCUGAACCCCAGGA
323979169	65492	TCATACTGTUGCCAAAGGTCUCAAAA	65493	CGUCTAGUCAAAGGAGCAAAGGG
323841591	65494	AATGCATGAACAUCTGGTTACAUACCA	65495	AGAATGTGTCUGCAAGATCAATGAUGA
325047986	65496	GGCTTCTTCATCAUCATCTTTCTTTTCUT	65497	TTTGTTTCCAUCCAGGCCTCUT
255173443	65498	ACTGGTTGACAAUAAGCGGUGAA	65499	GTTCATCCAAGGAAUAATACTGGUGGA
263178331	65500	CCAACAGTTAAUTGGATACCCUGGAA	65501	GTGAGGGAAAAUAACCAATCACTTUCAT
266767271	65502	ACACATCAGUCCAACACTTUAGCAAA	65503	GCAATACATTGGAGUGTACAGAGATUGT
269113526	65504	TTTATTAGCCUACTCGCCCUCCT	65505	GTCTGTTGTTUGGTGCCATTATUCAAAT
269076963	65506	GCCCTCAGGUACGTAGCTUT	65507	CCTCCACCCTAUTTTCATCTCCAATTTUA
268588979	65508	TGTATCATAAAGAGUGTCAGCUGAGAGA	65509	GGAACTUACAGCAGGUCCAGAAC
268457866	65510	TCATTCCTTTGTAUACAGGGTGAAAGUG	65511	TTCTACCUGGCTGGTTGAAUAAAAACT
268408474	65512	CAAGCTTGAGGAAUTTCATATTTTUCAGT	65513	ACCTGGUCGAGCUGGGAA
268867307	65514	TGTTTCCAUGACACCAGAUAACAAGAG	65515	CGTTCTTCAATTUCTTCACAAGTGTTUG
267122146	65516	CAGGGTGAGAAGAUCTCCCTTAATUG	65517	CGAGTCATAAAGUCATCAATCACCUCAT
267785091	65518	TGCAGGAGGAGAUTCAGTUGAAG	65519	CGATCTCCUCGTTGAGAGATUCA
235224752	65520	GCAAAGUCAACUAGAAGACAGGCA	65521	AGGGTACAUCCTGTGTCTTUGAGA
266535608	65522	AATCACAGCUGCAAACGTTAAATTCUT	65523	TCAUACACGGCAGCCACAUAAT
257545338	65524	GGAGCCUCACCGCTUCAAT	65525	GGGATGTTAAGGUCTCCTATCAATCTUA
328357382	65526	AGACTAUAGGACAGCCUGCGAA	65527	GGGTCAUGGCAAACTGTCTCUA
272296489	65528	GGAAACAAUACTGGCTGAUCACC	65529	GTTAGGUCGTTCTUCACGAGGAT
333782305	65530	TCTGAGGTAAAUCCAGTGGCCUA	65531	CCCCCAACACGUTGCAUGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
233175804	65532	TCTCTTTTCCCCUTGGGATTAGTAUCT	65533	AAGCTTCAACAATUTACTCTCCCATGUA
233123150	65534	AGTTTGCTGGUGGAGATAAGGTTAUG	65535	AGCAUTTCCAAAGAUGGAGCGA
232951907	65536	ACAGAGGAAGAUGGUCCCAAAGA	65537	ACAACAGAAGTAUAAGAATGGCTGUCAC
325203620	65538	GTAGGAGATCUTGGATGGGTUGG	65539	CTGTCUGAGCCACTCCGUAT
324076684	65540	TCTCCGUCCAGCTGACTTGUA	65541	GTGGAGACAGAUGACCAAAGUCC
323746002	65542	AGCTCTGGGCCCUGTATATGUA	65543	CGAGUCAGACACAGAUGACCAAG
325838581	65544	CAGCTCCAUGAGGCUAAGGAT	65545	TCCAUCCCAAACAATTCCUGCT
324307190	65546	ATUGACAAGGGAGTUGCACAGA	65547	CUCAACCACCTUGCAGGAGA
314658782	65548	GGTCGAACAGCAUGAAGGCUT	65549	GGGTCTCTTUTCAGATTGAGTUCAC
332050806	65550	GTCTGCAGUGCTTTCCATCTUG	65551	AGAAAGAGAAUAUCCGGCAGGAGAT
332054996	65552	ACCTCUCCAGCGCTGTUC	65553	GGGAGGACCUCCCUAACCAA
332165709	65554	CTTGGTUCCGGCTGAACTCUT	65555	CGAAGCUGGACAGTCUGGAG
332149722	65556	TGTGAGUGGGCCAGGTGTAUA	65557	ATGTCAGCUGAACTTTCCAUCCA
261200248	65558	GGAAAGAACTTCUTCTGCCTTACUGT	65559	AGGCCTAGCUAATATCTTAGTCAAUGGT
255423765	65560	CTGATCTAACAUGATGTCTCACCTUCA	65561	TCTGAAACATCUCAACCATCAGTUACAA
324973138	65562	CAGCTTGTAUTCCTCTTCTTUCCCT	65563	GATTCATCAGACGUCCATTTTGCUAAA
328834405	65564	CUGCCACGACGGUACCA	65565	TCCTGCUCCAGGAUGGAGAT
328760002	65566	CGCCTCCUCGGAGUCCT	65567	GCGGAAUCCGGGCTCUAAC
318222579	65568	AGCTGTCCUTGTAATTGCCUCAA	65569	CCTCTCTTGTTCUTGACAAATCCAGAUA
326442863	65570	GTAGCCGTUCCCCACAGUAA	65571	AGCCACUGGCTTTGUCAAAAAG
332618707	65572	CTTTTTCTTTGTCCUTGTTCATGGCUAA	65573	GGCTTCCAUACTTGGCTGCUAC
332856387	65574	CACCTGCGUCATCATCGAGUA	65575	GGUGAAACAGGCAAGCGTTUT
333715087	65576	GCCTGTGAUGAAGGTCAACGUA	65577	GGGAGTGCAAGUTCTAACCCUT
332958796	65578	AAUCTAATTTUGAGGGCCAGGACAT	65579	AGCCUCAAAGGCTTCAUCGT
319752995	65580	TGTTGTGGUAATAACCAAAATUGAACAC	65581	AGGCAGAAACAAAAAUCCCAGUCA
262386672	65582	GGGTACTTGUCAGGCGGUAA	65583	GCCATGTAGGTUAACGTCTTAAGGAAUA
262354325	65584	TCTTTCTTCAGUGTCACTTACATTUGGT	65585	CTCUGACACGCCGACTAUGG
267600493	65586	TCTTAATGTTTUCCTCCAAAGCGUAGAA	65587	GTTCACTTCCCAUCTGAGATGTCUAA
264120982	65588	CAGGACAAATCUAGCAAGTCTTUGA	65589	TGGAAATATGCCAGAAAUCCCTTACUG
269253460	65590	AGAGTAGAAAUCCTTAACUCACGGGAT	65591	GTGGTTGTGTUGGAAGTTCCTCTATUAA
290963202	65592	CCACCACAACUGTTACTTCTAUCGAA	65593	GCTTTCTCACUCTGCTCTTTTUCA
289588316	65594	TGACATGGCUAATTCCAAAAUCACAGAA	65595	TTCATGAAGCUTATATTCAATGUGAAGGAGA
223188131	65596	CTCATGCACCAUGACTGACGUA	65597	CTGATTTGCCUTGCTTCATATUCCAAT
222781947	65598	GCTCCAUCCAAGTTCUGCACA	65599	CTGCTTCCTGUGTCGTCTGAUT
222796208	65600	AGCTCCCAAAUAATGAAGATAGAGUCAGA	65601	TTTGCCTTTCTUAATTCAGCCTTTUCC
224584739	65602	GCCTCCAAAGGACUAAATCAGATGAAUA	65603	TGGTCTAGATGAUGGAGAAAGAGATUCAA
224578799	65604	GGGTTUGGAAAATCGCCUGAAC	65605	TGTGTTTGCUTGAGCTGCUAGA
326598924	65606	CGCGCGAGGUCUAAGGG	65607	CCGCAGCAGAUGGTGGUA
327011905	65608	AGTGGACCCUTTGCCTTGUAAAA	65609	GGACTACGAUTAGGGUCGACAAAAA
327565369	65610	CCAATUCCCAGGCCUCAAAAG	65611	TGTCCCTCUGTGTCCTGCUAT
236772532	65612	GGCCCTAUCGGCAGTACUAC	65613	TCTTTTTCTTACTUGCTTCTGTCACUCA
257621059	65614	CTCTTCTGAUACCAAAGGCTCUCC	65615	AGTAATGGTTTTGAUGGCTTTGATGTUC
238236245	65616	TGAAAAATTGGGUGAGCTGCUG	65617	TTGGAGGAAGACCGUTCGATATCUA
239847401	65618	GAGTGGGCAAUCTTTTAGGTCUCT	65619	TGTGCCAAUGTCTGTGUGCT
269267507	65620	AGCATCGGUATTGTTGGGTUGT	65621	CTCAUCCCCCTTAUGCACGAT
268985750	65622	GAGCUGAAGAAAACGCCCUT	65623	CTCCTCCUGAAACTCAGCTTUGA
265992653	65624	AGUACGATGACCUGAGGAGAGG	65625	ACAGTGAAGCUGTGATCAAGTATTUGT
263586784	65626	TGTCGUCCAAGGGCTUACC	65627	TCAAGGTAUAGCAACCACUCCCA
316134797	65628	TCCTCCAACCUATAGAAGGAAGUGAAA	65629	GCATCCATUGGCTGCTTAUCC
331698561	65630	CTTGACUCCCACCTGGAGTTUC	65631	GGCGGACAGCUTCAAAGUC
331783922	65632	GCCCATCUCCATTCCTGTACUG	65633	CCACCTCAGUCCTCTCTTUCCAT
331666340	65634	CCTCAGGCUCAGCTGTGUA	65635	GGTGAATUCGACTCCTTTGUGGT
331858283	65636	TCTTATATTTTCUCTCAGGCUCCAGGT	65637	AGATGUGACCCCCAACTCUGT
331552983	65638	CCCCTUGCGTCGUCGAG	65639	CCAGGUGAGGGAACCAGAAGUA
331572274	65640	TGUAGCCCGTGUCGCAAAT	65641	CUGGCGAGGACTGUGGT
267991895	65642	AGCCCCUGGTGGTAUCAGAAT	65643	CTCATCTUCCCCAAATGTCTGGUT
268689841	65644	CAACAAGGGCCUGAAACCCTUA	65645	ATGTGTTCTATCUCCATCTCCTTCUGA
327918863	65646	ACCGGTAGUCTAGGGUGAAGG	65647	TGAGATAGAAGAAGGGAUGGGTGUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
327767106	65648	GTGCTCAGGGAGUTGGCTAUT	65649	CCTCACAGGCAUCTGTTTCCUT
326753068	65650	TCTTCATGCCCACUGAGGGUA	65651	GCUCCTAGACCUGCAGAGAAAG
314396405	65652	GAACTCGAGGGUTGTCTGAATCAUA	65653	CCTTGATTCCAGACUCTTGAATCTUACA
270540959	65654	CAATGUGGCGGCTAACTTUCC	65655	GTCAGAAATGCUAAGTATGCAAAATGUGT
270055012	65656	TGCTATGAATUCCTAATGGCUGCAA	65657	ACTTTTTCTTCCUCCCTCCTCCUAT
271076114	65658	ATCAGCCCUCATTTGGATGUGAAT	65659	GAAAUTGGTGATUCGCCAACAGT
272257534	65660	AGCAAGCACUAGACCACAAUGT	65661	GGTATTCTGUGGCCTGTATUCACC
272626675	65662	CTGATTGAGAAAGAACUTTATGCCCUCT	65663	TGGATCCCCUGGATTTGTUGAAAC
269965409	65664	AGGAAATAGUGCCATGCTCTAACUG	65665	CCTACTCAACUCCCTTCTTUCCCT
270334169	65666	GTGGCATCUTTACTCACCAUCCA	65667	GTAAAGAAGGGAGAUTTGCCTGTAUGA
317376670	65668	GCTGGTTTGGGAAAUAGAAGTATACUCT	65669	CCAUTAUCGCCCCAGGAAGAC
315739262	65670	TCCACATGGUATCAACCCCTUG	65671	CCTCAGTTAAACCUTGATCAGTATUGGT
317532874	65672	GGCCCCACUAGCCAGAAAAUAT	65673	GGGAGGAAUACACAAATATGCGAATCUA
315562772	65674	CAGAAGAAAAUGAAUGCCCAGAAGT	65675	CATCAAAUCACAGGCTGCTGATUC
317948492	65676	GACATACAAATUGTCCAGGGAUGGT	65677	CACCACAUACTATTAGTUCAAGGGAGT
267241523	65678	GTGCATGGAAAAAUTGATAGCCGUT	65679	AACCACTGUGTCGCAATTTUCAAAT
262544760	65680	TTTAATACCCCAUTGTGUGAACAAGGA	65681	GGGTAGCGGCAAUACTTGAATATTUCA
323471596	65682	CCAAGATGUGAAGATGGCACAUT	65683	CCACAGCCAUTCGTCCCAAAUA
323819211	65684	TGGACCAGAAAUTACAGAAATGGAUGAT	65685	GGTGTGTGTGUATCAGTGTCACAUA
265363744	65686	GGTUCACGGAGGAGAAAUGGAG	65687	CTGTCTCCCCUGGGTAGTTTUG
268465474	65688	GTCAAACGAAAGGAUAATACTTCAUGCAA	65689	TTGAGGAGACAAGUGAAGACCATUC
267271847	65690	AGCCAUCTUCAAGAAAAGGAACACT	65691	GCACAAGAAGGUCAAGATTUCCA
258038234	65692	GCCTUAGAGCCAGUAGGAGGA	65693	AATCAAAAATCCACAGUTCCCTAGGUT
268054776	65694	AATTTGCAATAGCGUGCAAGAGATUT	65695	GACGAAGTUGAGACAGCCATGUA
268594749	65696	TUACACACUGCCCGCAAGA	65697	GTCCATCATGCUTAAGATTTGCTTGUT
266494527	65698	GACTCTATGTGUTCTTTTGGAGUGCT	65699	AAAACTGGAAACUGGTCCTGTAAACUAT
264376786	65700	GCUGCCACACAATUGCAACC	65701	TCAGCCTGAAGGUCCAGATGUA
325789501	65702	ACTGGAGCUGCTCCTATCTUCA	65703	GGTGGAGAAGAAUGAGAAAACAGGUAAA
327069070	65704	CCATGTACUTACTTCCTTTUGCACA	65705	TTCCCTTUCAGCGGTTTCTAAUGAA
232976845	65706	GCCTCCCCACUGTTCCTUAC	65707	GCAACTTUGACCCAGGGAGUT
230770022	65708	GAGGGTCCUTGGGAAACUACAT	65709	TGUGGCCATCUCAAGGACAC
224468965	65710	AAGGAAAAACUCAAGGAAGAACUAGGAC	65711	TGTCTGTCTAGCUCTCTGAATCTGUT
223512026	65712	ATCAGCTAACACAGGAAUTATTCAGCUT	65713	AGGACTACTTCUAGTTCAGGTTTGTCUT
222164979	65714	GACAGCAAAUGGAAAAAGAUAGGCA	65715	TCTTGCTTCUGGAATTCCUGCAT
321106450	65716	GGTGACATCUCACCTCCTTUAACA	65717	GCTGAAATUAACAGACAAGTTGGUCAA
262071929	65718	TTTTTACTTCTCUAGAACTTTGCTGCUCA	65719	GGCGTGGTAAAAUGTGACATAAAAUGAA
261074171	65720	CCATGTAGGGUGAACCTGGUG	65721	AATGCTGAAGGAUACAGTGATUAGCAA
268919490	65722	GGGAGUAGAGTGGGUCGGAA	65723	GATCTAATGGGUAGCTGCTGUGT
268154225	65724	GTGGGATUCACCAGCUCACAT	65725	CATTCCTTAGGUCCGTGATCTTCTTUA
266080801	65726	TUTAGTGTGCUCAGAACCACGAA	65727	CAACUCCCAGATUAGCCCCAT
264249771	65728	AAACTCTGTUCCACAAAGCTCUGA	65729	ACCTGTTGTTAAAAUGGAAATGAAGGUA
264589722	65730	GCCACTCUACAGGTTGCTGUC	65731	GTTGGGTATAGUCAAAATCACCTCTUCA
263152647	65732	GGAGGAGGAGUTTAATCATAUGGAAGG	65733	AATCCACCCCAGGUTTCCATUT
314219745	65734	CCCCAGAAGCUGAAAATGTUGGA	65735	CCTGAUGGAGGACUGCGA
313947041	65736	GGCCCGCUCCTACCAUC	65737	AACGCUCGGGUGGAGAAC
317158439	65738	CGAUACCCAACCGGUGACA	65739	GTCTACACUCACCACCAACCUC
317388673	65740	CATCCTTGTUCCCTATCGATGUGT	65741	CGGCACUCGGAGCAGUT
239999590	65742	GTTATTTGATGUGAACTTTGTGCCUGT	65743	CGTAACTATACACAAUGGATCCAGUGAA
228001477	65744	CCTCUTAAACCCAAUGCCCAGA	65745	GTCCCUAGGAGGAACCUCAGT
227982567	65746	GTTGATGCTCUGCACATCGUC	65747	GTGUGGCCAGCGTAATUCC
264124925	65748	GGCCACTGUCTTGGGTTTTUG	65749	CATCCATAAAUCCCACAGATCTGGUA
261167267	65750	ATCTTAATGAGUCATCCTGTTTTGTUGGA	65751	TCTTGCCTCAUCTGTTGCCTTUT
257247459	65752	TCCCTGATACUGTGGTTGTGAGUAA	65753	GTAGAATCCATCUCGGGTTTCATCUC
232636213	65754	GAGTGGAUCAGCGGCATGUA	65755	CTGCTTGCUCATTTGCCUGAC
231420020	65756	TGGCTCCUCGATGCCCUAA	65757	GGAAACTTGGGUGATTCTTGTGTTUAT
313104849	65758	ATGTAAGTATTGACUGTACACCCTCUCT	65759	GACACTGTAGCCUTTACGAATGTACUAA
313260309	65760	GCAGTATCUAACAGCAGCUGGAA	65761	GGTAACACTUTTCCTGTTTCUAGCCT
317186803	65762	CTTCAAUCACAGAATCACAGUCCCA	65763	GGAGGGTTGAUTGATGGACTAUAGAAAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326670255	65764	ACTGTCACTGUCAATGGTAATUACAACT	65765	GUGATACCTTTUCAGACAGCCGAT
326763089	65766	TCATCCCAUGGTGCCTGACUA	65767	ATTTATCAGTTTUGCCCGATCTCCUT
262515071	65768	ACACTGTGTCCUGGAACCCAUA	65769	GGCTGAGTUCAGGTCATAGAUGAA
315841114	65770	GCTAGAGAGCUCTGAGGACUGA	65771	CTACAGGCTUACCTCTCCGTUG
316641578	65772	GCUTGTTGGTGUCCCAGGAAGT	65773	TGCAGCAGAAGCUGTAAAACUGA
317212467	65774	GGAAAGTGTUGAGATAAAACAUGAAGCA	65775	GATCTCCACCCAGUTTGACAGTUA
298425714	65776	TCGCCGUGCGAACAGUAG	65777	TCTACAAAGGUCACCTGTUCGG
296013136	65778	GTGCTTGCCGUTCCTCTGUA	65779	TGGAAATTCTAGUTTGGGCATGTGUAG
327525115	65780	TCCGUGAGGCAGAGATTTAUCAAAC	65781	TCGACTTAATGGGUCTAATCTACAUGAGA
327702045	65782	CAGACCAAUGGAAAATGGUGCAT	65783	AGGAGAGTUCAGGCAAAGCUG
277938824	65784	TTUATGCTTGATTTCCTUAACAAGAAGAGAGA	65785	GGTAGGTGTUTCTTGGAAATGUGGAA
264186920	65786	GGATGUGCGCCTCCTUGT	65787	CCACTATCUTTGGCTGUGGGT
242563501	65788	GCCAGGUGAGATTCCAGTUCC	65789	GCCTTCTCAGUCCTTCTTACATTGUC
267986417	65790	ACTACACGCCCUCACCGUAT	65791	AGAAGGGAGCUCAGCATTGUG
269254892	65792	GAGCTGGUAAACCTGGCGUAT	65793	ACAAAGCCTUTCTCCACACUGA
333402915	65794	GCCUACGUAGAGCCAAAGGAA	65795	TCCTTTTCACAGUAGCGATCCTUG
258105607	65796	GAGGGTTTGUGACAGGCCUA	65797	TGAGAGAGGGCUCCAAAAGUCA
321127906	65798	CAACAAGAGGUTTGCCCGACUA	65799	CGCACAAAUGTTTCAGAACTUCAAACT
321147998	65800	ACTCTTGGCUTGTATTTTGGGUGAA	65801	CATGUAGACGGATCACTUAAGAGCA
318996586	65802	GCTCATTTCTAUCGATGGCTCTGUT	65803	GGACTGTCATGTUTGTACTTTGTTTGAUT
319898229	65804	CCTCTACCAGAAAAGUGATACTUGCT	65805	CCTGCATTTCTUTATTTTGGTAACGUCA
319174054	65806	AGGTATTTACAUACCGGATCATCUGGAT	65807	CTGTAACATTTCUGGTGTGCAGUT
259519994	65808	GCCAGATCAUGGTAGCTTGCUAA	65809	GATGAGGATGTAUTCAGACTTGGTCUC
254553900	65810	GGAAGGACGCACCCUACUAC	65811	CTATUGCAAGAGCCAGCUCAGA
254718634	65812	GAGCGCAUCGCGGAGUA	65813	CCTCATUAACAAGGGAGCCUGT
254466324	65814	TCAGGACCUAGGAGCTGAGATUC	65815	GCCGCUGATTGGGUCGAT
328346744	65816	CCAAACCACCUCTGCCUGAAG	65817	CATCCTTUCCGAGAAGACATCCTUT
313314880	65818	CAAGTTCUGGGAGCTGCCTUA	65819	CACAGTAAACGUTGTTCTGCTCTUC
315488736	65820	TTTTCGAAGCACUGTCTGTUCCT	65821	CATACTGCUCGATGGUGGACA
314438379	65822	GGAGAGAAGAUGCTCACAGUCC	65823	GGAGAAACUCACTGGCTUGCT
318495733	65824	CCTGAGCCACUCCTCACTUCT	65825	GACTCTCACTCUGACTACTGTCATTUC
319795090	65826	ATGACATUCCCCAAGCAUGGA	65827	CGCAGACGGCAUGTATGATAAACUA
321108379	65828	GACACCACCGAGCUGATUCA	65829	GGGATGAGGAUGCATTGTGGUT
238649441	65830	CAAGUCCGCCGGCUCAT	65831	CTCAGCTGTCUTCGGTTCTCUC
262327187	65832	CTCGGCUCCTGTTTGAUGAAG	65833	GACGUGCGGGACCUGAA
332443457	65834	CTTCCTCAGCUGCAGTCAGUA	65835	AGACAGCCCAUCAATAAUGCCA
332529902	65836	GCAGTCCGTUTTTCATTCACAAUCA	65837	GCCTCCCAGCUCAAGCATUAA
313345461	65838	AGGTUCCCACATCCUCAGGT	65839	ACCCAGGUACATCTTTGAGUCCAT
324813501	65840	CCCACTACUGGGTCCTTCUG	65841	TCTCCACCUTCTTCATTGCUGAG
323502649	65842	CCTGGAAGCUTAGGTCUGACT	65843	CATGTCTUCAAGACGATGTTUCAGG
266808198	65844	CUCATCCGCUACGCCAAC	65845	GACTTTGGCUCCACCCAUCT
260112541	65846	AGGATCGUCTCAACCTTUGCC	65847	GTTCTTCAGTGUGGACAGCTGUAT
332301214	65848	CACAGTUACAGCAAATAGAAACAUGACAA	65849	CCTGTTGCUATGGAGACUACCAA
314686828	65850	GCAGCAGCUGATTTTUAGAGCAAAC	65851	GGGTACCUGAGAATTTGTAGGCUT
223702876	65852	GCCTGATTCGAGAUCCTGAAACAATUAA	65853	GCAAGGCAUAATGATATAUAGGAAGCAAAG
317191864	65854	CCACACACAGCCUACTTUCCAA	65855	AATAGACGACUGAGGAUGGCAAC
317224974	65856	AATAATGAGCACCUGATTGATTGACUCT	65857	AAAGAGCCUGAGTGAATCCCTUC
332672668	65858	CGGAGGUACAUCCCCAAGAAC	65859	GCTCCGTUACACTTTCCAUCCC
332390528	65860	CCATCTGUGGCTTCCTACCUT	65861	CCGCTTCCAGAUCTTCTTGAUGAT
333094097	65862	GGCCAGCCAAUAGTCTATAGCUAC	65863	GCCCATCUGAAGCTTAAACAAAAGUT
319636228	65864	CCACGGAAAUAGAGAAGGAUAGAAACAA	65865	GTTACCTTTCACGUTTCTGTTTGCTUAT
313568761	65866	GGCTTGCTTUTGTTTCTGGGUAA	65867	GCATTGTACCUGGACAGACTTCTATUAA
279550605	65868	GUGAGAAAGAGAGCAGUCCCAAA	65869	TCCTATACAAAAUCCTCCAAGGCAAAUG
279380191	65870	ACCATTAACCCTAUTAAAATTTCATGGTUCCT	65871	ACACTGCATTCUGCCCAAAATATCTAUT
314021488	65872	GTGGTTCAACUTCAGGCTCUCA	65873	CGGGACCTGGUAGGTACTGAAUA
278494415	65874	CTGATGGAATCUGTGAGCCTTUCT	65875	TCCAAAGGAAGAUCCCATATTTTGCUT
279952653	65876	GTTTTGTTCTGUGGATACTCAATTUGCT	65877	GAGAAAATCTTTGUGCCACATCCUC
266121996	65878	GTTTCTTCTCCUTGCTCTTGCUG	65879	CCTGGGTCUCTCAAGCTTTUGT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
260783455	65880	GGAGGTCCUTTGGGTCCUACA	65881	TCGGCTTAAUCCTGTGAATGTTUCAT
320572388	65882	TCTGGCCTGATAUTTGACTACAGTAGUA	65883	TCATGTTUGGGAAGGATGTCUGG
314879247	65884	GGATGCTGAGUCCCGTGAUG	65885	AGGGACATTACAUTACAGGCAAATTCUT
312668647	65886	CCAGGCCUCAGAAGACGAUAG	65887	CACAACUGACACCAACACCUG
237934046	65888	CCTCTCCATTGGAUTTAGGAAAGCTUA	65889	CATCCATGAUGCTCTCCUGCT
332396327	65890	GCTATAAUGGCAGCGGTGCUA	65891	AGCAATTCCCAACCUCCTCTTUG
332397305	65892	CTTTCTCTCCUTTTGCACCTTUGT	65893	GCTAAGCCCAAAUCAAGTTTCAATTGUT
332426106	65894	GCATGTCCAGUCCAGGGAAUC	65895	CCUGAUGACCCCAAACACCAA
315381253	65896	CACAAAGGATUCAGAGACCTACTGUA	65897	ACAAGGUCAACAGCCTGUCC
313127704	65898	GTGAGCUCCGCGTTCAUCT	65899	GTCTAGGAGUGCCAGCTCTTTUT
314225855	65900	AGGGAGGACUTCTGGUACAGG	65901	ACCTGGGCAAGUCCAACAATUT
313620815	65902	GTAGGAGCAAGCGAGUGATUGT	65903	GCAGCAGGUGTACTACUCCAT
314053643	65904	GGUGACUAGCAAAGCCCAAAAGA	65905	CAAGCCAGGAGUCUGAGAACC
312692196	65906	GCGTGUCTCTGCGUCCAG	65907	CCTGACUGTCTGCCUGCAT
313177517	65908	TTTGTTCUCCCGCTUGAAGGT	65909	CCUGAGACAGACCCUGGACA
313377752	65910	CAGAGTCCUCCTGTGTTGUCAAA	65911	GTCCTTUCCAAGGCCAACUC
314711984	65912	GCCTGGGUCAAGGTCAGTAUG	65913	TGGAGGAUGAGGAGGAGATGAAUG
313070606	65914	CACAAACAUGTGGTGGTUGAAGAA	65915	GGCUCAGGCACAGUGGAC
324552404	65916	GUGGAGCAAGAUGAGGAAGAAGA	65917	CCACACTGGCUTTGAGAATAAUAAAACAA
330345784	65918	GTCTTGUCTTTTTGGAUAGGGCAGT	65919	GCTGTTGCTUGGGATTATTTCTGAATUT
327537853	65920	ATCAGTGCCTUGTTTATCTCATGAUT	65921	AGTACAGAGAGTUCACATTTGCACAUT
327852569	65922	CCTTTACCTTUAGAAGGGCAUGACT	65923	CACCAAAAUAGATTGGAGCAUGCAAT
320070153	65924	CCUGAAAAATTCCAUGAAGGAGAACC	65925	ACAGAAGCTUACCACCAAGAUGAAC
260954433	65926	GCCTGAATCGUGTTTTCTGTUGA	65927	AAGCTGCAAAUCACCUCCGA
315901666	65928	GACACCCGACACUCCTCAUT	65929	GGAACCTCTTCCUTATTTTTCCCTTTUC
317821743	65930	ATGACCAGCACCAACUGUGAA	65931	CCTGTGAACAGUGTCCCAUCC
316667432	65932	CACTGGAAACUCCCAAAGGUGT	65933	CCGACCAAAUCCTATCACCGTTAUAT
317050628	65934	GGAGGATGUCCACTTACATGUGT	65935	CCTGATGCTTTUGTGTTTGTATATGGUA
316984142	65936	CAAAAAGTCCAUGCTGGGAUGAT	65937	GGUACTGAGGAAUGCGAGGAG
315777472	65938	TGTUAACACACAGGCCATTTTUACA	65939	GCACCCTAGAAAUTCTACACAAACUACT
316344545	65940	GTCTCTUCCGGCATGGGTUA	65941	ATGUGAGAAAAACCCCTGUGCT
317888564	65942	CATCTGUAAAGGTCACUGGACACT	65943	CCAGAAAGGAUACATAGGGACUCAC
317650512	65944	GACTGGCUCTGGTTTCCTUCA	65945	CGGCAUCATGCGUCGAG
327092471	65946	GGGAGUAGCTCGCUGGA	65947	GGGTGATGGGUGTATCCCTUA
270319919	65948	GGCACCCUGTCCAGTCUAAC	65949	ACUCGGAGAGGGACCUCAA
316679210	65950	GCTTCACUCTGAGCAUAACAAGCA	65951	AAGTGTGAACCUGAAGGGTGUC
333255187	65952	GUGCTCAGUGGGCCAGT	65953	GGCUGCCCAGCCATCUC
333623221	65954	ATGAAGTACAUCTTCTTGCCAAUGGT	65955	CTCCTTCCCGUGTCCCAAUC
332644259	65956	AGGACCAAGUCGAUGAGGAAGAA	65957	TGTAACTTGTCCUCTCTCTCTTCCUG
319949057	65958	GCATCATUGGCCAGATCCAUCAA	65959	GTCTTGCCUCCTGTGGTCATTUA
241059673	65960	GTCTGACUGGAAGGTGCUGAAG	65961	AGAGGCUCGCAGTCTTTUGG
240328351	65962	CCUTGTCCATCUGCAGCGT	65963	TTCCCCAAGGAGUCCUGAGA
321341008	65964	CAGGCUCCACGAAGUCCAT	65965	GCTGCAGGCCGUGGTUA
319588125	65966	CGAAGUCCCACGTGUAAAGAACA	65967	TCCCCACAGGUGAGUACCT
241613566	65968	GATTTTGCAAGAAUCTCGTGGAAAUGT	65969	GCTCCTTCTTGUTTGCTGATGGUAA
239188299	65970	TGGTACCTUCCCAGCATAAUGGA	65971	TCTCTGATUCAAGCCCTACTTGUCT
235862638	65972	CCTTAACTAGACAGCCUCCTACCCUA	65973	GGATCCTGGAUATAGCTGGATTUGAG
258974210	65974	GTUCCCAGACAGGUGAGCAAAT	65975	AATAGAGGCAGGAGGUAGACUCAG
321438788	65976	AAGAAAGTCAGUAAAGTCAAGGTCUCAC	65977	GGCAGTUGACGGGCATGUAT
265442567	65978	GGAGATGGGUGGGAAATUGAAGT	65979	AGCTGCCTCUTTACTGACTGUG
259016388	65980	TCCCAUACCCGTCCGGUAA	65981	ACATCUCCAAACACCUCACCAG
258416945	65982	GACTTGUCCACCCGGAGUT	65983	GCGGAATGGUGTAGAGCUCA
240338133	65984	CATGAAGGCAGGAUGAGAAUGGAAT	65985	CTTACTTCUCCCCCTCCTCTGUT
263209938	65986	GGGACTGUAGATGGGUGAAAAGA	65987	GGGACTGACUTTCTGCTCTUGT
267654293	65988	GGACCUACGTGGCCAUGA	65989	CCGACUCAGGUCCCACCT
266626127	65990	CTTATGAGGUGGCTGTTGTCUCT	65991	TUCAAAGAAACTCTUCAGGAACCCAA
268023150	65992	CTGTCTTTCAUAGCAACTAGCCCTTUA	65993	TTTGTCTTAAATATUGGAGTCACCCAUGT
268366243	65994	GCACCTUCAGCCAGTATUCGT	65995	CACACCTCTTCAUAGAGCGTTTCAUA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
262405463	65996	AUTCTCCATAAUCCCAACCAAACCAA	65997	GGCTGATCUCAAAGAGGAGCTUC
267702329	65998	CGGGACAUAGAGGGATCTGCUA	65999	GTTGTCCUGAGGTTGCCCUT
264885042	66000	CAGTGTCTATUCCTGTCCTGUGT	66001	GTGTCTGUGGTGACCCTUCA
325551448	66002	GACTUCAAGCAGGAGGAGGUG	66003	CTGCCCAGGAGCUCACAUAG
325562343	66004	GCCUTCAAGUCGGGCAAG	66005	TGGAAGATCUCCTGGGTTTUGG
324928207	66006	GAAAAGAGCCCCUGCAGUCT	66007	GCCCUACAAAACACTGTGGUC
238570302	66008	AGGCATTTUGGAACTGGGUAGAAAA	66009	TGACACCAGTUGACAATAGAAGATGUAA
236466777	66010	CTGAAGAAGGAGAUGGTGUGGAA	66011	TCCTGTCAUGGGTATTATTTCTTUGCT
239153785	66012	TTCTCAGGAUGAACTAGCUCGAGT	66013	CUCAGCACACACAUACACACAAAAT
235370590	66014	GACCTTTGAACUCTTTGTTTTCATGUCT	66015	CAAGCCCCUTTCGATTCUAGGT
235180428	66016	TTTTCCATUACAGCAAACACAAATUCCA	66017	GGAGUCAGGAGGGATTCTUCACT
313518207	66018	ACTCGAGUCCTGGCTUCACT	66019	CGGCUCTUGGCGGAAGAC
226587306	66020	GCATCAUCAGCCCGGTAGUAG	66021	AAAGCACTUGGATGCCGGUA
226201195	66022	ACCAAACCAAGAGAAGUCAGAUGAG	66023	CCAGAGUCCCACCATGAATGAATUT
225643961	66024	TCCAGGCUGUCCAGGGAT	66025	ACCTGGCCUCTTGTTTCTTCUC
257428598	66026	GACCTGCUGAGCCCCAUC	66027	GGGCCCCGGACUTTAUCAC
333051402	66028	TCTUCGGAAAAGCCACTUGGT	66029	GTTGTCAATGUCCTGTTTACTCAAAUCA
328404063	66030	GCUGACCACGCUGAGCA	66031	GAGTTCTGGUGGTCGGTGUA
255059427	66032	CTGGTGACCCUGTTTCTCTCUT	66033	GCGCAGGUCTTGGTGUAGAG
261622465	66034	CTCTGGTGTUCTTGGGCTTUG	66035	ACATCCUCGCTGCCTGUG
256783873	66036	CCAGCCCTAAUTTTGCTTTTTGAUGAA	66037	GAGCTCCUTCTTGGAUGCGT
259872738	66038	CAACGACCUGAAGAAGCUCAAC	66039	GGAAATTACAUCCTGGUGCAGAAC
266538691	66040	CAATGCAGTAGGUTATTCATGAACAAUGT	66041	CCTGAGUCAGAAGGCAGAAATAAUCC
268792327	66042	ACTGTGGTACGUGATAAACTGGACUA	66043	TGAACTTGAGCUTGTTTTACAGGTTUG
312699815	66044	GACTCACTCCAGUACTGTTCTTGTUT	66045	AACAACACATTTTAUGGAGGTACAAGUCT
259745912	66046	CCTTTTCUCCCGACTGTTGCUA	66047	ACTGTUCACACGGCCTCTUC
265477332	66048	GCCCTACGUAGCAAACUACAGA	66049	GTGGACGAGUGATGAGUGGT
257590045	66050	GATGTAGGAAGAGUTAATCACGUGCT	66051	CCTGAGCUTCATGTATTUCCAAAGGAA
261750079	66052	ACGATACCTUCAGATGTGTAGAGAUGT	66053	CAGAAUCGAAGGATUGGGAACAG
324288298	66054	AGGTCTCUGATGGTGGCUCAT	66055	CCTCGGAGAUGCGGAUGG
324367140	66056	CTTCCUGGACCGTGTGTAUGG	66057	TGAUATGTCCACAAUCCCAAGAAAAACA
325102790	66058	TGAGCATACAATUGGGACTGACAUT	66059	GGTACAGCUCCGGGTCGUAT
325680639	66060	GGCCTAUGCTGATATCAUGGCAA	66061	ACCUCAAAGGAGACCUCAACCT
325310926	66062	GCTTCCTCCUCCCATCCTGUT	66063	CAGATCCUCAGCCCCUAGGT
324015835	66064	CTGGUGGCCTTTCTCUGCAT	66065	CCTGTCAUCCTTGCUGGAGAC
256221541	66066	CAGTCUGGCAGCGTCTTCTUA	66067	CCCTCCUCACCATAGTTGGUCAT
316402877	66068	AAAAGAGGCAUAGTCACAATAAAGUCAGT	66069	TGACACGCCCUTCTCTGTTUT
333239578	66070	GGAGCAGUAGCGCCUCT	66071	CGGGTGCUGCTGAGUCT
266852799	66072	CATATCUAAAAGACGCGGCAUGG	66073	CACACACCUGCTCTUCCAGAT
326053279	66074	CCATTCTCCCUGTGACAGTCCTUA	66075	TGCGGAGTUCTTCAGCATCUC
264610976	66076	GAACAGCTGAAGUTCATGGGACUA	66077	GGUCATGAGAGAAUGGGAAGAGG
255983609	66078	GCUACGCCGGCTTCUGA	66079	GGGACTAUCCCTGGCUCACA
263737951	66080	CCACCCUACCCCUGGAGAAAA	66081	CTGAGGCCUTCCTCTTGGUG
328931387	66082	TGTTTCAACAUTGAGAGCUGGGT	66083	TGTATAAGUAGAGCTGGGTTUGGAACT
315964458	66084	CCGAGGUGGTCAGTGATUCC	66085	GCCATGTGTCUTTCTGTCCTCUC
323945422	66086	GGTTGTTTCCAGUCTGGTCCUT	66087	CTCGGTGACUCGGTATGTTCUC
267760205	66088	TTCAGCTTCTGUTAGCCACTGATUAAAT	66089	CTAAACTCTGCAAAUGCAGGAAACTAUC
265924827	66090	CTTUCCCCAGGCAACTUCAGA	66091	CUTTTCAGGUAACAGAAAGAAAGCAACA
263807902	66092	AGCACGCAACAUAAGATACACCUAC	66093	GCTTTCAAAGAGGUCATAATAGGCTUCT
326278227	66094	TCGCCACAGAUAAGCAAGTATCATTUAT	66095	CCAATGTTGATGAGUTTTTCTGTGGAUT
318895855	66096	CCATGAAGTTAUTTAACCAGCGUGT	66097	GAATTAATGAACCUTCAGAGAGGCAUCA
240629784	66098	AGCCAATGAAGGUGAGTCCTCUA	66099	GAAGAAUCAGCACGCACCUC
262407971	66100	GGGAGCGCUTTTGGAUCA	66101	TCCTCAGUCCTGGCCUCAG
289538718	66102	CCTTTCTCTCAGUTGTTCTCCCCUA	66103	GGGTUCAAAACAGATCAUCACAAGGT
289530665	66104	CCGTTTACTCUGCTAGCTGCUG	66105	CGCCAGAGCUTTGTTTCAGTTAUT
289871915	66106	GCTTTCCUGAAACTCTGGCCUT	66107	GGGAGCTTCTUGGGTATGAAACUG
305123392	66108	GCACTGATCUTCTGGCTGAUGAAAA	66109	GATTAAGGGCAGUATCTGCUAGACAC
301932849	66110	AAATATCAGGGCCUTTGGAATUCAGAA	66111	CATAAGTGGTGUCTAAGAGGAAGGUG

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
303450337	66112	AGCAUCCGGAAACAAUCACAGA	66113	AAGGAAGTGGUAAATCAAACTCACAUGA
327935040	66114	GCTGTTGACCCUAGGCAGTUAT	66115	GTCTTATUCCACCAGAUCCCACA
257439361	66116	CACCAGUTAAATCCUCAGAAGGGT	66117	GGAGTGACUGAGCTTGCATTAUACT
266794344	66118	TTGGTTCUAGCTTCCATUGGCA	66119	AATTTGCCTCCUGGAACTACTTTAAUGA
256876968	66120	CCATTTCAGUTCAGGTUGCAGAAA	66121	TGCACAUCTTCUAAAACAGCAAGAGAA
268867691	66122	CCTATTCAGAAAUGACGCUACAGCA	66123	TCAAAACATTTGUTCCCCAGAAUGAGA
258410085	66124	ACTCAGAGTTUGCGGAGCTTTTUAA	66125	GCCTTTCTGUCCAGGTAAUCCT
318713589	66126	GCCTGGTGUGACCGAATUCT	66127	GCTGAATTACTGAUCTGTTCTGAGTCUAA
227474416	66128	AAGCAGATCTAUATTGGCGTTGTUGA	66129	GGAAGAAATTGAAGUGCCTTTCAGAAUT
313618960	66130	TGTTGGATAGCTUCTATAGGAGCATUGA	66131	TCATGCATTTUCAAACGCGTAAAGUT
263648980	66132	GCAGAUGCCATUGAGCGGAT	66133	CTTGAAGUGACAGCGCUGAAC
314387885	66134	CCTGATUACCCAGGCCAACUG	66135	AGTCCUGCAGAAGACCACAAUG
313525557	66136	GAAGTCACUCTGTTGTCCUCCA	66137	CGCTTCUTCCCCTAUGCCAAT
333671748	66138	GGCTGUGGGCACTCCUA	66139	GGAGGGUGACGGGAUGGA
316103034	66140	CTCTCAGAAUGCCTTTTACAATGUCT	66141	GGCCATCAGUGGACTCTCTTTUT
316048734	66142	CACTTCTTCCCAUCAAGACTATACAUGA	66143	CACCTGTAGCAAUGTAGATTCTTCCUAA
317672543	66144	TTGATCTGACUGAAGAGTAGUACGAGT	66145	TTGTCCCUGAACGCTTGUGA
318410723	66146	GCCCCGUCGCGAAGTUT	66147	GGCCTUCGCTCCCUCAC
318932681	66148	GCAGACAAGGAGGAUCTGGUC	66149	TTATCTTTUCACCAAGCCUGGGAAT
319605708	66150	CTTCTCTGUGACCCCACGUC	66151	AATCACCCAUCTCGCCATCUC
319100426	66152	TCUTGAACACAAUGAGCCAGGAG	66153	CCACTAACUGAAAATCCAUCACCAACA
324578014	66154	GCUAGCACUACCCACAAGGGA	66155	ATGGAUGGCGACGGAUAAAGG
254187862	66156	GAATGAATGAAUAGCACGCTTCAGTUT	66157	GCUCACAGGACGAGAACAUCT
253788318	66158	CUTGCTAGATTUCAGCAGGAGGA	66159	CCGTCTTGTTTGUTTGTTTACATGGUT
266805659	66160	CTGGGCACUCTGGCTCUG	66161	CATTAGAGAUCCAGACCTTATAGGCAUT
259960757	66162	ACTTCAAAUGCTGGTTCUGACAAAGA	66163	GCTGTCCAUGCAGATGAUGCT
253902719	66164	AACUTAACCAACAUGAGAGGCCAAT	66165	AGAGACCTTUACAAAGCTGAUGGG
257936313	66166	TCTCTCCAUAGGTGAGGGAAAUGA	66167	AATGAGGCTTUGTCCTTACAGCUT
258812152	66168	TCCCCATTUTCACCTTTTUCACCA	66169	GTGTAAGATTTUATCACATGTGGUCAAC
267916479	66170	CAAAGGAACAUACCTGTGGUCCAA	66171	GTCAATAGGUGACTTTCTTTTAATGUGACT
266484953	66172	TTGATTGCTTTTUCTTCGCTACCTTUAC	66173	GTTTTCCATTCCAUCTTTCACCACATUT
237217145	66174	CAGAATATGGGUAAAGATGAUCCGACA	66175	TGGTTUCCAACAGGTTCTUGCT
327350217	66176	GTTACCATGGCUATGACACATTTTTCUC	66177	TGGCCATTTUTCTGTCCCUGAT
327690105	66178	CCAGCCCCGUGTACTTTGTUT	66179	ACCCGTCTUGACTCTACGTAUCC
328292438	66180	CCCAGGCCAAGUGTCUGAAAG	66181	CTCTCTCTCTCUTTAAAGGGATCCUCAT
328432427	66182	CGTGACACAUGAACACGCTACUT	66183	AAGAGGGAAUTCAACCATTUCAGGAAT
326923627	66184	CACTCCTUGAGGCACATCTUCT	66185	TTCCAGAUGTGAACCUCAAGCC
327386757	66186	CGCCUCCGAGAGCTTTTCTAUC	66187	AATGCTGUGAGACTGAACTTATUCCAA
328426529	66188	GGATTGCATTUACCTGTGAGGTUG	66189	CTGTTGTCAGAGGUGTAATTGAGAAGUA
328302045	66190	ACTAAACUCACCAGGATCCTUCCT	66191	TGGTGAAGGUGTATTTCTCATCUCCT
326955211	66192	CAAGAATTCUCCCCAGTGTCATUACT	66193	CTTTTCTCTCTUTTCCGGTTGCUT
324586918	66194	ATGATCAGCGUCATCGTGGUT	66195	TTTTTCUAAAGGCGGCTGTTUCAC
325827373	66196	CCGCCTGAGAUGTGAACCTUT	66197	AGGCTGTTAGCUCCCCAAGAUA
333258046	66198	CCTCCGUGGGTCCGTTUG	66199	CTCATCCTCGUCGTACACGUAG
323952673	66200	GGAGTTTATAGUTACAGCACGAUCCA	66201	AAAAGCAUAATUCAGACAAACACACAGG
324856153	66202	CCCACATAGCUGCTGACAAATCATUA	66203	CCCCAGAACAACUTTCTTGATAAAUGAA
323693612	66204	CCCCTGAAAGAUTCCACTACGUAGA	66205	CTGCATAUACACCTAAGTCAUACAACAGT
325116784	66206	GAAGATGTCCAGGUGTCTTGTTAUAGA	66207	GGAATTTCAAAGGUCAATCCGGTTUAG
324074585	66208	GGAGGCAGAACUCCTCATCCUA	66209	ACGTTATGACCGAAUTGGAGAAATUACT
325638349	66210	AGATCTCGGAGUCGGACTUGA	66211	CCATGTCCTUCACGGTCATCTTTUT
325681096	66212	TTCATTGTAAGTTUACGTGGCAGGAUAT	66213	TGTGCTTTAAGAAAAAUGTAGAGGATUCCA
323827697	66214	GTCGGTCCUGCTGTTCGUT	66215	CAAGTCAUCATCAACCGUAACCCA
263343560	66216	GGAAGCTGUCTGTCTTTGCUGAA	66217	GTAGCTTGAUCTTGCCCGUGA
268881511	66218	GCCUGCGGAACAUGAAGAGT	66219	AUGTAGAACTTCUAGCCCCAGGA
264871928	66220	CTCTAAUCCCCATGTGUGGCA	66221	GCUCCAACACCACAGTCTUAGG
269185543	66222	GGGTAGTTUCGAGCTCTTGUC	66223	GGAGGTCATAGUCATAGAGAGTGATCUT
326843536	66224	ACTCCTGAGCCUGGAATCCUT	66225	CGTTTCTTTUCCTTCCCCAGUG
313456269	66226	CAAACCCATGACUGGTCTATTGGUA	66227	CCAGTGGGCAAACAUTTTTAGCUG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324878848	66228	TCATGTGCCUATTTAAGGTUGACCAG	66229	TTTAGGGCACGACCAAUCAAAUACA
263707543	66230	GTATCAAAGGUCCAGCUGGGA	66231	TGTCCAGTAAAATUGGTTAGGCAAGUAA
268099986	66232	ACTGGTCCTAUTGGTCCTCCUG	66233	ACCACCUTCACCCUGGAAAAAG
258991442	66234	ACTGGATGGGUTTGCTGAAAUACAT	66235	AAACCCTCUGTTAATTCTTTUGGAGACT
268304180	66236	CAGGAGCACUTCTCCCCTTUG	66237	TCTTCATGCAUCTGCTTUGCCT
262896490	66238	TCCCCAGAGCCUGTTCACUA	66239	TGCTGGAAAACUGTGTACTAGCTATTUT
259245594	66240	GGCUGTACGTUCCCCACAAG	66241	TCTTCAACTGAACUGAATTAAGTGUGGT
267841527	66242	AAGCTTTCTTUGGGCTGCUAGT	66243	CCTGGTACUCGCGCAGAUG
234916217	66244	CTGAAATAAGTAUCAACCTCACCCCAUT	66245	AGAGGUCGACAUCCACACCT
236777816	66246	GCCTGTCTTUAAGTTGAACATGAUCCT	66247	CAGCTGCAUCTCTCCTACAAUAGT
328197893	66248	CAGCTGUAATAGGACUGCCCAT	66249	GTACACTGCCAUCGCCTCTTUAA
270825483	66250	CTGCACAUGCCATTCTCAGUG	66251	ACTTGGTTGAAUCTTACTGACCTTUGT
332795995	66252	CACCACCTCUGGCATCCAUAC	66253	GCAGAAGAUCCUGGCAAAAGCA
325194809	66254	CTGGTTTGUGACTGACTGCAUT	66255	ACTTCCTUCCCACCCTCCTAUG
326317956	66256	CATAGCACAGCAUAGCAAAUGAGAT	66257	GCTCAGGCCUCCCUAAGAAAC
264834760	66258	GCTTCACCUCTGGGTTTTUCAGAAT	66259	GGCUACACAGGAGAGGAUGGT
266690177	66260	GGCCTGCUCTTGAGTCTCAUA	66261	CAATACTTCUGAGGGCCACCUG
260874475	66262	AAAATACAUGGAGGAGAGTTTGUCAGG	66263	CCAGUCACCCATGTTTAUCAGGAT
316667771	66264	TATGCTATCACTAUTACAGGGCAATTUG	66265	CATGCAATGUACTACCAAGAAUCAAAGG
332166520	66266	GGAGCUAGGAATTUGGAGGGAAG	66267	ACTGGCUCAGAGAUGGCAAAG
325737618	66268	GCUCAAGCCGGAGGUCAA	66269	CAGACCAUGGCTCCUCCAG
253895190	66270	TGGCAGUCACCCTAUCCAAAG	66271	CAUGTGGCCTTTUGGAAACACAG
328886463	66272	CCCAGCUCCCCUGGAGAA	66273	GGGACUGCCACTUGCCT
228572656	66274	CTACTCCTUCGACACCUGCAA	66275	GCTGAAGCCUCTCCACCUCT
318758766	66276	CACATTTCUAGCATTCTTTGTGUGG	66277	AAGGTATGTGAUCTTGCTGCTUCAT
320737470	66278	TGACCGCGAUGGUGAACT	66279	CCGGAUGCGCTGCAUCT
318283397	66280	ATTTTCTGTTAUTCGGCAGCUACCT	66281	CCCAAAACUCGATTAGCTTCCUCAA
333827433	66282	TTTACCTATCUTCCCTATGUCGAAGGT	66283	CAAGGCUTTAGGGCUGACAGT
332629268	66284	GCCATCAUGCCCTGTCAUAC	66285	TGCCTTCTAUGAGGCTTGAAAGAAAUAA
333732983	66286	CAGAGCUCTCGGTCUGAGAGA	66287	ACACAGGTATUCAGATCATCAGUAAGGT
333074387	66288	GTTATGCTAAUAGTTTGCTGUGGAAACA	66289	GTTTTCCAUGCTGGTCCTUCAC
333720225	66290	TGGACCACUGAAGGAAATTCCUC	66291	GTATTGCAUGCCAACAGTGUCA
315363005	66292	TGTGUACAAACAACCTUAAAGGACCA	66293	TGATTGTTCTTGUTCTCTGTGGUAAAGT
312987640	66294	AGATGGCAGAUCTGGTAGCTGUAA	66295	GAGTGAAAGAUACAGAAUGCAAGCAAG
312845641	66296	ACCTGACCCACUATGGCAUCT	66297	GGACTCGUCCAGGTGATUGAC
269051842	66298	TCUACGAAAAGGACTCAUACACCAGT	66299	CCTCCTGGCAGGAAUCCTTAAAAUT
262051857	66300	CTTCTGCCUCTTCTAAAGCUGGT	66301	CTGTTTGGTGAAGUATTGCTTGCUT
263598964	66302	CCCAATAGCACUTATTCACACCACUA	66303	GGTTTTGTAUCGAACAGCTGGUC
269321295	66304	ACAAAATTGGGCUTACTGAGCCAUA	66305	CAATTCCCTCUATTTTAGGCTGUGCT
290330615	66306	CCACAGACAAGCUCUGGGAAC	66307	GACATUCCCAGTGAAGTUACAAACAAC
289898789	66308	TGGCAAACACAGUATCGUGAAACT	66309	GAATCTTCTTCUGCATTAGAGTCCTUCT
291776449	66310	CTTTAGCTTGAUATGCAACGAGGUG	66311	CAAAACATGATGCUTGAAAGGCAAAAUT
292477743	66312	AGTATGTTACTTAUGGACACTTTTAATGTGTUT	66313	CAACAAGTTGAGUACAAGCTTTCTUCAC
293045069	66314	ACCAAGAGGACCCAAAUAACACTUC	66315	GATCACAGTGCCAUATAGCTCTATGTUT
292868571	66316	TGGGTAGACACUATTAAAGAGUCAGACA	66317	CCTGTAAATTUGGCTGCATGUACAA
224573714	66318	AGGAAAAACCUCATCTGTAACCAUACC	66319	GGTGAAGTUGGTTTCTTTTTCTUACCAT
224568800	66320	CTATTCAGGAAGGUGCAAATTCCAUAG	66321	CCAATGTACTTTUCTCCCCTGGTTTUAG
327584030	66322	GCGAGGAGUCAGACAGUGAC	66323	GGGAGUCCAGAAGGAGAATGUGA
328336428	66324	AGTGGTGAAGGUCCTGACUGA	66325	TCCCCTUGGAAGTCGUGGA
326646235	66326	TGTGCACCUCCCAACATUGA	66327	GGTCTGTTUTCTGGCCUGAGAC
324753141	66328	TGGAACTTGGCUAAAGCCATTUCA	66329	CTAGGCACTGTUAAGTTCTCCCTTUT
267738298	66330	CTTTTCUCCAAGGCTGCAGAUG	66331	CCAGGATGTGUCCAAATCCATGTTAUA
261160333	66332	AGGCAAUCCCATTTTCTCUGGAA	66333	CTCGCTTACCCUCAAGAACCUG
331819595	66334	GCAACUGTGUGGGACCGT	66335	CACCACGGGUGAGAUGGA
331984323	66336	TGTCACCCCAAUGACAGAGAUG	66337	CCCTCAGCCUGTCCUGGAT
331712772	66338	CCGTCCCUGTCTTTGTACUGG	66339	ACTATGCTTUGCTTTTGCCTCUCA
257858861	66340	GTCATCCCUAGGCGUCACAC	66341	GGACCAGGAGACUAAGAGCAUGAT
267971362	66342	GACTCTTGCUGCAGAGGAGUT	66343	GAAGGAGAGGAGGUTTTTGACTCTAAUC

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
260206591	66344	GAGGAGACGGCAUGAAUGGAT	66345	CAGCAGCUTTACCGTGUCCT
262650771	66346	CAAAAGAAGCCCCUTTCCAGAACUA	66347	GAAGGGTGAAUTTGGAGAGUGCT
263478813	66348	GTCAATCCUGCCTCTGATUGCT	66349	TTCACTTGAACCUCTTCCACCAUT
327404415	66350	AGGACAGAGAUGACGGGCUAT	66351	CCTCTCACCUGTCTCCCCTTUT
326195152	66352	GTTTTGGGCUAACCATCATTTUCCT	66353	TGGCCUCCAGGTAAUGGACT
269837079	66354	CATTCAGATATAGCUTACCTGCGTUGA	66355	CTGCTTATCAUGAAATGAAAGAGTUGCT
270897277	66356	ACAAAAGACUCCCTCUGAGGCT	66357	GACCATTGACUCCTCCATATAGTCUACT
271315665	66358	CCATAACACACAGCUGTCCCUT	66359	TCCAUCACCAGGUCAGAACCA
318817528	66360	GCUTTAAAATTGUGACAGCACAGCA	66361	GATAATGTCACUGGCACCACUCT
272123659	66362	TTTCAGAGGACAUTGATTGCCCUT	66363	CCAGAGCATTTACAUATGTCTCTTCCUT
316419601	66364	GAGTCATGUAACGTAGGTUGGGAAT	66365	AGAAAGCAGGUCCTGTTTAUGGG
320546655	66366	AAGAGGAAUGCCGAGAAAAGUGT	66367	GCATGGAGAAUGAACCUGGCT
316386692	66368	CUAACACACAGGCAAAAACUCACT	66369	CAATCCAGGCUATGTTGGGAUAAGA
317002662	66370	CAGGACCTTUATCTTGGCAAAUACCAT	66371	TTTCCTTTTTGCAGUATGTATGCATUCC
256933022	66372	CGGCTGCAUAGCCTGAGAAUC	66373	GCUGGAAAGTAAAAUGAGCCACCT
320977483	66374	AGATTATGACTAGAAAUGTTGGTGGCTUT	66375	ATGTTGCAGGUCCTGTTCAGUAG
268429739	66376	TGGAAAGACUGGAATTTGGUGGT	66377	GGATCCCAUGCAATGAAAAUGCAAA
257714694	66378	CTCATAGTGCUTAATGTTGCCTUCAC	66379	GTAAATGTGUCCAACCTTAUCCACCA
268015492	66380	CAATCCTGAUCACGCTTTAGTTTAUCAA	66381	TGGGUCAAAATUGACACAGAGAAGAC
258386463	66382	GCAGACTTGGUCATCTTCACTUGG	66383	CTAGAATAGCAUACAGCCTGTCTTUGA
258663146	66384	AAAAACTTTCAGCUCTTACCTCUGGAAT	66385	GCCAGCTACUCACTCAACAAAATCAUA
268831940	66386	GTGUAAGGAAAGAAGAATUGGGCAAA	66387	GACAACAAATGTUCTTTCCATAGCUGT
257342352	66388	CAGGCACCAGUTGTCACATTUT	66389	AAAGCCAUCUGGGACAGGAAG
268158442	66390	CAAGTTTTTCTUCCTCCCTCCCAUA	66391	GCTTCTGGTUAGGCTGTGGUC
258664938	66392	CCTGAACUGCCACCUCCAT	66393	CCGGATCAGCUCCAAACTGUC
230142763	66394	GGGCCACCCCAUTCACTAUC	66395	CTGTTCCTAGTUTCCTTGTCCCAUT
224482255	66396	AGTTACAAGAGGAGUATGCTUGCC	66397	TTCAACAACCUCACCCATTUCCA
222555269	66398	GATCCCCAUGATATACCAGAAUCAAAGG	66399	CCAAACATUAAGCAGCACTATTGCUAAT
223782441	66400	GTCATTAAACTTUAGGAGCAAGCCATUG	66401	TGTAAGTUGGGCAATATCAGUGAAGT
225156563	66402	GGAGAAACAAAAGAAUCAAACUACGCT	66403	GGGTCUACCCAGCCUAAGAAT
319201979	66404	TGACTTCTGUACTTCTGACATTTUGGG	66405	AGTGAAGATGACUGGAAGAATTTUGCT
318722120	66406	ACATTTATCTAGUCGACCAGGCCUA	66407	GTTAACCAGTUGCTGACTCAGTUG
319378884	66408	TCAAAATATGCCAUCATCTTAGCUGGAA	66409	CAGUACTTGTGGAUCGAGCCAT
318353146	66410	TCCTCACTGTTUTCTTCTTTTACCAUAGG	66411	CCTGGATGGGUACATTGTTATTGUCAA
259316950	66412	TTGTTCACUGGAAATTACTTCTUAGGCA	66413	GGACGAAGCCCUTTATAGTTCAAAAAUT
257857006	66414	AGTGTCAUGCCACTGUAAGCA	66415	ACAGTTCCAATCUTTCACATCACAGUAA
263054196	66416	CGCTGGUGAAGTUGGCAAA	66417	AGTAATTTGGCUCATTCTCTCCAUCAG
268412690	66418	CTCTCTCTGCTAUATTCTCCCTCCUT	66419	CACUAGGACCAGAUGGACCAG
266787551	66420	CTTCCAGGCCCUTGGTGATUAA	66421	CCAACUGCACCTACTTCUCCAG
267418452	66422	GGGAAGGTUAGCATTCCAUCGAA	66423	CACACAATGAAAUCCTGCTCAGTTTUAT
326202653	66424	GCAGCAGATTUAGCATGATACTUACAC	66425	GCTGGTGGTAUGGAAATAATGTGTTCUT
323487446	66426	CCGAGGUGCCCTAGUAGACT	66427	AGGTGAACGATTUTGTGAGGGATAAAUT
324499214	66428	ACACCACAAUACTUGCAGGCT	66429	AATTTATTTGAGGCUGCTGGAGGUA
325280261	66430	AATGTTTCTCCUGAGCAAGTAACUGAAT	66431	ACGGGAAAGTCUTACAGGTAGATAUGT
267876752	66432	GATGGTTGCCUAAATTTTCTTCUGACC	66433	GAATATCCTGTUCAGGAATGTGACTUCT
265591648	66434	GTTTATGGCAUGGTACCTATATGUCACA	66435	CTCCACTGTUGCAAAGTTATTGAAUCC
263718770	66436	GTATATGCCCUTTGAACACUGCAC	66437	AAATGTAACACUGCTCCCTCTTTUCA
268074220	66438	GTGTGGUTTTGAGCAUGGGAAT	66439	CAGCAAAGUAGGTGGAGGUGAC
313911326	66440	GGGTGGUCACAGCACTGUAG	66441	TGTCCCCACUTCTCUGAGCAT
314717636	66442	CCAGCAUGCACCAGTGUGT	66443	GGUCCCAAGGGAGGGUGT
319641360	66444	GGTGCCACTUACCATAGGTGATTUAT	66445	AAGCTCTTCTAGCAUATATTCTAGGCUCA
332808886	66446	CTGATTTGGGUGTGCTGACUCT	66447	CTGTGCCCGUAGTGAGAUGA
317386662	66448	CCAGCTGGUACCCAAGGUT	66449	GAACGCCCUTCACUGCAC
240024360	66450	CUTGGAAATAAAGUGGAACGAAAAGAAGA	66451	GTGCTTCCTCUTTATTTAGTACCUCAGT
241861104	66452	AGAGCAUAGCUGAGAGCAGGA	66453	GTGGATTGCUTGTTTACTTCAUCAAGT
266467136	66454	CCAATGAATCAGUCCGTACCAAGAUAC	66455	GAGTGCCUGCTGGATTACUCAT
259125762	66456	GACUGATACCUGGCCAACAACAT	66457	CAATGCAGAGGUAGGCTCUGT
261376550	66458	GCTCUACAGTGCAGUGAAGGA	66459	CCAGTTGGGAAUTCTAACTACTGTUACA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
257342502	66460	GCTACTGACUCATGCCCTTUCT	66461	GGAAAGGUTCAGGGAUCCACA
255170272	66462	AGACTCAAAUGGAACTGCUCCAAG	66463	CAGCTGUCAACACGUGCAAT
316478561	66464	TTTCTATTCACUTGGGTGTUGGCT	66465	ACCATGGTGAUGGAAATAAAAGAUGAAA
317171079	66466	CATATACTGAUGAAGAAACAAGGUGCAA	66467	TGTCAAATGGAAGGCUTCTTGTCTTUA
313753412	66468	GCTCCUGAAAGTACTCUGAAGGT	66469	GGCAGGAAGAAGUATCTCGTATCAUAAAT
313337527	66470	CATCTAAATCCTGUAGCTCTGGCTUAG	66471	TGCTCTGCTUTAAGTTTGGGAUGT
315738668	66472	CCATGUCAGAAAAGCGCAUCT	66473	GCTAATGGCUCTTTTTCCCTTUGT
317097085	66474	GCCTCUCCCATCTGCUAAGGA	66475	CTGATGATGATUTTGCTCTTTCTTUGCT
317910752	66476	GGGATAAGCUACTTTTGCUACCAC	66477	TGTGGAGTTUAGAGTTGATGTTTUCCAT
317086904	66478	TGCCCAAATGUTTTAGACAGATUACCA	66479	CTCCCACTAAUTGTCCTCCAUCAC
298420680	66480	GAACTCGTUCCAGCACUCGAT	66481	CCATCATGUACGGCAAGTTCUCC
281238800	66482	AAGCCAAGGAUGGTGTTAUGAACT	66483	GCCTGTCTTUGTGTGAATCTTTTUCC
281269601	66484	GAGAAACACUAGACCTAUGGCAACA	66485	CCCTCAAAAGAGUAATGACCTUGCT
261868606	66486	CGGAGAGCAGGCUCCAUT	66487	CUCCUCGGAGAGCAGCAG
259801061	66488	GAGAGGCUGTCCATGTUGAGG	66489	CAACUCCACAGGGCCAUGAT
265637038	66490	CGUTGGGAACUCCAGGAAGAG	66491	GGAGTCATTGUCATCACCTTATTCUCA
267503168	66492	GCTCCUCCTCGTCUGAAGGT	66493	CACAATTCTCUAGCTCCACACUGA
267210388	66494	CCGTCTCUGAAATCCAGGUGAA	66495	CTGCATAUACAAGAAATGCTUGAAGCC
333408955	66496	CAACCTCATAUTGCCACTCTTUCC	66497	ATCCACAAAACCCAGUATGCUGAA
264232239	66498	GGGTCUTGTTGTGAUCCCAGAA	66499	AGGCAUACAAGGCAGAUGCAG
253792759	66500	CCGCAAACACUGACAGCUAAGA	66501	AGGAGGCUAAGTGGCCTUGA
319692890	66502	GGTTTGCATUCTTGCTTCTGUCAT	66503	CCCTGUGGAAGAAAGUACAGACC
321191559	66504	CCAGACGTUGAAACGGAAAGUG	66505	CCAAACATCUCTCCTTCUGCCT
266613275	66506	GGGACATGUGGGAGCTUACC	66507	GGACTGUCAGCACAGAGGUC
266734686	66508	AGGACGCCUTTGCTGTGAAUAT	66509	GAAAAGAGAAGGACGGUTCUGGT
266915789	66510	GGAUCCCTTCTGUCGGAACCT	66511	CACCCCTUAAAGAACCCAGCUT
327644620	66512	GGCACAGCAGAUCUCCCA	66513	CUCACCCGGACGAGGUT
327025644	66514	GTGGTTCUGCCGGTGTGTUA	66515	TCAAGAGTAGGCUTTTTGTCTCAGATUG
324631472	66516	GGAAGGCGACAGUGCCUAAG	66517	TCAGGAGCUGATCAACAAAUGAAAAGA
314870567	66518	GACGCGUGTGGCCTCUAA	66519	CUCGGCGAGUGAGGAGAAG
263726631	66520	CCCACAAUTGCATGUCACCAA	66521	GGAAGGACCTCUATGCTAACAATGUC
332441250	66522	GGTACATCUCCATTCCGGUGAT	66523	GTCATCCCCCUGGATCTTGUG
313570127	66524	AGCCCGACACUGTGTGTTUT	66525	CCATGCCUGGAAGTTUCCGA
327057196	66526	CCACATCCAGAUCCACCAUGT	66527	CCTAACCCCUGTGCCTTTCUC
318911728	66528	GTACTCTGUACAAGCACCTCTGUC	66529	GTTCTGGCACAAUATGGAAAATCAACUT
239708127	66530	ACACTAGTCTTTUCCAATCCCTCUCA	66531	CGAGGCUAGACCTTCTCTGUCC
333405365	66532	CCTCGGCUGTACACCACATUAA	66533	AGCTTGGAGUCTGAAAAGCAUCAA
313484980	66534	CAGGCCCUGCCATATTGUGT	66535	AATCCUGGAGATTCCTAUCAGAGGAG
312675540	66536	GTCCAAGCCCUAAAGCCUCAT	66537	CGGGAGGAGACCUTCAAAUACC
314198545	66538	GTGATGAGGGUGCTGTGCUAT	66539	GCGGAAAAUAGGGAGGAAGUAAAGG
325767618	66540	GAGCCGGCUAACCTACUGG	66541	AGGTACGACUCCGCCAUGA
324150793	66542	CCAGCCUGACCCUCGAA	66543	ACAGAGAAGGCAUTGCAGGUG
262581321	66544	GCCCUGGTACCUGGAGAAGAG	66545	TTCTAGCCUCAGTTUCCCAAAAGG
265394242	66546	GGAGAAGUAAGGCCAGGTGTUG	66547	CACAGTAGTTUGGTCCTTGAGTTUG
267772497	66548	TTTCTATCCTGUGACAAGTCTUAGGGA	66549	TGATCAGGCUGCTTGTGUGT
313101276	66550	GATGAGGAGGACCUCTCUGAGT	66551	CCAGCAGUGACCTAGUGACAG
313364852	66552	CCAATCATGUTGCCCGUGAC	66553	GCGGCCAUACCTTGUCAAACA
328466719	66554	ATGGTGATCGUAACAATGGTGGUAA	66555	GGACGGCCCCUACCAUC
223777262	66556	GGTAATATATGCCUTTTGAGCTGTCTUGA	66557	GCACTAGAATTUGCTGGCTCAUGT
223107583	66558	AGATGTGUAAGCGCAGCCUT	66559	ACAGAAAAGCUGCACTTTAGGAUAACA
223557787	66560	CCATATGTCATUTTCATTTCAGCUCCCT	66561	TGAGAATACUCAGGGCAAGACUCT
224106118	66562	GTTCCCCUCTCUCAGCGAAG	66563	ACAGCTGTCAGCUTTAATAAGCCATUA
223100547	66564	GCATAGGCUCAGCATACUACACA	66565	TGAGATACACAGUCTACCTGGUAAGAAAA
333277358	66566	GGCTGTACUGTTCTTCCUCCAA	66567	GCTCCTUACACAGGCCTCTUC
333325087	66568	AGACTCTTGTTTCUCCTTATCTCCAUCT	66569	TGATCCAAUCCAGGTAGCCTTUG
333320632	66570	GCCTGGACGAUGATTCTGAUGG	66571	AGGAGGAGGAAUGAGGAGGTUT
332825411	66572	GGTCTTCUCACAGCACCTCAUT	66573	AGCTATACCCUCTCTCAGCTUGG
333424593	66574	GGCAUGAAGAAGGTCCUCAGGT	66575	GGCCGUCGCTTTGGTAGUAG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
333309506	66576	GCAGCAGGCGUCTTCTCTATUT	66577	GTGTGGTTAACAUCGTGTTTTTGTTTUC
333190734	66578	TGCAACAUGGAAAATACACATTUGCT	66579	CGCCAATTCAGUACTTTATTGCUACA
318871063	66580	ACGTTGTAGAAUATGTCAAAAUCGAGCA	66581	CTGTTTTCATGGUAACTCTGTGCTUT
278509725	66582	GCAGCGGACGUTCAUGCT	66583	TTCTATCTGTTTUCCTTCCTGGACATUG
280383037	66584	CAGTGGTCCCCAAAAUACTAACAGUT	66585	ACATTTAGUCGACAGAAACTAGTCTTUT
278122269	66586	CAGATTTUGACAGTGAAAGUGGAAGG	66587	CTTGGAACCAGCAAAUATTCTTCTCCUA
280421692	66588	GCTTGGACAGCUTAATTTAAGTGCUT	66589	GTCTTAACAGCCUGAGTGATGTATGTUT
278295799	66590	CCTAAGTGUATGCCTCCTUGGAT	66591	CTTCAAACCCUCTACTATTCTACCUCCA
261269959	66592	CACAGGCAGCUCTTCTCTCUG	66593	AGGCUCCCAGAACATCACCUA
268598628	66594	GGACTCAGUGCAGGACACTUG	66595	CCGCAGUCTCTGGACUAAGGA
267386604	66596	CTGTCTCCUCGAGCACCTUT	66597	CCTGGAUGAGGAAGGGUGAGAT
264560651	66598	CATGAGGGCCUGCACUGA	66599	CACCTTCTUACCCCAGCTCUT
269062967	66600	CAGCTTTGGUGAGAGGCTGUA	66601	GTTACCCAGGCUCCAUGAACA
267845368	66602	CCUGAGGGTCUGAAGCCAAG	66603	CATCGCTGAGGUCACATGGUAT
267728140	66604	GCCCACAACUGUCAGAGCAAA	66605	TCTTCATTTCAUCCTCCCTGTCUCT
265209356	66606	CTGAGGCAGUCTTTCACGTCUT	66607	CAGGAUGGGCAGAGGTATAAUGA
324673270	66608	CCAAGGACAAGGCCAUTAAGAAATUC	66609	GATACTGGGAUCCTCACACAGTUC
320379011	66610	AAGATUCCAAAGCAAGCTATGAAUGA	66611	CCACCAACUCAGGAATCCTACTAUGAT
317120200	66612	AAATAAGAGAAGGCAAACUGCATAUCCT	66613	CATCTCTGCAAAUGTTAGATACGGUACA
317078898	66614	TGTTACTATTGUCACTCGAGGATTGUC	66615	GGGTATTUCACATCTTCATAUGCCAAGT
318294422	66616	CACAGAAGGCAGGACUCTUCAT	66617	GCCTTGAAAAAUCAGGTGTCTCTTUT
255964901	66618	GGCTGATTUGGGAACTGCUGA	66619	CACATGTATTATGCUGTGGAGATACUGT
266867811	66620	TGGTACAGTUGCTGCTGCTATUT	66621	CTTGTGCTCAUGGCAAAAATGTATUACT
267026029	66622	CCGGGCUTGCGGACAUT	66623	TGCGAGCCGGUGTAUGG
326782141	66624	GGAGCTGUCACCCACAUCAAG	66625	GCAGCAGACTTUGTGGTCACTAAAAUG
236449885	66626	ATGTAAGCTUAAACAGCGTGGTCUA	66627	ACCAATAGAGCACUTGCATTTAAAUACCT
327435031	66628	GTCAAGGGAACUTTTTGTTTTAGCUGT	66629	AGGAGCAUAGCCAAATTTACCATUGT
242616297	66630	AATACAGTTTTAACAUAGTATCCAGTGTGUGAA	66631	CAACTGCTGCAAUAAAGATACAGATUCC
242315995	66632	AGAAGGCAACTUGACAAGAGAAATGAUA	66633	AGGTAGATGTUAAGAAACACCTCUCACT
242609956	66634	TGCTCATCTCUGCAAAATTGTATAUGGT	66635	AGGTGTTTGAAUAACTGCATTTGGAAAUT
333240641	66636	CTTGTAAGAGUCCAGACATTGAUCCA	66637	AGGTTTGUAGAATGACTTUGAACGAAGT
318776496	66638	GTGGAAGUGCAACATATTGGUCAA	66639	CGGAGATGTTCCUTTCAGGACTATUAAA
313445436	66640	GCCTCAGTUACCTCAGGGCUAT	66641	GAAGGAAGGCUACCTGTCACUC
312852465	66642	CTTCUTCTCTTGCUCCAGGGAT	66643	CCCCTATAUCTAGGCAATCUCACAGT
314854602	66644	GCAGAATCCCUGCTCCTCTGUA	66645	CTTCTCCCUGATCCACTAUGCC
314031052	66646	GAGAUGACTGCUGAGCAGACA	66647	GCCATCAUGCACTTUGGAAACAT
255904171	66648	CCACACTGTTUGTAGTCATCTTTAUCACA	66649	GCAGCCACCUGGTCTATUACAG
330253474	66650	CCAGCCCAUTCCAGTTAGGUA	66651	GCAGCTACAUTCCTGCTCCUG
326825655	66652	GGCUGCAAGAGGACUAAGCAT	66653	CAAGCAGGCUCTCCCTCTUC
319446198	66654	GTCAGCCUGGGTCAGCUC	66655	TGCCTTGUGGTTCTCCTUGAC
316902809	66656	ACTAACTTCUGACCCACCUCGAT	66657	TGAAAAACATCTAUGCTCCCCTTCUG
327871372	66658	GCGCACGAAUGGCTAACTCUT	66659	GTGCCCTUGAGTTTCTTTUGCAG
327457033	66660	CTCAGGUGGGAAGATGGAUGT	66661	GAGTCTUGGGAGAAGUGAAGCAAA
320416008	66662	GAGGUTCATGGACUGAGGCAAA	66663	GAGAAGCCAUACCTGUGGGAT
318469799	66664	GCTGATGUCAGGAGAGCATUCT	66665	GAGGCAGAGACCACUGGAUG
316640613	66666	GCCGAGCAUCAGCAGTTUAG	66667	GCACCAAGCUTACCCTGTCUT
333262742	66668	GCCATGGACUCCCCUGAG	66669	CCTGCCACCUGCAUCCA
318297780	66670	GACTCTUGAACCCAAACTCTTUCCA	66671	GCTTCCCUCTGCACTACUCAG
265786298	66672	CAGUGCCACTTCUCCAGGAC	66673	GUGGGTGACUGGCAGAAAGAT
262600380	66674	GAGGGUGCCTGCUGACA	66675	AGAGGAGCUGGACTTGCUCA
240855685	66676	CCUGGCGUGACCACCAA	66677	TGAGCTCACUATCAGGUGGCA
318280831	66678	GGCTCTCUACCAGGGTGUCA	66679	CGTGAGUGTTGCGUGGCT
320593826	66680	CGGAGTUGGCGGAGTUGG	66681	CTGGTGGACUCCAATCCCTUT
321342930	66682	GCTGCACAAACUGCCTCUCT	66683	ACTACCTCTUCGACTGGACCTUC
321337344	66684	CAGGTACACAUGCTCCACTGUT	66685	GGACTCAGCGUGGACAUGAG
241641206	66686	GAGATTTGTTCUGGAAGAAACCUAAGA	66687	GCAAAGCCUGAACTGTGTTTUCC
258881167	66688	CUTACACAGUGGGAACACCCAT	66689	GGTTCAGAUGGTCACCAATGUCA
327377723	66690	TGTCTGTTGCUCATGTGTTTGTTUC	66691	GCCAGCAUCTCGUGGACAA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
320304743	66692	ACAGGAAUCGCACCAGCTUT	66693	GAGTTTTGGTUCCTGACCCCUT
320318386	66694	CCAAUGACCAGACTGUGCGT	66695	CCTGAAACAGGGAAUTAGCAAAGTTAUC
321018493	66696	TCCAGGCTTACGUGTGAGTTTTAAAUA	66697	AGUGCAUCCAGAGGAAAAGAGG
267219509	66698	GTGGCAGUCCTTTAUGAGCCA	66699	CTCTTTACAAAGUTGACGTGTCATTUCT
268896821	66700	CUGGGCAAUGAGGAACAAGAAGA	66701	AACATCATCGUGCCCTGUGT
267473709	66702	GTTGAGUCGGTAATCCUGCCAAT	66703	CTTCAATCAUCCCCATCTCCCAUC
263953305	66704	CCACGCCCUGAATATCCCAUT	66705	CTAAGCUCCCCCAACCCAAAUT
258233661	66706	CCAGCAUGAGAAAATGCTCTGUGA	66707	AGGCCTUGGAGATGCTTTUGAA
242286013	66708	GGCATAACUGCACCCTUGGT	66709	CCTCTTGCTUCTCTTTTCCTAUCCT
261096879	66710	TTTCCCTACAGUCTAGCAGCCUA	66711	CAGACUCCAGAGACGGAUAGAAAAC
258830446	66712	CAAAGCCCGAACCUGTATTGUC	66713	CUGTCATUGGGAAGAGGAAGCAA
268192262	66714	GGAAAGGACGTUATGTGGAGACATTUT	66715	GGACACCAGAGGAUGCGAATUA
325576255	66716	CACCAACUACAGCAGCTATUCCAA	66717	GAGGAAAUGTACTUGAGGCGGAT
239268603	66718	TGTCATTTTCCUTAGGTTCAAAACUGGT	66719	TGCGGAGACGUTGTCGUAAG
332512861	66720	GAGTTUGACAGGACTCUGCCT	66721	GATGGCCCUTCGCTTCUCA
333181400	66722	GGGTAGTCUCCATCCATGUCCAT	66723	GTAGCTUGCAGACCCUAGGAC
333036024	66724	CCGTGATGUCGTCCTTGUCA	66725	CCTGGAGAGUGTGCTGAAGATUC
313372709	66726	CACACGTUCCTCTGCUAAAACCT	66727	CCTGGTTCTTTUCAAAGGTGGTTUC
226700560	66728	GAGTGAUGGAGAGAGGGCACUA	66729	CGUGGCCTACAUGGACCAG
225631151	66730	GTCTTCCTGCUCCCCAGAUG	66731	TTTCCCUCTGCTCCUAGGCT
328626251	66732	AACCCAGGACAAAGGUGTTAGUG	66733	TTCTCGCTGACAUCTCCATTTCAUT
266725963	66734	CCCAGAUCGGGAGAAUGAACT	66735	CCCTTCCTTUGTGGGAGGAAUC
265910699	66736	GACCAUCCGTTUCCGGAAGAA	66737	CATUCACACGAGCCUCACAG
257906818	66738	GGGAAAUACAGGGCCUCGAA	66739	CTGCCCTGUCAATGCAAGUC
257447369	66740	TGCCATTGAUGCCCCAGAAUA	66741	CGTCTTCUGCTTCCTCGUCAC
262698943	66742	CTGCAGAGCCAGUTCAATACCUA	66743	CTGCAACTCCUCCGTGAGUAT
257105290	66744	TCCTAATTTCTUACACTGCCTCTCCUA	66745	CAGGUCUCCAGAGCCCAAG
316342933	66746	GGGAACATCAAUAAACCCCCAUC	66747	GCCCUCCCCATCAUGCT
317467327	66748	CTUCGCCACAGCCGTUT	66749	GGUAGCGGCTGUCACAGG
316593560	66750	CTTCTGUCCCACTCCTUGGAA	66751	CCCATTCTTCTUCATGCACACGUA
330750501	66752	GCAAATTAAAGUTGCAGTGGAUGCT	66753	TCTAACAGTCCUCCCTGCAUGT
331384272	66754	CTTCTGAAGUACAAGACAAGGUGGT	66755	GGACTCCTACAUGGTGGATTATTUCAAA
331298112	66756	CACUTGATGCTAAUGACAAAACCGA	66757	CTTCTAACUGGGAGGTGTTTTCUAAACT
330680615	66758	ACCCCACUGAGGAAACGAAUG	66759	CTGTGATGAAGUCCACTAATGCTATTUCT
269365337	66760	CCTTATGCCACUGCTACTTCTTGUT	66761	CCATTTUCCAGAGAGGCTAGUCC
268036194	66762	CCAAGGAGUTTTCTAGCAUCGAACAA	66763	CCTCCUGAGAGGAGAAAGATGUGT
268674498	66764	CAACUCCATTTTCUAGCCACCCA	66765	CCCCGAGCCCUCUCCAT
266020640	66766	CACCCTCTGUGTTGTTTCTGAGUA	66767	GCCCTCAAUATCCTTCUGGCT
268001170	66768	GGAGTACUGGTTTGTGCUGACT	66769	CCCGGCGAGUTACAGTCCUA
257234322	66770	GGAAATAACACCGGUTAGAGGTGAUA	66771	GCUACCGTCTATTUCCAAGAGGAAT
319910724	66772	GACUGCACACCCGACAUCT	66773	GGTCCTCCCUCTCACGUC
324785400	66774	CCTGTAGGTGAUGGGCATCTTUG	66775	TTCTTCTTTCUCCCCTTCTGCUG
323869753	66776	ATGACATTUCCCGCCTTCTUGA	66777	GGTTTCTCTUCCTTCTTCTUCACCA
325609143	66778	CTTCCTCUGCTATTTCUGCCGAAT	66779	AGTGAGCUGGTGGAAAGUGG
323647323	66780	GGCTGATCCUTCTCTCCACAUC	66781	GGTGTCCUAGGTGAGTCUGGT
324240873	66782	CCTGGAAAUGCCCAGCUAGAG	66783	CAUGCGGAAGGUCCCAGAT
325308791	66784	TTGATTGCAGGUAAATGATGGGAUGA	66785	CAUCCCACAGCAUGGAAAAGG
264876196	66786	ACGTCACCCCAUGGTGAGUA	66787	GGUGCCAAGAGAAACGACUGT
319384802	66788	CCTCCCCAGGUGGGCUA	66789	GGCTTCUCCCCTCCAUGAC
316469040	66790	GGCAGGGAUTAGGCUCACAA	66791	AGAAACCGAAGGAACUGTCAGATUC
316810597	66792	CAGGGACAGAGCUCTCCUAGT	66793	GCTTTTCAATUAAGCCCAATTTCACUGT
333674495	66794	GCATCTCCUGGCAAGTTCUGG	66795	CCATCCTCACUGCTGTTTTGTUCT
320502171	66796	CATCCTTCTUGGGCTGTGUCA	66797	GAATTCATCUGCACTGTGTUGGG
324438661	66798	AGGCTCCTTUTTGATGACCTUGAG	66799	AUGGGAGACCAGGAGTAUCAGAG
257333926	66800	GCAGGATGCCUTCCTTGGUAT	66801	TGCCTTGGAGCUATGGATACTAUAACT
327372200	66802	GUTGCAGTCCUCGGAACCA	66803	GACCCGCUCCUAGCAAAGG
266999003	66804	GTTGGGCUGACCTCTTCTCTUT	66805	CTGAGTTUCCACGGCUCAAGA
226443845	66806	CATCCTTTTUACGCTCCCACTTTUT	66807	TCTACTGCAUGAATCTGAGGGUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
315797314	66808	CAGAGGGCACAGGUTTCTAUCC	66809	GATGTCTGTGUTTTGCTTGCAGUA
325039322	66810	CTTACCCCTUGTGCGTGAAGAUAT	66811	CTTCGTTTUGGGCACATATAGTTUCAA
265601143	66812	TCCAAGTTTUGACCGCCUCA	66813	AAGCTCACUCCTCCACTCGUA
265207924	66814	CACCTTGGAGUAGATCTTCCUACCT	66815	CAAGTCCTAUCTCTTGCTCAUGGAA
258489220	66816	GAGCCAGCAUATACGTAGAATUGAGAAA	66817	GGTGGAAGAUAAACTCAGTCTTCUGAAT
259825716	66818	CCTATTGATUATGCTCCAAAUGGAAGGA	66819	ATCATCGCTTUCTATAATCAGCUACAACA
268057653	66820	CTTGAATAGUAGCTGTCCTTUACACACT	66821	TCACTCTUCCAAGTTTTGCCUCAA
259413898	66822	CCATATCTTCTGCUGCTTACTCCTUAAA	66823	AACATTCACAAAAUGGGTAAAUGCACA
326216471	66824	GGTTCTTTCTGCUCCTTCTGTTTUAC	66825	GACAGCAATAUCAAATCCCTCGTTTUT
324248910	66826	TTTTAATGACTTTTCAUTGGAATTCAGGCUC	66827	GTATGGCAATUGAGAGCGGATTCTATUA
324873356	66828	CAGGGAACAGAACAGUGGACUC	66829	TGGAGAACCUGAGAATGGGAAGTUA
324724081	66830	GTGTCTTACTTGUTACAAAAGCTGAAUGG	66831	CCTGGCTACCUTTTAAAACCTTTUCT
318960536	66832	GUATTTGCCTTTATUGCAAGGGAAGT	66833	CAATCCCTCUCTTCAACACAAGUGT
316382437	66834	CAAACCCTCTUGGGTAATCTCUCA	66835	GAGAATCCTTUCCTGTTTGCATUGG
314594164	66836	CTTAAGAGAGUAGTCTGGAGAAUGAGGT	66837	ATCCTGCCCUTTCAGACATGTUAG
303250199	66838	AGGGAGCUCAGTAAGTCACTUCT	66839	CCAUTGATGTUGCCGAAAAGGAAAC
300421279	66840	CCUCTTTGGCCUCAGAGAAAGT	66841	GCAATCUGAGCATTCUCCACAGAA
303122675	66842	AAGGAATTCAGGUTTTTAGGAGTCUCAC	66843	ATTCCAACTCTAUACAAAGCCCCTAGUA
257080038	66844	TGTGCCTCCUGCGTACAUAAAA	66845	GGGAGTGCUGATTAAATAGGUAAGAACA
254116541	66846	CACACCATAAAAUCTTGGCCATUGT	66847	GGGAATTCCUACAGGAGATGACUA
260173884	66848	ACACCTUCGGAAGCTGAGTCUA	66849	TCCTCTTGACTGUCTCTCTTGATAAGUC
265488851	66850	TCCAAGGTTUGTGCTTTCCTUGA	66851	GCACACACAUTTTAAACCGATTUCCAA
257109859	66852	GCATTCGCTTTUCTACCATAGTAAGTUG	66853	CCTGGCTAGAGUGGAAACGAUAAT
255832155	66854	CUGGTATTCCTTUAGCCAGGACA	66855	AGGGTTAAAGAUGGTTTGTTGAUGAAGA
299083532	66856	TGTTGCAAATTTCUTCAAATCTGCTGUT	66857	TCATCTGGTTGCUTAATCCCTCTUA
315568657	66858	GGGAGCCAUCCAACAGTCAUC	66859	AATGGGAGGUACCTAAGTGTTCATUT
268453469	66860	ATTTCTGTATGAGCUTTGTCAGGAGUT	66861	TGTCCTTTTUCCCCTTTCTGUCC
268709093	66862	GACCTCCUGGACTTGATGTUCC	66863	ACATGGGAATTAUCTACCAGAGTCGUA
263504421	66864	CCTGAACTUAGGTCACTTUGGCT	66865	GATGATCTGCAUTGGTACCTGGUAA
269450567	66866	ACCAGAAAATGUGGATCTGATTGTCUT	66867	CAATGAGACACUGCATCCTAGGAATUT
315376390	66868	AAAGACTGAUCTCAAAATGCUGGGAT	66869	CAAGCACCAUCATGCTGGATAUG
313647056	66870	CACGTATTGATTAGUGTTACAGAGTCUGA	66871	TCTTTGACTUCGAGACATTCTTTTGUGA
314353537	66872	GGCUGAAGGTAGGAUACGCAAT	66873	GCTGGAACCUATTCAGTTAATAAUGGCA
320735979	66874	AGGAATGTUGAAAGAATGGCTTTUGG	66875	TGCAAUGACCAUAGCAACAAGGAA
320010519	66876	GTGTCUGTCTGTTATUCCCCAGT	66877	AGCAGAGACAAUGGUAAAGGGAAAA
321463395	66878	TTCTGTCTGUCAATGACTTTCTTTUCCT	66879	ACCACAGUTAAGTGTTAAUCAAGCACA
228149002	66880	TTTCCTTGAAGAGUTGATGAGATTGUGT	66881	TGAAGAAUCAGCTCCGCTUCC
333024166	66882	CATCACATTUGCCATCCATGGUT	66883	GCTATTCCAUACGCACCATAGACUA
333406372	66884	TCCCCAAACUATGTCCTTGAUACCT	66885	CAACTTTGUGGCTTTGTGTTTTUCC
261360686	66886	CCAGGAAGCCUCTCTGTGUCT	66887	ACCTGACUCTGAGUAGCCAGT
256378861	66888	CAGACUCCCCAGAAUGCAGAG	66889	AAGGGCUGAGGCTTGCAUAT
312983916	66890	CCCCUCCACCTCCCTUCC	66891	ACCUGGGCGAGGACCUA
313756595	66892	TCCACAGGCUCCTCTCTGTUT	66893	GCGTCUGCAAAGAGGAGAAGAUG
266449415	66894	CCAGGATCAACUCGTAGGCTTUAC	66895	CCAGACTUCCCTCCCCTTUCT
332260270	66896	GGGCAGGACUAATTGCATCUGT	66897	CCCCCAUAGGTCCCUCCAAAA
317695301	66898	TGTGAACTTTUGGAAGCAATTCAACTUT	66899	GGGUCCAAGAAAGCAGTCATTUC
317657241	66900	GCCAGACTGAUGGACTATTCTCAATUAA	66901	TCGTCAACAGAGAGUGGTAGGTUAT
317665047	66902	GCCAAATTGTCUGATGGAATTGTUGAAA	66903	GGAGCAAUAGACAGTAAUAACAGCCT
316800684	66904	GTCCTGAAGCUAGATCTCTCUCCAT	66905	TGGCTTGTTGTACUCTAATTGAGCTATUT
315547610	66906	GTGTGTCUCCAACTTCCCCAUAA	66907	CCTACCUAGAATTTTTCTUCCCAACCT
318584283	66908	AAGAUCCCCTCCUGGCAGAT	66909	GCCCUTGACGUCCACCAC
319825293	66910	GAATATCACAAGGAACUACTGCUGGAA	66911	GAGCTCTCACAUCTGTGACTUCAT
261857422	66912	CGGTAACCCUCCCAGCTTUG	66913	CGTTTCCAACAGUCCTACTTCUCT
258510600	66914	GCCAUCTUGAACCCACCGT	66915	TCCCAGTCACAUGTCTCACUCT
255241957	66916	CAGGAAUGCGGTGATCUGGT	66917	GGGCCATGTAAUTAGGCATTATGTTUA
264746971	66918	GGTTACTCTUCATTGTGTTTAGUCCCT	66919	CACTTGGCAUTTGTTCCCUGAAAA
268883613	66920	ACAAGCACAUTTGCCCCAUCT	66921	CCTTGGGATTACUACAGTTTCCTAUCCT
260938554	66922	GTCTTGTTUCAGGGAATUGAGGGA	66923	CCACTTTAUGAAACAATTGCACUCACAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
261556488	66924	AGGACCAGGAUCUCCAGGAAA	66925	TTGTCATGACTTUAACCTCTTCACCUC
266382837	66926	CCCTGGGUTCCCTGCTUC	66927	AAGCACTGGAGUCACTGATAGAAAAAUT
266869427	66928	GCTTTTUCACAGGATCTACUAACACGAA	66929	CTTGTAGCUGCACTTCAAAACTGUAAAA
268666431	66930	GATAGACAUGCACATGTATUAGCAGACA	66931	GCAGATGCUATGAGAAAGAATUCAAACT
267832844	66932	AAACATCAGCUGCAAGAGUACCA	66933	GTTGTTATUCTGTGCCUCAGGGA
266350613	66934	CAUCACCACTATACUCACAGAGGAAGA	66935	GTTGATACCAAUGGAATCACGGTTUT
268926269	66936	ACAGAAAAACAGGUGATCUCCCAAC	66937	TTTCTAACTCTTUGGCCTTTTCTTCUCA
316167692	66938	TCATTCATUAAATTCCAGUGCCAGGA	66939	GGGCTAACCUAGTGCCTATAGCUAA
314912383	66940	CTCAGUGACTGTGGTUGAGGAC	66941	GCCAGCGAGUAAAGTUCCAAAA
324451513	66942	AGCATGTCACUAACCACCAUGT	66943	CTACCCACUCTACCCCTACUCC
326226941	66944	TAGGCTTCUCAGGAGGTGUCT	66945	AGGAAGAACAGUAGCAGAAGCUG
315780084	66946	TGGTCACTAATUTCATGGTTGAATUGGT	66947	GCTGTCGGUAAATTGTTCTUGAGGAA
326730134	66948	TCAATAGGAGAGUCAGGUGCACA	66949	TTCTTCACTCTGUCTGCTTCACTUC
326645897	66950	GGCTCCCAGGAUTTCCACAUT	66951	CTACTGACAGUGTTTCCTGTUGCT
327848302	66952	TGTCAGGGCUCATCTATTTATCUGGA	66953	TGCAAACCAUGCAGGAGAAATTTUAAG
327019393	66954	CACAAGCTCCUCCCCTGAUT	66955	GCTGUACAAACAGTTCCUGGGT
327079807	66956	CGATGCAUGCTTCATCAGUCCAT	66957	CCTTCTGCAGCCUTTTTATATACCUACT
327036164	66958	GTTATTGCUTTGCAACUGCCAAAAA	66959	CCATGCTCAUGCCATACAACUG
328231341	66960	ACCATTTAAACUCTGTCCTATTUGCACA	66961	GTGCATCAGACAAAAAUCAGCTTCTUT
324176086	66962	CTTCTGGGCCAGAGUTTCTCUT	66963	GCAGCUGGACGCAUCCC
332976877	66964	CCTGGGAGGUCTGTTUCAAAAGT	66965	GAUTCCACTGAGAAUACAAGGACCAG
326279953	66966	TCAGCTCCUCTATGCCATUGAGA	66967	GGGTGATGCUCTTCGTCUCC
326231525	66968	CTTTTCAGATGATUTTGTGGCTAAGCUC	66969	GCAAGGCAGAGAUCCTGAAUGAC
325206395	66970	TCACAAGGCAGCCAUGGTTTUA	66971	AGAGGAGGAAGUCCAUCGCT
323977868	66972	TGTGAGAATAAGTAUGATGTTCCTGCUG	66973	CCATAAGCCCAUGCTGATCCTTTAAAUA
327621392	66974	GTGAGAACTAAACUAGACAGCCGUT	66975	CCACAGGATCUGCTTCTGTATCATCUAT
328121251	66976	GTGGGAGGUGAACTCTGAAATGUA	66977	GTCATCCGTGUGACTTTAAACCATTTUT
326795337	66978	AGAGAGCAAATUCTTTCCCTGTUCA	66979	GCAAGTTCATCCUACTCTCGAGUC
239694657	66980	TCACTGTCUGCGGTAATCAAGTTUT	66981	ACCTGAAAAAGGUTAAGGGCTCUG
320118125	66982	CAGTAGAATTTGUCATAGCACCAGGUA	66983	ACTGCTACTUCCTGTCTGCUG
265457620	66984	CTTUGGCGGCAAGAGTTUGAT	66985	CCUCCAGAACCAAAAUGCAAGGA
262440751	66986	TGGCTGGGUGGAGCATUG	66987	ATCTGGCAUCCTGCCCTUG
264812016	66988	GACCCUTGCCUGCCCAT	66989	ACUGCTCACUGCCACACA
267813068	66990	GGAGUTGTCAUGGAAGACAGGAA	66991	GTCTTGCGGUACTCGAGGUG
327260656	66992	TCCTAATUCAGGCTCAACTCUCCT	66993	TCATCTTGATTUCTGCCTGCTCUT
327324458	66994	CAGCAGAACCAGCUGATTTUCAC	66995	AGGCAGATGAAGUATTGGAGATTTUGAA
327952545	66996	ACACUCACCTGGUCCCCAA	66997	GAAAGGTTCUGCCATTCAATAUCACAT
313055723	66998	ACAAAGAAGTUGAAGAAGTTTCCAUCCT	66999	TTCTCTGGCAAUGGGACTCUG
314089952	67000	ATTATCAAGUGAAAGAAAACACGCUGAC	67001	AAACTGCTACCTUCTTATCCCACATTUT
313874326	67002	CTTTTCUGGTCACAGUAACAAGGACT	67003	CACATAAGCCCUGAGAAGTGTUCA
314370964	67004	GGACTTGAACAUCGACCCUGA	67005	CTCCCCCGGUAAAACACTGUT
326312313	67006	CCTCATTCCUTCAAATCTAGAUAAGGCT	67007	TGTTCCTGTUGAGTTGCTTTTAGUGA
324101447	67008	AGCTCAAGUAAAATTTTGTCATUGGCA	67009	CTGCTACAAGAUTGTTGAACACAGUT
324742862	67010	CTCATTTCAGCAAGUGTATGGTUAGAAA	67011	CAGCAATUGAAGAAGACCCTGAUG
326388590	67012	TCCTATATCTCTUCCTCTGCCTTUGAA	67013	CAGUAGGTGCTUCAGCAACCA
267193435	67014	GAATTUCAAGCCACGAAGCTUACAT	67015	CACAAUGAAAAGACCAUCCAGAGAAAAG
264451323	67016	CATGTATAUCAAGGAAACTGGGCUGAT	67017	GTATCACACUCTTCATCTGCTUGAAAAA
261686276	67018	CGTGGUGAACGCGTAAGTUT	67019	GTTCTCCAGGUGATCCATCCTUG
267900913	67020	GATCTCCTCUTTGTCCTGCAUCT	67021	AAAATAATATCATGGUTATTCTTGTTAGGGUGA
264300555	67022	ACCCTTGAGCAUTTTGAGCUGT	67023	GACTAGCTAAAUGTCCTGGTTCTUACAA
267956167	67024	CATCCGGGCUCAGTAUGAGAC	67025	GCTCTCCUCCCATGGATGGUA
267390626	67026	GACTTGGUCAGGCTGAGUGT	67027	ACUAGCCAGGGACCUAGACC
261715605	67028	CCTACTCCUGCAACGTGCUT	67029	GTGCTTCAGUCACCTTCTTUGG
264380150	67030	GGCAGGCGUCGAAGAGUA	67031	GCGATUGCAGAAGATGACCUG
333181143	67032	GGUCCAGGCGGCUACAT	67033	GGGAGAGGCGCUTCCUG
232268195	67034	GAGAACTGAUAGAAATTGGATGUGAGGA	67035	GTGGATTTCCCAUGTGGTTCTTTTUAA
324427562	67036	CCTACAGTCAGGUGAGGGCTUA	67037	TCTTCTTCATGCUTGTCATCTTCCUG
261771496	67038	CCAAGGAGUGGACCACTGUAAA	67039	GACACCGCUCTATGACTUCCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
326893324	67040	CATAGGCAGCUCTGGGUGAAG	67041	ACAUCGAGGAGCTCAUGAAGGA
328366316	67042	GCTACUAACCCCGCACTCUCA	67043	GGGCAGGGCUATTTAAGUCAAG
262001994	67044	TGTGCAGUATGCAAUCCAGACA	67045	ACTGCTACUGGCATTTTGACAGUT
316530223	67046	CCCATTATGUTCAAAAGCCUCAGAAAA	67047	TCCTCAACTGUTGTGAATTCCTUAAGAG
315641122	67048	AATTTUATTCTTGCAATTUACACGACAGT	67049	GCTTGGUGGAGAAGGCTAUCT
317530279	67050	AAACCAAGACACCAGUAATGGCTAUT	67051	AGCTGGGAAATUTTAAGATTCCTTCUGT
316719050	67052	TGATGTAAAAUACGCAACTGTCAGUGA	67053	AGTATGTGGTTCGUGAAGGTGATAAUG
316259063	67054	CACCTTCATTTUCTCCAATGTTCTUCAA	67055	TCCTACCAGGUAGCCTCUACT
332038796	67056	CAGTATTGATTGUCACTGTCCGGUA	67057	ACTAATCACCUGTGTCCTCTCUGT
332181540	67058	TGAGAAAUGGGACCCCTGTGUA	67059	ACCTGGTTCACUCCACAATTCTUC
227587450	67060	GCATTGGTUGCGGCCAUC	67061	GACCCCAGGGAGGUTGTUC
228335196	67062	GCCAAGCCUGTCACCGUAG	67063	CCCAGCAGGUTGATGATGTTUT
325534561	67064	GCCCACUCCTTTACCUCCAA	67065	GTGGGCAUGGTGCUCAGA
320321779	67066	TTTTGCCTGUACAGATCTGCUGT	67067	GGGATGTAGTTGCUGAGCTTTCATAAUA
318043211	67068	AGGAGACACUCACCAGTATGAAUCAT	67069	CCATGTTTGCAAAUGCATAACAAAGGUA
320764309	67070	GGGCTAACUGTTCTCCAAGUCA	67071	CTTGGTGCAUCCATCAAGUGAA
321302139	67072	GGCAATAAGGCUAGGGAATCAUCT	67073	GGGAGGTTUCACAGAATGTTCTTUT
320009385	67074	GGATCTTTCUGTGTTCCAGUGACC	67075	GCATTGAAATGAUGAAGCCAAAUGAAC
318294266	67076	GCAGCCTGUGAGATTATCTTTTGUT	67077	GGGAATATCAAGAUCCACAATGCUGA
320970142	67078	AATACTTTCCCCAACUTTGAGCAUCT	67079	GCTTTGGCUGGTCACTTGAATUT
319029606	67080	GAAGTGAAAUCTGACTUGGCACAG	67081	CTGGGTGAAACAAUGCTCATTTTAUGT
333002295	67082	CAGGGAGACCACGUGGAAUG	67083	AGUTAATGTGGACUGGGCCAAG
332716298	67084	CTCCTGCUCGGCTCATCAUT	67085	GCAAAGACAUGAAGGCAAAATGUCA
333140278	67086	AACAAGCATTTUACCACCATGCAUT	67087	TGGAATAATGATUCGGAGCCCAUT
333679208	67088	CCCTGAGGCCUTGTGGATCUA	67089	CAGGAACTTCATUAACCAGGTGACUT
333706847	67090	CAGGGAAGAGACUCTCTCUGAAGA	67091	GTGGAGGCUGAAATCCCCAUT
333034625	67092	CGTCUCAGAGGAAGACATTTCUGT	67093	GGTATTACATTUGACAGGCTTTCTTUGG
317802266	67094	AGAGGGCATAUCAATGTAAGTCTUCCT	67095	ACTGACTCACCAACAAUATCAAGCUG
265769891	67096	CTTGGTAAAAACUGAAATCTGGUCCAA	67097	AGGGAAATAATAAUGCAACGGTAGUCA
266317976	67098	GCATTTCCCUGAGGAGUACGA	67099	TCTGATCTUGAGACACCTATATCTUCCAA
268698660	67100	GGATGGAUCATGGCUGCCAAA	67101	GGAAACACUCAAGGAGTUAGGCT
263805334	67102	ACGTGGACCUTGATATTTTGUCAACT	67103	GCTTTGCAGAGUAATGAAGACAGUGAT
265962112	67104	GCTTAGATUCAACCCATCTGCCTUA	67105	AGAAGCCAAACCUATAATUCGCAGT
267245941	67106	CTGTTTCTGCTUCCTCCACATCUT	67107	GGATACATTAGAUGCAGTCCTGTTUGAAT
291007794	67108	CTTCAAAAACACCCAUTACUCCACAAG	67109	CCTGTTGTGATAUCTGTTGTTGATTCUG
290302847	67110	TACTTGAGGTTTAUATATAGAGGCGTCUT	67111	TCACTGCCAAGUTCATTAAGCUGAT
318895717	67112	ATGGACTATACACUTAACACCTGUACT	67113	GCATTTUCACCAAGAACTCGUAGG
320935596	67114	GGGAAAGAAGUACCTGCTCTAAUG	67115	AGACTTGGAUGCTGAAUAAAGGCAA
291053541	67116	AGGAAAAUGAGUCAAGCGACAGT	67117	GAGAAGTAAUAAAATACCCUGGGACACAT
223255170	67118	CACAGTTCCAUGCCTTTATCAGUCT	67119	AGTTGCCAUGTTGATTTCUCCCA
325958154	67120	TTGAATTGAACATUCACTTGCTGTTUCT	67121	GGATCCAUGAGGCAGTCUAGGT
332031410	67122	CGACAACACCAGGCAUCTUACA	67123	CCTTCTAUCCACGTGCCUACAG
236728899	67124	TCCTCGAGCUGTTCCTUCCA	67125	GTCTGUGTTTGCCUGAGAAACAA
235330795	67126	GCTGCTTTGGUGATGGATCUCA	67127	GGATCUGACACACAGCCTTUCT
269233292	67128	TCTGGTTUCTCTGTGTTUGCCT	67129	GGGTGUGGCCAAGGCTUT
265189179	67130	GCTGGGAUGAGTUCACCAAAC	67131	GGTCUAGAAGACTCTTTGUCACACAA
259090081	67132	CCGACTGACTUATGAGATTGAAGAUGA	67133	CTGCAGUAGAACCCTCAACCTUT
268978677	67134	TCUCAGGAGGGUGGAAGAAGAC	67135	GATGGTTTUGGCAGCATCAUCA
265547275	67136	CTCAGGUAGCCGAUGACAGG	67137	TCCCCTUCTACCCUCAACGA
265550869	67138	GCTGCTCUCAGCTTTCTUGGT	67139	CCCAGCAGAACCAGUACGUC
331814878	67140	GTCCCTGUCCTTGTACUGCAC	67141	GGCACCTGGCAUCCTCTCTAUA
331759750	67142	CACACCTGUCCTGAGCCTTUA	67143	CTGUACGGCCUCCACGAG
331834414	67144	GGAACTTCCUCCAGGAGGUGA	67145	AGCTTTCCCUAACCCATTCTCTUG
268581784	67146	CTCUCAACCCCCACAACTUCC	67147	GACTCCTCTUTGCATTCTCTUGACT
267342915	67148	AAGTGAGAUGGCTGAGCAUGAA	67149	CTGGGCCCAUGTTTTGTATACTUG
267367169	67150	CCCATAATCUAAACACACTGUGCCT	67151	CCAAUCCCAGCCCACUGA
325460483	67152	CGCAGCATTUGAACTCGATCUG	67153	CGTACCTGGCUATCTGTGTTCUCT
314889746	67154	CCAGCTCTCAUCTTTGCTATTTCCAUAT	67155	AGTTACATAAATGUACGTGCACTGATCUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
272203438	67156	CTCTCUTCTTAGTTGUCCCAGCAG	67157	TGAGTAAGCAAAGUGGCAGCUT
271523537	67158	GCUTCTTTUAAGCCAACAGCACA	67159	CCCGCCACAGGAGUCAAUT
269506866	67160	GACGTTGUCGCCATCTTGUG	67161	CTTATACTAUCCCGCCCAAAAACAAUG
271925528	67162	GTCATCGCTCUGAGAAATAGAGAUCAA	67163	GACAGAACACCACGUCAGUCT
270818306	67164	CCCATCUCAGAGCCAAGUGAC	67165	GCTTGGGAGCACUTCACATATACTTUAT
318539449	67166	CTCAGCCACUCAGTGUCCAAAT	67167	AACATCCTUCTCCGGCTUGG
320101654	67168	AAGCAAATACCUTAACACCTGCUCT	67169	GCTGATCTCUCTGATGAGTATUGAAGT
316063791	67170	AACTTATGTAACCUCATTTTGTTCATCUCCA	67171	TGGCTCTAAACUATGATGGCATTTGUT
316471732	67172	TTACTTGTGTATATGGUTGTATACATATGCAUT	67173	CAGTGTCAACCACAUGTCTGTTUC
317617557	67174	ACAGCTTGATUGCCTGAAGTATCTATUT	67175	GGAAAAACATGUAGACGGCAATUGG
263237282	67176	CTTTUCACCAGCAACACCCUT	67177	CAGAATTTGGGAACUAGGAAGCATCUT
258838822	67178	CACTGAGTAGACCGUTAGTAGGAGAAUA	67179	ACTAAGTATAAACCUCAAGCTATAACCATTUT
256865980	67180	GCCCTTCTUAGCAGCGAGUT	67181	AAATCTTTACCUGCTGCCCUGT
318276391	67182	TCCCUTTTGGACTUGGAGCAAA	67183	GGTTATGAATUAAGCACCTGCACUG
327666891	67184	GGTCTGAATCUTGCTCAGCTUGT	67185	CAAGAAGTCUGCGGGCUGT
257477637	67186	CCATGCTGUGTCTTCCGAUGAA	67187	ACACTCTAAAGUCCTCAAATTTGCUCAT
268019140	67188	AATTGAAGTAAUTTCGCATTTGUGCCT	67189	TTTTCCTTATAAGAGUGACTTCCGCAUT
266525595	67190	GACTGTGATGTTUGTGTTTTCTATTGCUT	67191	ACTTTGTAGUCCATTTGCTCUGAACA
267670116	67192	CTTCCGCTAAUCCTGTCTGUGT	67193	AGGAUTTTCATCTUGCCAGGCT
267362901	67194	GTAAAGCATCCAUCCTATCTGGGAUT	67195	TCTTGGGAACCUTTTCAATGTCATAGUT
314859671	67196	GAAGCGTUGCCATGTATTTTACUACAG	67197	TGUTCAGTGATTUCAAAGACAACAACAA
323686940	67198	GGCATTCTTUGTCACCCGTUC	67199	GGGAAGCAATUAGTTTACCTCTGTTUC
327457508	67200	TGCCAGAUCCTTCATTAUCCAGACT	67201	TTGTCTTUGAACTGACGATUAAGAGGT
264423954	67202	GTCGTCAGUCCGGTCTUGT	67203	CTCTCTCCUTTGGAGGCUAGGA
256326927	67204	CTGCTGAUGCCTGCUCAC	67205	GTAAACAGAAUGGTGCTAATGCUCAAA
258846251	67206	CTGCAGGGUTCCAGTGUCA	67207	GGTCCUCCCCTCUAGCACAG
261980469	67208	CTGGTCACCAUGAATCCCUGT	67209	CCCATAGGCAAUGAATGAAGGTUT
231478902	67210	CTTUAAACACGGCUCGGAGGA	67211	CTTGGUCCAGGCCATTUCAGT
224095523	67212	GAGAAAAACGUCAAGCAGTAAACAUGAT	67213	GGGAGAAUACTTACTUCCACAGAGAAG
332408412	67214	GTAGGTTGCCAUACCATAATCTUCCA	67215	CCAACTCACTUTCCATCATCTCUAGAT
332281896	67216	GAACAGCUACAAGAAGAGATUAAGAGACT	67217	AGTATAGAGTGUGTTCCTGATGCUAA
223519387	67218	TGCTCTTGUCAGTCAAAUCCAACT	67219	TTCAACAACCTGGCUTTCTAATTCTGAUA
224076414	67220	AGTTACUGAAAGAGGAATGTGGUACCT	67221	TGAGTTGCATUTTGGTTTGTCAUCT
332303574	67222	GCACATTCTGAUGCTTACCAGACUA	67223	CTGATGCTAUGTCAAATCCCUGACT
222353013	67224	AGGTGCTTTCUCTCACTGAGUCT	67225	CATAGTATTCTTUGGTTACCTCGGCUT
319459898	67226	GAATGCTTUCCATATGTCGTAUAAACCC	67227	GTCTCTTGTUGCAGGACTUAGGAA
320207465	67228	GACCCCAGGCUGAAGAUCA	67229	CGCUAGGGUGGGCGAAC
264894192	67230	GCATTTAATGUGTGCTGCCUCT	67231	GUATTTCAGGATGAUGAGAACCACAGT
265450408	67232	CCAGUGGUGAAGAAGGAAAGAGAG	67233	ACTGATTTAAUAAGGCAGAUGGAAAGCA
325309676	67234	GCAAGGGUCAGGGAAGUAAGAG	67235	CATGTGGTTTTUCTTCCTTTGCAAAUG
326145898	67236	GAAAATGCUCACACAAGUCCACAC	67237	TCCACAAGCTACUGACTTTTGCTTUAT
325916697	67238	GTGTTGTTTGAUGCTGATATCATGGUT	67239	CATACAGACGACAAUGGUGAGCA
323907837	67240	CCTAGGTTATCUGGGTGTTTACGUG	67241	CTCAGAGTGUGTTGTTCTGTTTAUAGGA
263738968	67242	TCTGTGATACAAUGATGTTGGCCTUT	67243	TCTTCTGCTCCAUCATCTTGTCTAAATUC
268633776	67244	ACAGCTGUGATTTGCTUCGAAT	67245	CAGATCTGAACUAATTCCGTCTAGUG
317836959	67246	GACAUCGCCAGTGGGUGT	67247	ACCCTCUGACCCTGTTCUCT
317150451	67248	GCCAGTCACAUGGATGCTCUG	67249	CCCCTGAUGCCTGAGCAUA
265753063	67250	GTTGAATTCCAUGTTTGGGTGCUT	67251	GCAAACCTTUGCACAGTATCAUCC
239970449	67252	AAGAAATCCUACTTAGCGACAUGAACAA	67253	AGCAAATTTCTAUGAGTCAGCCTTAAUGA
228876952	67254	GCAAGCAAGGAAUGCCTUCAAAA	67255	GCTCTAGGGUGACCCCACUC
263764419	67256	ATTTTTCTUCCAGGCUCAGGCT	67257	GGTAGCATTTTCUCTTCCACTCAUAGAC
258822682	67258	ACCAGGAACUTTTGUGACACACT	67259	TTTCACCTTCUTTCCCTTCCTUCC
258142843	67260	GGTCAGUCGGACGGATTAUCAC	67261	TGTTCCAGTACCCUCTCATCTTGAAUA
316330561	67262	ACCAGGCGGAAAUTGCUAAGT	67263	CCTCACATGTAUGTGTGCCTCUG
232197308	67264	AAGAUATCUAGGGCCAAGACCCA	67265	ATCCUACCCCAGCCATCTAAUGA
317518704	67266	CCTCAGUTGAGAGTUCGGGAGT	67267	GGACAGATTCUGTGATGCCAUGAT
320399816	67268	AGTAGTCTATTUAGGGCCACTCCUT	67269	TGACTTTTGCUTTTGGCCCTUG
316175289	67270	CCACCATTCUTCCAGGCAUCA	67271	CAACCTTGTTCCUTTTCTCTCACTUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316411497	67272	CCCTGTTUCAGATTCACCUCCA	67273	TCACGTTGGAAUGTGCTTTTTCTTUT
258292933	67274	CAGGAGCCUCCCTGAAAUACT	67275	CATCTTGCUGAGAGACCATGGUA
268827396	67276	CTCTGTGUCCCAAACCTCCAUC	67277	GAGGTGGGUGGTAAGAGGTTUC
268727811	67278	GCTGCTCUACAGCCUGAAGAA	67279	TCTGAGTGCUTGCCAGACTUG
315553045	67280	TGCTGGCGAAUGACGTCTUT	67281	TGATTTTGGCTUCTCTCAGAAACUCAT
316637800	67282	TTATGGAATGCTUAATGTCAGTGGUCA	67283	GATGCCCUGTTCACAATTUGACAA
327910931	67284	TGAATCCTUCAAACGTGCUGACAT	67285	TGAACAACTTCUGCTCATGACAAACUA
277892366	67286	TCACCTACUGAACTCTGCCUGT	67287	GAUCATCCAAGAAUCGCCGAAAAG
315926031	67288	GTGTGTCUAACAAGAAAGCTACUGCT	67289	CCCGGTCTGUCATTCACCATUT
261900150	67290	CGGTTTTGGGUATGGGTACUGT	67291	CTACCCAUGCAGGTCAGAGUG
259251985	67292	GGCAGGACCCUGGTGAAUAA	67293	GCTTCTGGUCCTCAGTGUAAACAG
263223470	67294	ATTTCAGAGAGAAAAGCAUTCAGCTUA	67295	CACTATGGUAACCAAGCUCCACAG
262455653	67296	TGCTGCCTCUTAAAACGCTCAUA	67297	CATCTGUAAAAGGCATTTCUGCCA
257744133	67298	CCTTCTUCCTGTGTCUCGAGGA	67299	GCCAAACACGAUGATGCCATUG
265185616	67300	CAGATCUGGAGGTUGCGGAA	67301	GGGACCTCUGTGGTTTCTTUGG
258384504	67302	TGGCCAGUTGGAACTUGGAC	67303	GATCUCAGGAAACACAGUCAACCT
258029260	67304	GGCUGGCCGAGGAGTAAAUA	67305	CAUGCAGGGATTUGACAGCAAG
333760617	67306	GCACCTAAATUGTGCATGCTTATUCT	67307	GTTTTCCACTGGUCTTGTTCATCUG
332855623	67308	TTTACAGCGGAAGUTCAGAGUGAA	67309	GATTATAGAGCAAACAGUAGCAGUCCT
321216885	67310	TGATAACAATGUGAGTGCAAATCTGUCT	67311	CCCCUGGAACAACCTCCAUAT
321143403	67312	CACUCAGCAGGAGAACTGAUGA	67313	GGCAAGGUGAAACACTGATGAUAGA
320336205	67314	CCTGTUGAAGAAAAGAGCAACACUT	67315	CUGGACAGGGAAAGCACUGA
318040006	67316	ACTGCCUACAGTAGCGTCUACA	67317	GCATCCUAGGACAGCAGAACTUAG
320223276	67318	CAAAGACAGACAAGCAAUGCUCA	67319	TCTTCCATTTTTCUGATCTGCTTCCAUT
259402335	67320	CACCCCACCCUGACCUT	67321	GGGAUCCCCGGCTUCCT
265715738	67322	CTACGCCGUGGTGACCUAC	67323	GGGACTCUGGGCTGUGAAAAAT
256716997	67324	GACTGACCTUGGCCTACTCUC	67325	GTCCTTCCCACUTCCAAATUCCA
328242879	67326	CACTGCTUGGCTGTTAGCTAUC	67327	TCACCAACTTUTCCAGCTTCAUCT
328356800	67328	GATATGCTTUGAGGATGTATCUGGACAT	67329	CTGACAGAAAAAUGGAAGACCUCAGA
324255244	67330	GCCGUAGGCAGCCTAAAUCA	67331	CCACGGAUGGCTCGGAUAC
314808437	67332	TGATTCCCGGCUCTGAGTUCT	67333	CACACACAUGCTGTCCTTUGAT
314935247	67334	GTGAACACATUCCCTAACCCCUT	67335	GGTGCCAGUTGCGCAATUT
313344591	67336	CCAACUATAACCCUGCACCCT	67337	TGATGGAGGUGGTGCTCTUG
333530329	67338	GGTGCACCCUTTCCATGTCUAT	67339	CTCTCCTUACCTCAGGUCCGT
327024814	67340	CATCCTATUGTGAGACCUGGCT	67341	AGTTGGCCAAUCAGCCUCAT
327799048	67342	GGATAGTAGAACAUGTCCAAAGGGAUG	67343	CTCTAAGCAGAGUGACAATUACAGAACT
326628301	67344	GCCAGCCGGUTGATCTTUAG	67345	CTGTCGACACUATTTCTAACCTTTGUCA
313869257	67346	GCAGGTGUGACGTCGUCAAT	67347	GCCTACCTCUGAAGGCACATUAAA
314196251	67348	ACTGCTCCAGAAGGUTGCTAGUA	67349	CAGGTCCAUCCACACAUGGT
314427248	67350	AGTGGCAGCCUAGTCCTCTUA	67351	CAGAGGGACAGAAGUCAUGGAG
314673980	67352	AGGCAGGGUCAGTCUGGAAT	67353	GCCTUGCGCACCAGAUAGG
326891326	67354	ATGATCTGCTAGUGAATGAGATAAGTCAUA	67355	ACCTACTTACUGTACCTGGUGACA
223080829	67356	TGTGAGAGAAUGTGGTAUAGAAAAGCAC	67357	TCCTTCCTAACAGUTTACCAAAGTUGAA
222204633	67358	GGTGTAATAGCUGAAGAGGAAGCATAUA	67359	GGTTAACCTGCAUAAAATTTAATGTCTUCCA
222204141	67360	TTGAAGCAGCAUATATATTGGCCCUAA	67361	CTGCAATGTCAUTCATTAGCTTTGAUGT
222421677	67362	TGTTCTGGAATAUGCTTTGGAAAGUAGG	67363	TCATTCCTTCCUGAGCTTTCAAGTAUG
223584970	67364	AGAGGUGTTCTTGUGACAAACAGAA	67365	CATGGCATCUGTACAGTGTCTAUAACAA
222233512	67366	ACTCCTGUTTAGGCCTUGCAG	67367	TUGTTTAGAAUGAGGAGAGAGGCAAAA
222167249	67368	AGTTCTGTTAAAGUTCATGGCTTTTGUG	67369	AGCGTTTACGAUCCTCTTTCAGUG
333146316	67370	ACAGGAGTGUGCTCCAGAUCA	67371	GCCTTCCCUTTCCTCCCUACT
320576791	67372	AAAAAGAGGCCAGACUCACACTUAG	67373	CAAAGGGAAGGCAUATGUCACCAT
316552694	67374	GTGCAUCCCAGGTTTCUAGGT	67375	GTGGGATTTGGUGAGAACAAGAGATUAT
332362864	67376	CACGGCAUCACCAACTTUGAC	67377	CGUATGUGACCCCAAGACCAT
333614007	67378	AATTTCCCUGGGACTGTUGACC	67379	GCCCTTACACUACTGGCAACUT
332957077	67380	CCUGAGACCCCUGAAGAGACC	67381	GTGTGTATCTGUGCACCTATGTCUT
332912649	67382	CCCTGTTTUCCTGCCCTGAUG	67383	CAGGATUTGTCCGUCACCCT
319422726	67384	ATTGACCCUGATGTGCAGUGT	67385	AGTCATGTCCCAUTTCCATTCCUC
332508921	67386	TCACATCTTTUCCGGTGTACATAAUCA	67387	GTGAACAGTUTCCTGACTAUGGAGT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332538808	67388	ACCCACACATUCTTGCTCATAAAUCA	67389	CTTCCTGTCUTCAAAGAAAGTUAAAGCA
321583993	67390	CCAGCUTCCCUCAGCGT	67391	CAUGGGCAACCTCTUGGAGAA
321573367	67392	AATCGCTGUGCGTGTAGUGA	67393	ACTTTATTUCTCTCATGUGCAGGCT
314688430	67394	GCTGGGCACUAAATAATCTCCTTATGUA	67395	GCAGCAACATCUAAAACTAAATGCCUAT
279067787	67396	AAAGAAGAATGUGTTCATAGGAACUGGA	67397	TCCAAAAGTGAAAUTCGCACAAGUT
278203587	67398	CCTTGAGACUGAAGGAACTGAAGATTUT	67399	AACTUAGAGGGCCTGGUAAGGA
280809382	67400	GGATTCGUCCCCGGATGTUG	67401	CACACTTGUCATGCACTGAAUAGAAAA
279070544	67402	TGTAGGTTTTCUTATGCAGCTTUCAGT	67403	GTGACACATGAAGUGCAAAGATAATUCT
267884790	67404	GGGACTUGTCCTTGCUGACC	67405	GCACTCATCAUCCTTGTCTCUGT
266605460	67406	CAGGUAAGUGCAAGCAGCAA	67407	CTTCCCATTGAUGCCTTTTTCTCTTUAT
324733852	67408	GGATGCAGAGUAGTGTTCUCCCT	67409	GCCTGTCTUCAGTCTTTAAGAACUCA
318836986	67410	GCAACUGGTAGCUGGAGGAC	67411	GTGATGAGCTTUGAGTTTTCTTTCTUCT
320004105	67412	GCACCAAUGTCATGCCUCAAG	67413	CTGCGTTAGUTCCAGTGACUGT
260312948	67414	CTGCAAGUGAACTGTTAGCATUCC	67415	AGTTTTCTGTTTCAAUGTTCGCTTTTCUT
263621066	67416	CTUTCAATAATTTGACUGGCACAAGGA	67417	AAATGCACACCUCAAAAGGCTAATTUAC
235035551	67418	TCTTGAAAGGAACUGAAATACGACGUT	67419	AGCTTGAGCUTTCCAATCUGCT
242692069	67420	CGUCAUGCCGCCCAAAA	67421	CGGCTCUGCTCGCUCAC
332431566	67422	CCCGGAGGACCCAUGAAUC	67423	GTCCACGCUGGAGATTACUGT
333514452	67424	CTGCCGAAAAUCAGGCCTTCUA	67425	CACGTAAGCACCUTTGTGTTTTCTUT
333832580	67426	CACTTGGTCCUGGCAGAGAUG	67427	CTGATGUGAGCTTCTGTCUGGT
333054255	67428	GGTGAGGUGGCACATGTTCAUA	67429	CCAACTATCAAAGAGUTTTCAGCTTCUT
320131477	67430	GGAACGGCCUGGAGUCT	67431	TCCCUCACCGGGTCCUC
319102287	67432	AATGACAATTCUTTTCAGGTTUGCGT	67433	ACAACTAGAACAGCAAUGGACAUAGG
313198915	67434	CTCCACGAUGGCGATGTUCT	67435	TGGAGAAGCAGUGGTGTCUG
313288429	67436	TGGGCCATUTCACAAGTCAUGT	67437	CACACTCACCCUTCCTGTCTUG
313256998	67438	GGUGUGCAGCAGGGACAG	67439	CACCTTTTTCUGGCTCTACTCTCTUT
313175550	67440	CGGACTTCUCTAGCGCCUCT	67441	AGGCTCAGCACUCCTTTCAAUG
257331590	67442	TCTGTGGCAUTCATGGCAUGT	67443	ACTGTGGCTGAAUCTCTCAAAGTUG
266078111	67444	GTCUCAGGGAACCAGCAUGAA	67445	AGCCATAAGCCCAAUAGATAAAAUGACAT
323640633	67446	GGAAGTGTTUAAAACCTATAACGTUGCT	67447	GATATGCCUGCTGGAGUCGAA
325954430	67448	TCTAGATTTAGUGGCTGTTTTGTGUCC	67449	GTGCTTCAGTUCCGATAAATTCUACAC
328028310	67450	ATGCAGTTGAUGACTGTCATAUCGAA	67451	AGGCTGCAUAATCCACACUGG
328074755	67452	CCTGAAAGUAGACTTAGGCUGCAC	67453	GGTGAAGGGAAUATCTCGTTCTCAUC
324404925	67454	AGAAAACTGAAGAAUCCACGCUGAA	67455	ACAGTTTTTGCUCTGGTGAATTACAUCT
324493652	67456	GAAATTCAGGCCCUCCAGGAUT	67457	AGATACAUCCCACCATGAUCAGGAT
319466773	67458	GGGAACAGGCUCTGAAACCTUC	67459	GAGTAAATGAGCUGTGGTTTCTCUCT
321205672	67460	CATGAAATCUGAGCCTACATGAGGUT	67461	CTGCCATTTCAUTTCCCCTTGUT
320085158	67462	ACGAUGCTCAUGGAAACCCAAT	67463	CGGACTCGCUGAACTTGUGG
265374131	67464	AAGGAAACAGUAAGCCACTGCUT	67465	ATCCTGCAUGGCTTTGGAUGA
317737479	67466	GCCACTGGCUTCTTCTTTGUGA	67467	CTCCTTCCAGCUCTTACAACTCUG
316937787	67468	GATATCACTGCUGCATATCTGTCUGT	67469	GCCTTUGCCACACTGGTTTUAA
317737385	67470	ACATTTATAGGUCCCACGAAGGTTTUC	67471	GACAGAGTGTUCTCTTTCCAGUGAAAT
316581197	67472	AGTTGGAAUGCAGCGUCCAT	67473	GACCTTUGCCCAAAGAGTAUCCT
319752627	67474	GGGCTGGGAUGGGATATTCUG	67475	GATGTUCGCCCAGGATACUGT
317345093	67476	TTGTCATTAAACCUACCTATGCATCUGG	67477	TGAGTCCTTCUACTGACGAATGGUT
316081217	67478	GACATGTTAGACUTACTGGATCUGGAG	67479	CATGTGCUAACAGACCTCTGGTTTAUT
319190726	67480	GGCCCCACACCCAUGUC	67481	GGAGGUGGCAGGGAGTACUT
320422474	67482	CACTCACATCUCCTCTTCCATTUCT	67483	TGAGTCTTTACTCUGCCTCTCTACAUC
320021523	67484	GACCCCUCCCTCCATCCTUAA	67485	CGTGGAATGAUGGTGATAACACUG
240603774	67486	CTCCCACAUCCCCGAGGAUA	67487	CCAUCCGGTCACUCGAAGA
321559349	67488	GCTGGTAGACGUCCTCTGUG	67489	CCAAGGTAUCCCCGGATGUG
319432069	67490	GCGAGUGAAACGGCUACGA	67491	GCCUTCUAGGCGACGCA
320142422	67492	ACGTGCUCCCCCUCACT	67493	GGTGGACUCTGGUGCCAAC
238712230	67494	GCCGGGUTTCTTCTUGAAGCA	67495	CCCTUAGAATGAAGTUGAGAGCGT
235132139	67496	CCACUGGGCTGTTGAUGAAGT	67497	GTCTGATTCUGACCCTGTTACCTTATUC
267364687	67498	ACGAAAGAAAAGUTACATACCUGGCT	67499	GUGACCGAAACGGCAGUCT
267686859	67500	TGUGGCAGAAACCACATCUCAT	67501	GTCATTTCACCAUCATCATTCCCTTUC
268063545	67502	CCUCCCCGCAGTCTTUCAAT	67503	CCCCTTCCACAUCTGTGTCUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
260636875	67504	CCATCCUGCCCCTTGTTCTUA	67505	TGAAGGGCGUAGAGAAGGUGAT
316040325	67506	CCAGGGAUCCCAACAGAAAUAAGA	67507	GCACUGGACCCGCTCUG
327053934	67508	TCACGUGACACCGTCUGAG	67509	CTTAUGGGAAAAGTATUCAGCAAACACA
318161567	67510	CGGCCCCAAGAGUTGATTTUT	67511	CGACTGGCUCAAGACTATTTCAUCT
319188277	67512	GGGCCCTUAGCTTATGTCCUT	67513	CTCAGCAGUGTACCTGGTCUG
318827300	67514	GACATGAAATUAGCCTCCCGCUA	67515	CCACTGUGGACAAGACTGTTUG
318202874	67516	GGGAAAACGCAUCCTCTUGA	67517	GTCAATGAGAUTCCCTGGGUCAT
255741760	67518	CCGGCCCAGAGAUGTTTTUAGT	67519	AAGAACAAATGTUACCTGCAGATUAGGA
260655723	67520	CTTCAGCCUCCTGCAGATGUT	67521	AAAACCACAAAGCCUCCAGCUA
259187102	67522	GCTAAACCCAGUTGTGGAAGUCAT	67523	AATGCCGAAGAGGUGGAGTUC
268330893	67524	GGACAGCUCTCACATCTGUGT	67525	GGCCAGAAGAGUGATGAGGAUG
257619571	67526	TTTTTGTGAAUTGTCCCCAUAGGGT	67527	ATCCTGAGAGAAGCCUGTACAUCT
257720537	67528	TCCTCTUCAACACTGTACTUGGGA	67529	GGTTGUACAGCCTCCCUAGAGAT
325584499	67530	CCCUACCCAGGCCGCUAT	67531	GGCACTGCUGTCTTTTTCAUCA
325561638	67532	CUTCCTACAGTUCCACACCGT	67533	CAGGTTCUCAGGGAGCTTGUC
325566176	67534	CCTCCAUGCGCUCAAAAGGAA	67535	TGGCTTTCTUGGGAGAAGACAUC
323644338	67536	CTCTCCUCCACGATGCACUT	67537	CCTTGAGTTTUGGCTTCTTTTUGGG
235554636	67538	CTGTTTGTUCAGAAGACAATGTTGAUGT	67539	AGTTTGGTGTTCUAGTTCAGCACAATUA
237215961	67540	GAGTCUCAAACAGGAAGACAACUCAA	67541	CATGATCCAUGGACATTTGACTGGUAT
235504478	67542	TGGTCCAUGCAATTCAAAUAAAAACGAA	67543	CCTCCUTTCTACCAAUAACCGCAT
237203200	67544	ACTTCAGAGTATUGCCAATCATGTTCUC	67545	AGCAACUGAGTAAGUGGCAAGAAA
239661439	67546	ACTTGCAUGGACTGTGTTATUGGT	67547	GAGCTAGTTCUGTCCACTGGUC
237076660	67548	TTCTGTTTTCCUAAAAGGCACTUGAGA	67549	ACACTGAUACCCAAAATGAAUGCACT
332292146	67550	CAAGAGGGAAGGGUTGGTCUG	67551	CCCCCAUCTGTGCCTUAAGAG
332995471	67552	CCGCCCUCAAGGCCAUC	67553	TGTCATATUCCCCGTCCATCUCA
328596651	67554	GGTTAGAAGACAAGUCCCTGUCA	67555	CTACAGAGGGAUCACCAUGACC
253669697	67556	GGGCAGUTCTTGGTCUCGT	67557	CTACUGACAACGCCCCTCTUC
318622343	67558	CCATAGCTCTUCCTCCCTACTCUT	67559	GAUACGGUGCACGCACAG
262854776	67560	GCAAATCAGUGCTGCAGAUACGA	67561	CCTAAGACUCCGTGGGAUGG
316252452	67562	ACCAGGAUCACCCTGUGGAA	67563	GCAUTGCTGTTUAGCAGGAACAC
317029078	67564	TGACAGGGUTCCCGAGUGA	67565	GCAGCCCCUCCTGGUAG
317466513	67566	GCACUCAGAGGGCGCAUC	67567	GGUGCCGAGGCATUGAC
331165143	67568	CCUATGTAACTGAGUAAGACAGGGAGAA	67569	GTTGGTAAAAGUGGTTTCUAACACAGT
330503740	67570	GAAAUAUCGCGCCCAGGGA	67571	GCAGTGGUGACAGGAUGAACAC
264230730	67572	CCACCGAUCCTCTTCCTUCAT	67573	GGAATCCATUAGAGGACACACTCUG
257903698	67574	CTGCTGGGCUAAATCATCAGGAATUA	67575	CAATCCAGGAAAGCUGTCTTCTTUT
262972438	67576	AGAGACAAAAUGGCCAAGCAUCA	67577	TUCAATCUGACACGGCCCAA
267891462	67578	ATGATTTCAGCUAACAGGTUACGCT	67579	CCCAACAAAGACAUCCTGTGUGA
315123420	67580	AACAACAACGACAUCATCCAGGATAAUAA	67581	ACCAAATAAUCACAACCGCCTUCA
268408182	67582	CGGUACCGAGAGGAACUACAG	67583	CACCCUCCACUCCAGCAG
266015289	67584	ACCCGACAAACUTCCCGAUAG	67585	AACTCUAAGGAGTGCCUGCAAG
268199234	67586	GCTGGACAGCUGTTGGTUCAT	67587	GCTTCCCCGUGTTGGAGUC
268502517	67588	GTTUGCCACAAGCATCUCACA	67589	GGTCGGUCAGGCTTCAGUC
255820178	67590	TCAATACTACUACAAACCTTGGAUCCGA	67591	AGGTCTTTCCUGCAGACATUGAC
325090951	67592	GGCAAGUGCAGAACTCAAGUC	67593	TGCTCACTUGATGAACTGGTUGT
323881149	67594	CCAGAUCCCCAGTCCTATUGGAT	67595	GTGCCCAGAAUGAGAGGUGAA
324648804	67596	CTTTGGATGTCUGTCTCTCTCUGG	67597	CGTCCACCAUCACCTCAAAGUA
323466011	67598	CGACCCTGACUACGAAAACCUG	67599	ACTCACCCTCUCTTCTTGTTCTUCT
323346137	67600	GTCCTTCTAUGCCGCCTUGAT	67601	CTCACUCCGTGUCACCGA
323421920	67602	TGGGATTCCUGCACGTGTUC	67603	GAAAGAGGAUGGATTUGGCCACT
326283601	67604	GGTGGCCGUGACCGAUG	67605	TCCAAUCCCCCATCTTUCCAAAA
323484623	67606	TCTACACAGCCUGATGCTCUCT	67607	AGTGTCAGACUCCAGUCACCT
325914051	67608	GCTGUCGCCGGTTCTUGAA	67609	CGCAGUGGACAAGTAUCGAC
325917996	67610	GCTCTCGAGUAGCCGGUAGA	67611	GCUTCUCGCCCGAGCAG
316870189	67612	GCTACTTAAAGGGAAUGGTGGCTUT	67613	GTAACCAAGGUGGTCTTTGCTUT
332640477	67614	GGGUAGCAGAGGACAAGTCTUC	67615	AGTGTTGGAGTAUCTGCCTAAGTCUT
316122240	67616	CAGAGCGGGCCUTAATCTCATUA	67617	GATCTGGCUGGGAGGTGTUC
266925618	67618	CCCAAGAAUGGAAGGGCAUC	67619	TGTCTGCCAUTCTGGCCTTUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
263054682	67620	GCCTGCTTCUGGCATAGAGUAT	67621	CACAGCGUCTACCTGACUCA
266875858	67622	CAGTCACUCAGTTCGCCAUCA	67623	CCTGAGACCAUGCGTATGUCC
257929963	67624	GGCUGCGGGAGCAUCAA	67625	CCGUGGCCGAAGTCCUG
326132618	67626	GGTACUGACATGCAUGAACAAGAAC	67627	GGCATTATGGGACUCTTCACCAATTTAUA
326102961	67628	AACAAATATCUACTCCCCGCUAAAAACA	67629	GCCAAACUTGGAAUGCCACA
323668436	67630	CCTCCCCUGAGAAAATCCAAAAUAAGAT	67631	CCACATGGAAACUAAGATAAATCAGTGGUT
323949621	67632	GTGTGGCCTUCTTCAATACCTUCA	67633	GCAGGGTCTTATTUTAACAAGGATATAGTTUAT
267638594	67634	CAAAGTCCCUGTGGGCTUCAT	67635	TGAAATGTTGCTUTAGTGTTCTCAGUCT
258869294	67636	ACCTTGGTTTCUGTGATTTTCTTTUGG	67637	ACAATGGCUGGAAGCUAAGGAAG
268416366	67638	ACUGTTGGAAUCCCAAGCACAT	67639	GCUTCTTTCTGCUGAGGACAC
315897533	67640	ACTTTCTTGGCCUTAGCTGCUAC	67641	GGGAATGACCACAUATGCACACAUA
317034341	67642	TCATCTCCCCUCAACCGACTUA	67643	CAGTGTTTUGTGTTCAATGUCGAGT
290517850	67644	GGGAGTCUAAGAAGAATTUGAGGAAG	67645	TGCTTGTTGACUGAGCAGATAUAACA
290160439	67646	GCACACACAUAAACCCACAUACAG	67647	CTTTCTACTGUTGGCTGGTUCAGAT
289320371	67648	TGAAAGGTUCAGGCTTCACUGT	67649	CAUTTAGGAGGTGUGGGAGGAAG
292984093	67650	CCTGCUAGAGCCUGAGAAAAAGG	67651	AAACCGGAGCGUCAUGAAGT
300435889	67652	GGACAAGACAGGGUTACTATATUCGG	67653	ACAACCCAAUCCCCTCCCUAT
255881169	67654	TCCTTATACTGGAUGAAATGGTCACAAUG	67655	CAGCCCCAUTACAGGAAUACAGAAAA
315749178	67656	GAGCTCUGGCACATGGAGAAUAA	67657	GGTTGTTACUGTGACAGTTUGGAAAAT
262474135	67658	CTAGCTCTCUCCATATAAACCCUCAAGA	67659	GTGAAAGAGCGGUGAUGGG
257472025	67660	CTTCTCTTCUTAGGGCCCUCCT	67661	GGCTGAAUAACCAGCTCTCTTTCUT
267405985	67662	GATATCCTCACUTTTCCAGGAAUGAAGG	67663	AGCATCAGUCCCATCCTTTGAATUAA
267547327	67664	ACACTATACTGAAAUGTCGTCATTUGCT	67665	ACACCCACATTCUTCTCTCATCAGAUAT
313738912	67666	TCTAATCCTUCAGGGTAAUCCACAGT	67667	CGTATCTGTTATCUGTAGACAGTTGUGA
227394130	67668	CTAGCGCGCUCAGGGUA	67669	CCGCUCCTTCTUCCAGAGACT
332741648	67670	CTGTGUAACCCCCAAAGCCUA	67671	GCTACCCATGUTCCCCTGATAUT
313251633	67672	GTAGTCCAGGCUGTGGAUGAC	67673	GCAGAGUGGGAAAAGCUGGAA
314511840	67674	GGCCCATAUAGATGGCTCUGG	67675	ACTATGTCACCGUGGAGGGUAT
263914501	67676	CCCTUCCCAAGGCTACAAUGAC	67677	GATCCCCTAGGUTGTACCCAAGUA
267265372	67678	CACTCCCTUGTTGTCCTCCUT	67679	CATCCCCUCTTACCCAUGCAG
315565956	67680	CCAGGCATUACTCCTCCCTUG	67681	AGCATGTCCTTGUGATAACCTTCTTUT
316752929	67682	CAAAAAGTGGUCAGCACAAUAGACA	67683	CGTCCCTATTCCUTCTATTCTAGCCTUA
317258200	67684	GGAGCCAUCAGTAAATTCCUGGAAA	67685	GAGGCATTTCUACCCACTTGGUA
317680098	67686	GCTGAAATATCTUCATAACTGTCCUCGT	67687	TUATCTGGGAAUGGGAGAGAACCT
318267065	67688	CTCCAGGAGCUTCTCACACUG	67689	TCCCCCGGACUAATACTGTTUCT
319532258	67690	AAAACCAGUGAGAGATGUGAGAAAGAG	67691	CGCGTGGCATUTTAATTACTAGAAAGUG
320923398	67692	TGCAGCUATGGACACUGACAAA	67693	CAATCAAGGTUAAGCAGGAGTTUGAG
318461291	67694	GGAACGTCUGTGCCTGUGAAT	67695	ACAAGAGUGAAGGGCACAUGG
318777703	67696	GGAAGCUAAGGGTCCGTCTUG	67697	CUGTTCCCGUGCAGCCT
319461015	67698	GATGUGAGCAGCCACCAGUA	67699	GGCCAGUCCTGAGCAGUG
263026018	67700	GGAACGAGGUCACCUCCAT	67701	CCCCTGUCACGGAAGGAAUC
258495568	67702	GAGGCATAUCTGAGCCTUGGA	67703	TCTACCTAATCUCGCTCTTCTCTUACC
266659654	67704	GCACCAAGGUTAAGUACAAGCC	67705	TGCTGUACACCCTTUACCAACAAT
257702064	67706	GGAGCCAUGGATTTGCCAUCT	67707	GCTTTTCTCGUTGTCCCAUCCT
261325847	67708	CCAAAGTCAGUGACCCCACUT	67709	GUACTTCTTUGACAACAGCACACAG
256098528	67710	CCCCACACUTCCAACCTGTUT	67711	CAATCTGGTCUTCGTGTGGUCA
268216218	67712	CACCCCAUCCCCTTTUGCT	67713	TCTCTGCCTTUCAAAGGGACAUC
266634864	67714	GCCAGGGUCACCTTUGAGA	67715	TCCGTATTTTCAAAACUAAACTAGGTCUGT
257911326	67716	GAGTGAATAGGUGACCCTTGAGUT	67717	CCAAGAGGCCCUCAAGGUC
263550626	67718	ATCATACCCGUGCACCTTTCUC	67719	GCTGTGTGAAAAUCACTCTGTUCCA
285261469	67720	TTAAAAAGTGGGACUGTGATTTAATACTGUCT	67721	GAATTTACCATUAGGCAAACATCGTUGA
332836709	67722	CCGCTTAUGCAAGAATAATUGCAACT	67723	CCTTAGCACACUCATCTTTCCATTUGT
315825533	67724	CCATACUCAGCTCCAUCCGT	67725	AGATGTGTCCAUTCTCCATGTCTUC
314281496	67726	TGTGACCCCUTTTCCTCATCUCT	67727	CCAGCCCAAGUCTGTCAUCAC
313277097	67728	GCCTTGACUAGACCCCCACUT	67729	CTCCAGTTUGCGCTTTTUGGT
323508967	67730	GAAAAGCUGCUGCAGAAGAAGT	67731	GCCTCACUGGCGTCAAGUC
314927061	67732	GTAGCUCCATCTCGAUGACCA	67733	GTCGCUCGGTGACTGAUGT
315639601	67734	CGUTGAAACCCAUGCAGACAC	67735	GAATAGAAAAGCAGGUGGTGTGAAAAUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328025938	67736	CTCCATTCGUGCAGGCUACA	67737	GGCTGCUCCATCAGAAGUCAG
328029631	67738	AATGTCCUCACCACATUCCAAGAG	67739	CGCTATGAAGUGATTCGCAGAUG
327154185	67740	CCAGCACAGCAAAUCTGGTTUC	67741	TTGGGATCUGCAAGATGATTGTGAUAA
328165894	67742	CCCAGCUGATAGAAUGGACAAAGT	67743	AGTTTTCTCTGCUCTAATTCATCTGUGT
326779272	67744	GAUGAGCACCCAAAGGTTUGT	67745	CATGTAATGCCUCTTAGAGTGGUAAAGT
326569443	67746	ACTCACTGTAUGGGTATTGATCCUCT	67747	TGCTTTTCTGTUTATTGATTGCTTUGCT
328137348	67748	GCAGTGTTGAAAAUTGTCAATGGUCAAA	67749	GGGAGACAGUGCAATAAATGTTUGG
327217447	67750	CTGGGAGUCCACATACTGCTUG	67751	AAATGCTTTAUCAGGAGGAGAAUGCT
324225300	67752	TGTTTGAGCAAGUAAATATTCGCAGGUA	67753	GGACCTAATTCUGATGGCTTCUCC
324560567	67754	AGCAGAACTUCGTTGTACAGAAUGAAA	67755	ACCAAATCTGUCAGATTCCAGTUACAAA
323342042	67756	GAATGCCCCAAAUTTGTAGCAUGT	67757	TGGCTTACCTUGCCTTGTAAATGAAUAT
323831924	67758	GCTCTTCTATGUCTAATGTTCTTTUGCAC	67759	AAAACTCTUCACTTCCTCTUCACCAT
325635237	67760	CCATAAGCACUACACGCAGUCA	67761	CGCUCTCTGCTAATUCCAGAAAAGT
325634749	67762	CCGAGGATCUGACCGACTUAAAG	67763	CAGAGAGAATGCUGCTGTGACTUA
324800155	67764	GCGTTCTGTTTUCTGACATGTTCUT	67765	CTGAGGACAAGAUGGTTCTTAATGTCUT
323914125	67766	TGTCCCUCCAAGAAGTGAUACCA	67767	TCATCAGCTUCAGTGAGGAGGAUA
324149676	67768	TTTCCATACCGTUCATTTCTGATCAGUT	67769	ACTGTTTAAUGCACACATTTTGTTCUGA
326610423	67770	TGGATTAAUAGACCTGAGTTTUGCCAAAT	67771	GGGCGTTUCTGTTAGCCUAGT
237721752	67772	CTTAGGCTTCUCCTGGCAATCUC	67773	TCAGGGAATUCACACAGTCCUAGT
320194660	67774	GGATGCTACCUTTTCAGCTGTCUA	67775	GCCACAGTUCCTTCACTCTCUG
266658808	67776	TCAGATCAGGGUCCAGGUGAT	67777	ACACTCUTGAATGAATUGCCAGGT
262827425	67778	CGATGTGAGCCUACTCAGUCCT	67779	GGATGTGTAUAGAGGCTGTGTGAUAAT
262934671	67780	CCCTAACCAAGUGCTCTCUGT	67781	TCCTGGACUGTGGCCTAUACC
327602107	67782	AAGGAAATGUGAGAGAAGCUAAAACCA	67783	CATGAUCGCCGCCTACTATUACA
327973964	67784	ATTTCAGGCAAGGAUACTGAUCCC	67785	GCATCTGTTCTCCUCATTACCTTGTTUT
314483962	67786	GTTTCTCTGCUGCTGGTCUCAT	67787	AGCUCCCAGAACATGCAUGG
324715800	67788	CCAGATGAATCUTCAGGAAGCTGUT	67789	GAGGAACTUAGCAGTGATUCGGAT
324554315	67790	GACATAACCAGAAACUTGACTCUACACA	67791	GGCUAUGGAACACCACCCAA
324163484	67792	CAAATAGTTGGAGUTATGAGTGGCCUA	67793	CTTGACTAAAGGCUCAGGTAAGTAUCAT
323637245	67794	ACCAGAGUCTTTCAAGGUGCAAA	67795	GTTTCAAUGCCACACCTGCTTTAUAT
263795998	67796	CATCAAATCCCUGGAGTTCACATUC	67797	GCCAGAACAAGUTAAAAAGTGTGAUCAT
267577652	67798	ACATACCACAUCTTTUGGCACACA	67799	CTACTCCAGACUTGACATCATATGAAUCA
267828505	67800	CCTTCUACCAAGAAAGCTGATCUCA	67801	TGCUGAAGACTCACUGGAGGT
266931078	67802	GCCCTCCUGGTCCTCCUG	67803	CTAGGGACAACACCUCTTTTAGAAUCAA
257663835	67804	ACTGGCTUCTTTTGCATTTUGCAT	67805	CAAGGCAACUTACUGCACCAC
265928841	67806	GGAATGTATATGUTGGCCTATCCTUGA	67807	GGTCGACCACUTTCTCCTUG
267648809	67808	TCTGGACCAAAAGGUGATGCUG	67809	CCTGGAGCUCCCTAATACAGATAAUG
268160090	67810	AATCCCUCGCGTGCAGTUA	67811	CCTGATCCATGUATGCAATGCTATUT
268083085	67812	CAAGGTAAAATUGCCCCCAGTUC	67813	GGACGAUCAAGCTAAGAACCUCAAAA
268081497	67814	TTTTACAUGACCAGGAAGCACUAGG	67815	ACATTCAGCCUCTTTTGCTTCACUAT
315715925	67816	CTTACCCCACCCAUTGTAATUCCA	67817	GTCGTCTTTGGUGTTTCTTGCTAAAAUT
267659656	67818	AATGACCGCUTCGCCAACUA	67819	CTGGTTAGUGAGCACCUCCAC
235289854	67820	AGGACGTAUGGAGCCAGUCT	67821	CAGCUCGGCGGTGTTTTUAT
264860996	67822	CCTTCUCACCCCACTCTCUCT	67823	CCTAGAUGAAGCGCTTGTCCUG
236167121	67824	CCAAGCTUACCGTGCCATUT	67825	TTGATCCTTTGAUGCCCTCATTAUCA
333586429	67826	TCTTCAGTATUCCAGTACCAGUACCC	67827	GACUCTCACTCUGCACAGGAA
263683168	67828	CAGAGACTACAAGGUGAAGCATGUT	67829	GGTGACTTTUGGGATTTTCCATGUC
263557252	67830	ACCTTAUCCAAAGAGCTGTAUGCC	67831	GTCATCCCUGAGGUCAGAAACAAA
233225397	67832	CAGGCCAUTGUCACAGAGGAT	67833	GGTAGGCUGTACTTTUCCCAAAAGG
234742951	67834	GGTATTGAATTTCUTTGGACCAGGUG	67835	AAAGATTGTAUGAGGTCCTGTCCUAGT
324704084	67836	GGGAGGAAGGAAGUCCCTUCT	67837	TGCCTTUGAACTACACCAUCGT
325322157	67838	GGGTTGAGAGUTTGTGAGCTGUT	67839	CTGGTTCGAGACAUTCATCATCTUCA
260828456	67840	CCAAAACCCUCACGGAGUGAT	67841	AUCTCTGAAGGUGGGAGAAAGAGT
316030884	67842	TGCCTTCATGTUTTTCACTCACGUA	67843	GTTAGGTACAGCAAAAUTGTAACATGTUC
263794704	67844	GGCACATGTUGAATATTGCATAUGAAGG	67845	AACCATCTAGUTAAGCAACATUCACAGA
332124095	67846	GCCCTGTGCUTCCTTCTCAUAC	67847	CCTGAAGGACUGCGCTGTUA
324627543	67848	CCTUCGCAGCATTCTUGGGT	67849	GCACGAUCAGCAGAAACATGUAG
256789054	67850	TTGGUGGAAGAGCAAGAGAAUAGAAG	67851	TCTACATTTCAGGUGATGAGTATGAGCUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
227974265	67852	GTGGAGCCUGGTCAUGGAAA	67853	GGGCAGAUGACGCUCAGG
227608653	67854	GACAGCCUGACCTCACCUT	67855	CCUGAGGACCCAGUGGAG
326422178	67856	GCCACGUGCCTTTGTCCTTUA	67857	CCTCCTACUGTGCACCCUAC
264490187	67858	CCCTGCGAGCUATTTTGAAAGUGA	67859	CCAGCCACCUACTCTUCCACT
262509004	67860	TGCAATGATGUCCTCGTCTUGG	67861	TGACCCCACACAUCCGTACTUA
320879421	67862	ATGCTTTCUGCTTCTGUGCAAAG	67863	CTCCCATAAAGCUGGACCCAUT
319704002	67864	CTCACTCAGUGACCCCTUGT	67865	CAACGCAAATTCUGCCAATTCCTTTAUA
332375804	67866	GCTTTTCTGACTUCAGTGTAAACATTCUT	67867	CACAGAGCUAGCTGCCAUGT
333690688	67868	TCTTTGAGGAGAUTAGTGAUGAGGCT	67869	CAGGTGGCAGAUTTTCAATTACTGAUAC
314543643	67870	CTGGAACAAAAGGUTCTCATUGGG	67871	CAAGTTTUCAAGCATGGGUCACA
314406444	67872	TCTTCTTGGGUTTAGCCACCTTUC	67873	ACAGACTAUAGACGCCAAUCCCA
316022702	67874	ACACACATACGCAUGTCCTGTUT	67875	GCAUCUGAACGCCCAACAAC
257281420	67876	GTTCTACTGGGUAAATGCAGATAGUGT	67877	CATGCAGAAAACUAATCAGGCTTUCC
259070511	67878	AATAAATCCCAUGAGACCTTGCAAUCT	67879	GATGATTUCAGCGAGTGTUGCC
259166035	67880	GATGATGTCAAGGUGTCAAAATTTCCUT	67881	TCCTACTTTTTGAUGTCCTCACTTCCUA
268482733	67882	GATTTGCTAGAAUCAGCCTCUGACAT	67883	ACCTCTGAGAAGAUCACATCTCTGUT
292194284	67884	GTCTGTTTTGUGTGTTGCAGUGT	67885	GCAAUCCCCGCAAGAGUAGT
291330442	67886	TCTGTTTGTTTUTCCAGACTCUGACAAT	67887	GTATGGTTGCAUAGTCATTGCATGTUT
289875093	67888	TGCAAAACAGGAAGACUTAAAAGAAAUGG	67889	TCTTTTAGTAAGUGCTGCTGCCAUAA
223858254	67890	CCTTTCTTUAAAAACAAGCAGCCACUA	67891	CAGTGCCUCAACTTGCTTUAACAA
222847255	67892	ATCACTTAATTGGUTTTTGGCTTTUGGA	67893	GUAAAAGCTGGAUGAGGAGAGGAAG
222509664	67894	TGCCAGCUCCTGTUGAACAT	67895	GTTGGTGGCCUTATATCCTAATTCAUCA
224582664	67896	GCCCATACACAUTCAAACACTTACAAUT	67897	GGTATTGACCAUAACTGCAAAACTTACUT
224555371	67898	CCTTAAGACUCCAGCCUCCAA	67899	TCGGCCAGGAGACUGTAUAGG
327231801	67900	CTCACACUGGGACTCTGTCUAC	67901	CTGCTCUCCGAGTTGUCCAT
328182079	67902	GACTTCUCCAGCAGGCTCAUC	67903	AGGAGUCCAAAGGACCACGUA
323870453	67904	TTTTCTCTTCTCUCAGCGGTTTAAUGT	67905	AGUATTAAAATCAUGAGGAGCAGGACAAA
235830815	67906	GGATGAUCCAGATTCCAGUACCAGT	67907	CAAGTTTCCCTTUAAGTGGCCTGTAUAT
242586924	67908	GGAGATGGCACUCAGAACUCC	67909	TGTGTTCTTUACCATTTGGGCUGAA
238520908	67910	ACAGTGGGTTUTCCTGAAGCTUT	67911	GGACCAGUGAAAGTTTGCTGAAAUT
258602616	67912	GACAUGTGTGTTAGUAGCCAGCA	67913	GGCGTGAAAAGUAGCTTCTCTTUAGAA
258741128	67914	CTCTTGGGAGUTGGTATCCTTUGT	67915	CCAAAGCAGAAGUCUAGAAGGGT
316593973	67916	TGGAGCCAUCCCCGTTUC	67917	GCGCAAAGAAAAAGCUAGTTTCGAUT
316573377	67918	GGACCTATTCCUTTGGTTGCAGUT	67919	CTCTCCAAUCCAGTGTGUCAGG
331720661	67920	CGTTTCCCAUTCTGGAGUCCAAA	67921	CGTGACCUCGGACTCAGUG
331742136	67922	GUCACCCCAAUGGCAGACA	67923	CCACTTCCUGGTCCAGUACAG
331647540	67924	GAAGCCCGUAGAGGTTCAUCT	67925	GCCCCTUCGACTCATTCAUGG
261136625	67926	TGGCAGCCAUCTCTGAATTCUT	67927	CCCTCTCTCUCCTTCCAGTTCUC
267461591	67928	GAGGAGCAUCCCCACACUG	67929	CCTCTGCCAUTCAGGACACAUT
257282256	67930	GGAACACAGCACUGGAACUGT	67931	GGTGCCCTCUCACCTCTATCTUT
266569983	67932	CATTGCTGTCUGGGTAGGGUT	67933	CACTGGTCACAUTTTCTATCCCTUACT
269317089	67934	GAACAGAAAAUGACAAGTCACAGAUGG	67935	CCCTACGATUACACCTATGGCTAUG
261807702	67936	GCCUACCCCACCATGUCAC	67937	GCATGTCCCUTCTCCTGATAAUCAT
324833544	67938	CGCCCCCAUTAGACCCAAAUG	67939	AUCACCAACAACUCAGCACACT
324623989	67940	GCAACUCGACGGGCGUT	67941	GCCCTGCGCGAUGTAGTAAUC
269750958	67942	GGGCCTTATTTAUCATCTGTTCTGUCT	67943	TGATGGTGTCUAACACAACCTTTGUT
316208599	67944	CATGTTCAGGAUCACAGGUAGAAACT	67945	TGTATCCATCUCTAAACAAGTGCUCAAAC
317237024	67946	CATGACAGGCUCTTTCTTCTCUGT	67947	CTTCTTCAGAAUGGTCCAAAUGGGA
315577902	67948	CTAGAGACAACUGGAGTUGCACT	67949	GCTACCCCAACGACUTCAGUAAT
317137569	67950	GTCATCTTAAATGTACUTAGCTCTTGTTTTAUG	67951	ACTGUGAAACAAACGCCAATGAUT
317529702	67952	GCCAAATAAGAAAUGAGACAACAAUACCA	67953	GCAAATCUGCGTCCUGCAAAA
317369263	67954	GCCUTCATGUGGGAACCAACAT	67955	CUGAAGGCGAAAAGUGCCAAG
316855570	67956	ACCTGCAAGGAUAATCTTTCTCACATUT	67957	CTTCTCCAGGUAAGAACCCATTCATUAC
266679745	67958	TCAAACAUCAGACAGCATTCAUGGA	67959	CCTGAAGTTCUAACCTGTTGTAAUCAGT
268595215	67960	TGCAAGTCAATGAUCACTGAAAAATGUG	67961	CATCTGCTGATUATGCTGATCTCTTUGA
325203845	67962	GGAAAGATCTTGGGUCTGGAAATGAAUT	67963	TGTTGGCACCUGTTCTACTTTCTUC
325178377	67964	GAAGGUGGGCGAAATAGCTTUG	67965	GGCCTTTATTTUGTATGTCTTTGUGCAT
268957327	67966	TTGTTGCCUCCTGAGATTGUGT	67967	ACTCAGCCACAAUTTGTTTTTGAAUCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267474380	67968	AACAGUCACACCAACCCGUT	67969	ACATCTCCACAGAGUGTCTTCTCUT
267299162	67970	AGGGAAGCUTTCTGGAUGACAC	67971	ATGTCTCATUCGAACAGAGCATUAGAA
259326687	67972	TGGTTCTCUGAGTTTTCAGUGCAA	67973	GTGCAGACUCAGCACTCAUGAA
261154713	67974	GGCUGGAGCCGAAGCTAUC	67975	GCTTUGTAAACTCCTUGGAAGAGGT
314245585	67976	GAATGCCGUGGTTCCUCAGT	67977	GCCATGGTAGAUACCAACATTACTTCUC
313177797	67978	CTCCCCACAUTGTCAAAAUGCT	67979	GGACGTTCATUCATGTGCCACUAA
327003158	67980	GTCCCTCUAGAGTCCCCACUT	67981	CAGAATTTCGTCTUCGTTCAGTTCATTUT
254719523	67982	GCAGAUCAGGGCAUGGAGAAA	67983	GGCUCACTTCCUAGGAGGCA
231534675	67984	CATGACTUGGCTTCTCTUGGCT	67985	CAACGTTGAUGAGGTCGUGAGT
224471011	67986	AGAAAAGGGTACACUTGAACAAGAAGUT	67987	CTTTCTTCTTGGCUAACAGGAGTAUGT
222654214	67988	CTGTCACAGAGACUGTCTGATCTUT	67989	CTTGTCATGGUCACAACTCCATCTAAUA
223209441	67990	TGGAGAAACAGGAUTGCTGCUT	67991	TCTAGGGACAATUCTGGTTTAGCTTCUA
332432928	67992	GGAAAGAGCAUTGATTTGTUCCAACT	67993	GCTCTAAGAGCCUCGAGTTCATUAAAAA
319696036	67994	CTTCCAAAGUAGAGCCGGTACATAUT	67995	CATCTTTAAACUGGTTGTCCTTTTGUGT
318425291	67996	CTCGTGCAAUTACCCCAGCUA	67997	AGCTGCTACTUAGTCATTTCTGTTUAGAC
320163526	67998	AAAUGCTGACUGACAAAAGAACAAGAC	67999	CCATCTGTUGTCCTGCUGGAT
258719747	68000	GCATTCTCGUGGGCTTCACUT	68001	GTGTTGCAAAGAAAUCTTCAGCATGUA
324123358	68002	GCTGTATTTCCAUTTTAACGCAGUCT	68003	CCAACGATCAACUGGCTCTTTUG
325105793	68004	GGCTGACACUTTGGGACTTTUT	68005	GGUGGCTTUAACCAAGAGAGCA
323434511	68006	CTTTCTGCATACUGTAACTTTGGTTUGT	68007	CCAACTGAGAUATGTCTTGATGTUCCA
324373678	68008	GCTAGAGTCCUGATTGCCAGUG	68009	CTTGCTTACTATTTUAGCACCTGACCUA
323664757	68010	CUTCCTGAAATACUCAGCGAAGGT	68011	CTGAGATGGATAUCATAAGGCTGTTGUT
259672034	68012	GCAGAGCATUGAATTCTGCCAAAUA	68013	TGAAGCCAGCUCTCTATCCCAUT
263060752	68014	GCTTCCTAUGACCCGGAUAACAA	68015	GTACGATACAGAAUATATGTGCCAUGGG
259606613	68016	ACTTAACGACUACAGAAGTAGTGAUGGA	68017	CCTCCTTCCAGUTCTACCAGTTATAUCA
255995424	68018	CTGCTUAGGATGATAATUGGAGGCA	68019	TCCAGGAAAACUGAGAACAGAAUGAAAT
263227514	68020	AGCTATAGCAGUTGTCGCAGUT	68021	AAGATGAGTAUCGCACATTCACUGT
257524696	68022	AUGTGAGAAAUGGCAGGCAGAT	68023	GGTCTGTGAAGGACUATTACTGATTGTUT
263136299	68024	TTCCTTUCCCACTGCTCTUCAG	68025	CAATCACAUCCCCTGTUCCAGT
319928146	68026	ACATTCUTAACCACTUGCAGCCA	68027	CTGTTACCAUGAGCTTTGAAACTTUCAT
319516774	68028	GGCGCACUCACCTUCGT	68029	GCGUCGCAGCTCAUGCT
319206655	68030	GCACCTCAAGUGAGCTGUGAG	68031	TGACACCCACGUAGAGTUCCAT
333578789	68032	GACGGGUCACTATCTGUGCAA	68033	GGGCTCUCACCCACGTAAUC
316012798	68034	TGCCUGCGGCCTTGAUT	68035	GGCAGCUGCTACCUGGAT
316810940	68036	CAGAGGCGAUCUGGAGAGAG	68037	CGGGACUTCAGGACAUACCAT
242324749	68038	TGTTTAAAUGCAGTCTAACTUGGAGAAGT	68039	CCCAACATCUGACAGTTCTTTCTCTTUA
239369610	68040	GGGAGAAAGGAUGGGTGTGUA	68041	CCATTAATTTCTUGCTGGTATCACTUCC
266522177	68042	GTGGTUACCCGGAAAATCCAGUA	68043	GGAGACGCGAGUCCGTUC
266396398	68044	CCUCAGCACAUGCAGCAGAT	68045	CGAGUGACGCAAGGAAGGUG
258526395	68046	GTGACCCAAAAUATTATTGCTTGGUGAA	68047	GTTGCCTGAAUCACCACTTTGUAAT
255784858	68048	TTTTAACTUGCAAGCAAATCAUGACACT	68049	TCTTCTCAAGGAUGGCTCGGTAAUAT
261837813	68050	GGAAGTGTTTTAUCCTGCCTTCTUCT	68051	AGGATTTTCTUCCAGCCACCUG
326713731	68052	CTCGGATGUGATTAGACTTACUCGAA	68053	TGGACGCCAGUTGGATTTATTAAUCAAT
316575196	68054	CCAUGCGAUAACGCCACCA	68055	GCATGGGCTTUCTATTTTCTGTCAUT
313926761	68056	GTGACAAGAAGUCCCACGUAGT	68057	TGGTGTUGCAACTTGTUCCCT
312835344	68058	TGAACCCAGGUTCCTCTGGUA	68059	CTAGCAGACAUTGAAGCCCACUAT
314015921	68060	GCGCTTCACAAGCUCTTTCCTUA	68061	GCCATCTTTCCUCTGGATTTCGUT
314081726	68062	TCCTGGGCUGAATTAATGAAUGAGG	68063	CCTAGGAACATCUTCTTACCGTTTCTUT
265346919	68064	GTCCTGCAUAGAAATCTUCAAGCC	68065	GAGTGAAGCAGAGUCAAGTGAATCUT
263596746	68066	GCCTCTTCCUCAAACTCTACAATATAUGG	68067	CTATCTTACTGUAGGTGCTGTTGCTAUT
255443382	68068	CCAGTUACCTTGCTGUCGAGA	68069	CTCGTGCTAGUGGATCTGTTTTTCUA
316273491	68070	GAGGGTGGCUAGACCTCTUG	68071	CTGAGTCUCCAACTCTGGTTUGAAA
316269506	68072	GTAAAGGACCUGCCTGTTCTUCT	68073	GATAAGAAAGTUAGGGACTCCTUGGG
315796280	68074	ACTCACGTATGUATAAAGCCTAGUCAGT	68075	ACACGTCCCAUTTGACCAGTTUA
317501740	68076	CGAATAGUGCTAAGCUGGGAAGT	68077	CUGGGUGACGCCAGGAG
317875869	68078	CTTTGGCUTTCAGAGTUCGAACC	68079	GATACCTATGACGUGGAAGGTGTTTUAT
295780780	68080	GGTGGCUGGGAACCTTCAUAT	68081	GGAUCATCAUCCGGAAGACAGAA
278633307	68082	TTCTGTTGCUGATAAGATGCCAUGAT	68083	GGCCTTTGGUATTGGCAGTCUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
315857673	68084	GGGCAAACACUATCTCUGGACT	68085	TTGTAGTCAACUGCTGCTTATTGUCT
279789336	68086	TCTGTATCATCUGTATCCATGTGUACCA	68087	TGTATGTGTGUTTGACTCCACUCC
261869229	68088	CTGGAGGCAUGAAGUGAGACAA	68089	GTGGCACAGACUGTGUCCAT
265403355	68090	CCAAGTCTTUGCCCAGTTCUGT	68091	CATTCAGCAGUCGGUGGGA
239939495	68092	CAGAGCGAGGGUCAGGTTTUA	68093	GCAGTTTTACACUTACAGGGATUACACT
263719001	68094	CCCACCAAGCAGCUGUACC	68095	ACTGTTGCAACUGCCTTTUCAC
269173977	68096	ACCTCCTTTUCCAGAGTCUCCT	68097	CCAGCTCUCAGATTTGCCAAUGA
269074699	68098	TCAGTGCCTUTGCTCTTGTCUC	68099	AGGTCCTAGTCUCCCTCCAGAUAA
266458891	68100	GGUGCACACAGGCAATATTUGA	68101	GCUTACCCGTUCACCAGGAG
268293245	68102	ACAGGAUTTCCUGGACCAAAGG	68103	CCUCATCUGACCAGCCAGAAT
268646493	68104	GACCAGGGCUGTCCTTAGATTUAG	68105	CUGACACAGAAGGCUCCAGAAA
332569971	68106	CTAGGAGGCAGAAGCUAAGTGAUT	68107	CCAGCTGCAAUTCTACAGCAAUAGA
257731247	68108	GCTGTCAGGAUGGGACTGTTUG	68109	GGGTCCCCAGGUTATGAGCUA
254974328	68110	AATACTATGGGCUCTTCTCCTCCUAC	68111	GCCCCCUCGGAGAAGGUAAT
257802553	68112	GCCCACTTCUCATCTCCTGUT	68113	TGACTACACTACUCTTGGGCGAUAG
319444996	68114	AAAATGGCCCCUTTGATAATGTGTUC	68115	GTCAGAGAAACCGUCTUCACCA
321426053	68116	CCACTACAAATCCUTCTTTTCCCTCUT	68117	GCCATTTCAUAAGGGTTATCTTTTCCUG
318643730	68118	CATTTCGUGTATTTCAAAAUCGGACAGA	68119	TTGTGCTGTUACGCTGTTCTTACTUA
320090567	68120	ACTCACTTACAGUGACTTAATTCTCTCTUCT	68121	AGAAUAGTAGCTCUGGACAAGGACAT
320008395	68122	AAGAAACTGTUGTTGCTATACUCAGGAAA	68123	GGTGTTGAUGGATCCTGTUAAGCA
256421425	68124	CAGCCCUCACCCTGUGT	68125	GCACCCCAGGCCAUCUG
254491316	68126	CTCAACCUAAGGCTGTGTGTUCT	68127	GAAGGGACUTCUGAGAAGGAAGG
254942131	68128	GCCTGTTTUAAACCACGGTGUT	68129	GCACGTTGUCGTTGACAUCC
266897879	68130	GGAAGGAAAGGAACUCTAAAAACCTCUT	68131	AGACCTTUGGCAGCCUAGAGA
327202891	68132	GCAAGGGUGCTCTGGTGTTUA	68133	GCTCCAATTTCUCAGAACTCATTCTUCA
325798477	68134	TGCTGCTGAUCTTCCCTGGUA	68135	CTTTCTCTTGCCUTCGAGTTCTUC
258159423	68136	GGCAGCGGAAACGUTCATUT	68137	GTTTGCCACAAUGTTTGTATCTGGUT
314079141	68138	ACUCTGTCCCUGCAGGAGAT	68139	GGTCCTUCCTGGTCUGGAAAC
327180831	68140	GCCAAAGGGAGUTTGAGATUCCT	68141	TGTATCCACCUGGGCTGTTUC
327791842	68142	GCAGTTCUCCCCACTCTTCCUA	68143	CAGGCAAUCCAGUGGAGGAC
333436022	68144	ACTTGTTTTCATTGUTCTCAGGTACCUC	68145	GTTTCCCCUCAAAGGAATCCTTCUT
333384648	68146	GGAGTGTGUAGAGCTCTUGCT	68147	GATTACATGCUGCCCTACTTGUG
333395971	68148	CCATTTCCCAUGTTGCTUCCAAA	68149	AGTCTUGCCAGGAGGAATCUCT
314074949	68150	AGTGAGGGACUGGAAAGGGAUT	68151	GCAGGTGAGGAUACTGAGTCUAAC
324139901	68152	TGGCCAAGGUTAAGTGTTUGCT	68153	GGAGGAGACGGAGCUCTACUG
323400300	68154	GAGCATGGCGUCATCATTGUT	68155	ACGAGAAGCUGTGCGAGTUT
268002988	68156	GCAGGATGGCCAUGTAGATGAUG	68157	AAGCCCAAGGUCATCGAGUG
315397942	68158	CCCACACTUAGCAGCCAGTUC	68159	ACCCTACCTTATUCTTGACCTAGCUC
315382889	68160	GGCUGCCCTCAAAAUCCACAT	68161	CCCATUGACAAAGGTCCTTCUCAG
327733337	68162	TTCATGGGAUTCAACTGUGGAAACT	68163	TCGTTAAACAUGGGTGTTGAUCCA
222445156	68164	TGCCATTCCAAGUGTCTTATTTTTGTUC	68165	TGTTGCTGAGATAUTTCACACCAGTAUT
223395325	68166	CCCTCCTACCAUCTTAGTATCTAAUGCT	68167	AAAGAACACACAUTGCTGTGGUAAAAA
333114222	68168	CGGATTCACCUGTCAGGACATUC	68169	GCTGGAGACUCCCUACCCAA
333099715	68170	TCACGGACACAAUGTGUAGCAT	68171	GTCTTTGTACGUGATGTAGTUGCC
333243422	68172	CACAUGTCUGCGCGAACAA	68173	GTGCCCTGAAAUGTGTAACAAAUACAT
332440569	68174	TGGGACACTUTCACAGAACTUCAC	68175	GCCTCAACTTGUGTTCTTTTCCATUT
319918108	68176	GGAACGGCCUCCAACAAAAUC	68177	CGTTTAATACTTGUTCTTGGCCTTCAUT
279765271	68178	CACCTTATUGCAGCAATTAAUGAAAACC	68179	GCTCAGTTTTUGAATCCCTGTUCCA
279399776	68180	TCAAGUGAATGUCACGGAAAGCA	68181	GCTTATTCAGGAGUTCCTTGGTGAUT
313978413	68182	GGTGATCTAGUTGGGTTCCAGUT	68183	CAACCATGCATUCAACAATTACGTTTUT
279481389	68184	GAGGCCATATUTTACTCCTGGAUCT	68185	TGACACTGGAAAGUTCAGAGAAAAUGT
317190716	68186	CTTGCAACTCCUATCTCTCACUCA	68187	TCGTACCAACGUTTCTCATGUGG
316207432	68188	AGGCCAAAAUACAATAGCAGCUGT	68189	AAAAACCCTTCUACCAATGTCTCAGUT
265802459	68190	CACAGCUGAGATTATGGAUCCAGAA	68191	GTATTATTCCAACUGAAGCTGTUGCC
265645147	68192	AAAACCCACCUCTTTTTGCATAACUG	68193	CTTGAUGCCGCACAUGAGAAA
317883990	68194	TUCGAAGAUGACCCGGAAGAAG	68195	CCTGCAGCUGATCTTCGUGT
326771467	68196	TCTACTGAAATAAAUTCTGCATTGGUGCT	68197	GCAGAGAAUGAGGGAGGAGUACAT
241676023	68198	CTTCCTCAGACAUTCAAACGTGTTUT	68199	ATGTTTTGGUGGACCCATTACAUT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
332357524	68200	CGCAGTGTUTCACTCGCUACT	68201	GTGTCCTTCUGGGACCAAAATUCT
332289863	68202	TCGGTCUCCTGTGGUGAGAAA	68203	TCCTTCATCGUTTGTCTTTGCUCT
313478517	68204	CGGATCTGCCUCTACATCTCUAGT	68205	GCCTGTTGCAUCTACCCCTUG
313858123	68206	CUGCATCTTCTTUCCCAGACCT	68207	CCCGAUGACAAGGAAGAGTTUG
314618550	68208	GCTGCACCCGCUCACUA	68209	CTCATGCCCACUCTCCUGAT
314327004	68210	GAGACUGTGGUGGGAACCAT	68211	ACATCCATCATAUAACTCTCCTTCCCUT
312758691	68212	CCAGGTUGCCATGGAGAUAGT	68213	CCCTAACTTTTCTUTCTCTCCTTCTTCUC
326410373	68214	AGAAGGACCGAGUTCTGGUCT	68215	CCTCCCTCCAUCTCACACTTUT
324123059	68216	AGAAAGGGAGUCACAAGACACUG	68217	AGGAATCCAUGACTTTGCAACAUAGAG
320914543	68218	TCCCTGCTGUGCCTTTTTACAUAAT	68219	CTGATTCUCACCACACATCCTTUCT
319531252	68220	CCCTAGGCGCUGTGTCTTUA	68221	GGATTAATTGGCAAAUTTGTGCTTUGAT
318047352	68222	GGGAGCAGGUGTGAAAGTUACC	68223	GAACAGTAAGGUCGTTGTTTCGTUC
318198318	68224	TCTTCACGCUGCTGGTTUGAA	68225	GGGAGCGAAGAUACCTGCUAAG
266823593	68226	GGGTTGATTUGGAGATTCAGUGT	68227	GTAGCCTAGUCCCCTCCCAUT
320429480	68228	CATCTCCCCUCACAGATAAAGCTUC	68229	GCTGTCCATGAUCCCTTATTTACTUACT
316957965	68230	AACTTTGGCAAUGATGTCATUCAAACA	68231	CCACCTTTAACAUGGTCATTTCCATUT
316001418	68232	GGCAUAACTGTCTAAAAUACAGGAGACT	68233	TCCTTTGTGACAAUGGACAATGUAGAAA
272300790	68234	CTGGUCTGGCAUCGACACT	68235	GCCTACCUGGAATATTGCTCUGG
318339087	68236	CGGGAAGCACUATGGCATCUAT	68237	GCCATGGGCUTGGACATTTTUG
333725421	68238	CGCCTCCCUCCACTTUGAT	68239	ACGGACACCUGCATGACUC
319252384	68240	CAGCACCAUACCTGGAAGTUCT	68241	GCTGATCUGCCATGTCCCTUG
320241834	68242	AAACAAGTCACUCTTCATCTGUCCAA	68243	CCACGCUGAGGUGAGGAC
242158745	68244	GCTTGGAGAUCCCTTTCGAACUG	68245	TTCATGAAGTUGAGCCTCATAGAAUG
241726329	68246	CCGGCCCCUACTCACTTTUG	68247	CCAGAUCACCACGAGAGTAAAUCT
257560335	68248	AGCUCACCTTCTUGCACACAT	68249	TCGTTAGCAAAGUCGCACTCUT
327810584	68250	CAAGGTCTTCGUCCTGTGAGUC	68251	GGGCUCAAGTCACUCAAAAAGGT
328203623	68252	CCAACUCAUACCCCGGCAT	68253	GACUCCCCACCCACCTTUG
326914028	68254	GTCCTCACUGTCCAGCTUCA	68255	CCAGGUGCCAUCCCAAACT
318126732	68256	CTGGCCUGAAAATACATGGUCCT	68257	GGCCAAGUTCCTGGACUACAC
319708397	68258	GCCTCCAGGAAUGGCCATAUT	68259	CTTGAGGUGGGCCTTTCATTTUT
318091399	68260	TCAGGAUGTTCCTUACCCCAAGT	68261	GGCCTTTAAACUGAGGTGCCUT
318188499	68262	CCCAAAGGAGGGACAUACCACUA	68263	GAAGAGACCUCCCAAAGCTGTATTTUAA
262043335	68264	AATGAGCUAACCGGAGTATTTCUGG	68265	ACCTACCACTUTTCACACAACAUACAT
262328803	68266	GCCACUGACAACCACCCTUAA	68267	CCTCTGATUCCTCACTGATUGCT
263746824	68268	GGGTGAAGAGGAAUCCCAAAGUT	68269	CCCTUCCCAGAAAACCUACCAG
264767784	68270	CATCCUACCGCACCTUGACA	68271	GGATUAGGACCCAGGUCCCAT
269264267	68272	CTGTTUAGCAAGACAAGCCCUAGA	68273	CCATCTTATCCCGAUAAACTCGATTUGA
266868044	68274	GGTGTGGAGACUGACAAAGUGAG	68275	CCTGAGGGAUGAGCAGGTAUG
265373990	68276	CAGTCTCATACUCCCGGACUCAT	68277	TGATTCUAACCAGGGCCAUGAAC
267339142	68278	GCGGGUGGCCAACCTAAUAG	68279	TGTCTGGGCACUAAAAATAACCTGTUT
260854576	68280	ACACAAGAAATAAUAATGACGCCUCCA	68281	ATGAGGCAAGUATGGGTCAAGAUAAC
325555024	68282	GGATUCCACCACCUCGGA	68283	GUGCAGGATUCAGGGAGCAA
235100920	68284	AGTATGAGTTTUAGAGGCTGTTAATTUGCT	68285	TCAGCTGCCUACTTCCUCCAT
236497505	68286	TTTCTATTTGCTGUTCTTTTTGGCTUCA	68287	CCTTTTGGACTUACATTGGTGATGATUC
236052142	68288	CAAACTAGAAGUGGCCCTGUACAT	68289	TCATATTGCUGACAGAGGCAAACUC
238959215	68290	ACTCATCUCCCTTTAATTTUGGCACAT	68291	GCACAATTCCAUGGATTGGATTUAACA
226050915	68292	GAAGCCTCUCTCTCCTCTCUGA	68293	GGTGCTGAUGGTCCTGCTGUA
329557948	68294	GGGAAGUCACAGGAACAGTUAGG	68295	GTGTGUCGCGGAGTUCACT
327148602	68296	ACTGACCCCUCTCCCTCTUT	68297	GGGAGATGUGCGTCTGCUC
327621967	68298	CAUCGGCGAGCUGAGCA	68299	GCCTGCUGCTTGGACAUC
261120133	68300	CCTCTGTCCCUCCAACCAUGA	68301	TGAGGACCUGGAUGCACAAG
262108782	68302	CUGTCCCCUACCAACACCAAC	68303	GGCAAUACCAAGAGGUGGGAAA
262618256	68304	GGTTCCAACAAGUAGGTCCCUT	68305	GGGCAATGUCACCGTTGATUT
262086822	68306	CAGCAGGTGUCTTTCTTCTGGUT	68307	GATGAGAGCCAGUCGCTUGT
316866446	68308	CTACTCCATGAUTTCCTGCTGGUT	68309	CCTGGGTGAUGGCCTTGUC
316739227	68310	TGGGATCCUGGATGTCTACATCUT	68311	CGGCAUGAACGGGTATCCUG
331254012	68312	GGAACCUCCGAGCTCUCCAT	68313	CTTGGCCUCCTCCTGCUG
267626400	68314	GCAAGTGGTCAUTTACATCATCAATGUT	68315	TGGTGCTTUCCCCCAATAATTAAATUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
315042838	68316	CAGACCGGUTGCGATTGUG	68317	CAAAUTTAGCGTUCAGGAGAAGCAG
268950787	68318	CGAGUCUCCCCGGAGAGG	68319	CAGCTCGCUGTTCTGUGACT
267435318	68320	CGACAGCCCAGUATGTCUGAG	68321	CAACTACACAAGUGCAGGACTCUA
262390017	68322	GAGCUCGGTGCUGGAGAA	68323	CAGGGAGUCCTCUGCCC
259627294	68324	CGGCATCUTGTCCACGUGAA	68325	CTTAGCTGTCACUTAGCGTCCUC
268022486	68326	CCCCUCCCCACCTGTCTTUAT	68327	CCAGACCACUGAAGCTCCUG
321489318	68328	GUCTTCUCCGGCGGAGT	68329	TGTTGTCGGUCTTGTGGTCAUC
320908213	68330	ACTGATTTGTATTTCAUTAGTATATTGGAGUGA	68331	CCTTCCTTCATGAUTTCCTCAGTCTUT
324580408	68332	CGACTCCAUCTTGAACCCAUCAA	68333	CUCGCCAGAAAACCTTUGCAG
323339414	68334	GGACTUGGCCACTGGCTUAAT	68335	CATCTATAAGAGCUGTCCTGGGAUG
325411553	68336	CATCACGCUCTTCCCTCCUG	68337	CAGCATCCUCAGTGCCTUGT
323863633	68338	CGUGGGCCAGAACCUCAC	68339	GCTTACAGCAAGAAAUCCACACATUC
323811168	68340	GGGTGAUGGCTTGACATUCC	68341	GCAGCGUGATCTCGAUGACAT
326286850	68342	GGAGUCCAAGCGCCAGUT	68343	CCCUCGGGCUCCGAGAT
256367365	68344	GGTGGTCTCCUCTGCTCTCUT	68345	GGATTCCAGAGAUGACGTUGGG
256123264	68346	CATGTCAAUCCGCGTGGAUG	68347	ACAGTGATCGATAUGAGGAAGATGCUA
325602292	68348	CAGGGUCACCACCTGUGA	68349	GGCTGCCACCUTTCCTCUG
318629426	68350	CCACCTCTCUGCTTTCTTCUGA	68351	GTGGTAGATGUAGCCGGTGUG
319123277	68352	GGCCUGGTCGCUGAACT	68353	GGGTCUGGCCCATACCUG
327645260	68354	CGGTTGUACAGCACGTTGAUCT	68355	ACCAGCUGGAGTCUGAGAAGT
328333121	68356	GAAGGGTGGUCTTGGAGGTUG	68357	CTCTCACGUCTCTTCCCTCUCT
327748260	68358	CCTGCCUAAGCCCTGGGTAAUA	68359	CTAACCTCTGACUCATCGCCAUC
319892457	68360	CTTTCTGCUGGTGTTTGUCCAT	68361	CAGCUGAACCAGAUCAAAAACCC
316114527	68362	TCTCCCCAGCGUGGTATCUT	68363	CATCCCTCUCTGACTGCCAUC
316066435	68364	ACTCCACGACCAUGTCCTCAUA	68365	GCCCACGAAUCATGCAGUCAT
264267178	68366	GAGAAGCAGAAUAGAGCCAAGTAUGG	68367	TCAATCUCCACAGCATGGUCAAG
261995280	68368	CTCTCTCTCTUGCACACACGTUA	68369	TGCTCTCAUGCCATCTTUGACC
256168026	68370	TCCTAUAGGGTCAGUGCACAGA	68371	CCATCCCCACUTTGTGATUCCC
314104909	68372	CGTTTTCCTAACCUTGTTCGCCTAUT	68373	CCATGAGGUACAGGATGACATAGUAGA
315525228	68374	CTTTAGAAAGGAACAAGUGGCAACTUT	68375	CAGUTCCAAUGGGAGGACGAC
324087316	68376	CCCAGAGTCUGGAAAAGATTTTCUGA	68377	CCCCUCCAGAAACTGTAUAGAAGAGAA
268451559	68378	CUGTAGAGAGGUAGAAGGAGAGGAC	68379	GGCTTCTAAAGUAGGAAGGGTCAAAAUT
265699328	68380	CTGTGCTAUCCTACCTCTAAAUCCC	68381	TTTTCAGGAATGUTCGATTAGGTCTUGA
264697306	68382	CATGTAGTTCCCUCCAACGAGAATUA	68383	CTGAGCATTUGCTGATAATCCAAUGT
267300908	68384	CATTTATGCTTCTUTGCAAACTACTGUGA	68385	CCTACUGGAGCAATAAAGTTUGAAGAAC
323558458	68386	TTTGTAAACCCUCTCCATCAGTGUC	68387	GGGAACUGACGCAGGAUACA
318809334	68388	GCTCCCUCACTGCAACUGAAC	68389	CAAACCCAAGUCTCTGACCAUCA
316904791	68390	GCAGGUGGGTTGAAUGAAGGA	68391	AGCCAGACUACAGUGAACGAC
290883853	68392	CCUTATCGAUACCAAGGGCAACAA	68393	AGCTGAUGCAGGCAAAGTUCT
301125178	68394	GTCTGUAGGAAAGGTGAATCTUCAGG	68395	TCTTCUAAACACCAAGCCCCTTUT
263909434	68396	TCTAGGAGCAAUACAATGTAGTGACUGT	68397	CATTTCTAATCAUCCACTCCCGGUT
262308310	68398	TTTCTGCATGUAGCGAGCAUCT	68399	CTATAATUAACAATCCGGUCCAGCAAAC
253786879	68400	ACTGAATTTACCUGTTGATCTGAATCUGT	68401	AAACGTGCCTUCTGGTGGTTAUAT
259671123	68402	GCAAAACCAGCAUATTAACGUGACT	68403	GAAGCCAUTGCTCTUAGCAGGA
253964373	68404	GCCAGCAACUGTACATGAUGGT	68405	GCTATCCAAAAAGACUGCAAACCAATUT
316997749	68406	GUGTGAUGAAGCAGGCAGGAT	68407	CTAAGCAACCACACUTTCTUGGT
262495193	68408	CTTCTTATAGGGUCCTCCTGGACUT	68409	AATGGATGGAUCTCACCTTGGTUC
265798660	68410	CAAUTGCATUGAACAGGGCCAA	68411	GGAGUATGCGATUAAGGCACAAAA
263434055	68412	TCATGGGAGTTUTTGTTGTGTTTTGUC	68413	GTTGAGAUGCAGUGACAGCCT
313079850	68414	GTGCCATTTUGGACAAAAGCTTGUA	68415	CCTACCTTCTUGGAAATAGCCATTGUT
318776572	68416	CACCAUGCGGAAGCTCTTUG	68417	ATGTCTTAAATAUCAACAGGCCACUGT
321106207	68418	ATTAACCUTTTGTAACUCCCCGGAA	68419	CAAGCAACTGAACUTTACATGAACAUGA
317673231	68420	CTGCCTAAGUCGGTAACAUGGAA	68421	CAGACTACUATGCTTTGTAUGGCAAAGA
315645718	68422	GATGTGATTGAAAUGGATTCTTTGTUGCT	68423	GACTTGTGTGGAAUACCATGCTTUC
229096102	68424	GACCAAGCAGUACGTTCUCCAT	68425	CAGUAAGGACTGUGGCCGAA
229076944	68426	CAAACTCAAAAGCUTGTGGAGUCA	68427	GGGACCUTAAUCACCACAGCAA
317907209	68428	GCAGAUGCGAGCAGTTTTGUA	68429	TCAAAAGGAAGCAGAUTCAAGUAGGAAT
333585219	68430	GCATCTAAGACAGAGGUCTCAGGACUA	68431	CCATCATTGCAUTTACCTCGGAUCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
314791122	68432	GGCCTAGTAUGGAAATAGAACCTGUAAA	68433	GACTCATTCUCCAAGGAGTGTGAATUAT
312871723	68434	CGTCAUCACCCTGTGGUCAAA	68435	ATCUGAGGCACGAUACGGAAC
313198147	68436	ACTGTATTGCUACAGGCUGCAAA	68437	CCAGAGTUCCAAGTGACGCAUAC
266769400	68438	GCCCACAAAGUCTACCCCUT	68439	GGAGCCGCUGCAGGAAUAC
315068283	68440	CTTACCTCUCCAGGGACCUGAA	68441	AGAAGAAGCUGTCCCTCTCUGT
313958463	68442	AGACAUCAGCCCCTTCCTTUG	68443	AGGCTGCAGCAUTGATGTGTTAAUA
314497788	68444	TCAUGACCCCGUCCAGGAA	68445	GTGUCAGCCCGTCTGUCC
332599021	68446	CCCCCAGUAUGAGCGGGAT	68447	GCUACAAACACGCCCATCUAC
267765766	68448	ATTAATCTUGACAAGCCCTCUAACCC	68449	GCTTTTCACTCUAGCCAGTCCUT
316543055	68450	CACATGTCCACUGAAATGAATAGAAUGG	68451	TGGTGGAGUGGAGAGAAAGAAACTTAUA
317661638	68452	AGAAATAGGTUTCTGCTGCTUGGAAA	68453	GCCAGAAUCAGCAAGGUGGAT
319904258	68454	GCCUGTCCUCCCCAGGAT	68455	TGCUCCCAGCCCCTAUGT
314327943	68456	GGAAGAGCACCGUGATCAAUG	68457	CGTGUCACAACGGAGGACTUG
313552987	68458	CCCTCTTGCUCCTCTGCTUAG	68459	CCAGAATGCCUCCTCCTCATUT
315038427	68460	GGTGGGAUCAAAGGAGACATUGAA	68461	ATAGACGUAGAGGAGGCCAUAGAG
319300319	68462	GCTCACGGUGCATTCTTTTCUC	68463	CTCTTTGUCACCTCCAGGTUCT
318352283	68464	GTTCCTUGGGACAGAGTUCAGA	68465	CCGUAGAAGGGATUGACAAGCC
264055185	68466	GCUGGGAAAGTGUCCACACC	68467	GGCTTTCTCGUCACTCTCATACUC
256622079	68468	CCAGCAUGACCCCUGAACA	68469	CCTATUCCCAAGCCCAUCCC
323980783	68470	GATGACAAGGAAUGTTATTGCUGCAT	68471	AGATTCCCCUCTCCUCACAGAC
316017202	68472	GATGGTTTTUCCTCTAATTCTCUCAGGT	68473	TGGTGTTGCAGUCAAAGTCCUT
321426061	68474	CUAGGAAGAGAGAGAAUCGCCAAA	68475	CGCGGUCATGUGACACAG
314024587	68476	GAUGGGAGGAGCUGAGAAAGAAAA	68477	CTTCUCAGCCAGGUAGACCAG
315485872	68478	GCCTTCCUGGTACUCAGCAC	68479	GCCCTAGGUCTAGATCCUGCAT
263090543	68480	AACAGTTACTTCUCTAATCCCTTCUCCA	68481	CCTCTGCCUGAGAACATTCTCTAATTUT
268891891	68482	GAGAAAGUAAAACACCACTCCUGGAT	68483	CGAGGAGAGUCTCTCCAGTTUG
264528733	68484	ACCGACUGAAACGGUGACAT	68485	GCAAAATTTCACCUACCACTGTCAUC
257302244	68486	CTTACAGTAGAGCCUTTGTTACCCTUT	68487	TCTCTAGGGAAUTCCTGGTCCUG
268786914	68488	GGAUGCCCCGAAGACCUT	68489	GTATTTTCTCAUCACTAATGTGCUCCCA
268583156	68490	CCTCAAACAGUTTTCCCTCAUGAGA	68491	CAGGGTAUGGCAGGTGTAGAUG
264578556	68492	CGCATGGCAATUATCTGGTTAGCTUA	68493	AGAAATUGGACCAAGAGGTCTUCC
269277244	68494	TCAUTCCATCAUCACCAGGAGGA	68495	TCCCTGCCAAAUGTCCTGTUT
286215364	68496	TGAGATATCAUGTCCATTCACTUACCCT	68497	AGGGCAACUGTTTAGAACTCUAGT
333294606	68498	CTTCTGAAAAGGCUGGGCUACT	68499	CCTCTGCCTGCUGTCTAATCTTATTTUT
316557611	68500	CGCCACAGGUAGGTGUGA	68501	CTCTGCTGUTGTGGTCGUG
316613638	68502	TGAGTGACCCCUTCCCATUCA	68503	GGTGGAGGCUAATGGCUGAAC
312796180	68504	AUCAAGCGCCAGAAUGGAGAT	68505	CTTCCACACCAGGUCGGUAG
319601926	68506	GAAAAAGCAGAAAUGGAAGTUCACAAAC	68507	GTATACCTGCUCACCTCTTACTTGUC
320214627	68508	GGAAGCCAGUTCACTGUCGAA	68509	CTGCCTGUGGCTTCTAUCAGAG
314046814	68510	GAACGACCCCGUACCTAGTUG	68511	CCCGGCCUAAGGACCTTUAT
317578753	68512	GGGAAAATUACAGGCTGGTCCUA	68513	CAGTTCCAAGCAUTCATAAATTCTCACUT
327555936	68514	ACTTGGAGUCTTGAGUGAGAAAAACA	68515	GTATCCAUGCGCTAAAACUCAAAAGT
326721485	68516	AAAATTTTGTACCUTGAAGTGAUGCC	68517	GAAGGTGGGAUTCAGACTATTGTUAGT
326887206	68518	AGGCTATCACUCGATACAGGTATUCT	68519	GGGAAATGACUCCATCCTGGUT
326490267	68520	CGTAGGAAACACAUGGCUGACC	68521	GTTCAACAAGGAGUGTAGCTGUCA
323878149	68522	CTGGTTCCAAAAAUCCGTGCAUT	68523	CAGGCACAAACAGCAUGAUCAC
332636808	68524	AAAGAGCAGAUCTTGCUGCAGA	68525	TTTCTCUCCCCTCTCTGUGGAAT
333138106	68526	GGAGAAATTGCUAGAAACCATTGAUCAG	68527	TTCTAATGCAUAGGGCATACAGAGTUG
333216294	68528	ACCGTCACCUTCCAATCCTUC	68529	AGGATGTAGUGGACTCCTGCUAAA
323387420	68530	CACGTCTCACTUATTTTTCCCTCTCTUT	68531	CTTCAATGCCACUAGTAAAACTUGCAT
324813273	68532	GTTTACUCACAGGCCATTTGCUT	68533	GTGCATTAGGCUGTGTTTAGAAGUT
326385314	68534	GTGTTGCCUCCTCATCUAGAAAGAAT	68535	GUCACCCCAUAGCGGGAAAA
325254752	68536	GGCTCAAGUGGGTAGGAUGAA	68537	TCCTGCTTTTUAGAAATGGCCUGAT
324954168	68538	GACTTGGAAGATUATGATGCTGATTCUGA	68539	GGACTGTAACCUTCCTCACATAACUAC
326127151	68540	TGCTAGCAATUAGGATTACATTTUGGCT	68541	AGGCCUCCGAATGAGCAAUC
324717667	68542	ACACGCACTUAAACACCTGCAUA	68543	AGCTTATATGGCUTCATTAATGGCUGAA
325026334	68544	CACAAGGTTTTUAATGAGGCACUGT	68545	GCCAAATATAUGCAGGAAAGCATUACAT
324050313	68546	TTGGAAGATACGAGUCCTCCCTUAT	68547	CCACTGTGGTGUAATTGATAATCTGAGUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
324655843	68548	CAGTCTCCCUATGCCATUAAACAGA	68549	GCAATTCCAAGUTTCAGAGTAGCUG
324209052	68550	GTCCAAGACUGGTTAGTCAAUGGT	68551	GGATAGCTTUGGAGAAATTCCGTUG
326875592	68552	GATGCCTCAUGGTACCTGGUC	68553	ATTAGCTGAATTTUACCAGGCACATAUA
326500861	68554	TCTGATTCTACUCGTAAACAGUAAGGCT	68555	GGCAACCCUGAGGTCCUAAAA
327597525	68556	GGTCTAGTCTGUAAACAGGTGATGAAUT	68557	GAAGAAAGAGUAGCTGTGGUGAGT
327847006	68558	CATTGCUAGCACCAGGAAGUC	68559	AGCAATCAAGAAGAUGAACGAGATUCA
327115631	68560	AGAAAAGCTCAGUTTCCTACCTTGUC	68561	TTTTAATTTTGCAGGAGGUCCTAGGUT
258191416	68562	GTACCTTTTGGAUCAAATGATGCTUGT	68563	CGAAGATCAGUAAGAGGAGUCACAAA
257301051	68564	AGAGGGAUCCAGGCCTCATUA	68565	CTGACAGCAGCUTTCTAGATGUAGG
267654255	68566	CTGAGUCAGAGGTCAGCUCAC	68567	TTCCCACAATUCTTGCCACAGUA
267331231	68568	CCTTTCUAGGGACAGACUCCAC	68569	AGATCUCAGCCCACAGTCUCT
327790026	68570	GTGGGCUCAGAGCACACTAUT	68571	GACATCAUGGAGATGGAGGAUGAAG
327211833	68572	TCTGGTATGCUGTAGAGAAAACACUG	68573	TCCGTACCUGGAGAAGCUAAGT
267980719	68574	TGCTGATTACATUCACAATCCTGATTUCT	68575	GACCAGCTUGCCCAGGUT
262028298	68576	GTATCTAGGGUGAAAATGGTCTUCCAG	68577	CCCTCTUGGACCCUACAGAGT
264235794	68578	CCAGCUGGAAAGAGTGGUGAC	68579	TTTTGGTTGGCAGAUCTGACATTCUA
268922780	68580	GGTTTUGCCCCGTATTAUGGAGA	68581	TTGCCATGAAGAUGAAAGACUACCAA
268011178	68582	AAGCUCAACUAGCACAAACAAGT	68583	TGGGCCAACUGGAGCUG
260231802	68584	GTAGCTTACATCUTCCCCAGGTTUA	68585	ATGTTTTGAATTGUATTACTGGCAAGUAAAGG
269054852	68586	GGCTTTTAACUGGCATACAGUAGAGT	68587	ATGAAAAATCUGGACTTGGGAGUCAA
317835663	68588	CCTGCTCCCUTTATAATGAUCAGGAAAG	68589	TGAGATTCGTTCTUCTGGATATCCCTUA
265478255	68590	ATTCATGCUGCCCAATCTUCCT	68591	TGCATCUCCAGCTCTGCAAUC
236031729	68592	TCATTACACUACTGCCUCAGGGA	68593	CCAGGCAUGGATTTTCCAGCUA
235049836	68594	CTGCCGGGCAAUGTCAATUAG	68595	AGTAGACCUCCCTGAGCACTUT
333212703	68596	GCTTTCUGGGCTGACGUGAAT	68597	CTTUACCCCAACAGAGTTTUCACC
333145512	68598	CCCATCTCUGACAGCTTCCUCT	68599	GCAGACTGAUCCTGTGCCTTUA
325225995	68600	CCCGAGAGCCAUTGCTGUT	68601	CATCTTTGGCAUGGCCAACTUC
325681420	68602	GGCATGTUACATCCCUGGACAC	68603	TCAUTGACAACTUCAACCAACAGAAGA
327068995	68604	CCTGTACAGCUCGGCTUGA	68605	ACCTACCCUGGCCTCTGUAAC
255569944	68606	GAACCAGAUGAGTGAGTGAUGCT	68607	CCATCACTGTUCCTTAGTTTAATCTUGCT
267169728	68608	AATAGAGTGCAGUGTACAAACGCTUA	68609	CCGGCAGGUTTCTACCCTUG
316827780	68610	ACTTTTCAAGGUAGCGCCUGT	68611	GCTATATGGGUGGACTAATATGTGCUT
257760371	68612	TGTAAAAGTGTCUCAGTTGCTGUGT	68613	GCTTATAUGCCACCATGTTTGAUCACT
332114853	68614	CACCCACUGGUCCACCAAG	68615	CCGTGATGUGCTGGCAATTUAT
332083699	68616	GCTAGCGGAUTTCAGGTTCUCA	68617	AGAAATUACCAGCAGAGAAUGGCA
332050049	68618	GCACGGAAAUCCATCTGCUC	68619	AGGGUTGGCUAGAGGAGGAA
261960356	68620	TGATGCTGACUAGTGAGATGTCUGA	68621	CCUACAGCUAGCACAAAAGGCA
257038973	68622	GGAGGGAAAGUTGCAATATTGTUGT	68623	CGCGAGCGGCUAAGTAAAATUG
265571134	68624	GCAUGAGAAGAGGUCCAAAACCAG	68625	ACCATGTCTGUAGAAGAGAAAGCTACUA
260816907	68626	TGUCGTGAACAUACAAGCCAGT	68627	TGAGATTGGGAAUAACACAGAGTTUGAG
227469618	68628	CCTGAGCCGGGUCTCUT	68629	TTGGAGCUGGAGCTCTTGUG
328929345	68630	AGACTCACUGGCGTTACUGA	68631	AGGATGCCUGCATACACACUG
323332802	68632	GTGTGAGCAUCAAGGGACCUC	68633	GCAGUGGAUGCGGAGAAAGAC
261691232	68634	CACUGGCAGCCACTCCUC	68635	GCTGCGUGGTGTGTCAUAGT
261792051	68636	GCTTTCTTTUCGGCATGUCCAG	68637	CACAGAGCACCAGUCUGCAA
320740006	68638	GGCGGAGAGGCUGGTUC	68639	GCGCTGGGUACCGGAAAUA
332945350	68640	AACTGATACTCUACCCAGTCCTTCUC	68641	GCTTCAGAAGAAAGUTGACCATTTUCAC
332604813	68642	ACTTTGCAGUGGTGTCTCGTAUC	68643	AGGTAACAGTCCUTGACAAAGCTAATTUT
332930461	68644	CTAGTGCAGAGAAAGCUGAACTUAAAAA	68645	CTTGCTTCGACCUTTCTGTTCAUC
333700423	68646	GCCCCAGUGAAAGCTTTTCAUC	68647	ACGGGAACAUCCATGGAAAATCTAUC
314535939	68648	GAAGGAGCGGGAUATGACATAATTCTUA	68649	CTGCTGAAUGAACAAAAATAAGTTGUCACT
267625325	68650	AAAAACCCGUCAUCCAAAAGCAG	68651	AACATAGCTGGUTTACACTGCAGUAT
267906986	68652	GCAACCCCAGCUGACATTTUG	68653	CUGACATCACCUACCAGAGCAAG
268438055	68654	CCAAATGGAAUTTTCCGGGCUT	68655	CAATCACACGGAUGAACGTAAAGTATUT
267921316	68656	CCACTTCAATAGUTTACCTGCAGCUT	68657	ACCTGGTTTGAUAAGGCTTTAGTAAGTUT
261859514	68658	CAGTTTCTAUGACACTGTTGUACAGAGT	68659	TCATTTTGATGCGUTTTCACTTGTGUT
269360142	68660	ACCTCAATAGGUCCTACTTGAAAGUCAA	68661	CATUGGACGCCACTGUAACAAAAA
262701022	68662	GGCTCAGCAUTAATTTCCTGCUC	68663	TGCCTTTCAGAUTCTTCCTTCTUAACAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
259108236	68664	CCCCTUAGGGACACTGATGAUG	68665	GTGAATTCTTCCUTGTTTTGGGTUAACT
267824186	68666	CACAGAGCACUGCAAGUAGAGAAA	68667	GAGTTCCGCAUTGATGCCATUC
293612979	68668	CTGCCTCTUCCATCTCCTTUACC	68669	TTCTCTTAGUAAGGCCAAAACTTTUCACT
290172613	68670	TGACTCACCUCGGTTAAAAUCAGAAC	68671	GCCATGTTCATTUCTACTAGAGGATCUCA
292709286	68672	CCCTGAACUCCTGGCAGAAAUT	68673	AATGAGAAAAACACAUCAACCTGCTTUT
290463323	68674	ACACACAUCATAACACTTTUCCACCA	68675	CCGCTGATTTTGUAACTCTCTCCAUAAT
292191379	68676	CACATCAUGCAAAGGAAATUGAGACA	68677	GAGTTCATCCUGCAACAAAAAGTCATUA
290296928	68678	AAACAATGAAGCUAGCCTCAGAATGUAA	68679	CCTGTTGTACCUGGTAAGACATCTUC
222399018	68680	CAGUGAGGGACGGGCAAUAG	68681	ATTCCATAAGGCACUCAATACGCUT
224517330	68682	TTTGTTGTTACUGCATACACATTGUGAC	68683	TCTTTAGGATTTCUTGCTGAGAGATUCC
222829631	68684	TGATAAACACCUCAAGTUCCAACCAC	68685	TCTCTTCTTCTTCAUGCTGTTCTTCTUC
328223626	68686	CCTGAGAGCUCAGATGACAGUGA	68687	ACAGGTGCAGAAUGAGTCTGAGAUA
240608097	68688	CCTTGAGTCCUGGTGGTCCUA	68689	TCTGAGTTTCCUCAAAGATCTCCTCUAT
269285627	68690	GAAATTGCTCAUTGAGTTGCTGTUCA	68691	GCTGAGGUTCTGGGTCUGAGA
267454535	68692	ACTAUGAAGACAGAACUACAGAAAGCC	68693	TCAAGTGACAUTATCTTGUGAACAACCA
266167855	68694	GAGGAGCUGAATCGGCUGAA	68695	GAGGTCATCCUCACTCCTCTUCT
268497138	68696	TGAGAAACAGCAAAUTCAGAAUGACCT	68697	TGTGACTGTGUCTCCCTGGUA
268492092	68698	GAACCACAUACTGGTCTGCUCT	68699	TGAACCCUGGAGGAAGTCCTUA
268511771	68700	CAGGGUGTGATUGACCAAGACA	68701	CTTCGGUGCTTATCCUCCCAT
265516853	68702	GTGCTGGAGUCGATCTUCAGG	68703	CTGCCUCCCTACTTCAUGAAAGG
331600621	68704	TGCACGGUGAAGGAGUCAAAG	68705	AGCAAGTTGCCCUTAAACCCTUA
331682870	68706	GGGUCAACCACACAAAAAGGUA	68707	GATGAACCUGTACGGCTUCCA
331875093	68708	GCAATACCAAAGUCTCGGAGUGA	68709	GATGAACCUGTACGGCTUCCA
331762124	68710	GGGAGGAUCCTGTCACTGTUAG	68711	TCTCCCUCCTTTUCCCCAGT
331888875	68712	GCAGTCCUCACCGCCAUA	68713	ATCTGTUGGGAAGGCTACGUG
267483453	68714	GGCAAGAGACAAGGUTGGUGT	68715	CCCTCCATGACCUGATTTATTCCUT
269205823	68716	GGUGGGAAUGAAGCAGAGAGAAC	68717	TCCTGAACCCUACCTTTCATAACTUCT
324557804	68718	ACCCATACUATATGACAUCCCCACAA	68719	CAGTGAGTTGUCTTCCCTTGTTCUAT
314993581	68720	TCAAAACCAAGAUCAGCAAATCCTGUA	68721	AGGGTTCATAAAUTCATGGAACGUGAA
313274742	68722	CTGTGTGCAUCCATGTATGUGAAA	68723	TGAAGAAUGTGCUGCCCGAA
269708801	68724	GGCCCCUCCAAGAGAGTTGUA	68725	CGAGGAAAGUTCCCAAUGCCT
270735979	68726	GACCTCACUGGCAAATTAAUCCAGA	68727	TGGCTTACTCTTUCTTATCTCTCTCUGT
271842756	68728	GAATCCUCCCAGCTGACUGAA	68729	GCTTCTTGCACUAATAGAACUGAAGGA
269483210	68730	TCAAUAACACAAGCACACCCTUAGAC	68731	GCTTTGGGAATUCATGGTTTTTGATUCA
257740555	68732	CTATTCACCATACUTACAGATCCCTTUGG	68733	CCGGAGTTAAUCTGTTCATGGTTUT
267241116	68734	TCATCACCATCTUACTTTTTCCCCTUT	68735	CATTGTCTAGAUCAGCTTTTGTGAUGAG
269050431	68736	CCAAATTCCAUCTGGGACAUGCT	68737	ACTGCAACAGGAUTGAATCTTTACCUAT
262020108	68738	GAAAGCATGCAUTTTCAATAGGGUACA	68739	AGAGTGGATGAAGUAGAATGACATGCUA
264162624	68740	CACAGGGCAAACUCAGAAAATGAAUC	68741	TTCTGGAATUAACACAGCUACCACAAT
319918256	68742	CCAGATGUCCAACAGCAGTATTTAUCA	68743	GTGATCAATTCUGTCAGGCCTATUAAAGA
257281653	68744	ACAGTTTTGTUGCCAATTTTGUACGA	68745	AGTTCTTCTAGACAUTTTGCCCCUAAAA
269310968	68746	TTTAACTTAGCUTCAGGCACCUGT	68747	GATATTGAUGCCAGGCUGAGGAA
262180545	68748	CGAACTCACUAAACGTGTCCTUGAA	68749	CTGUCTATCCAACUGGCCACAT
268012726	68750	TCAGGTCTTUGCAATTTTCTGGUACA	68751	AATGCTTGCUGTTGGAAAUGGAAG
264980118	68752	GCAGGAGAAAUCCCAGATCTGTUC	68753	GCAATAGCAGGUTTTAACTAACAUGCAA
268683717	68754	TCTTGAATTGGAUTTCCTGCTUCGAT	68755	GTTTACATTTCAACACUGGAGAGAGCUA
262913128	68756	CTTCTTGUCAGGGTCTTCUCGAA	68757	AGGAAGCATCUCCTCTATGTACUGG
314451874	68758	TGTTTTATTCTTTUGAAGGTGGTCUGGA	68759	CCTAAUCGACCAACACCCUGAA
227906350	68760	GGAUAAAACGAGGUGCGGAGA	68761	GUCTAGTCACCUGGCCCAAAG
229086242	68762	AGGGAGACCCAUCGTUCAGAA	68763	GGCACTCTGUACTGGTTAGATUCC
223420515	68764	ACAAGAATTUGAAGCTGCCATUAAACAA	68765	CTCTGTTCTGUCAACTCTAAAAATTCTCUCA
222262238	68766	TTCTCATGAATTTTUAAACTCTTGTAGTCAGUA	68767	CAAATGCGUTGGGCTUCCAT
223043830	68768	GTGTGGTGUAGATTTTGCAUGAACA	68769	GTACCATCAATATUCTTTTTCACACAACTUCC
223889694	68770	GCCATGTCCTUGGGATTCTAGAUAG	68771	TUGAAATGATTGTTUCCACAACACAGAA
224492847	68772	CAATGTCAAGCUGAAAAAGTACGUGAT	68773	GCTTGGTTTTGCUGTCTTAAATCCATUA
224425364	68774	TTGTACGTTATAGGCUCTGATTTCTTTUGT	68775	GCATCAGATTCCUTTATGGCAAGUC
223639004	68776	AATTCTGTUGTTCTCGGUGCCT	68777	TCAGCATTTTGUCTCAGTAGTCTTUCA
223238062	68778	GTTTTCATUGAATGGTGGUGCCAA	68779	CTGTGATGTTUAGATGGGAGATGUCT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
320109763	68780	CCATGACTGAGUTAATGTGTTCUGGT	68781	TUGCCAAGAACTUACACAAGAACAAAG
263722914	68782	GGGAGGGAAGGAACUGTCUAA	68783	CTTTGATAGCAUCCATAGTGCAUCCT
323304496	68784	TTGGUGCAAAACAGAAAAATGGTUAAGT	68785	TTGAACGGAUTGCTCCTCUGG
323753502	68786	GCTAACAGGUGATCCCGTUCT	68787	TGCUGTTGCUGGAAAGCGA
259658195	68788	CTCCCGGGUGATGACGUA	68789	CTCAACACGACCUCACCTACUC
267255957	68790	GGTCAATTTUAAACCTCGGAGCTUCT	68791	CAACTCCACCUACATGACCTAAAAATUC
267905250	68792	CCAGTCTTCUGGTCTTTCCTTUCC	68793	GCCATCTGUGTCAGCATTTGUC
266693851	68794	GAACUCCAAAATCUACAGCCAGACT	68795	ACAGGAGCAUCTCCTTCTAAUGAGAA
263115945	68796	TTATTTGGGTTCUGAATGCGTCUACT	68797	CCTGGATGAAGUCAAATATGGUAAGAGG
257686509	68798	AAACTTGGAUCCCTATGAACAGUGG	68799	TCCAGTCAAAAGUACCTGTUGCT
266819342	68800	AAGCTGATTGUGGCTAACGCUAT	68801	ACAGAGAATUACTGTGCAAUCAGCA
265304540	68802	ACCATACTTCCUGTGAGGGTGUA	68803	GTGTGACCUGGACTGTCTTTCTAUC
259892710	68804	GGGACAGGUGGUGAGAAGAAAA	68805	GTGGGCAAAGGUCCAGGTUAA
313018739	68806	CAGGACUCCCTTTGCTTUGGAT	68807	GTTCCCACATUCTCCTTCCCTUC
313987312	68808	CAGCCUCAGTTTCCUCCAACT	68809	CCCCTCCAUCAAGGACAAGTAUG
314902223	68810	GCUGGCGCAGCTTTCUC	68811	GGCCCUGGACGAAGUGAC
321437801	68812	TCAGAGAGTAGUAAGTTGAGAAACUGAA	68813	ACCCACAAAAGAAUCCTCAAGTUCC
316945753	68814	CTGCCUCCAGTGCTCCUG	68815	ACCAACATCCUGGACAGCAUT
241452310	68816	CTTGGCAAAGUTGCACTAATUCAGT	68817	AGAACGGCCAGCUAATAAAAGAACTUA
262969364	68818	TTCAAGGATAUGGAAAGAGTTTGUGCT	68819	AAAGAGGGTGAUATTGTGGCAATGAUAA
264519159	68820	TCAGGTTCCAAUCGTTGCACUT	68821	GTTTTGACAAGAAAUGGCUGCAGA
240509797	68822	TCTGTAGACAGACCUCTTTTCAAGUACA	68823	CCAAAGGCATCUTCTTTTCTTGGAAUAA
266933831	68824	TTTGGTAAAGAUGACTTCCCTGGUG	68825	CGTGGCAGUTTTTGCTTTCTTUT
262411707	68826	ACAGGUACAACAGCTTUCCAAGAAA	68827	CTATGGAAAACCUGGCCTCTTUAGAT
254226882	68828	GCTGAAGCUGCACCCTACUT	68829	AGACCUGGGAAATGTTUGAGACC
267079227	68830	CAGGGTTTUGTTCCTGAGUCGAT	68831	CGACTGGAGAUTCTGGAGATTCUGA
326980928	68832	CCACGCCGGGUGGTUAG	68833	CTCCTTCCUGCTGCGGUT
316260717	68834	AGCTCACCTATUTTAGTTGCACTGUAAA	68835	GCAATGCUCGTGCTTGTUCA
320357420	68836	ACTACTAAAAGCCUTAGGAAAGCTCUCA	68837	GGTAGCAGTUTTACAACATCAUCAGGAA
231344745	68838	CCAACUTCACACCUGGACCAA	68839	ACCAGGAAUGCCTTATATCACGUC
314049893	68840	AATCAUAAAGCACAGAAGCCTGUCT	68841	CCTGTTGAGUCCTAACATCTCTTUAAGG
312854046	68842	GAGGGAAGUGAAATCAGTCTGTUAAACT	68843	GTAAGCUGCTTCGAAGUACAGGT
327909152	68844	CCAAGCATAUAGGACACTTAGAAUCAGG	68845	AGATAATGGCAUCAGCTGCUAAGG
259520847	68846	TGCAATAUGTGCCCUCAGCAA	68847	ACCTTGAACUCCTTAAGCATAUGCAC
316827223	68848	CTGACUATTGCAACUCGGAGGT	68849	CTGTTCCAAGGAUTTTGAAGTTTCUCAA
316406409	68850	CATGATATCAGGCUTCAGGCGAUT	68851	TGTTACGGCUCTGTGTTUAAGAACAT
296704661	68852	GGGCGTTCUGTGTGTCAUCA	68853	CTACCUGCCCAACTTCUACCC
295533967	68854	GAAGGAUGGGAUGGCGAACT	68855	GGGACUGGATGAATGUCAAGGG
297004150	68856	GCUACCGTCUGCGCACAA	68857	AGCGGACGCAUCGUAGAAAG
280204795	68858	CAATCTAGACAAUGTGTGGCGUT	68859	CCTCATGCTCAAACUATTTTCCATTCUG
279552721	68860	GGCATAAAAGUAAGAACTCCACAUACCT	68861	CCCCAAATGATUGTGTTCTGTTTTGUT
278350091	68862	TGTCTTCACACAUAAATCACAAGCUAACT	68863	GTTAGGTAAAATGGUGTATCCTGGCUAT
267338620	68864	GTACCAGAGUGCAGCAGUGA	68865	TTCAGAGAAGUCGAGGGUCCA
262586949	68866	TCCTTACAAACAUCCTACCTUGAGACA	68867	AGGACTGCCCUTGTTCTTTTACAUT
268074815	68868	CGGCGAACCAGGAUACCAUC	68869	AGGCACCGAGGUCTCTTTAAAAAUAA
268459408	68870	GGACCCTUCCCATCCUCCAT	68871	CCAGCTUCAGAGAGTUGAGAGAG
332728911	68872	TUCTCTGCTUCCGAAAAGCCA	68873	GGAGAGUCGGCATCGUAGAAAG
319789889	68874	CCAGACATCUCTTTCAGTTCCAUACA	68875	CAAAAGACCCAGAGCUTCACCUT
257002196	68876	TCAAGTCTGCUTACAGAGGGAUCT	68877	ACTCACCAUCCCTTACACUAGCA
263235152	68878	GCCGGGAGCUCTGTTUCC	68879	CTCTGCCCAGAUCACTGTGUT
266378837	68880	GCTTTAGCCCUGACTCCAGUT	68881	CCCCCGTAUGTCCAGCTATAUG
260307652	68882	GAAAGCAGGGAAAAGGUCUCCAT	68883	TCTCTCTCCAUGCGCCTCUA
261853939	68884	TGACAAUACGCCCCAGTUCAAG	68885	CCAGCCCUCCTCTGACAGAUT
327966625	68886	CAAGCACAGCGGUGGATUG	68887	TTACAGGACCCCUATCAACAACTUG
327094893	68888	TCTTCTCTGTGCUTCTCCTTCCUT	68889	GTCACCTCAUCTGAGGCCTUG
323733567	68890	TTAGCGAUAAGCAGCTTTTUACCA	68891	GTGCTTACAATCUCAGTACCTGCUA
333229016	68892	CGUCACCCCCGCCTTUA	68893	CAAAGGGUCGCGGUCAC
314371647	68894	GGGAGCTGUAGCTTCCAUAAGG	68895	CCACAGACUTCTTGGGTTUGGG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328164846	68896	GGCCCAGAAUGCACCACTAUC	68897	CCTCTGCUGTGTTGCCCUAAA
319066981	68898	GCTCAACUGTTGTGUCCCCAT	68899	TCCATGTCTGTTUCTCAAAGGGAATAUC
318239177	68900	AGACCCCCUCGGACAGTAAUC	68901	TGGTTTTCTGUCCACTTCCCCUA
262310331	68902	GGGTAAGAGCUGCGGUCAA	68903	GCCCGCUATTCGCAAUCAG
332416328	68904	CCAAGGTTTUCCGGATCGAUGT	68905	GCTGAAGACUCTTCCTCTUGAGT
313408623	68906	TTGGCATCUCCACCCCTACUAT	68907	GGUACACAGUGCAGAAAGCC
312705071	68908	GGGTTCUTCACTGUGACCGT	68909	ACTTGGATCUCACCCCAACUCT
313192410	68910	CCTUCCCACCCCAAUGCT	68911	AAAGCCUTTGCUCACAGGGT
324764340	68912	CCTGCTTTGAGUATTTTAGAGGACUGT	68913	GGTTGUCGGCAAGCUGGAA
265747724	68914	CGCTGCGUCCACACAAUT	68915	GCAGCTCCUCGTGATCCUC
265504675	68916	TTCACAGTGUCACAGGCAUAGAC	68917	TGTTCCAAAGGUTCTTTGAGGTGAUT
265317849	68918	GCUGTACTGGUCACAAGCCAT	68919	GAGCAACAGUTCUCCCACACA
314682901	68920	ACATTTUCAGGCCCTGGAUGA	68921	GTAGCCAGCUCCCTACAATCCUA
313393635	68922	CAGGAUGCCCTGGACAUGAT	68923	CCTATACTTGAAUTGGCCCCUGA
313228209	68924	GTGUCTTCTGTGUCACCCCAAT	68925	CCAAACATCTUGTCCACCATGUCT
313337983	68926	GGGACACCCUGTAAGCTUCA	68927	CCTCTGTGAGCUTGGACTTCTUT
312669050	68928	CATGACTGACUCAACTGGCCUT	68929	GTATTCGUCCCCCTTGAUGGT
314966637	68930	GCUCCCTCTATUCGGCACAA	68931	CCTGATGUGGTTGTCGGUCAG
313650595	68932	CCTGTGACCUGCTCTGUCT	68933	CACCCGCUTCCAGTCAUCA
313239648	68934	CCACCGTGUGCTCGCTUAT	68935	GGTAGCUGATGGGCCUGAAC
222538257	68936	ACAAGATGTTCAUAGAGTTTTAGUGGCT	68937	GAGATTAGATUACCTCGCACACUGAAT
222995339	68938	TCTTAGCAGCUCTTACTATCTTCCUCAA	68939	CTTTTTCTUGGGTTTTGGCUCCT
223542933	68940	GAAGUTGCATTGTGUCAAGACAAGAG	68941	CTACCCTGAATUATGGCTCCAAGUAAG
223582379	68942	AGTTUAGCACAGAAAGACATATUGGAAGT	68943	ACCTCAAGCAAAGUTTTAAGGCAATUT
328813149	68944	CATCTTAAAAGGUAAACATTGCCUCCAG	68945	CACAGATTTATAUCATCCAGGCCTUCA
223038506	68946	GTCAGACTGTACUTCCATACTTGATUCAT	68947	GGTTGTGGAUCGGCTCGTUT
328931168	68948	AAGATGAUGGGAGGCCUAGGA	68949	TGAGGAATUAGAGAGAGAAAATGAGUAACT
329033073	68950	GAAGATGTTGTUGTCCCTACTAUGGAA	68951	GCTTGGGCAAAGGAAAUATAATACUGAGA
224361111	68952	GAGGTGCACAGAUGCTCAGAUT	68953	GACAGCATCUTGTCTCAGGUCA
317805992	68954	ACTGGUGGCAGAAAACUCAAGAA	68955	ATCCCACCAAGCUGCCTAUC
332442117	68956	TCTTTTGCCACAGGUTCCAACUAT	68957	CCATATTGCUGCCGCTUCC
332272910	68958	TCCCCACCCUGTTCCTTTTUG	68959	AAGGAGCAUGTGTGTUAGCGA
332765724	68960	GCTGUACCGCTCCAUCGAC	68961	TCCTAGGAAGCUACCTGGTUCT
332418432	68962	CACTGCCACUGAGGTCTGTATUT	68963	GACUTGATGAAGGUCCACAGCA
333739746	68964	GTTCUACGCCACGTTCCUGAT	68965	GUCAGAGGCAAUGACCAGGAC
319541620	68966	ACCUGAGAUGCAGAAGGAGACA	68967	ACCAGTCAGUCTCATTATAATCCUGAGT
332831921	68968	TCAACATTAUCCCAAATCUCAGCCA	68969	ATGAGCCTTUCATTTTGTGGUAACAAC
318606677	68970	GATGAATGGAAGAUCTTAGGCUCAGT	68971	TCAGAGGAACCAUTGCAGATUACC
318478911	68972	CAGCCGAGGUACCCCATTUA	68973	CATTGAAUGCCTTGAUGCCACA
279394327	68974	ATTATGTGTGCUCTTGTATATGCTTUCCT	68975	GCCACTTCAGGAGAAUGTATATGCUT
280769224	68976	GCTAGACTTAAGUTCCTCAGATGGTUCA	68977	TGGACATTTCACUGTAGGATCUAAAACC
312861313	68978	TGTCTGCCAAUTAACTCATTTATUGCT	68979	CAGGAAGAUGCACCAAGGCUAA
268631126	68980	CTTGCCUCCTAGGCAUCAGAA	68981	ACTCCTTTGCUAACGCTTGUCA
262987658	68982	AGTCTCCUCCAGGCATAATCUGA	68983	TGTGAGGACCUGCCTCTCTUT
266129781	68984	CAAATGGTGGUGTTTGGCTTUG	68985	CGTAAAGCCAACUCATGCTUAGG
257721727	68986	CGTCUCACACAGACCTTGAGUT	68987	GGAAGAAAAAUACACAGCAGTUCAGAGA
316454240	68988	CGAACCTTCTGCUTTTTAATGTCCTCUA	68989	GCAACCGGGAUGCAAAAAUGT
240121618	68990	CCAGTACCAAAGUTGATAATGCTATGUCA	68991	GCTAACATUAAAAGGGACAAGTCUAAGA
332574745	68992	GGTCATCUGCCCATGUCGAA	68993	GCAATTACUACGCAAACGCTUACAG
333486015	68994	GCUTGGCCAUGAGAAGCCT	68995	GCTCACCAGUGCCTTCTCTTUC
332456602	68996	CATTTCTCAAUGCTTTGCAGAUCCA	68997	GTTTTATTTCGACUTGCGGCUCA
332647021	68998	AAGACAAGCAACUTTCCAATTGUGG	68999	TGCCTGGGTUACATTTTCACTTTCUT
314938521	69000	CAGAACUGCAGAGTTGGCTUG	69001	CCAGCCUCAUCAACCAGAAGAA
315107148	69002	GGTCUGCAGCGAGUCCA	69003	TGTATCTTCTCAUCCTCCCTCUCAAC
315440326	69004	GCUCCCGAGACAGGTCUGA	69005	ACCTCTCCACUGGAAGAGCUA
254091720	69006	AAAGCCAAGAAUTAAAACTTUGCAGGT	69007	CTGGTTACAGUCTTCAGGAAAATCUAGT
325010512	69008	GCGGCAGUGGAAATTTUCGG	69009	ACAAGAACGAGAGCGUACUCAAG
331174334	69010	AUGAGACAACCACUGAGAACCAG	69011	CCACTGAGCUGGGACATUACAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
328073082	69012	TTAACACATCACCCUCCCAATCUG	69013	TTGAGTTACUGGCCATTTGAGGTATUT
253849454	69014	TCCCCTGUGTTGTTCCCUACA	69015	TGGTCAGUTCTGATAAUCGGAGGT
266345702	69016	CCCTTTTTGGCUCCATGTGAUT	69017	CTUCATGCTCTCUACCCACACA
257325658	69018	TTUACAAACACAGCCAGGUGGA	69019	TGAGGAGCUGCTTUGAGACAAC
315609864	69020	GCTUCAGAAAGCAAGCAGTGUT	69021	ATCATGGTGGCUCTGCTTCTUT
319794966	69022	AATCCCTTAAAAGAAUCGCTACAAUCCAT	69023	GCTTGACTCAAAUGCCTCTCTUG
316859108	69024	CATGTAGTCUGGAGGACAGAUACAG	69025	TCAGGCCAUTCCAAAATGUGAAGT
316232267	69026	ACAGGUCCCACTUAGGCAGAT	69027	GAAGAGCAAATGUAAATTGGCCTCUAAA
317768220	69028	GGAACCTACUGAGAGATTCAACAUGAG	69029	ACATTGATGAAUGCAGCATAATGAAUGG
315832481	69030	AAAAAGAGAACUGACCCTGTUGGT	69031	CAACACTGAUGGCTCCUACAGAT
328191331	69032	CAGAGGTUCCATTACCTCCUAAGAGA	69033	TTGGCTTCAUCCACAACTCUCAT
319953695	69034	CCACTTCAUGGCCAGCCTTAUA	69035	AGAGGUCAGGGACAGATGAGUG
332647807	69036	CTCTUGGGAGGGACCAATGUG	69037	CATGUCCGACGTCUGGCT
319888334	69038	AGAAGGCUGGAGCAATCCTUT	69039	GGACCUGCAAGAATTUAAGCAGAAGA
318942452	69040	GAGTACCUCCCCTAACCACUGA	69041	AGAGACUGGCAGGAGCAGTUA
321588710	69042	CAGACCUCCACGUCGAACA	69043	ACAACCUGGACCAGCACTUC
316606181	69044	CCTGGACAAGUTCCTGGCTUC	69045	ACACCTCCAUTGTTGGCACAUT
262473081	69046	GATGTCCCCAUTCCTGTTUCGT	69047	CTAGCAAAGACACAGGUAGCUCA
238394789	69048	TCTGCTGAUCCTGTGGCTTUT	69049	TGAUCGUCAAGGCCAGAGAAAC
239049443	69050	AGCAAACCAGCCUCUCGAC	69051	GUGCCAGGCAAGGCUACA
240424518	69052	TCTCTGCUCGACCTGTGTGUA	69053	CAGCACCTAUGAGGCAGAGUG
321283310	69054	GCTGUGGAAGCCGCCUA	69055	CTCCTGUGCCGTGTAUGACA
320319320	69056	GCCCCTCCUCTGGCAAUC	69057	CCCACCCTAUGCCTCCTGUA
320080970	69058	CACAGGGUCACUCACAGGAA	69059	AGUACTUCAGCGAGGAGGACA
318025066	69060	GTCAGCACCCUGGAGUGA	69061	TCUGCCCCAGGCCACUA
319572261	69062	TGCUGAGGAGCCGGUACA	69063	TCTTCCUGGGAAGTTCGGGUA
318729651	69064	TTGTTGCUTATATCCCUGGAAGAGAC	69065	GGCCACUCACTCCUCAGAGA
235710460	69066	ACCCTCTUGTCCCTCAAUCCA	69067	GCAACAUGGAGGCCAUGAG
235076112	69068	GAGCCACGCGUCATACUCT	69069	CCGCUTATGATAAACUGGAAAAGACC
237077663	69070	TGCGCCUCCAGCTTCTUC	69071	GTTATCCCUCCCCTCTGCTUC
238061913	69072	AUGCAGCGCACGAAGTUG	69073	GUGGGCCAGAGGCUGAT
316172588	69074	GGAGAATAGAGTUCACTAGCAGCTUT	69075	GCTGTATGACAGGAAUCTACTTTTUCGT
319579861	69076	CGATGGCCUCACCTTATCCCUA	69077	CCCCCAGUGGCTACGAAUG
318708359	69078	CCCAAGAAUAAGAGGCAACAUGGT	69079	TTGTGUAGGCCATGCUAACGAAT
319948837	69080	ACATGGAGAGUAAGAGUCAGCCT	69081	CCAAACTCTGGUGGGCTTATTUT
318833954	69082	TCCTACATACAUAGTTGCAAAAUAAAGGCA	69083	GGTCCACCUGACGTAAATTCTTCTUT
264071642	69084	CCCTGCCCUGTCTTGUCC	69085	GCCATGUGGGCAGAGATGUA
262125764	69086	TCCUAGGGAGACUGCAGAACC	69087	TCUGACCCGACUGGGAAGAAA
266558051	69088	CAAGGCTUGGTTGAGATCAUGG	69089	CCACTTTACCCCAUTCTGAAATCCUAA
258633276	69090	GCAGTAGCUGAGCTGCAGAAUC	69091	AGCTCCTTUAAGGTTTTCTCCAUACC
267943376	69092	GGAGTGGUGGTTAATTGCTUCCA	69093	GGGAAAAGGAAAUGATGCCTTCTTATUA
266641087	69094	CTGGTCCCUCTGGCTGAATUT	69095	CTCATCATTUGTGACTGCTTUGGG
267287487	69096	CACCTGACUGTCTCTTGCTUGA	69097	CCUTCCCAGACUAGCCAGAG
325554260	69098	GACTCCUTGCAGCUGGACAA	69099	GGUTGTGUCCGGGAAACAGT
258121305	69100	CACAGGCCGGUGGAAUG	69101	CTCCTACCUCCCCTCACCUA
236388202	69102	AGTCTTTCACTTUTCAGATGTGTGTUGA	69103	ACAAAGCCTGCCUACTTAAGATCAATTUA
237068798	69104	AAAACCTAGAGAACUGGCATGUAAGAG	69105	TCAAACCGAUCAGCCAATACTGTUT
238333700	69106	GAGGCCTCAGGUAAAATAGAATTTUCA	69107	GTATCTGCCAUCACCTCAGCTTUT
237994918	69108	GGAAATCCAUGAGCCUGGACAT	69109	CAAAAACTTTGCUACACTGACAUGGAA
333062855	69110	GGGCAGUAGCTTCCTGUGAC	69111	GGGAAGUGAGTCCTCCUCCAT
333358745	69112	GGCCTCACUCTGTTCCAAAGUC	69113	AGTCAUGCAGCAACCAAGUCA
313402560	69114	CTCTTCTTUCCCCAGGTGAACTUT	69115	CTTGGCTUGCAGTGATCUGG
314875183	69116	CCTTGGTATTCTUGGGATGTGACTTUC	69117	CATGGCAGGCAAUTCCAGTUC
312934620	69118	AAAAGAGGCUGACCTUCCAGAG	69119	CGATTTAGUGGCGTCCUAGGAA
253629491	69120	CCCUCCTAUCCCACAGCACA	69121	CTGACAGTTTGUCCCTTTCTCUCT
225495550	69122	CTGGCTCTUCATGGATCCUCA	69123	CTGTAAGTAUCACTCCCCCUGAAC
264935758	69124	TCTGATCCUCCTGTGTGTGUGA	69125	TCTCCATUTCGGCTUGCGT
266201199	69126	GACAATGUCCCATCTGGGUGAA	69127	CUTATATGGCAAGUCGGACCAGT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267986228	69128	CUGCCCCAACCAGATUGAGAA	69129	TCAGGGTUGGGCATGATGUC
317476059	69130	CTTTGATCUGGAGGAGAGUCACC	69131	AGCCCAGAACAGACAUGUGAAC
268673006	69132	ACATGCCAAGTCUATCTCTCACTGTUA	69133	TCCCATCAGGAAUATCTGTTTCUAGGAA
268820610	69134	ACTGTTGGCTUAAACACTGAAGAUGT	69135	TCAATCAAAGTUTTCAGAAGCCUGGAT
267348791	69136	ACAGAGAGTUCAACCTGAAACATUCC	69137	TCTTCTCGAUCAAGAATGCTGGUAAC
269313953	69138	GGTTAGTACCTUCTCCACTCCAAAUT	69139	CAGTTGTCGTUGATGTCTTCAACAUT
313909453	69140	CCAAAACAACCGUACTTTAACTGUGT	69141	TGGTTTAGCUGCTGGACTTGAUT
333664496	69142	GGGCUACCCCCTUAACCCT	69143	GGCAGCGAUCTTCTTGUAGCA
325924063	69144	GAGCATTCUGGGAAGCCAUCA	69145	CGCAATGGCUCACCAGGUAG
323566784	69146	GCCTCCAATAUCTGTCCCTTTUCT	69147	GGACUCAAAGACACCCUGCAC
323815332	69148	GTGACCUGTCGCCUCCA	69149	CUCAGCCUCCCCACAAGAC
325153981	69150	AGGAAGGCUTCGAGCCATUT	69151	CACTGUGGAAGGAAGGAGCTUT
324320905	69152	GTACACCATCUCACCGTCCUC	69153	AGGGAATGTTATUGTATCCTGAGGGUAT
324929983	69154	CACCCCAGAAAAACCUCTUCAGT	69155	TCUTTTGCTUGCAGAGGAAGGAG
324274710	69156	GCACACTCTUAAATCCCCTTCUCT	69157	TGCCTTCTTCUGAAGTCCCTTUG
323672232	69158	GCCAGGCCGUTGATGAUGA	69159	ACGACUGAGGACGAGUCCA
319404570	69160	GAGGAGACACAGCUGGATCTTUC	69161	GAGAAGACAGUCAGAAUCCAGCA
319405720	69162	GCCTTCUCCTCACCUAACCCAT	69163	GGACCTCUGTGTCCCTUCAGT
320458773	69164	ACCCUCCCTGAGTAUCCAGAAA	69165	GGTGGCACCUGCTATGAUGAG
316229103	69166	TCACGUTCTGCAUGGACAGG	69167	AGTCCTUGAACGTAGTTUCGCAAA
332827450	69168	GTCTUTCCATTGGUCCCACCA	69169	CGAGGCCAAACACAUGTCCUT
320478284	69170	GCTTUGAAAGCCCCTCCATUCAT	69171	CCAUCACACCCCACGAGUA
325586375	69172	GCCAGGAUTTCCTUGGGAAAGAT	69173	TTGCCAGTGAGCUTCAAATCTCTAUT
314723961	69174	GGTCTTCTUCCTGGCTAUGCT	69175	GAAGAAAAUGCCCAGCAGGAUG
313034049	69176	CUGGCUGCCAACCAGACA	69177	ACGTTGCUCCCGCUCAC
229752887	69178	ATGAAGCACUCGTUGAGGCT	69179	TCGTACGUGGCGCTCAUC
229746185	69180	GCTCUGCACGCGTGTGUA	69181	CCCCAAGUACCTGCAGUCT
267857483	69182	CTGGAAGAUGGTTATGAGGTUGGA	69183	GCCTCTGATTACUGACTCTGTCCTAUAT
264059625	69184	GGCAGTCAGGAUCTAACTCACUCA	69185	CCAGGGCUGACTCTCATGTUT
268040976	69186	GCCTCTGTUCACCTCTCGAUG	69187	CTGTGUCAGGCATCCTUCACT
320645884	69188	CUCCTUCAGCGGCAAGAGA	69189	CGCGGCCUCTTCGAUGA
318017395	69190	TTCCAGCUCCTGCCGTUT	69191	GCGGGAGCUGGCUGAAC
320499907	69192	CAGCGCUCAAGCAACUGG	69193	CCUCCTGUCCCCAACAGAA
318034458	69194	CCTTCAGCCGUAGGTTGUACT	69195	AGCAGATGUACCGCAGGUG
318294686	69196	GCTGGTAGCUCCATCTCCUT	69197	GAGUACCGGGAGCTGGUG
320341086	69198	GAGGTAGUCCAGGGCAATCUG	69199	GGAGGGUGAACCTGGGAUGA
318552755	69200	GAUCTCUGGCGGCAGGT	69201	GCTUGCACCCCCATGUG
229521494	69202	CATAGCCGACGUCATGCAAGUA	69203	ACTTCTTGACTUTGGGAGTGGUC
227929253	69204	AAGTGCTCTTGUCCAAAATACTCUCAA	69205	ACGTGTTCUGATCTGACTTUGCAT
235585662	69206	GAAAGUGGGAGGAGAGAGTCUGA	69207	GCAGCGGCUGTAUCGGT
231863204	69208	CCTTCCTCCUGCCATCCCUAAT	69209	ACGAGGAGATCUACAAGGAGTTCTUT
232458215	69210	CUGCAGAAGCUCCAGCGA	69211	GGTGGGCCAUCATGAGACAUAAT
324030532	69212	TCCAGTAATUTTCAAGCCAUGAGAGAA	69213	TCCTGTCTATACUCTTCCCTATGTTUCAA
269227472	69214	AGATTCCCCTUACCAGCTCCUT	69215	AGCTCCACACAUTCCCCATUG
266703310	69216	CAGCGAUGGAGAGTGGCAUT	69217	AGGAGTTCUGAAAAGCACATATTGATUGA
312867261	69218	GGCCTGGATCUCATTCATCTTCUG	69219	CCTACAGTCAAAUGCGTGTTGUCT
313414123	69220	CACUCGACCCAGACCCUAC	69221	GCCCTTCTTUGTTGATTACTCCUGAT
254434273	69222	TGCTTTCUGCAAACTGCAATCUC	69223	GCCCCAGGTUATTTTTGTTTTCCAAUT
262082955	69224	ACTTTTCATTTCUGGCTTATCACUGCT	69225	CCTTTTCTTTTCAAUGGCTGTAGCUAT
253786129	69226	ACAAATCTTCUCTAAAAGCAATCUACCACAT	69227	AGCTCCAACAACUACAATGAGAAAUCT
263800070	69228	CTTACCCAAGCCGUTTGTTTGAAUT	69229	CGAUTTTCTGUAAAACAGGAGCAAAGA
257014785	69230	TTGGCAAAUTTCATTACGUAAAAACCGA	69231	GCTTGTTGUTGACTCATTUGAACCT
254078606	69232	CCTGGAAGUCCGTGCAGUAT	69233	CCTTTCTCTCAGUTCCCGCTTUC
264105146	69234	AAACACAACCACCAUAUAGCCCAA	69235	GGTTGTAATTUCCCATGGTCTUGGT
324213893	69236	TGCTACAACTUATGTACACGTTUCAGA	69237	TGTCCATCCUCAGGCGUAGAA
323354613	69238	CCAGACAGUGGATTGGAGAUGT	69239	CTCGTATGCAAUGATTACTCCAGTGUA
323442239	69240	TTTTTAACGTATCUTAGTGTGAGCUCGT	69241	GCATGGCCCUTTGGAGACUAAA
325561249	69242	GGGACTCCUTGCTAACCAUAGG	69243	CTAAAGAAAAGAUAGTGGGTGTACCUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
227858245	69244	GAGAAGACGCGACUGUGGAA	69245	GATGTGGGUCCTCCUGCAC
228914735	69246	GUGGTGUAGCACAACAGACACT	69247	ATTGTUTTCCTGTGAUCCAGAGCA
228553284	69248	GCGAAGCACCAGAAAUCAUGGA	69249	CUCCTTUGGGAGCACACGA
315691991	69250	CUGGTCTCTTCUGACGGAACT	69251	GGAAAGAAGACAACUGGCTCCUG
317089627	69252	TGGGCAGAAAAUGCAAGUCAAC	69253	GAGGGAGGACUTGAACAUCCA
278595310	69254	GAGCUCACCAACCTGUACCC	69255	GGAATACAGGAAGAGUGCTGUCA
278192836	69256	CCUCACACGGGACUACAACT	69257	GAAGAGAGGAAGGGUTAGUGGGA
278430136	69258	CACTGTGACUCCCACUGAGA	69259	GCCUCACCGCCGTUCAG
263540385	69260	AGATCTCUCAGGATTAACACUGCAGA	69261	GCCUGCCGCUCACACAA
326808571	69262	AAAAACTGTGUTGTGGAGUGCAA	69263	GTCCACGTAUCCATCAACAGUAACA
236021889	69264	GGCCAGUAGGCAGTGAAGUAA	69265	ACAGTGACAUCATCAGTUAAAACAAGGT
264807116	69266	GCTCCCTCUGTCTCCATCTTTUC	69267	CCCTGACAUCCGACTTGTUCT
260921447	69268	CCCACCTGUTCTCCACGTUC	69269	GAGCCUGGAAAGCCTGGTAUT
268613659	69270	CUAAAACCTGTGUGCCAGGGA	69271	ATGACCATGAUGAACTGACTTUGAGT
257565423	69272	GGUCCCCGAAACCCTUCAAT	69273	CTGTTCCUCAGCAAGCTTATCTCUG
258176422	69274	AGAACAGCAGGUCAGGGAAUG	69275	CTGGTATCTTUGGGAGTGAGGUG
269343243	69276	CACCAAGCUCCCAGTGGAUA	69277	CCTCAGGCUCTGTGTTTCCTUC
268257037	69278	GCCTTGCAGACUCAGGACTCUA	69279	CATGAAUCCCTGGUGGGACT
268640171	69280	ACTTCCCGUCTGTGAUCAGGAT	69281	CCGUGAGCTTAGCUACAAGGG
316598233	69282	GGCGCTUACTTGTAGGUGAGG	69283	CCGCGCGGGUGTTTAUG
318325376	69284	GAGAGCAUGUCGGCGAACT	69285	TCAAGUCCATGATCAUCGACCG
320634004	69286	GACAGCUGGGCGUCCAA	69287	CGAGTTTCAUGAGAAGCTGCTAUCA
320640040	69288	GGTCAAAGAAGCCCUTGGUGT	69289	CCAGCAGAUCTCTCTCTUCCAA
320648533	69290	GCCCTCCUCGGCCUCAT	69291	CTGCAGCAAAGCUTCCTCUC
320341693	69292	GCTCGGCAUCATGGUCACT	69293	GCTGGAGAUGAGCGCUGA
320209737	69294	GCAACGGUCCCGGACUT	69295	CCACGGCUCUGACCACAC
318321136	69296	AGACAGGAGGGCUCCUGAT	69297	GTCCCGCAGUCCTUCCA
320714729	69298	ATCTGCAGCUTGGUCACGAT	69299	CAAGCTCCCACUCGCCTUA
318906410	69300	GACGTAGGTGAUGATGGACTTCUC	69301	GGUGUACCGGCAGACCAAC
229651784	69302	CATAATGCUTGTGGTTUCCCCAAT	69303	TCTATAGCCCUCTCCAAGCUCAC
237942590	69304	GAAAGAGUTCTCUCACAGCACCAT	69305	GCATGTTGGUGACCTCTGAATTTUT
239637376	69306	GGAAAAACUCUAGGAGAAGGCGAA	69307	CCGCTCUAGAACAGCATUGG
223123572	69308	TGAAAATTGUCACGAAACAATGAGCUT	69309	TTTCTGGTCGGAGUCTGATTTCAUC
222673095	69310	GCUGGACGAAAGCCUGAACAA	69311	CAGAAACUACTCAAACUCCCACCT
231175888	69312	GAGGGTTTUGAAGAAGTGGGUCAT	69313	GTCCCUCTATCCUCGAGAAGGG
323892305	69314	CTTGACTAGCAUATACTCAAAGCACUGT	69315	AGAGTTTTCCUAAGCATGTGCTCTATUT
262480637	69316	GTATAATTTTCGTCUTCCATCCCTTCUGT	69317	GGTGTCTCCAUAGCTCTCAUCAAG
313350389	69318	CCCAATAGUCCATGCCCCUA	69319	TGACAATGACACUGAGACTATTCUACCT
313847203	69320	CAATCTCCTCAUACTGGGCCUT	69321	CCAGAUGACCGACTCCAAAUCT
261987923	69322	ACAAAAGACCCAAAGCUTAUCAGGAA	69323	AGCUAACAAGGACCAAAGUGGAG
256204296	69324	TGGCTTTTTCUAGAAGACGTTGATACUT	69325	CAUAGCTGAGCUAGGCAGAAAAGAG
262129826	69326	GAACTTUTCCTGTTGUGCCAAGG	69327	AGTGAGGCUACTGCTCTTGGUA
256688832	69328	AGAAAAGTACTAUCTGCATGCTTUGGT	69329	GAATTGACTUACCTGATGGGAUAGCA
255417541	69330	CTTTTAACCTCTUCAGAGCCTCAACUA	69331	TTGGGATCACUGATTTGAAGGAAUAAGT
264461666	69332	GGCCAGTGCUAGCCACTTTTUA	69333	AGGTTCTACAAAGGCUGTAATTGTTUCT
266180360	69334	TTTTATGAGCUTTACACAGTTUGCAACA	69335	AACTTGTGUAGCTGCTGAUGCT
258133849	69336	CATGTGACCUGACAGCTGCUA	69337	CCATGTGAGUGATAAGTGGCGTUT
230482086	69338	AATACAGTGTGUGCTGCTAACCUT	69339	TCTCAGAATTGAUAGCAGTGTTUGCT
266982472	69340	CGGGCACGCACGUAGUAG	69341	GGAGAGGAGGAGGUACTGCUAT
317946387	69342	GTCTTCCUGCCCTUCGACA	69343	CUCCCGGGACCGTCUAC
316016993	69344	CCCCACUCTTUGGCACCAT	69345	GGCAAAAAGCCGGUCUCC
315689630	69346	ACCAUGCCGCGGTACUG	69347	AGAAUCCCCACAGTGCUCAAG
281232165	69348	CCCCACAGAGCACUGAUCAA	69349	GGCGCUGTGCCTAUCCC
264360000	69350	CATTGACTUACCTTCACACCUGGA	69351	ACCCTCUCAAATGCTGTTUGCT
265699574	69352	CCAGAACAUCTGCTGUCAGAAGT	69353	GAGGAGGAAACUCACTAGCATUCC
267564452	69354	GCTCCCCTUTGGATCCAGUCT	69355	CCCCTTTGUGTTCTGCCGUAT
264437076	69356	CAGGACTUAGTCAGGGUCCCA	69357	TGTCTTCCUGACTTCTTATCCTUCCAT
268354367	69358	GGGTCUGAAAGAGCAAUGGAG	69359	CATGCCAGCAUTTCCCTCUGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258307700	69360	CCTACTCACCGUGGGTCAUC	69361	GAAGAGGCCCUGATCTCUCCT
316891038	69362	TCACCTCUCGGGCTCGUA	69363	GGCCACUCACUCCACCAC
320607951	69364	CGUAGCCCGAGGAGGAGUA	69365	GTCCACCAAGGGCUACUACAG
318310998	69366	AGGTACUGCACCUCCAGGAA	69367	GGTGGACAAGAUCATGGUGGA
318157455	69368	GCTCUGACAGCTGGUCGT	69369	GGCTACCGUGACCCCUACA
320640056	69370	GGCUACGTCUCGCACAGA	69371	CGGATCACAGUGGAGAAGAUCA
320340695	69372	CTCGCUGTCCGAUGCCT	69373	CGGGUGCTUGCGGAGAA
320078896	69374	CCCTCCUGCAAGGUCACA	69375	GGCAAGCUGGAGCAGGUC
228770475	69376	CTTTTTCAAGGCUGGGAAGGUG	69377	AATTATTAGCCACUGCTGUGACCAT
328885928	69378	ACTCAGCAAGAUAATGTAACAGUGAAGG	69379	TGGACAAUCAAAACTTAACTCCUGGAT
239396236	69380	TGATTTCTAAAACAUGTCTCCTUGCACA	69381	GCAACCTGAUCTTGTGAACAUCCT
234949708	69382	TTTGACTUCCACAAAGCCCCTUAT	69383	AGUAAGGACCATCUGCAGCAAC
236320880	69384	CGCTACTTACTUCTCAGCCTTGUT	69385	GGCCTCTGUTCTTCCCGTTUT
241717895	69386	GTGGGCUGTCCTTCUGAGAC	69387	GCCACTTUCAGCTTGUGGGAAT
223057641	69388	GACACCAGAGCCCUGCTUAA	69389	GGCAAAGAACCACUCACCUG
326241167	69390	TTGAACAGUCCATGAAAGGUGACA	69391	TGACATTCAATCTAUAGCTTGGGCTTUT
268008206	69392	GTCAGTGAAUGATGGCACAUGG	69393	CACCCTUGCAGGCCCTTTAUA
314057393	69394	GAGAGACAAGGACACUGUGCT	69395	GACAGTCTCTGGAUGACAGTTTCTATUT
314905239	69396	TGCUTGCACUGAAGCCAGA	69397	CTCACTGAGUCCTCCCTCCUT
262028671	69398	CCAGUTCTAGTUCAGACAAAGAAACACT	69399	TGGCUAGTGCTUGACCAGAAAAA
262332830	69400	ACCCACATTCGAGUTGGAAGTACUA	69401	GCAGGGTGUGGACAAAGAAACUT
254503647	69402	CCCAGGUAGAGGAAGGGACUT	69403	CCAAGTACCUTCCTCCTTTTUCCC
325625148	69404	TTTCUTCCAGGCAUACGAAACCT	69405	TCTGGTGTTAUGTTACTTGGAGAUGAAC
326351312	69406	TGGAUTATTTTUCCCCAGCCCAA	69407	TGCAGAGUGGACTAGTTTGTTUAAAGAG
230575658	69408	TGTGUCCCCCATAGTCUGCAT	69409	TGGACATGTACUTGAAGCTGGUC
232788574	69410	CATCAGAGCAGAGUCTGCACAUA	69411	TTCTTTTTCCTTUCCTCCCTGTAUGG
232467100	69412	GCGGAACAGGAUACTGCAGUG	69413	AGGGAGGTGUCTGCCAAATUAAAG
328562978	69414	ACAAACATCCCAUAGAATTTGCGACUA	69415	GCAAAGTGATUGACTGTGACAGTUC
265584800	69416	GGGCACACCUGGAATGTUGAA	69417	GGTGAGATTAUCTCCGCCTGUG
315913987	69418	CTGCTUCGCGCATUCGG	69419	CAGGUCCAAGGGCUCCAT
317929019	69420	CGGATGCUGGAGCAGTACTCUA	69421	CUCAGCCACAGACCUAGGGA
316191373	69422	GCAACCTGGUTCTGCACUAAC	69423	CCACGGCACUGAGGATGUC
315334412	69424	CCTCCCTGCAUTTCTTTTAAGCUGA	69425	GTGGAAGCCGACAUCAAUGG
279394023	69426	GTGGAGGCCUCATGTGUCAAT	69427	TGTTTAGGUGAGACACCGUGAGA
280296074	69428	CAAGAAGAAGGGUGAGCUGGT	69429	CCCTGGGUGCTCACCUT
315899233	69430	TGAAGCTUACAGAGAAGCAGGUG	69431	CCCTCCUGGAACUCCACCAT
238604713	69432	GCUCTCUCAAGAGGAAGCAACC	69433	TTCTGCCCGUCTCTAGCUACA
237136482	69434	CGTGAGGCCAUCTGTTGUGAT	69435	CCAAATUAACGCCCAGGAAAAAUACA
268130540	69436	ACTGGGTCACTAUAAGGTCAAAAGCUA	69437	GCAUCTGAGUGGCCACACAT
266735225	69438	GGCTGAGGGUTAGAGCCTGUA	69439	CTCAGCTCUGACCTCTTCTTTUCC
318329266	69440	AGAGCCUGGTAGATGCUCAGT	69441	CTGTTCGAGGCUCGGATCAUC
320625284	69442	TGTGTCTCTUCAAATGCCCTTCUT	69443	GGAGAUGAACCGCGTCCUG
320626599	69444	CTTCACGGCCUCGUGGA	69445	CUCGCCGGCATCUACCT
318019482	69446	CTCCGCCUGTGCCTTUG	69447	CTCCGCGCUGTCUGAGT
319787490	69448	CCGACCCCCAUCUCCAAGA	69449	AGGACAACCUGTACCUGGCT
228472846	69450	GTATGTGCTUGGTCTGGCUCT	69451	GTATAAGGAAGTAUGGCTCCCAAAGAUT
232187763	69452	GGACCTGGCUCTGCATTTUGT	69453	GCTCCUTAAAGAGCUGCGAACT
237365822	69454	CCACGUCCTGCAGCUCAAT	69455	GGCTACUGCCAGCCCAUC
261512021	69456	GCAGACGUGGTACCTGCAUC	69457	TGAAGAGCGAGCACCUCATTUC
240756507	69458	GCAGGAUCTGCCUAGGAGGT	69459	CCTGTTCCCAUGCCCTGATUAAA
234684087	69460	GCTCCTCUGGCTTGGACUC	69461	GGCAACCTUGCTCTCACCUT
231208212	69462	CACCACGUCGTCGAUGGA	69463	GGGCGGGUGGAACCTUAG
264310030	69464	CTGTGAAACUACCATTGGTTCCUGT	69465	CCUTGATATCCUGGGACACAGAAG
262559338	69466	CGTGGAAAAUCGAAAAGGGAGAUGT	69467	CATTACCTUGCAGCTGTTGTCUC
268823468	69468	GATTTCTTTUCTGCTCAGUCCAACC	69469	TGGTGAGATGGUAGGTTTGAACTCUA
260212607	69470	GCCTACCACUGCACATGUGAG	69471	CAAGAACAGTGAUGCAGAGTATAGCUT
313256547	69472	AGGTGTCCCCAGUAGACAAGUAT	69473	TTTGCTGTGUCCTAGGAAAGGUC
314822582	69474	AGGAGACTCUGGTTGACAGUGA	69475	CATCAGCACUAGTGGUGGCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
266666741	69476	CTTGTTCTGTUGCACAATTTCTTCTUCA	69477	ACTGGCATAUGAAAATAGAAGAACTUCGT
263718970	69478	CTGAAATTTGGCUATCACTGTCCUACT	69479	GCTGCTATGTCUTCATAGCTCGTTUT
266752353	69480	GAATAACTGAGTAUACCTGAAGTTGCACUT	69481	AGTACAGAGCUGAAAACCAGATTCTUT
254923382	69482	GGTGATGTAGAUATTACCAGGTATTTUCACA	69483	AGTTGCTTTTCUGTTTACTTAGGUGGAA
264753303	69484	GAGGTGCUGGGCCACUT	69485	CGGUCAGCCATCTUCCCT
263296815	69486	TCATCTTGUGACCAGTTCTCTACTUCT	69487	CCAGACUGCAATGCAAAUAAGGGA
254732927	69488	ACATAGCUGACCTGGUCCCAT	69489	GCCTTGTTUCTAGAATGGCUCAGA
263303598	69490	CCAGTCTTGUCAAACATCACAGTCUT	69491	GTTTCCTGTCUGAGGCAGGUT
325241882	69492	CCCTTTAACGGAUAGGCAGCUT	69493	GGGTATCUCCAGCCTGAGCUA
324216612	69494	GAAGGAAGUAGATAAGGTGCUGACA	69495	GTTGCACTUGAATAGATCCGTUGG
227990399	69496	GGAGGGCUCGTTCTUAACCAT	69497	GCCATTCUCAGGGTTGGTCUC
229066910	69498	AGACACGTAAAUACATTTCAACACTUGGA	69499	AGTTGCTUGGAGACCATGAUGT
281031221	69500	CCTCCGGAGUGACCCTCUA	69501	CGGACAUGGAGTUGGAGAAGT
280077460	69502	CCCTGAGGAUCTCTGGGUACA	69503	GACUCACCGGAACTTGGUCT
316350568	69504	CCTACCGCUACACGGUGAA	69505	GGCGUCCACGATAGGGAUG
239080634	69506	ACCACGCGGUCTTTGUACAG	69507	CACCCAGAUTTCAATTCTTTUGACAACA
261601407	69508	GCAGAGAAGUTATATGCUGAGGAGAAT	69509	AGCCTTUCACAAAACTCATCCUGA
269262720	69510	CAGGUGCTUCAGCCACCA	69511	GTCTGGGTCCUGACTCTGTCUA
267436226	69512	GGATGAGAUGTCAAGTCAGUCCCT	69513	ATCTCTCCCCUGTGACCTUGT
257311772	69514	CAGGCUGGAACTTCAGTGUGT	69515	CTGCCTCTAUGCTGTGCTCUC
315560982	69516	TGCUATGAGGUAGGGCACGA	69517	GTATCCCGUTTTTGCCCTUAAGAG
315848815	69518	CACTCGCUCACCTCCUGAC	69519	GGCATCCCAUCCTCACATTGUT
320345969	69520	GCCACCUGCTTCATCTTCUCA	69521	AGGAGGAGCUCTTCUCGGT
320345125	69522	CCACAGCCACGUGTUCCT	69523	GGTACAGGUGGCCCUGGA
321420896	69524	CCCUGCACAACGCCTCUC	69525	GCTGGUGACGCTGACTGUA
318025163	69526	GCTCACCUCCACCTGCTUA	69527	CATGGCCCUCGTCTGGAUG
318694931	69528	ACAGCAGCAGCUTCTCCTUG	69529	CCCCTGGGUGCTGAGCUA
228788812	69530	CTTTTCUGGCATCTUCCCACAG	69531	TCATGCCTTUCAAGACACTGCUT
232655913	69532	CCATAGTCTGUGCTCTCTGCUG	69533	AGAATTTAGGTUGTCAACTGCCAUGT
232095859	69534	ACAACCATAACUGAACATCCATTUCCT	69535	GTGAGTTAACCUGCAACTGATTTTGTUT
329211858	69536	CGGAGACUAGGAAACCAGCUCT	69537	TCCTAAGGAAGAUGTATGAAGCCTUGA
242191185	69538	CCCCACAGACCUGACTTCUCT	69539	GCUGGAAAGGAGGTGTUGAAGAA
223979161	69540	GGCCCCUTTCACTCACUGAAAT	69541	GGTTACATAAATUGGTCCGACAACATUC
266197333	69542	GTTCGGAGAACUGCTTATTTCCAAGUA	69543	GGGAGTTGAATUAACTAGCCCTGUT
264091007	69544	ATAAAGCTATATAAUTTCCAGGTCACUAAAGGA	69545	GCCAAAAUAGAAGGAATUCGAAACAAGT
336400667	69546	TTTGCCTATTTTTACAAUACATTTCGAAGACUT	69547	TCTCTTTCCTCACUCTTGGTCAAACUA
265283692	69548	TTCATCATTCTAUGCATTGCCCUCA	69549	AGTTTGCCCCUTCCAAAUCAACT
257353991	69550	CTCCATCUGCCTGTCCATGUC	69551	ATCTGGAAGAUGAGCUGACACAC
259203830	69552	GGCACCUCAGGGACAGUAAAT	69553	CACCCTTACATUTCTGCAAAATGGUT
265779537	69554	CCTGUAACCCCGUAACGCA	69555	GTTACAGCCAUGACCTGAUGGT
254898885	69556	GCCACTTCCUGCACAGATGUAG	69557	CCTGAAACCUCTTGTTCUGAAAAACAT
256436741	69558	GGCTCCAUCAGGAAGAGAAACTTUAA	69559	GTCACCCUCCAACTGAGAATAGAUG
265387225	69560	CTCTCACTACUCCTTGCAGTTUCC	69561	TGAAATATGUGCCATCGGTTGUGT
325108971	69562	CATCTGTATUCCCCCTGCTTUCA	69563	CUGAGATGCCUCGGCACAT
229299501	69564	CUCUGGCGGGAAGGGAT	69565	ACUCGTGGGUCCCGAACT
316523530	69566	GCTGAAGUCACGGAACTGCAUA	69567	GGGAGAAGCCCUTGAAATAAUGG
317105408	69568	CCTCCCACAUCTTGGTCTUCAA	69569	CCCAGCACUGCTTCAUCAGG
313092870	69570	CAGAGGAGGAGGGUCTUACCAT	69571	GCAGGAGAUCGCCACCUAC
314485131	69572	ACCACCCTUCCTGGCACUA	69573	CTGGTGTGAAUGGCATTCTCTTTUT
313183271	69574	CTGATCAGUCTTAGGGCAUCCA	69575	ACTACAGUCCCTACTUCAAGACCAT
279696725	69576	GAGAGCGUGAGGGTGTCAUC	69577	GCACUGGGAGTGCUCAAAGT
238060087	69578	GGTGAGUTACACTTTTUGCCCAT	69579	CTGAGGCCCUGATGCTAUCT
235133367	69580	CGACGUGGCTCUAGAGGAAT	69581	CAAGGAGCUCAGAGAGGTTUCAA
239403415	69582	CCACCTTUGAGGTGAGUCCAA	69583	TGGCTCTCUTGATATCTGGUCCAT
267262803	69584	AAGGACUCCUCCCCCAGAA	69585	CTTTTGTCTAUGGTGGCTGUGGA
265162915	69586	CUGTGGAAUCACAGCCCAGAT	69587	GCAGATGGGACACUGGGATTUT
268375453	69588	GGATGGAGCAGUGGTTGAUGAT	69589	TCTTCCCACCCGUGTGTTUC
262358715	69590	CCTCACGCGGUACTGTGUC	69591	GGTCAGTGAGGAUGAGGAAGAUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
317581212	69592	TGGAGAACCCGUAGTGCAAAUC	69593	GTCCACACACCCACUCTTGUT
318018149	69594	TCCTCCACCUTGGCTTUCAG	69595	CUGGAGCUGGGACGCAT
319115673	69596	TGCCGGCUCTTTGUCCAG	69597	CGGUGGAGUGACCCACAT
318573674	69598	CTCCCCUTCCCUAGGCACT	69599	CCGACGAGCAGGACUTCAUC
230445022	69600	CCCGCTTUCAGGGATCTUGAG	69601	CCTTCCTAAGUCCGCTTCUGG
235661651	69602	TCTAACGCUCTCATAATCAUGACAAAGG	69603	ACGTGAAGUATGTCATGTUGGAAGAAAA
237864243	69604	GAAAGGAAGAAGACUACAGGGCAUA	69605	GTGACCTGCCUACTAATTCCCATAAUT
240365924	69606	TCTACAGCACUCCTCTGGTUACT	69607	TGUAACCUCCACCCCAAGAGA
222908297	69608	TTTTTGAUGGCAGCATTCGAUGG	69609	ACAGCGGTUGACATCTAATATTUGACA
223140586	69610	TGGGTACACCAUGCTTTTTGAUGA	69611	TTCTCCATAUCGGCCTTUACCAAC
261051676	69612	TGTTGGUCCCAGCCTTGTTUAA	69613	GGAGTTCUAAGCCAAUCACCCAA
266727165	69614	CCACUGCGAAGAAGACGUCA	69615	AGTGAGGGAUGCATGTTCCATTATTUAG
314815588	69616	CCCAAAGGAAGGCAUGGTAGUAG	69617	GAGCCGTTGUTCGAGCAGUA
265321852	69618	CAAGGAACATCTUGCGATATTATGCAUT	69619	CAAAGCATTACUGACCTTAAACAGCUT
265735203	69620	CTTTTGGCCAGAUTAAGAAAGAAGTUGA	69621	GUTGTTCAUAGGGCCCACCA
254314838	69622	TTCATAGGTTTUAGGTCTACTTCCUCCA	69623	GTCAGTGATAGCUTCAGAAAGTTGCUA
255323413	69624	GGTTAAGUACAGGATTATTCATCUGCCT	69625	CCAAGGAAAAACUTCACACTATUGAACA
253977956	69626	CATCCGAAUCCATCUGAAGAGCAT	69627	GGAGACCUGGAAAACAGAATCUAAAACAA
266929838	69628	TCTAAGTGCCUCATTTTCAUCAAGGAA	69629	ATTAAATTGGATATTUTTCAGGGAGTATAUGGT
255990770	69630	GGACAGTTCUAGAGCTTTTCUAACCAAT	69631	GAAGAAGATGAUCCAATTATGGTAGCUGT
266804091	69632	AGGAAAGAAATGCUGAAAATGCCAUC	69633	GCCTUGAGAAAAGGACTACATUCAGAAA
263724722	69634	AAGAGGTTGTTUGCCTTTGTCCUA	69635	AGATCCTTTAAAUGAGGAGGAGGGUT
260514877	69636	ACAGGCAAAGGGUGTGTAUGAAA	69637	ACAATAAACCAGGUTCAAATACTCACUGA
324860336	69638	CAGAUGCACCGACUGCAAG	69639	TTCCCAGTGUCTTAGCCCTGUA
323675175	69640	TCTCAGACACUGGAGATGGUGA	69641	CTCTGGGACCCAAAUGTGGUA
323662926	69642	GGGCTCACACUGCAACAGUAT	69643	CAUCAGCACAAAACCAAACUCAAACT
325109963	69644	CCAAGTATCAAAGUGTTCAACTGAGUG	69645	CTTTTTACTATGGTUCCCTCAGAGACUT
227694259	69646	CAGGGTGTTUAGGAGATGACCUT	69647	CATCTGTGUGCTGGTGCUCT
232899129	69648	CGGTCAGUACACGCAUGGA	69649	CCACCAAUACAGCCCCTTCUT
230398852	69650	CGGAGACGAGCUCAUGAGT	69651	CACCACGCUCATGAGAACUGT
263736629	69652	GCTCGUCCAGGTCCTCGUA	69653	GCTCTGAGUGGAGGCCTTTUAT
320597683	69654	CCCCATUCCCCTTCCCUGA	69655	GGCTTGGGUGGGACGUT
316553874	69656	GGAAUGAAGCAGGACTCCUGT	69657	CACACGAAGUCTCCGTUGAAG
278335516	69658	GCCCAGCACACUCUGACAA	69659	GCACCCUCGACCCTGUG
261778730	69660	TCTAGGUGGCTGGUCGGA	69661	AGTGATATGGATUCACACAGACACUA
264603924	69662	TCTCACCAUCACTAUCCCAAGGAG	69663	TGTGCACACAGUGGAAAUCAGT
265552015	69664	CAGCACATGUGTCCTTCTGTGUA	69665	CTTTATGGTCCCUGTGGTCTTCUG
267567763	69666	CCCUGTACCTUGGGACCGA	69667	CTCACCCCACUGCCTGAUG
257796827	69668	CTGGGAGTTUGAGCTCTCAGAUG	69669	TCCCGACUCCTCTGATTCCUG
264516832	69670	CUAGGGAGGAUGGCAGAGAGT	69671	CTGAGTCAAUGAACCTAATGUCACCA
257722831	69672	AGAGCTCTCAUCCCAGGTCUC	69673	GCCCTUCACCCAGACTTUGT
268001523	69674	CCTGCAAGAUAACAGGGUCAGA	69675	GGCCACUGACATCCCATGUG
316927520	69676	CAGCTGCTUCTGGGAATCCUT	69677	CAGTGGAATCUCTGGAGTGGUC
320641148	69678	CTCCACCGUCAGCTUCAGT	69679	GGUCACCAAGAACTUGCAGAAGT
320640785	69680	ACCTCCUCCACGATGGTAAUGA	69681	CTTUGAAAAGACCCCGGTUGAG
320645950	69682	GGCGTAAACACUCAGCTTCUCAT	69683	GGAAGGUGTCAGCUCAGAGG
318144050	69684	CCCCACTGGUCTCTGACCAUA	69685	CCGCCACUAAGGAGCTAAUGT
318376855	69686	CACAGCTGCUGGTAGAGGUA	69687	CGUGGGCUGGAAGCAGA
321305154	69688	GGCCAGGAUTTCACAAGGCUT	69689	CCACAAGCUGCTGCUGACA
230956472	69690	GTCTCTAGUAACAAGGCCAGGUC	69691	TGTGTGTCTATGUGTGTGTGTATACUC
230201006	69692	GCAGGAAGTUGAGGAGAAGGUG	69693	TTCCTAACCUCTCCCCTGUGAA
235184774	69694	CACUACCACGGUGGGAAGAC	69695	GGGTCTGATUCCTCCGACUC
235315358	69696	AAAGTAGAAGCAAUCTGATGAACUCCAA	69697	TCCACAAGGGACCUGCUCT
235832485	69698	CAUTTGUCAACGGACAGCAGAT	69699	TTCTGUGCCCCCATTGTUCT
235564482	69700	TGAAAUGGAACAAACAATGAUAAGCAACA	69701	TTAACCTAACGCAUGGCCTCUT
237018918	69702	CAGGTGTTGUAGGAGCGCUT	69703	CATGAGTTTGCAGUGATTTTGCTATUCT
242042504	69704	GCCCCUGTCTGCTUGGT	69705	GGGCACCAUCACCACCUC
241510364	69706	GCTACCUGGGCAGUGGA	69707	GCTGGGUGCAGAGCCAUA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
262763241	69708	GGGAGTTTUGCCAAGGCCTUA	69709	GTTAGTGCCAUCAGCTCUCGT
233058664	69710	GTAGCCAGCCAGGUACATGUAG	69711	GAGAGGACUCCCTGGGATCUT
323500249	69712	GATTGAGUGCAGCAGCTCTGUA	69713	GGTTTGGCUTCATATTGCUGACAAAA
323908246	69714	GTGATCAGGATUGGTATCAAAGGUAGG	69715	CTCTTCCAAAGCCUTTTAAAACCACUT
269293862	69716	TCTCUGAGACAGACAGGGAUCAG	69717	AACCAGGAAAAAUGCCCAAAGUG
269254690	69718	CTTGGTCTTTTUACAGTACTGAGTGGUA	69719	GAGGAUCAGUAACAAGGCGACA
313315601	69720	CCACCCCACGUCAUGCT	69721	CGGTGGCUGCTGTTGUCT
314596450	69722	CCAACCACGUTGACAAAAACAUGA	69723	TCTTCTUCAGCGCTTCTCTTUCC
257348984	69724	TTGTTGAAAAAUGCATGTGTGTGUCT	69725	AATCGTTGATCGACAUACTAGAGAGCUA
264945352	69726	CTAGCAGUTGCATTCUGAGGGA	69727	AGAAGAGATAGAUGCTGAAAACGAAUGG
260189127	69728	GCTCACACTAUCAGCTAATTCATCTCTUA	69729	TGAACTAAGGCCAAGUAAAGAGGATUG
261994943	69730	TGTCTGATGCACAAUAGCTTTCATTCUA	69731	AGGACACTTAUGGCTGCGTTUAA
263546919	69732	GCATCTUCGGGCAGGAUGAG	69733	TGTGTAGCCUGAGTCACCTGUA
264945513	69734	CTGCAAUGGGTAUCCCAACC	69735	GCCGACGUCGTCCTTAUCA
257948552	69736	ACCACCAGGAUGACCAGAGAAUA	69737	TGAACTCTCCUCCCTACTUGCT
266927653	69738	GAAAATCCUCCTGGUGGGAGT	69739	CGACCAGGUGACCTTTUGCT
325851459	69740	GAAGCUGGCCAGTATCGAUCT	69741	CCCACAATTTAGUGCTTCAGAGTTTUT
324138640	69742	CCCTGATCTAAUTGTGCCCTCTUT	69743	ACCTGAAGUACTTGCCACUCAG
228971716	69744	TCCTCTTUCAACACCTCUCGGA	69745	GTGAAACUTGCGCAAUGAAGAAAC
230585670	69746	CCCUACACACACTCTUGACCA	69747	TTGAAGGGAGCGGAUGCTTTUAT
329081687	69748	TGCCTTGUACGTGAAGAUGCC	69749	GGCTCTAAGTTTUTGCTTGAGGTTAAUT
266827502	69750	GGGAGAAGGUCAGCCAUGAC	69751	GAGAGGGAAAUCGGCTCTUCAA
313213468	69752	CUTCTCACUGCCCACCAGAA	69753	GCGGCCUGTCTGTCUCA
278533815	69754	TGCUGGTCTTCUCCACCGA	69755	CTATAGGAGUAGTTGGUGACAGCAAA
281266945	69756	CCCAACACAGUGCCTGUCT	69757	GCUCUCAGCAACCCCAACC
317450681	69758	GCUGGAAGGUCACCAACAACA	69759	GTTCAUAGCACCAUCAGCACAG
279848819	69760	GCAGACGCUGAAGGCATCUT	69761	GGGUGAAGGAAAGGACAGGUG
278083961	69762	CTUAGCACCCACAUGGACCAA	69763	GGTGCAAGGAUGGAGTAGCUG
264300513	69764	GGACTGGAAGUAGGACUGCAC	69765	GCCCTUACAACAAAAACAAGAGCUT
241339762	69766	GCCUCAAACCCTAGAUCGCA	69767	TTCAGTTUCAAGGCCTCGATTUCT
267247971	69768	CCCCAUCCTAAGTCCUCACGA	69769	AGGGTUCCCAAGTCACTCUCT
266024106	69770	GCTCCUGGAGCTCATCCUCAT	69771	TGTTAATCCCUGAGCCCTGTUC
261661626	69772	GTCAGAGGUTGCAGAAAACUCC	69773	TGAATGTTUGGGCTGATGUGAGT
266879583	69774	CTCCAGACCCCUTGTGUGAAG	69775	CAAACTGCUGCCTACCTUGAG
267858398	69776	CUGGAAGAAGCCCCUAGACAT	69777	CACGTTGACAUTCGCCUGAG
265545425	69778	GAGGAGUGCCUCAGAGAAACC	69779	AGGGCCUGAGAGGACAAGUT
267131714	69780	CTTCUGCAGGAGACAGAACTUGA	69781	ACCTCGTGUTCCAAGCATUGA
268377195	69782	GGTGGGCAUACAGCAATGGTUA	69783	CCCCTTACCUTGCCTCTGUC
266571112	69784	GGTCAGGAGCACAUAGGAUGG	69785	TGACTTCTTCTTCUTCGTCAATGACUT
315853071	69786	TCTCAGCAAGAAAGUCGATGTCUC	69787	GGCTTTCTUCCAGCCTTTUCCT
316369862	69788	AGCCCACCAUGGTCAGTUC	69789	GTGATAAACTCUTTACGTGGGCUGT
320350249	69790	CGTCTGCUCGGCGAATTTCTUAT	69791	GCUGAAGCAGUCGGCAGAG
318021112	69792	GCAACAGAUGAGACGGUGAGG	69793	CTGCACCAGUCCAUCGAAGA
237350243	69794	ACAAAAGGAACGGAAAGUGUAAAAACC	69795	TCGAGTTTACUTTGCTTTCCTUGAGT
238688959	69796	GCTGCCUGGCTAAGGTGTUC	69797	AUGTAGTGAAGTUCGGCACACT
264074492	69798	GCCTTCTGCAUCCACTGCUAC	69799	GACCCUCACCAGGATCTUGAA
233335526	69800	CACAAGCGGUCCGAAGUC	69801	AGATCAACUCGAGCGCCAUC
325276214	69802	TUCCCCACCAAAATUCAAGGGT	69803	GAACTTCCTTCUTCATTCTGCAGTUG
313956077	69804	GACCAGAAAAUCCAAGGCCCAUA	69805	CCUTCGGCTTAUCCAGGACAG
314396542	69806	GGATCTATCCUGTCTGCCUCCT	69807	ATGCCCTGGUGAGCTATGUC
314052871	69808	CCCUGAGCTGGUCCAAAAGG	69809	TGCTGAUCCTTCAGGUGAGGA
313435719	69810	ACTGGAACCCCUGGAGCAUA	69811	CCGGATCCUAGATGCAAAGAGUAAG
313688429	69812	CGUCCCCCAGGCTTUGAG	69813	AATCTAGGACACAGUCCCUGACA
312912605	69814	AAGTGGCGAUCTCCACGUC	69815	AACCCCACTCUCCTCCTTTCUA
263871094	69816	CATTTCTTCCGGUAAGCTGAUCAAC	69817	GCTTGGCAAUGAAAATAGGAAAATGCUT
264868488	69818	TCAUTCTGAAGGUAACCAAACACAACA	69819	TCATTTCTAATTACCGUTTTCCTGTCCUT
264590014	69820	AGAAGTCATTUGGGCTCTCTTUGT	69821	GCTGATCAAUGGTTCCTTUGGG
266329898	69822	CCAGGGCTUCTCCGAGAAAUT	69823	CGGGTTGUCCTCTTTACACUGT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
325294550	69824	TTTCAGCAGUGTCATAAGTAUGGCT	69825	CGTTTTGGUTTGAGGCAUGGA
279735502	69826	CUCCTTCTAGTUGAAACGAGCCA	69827	TTATTCCGGAACUCATCCACATCTUC
279414016	69828	CGCUACGAGGGTCAGTUCT	69829	GGTCCUGACGGGAAAGUCAT
278019155	69830	GGGTGTTGAAGUGGGTCTCUG	69831	CAGCCAGTUGAAATGGATCTUCCT
238729728	69832	CAGGAAAUGCAGCGCAUCAA	69833	CAGCTUGAGGACAACTGCTGUA
232964567	69834	CAGTTCCAACCCAAAUGCCTUT	69835	GTGCTAGUCCACTGGCTTCUG
230573648	69836	GACGTAGGUAGTGCTUGAGACC	69837	AGAGUCAAGGAACACGGAUAAAGAC
230654190	69838	CATCAGAGAGUCCTCCTGGAGAUT	69839	GGGAUGCAGCTCGTUACCAC
230744155	69840	CUAATGATGGUGAAGCAGAAAGCC	69841	TCACCCTUAGGCATCATCCTUCT
231407847	69842	CCCCAGACUGGACAGACAGAAUA	69843	GGTGAGGCUTATGGGCTTTUACT
228425956	69844	GCATGAGTCUGGAGGACCACTUA	69845	GGAGCTTCTGGUTGTCCTTCTTUC
232431157	69846	GCAGATAUGGCAGCUGAGCAA	69847	CTTGGCTUCCATGACACCUGA
228877099	69848	CCAGGAGTUAAGTTTTGATTGUCCAGA	69849	CAGGGATACTUGTTCTGTGAACTUAGT
242208630	69850	CTGTGCCCGCGUATACTUCT	69851	CCACAAGGUCGGCACUCAC
264082246	69852	AGAACCAGGUCTCCGUGGAT	69853	GCAGAACACAGGCCUCGUC
260350819	69854	ATCTGTGAGCAUCTGTGCTUGAA	69855	CCTAGGGUCACGATCUCCCA
223980312	69856	CCAGCUACGCCGGACAAUA	69857	AAGATATTUGAGAAGCATGCUCCGA
231871856	69858	GGGATGACAUCATTGGCTACTUC	69859	GCAGUGAGGACCCCACCUA
232652555	69860	CCCCAACACACAAAGUTCTCTUC	69861	GTGGCAGCCUGAATTATGAUCCT
314232256	69862	CCCTTCCTUGCCCTCTTUCAAT	69863	CAGAATCTTUCCTCTTTCCUGGCT
314826900	69864	GCACCAAACCGGUTCCUGAA	69865	CCAGCTUCACCTCCGTGUC
257046750	69866	ACAGCTGTTTUCACAAAACGAUACT	69867	TCAACAGAUGCTGATCAACUAAAGGAAA
253789588	69868	CTAATTGGCTCUTTAGCCGTTCUACT	69869	ACATCAGGCTUCAAGAAAACCAUGA
262251391	69870	TGCAGTTTAGAUGTAATTGACUCCAACT	69871	GCCACTGTGTUAAAACTTTGCTTAGUAA
265566086	69872	ACATCAGGATCUTTCTGCATTTCCUT	69873	ATCTGATCATCCAAUGAGAAAACTGUGT
258798047	69874	TCCTTGAGAAATGUTTTCAGTTAGGTUCA	69875	GCTATGTAGAATUTTGGAGGGATTTUGG
254848812	69876	GGGCGGGAGGAAUCAAUAGT	69877	CTTGAACUAGGAACAGCCATTCCUT
263970846	69878	GCTGACCCAACCAUTGCTTUC	69879	TGAGGTAGCGGAUGAACTGTTUC
265315339	69880	AAGACGCAAGACUTACAATGCATUC	69881	AGCUGCCAUCAAGAGCAAAGT
325250909	69882	CTAGAGAGTACCGUAATGGGTTAATUGG	69883	CATCACTTCUGCCTCTGGGUAG
228494722	69884	CGGUCCGAAAGCTGCGUA	69885	GTTTTCTTCCCAGUCACGAGATACTUT
231797331	69886	AGACAUGAGACUGGGAAGGCT	69887	ACTGCTTTGTTTUCTTGTTCTCATTCUG
328769875	69888	TTCTTGCUGCAGCCATGGUA	69889	CTGCCUAGGTGGGCTUCAC
319885604	69890	GTCCCCGCUTCGAGGUA	69891	GCUTCTUCGGCGAGCAG
316334303	69892	CCAAAACUCAGCCTGACCUCAA	69893	TCTTCCCCCACUGTCTCTCUG
280280368	69894	CCCTGCTCCUCTCACTCTUGT	69895	CAGCCAGGATUATAGAGTCTCGUG
326977243	69896	GGTTCCTUCAAGCTGCCCUAT	69897	ACATGGGAAAACAUAACCTTGAAUAAAAG
238601985	69898	AGGTCTTTGAUTTGCGTCAGUGT	69899	GGAGCTATUCCACCTACTGAUCCT
236008296	69900	GAGCUGGGAGGGAATGAGATUG	69901	CTGCUATGTCTTCCUGAAAAGGGAAT
241506017	69902	GGGTGGTGUCTTTTCCTGCUA	69903	GAACAUCACCAGGACUAAGGCA
266823542	69904	GGCTGUACCCATCAGCAAUGT	69905	ACAGTCTGAAACCUGAGGGCUA
266750871	69906	AGCTCCTACUCCACTTGAAAGUGA	69907	ACATTTAATGAUGAGCCAGACGAGAUG
313750751	69908	GGTGGUCCAGGCTGTACTTUAG	69909	GACCUGACAGGACUGGAGAAG
266689076	69910	GGACCCCCAGGAUATGTGUGT	69911	TGACTGAAUCCCTCTCCUGGT
267388986	69912	GACCCUGACGGAGAACAAGUC	69913	GCACTGCCCUGAACTTTCTCUT
267040651	69914	GGAGGGUTGCCCATUGAAACA	69915	TGACTCCACUCTTTTCTGAGGUCT
268257315	69916	GGCCTCUTCCAAACCUGAGT	69917	TGAAAAGGCUATCAUGCAGCCA
267952000	69918	CCCAATGGUCCCTAACTUCCT	69919	CTCCCTGATUCCTGAGCTTUCT
268305518	69920	CAGGTCTGUTACAGGGCUCAC	69921	GACCCGCUACCAGTUGGAT
267692223	69922	GCAGGGUCTGCUCAACAGAAG	69923	TGGCACGGACUATGAGGUGA
267901627	69924	GGTCAGAGGCUGGCAGAAUT	69925	CTGGGCAAGAUAAAGTGACCTCUT
316024655	69926	CTCAGTCTGGUTGCTGGGAUA	69927	CCAACCUGCAGGCAAATGTUC
316696142	69928	CUCCACUGAGAGGAAGGACAC	69929	TGACCACACTUCCCTTCTACAUCA
318016839	69930	GCCTCCTUGCGCAGCUT	69931	AGCAGAGCGUGCUGGAC
232207121	69932	CCTGCGUGCCTTCTAGACTUG	69933	TTTAATTTGCCTUCTCTTCTGTCCUGAT
237371796	69934	CAGAAGCCGUCACAGUGGT	69935	GCGCAGAGACGCUTTTGAAAUT
236779679	69936	GCCUTAGGTCUCCAGAGAGCA	69937	ATGCCAAACAAUTACAAGAATGGAUCAG
235686237	69938	GCCACATTTUGGGAAGCTGTTUG	69939	CGGACAUTGTACCUCGGGAAA

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
235884867	69940	AGAAGAGGCCAUGCGTUAGG	69941	CTGCTTTTCATUTTATTAGGCAGUGGAA
238099727	69942	GCATGGCACUGTATGTGUGAAAG	69943	CATGGUGCGGTTCUCCGA
223164219	69944	CAGAUTCAGATGGUCCGGCAA	69945	ACCTCACUAGCCTTGTCAAAAAUGAAAT
223061587	69946	CTGGGCCUTGCTGTTAAATUCAA	69947	AACAAGCATAUGCACATTTTTAGAATUCCAT
223003751	69948	CAGCAACCAUTTTTGUGCCCAT	69949	GGTGGCATTUACGAATCACTTCTUC
234682094	69950	TGCCGTGAGUTGCAGCUT	69951	GCCAGGGUGCAGTGUCAG
233521715	69952	CUGGGCCAGAAAAGTCUGACAA	69953	CCCACCUGCTGCGATTCUAC
253794539	69954	CTTTACAGACACUCTCATCAAGGAUCT	69955	GAAAAACTUAAAGCTCATCTUGGGCAT
253988776	69956	GCATCTTGTUGGACTTGATCCUCA	69957	GCTATGAUACCTCTTGTGTUGAGAAAACT
266766107	69958	ACTGACUACCACACTTGCCUCT	69959	ACCAGTTGCTTGAUGGTATATGACATUT
260685539	69960	GAAGAAAUAAAACACCACAAGCAUGGA	69961	CTCAGATTGUGAAACTGGUGGAAG
323987101	69962	GGTATTCTTACUAGGGCATAGUCAAGGA	69963	CCAAGAAAGCACAGCUGATGAUG
324143270	69964	CTCTTCUCCCCCTTTGUCAAGA	69965	GCCCAACCCAAACCUGGAUT
230129014	69966	CCTGCCCAGGUGGTAGUAG	69967	TGTGCCAGCAUACTGCTCTUT
230338959	69968	ACAGAACAUTGCCUGGAACACT	69969	GGTTGGGAAAAUAGGACATAGCTTTAGUA
266838502	69970	GGCCTCCUGGTACTUGGAAGA	69971	TGTTTTTCGGGUCTCTGAUGGG
317953823	69972	CTGCCCTCUGACCTCAATCUG	69973	CCUCGTACACUAAGAGACCCCAA
316508178	69974	GCTCAGAGAGAAAUAAAGCUGGAC	69975	TCCCTTGGAAUGGGTAGGGUAA
281042172	69976	GTGGACCTGUACATCCTCAUGG	69977	CTCAAATGTCCAGUGTTTCCTTCUG
278542110	69978	CAAGCACAACAUCATCCCCAUC	69979	AGAGGTGUCTGAGAAGCUCCAT
279777522	69980	GTGAGGCAGAUCGCAGAGUA	69981	GGTGTAGCUGTAGGTGCAGUC
278851751	69982	ACAGGCTGAUGCTCTTCCTCUA	69983	CTCCTUGGGCCATCUCACAG
324576087	69984	ACAAGACCTGAUCAAAAGATGAAAATUCT	69985	CCAGATGCCUTGGAAGAAGAUGAT
323632439	69986	GGTTGAAAGGAGAAGUTCTGTATTTATTATUG	69987	AGCCAACTACAUGGATTGTTTUGAGT
312678683	69988	CCTCACUGGCCGTACATCAUT	69989	CTGGUGACAAGCAUGACCAAG
314054805	69990	CGAGAAGCAUGAGGAAUGGAGAT	69991	GCTTCAATGGTCUCCTTACTATGTAUCAG
258828136	69992	CCCTGUGGAGAGAGGAUAGGAG	69993	TCCTGGGCUCACACTTTCTCUA
269273651	69994	TGGCACCCAUACCCTCATUG	69995	TCTGACTTCUGACTTCTGTCTGUAACT
320635498	69996	CCCTUGGTGTCGUCGCT	69997	GCAGCACCAUCTCCCTCTUC
320644730	69998	CGAUGAGGCCCTTCUGCAT	69999	CUGACCGUCAACGAGGCT
320344628	70000	CCTCAGCGCUCATCUCCA	70001	GCAGAGAAGAUGCUCAAGGAGAAG
318914242	70002	TCTGCCGGUACACCTTGTUC	70003	ACAGTGTATTTTUCAGGGTGAGUGT
319031808	70004	CCUAGCCAGAAAGCGGAUCAA	70005	GTGAAGCUGGTGAACAUCAGGA
318550723	70006	CTACTTGCCACCCAUCATGACUT	70007	GGUCTACCGUCGGAAGGAG
329107672	70008	CCAAAACCCCAAAUCCTCCTCUA	70009	CACCCCTGUTCTGTGTCCUAC
230062958	70010	CTAATUTCCCCATGAUACAGCCAGA	70011	CAAGTTTCTGAGAAAGUGCTTGTGAUAT
232569651	70012	TTCTGGTCCACUACTTACCATCTCUT	70013	GGGACATCACCUTTTCGCTTTUT
236557004	70014	CACAGGGAGAAUGCAAGGTUC	70015	GGTCATCCUGATCGCTTCUGT
235328531	70016	GAGGCUGGAGUCGGAGAAC	70017	CUTTGCCCAUGAAACGCAGAT
223128731	70018	GGATAGTATGCUTCATGGCACUGG	70019	CCTAACTCTUAAGAAGGGCTGCAUAAAA
314830474	70020	CTGCCTCCUGAGGTTGTUGAT	70021	GGGAGGCACCUTAGTGAGTUG
265322073	70022	TGGCAATATCAGTTUCCAATTCTTTTAACTUG	70023	ATACCTTATCTCUTGCCACCACTTUT
256206651	70024	TGTGTGGUGAGATTTTGGTUCCAT	70025	TGCAGAAACUAAAAGAGAAAGAATCUGCT
260179072	70026	AGAATTGTATACCUGTAATTGGGTTTCUT	70027	GATGCTGAUAGGCAACGGATTCUA
259342823	70028	GAUATTTCAGAGAUCCAGACAAACCACT	70029	AGCGGGCUGAACATTGUCAA
258544841	70030	TTTTTCACAAACTUCAGCCTCCATUG	70031	CTCTTCAGATGGAUTCGGATGAAAUGAA
255104064	70032	TCTATTTCCCUGAGACAAAGTCAUACCA	70033	TTTTAGTTGGCUCTTCGAAAUGAGGA
265639097	70034	AAAACGAAGTGCUAAAATGTCTCTCUCT	70035	AUCTTACCAUCAGCACACCAACA
257378730	70036	GAGGCGUGACACGTCTUC	70037	AGGAAAUCCCATCGGUGCAT
265859053	70038	GGGAAAUGAGAGGCAAGTUCCA	70039	GTGTGAGUGCGAGTTCTTTCTUC
266321807	70040	GGAAAGCUGCAATAAAGUGCCAT	70041	CAGGACTGTCCAUTCTAAATCTCATCUT
256342315	70042	CAAGCUCAGGACATGCCUCAA	70043	CCATUGAAGGCATGATCUCCCA
325703437	70044	TGTTGTTCTTATUCTGAAGCAGGUGA	70045	TCAGTGCTGAAUGGGATAATGTCATUT
326355335	70046	CAUCAAAATTGGTUCACACCCAGAA	70047	AAGGGAATCUTGCCAATGUGGT
229832790	70048	GGCCAGGGUAGCTCTTTUCAA	70049	GGATTGTGTGTUCTGTCCTCATTGUAT
227864654	70050	GGUCAGGAGGCTGUCAAAGAG	70051	CGTCTUCAGTGCCCUGGAAAAT
230094656	70052	TGAAGACCCCCUGCTTTGTUC	70053	GGTTCTTGTCAUCCCTAACTAGTTTCUT
230538666	70054	GCTGCTGAAGCUCTGGAAGUG	70055	TGCTGACAUCTGTTTTCTGTUCCT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
316021947	70056	CCATTCGUGCTGCUAGACAC	70057	GGTCCAUGGCGATTGTCUCA
316733287	70058	GGTGAGGGUGGGAGTCTTUC	70059	CGGCACACUACTTCTTGCAUGAT
317109421	70060	CAGGCACCUGTCGAGTGTAUC	70061	GCTGTCUCAGGTTGCUGACAA
314246050	70062	GAGGGCCAAGACUCACUGG	70063	ACCAAAGGUCGCTACUGCAT
313201279	70064	ACCTTGTTCCUCAGGTCCUCA	70065	GGCAGUGAGAAGGUGACCAT
279808701	70066	CTGCCACUGACAGCACTCUT	70067	GGCAGGAAAGAAGGAUCTGGUT
268143017	70068	TGGGTUGATAGACAGTUGAAGAAACAG	70069	CCAGCAGUGACAAGTGTAATUGT
315298544	70070	ATCCTGACUCACAGCCAAGTTUT	70071	AAGAACTGUGAGCGGTGUCA
262527652	70072	AGGGACTAUGGTGAGACUGCAT	70073	TCCCTGAGGUCAGAGGUCAC
257800538	70074	CCCAGGAUCACAGCTGAGUCT	70075	GGCGGGACUCACACTCTTUT
258981365	70076	CTTCACCCUGGATGGTGACAUT	70077	CCACTGATUCCCCTCACUGAT
265743726	70078	GCTCCUGGATGTUGGGACAT	70079	GAGAAGGCUCAGUCCAGACAC
262588983	70080	GGCATTUGGAAACAGGCTTGUG	70081	AGCTGUGGGCCTGAAATAUGAG
266679331	70082	GGGTCTAGGGUCCTCATGUGAA	70083	TGGTGGCCUCTTACCACTCUAT
263763404	70084	GCCCTGUGGATGGAAGGAUAAGA	70085	AGCACTGAUGGTCTTTGUCACC
266596575	70086	GCAGTAGTGUCCTCAAGATGCUG	70087	CAAGCTATTUGCTGTGGGUAAGGA
317165765	70088	CCAGGAGCCAUACCATCACCUA	70089	CCAAGCTCUTCCGTCCTTUCT
318323320	70090	CATCCAGCUCCACUGCGT	70091	TGGAGCUGAAGGAGAAGAAGAUCA
240735446	70092	TCTCACCAUCCCTCACTCACUT	70093	CAGATCCAGUTGTTCTCAUGCAG
261994469	70094	ACATTACCAGGUATGGTGCTTUCAG	70095	TTCGATAAAGGCUAGCTTGTTCTGAUT
253786203	70096	TTGTTCTACUTGTTCGGUGAGCAT	70097	GGTAAAAGGCAUACTTGUACCCACAA
264155120	70098	ACCTTCAAGCAAAAUATAAGAACACTUCCA	70099	CCGTCAAGAAGAACUGGCAGATAATUT
263367748	70100	GGGAACAGCUTTCCAAAGUCAT	70101	CCATTCUGCGAGTUCCAAGAG
264618117	70102	CATCAUGAATAAACCUCCCCGGAA	70103	GCATCTCTGTCUTTTGCTACCCTAUAC
262253781	70104	AGATACTACTTUCATCTCTCAGGAUGGG	70105	AGGTGATCAUCCGGTTTGCTUT
254845504	70106	AACACAGTTGCUGGGTATTCUGAA	70107	CATCCTGUGTGTCTAACAUAGAAAGGA
258720958	70108	CCCAATTTGAUGGCAAACCTGUT	70109	GGCTATGAAGGUGGTCTGGAUG
325049550	70110	TCTCUGGACAAGATGTGAUGAGACA	70111	GTACCTTTTGAUCTCATCCTGTUGCT
323686793	70112	GGTATCCATCUGAGAGCTTGCUT	70113	CACATTUGAGAGAGCTCTUCAAGGT
324321742	70114	CTCCCTTTUACCAATGCGTTUCC	70115	CCCCTTCCUGTACCATCTTUCCT
231337417	70116	AGTGCAACAAGAGCUCCAUGT	70117	CTGAGGACCUGCTCCTCUCT
231478428	70118	GCTGTGGAGUCTCCCACUCAT	70119	CACTCTACTAGUTGTGGGTCCUCA
228350229	70120	ACAGAAGATCCACAAUTCTTCGCAUT	70121	TTGTGACCAGUTGTGUAGAAAGCA
279741631	70122	CAAGAACGUCATCAGCCUGACA	70123	TGCCCAGAAGUGCUCACC
278949328	70124	CCGGCUACTACACCCUCACT	70125	CGTCATCCUCAGGCCGGAUA
324892414	70126	CCCUACTTUGAGGAGGAGGAGT	70127	GCAATGTTCUGTCTCCCCTUCAT
264072914	70128	CAGGATGGAAUTGATGGTTACUCCT	70129	GAAAGAGCTAACUACACCATCTGUGA
268296011	70130	AATGUAACCCAAGGCTGUGCT	70131	GGCTCAATGUAAATTTCACAGTCTUGT
269290940	70132	TTCACCACTAUTGGCTCAGUGAC	70133	TGTGTGGAUCCCCATCUCGAA
313427569	70134	CCUAGAAGGGCAGCAUGGA	70135	CCTTTGTCUGCCCAACGUG
262881416	70136	GGATTCACCAUGCCCCUACA	70137	GCATTGACCAUTCCCTCCCTUT
258815871	70138	ACTATGTTTCTGGAUGCATCTGTATGUC	70139	ACATCCAACCAGUGATCTGTUCC
268799431	70140	TUCGCCCTGAUGGAAAAGAAGA	70141	GTTGGAGTTUGGGACCCCUT
268645214	70142	TGGTCAGCCACAUGGAGAATUG	70143	TCAAGAGAGCCUGATACCCGUA
316385407	70144	AAGGACTATATCCUATCCACCCATUCC	70145	GCACCCCUCCCCACTAAUAAC
320617787	70146	TCGGTCAGGAUCTCGTTCAUCT	70147	CCTACTCUGGGAAGCTCATCUCC
320630592	70148	AGATGGACACCUTCTCCTUGGT	70149	CCCAGTTUGAGCAGCUCAAG
320647373	70150	CACCACCGUGATGATGATCTUGA	70151	GCTGGTCUACACTGACUCCGA
318016810	70152	CTGCGCCUGTCGCTTUT	70153	GAGGAGAUCCGCGUGGT
320274646	70154	GAACGUGGGCTGCTGUG	70155	CCACCAAGGCCUCTCUGA
318198054	70156	TGCAGCCGGAUGTCTTUGAG	70157	GATGGCUGAGCGCGAGUA
318024056	70158	CUCGATCTUGGCCCGGAAT	70159	GAGCUGGAGGACTCCACUCT
321041065	70160	GCGGGAACUCAGTCAACCUC	70161	AGTCTCTGAAGAUGTCTCCAAUGGAA
231247220	70162	ACTAGTCAAGUCACCCCAUCACA	70163	CUTTAGGGAAAUCCACAGAGAGCA
237667013	70164	CCACAGCCUTCAUCACCAGAA	70165	ATGTCCAGUGCAGCTCUCAG
236664964	70166	GACUAAAACAACCAAACCAAACUCCA	70167	GGCATTTCGCAUTCTGTTGUGA
237782565	70168	CGCUCTTACCTUCCACCCA	70169	GAGAGCGAAGTUTCAGAGACTCTTAUT
242042835	70170	GGGAGAAGUACGAGCTGGUG	70171	CGGAGACAGACACUGGGUAGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
238720513	70172	GATCCUGTTTGTGAAUGACACCAAG	70173	TGCAGCTGUACTGCTTTTCUCAA
233659805	70174	GGTGUGGCCCAAGAAAAUGGA	70175	TCATGCCUGGGTAGTGTTUGG
265291961	70176	CTCCTTAATTTTCCUTAGAGCGATCUCA	70177	CTCTCAATGCUGCAACTGCTTTUT
266929850	70178	TTCAACGACAGCAUCTTCUAAACCA	70179	ATAGGCATATGTACAUTTTCCTTTAGACTUAG
254009311	70180	TTTAGGAACCAUTGCTCTGAATUGACT	70181	CCTTCAGAAUGAACAACTTTGUCAGGAT
263522986	70182	TGCAGAAACCUGTCTCAATGTTUAACT	70183	ATCATGAUGACCCGGAUGCC
254703758	70184	AGGGCAGGAUGACTGGACAUAT	70185	AAGTGGTCTCUGCTCCTGAAUG
323593159	70186	CCAGCCCTUCATGTTCCAGTUT	70187	GCAGGAAUAACAACATGGGATAAAUGAG
323848814	70188	CTTCCAGAGAAAUGCTAGGGUGAA	70189	CTGCACUCAGGATTCCCUGAT
324854256	70190	TTTTCCTCAAUCCATGACCAACAUCT	70191	GGAATCGAGCCUGGTCTCUAAA
230679175	70192	GTCTGGAAACCCUGACTUGGA	70193	GCCTTATTTAGAAUGACAGCACAGGUAAT
230691580	70194	CAGGCAGCAUGACAAGTACUAGG	70195	TGATCTCTGACUTGAAGTTTTTGTCUGT
227685428	70196	TGAACTAGAATGAUTAGCATAGGCCUCA	70197	CTGGCCUGGAGCTTGAATTTUT
255497833	70198	GAATAAGTTUGCAGGACTGGCTUT	70199	ATGTTCAAGCUCGAGGTCUGG
315914675	70200	GTCGCCUCCGTGACTUCC	70201	GAUCACTGCUGCGGACAGA
281062873	70202	ACTGUCACCCCTCTUGACCAT	70203	CAGCUCAGAGAAAGAGCAGUCA
280591251	70204	ATCCCCTGAUCCTAGCAUGGT	70205	TCCTTACGTTCUCCTCCACCUC
317112833	70206	GUGTAAGTACUCCACCCAGCAA	70207	AGTCAACTUCTTGCAGCUCCAG
316669523	70208	GGGCTACAGUGTGGAGUACCA	70209	GCTTTAGCGCUCAAGGGACUT
261793982	70210	GTCAGTATGCGUTTGACTTAAAATGUGA	70211	TCGCGGGCTAUCTTCCAAATTTATAAUT
237942095	70212	TCAGCUGGCGCTTACAGUAG	70213	GACCCAUCTGCAGUACACACAT
241362258	70214	GAGCAGCUCAATGAACUCAAGAC	70215	AUCAGCAAAAUACAAGAAAGAGACCCT
325251846	70216	ACACTTATTTUCAGAAGAGGACAGATUGG	70217	CTCTCAACUGGAGGACATTCACTUT
264183644	70218	CAGCACAAAGGUCACAAAGAAAGAUT	70219	CATGTTGTCACAGUCTTTGTCCAAAUT
267755274	70220	GAGATGAACAAGAUGAACAGCTGUG	70221	TCTCTTCCAGAAGGCUCTAATGUGA
313092774	70222	CTTAGATTTAGUGCCCTTCCTGCUT	70223	CTACTATGCTGUGTCCCAGCUC
263824908	70224	CAATACATGUGAGAGCCACCTUCT	70225	CCATAGAGUCCCCCTCCTTTCUG
268023044	70226	CTTCCUGCCTCUCCCACAC	70227	GTACAGCCACCAGCAUTCUCT
264235062	70228	GUGGGCUACAAGAACCCCAA	70229	GGTTCCTAGCAGUTTGTCTTCATCUC
268352951	70230	GGCCUCAGGGAGAGGUAGAAT	70231	CGCTTCAGUAACTTGTTCCCCUT
267827932	70232	GCTAATGCGGUGTGGCUAGT	70233	TTTGCTAGCCCUGGAGCUG
320611654	70234	GAGCCGCUGACGCTGUA	70235	GCCTACUCCAAGTACCUCACCT
320648864	70236	CTCCUCCGCACUCAGGAT	70237	GCUGGCGCACUCAGAGG
320347530	70238	AAGATGAGUGCGCGGTUCT	70239	AGCAGGAGCUGACAACACUG
320896261	70240	GGACACAACAGGUGGUGAGAT	70241	AGCTCUCGCAGGGCUAAC
318147128	70242	CTCCTCCTCCUCCTTCTCATUCA	70243	GGACCUGCAGUACGCCAA
319966208	70244	GTTTCCTUCCCAGGCAGUGA	70245	CCTATAGGGCCUGAGTGUGG
318300600	70246	TGGTGUCGCATCCACUGAAG	70247	ACCTACGTCUCGTCGCTGUA
318017587	70248	GGCAACACUGCTTTCACUGA	70249	CCTGTTTCCCUCCCTGGUG
318556506	70250	CCAUGGCACGCAUGACCT	70251	CGGGCCUTCTCGTGGUA
262811156	70252	TGGAGAGAGUCCTGTACCACUC	70253	GTTTCTTCCCCUTGTGAGTCCATUA
222389872	70254	GGAUAGGATTCTTTCUGAGGGAAGGA	70255	CTGTTCCAAAUCACGATTGUAACGAC
258857436	70256	GGGTCAACCAGUTTTTCATTACAAUGG	70257	ATGACTGTUGATCAGGTTTUGGGAA
336401109	70258	GTTCCATCUCAGCCAGACGAAUA	70259	ACCAAATTAAAAATAUGGAATAAGTATGGCAUT
255990823	70260	ACCTTCCATTCUTCTACTTTTGCATUGA	70261	GTTACATCAGTTUGCAACAACTCTUGAA
261890485	70262	GCTCATTUCAGCCGCCTTTUT	70263	CGAAGGTCTUCAGAAATTCAATGACUT
254939221	70264	AGUTCAGAAATUGCCACCCAGT	70265	AGAACATCTCAATUGCAATCTGCCAUA
255712361	70266	CUGTATTTCUGAGAGAGCGGAAGG	70267	ACCATTTAGAAAUAACCACAGCCTCUT
255317963	70268	CCATGGGAAAAGUTGAAGAATTTTGGUT	70269	AGCAAAGCCCUTGTTAAGTTUGAC
325017659	70270	CAGCAAGAAGACUGAACAGTACUACT	70271	CAGACTCCCCCUTCAGTACAUC
257749532	70272	GGAAAGAAAAGUCCAGGAAGGCUAT	70273	GAAGCTGGAGAAGAUGATCAATACTCUG
316195671	70274	AGAGATCGCCAACAUGTCACUG	70275	AGTTGCCTCCUCTACAGGAAAUCT
315880890	70276	GCTTACCGCAUCCACGUGAA	70277	ATCTCGAGUCTGCGUGGAAC
313916389	70278	GAAUGCCATUCACACCAGAAGG	70279	TGAGCCGCATUCUGAACGA
278482519	70280	GTGGGAAAGUGCTTGCCTTUG	70281	ACCCTAGATTCAUTTCCACCAGCUAT
279644234	70282	GCAGTCCCCAUCATCCCUGA	70283	TGGACUCACTCTGUACCCAAGA
260738028	70284	AATTTTCCTUGCAACGTTAGCTGUT	70285	TGCTCTTTTTGCAAAUGTTTCACTCUC
240139242	70286	ATGATGGUGAAGGATGAATATGUGCAT	70287	GCAGTGCTGGUAGCATTAGACUC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
323787288	70288	AGAAACATTTGUTCACTCCCGUGT	70289	CTCACTGAGGUTTCTGTTATCTTCUCT
269258245	70290	GCAATAGUAACCCCTGCCAGUC	70291	AGAAAGTCAAGTCAUATCCCATCTCCUT
262516404	70292	TGACTCCACUGGTTATGTCATCTTUACT	70293	GGGAGAGTTUGGAGTCAGCATUG
313318839	70294	ATTTCUCCCCAGGCCTACTTTUC	70295	GATUGAGCGCTCCUCAGACT
268226363	70296	GCTCTCCCUGTGGCAGAGAUAA	70297	GCCATTCTTCUCACTGGTCATUCC
268842715	70298	GTCAGCCCUGGTUCCAAGAA	70299	ACUGCTTGCTUCGAGCGT
267159537	70300	GGTGUCCACCACACGUAGT	70301	CCCAUGATGCTTCAAUAAGACAAACC
318315971	70302	CCTTCUGGGCCAGGTUGAT	70303	GGCUGGCATCCUGGACAC
318334464	70304	GCAGGTUGTAGGTCUCGAGAGA	70305	CCAAGGAACGCAUGATCATCAUCA
320629976	70306	GTCCUGCCCTUGAAGCCA	70307	CGCCAAGGCCUACAGUGA
320655542	70308	CTGTAGCAGGCUGTCCTTTUCA	70309	CAAACTGCUGCAGCTCAAGUC
318016816	70310	CCAGCUTCUCCGCAAGCA	70311	CGAGGGCUGAGGAGGAGUC
320498829	70312	GGGTGAUGGTGTGGUCAGA	70313	CUACCGCGAGAGUGCAGA
320082493	70314	TCTCCAGGUAGAUGGCAGACA	70315	CGGTGAUGAGTGCGTUCCC
319850440	70316	CCGUGCAGCCCAGACUC	70317	GGAGGCACUGCGUAGGAA
235586852	70318	GGCCGGUGCAGATAGUCC	70319	ATGGCCUCGGCTGGUAAC
240421317	70320	GGCTGAGUGGGCTACGUC	70321	GATGTGCTGUTGAGACCTCUGT
241626667	70322	GCCTGACGACUCGTGCUAT	70323	TCAUAAACATCUCGGGACAAGCC
313130827	70324	CCACCACCCACAACUTACTAAGUG	70325	TTGGGAGCTGUTAACCCTTAATUCAAT
315080186	70326	TGTCAGTTCCAUTCAAATCTTTCACUCA	70327	CAGTGCCAAUCATCCCTGTTUC
262698536	70328	AACAACTAAGGAAGGAGUTTTAGGCAUT	70329	GAGTCAGAUGATCATTGUCAGAGAGAAC
264092387	70330	AAGACTTCCCCCUCTTTCTCTUT	70331	CTGGTAATTTUCCTACCTCCTUCGT
266666952	70332	AAGACTGCTGAUTGTACGTTCATATUCA	70333	TAAATTGTAAATCTTAGGUAATCAACTGGCAUA
255323449	70334	TTTCCTGTUCCCAGGCTUGT	70335	CAATGTCATTTTGUGGTATTGGTCUGAA
266325855	70336	GACATACCTCCAGUTCATTTTCCAGUT	70337	TCTAGACTCCUATTTTATGGATCUGCCAT
266342306	70338	TGGATTTTCTUGCAGAGTCATTUCCT	70339	ACCGTGACUACACACAATUCCC
263256119	70340	CUGCAGAAGGGCCCTCUAAG	70341	CGTGGCAGUCACCAAATACUGT
325261866	70342	CTTTTTGAACUGCACAUCCACCAG	70343	CTGAAGCCTCUTGAAGGTAGTGUA
324224185	70344	TCACUGACCCUGCAGAGAAAC	70345	GATTGGCAGAGAUCTGCUACCT
230585232	70346	TUGTAUCCCCAGCCACGAAG	70347	CTTTCCAGCAGUCTGTAGCCAUT
278696811	70348	GGATCCAGACAUCTCCUAGGAACT	70349	CCGUCGGAGAAGGAAGGTTUC
316560903	70350	GCAAAAAGAGGUGCGGUCAG	70351	CGCCCTUAGCCGTTTCTTUGAT
279048269	70352	CAGGCACAGAUGTAGCTCUCAT	70353	CCATAGGGUTCTCTCUGGAGAGG
238074839	70354	GCAGCCATAGUGAAGGACTGTUG	70355	CAGTCCUACTTCCAGUCCAGGT
261673372	70356	TGACCTTCGUCGCTTATGCAUAC	70357	GTUAAGGGCCCCAACGGUAAA
240856033	70358	CTCACAGTGUCCTTCCCCAUT	70359	CCCACCAGTUTCATCGAGTTCUA
314449350	70360	CCATGGUGCCAAGGAGAAGUG	70361	CGCUCCCAGAUGGAGGAAGAT
314404310	70362	CAGGCTGUGCCATTGTCTUG	70363	AGATGTCTGGCUGTTTCTGGUG
314683640	70364	CCAAAGGGTUATAGGGCACCUT	70365	AGTGTCTGCUATCTCCCTCUCC
262747581	70366	GAAGATTGGGAGGGUTTAGCATUACA	70367	CAAAATATUGGGAGGGTCTGTCUCA
267524184	70368	GGUCACAAGGGCCAGAGUAAC	70369	GGTTGCACCUTATACTTTGTCUCCT
265641210	70370	GTGGAGTUGGCTGGGTUGT	70371	TCCTAGCUGACGGCTTTTACUG
317503231	70372	GAAGGGTTGUGGGCTGAUCT	70373	GCTGGAGGCACUAATCCCTUG
316891062	70374	CTCGTGUCCCGGGTGUT	70375	CCTCCUCGGGACUCGAC
320624529	70376	TGGCATCAUCGATGTCGTACUG	70377	AGATGTCAGTGUACGAGGCCUA
321423191	70378	CAGGGCUACAGUCAGCGT	70379	GCACAGCCGUCCCACUG
320197921	70380	GCAGGCAGAGGUCUCCAG	70381	CCACUCAGGGCCTATUGGT
319789605	70382	GGAGCCCUGCTACCTTTCTUG	70383	AGAGCACCGUGCCUGAG
227746753	70384	GCAATAACTUAAACCCAGACTGAAGAUG	70385	AGCAGTCTGUAAGACCAACATTGUT
230596386	70386	GTCCCAGACCAGUAATGCCUT	70387	TTGCCCTCUGACGTATCTCUCT
232122924	70388	CTGCTGTCGUACAGTCTTUCCAA	70389	GCCAGAGTTCUTTGAGGCTGUAA
229973491	70390	TCUGCCCAAGGUAAGAAGAGAT	70391	GCACTCAGATTUGATAAAGAAGTTGCUC
235195980	70392	ACTGTCGTCUGGGAACTATACUCC	70393	GCAGGTAAAUGGACAAGAACACTTTUAA
234957680	70394	ACAGCCCCAGGCUCGTAUA	70395	TCCTAACCUGTGCCCTTCUCT
237549971	70396	GTGTTTTGCUCTCCACCCTUCT	70397	GAAATGCTGAAUAAGGCTGAGGTUG
238818258	70398	CAGGAGCGAUCGTTUGCAAC	70399	GGGAGAACAGGGCUGTAUGGA
238886903	70400	TTGGAGAGGUCAGGAGATUGGT	70401	TCTGAGAGGCCGUCGTCAUAA
231197582	70402	GAGACCTTCUTCACCAGCUCAC	70403	GGCTGUCAACCGCGUCAT

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amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
258522617	70404	ATGCTACTCUAGAACTATAAACACAAUAGAAGT	70405	AGGCAAATUAAAAGACTAACCAGUGGAT
257364253	70406	ACACGTGTUGATGTTCACCUT	70407	GGCACUTAGUCGGGCACT
263800397	70408	GGTCTTCCTCAUGTTTCTTCACAATTUC	70409	GACATGCAUACCAGTCTAGATACAUACAT
256690543	70410	GAGAATTAATGAUACTGGCACTAGAUGGT	70411	GAGTTGTGATTCUCATTGCTGGATTUT
264475935	70412	TGGCTTGGUTTGAAGAAGGUGA	70413	CCCGCAAACAUATTTTTACUCAACACAT
265643103	70414	TCUGAUGGAGAGGAGCACACA	70415	AGAAUAAAGGGAAGAAAGUCGCCAT
265257730	70416	CAATGTCAAUACAACATGGGCAUCT	70417	CGATAGCTCTCAUTTCACATTCTGGTUA
326097882	70418	AAGCATTAAGAGUATCAACAGTGCUGAA	70419	TGACTCACUGTCTAGCTCTUGCT
229172773	70420	GAGCAGAAGGCAUTATCACAGAUCA	70421	GGGATTTAGTUGAGCCTTACGUCT
317795818	70422	GAAGACAGACCGGCUGCTUA	70423	GTCACTAAAGUACAGTGTCACTUGCT
314714909	70424	GGGATCTUCCAGTGGGATCUGT	70425	CCTCTGGUAACGTCCTCTUCC
315353271	70426	TGCATCUCCAGGTCAGCUCT	70427	TGTGATCAGGAUGGGTGTCTCAUA
316832733	70428	GATCTCCGGUGTACACAAGCUC	70429	ACCCACGAGUCTTCTACTCACUT
315976071	70430	GCAGAACCCCAAUGCUAAGG	70431	CCCTCUGACCACCTGTGCUA
279281759	70432	CCACCCTCUGACTGGCCUAT	70433	GAGAGCCGGGAUCCCCUA
239527302	70434	GCATAAGCTTGUTTTAAACAATTCCUAACCT	70435	AGGCTGGAAUGCAAGCUCAT
237089025	70436	GTCTCGAGCCCUGTGATUCAA	70437	GCCAAGGAAGUCCCCAAGUAG
267997200	70438	CCTTCTCTCATUAGGTATTGCAAAUGCT	70439	CAGGCTCTTTTUCTGCATGCAATATUAT
260009669	70440	TGUGGGAGACAGAGCTATUGACAA	70441	TCACAGTUTCCTCCAUGCAAACA
313966381	70442	CATAATGCCUCACCUCAGCAAC	70443	GAACCACACAUTGATTCACTGTUCA
313445591	70444	GAACTGCUCGGATCTGCUCAAT	70445	GAGGCTACUGTAATCGCUACCC
267270069	70446	CCAAAACGGUTGGCATUCCC	70447	GACCTTTCAACCCUCTCTGATUCC
266333449	70448	TGCATTCAUGGACACCCAUGT	70449	GCTGCCCAUGGTGACTUCAG
261406601	70450	GGGAGATAUAGGACAGAGTCAGTAAUC	70451	GAAGGTCTCTCAUGCTTCTTCTGUT
262244074	70452	ACACTCACCAUCTCTCCTTTGUG	70453	TGGGAATCACTUCTTCATCTGCTTUT
268930773	70454	GGGAACAGGGCUCAGGGATUA	70455	CTCCCCCTCAUCAGACTCTTTTUC
261781026	70456	CAGGAUCACAGAGGGTTAUAGGGT	70457	CTGCCACCCCAUTTTCTTGTTUC
267990368	70458	CCTCAGAGUCACCCUGAAGGA	70459	GGCTTCATAGTUCTTGGCTCATATTTUT
260804796	70460	GAAGAACCCUGGGAAGACACUT	70461	CTAAAGGUGAGCAAGCCTTGUC
265545987	70462	GGTCTCCACACUCACCCUCT	70463	CAGCACAGGUCTCACTGATUACC
316581658	70464	AACCTCAGCUTGACCUCAGAAC	70465	CCTGATCTGCUCCACCTACCUT
316916378	70466	CTTCGGAGAGACCUTGAGGUG	70467	CTGTCCGACUGACTTGGCTUA
320646460	70468	GUGGCGUCCACGAAGACA	70469	CGCAAGCUGACCTUCCGT
318160656	70470	CTGGAAGAGCGAGAUGGTCUG	70471	CTCAAGAAAGGGCUGCUGAGT
320636979	70472	CTGTACCCUGTCACAGCCTUC	70473	GGGCAGAAGCUGAGTATCUACAAT
320338849	70474	GCCGCCAGGCUCTTCUG	70475	GCGCUGAAGGCGAGCUT
320344350	70476	GCCTCCTCCUTCTGCTTCUCA	70477	CUCCCUGCAGGAGGAACAC
319394198	70478	CCGTGTGUACCTGGGCUT	70479	CUCCGAGTCAUGGCAACGA
232902356	70480	GGACACACGAAGGCAUATATTUGGT	70481	GAAGTACCTGGUCTTAGCATCUGG
230646917	70482	GCAGCAAAGACUTCCGAATUCC	70483	CGCTTGCCUCAGAACAACTUC
230564557	70484	GGAAAGAGUTGCUGCACCAG	70485	CACATCCAUCGGCGCTTUG
238703788	70486	CCAUCTCAGTGTUCAAGGCAGAT	70487	TCTCCUCCTCCGUGCGAA
315114129	70488	GATGTGGUCACGGATCUGCT	70489	CCTCTACACAUGCTACCTCCAGUT
257539733	70490	CTCACCTTGUCACCCTTTAGUCC	70491	GTAGCTCACGGUCACCTTCUC
265267947	70492	GAGAGAATGCUGGTGGCUGT	70493	CCGCTCCUCTGACCTCTUG
257547016	70494	CTGAUAACCCAGGCTCATGUCC	70495	GCTCTGATTTCUTCCTCCCCTAUC
264393013	70496	GGGAAGACCCUAGGAAGAAGUG	70497	GTTCATTCCCUGACCTGCTGUT
262345535	70498	GGTACAGGAGGAGUCACUCAGA	70499	CGAGCUCAGCAGCTAUCACC
320629917	70500	TCAGGAUCAGGCCCTTCTUCAT	70501	GTTACGTCAUCGACCCCAUCAA
320756515	70502	CAGCCCCUCACCCAGTUAG	70503	AAGCCCAUGTGAGGGTTUAGG
318020525	70504	GGAGCTGCUGAGCACCUT	70505	CTGGCCGUGTGCGACUA
321585115	70506	CCCAGCAUTTTGGAGCUCCT	70507	GCCGUCCCCTATGGUCAGA
319034902	70508	GCCGUCAGCGATGTCAUCAT	70509	GTTTCCACAAGCUGCAGAATGUC
230667946	70510	CCAAGGACUCUAGGACACCAACT	70511	TGTCAAGTTCUAAGACTCTGTACTCUGG
230981295	70512	GGAGAAAGGTUCATAATGTAAGCCUCT	70513	TTGCATAATGCCUTTACTGACCAAAAUT
237376621	70514	GCCAGAAUGCCCTTCAGUAGA	70515	ACCCTTCUAACCCACCCUCA
236304261	70516	GGGTAGCGUCAACGGAUGA	70517	CAAAGCCGACUACATGCCUGA
237010380	70518	CUGCACGCCGATUCGAAG	70519	TGCTTCCUGGGAATACTGATGAUG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
242225366	70520	GCAGUTCTTGUGCCCCAACA	70521	AATGAACTGAUGGCATGAAGGUGA
234683263	70522	GCUGUGCCAGCGACAGT	70523	CGCAUAGUGAGCCGAGAGG
314805685	70524	CTTCCTTCTTTCUCTCTCTTTGGCAUT	70525	CCCTCCUGGAGGTAUCCAAGA
254412240	70526	CCAAACAAACUGTTCAUCAGGAAGAAA	70527	TGACAGTTCAACUAGAAGAGACTGGUAA
263532772	70528	TTTCAACTGTUCATTTTCTCTCUGGACT	70529	GCCTGTTGTATTGUTGGTACTTCGTAUT
258870436	70530	ATTCTTTTTCTGACUCCAAAGCTCGUA	70531	AATTGAAAAGCCAAACACUGAAUGGT
257373173	70532	TCTGCCCGGAGUTCTAAAAGUG	70533	AGTTGAGTTGTTAAUTTGTGAAATATGTUCCAT
336400623	70534	TTATCATTTGCCUATTTTTACAATACATTUCGA	70535	CTCTTTCCTCACUCTTGGTCAAACUAAA
261270235	70536	CAAACTTTGTUGATGACGAATUACAGCA	70537	GTGTTGCTTACAGAUTTGGTGACTTTUA
264865511	70538	TCTGTGAATCTATUTGTTTCTGGTAGUCA	70539	ACCGTTTTCCUGTCCTTTTCUGT
263415174	70540	GTAGCAGCCAUTCCUGAAGGT	70541	AACCACGACACGGAAUATTCTAAATUACT
324890300	70542	CCAGCCAGUAACAACCCCUAC	70543	GGCGTGAAGAUGTAATAACCUCGAA
325258276	70544	ATTGAAATTGTCUCCCTGGCCUT	70545	GACTTCCUCACCCCAGUAACC
329574492	70546	CCAGGACUCTGCACAGUGAAAC	70547	TGCAGGTAUCACACAAATTACAGAAGAUT
230673113	70548	CGGGCAGGUTTCCTCATCTUT	70549	GTCTCATGTGTUAAGAGAAAGCTAUGGT
313089502	70550	ACAAGGGAAACUGGGUGACAG	70551	CGGCCCCACCAUGTATCTAAUG
314255787	70552	CTGCCAATCAUCTCCTGGATCUG	70553	CATGGUAGGAATAGUGCCAGGAA
313212016	70554	CAGGCGGUCATTGAGGTUCT	70555	GTCTCATCCUCCCGCTTCUC
278700239	70556	CCAGAAGGGCAACAUCCAUCT	70557	AGGAGTCCUGCTTCATTCCUCA
278719167	70558	TGGAAAGAGCUGCAGGUGAAG	70559	GTCTTCCCTCUCCTCCTGCTUA
278318901	70560	TGACCCTCUGAAGCACTCUCT	70561	GGTGGCCAGGUTGATGAUGG
326795490	70562	CGUGGCAGGAAACAUCCCT	70563	ACTGCTCAAAGAAACUAATCAACUGA
266924221	70564	AACCAAGGGCUCAGTTTGUAACA	70565	CCTCTGCAAAUATTACCUCCACGA
268817200	70566	GGAGTTGGUAATGGCAGTAGUCAT	70567	CAAACACCUCCATTGUGACAGG
260070381	70568	GTTAAATGUCTGCAACUCCAACCC	70569	TTCACAGTUCACACCAGTGTAUCC
314046978	70570	TCCAGGAAGUGGGACUCCAT	70571	GCAGGTCUCCGACAGCUC
313326684	70572	ACUCGCCAGGTCTUACCGA	70573	TGTGGTAUGCCAGGAGGTTUG
264583071	70574	GGTCAAGUCAGCAGGGTTUGT	70575	AGGAGUACCAGGACCCUGAAG
264795633	70576	TGCTGCCCCACUCCTCAUAT	70577	CAGCCCUGACAGAGCTCTUC
260899590	70578	GGAAGUCCCACAGCTCCAGUA	70579	CTCATGCAGUCTCTGGGTTGUT
267683160	70580	ACATCTCCCUGGAGGUGACAAA	70581	GCCAAGCUGTATCTGTCCUGT
264293767	70582	CCCACUACACATCACTUGCCT	70583	CGAATAGGAAUAGCTGGACATGTCUA
267212391	70584	ACCTTTCUGCCCTTCCCACUA	70585	TGGAGACAGCUTTTTAATCAAGTTCUGT
316789740	70586	CCCAAUCCCCAGCACATUCT	70587	TGTTGACTCTUCTCTGCCTTGUG
316909762	70588	AGGTGAACCUGGGTCCTCAUA	70589	AGAAGAACCGAGACUACCCTCUG
316365871	70590	GTGAATGAAACCAAUACCTCCCAUCA	70591	CATTGCCAUGGCTGTGAGTUAC
316597329	70592	GCGGGCCUCCTTCCTUC	70593	GCUACGUGCCCGAGGAT
318325793	70594	TCCAGCAGGAAGCCUGUG	70595	CTCCGTGGCUGGTGTCUA
320649773	70596	CCACCACACCCUCCTUCAC	70597	TGUTGCUGAAGGCCACCA
319113940	70598	AGUGGGAACGCACTCAUCAC	70599	GCUGGAGGCCTGUGAGAC
318030589	70600	CAGCAGGUCCTGCAGGUA	70601	GGTGUACCGTCUGCACGAG
228762684	70602	GGTCCCAAUCAGAAAATCAUCCCT	70603	CACATCAUCTCTGCUACCCAAGAT
230193234	70604	CAGACCCUCGGACAGGUAAC	70605	GCTCCUGCACAACAGCUGAT
329438869	70606	GGGCCTGAUGAGGAGGTCAUA	70607	CCGTTTCAATCTUAATGTTCATGCTCUT
228759355	70608	AGAAATGATUCCAAGCATCTCCTUCAA	70609	TGTCAGCTGUAGTCTGCCUCT
238120409	70610	TCUCAACCGGAACCTCUCCAT	70611	TCCCCAGACAGGCAAUAGGUA
241505630	70612	CCCUGGCTCCUGGAAGAC	70613	GTGAGGGCCCGCUCAUC
222176902	70614	TGTACCTGTUCACATTCAGACUCAAAT	70615	CTTCTTTGUCTCATGGGUCCCAA
224580728	70616	CCTGAAGAAGUGATTCGTAAAUGCC	70617	TCTAGAGTTTCUCCTCCGATGGTUT
233055134	70618	CGAGGGUGGTTGGAAACUGAT	70619	CTATCGGGAUGAACACATCUACCC
313259503	70620	GGGAAACAGGGAUGATUGGCA	70621	TGCTCATCCUCTGACAAACACTUC
258522853	70622	AGGCTTTTTGTUTCTTTTGCAGTUCA	70623	ATCATTGATACTTCUTGAAGAGTCATGAAUAA
256206705	70624	CTGCTAACCTUAAAGCAGATTCTTTCUCT	70625	GCATGCAAAUAACTGCTGTCAATUAGAA
262012757	70626	TGGCTAATTUCACAAGGTTCAAGAAUCA	70627	TGCAGCTCUCCAAAAAGTTGTAGAUAAT
263717271	70628	AAATCAACTGGAUAGTGACAGACUGA	70629	AAGAGATTTAGAAAGGAGUAGGACAGUGA
261110657	70630	GGGACCAGGUGGTAGAAGAAAUT	70631	CCTAAGGGAGAAACUTAAGAATGCUCA
264122812	70632	TGTTGGTGUGCTGATGGUAAGAT	70633	CCCAATGGACAUCATTTGTTTTCTGAUT
263531509	70634	CATGCUGGATCCUCCGAGAAT	70635	CCTGTGAAAGCUTTTGACGUCAC

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
264016644	70636	GCGGGCAAUCUACAACAACAT	70637	ATGACCCATTUAGATAAAGGCGUACAG
264919889	70638	ACAGCCTTUCTAAAACGCCUCT	70639	GGTCCUGGCACTGATTTAUAACCT
265652469	70640	GGGAGTCAUTGACCCCAUCC	70641	GGGCAAGGGUAACTTGAGGTUT
255318384	70642	GATAATATCCCGUGGACCGATAATTUCC	70643	GGCTTUCACAGGCTTTCCTUGA
325288844	70644	GATTTTCCUCGACATGUACCAAGGT	70645	GCATGCAUAGACCAATGGGTUT
325294026	70646	TGATGGAGACAGAUTCGCTTTUCT	70647	GAAATTCTGCAUTGGTGCTUAGGA
326098429	70648	GGAGUCAGGAAGAGATATTCUAGAGCAA	70649	TCAATCCACTTTGUGTCTTATCAACTUCA
325048169	70650	CCGAGTCUATATTGCCUGCAGA	70651	CCTGCTTTTCUACCTACCCAUCAG
230710528	70652	TGGAATTTUCCAGGGCACUGAA	70653	ACTGATGGTTUCACGGCTGUC
230162479	70654	GGCCTTCUGGGAAGATCAGGUA	70655	TTGCTGTGACUATGTCATGGTTCUT
257758857	70656	GCACUGGCAGTAGTUGAGGAT	70657	CUAAGGAACCUGCAGACCAAGG
255521640	70658	GCATGGAGGUAAGCAGGATCUC	70659	TGAACAGUGTGTCUAGAGCAGAGT
316739954	70660	GACGTCTTUAGCTTGGCCAUC	70661	AGAGTGAGGCUGGCTCTTTTCUA
317921586	70662	TCTTCAGCAGCUTTACCAGCUT	70663	CGGATCAGAUCCTCCAGGTUAC
280307613	70664	GCTCAGCTAUCCCCTCTCUGT	70665	AAGTTGTGGGUGAAAGAGGAGUG
316840287	70666	TGCATCTTTCAUGAGGGCACUT	70667	GCCTCATAGUGGAAGGCUGAC
239529723	70668	TCTTTTCTTUAGGGCCTGTUCACA	70669	GTGCGTTTCAAUCACCACTAAAUCAAT
326246617	70670	TGCTTGCUCAACTCAGTGCUT	70671	GGCTGAAGUGGAGATTAACAUCCC
323464349	70672	AATTCCTGAGAGAGAUGAAACATTCUGG	70673	TGCCTGTGCUCATGTTTGACUT
326163334	70674	GGGAGUCTGCACUGAGAGAC	70675	GGCTTCTUCCTTATTCTUCCACCAT
262528523	70676	CUAGAGCGCGGCAGACUA	70677	CAGGUAGGCCACCAATGTAGAUG
312699224	70678	CATCCGTGUCCAGAAGUCACC	70679	TGAGAGGUGGGCAATTGTGTUT
312855913	70680	GCUTAATCCUGGGCAGAGAGAA	70681	CCACAGACUCAGCTACTGTTCUG
315315983	70682	CGGTUCCGGAAATAGUGCAG	70683	TCAGCCCUGGGACTCTCTUT
266338123	70684	TCACCAUGGGCAGCCAUC	70685	TGCCAGGGCCAGUTCAUC
262377862	70686	CCUTCCCCCUAAACCCCAGA	70687	CCGUGACTTCTUACCCAAACCAA
260050011	70688	AAAACCACGACCUCTGACCUG	70689	CAACCACUGCTCCATCCUCAT
315845253	70690	CAGCGTGAGGGUCCTCTCUA	70691	GGCAUCCCCATCACUGAGAC
320615834	70692	CCTTATAGGAGAUCTTGAGCTTGGTCUT	70693	GAAGAAGGGCUGGCTCTACUAC
318017000	70694	GCCAGCUCGGCTUCCAG	70695	CGGGAGCUGGCUGAACAA
318020797	70696	GUGACAACGUGACCCACAAC	70697	GGGCTGUCTAGCCUGGA
235339049	70698	GGACAGUGGACTGCATGGUA	70699	GTTTCAGCATAACAUTGCAACATGTTUC
238023974	70700	CCCTGUGACCCTGCTTGUC	70701	CTCCCTUGGGCGTTUCCA
264060723	70702	CAGAGCAUACGCAGCCTGUA	70703	GGCTTGUGGGCAAACTTGUG
231999899	70704	GCTCCTCTAGAUCTGCCAGGUT	70705	CGTGGCTCAUAACTCTCTCCTUC
313360462	70706	TGCCUAGAAGAGGCAATCUCCAT	70707	CCTAGGUGGTGGGCUCAGT
257052846	70708	GACATTTTGAGCUGTGTCTCTAGATCUT	70709	GGAGGCAGCAUTAAGTGTTTACAUC
263797526	70710	GGUGAGCUACAGGAGGAAGAAT	70711	TCACAGATTAGAACUACAGGCTGAUAGT
257157294	70712	TCTGTGAGTUAACACTCTAGACTAUGCT	70713	CCTGATGTCTUCGTGTATGTGTCUG
257010803	70714	AAAGCCAGGUAACTTGAACAGUGA	70715	GTCTGCAGGUGGACGAGAUAC
260610601	70716	TGGCAGATCCAUAAAATAGGAGTCUAGAA	70717	AGCTGGCTUTGGAAGAAGUAGAAAA
264156791	70718	CCAATTAAGCACCUTGGATAAGGAAAUC	70719	TGTTTTGTUACAGAGGUGGAGCA
266764781	70720	CCTTGTGTCUGTTGCCTTAGAUGT	70721	CAGGCTCATATUCCTTAAGGGCTUC
260491702	70722	GGGUCACCTGTTUCAGAGGAG	70723	CAGTCTCTGUAGCTTCTCCAACUT
254718370	70724	AGTCATCAGAUGTACTGCTCCUCAT	70725	ACATAGGCAUGGATGACAGGUG
230804203	70726	GCAACAGCAAUCCCCAAAAUGG	70727	CCTTTCCUGACCCCTCTTTCUG
263730223	70728	CAGAAACAGGGCACUGUCCA	70729	GCCAACAUGTTCGCCUACCA
317811584	70730	CAGUGGAGCCCGAGTACTTUG	70731	GCTGGUGAAGCTGAATUGAAGGT
277849702	70732	TCATGGAGAUGCTTAGCCUGAGA	70733	CCACCGUGAUCCAAGACACC
317216289	70734	GAACCTGCUGAAGCCUGACA	70735	GAGACCCCUCTCCCCTAGTUAA
280065868	70736	GCCUGAACCTUCCACCCT	70737	CGTGGAAGGCCCUCTGTUC
278953812	70738	GTACGGGUGCCCCTCUT	70739	CACUCUCCCCACCCAGAC
280286172	70740	GAGTCGGGCUCAGAUGAAAGG	70741	CTATGGUGGCTGGAUGACAGAT
239063375	70742	CACAGGAGGAAGUGCCAATAUAGT	70743	TCCTGGGCAAGUTCTCUCAGA
264217566	70744	TGUTCTTGTUCAGACACAGCCAAT	70745	TCCATGTUGGCAGGAGTTCTUG
261030069	70746	GGTAACAGAACAUTTGACAAGUGCT	70747	GCATCCUGACAAGTUGCACCAT
314227812	70748	TTTTTCAAACUGCTCCCTCTUCCT	70749	GGCAAAACTCCCUCCTATATTTTAGUGT
313455109	70750	TCAUAGGTCUGGAAGCAAGGGT	70751	ACCCCTGUCTCTGACTGUCAT

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
267566178	70752	CCCATCCUGACTCCCTGUCAT	70753	GACACAAAGGAGAGAUGGUGAGT
265799248	70754	AAGAGAGAGUCAGCAGCACTUG	70755	TCCTCGUGAGGACTTAGGAUGG
267937034	70756	CACCCUGTTGUGGCGAAAAAG	70757	CCAAGUGAGGCCCAGATUGAG
266385969	70758	GGGAAGUGGGAGTTAGUGGAAG	70759	CCTGAGGGCUCCTATTGACTATAAUCAT
257710004	70760	CCATTACUCCAAAATCCACAUCAGAGG	70761	CCTGTGCAGTAUGACTTTTCTCTCUAT
260813984	70762	GGAGAGCCCUGCAAAUGGAG	70763	CCCTTCCTGUCCTGACCTCUT
265413055	70764	CACTGACACUCAACCCATTCTCUA	70765	GTTCAACCUCAAAGAGACCCTATGUC
257320805	70766	CCCTATUCCCAGACCCCTUC	70767	AGGGTTCUGACATGTCCTUCCT
261895822	70768	CCACCACCUATCACTCCUGACA	70769	TCCTGCCUGATCCCCUGAT
315719151	70770	GCGAUCCATCUGGACACCAAC	70771	GGAGAGGGAACAGGUCGUAAAAAC
318323604	70772	GACACCTUCTCCAGCGUCT	70773	CGGCACGCUCTCCAUCAC
318341315	70774	TCTCTGTCTTCUCAATGATCTCGAUGA	70775	AGGUGTACACUGAGGAGGAGAC
320632667	70776	GAAAGGTCCUTGACCGUCGT	70777	CCGTGGAGAAGGUCATCAAGATUC
320275634	70778	AUGAAGCCCAAGCCUCGAA	70779	CTATTGCUCGAGCCCCAUGT
320713379	70780	AGCCCCCUCCTGGCTTUA	70781	GCAGGCUGGAGTGTCTUCA
321049913	70782	GCTGCGTTUTCCCAAGGTUC	70783	GGGAGAGTUCAGTGTCTAGGTUA
228458041	70784	CATTCAUCCCCCAAGUCACAAGAA	70785	ACCCCTTCAUTGTGGCACUC
231279030	70786	GGCUGCAACCAAGUACAACAG	70787	GTAAAGACAGUCCTAGGGTGGATUG
230553247	70788	ACTCCCUGCCCCGAGTAATUAT	70789	TGACAACCCCUCCCTCAUGT
261489208	70790	GGACGUGCAGCATTCUAAGGT	70791	CTTGTGUACCGCCUCACCA
239566285	70792	GCTCAGAUGACAGCCGGTUCT	70793	GTTGCCTUGACCACTTTUCCAAA
223430134	70794	AGCAAGACCAAUTATTAAAGGUGACAGT	70795	GGAUGAGTUGAAAGAACAGAAGCAAG
314830220	70796	CAUAGCCACCCACUCCACAAG	70797	CUCTTGCUCCACCAGGAACAA
262699129	70798	TTCAAGTTTTCCUTCTGAAGCUCCT	70799	GCTTTCACCAGAACACUCCGATUT
256200857	70800	GTGTAATCCAAUCACATGCAAGUAACAA	70801	ACAUGCAAGCAAGGTTAAAUCAAAAAGA
258559163	70802	GTCGCTCCAATUCTACTAAGGTTGTAUAT	70803	AGTAATATGGAUGTGTCTTTGUGCAGAA
255474517	70804	AGATTCAGGACUGAACCCACUGA	70805	GUCAAATGGCUCAAGAAAGAGGAAAAAG
263269505	70806	CCCAAGUCCACGTACCTCTUT	70807	GAGTTGTGGTUGTTTTTGGCAGAUA
260697217	70808	CTTCATTACCUTTGACATCUGAGCCT	70809	TGAGCAAGUGACAGTTGTCTCTUT
256392516	70810	GATATTTGCUGCACCCCTUCC	70811	GGCACTUCCACCTGGGAAUT
325625084	70812	CAGACTACUTGGCAAGCUAGGG	70813	CAATTCTCATUAAGTACCTTCUGGAGCA
323866485	70814	GAGGUACTTTCCTTTUGACCCAGA	70815	CATCCCTGAAGTUGAAATGTAGATGGUA
326339242	70816	CTGAGTCAAUAAGCTAGAGTCCUCCT	70817	GTGACTTCAAGCUTCAGATCCTCAUT
325826131	70818	TCUCAGCTCCAUGAGGAGAGAAAT	70819	CCCCAUGAGGAGGTTTTCTCUT
325286954	70820	AGCAACAGCAGCUACAGAAGUT	70821	CTTTGTAAACGAUTGTTTGAGTTGCUGA
228498560	70822	CCTGGAGAUAAGCAGCUGCAC	70823	TCCAGTTCGGAAUGCACTAAATUCA
230799413	70824	TGAGAGACUGACAAGGAAAGUCCT	70825	GATGCACTGUCTGCTTCTCUGT
229932120	70826	GCCAGAAAUCAAACCCGTCUGA	70827	CTTTGTTGCUTGAAGCGGUGT
316281608	70828	TGGCAUGCCTCCCUAGAGAA	70829	GCTCACTTCCUACTTACCTCATUCCA
315027573	70830	GGATGTTCUGGCCCACCATUT	70831	TCCATTTGACAAAUTACCTGUGCCT
278181212	70832	ACCAAGGGACCCUGCUCT	70833	GTGTTCUGAGCGGGUCAGT
317134186	70834	GATATCGUCGGCTACCTGGUG	70835	CCTTGAACTTGUAGGGCACGUT
278080208	70836	CCCCAAGCCAGGUCATCUAAT	70837	TGCGGUCAAGTTUGGAAGAACT
268144176	70838	AATAATGCTACATGUGAGGACAGTGUT	70839	GCAGTAAATAUGTGTGAGCACUGAAG
268003725	70840	GTTTCAGAACAAGGGAUGCAAATGUA	70841	GTCAUGGAAAGGGTCACTUCGT
264905293	70842	GTATTCAACAGGGACCUGGGTUT	70843	TGCCAGAAUAAGAGAGAGACAUAAAAGGA
267390340	70844	CACGGGACCAAGUCACUGAAA	70845	CUGACGACCGTTUCCAACC
268268222	70846	GCATAUGCACACCACCTCUAGT	70847	GGACTGACUTGACATCTCAUCCC
264252976	70848	GCCCUGGAGAGAUGAAGACAAA	70849	TTTCCCCACCUGGTCATTCTUG
261647792	70850	CAAGGAUACCAGGAGCUCCAC	70851	TGCCTGAAGCAUCCTTGTCTUC
267980943	70852	GCUTTCCCTGUGGGAACAGAT	70853	TGTGCCCCAAGGGAUATCUCA
268293174	70854	TGAUGCAGGACGCUCGAAG	70855	CGGGTGAAUCAATGTGGGAAUG
265735642	70856	GGTGGCCCCUGAATGUAGAGA	70857	TCTAGCCCUGTCTGTCCATAUCC
267995835	70858	AGAGTGUGAGGCGGTACUCA	70859	TCTGCTGGUCTGACCCTGTUA
315542977	70860	GAGTACAUCATGGACCUAGGAGGAA	70861	CAGGACAAAGGAUCCATUCAGAAGT
320635554	70862	GTACGTCUGGTGGTCAAUCAGG	70863	CTGATGGAGCGUTGTATCACUGA
318156048	70864	CTCCTCCAUGGTGATCTGCUT	70865	TGGCUACCUCAACAAGGACAC
320651300	70866	CACCUGCGAGGCAGUGA	70867	CTGGUGGCCAGCAUGGA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
318201371	70868	GTAGUGGTGGCUGCAGGAG	70869	CTCAGCCCCACGUGCUT
318302503	70870	CACCAGCUCCCGGTACUC	70871	GTGGAUGTCCCUCAGCCC
318686539	70872	CCAACGUGTCTGAAGTUGCCT	70873	GGCAGUCGGAGGACAUGAC
318376529	70874	CCAGCCCCACUAGGUGAGA	70875	CGAGGGAGGUCTTGCUGGA
318551435	70876	TCTCAGGUGACACCTCCUCAA	70877	CCACCUCCGCCAGUACC
321491808	70878	CAGCGACCCACAGUGUCA	70879	TGGACTCUGCCTGGUGGT
229976759	70880	GCATACCCAAGACCUTGAGUGAAAA	70881	GCATTGTACAUAAAAGGCACTUGCAT
236582605	70882	GTGAACUCCACTCCTAUGCCA	70883	GATCUGAACCGAGGACACCTUAG
235708085	70884	GTGCAGCAAUAAAGTCATATTCTCUGG	70885	CTGACCTTGUGCCTCTTCUGT
237339958	70886	CCTCCGTCUTCTCCCAGUCT	70887	GAAACAGGCTUGTAATTGTGAGUCC
238920142	70888	CCACTCCAUCTGACTCCCUGAT	70889	GAGAGGAAGGAUAGUGCAAAGGG
260179443	70890	TGCTTATATGCACUTACTTTGACACTUCA	70891	GCACAGAAGGUGGAACAGAUGT
266925051	70892	GACTTGUAAATCAGGTUGCGCAAA	70893	TGGTTTAGAAGAUGCTGTCGTTGAAAUA
261993725	70894	GACAGACAAAAAUTCACATCCUAGAAAAAGT	70895	CAGGAAAUGGAGAAGATGACTGAUGAA
254975735	70896	CACCAAAUAAACCAAGCAGGACAUC	70897	GACUCCAGAGGTCAUAGGAACCT
266025745	70898	GCCACATUAACAGCCGCCTUA	70899	GACATAGAGGAUCAGGAAGUGGAGT
324857358	70900	GGAGAAGCCACGUGCTCUA	70901	CGACGCAGUGGAAAUGCC
326429717	70902	GGCCACUGAGATAGAAAAGTUCAGA	70903	CGAAGUGAGGAGAACAAAGGACUAAG
326383224	70904	GTTAATGTGUCCTCGGUGGCT	70905	CAAGTTGCTGUGGACCTCTAATTUG
229505118	70906	GCACAGACAACCCUTCCCAUC	70907	GAGTTGCCUGAGCCACTTCUT
317943657	70908	GAGGAGGUCGGCTGGUC	70909	GGGACAAGGCGUAGUGGAT
315685701	70910	GGCTGGUGGAGATAAUGGGT	70911	CGTCTTGUCCCCGUCACA
263539942	70912	TGCTACTTCUGAATTGAAATGGTUCA	70913	GATTACCTACCAUTACTCTGCAGTGUT
235167895	70914	CACTCATCACGAUTTCAGGCCUA	70915	AUAGAGAGTACCUGGGAACAACCT
266706093	70916	TCCATTACAGTCCUAAACCTGAGCUA	70917	GGCAAGGGUTTGAAGAACATUCAT
266814611	70918	GATTGGAAUCACATTACCCUGGAGAA	70919	GGCACUCCTAGCCAUAGCAC
264214798	70920	TCTGACCCAAGCCUTGGAAUC	70921	ACCTCAUAACCATCTUCCAGCCT
268689578	70922	CCTCTGACCCAGUGCCCTAAUA	70923	CCTCCTCUGACCTCACAUGGA
264334519	70924	GCAAAGGGAGGGAAUGGUCAAT	70925	CTTGATCCGAUGCCTCTTTUCCT
260114075	70926	ACCCAUCCGAAGCTCUCCA	70927	GACTGCUCACCCCTAACCAUT
268548206	70928	CAGGCAGCUGTCCUCCAC	70929	TGCCCACCUACCCTGACUT
267698470	70930	ACACUGCGGCCAAAUAGGG	70931	CCTCAGTGGUGAGTGAGAGAUGT
258287370	70932	GGGAATCCTUACCTCTGTCUCCAA	70933	CTTTGCCACAGUGCAGUACAG
320632599	70934	GGATGGCAGCAGGUCTTTCUT	70935	CAUCGACCGCGAGCTCUAC
320339654	70936	CCGCCUCAGCCTTGAGUC	70937	ACAAUACGCAGCGCTUCCT
320339232	70938	CTTCTCGAAGCUCGCCTUCA	70939	ACAAGGCUGACAUCGAGGAG
320344732	70940	CCGUAGCGCCTCGTUGG	70941	AGCAAACGCGCCUCCUT
321184283	70942	GGCUCCGGAAGAACCTTUCA	70943	CTGTGGTCUCAGTTCCTGAAGUT
318181312	70944	CAGAGAUGAAAGGUGAGCACACA	70945	CCAGGTAAGCUGGTCTTGTCUC
329534535	70946	AGTCCCAGAGAGAAUCCAGGTUT	70947	GTTGAGTGCUGACCGTCTUG
237357245	70948	GGAGAACCTUGTCCTCCTCTTUG	70949	AGGAGGGAUTCGAAGGUGGAA
236794396	70950	TGTAGGCAAGGACUCCAUCGT	70951	GCTGCGAGTUATAATGTGTTACAAUCAT
237793618	70952	CCAAGAACTUGCCGCAGTTTUT	70953	ACTCCTCCCUTCTGCTUCGT
242440430	70954	GCAGATGGUCTTTTGGTGUCCT	70955	GGAGGGAAUGCACACAGATGUC
233524291	70956	TCCTCCCAUTTGCAGAUGCC	70957	TTCCCAACCUATGCTTACCTTTUC
262084306	70958	ACCTTTTGGGCUCCTTTGGTAUC	70959	CGACGACAGTUTAGTGGAGCTTUAC
263868400	70960	CTCACCTTUAAATTAGCTTTUGCCAACT	70961	GAGUCTGCATTUGAAAGCCCAA
261087687	70962	GTGGGUCGCAGAGATCTGUT	70963	GGTTGGCAGUGAAAAACATAACATTUGA
254006626	70964	GTGGTTUGACCCACCTCTACUT	70965	AACTUGGAACAGAGACCTUGGG
228334311	70966	TCUATAGAAACCTUCAGGGAAGACAC	70967	TGCTGCGCUCTGCTATCTAUC
228467884	70968	GCUGGACUCAAAAACCCCGAA	70969	TGTGTGAATUGTGCTGTGAUGGT
316010765	70970	GGAGGGATCCUGGGAACAACUAA	70971	AGCAAGAAGACCGCGUCAUAG
316514454	70972	TCCCTCCUGCTGGACCTUAT	70973	TTGAGTACGAAUCTGCCAUCCAC
280796666	70974	GCTGUGCGGGTCUAGGGA	70975	GCGGCAUGAGUGGCAAAG
278589431	70976	CTCATCTGUGCAAAGAGGACAGUAA	70977	ACACCTTCATCUCATAGTCGCAAUAC
260793641	70978	GATGTGCCAUAGACAAGGUGGA	70979	TGCCACCAUAGAGGGTAUAGAAAAACT
240170708	70980	CAGCTCTGUTAGCCCCAUCT	70981	CAATGATTAGGAAAACUCAACTTGCUGA
258245320	70982	GCTAAAGGGCUCAGAGUGCAG	70983	TCCTCACGGUGAACGTCTUG

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
239329642	70984	TGACCCAAGCUCCTAAUCCGA	70985	CCCAATCACUCAGTCTAGTUCACA
323635193	70986	TCTAAGACTUACCCCCATGGTTUCA	70987	CCTTTCATUCACAAGCCCATTUGT
324575720	70988	CTAAATTCCUGAACATCACCUAGCACT	70989	CATGGCTTGAAAAUTACTGGACUGAAAA
314456893	70990	GATUAGGAGCCGTGUGCGT	70991	CTTCCTAGGUAGGTCTTGGCAUAG
313436764	70992	GAGCACACUGGTCACATTUGG	70993	TTTTCAUGGAGCGTCUGCCT
313098172	70994	AGCAUGGCCGUGACAGAAG	70995	AGACTCTATGUGCCTCTAACTTCCTUT
260919681	70996	CCCUGCAGGAAACAAGAAAAUGG	70997	CCCUCACCCGCTATTUGCAT
269077792	70998	CCUGGACCCCCAAUAAACCC	70999	GTTCCAGCAGACUCCCCAUT
320606658	71000	AGGAAGACACCUTTAAGCGTUGAA	71001	TCTCCATGACCUTCTCTTCATCCUC
320634553	71002	CACGGUGGCCTTCUCAAAGA	71003	GGAGAUGAACCGCGTCCUG
320349721	71004	CAGCAGGUTCTTCTGGUGGT	71005	CUGACGCGGAGAUGGAGAA
318016947	71006	GUCCAGCACGCTCUGCT	71007	CGGCGCUGGAGGAAGUC
318017104	71008	TCCTGAAUGCTGCGCTUCT	71009	CAGAGGCUGGCUGAGCA
320499473	71010	CGGCAUGGCCTGGATCUG	71011	CGGGACGUGGAGGUGGA
329893949	71012	CCTGCAGGUTGCCATGACAUAT	71013	GCTCTUGGCCTTCTACUACGG
235857677	71014	GGGAGGCACCUAAGTAUCGAA	71015	GTGTTCCCGUTTCCTCTTGAUCT
237901478	71016	GGGTCAGACUGAGGAAAATUAAAGGA	71017	ATGTCTAAUGCCACCATCCTCUG
241633877	71018	GCGGAAGAUGAAGATTTCGGATTUC	71019	GGTATCTTUCCTAGGCTUCCCAA
328895758	71020	CCCCTGTTGUCATAGGTAGGTUAG	71021	CAGCCAUAGAAAUGAGCAAAACCAG
223038391	71022	TCCAGAAUGAGCATTACTTCUCCCT	71023	ACAGGCAGCUGAAUAAGCCAAT
222658484	71024	ATTTTATTTTUGGCCCTCAACTUGGAC	71025	GATGTAGGGCUGGAAGTGGTUT
233661775	71026	GTGACCUCAGCTGTCTGCUC	71027	ACAGAGGACCCUCTTTCATUACCT
231207483	71028	GAGCUCGGGAACGTTGGUA	71029	GCCCAGAAGACGCUGTUC
312901721	71030	GGCCATGAGUCAGACTGAAAUAGT	71031	GAGCTCAUGAACACCAAGCUG
254310757	71032	ACAGAATTAAUACAGCCAGGTCAUCAAAT	71033	ACUAGAGAACCAATUAGAGGGAAAGGT
259357418	71034	ACGAAGTCCGUAAGTGTTCATACATUT	71035	TGCATGTAGGUAATGAATCTAGCAUGG
255415664	71036	ACAGAATAGUCTGTGAAUGGCAAGAA	71037	GCTGATGCUAGGGAAAAGGAUAAAGAAT
262836401	71038	CCCATGTCUTTGATCTTCGUCCT	71039	CATGTAAGGUACAGAAAGAAAGGUGACT
258809333	71040	CCACCAAAUCCTGCTCGTUC	71041	GAAAATTCAGCAGAAAUAGACAGTUGCT
262284623	71042	CAAUGCACAGCACCGTGAUG	71043	AGAGCAGTGUGGAATACCATCUG
257864635	71044	CATGGTGTUCAGAGGAAGUGAGA	71045	GGCCACAAGCAUTGCTTATGUT
258764375	71046	ATGCCCAAGAUCCTGACTGUG	71047	CCAGAGAAGCUGGGATGTTGUAG
325709091	71048	GAGTGGAAGUTCTCAGAGACUAACAG	71049	ACCATTTACAGGAUGTAGAGGTTCCUT
324900064	71050	ACTGTCTTUCTCTGCCCUCCA	71051	GGCATGGATUGGGCCTGAUAA
228875513	71052	GATTGAAACCAAGCUTGCGAGAAAAUA	71053	TGCAAUGACCCCGTTCTCUC
230455340	71054	CGCCTGGCAAUAAATATCTTAAUAGCA	71055	GGCGATACUGAGGAGGATTTTATTGUAT
319885916	71056	TCGTGGGUCCGGUGAAC	71057	GCCUCCACCCACAGGUC
317354860	71058	ACCCCAGUCCGCCUAAGT	71059	CCACGUCATCGCUGCCT
281054791	71060	CCAGUGACCCCCTGTCCUT	71061	CCCCATAAAUAGCCAGGCUGAG
278521940	71062	CCCTCUCCAGAGAGAACCCUAT	71063	CCCACACCUCGTAGGTCTUAG
279690394	71064	GTGGGAGUAACACTGCACUACT	71065	GTGCACCUGGGATTCAAUGG
264277681	71066	GGATTTACTGGUCAGCCAGCUA	71067	TGGTGAGGCAAAUTAGGTGTGTAUG
239063567	71068	TTCCTAAGGUTGCACAUAGGCAAA	71069	CCCAGCTTCUCTGTCTAAGTAGUAACT
235099002	71070	TGGCAAACAAUACCAAATTTACTTCAUGT	71071	GCCCATAAAGGAAUGTAAACCAACAAUG
257979284	71072	AGGCTGUCGGACTGAAACUG	71073	CTTCACAAGATGUCACTCTGATATCCUT
324581684	71074	TTCAGACACAACAAUTGCTTTCATUACC	71075	GAACAGTGCTTUGAGTATATGCTAGUCA
312994770	71076	TCCTCCAGUCCTGGGAAGUAG	71077	CTGGACUGCTCCAUCACACAT
265749682	71078	TGAGCCTTCUCTGCTCAGUAGT	71079	TCTGTGACTGAUGCCTGTGTUG
257296336	71080	CGACCCAUCAGGACTCAGUCA	71081	GTGATTUGACCCCUGCACCT
320640783	71082	GGAGAACCAGGCCCUTCUG	71083	CGGAACCAGCGCCUGUAT
320631809	71084	TGGAGCUCGCCGUAGGT	71085	CUCATUCCCCGGGAGCAG
320337968	71086	GCCCGUCGCACGUAGAG	71087	CTGGUGCAGACACUGGAGAT
319855583	71088	GCGGAGCGAUCACAACTGUAT	71089	TTTGCCACUCCTTCCTCAGUG
318148558	71090	GGCCTUGGAGGAGTTCTGUG	71091	AGACCTCACCGUCTCATCUGT
232134571	71092	ACTTACAGCAAAAUGGCCUCGT	71093	TGCATGGCTCUTAGATTTGAGTGAUT
237563902	71094	GCGGTCCAUGTAACCAUGAC	71095	TCTTTTCATGGTCUCGTCTCCTAATTUC
236992287	71096	GAACTAATACUCCAGGTGCATTUCCA	71097	GGTGCUAATGTCCUGACCACAG
240745868	71098	CAGCATCTCUACGGCACGUA	71099	CCATGCCAAGCUTCAGTGUCA

TABLE 15

amplicon_id	SEQ ID	fwdUseq	SEQ ID	revUseq
222393209	71100	GCAAGAGCAUCUCAAGCAGAC	71101	AGGACACATTCUAAATCAACACACCAUT
313832034	71102	AGCCATTCCUATAAAGCAUCCCAAT	71103	GGATAGCATCAUCGCTGAGGUC
263014058	71104	AGTCGAAAAATGCUTGTCTCTAGTUGT	71105	TCCATGGCAAACCUTATCTTCTAACTUT
264942688	71106	CATATCCCACUCCCAACATCTAAUGT	71107	CAACAATCUAGGGACAAGGAAGUAGAG
266327620	71108	ACCTGGACAAAGGUACACAAGAUAAAG	71109	CATCTGATATATCUGTGTTGCTGCATUT
254873980	71110	CTCTTACCAGCUTCTTTCUGCAGAT	71111	TGGTGCAAACUACAGATGGUACAC
265358606	71112	CTCAATATCAATUGGTCCCAGGCTUAA	71113	AGCTCCATUGAAGGCAAGGUC
329540886	71114	GCAGAAATAGUCGAGTTGTATUGCCA	71115	CCTGTGAGTTUGCCTGTTTTCUC
229359560	71116	GGUTTGUGAGGACCCACAAC	71117	GCTTTTCTTACCUGCCTTGAACTCUT
228953917	71118	GGGAAGGAACGGUCACCUAC	71119	TCUCTCUGGACACACAGAACCT
229671282	71120	GCACACAUGAGACACAGCAUGA	71121	GTGTCTTTCCAUCTGGTTTCTTCCUT
262982703	71122	CACCCUGGCTCAGCAUGT	71123	CCCCACAGGCAUCGUGAAG
317366529	71124	GACAGUGAGCCAATGGAAAUGAG	71125	GAGAAACCGAUGGCCACCUA
313938660	71126	ATCTTCTCATACUGGTCACGCAUC	71127	GCAGTAUTCAGGCCUAAGGAACAC
279406389	71128	GCTTTCCTCCUGGGCTGTTUC	71129	GGGACACUGGAAGTTGTCATACUC
279779170	71130	CCTUCCGGGACGAGGAUGA	71131	CCUCCCCACCGAGCUCT
232936268	71132	ACTACGAAGAGCUAATAAGAGGTCUGT	71133	CAACGTTUGCACTATGACCTUCAG
230567237	71134	CTCTTGCCUCCACTGGTUGT	71135	GGATCGCTUTTCCGAGCTUCT
230651561	71136	GCCACCGCUATCACCTUCAG	71137	CUTCAATGGCTAUAGAGAGAACCCA

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256098528	chr1	94586470	94586628	94586491	94586606	ABCA4	NM_000350	1	50	1	-	94586536	94586705
262985410	chr1	94578446	94578662	94578468	94578636	ABCA4	NM_000350	1	50	2	-	94578529	94578622
262156604	chr1	94576965	94577165	94576986	94577140	ABCA4	NM_000350	1	50	3	-	94576994	94577135
257936313	chr1	94574081	94574293	94574105	94574269	ABCA4	NM_000350	1	50	4	-	94574133	94574272
265846516	chr1	94568510	94568733	94568530	94568705	ABCA4	NM_000350	1	50	5	-	94568571	94568698
255685555	chr1	94564226	94564404	94564247	94564379	ABCA4	NM_000350	1	50	6	-	94564350	94564547
255708348	chr1	94564357	94564578	94564380	94564553	ABCA4	NM_000350	1	50	6	-	94564350	94564547
254482339	chr1	94548884	94549069	94548910	94549041	ABCA4	NM_000350	1	50	7	-	94548908	94548997
253902719	chr1	94545983	94546206	94546008	94546182	ABCA4	NM_000350	1	50	8	-	94546034	94546274
253948540	chr1	94546162	94546314	94546183	94546286	ABCA4	NM_000350	1	50	8	-	94546034	94546274
262836861	chr1	94544835	94545048	94544855	94545022	ABCA4	NM_000350	1	50	9	-	94544878	94545017
261325847	chr1	94543966	94544185	94543987	94544160	ABCA4	NM_000350	1	50	10	-	94544146	94544262
261392701	chr1	94544137	94544291	94544161	94544267	ABCA4	NM_000350	1	50	10	-	94544146	94544262
256390256	chr1	94543109	94543315	94543134	94543290	ABCA4	NM_000350	1	50	11	-	94543246	94543443
256406432	chr1	94543270	94543475	94543291	94543448	ABCA4	NM_000350	1	50	11	-	94543246	94543443
255020306	chr1	94528582	94528732	94528606	94528706	ABCA4	NM_000350	1	50	12	-	94528668	94528873
255056279	chr1	94528684	94528904	94528707	94528879	ABCA4	NM_000350	1	50	12	-	94528668	94528873
264463960	chr1	94528023	94528245	94528045	94528224	ABCA4	NM_000350	1	50	13	-	94528133	94528309
264509396	chr1	94528204	94528358	94528225	94528338	ABCA4	NM_000350	1	50	13	-	94528133	94528309
263224151	chr1	94526040	94526237	94526066	94526215	ABCA4	NM_000350	1	50	14	-	94526093	94526315
263296299	chr1	94526195	94526418	94526216	94526395	ABCA4	NM_000350	1	50	14	-	94526093	94526315
261720017	chr1	94522035	94522255	94522063	94522234	ABCA4	NM_000350	1	50	15	-	94522157	94522378
261744404	chr1	94522212	94522407	94522235	94522386	ABCA4	NM_000350	1	50	15	-	94522157	94522378
259960757	chr1	94520548	94520743	94520574	94520722	ABCA4	NM_000350	1	50	16	-	94520667	94520871
260031094	chr1	94520701	94520923	94520723	94520899	ABCA4	NM_000350	1	50	16	-	94520667	94520871
258653893	chr1	94517072	94517294	94517094	94517266	ABCA4	NM_000350	1	50	17	-	94517189	94517254
265685001	chr1	94514327	94514545	94514348	94514519	ABCA4	NM_000350	1	50	18	-	94514424	94514513
255215397	chr1	94512387	94512550	94512409	94512526	ABCA4	NM_000350	1	50	19	-	94512475	94512649
255241957	chr1	94512507	94512703	94512527	94512676	ABCA4	NM_000350	1	50	19	-	94512475	94512649
260105752	chr1	94510143	94510348	94510163	94510324	ABCA4	NM_000350	1	50	20	-	94510169	94510300
257702064	chr1	94508841	94509058	94508862	94509036	ABCA4	NM_000350	1	50	21	-	94508892	94509031
259023602	chr1	94508148	94508349	94508171	94508326	ABCA4	NM_000350	1	50	22	-	94508317	94508454
259079447	chr1	94508306	94508485	94508327	94508461	ABCA4	NM_000350	1	50	22	-	94508317	94508454
266632807	chr1	94506629	94506848	94506651	94506827	ABCA4	NM_000350	1	50	23	-	94506765	94506958
266659654	chr1	94506806	94507030	94506828	94507006	ABCA4	NM_000350	1	50	23	-	94506765	94506958
254228995	chr1	94505492	94505711	94505514	94505688	ABCA4	NM_000350	1	50	24	-	94505599	94505683
263105983	chr1	94502667	94502838	94502690	94502810	ABCA4	NM_000350	1	50	25	-	94502701	94502906
263165604	chr1	94502783	94502940	94502811	94502917	ABCA4	NM_000350	1	50	25	-	94502701	94502906
263060775	chr1	94502219	94502424	94502240	94502397	ABCA4	NM_000350	1	50	26	-	94502296	94502344
266798459	chr1	94497301	94497523	94497321	94497503	ABCA4	NM_000350	1	50	27	-	94497334	94497599
266805659	chr1	94497441	94497659	94497459	94497631	ABCA4	NM_000350	1	50	27	-	94497334	94497599

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266724180	chr1	94496515	94496713	94496536	94496685	ABCA4	NM_000350	1	50	28	-	94496552	94496676
258510600	chr1	94495911	94496110	94495930	94496088	ABCA4	NM_000350	1	50	29	-	94495984	94496082
264610153	chr1	94494912	94495136	94494937	94495115	ABCA4	NM_000350	1	50	30	-	94495001	94495187
264641433	chr1	94495093	94495233	94495116	94495205	ABCA4	NM_000350	1	50	30	-	94495001	94495187
261967053	chr1	94490451	94490637	94490479	94490611	ABCA4	NM_000350	1	50	31	-	94490510	94490604
266851761	chr1	94488805	94489019	94488826	94488990	ABCA4	NM_000350	1	50	32	-	94488942	94488974
257257252	chr1	94487340	94487537	94487369	94487514	ABCA4	NM_000350	1	50	33	-	94487402	94487507
253788318	chr1	94487079	94487302	94487102	94487275	ABCA4	NM_000350	1	50	34	-	94487196	94487270
261250178	chr1	94486606	94486822	94486630	94486801	ABCA4	NM_000350	1	50	35	-	94486796	94486965
261392641	chr1	94486781	94487003	94486802	94486981	ABCA4	NM_000350	1	50	35	-	94486796	94486965
264417358	chr1	94485054	94485217	94485075	94485195	ABCA4	NM_000350	1	50	36	-	94485138	94485315
264464740	chr1	94485175	94485399	94485196	94485374	ABCA4	NM_000350	1	50	36	-	94485138	94485315
254285816	chr1	94481167	94481377	94481187	94481354	ABCA4	NM_000350	1	50	37	-	94481295	94481410
254321630	chr1	94481330	94481554	94481355	94481527	ABCA4	NM_000350	1	50	37	-	94481295	94481410
260628640	chr1	94479970	94480142	94479993	94480113	ABCA4	NM_000350	1	50	38	-	94480099	94480246
260697372	chr1	94480089	94480277	94480114	94480251	ABCA4	NM_000350	1	50	38	-	94480099	94480246
261857422	chr1	94476757	94476972	94476777	94476948	ABCA4	NM_000350	1	50	39	-	94476818	94476941
256966336	chr1	94476301	94476518	94476321	94476494	ABCA4	NM_000350	1	50	40	-	94476356	94476485
258536143	chr1	94474243	94474456	94474265	94474434	ABCA4	NM_000350	1	50	41	-	94474307	94474427
257820961	chr1	94473734	94473882	94473754	94473858	ABCA4	NM_000350	1	50	42	-	94473791	94473853
256496985	chr1	94473111	94473323	94473133	94473301	ABCA4	NM_000350	1	50	43	-	94473190	94473296
254187862	chr1	94470887	94471066	94470914	94471045	ABCA4	NM_000350	1	50	44	-	94470997	94471138
254223135	chr1	94471025	94471182	94471046	94471155	ABCA4	NM_000350	1	50	44	-	94470997	94471138
264094092	chr1	94467360	94467581	94467383	94467553	ABCA4	NM_000350	1	50	45	-	94467414	94467548
263837235	chr1	94466502	94466719	94466523	94466697	ABCA4	NM_000350	1	50	46	-	94466558	94466661
266937926	chr1	94466308	94466524	94466333	94466503	ABCA4	NM_000350	1	50	47	-	94466392	94466484
260217273	chr1	94463327	94463549	94463351	94463527	ABCA4	NM_000350	1	50	48	-	94463417	94463666
260269252	chr1	94463507	94463718	94463528	94463695	ABCA4	NM_000350	1	50	48	-	94463417	94463666
258495568	chr1	94461563	94461783	94461584	94461756	ABCA4	NM_000350	1	50	49	-	94461665	94461751
266135297	chr1	94458601	94458825	94458625	94458803	ABCA4	NM_000350	1	50	50	-	94458394	94458798
332831921	chr12	22089388	22089608	22089413	22089581	ABCC9	NM_005691	1	38	1	-	22089467	22089628
332833536	chr12	22089582	22089775	22089608	22089749	ABCC9	NM_005691	1	38	1	-	22089467	22089628
332640005	chr12	22086567	22086757	22086593	22086732	ABCC9	NM_005691	1	38	2	-	22086716	22086857
332653218	chr12	22086709	22086905	22086733	22086877	ABCC9	NM_005691	1	38	2	-	22086716	22086857
333489365	chr12	22078769	22078992	22078795	22078972	ABCC9	NM_005691	1	38	3	-	22078876	22078997
333490847	chr12	22078952	22079176	22078973	22079151	ABCC9	NM_005691	1	38	3	-	22078876	22078997
332628480	chr12	22069685	22069904	22069708	22069881	ABCC9	NM_005691	1	38	4	-	22069871	22070037
332632401	chr12	22069858	22070053	22069882	22070028	ABCC9	NM_005691	1	38	4	-	22069871	22070037
332636933	chr12	22070004	22070224	22070032	22070198	ABCC9	NM_005691	1	38	4	-	22069871	22070037
332346346	chr12	22068548	22068770	22068569	22068743	ABCC9	NM_005691	1	38	5	-	22068602	22068844
332358829	chr12	22068721	22068945	22068744	22068916	ABCC9	NM_005691	1	38	5	-	22068602	22068844

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332960723	chr12	22065707	22065880	22065736	22065855	ABCC9	NM_005691	1	38	6	-	22065806	22066000
332968765	chr12	22065832	22065975	22065856	22065949	ABCC9	NM_005691	1	38	6	-	22065806	22066000
332972337	chr12	22065930	22066146	22065950	22066117	ABCC9	NM_005691	1	38	6	-	22065806	22066000
332865245	chr12	22063675	22063814	22063701	22063786	ABCC9	NM_005691	1	38	7	-	22063760	22063912
332868694	chr12	22063767	22063980	22063787	22063952	ABCC9	NM_005691	1	38	7	-	22063760	22063912
333369188	chr12	22063090	22063230	22063110	22063203	ABCC9	NM_005691	1	38	8	-	22063091	22063246
333369798	chr12	22063181	22063398	22063204	22063370	ABCC9	NM_005691	1	38	8	-	22063091	22063246
333190734	chr12	22060856	22061066	22060882	22061040	ABCC9	NM_005691	1	38	9	-	22061011	22061145
333197793	chr12	22061019	22061183	22061041	22061154	ABCC9	NM_005691	1	38	9	-	22061011	22061145
332334688	chr12	22058949	22059152	22058977	22059127	ABCC9	NM_005691	1	38	10	-	22059060	22059222
332344084	chr12	22059101	22059260	22059128	22059232	ABCC9	NM_005691	1	38	10	-	22059060	22059222
332538808	chr12	22048131	22048351	22048157	22048323	ABCC9	NM_005691	1	38	11	-	22048209	22048249
332677591	chr12	22046944	22047143	22046964	22047116	ABCC9	NM_005691	1	38	12	-	22046966	22047108
333515883	chr12	22040698	22040921	22040720	22040893	ABCC9	NM_005691	1	38	13	-	22040760	22040868
332440569	chr12	22035618	22035842	22035642	22035816	ABCC9	NM_005691	1	38	14	-	22035700	22035807
333827216	chr12	22028442	22028661	22028462	22028635	ABCC9	NM_005691	1	38	15	-	22028588	22028660
332918824	chr12	22025521	22025714	22025547	22025687	ABCC9	NM_005691	1	38	16	-	22025559	22025664
333249533	chr12	22017241	22017437	22017267	22017409	ABCC9	NM_005691	1	38	17	-	22017373	22017411
333508702	chr12	22015817	22016037	22015840	22016010	ABCC9	NM_005691	1	38	18	-	22015887	22015988
332384463	chr12	22013780	22013999	22013807	22013976	ABCC9	NM_005691	1	38	19	-	22013905	22013989
333665053	chr12	22012405	22012607	22012434	22012585	ABCC9	NM_005691	1	38	20	-	22012520	22012600
333667089	chr12	22012552	22012773	22012573	22012752	ABCC9	NM_005691	1	38	20	-	22012520	22012600
332547732	chr12	22005116	22005337	22005141	22005311	ABCC9	NM_005691	1	38	21	-	22005302	22005439
332559581	chr12	22005286	22005471	22005312	22005444	ABCC9	NM_005691	1	38	21	-	22005302	22005439
332547732	chr12	22005116	22005337	22005141	22005311	ABCC9	NM_005691	1	38	22	-	22005031	22005156
333167238	chr12	22004984	22005186	22005008	22005161	ABCC9	NM_005691	1	38	22	-	22005031	22005156
332573108	chr12	22000989	22001213	22001015	22001185	ABCC9	NM_005691	1	38	23	-	22001084	22001180
333082592	chr12	21998433	21998634	21998460	21998608	ABCC9	NM_005691	1	38	24	-	21998537	21998766
333094097	chr12	21998585	21998804	21998609	21998778	ABCC9	NM_005691	1	38	24	-	21998537	21998766
333185287	chr12	21997576	21997745	21997601	21997718	ABCC9	NM_005691	1	38	25	-	21997701	21997849
333190474	chr12	21997691	21997877	21997719	21997854	ABCC9	NM_005691	1	38	25	-	21997701	21997849
332383389	chr12	21997264	21997457	21997297	21997431	ABCC9	NM_005691	1	38	26	-	21997417	21997486
332384318	chr12	21997404	21997545	21997432	21997517	ABCC9	NM_005691	1	38	26	-	21997417	21997486
332605628	chr12	21995213	21995358	21995237	21995335	ABCC9	NM_005691	1	38	27	-	21995248	21995405
332611390	chr12	21995312	21995458	21995336	21995430	ABCC9	NM_005691	1	38	27	-	21995248	21995405
332895758	chr12	21990962	21991136	21990990	21991109	ABCC9	NM_005691	1	38	28	-	21991012	21991104
333309506	chr12	21981837	21982027	21981859	21981999	ABCC9	NM_005691	1	38	29	-	21981892	21981994
333687653	chr12	21971073	21971238	21971098	21971210	ABCC9	NM_005691	1	38	30	-	21971084	21971185
332508921	chr12	21969958	21970169	21969985	21970144	ABCC9	NM_005691	1	38	31	-	21970121	21970241
332527268	chr12	21970120	21970307	21970145	21970279	ABCC9	NM_005691	1	38	31	-	21970121	21970241
333293604	chr12	21968640	21968855	21968661	21968832	ABCC9	NM_005691	1	38	32	-	21968697	21968827

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332335364	chr12	21967488	21967687	21967514	21967661	ABCC9	NM_005691	1	38	33	-	21967578	21967656
332589004	chr12	21964930	21965125	21964957	21965096	ABCC9	NM_005691	1	38	34	-	21964983	21965091
333665912	chr12	21962608	21962832	21962631	21962806	ABCC9	NM_005691	1	38	35	-	21962786	21962889
333635827	chr12	21960186	21960391	21960210	21960367	ABCC9	NM_005691	1	38	36	-	21960280	21960413
333641816	chr12	21960347	21960535	21960368	21960509	ABCC9	NM_005691	1	38	36	-	21960280	21960413
332938038	chr12	21958894	21959090	21958918	21959062	ABCC9	NM_005691	1	38	37	-	21958932	21958994
333158752	chr12	21958069	21958288	21958090	21958259	ABCC9	NM_005691	1	38	38	-	21958108	21958245
332831921	chr12	22089388	22089608	22089413	22089581	ABCC9	NM_020297	2	38	1	-	22089467	22089628
332833536	chr12	22089582	22089775	22089608	22089749	ABCC9	NM_020297	2	38	1	-	22089467	22089628
332640005	chr12	22086567	22086757	22086593	22086732	ABCC9	NM_020297	2	38	2	-	22086716	22086857
332653218	chr12	22086709	22086905	22086733	22086877	ABCC9	NM_020297	2	38	2	-	22086716	22086857
333489365	chr12	22078769	22078992	22078795	22078972	ABCC9	NM_020297	2	38	3	-	22078876	22078997
333490847	chr12	22078952	22079176	22078973	22079151	ABCC9	NM_020297	2	38	3	-	22078876	22078997
332628480	chr12	22069685	22069904	22069708	22069881	ABCC9	NM_020297	2	38	4	-	22069871	22070037
332632401	chr12	22069858	22070053	22069882	22070028	ABCC9	NM_020297	2	38	4	-	22069871	22070037
332636933	chr12	22070004	22070224	22070032	22070198	ABCC9	NM_020297	2	38	4	-	22069871	22070037
332346346	chr12	22068548	22068770	22068569	22068743	ABCC9	NM_020297	2	38	5	-	22068602	22068844
332358829	chr12	22068721	22068945	22068744	22068916	ABCC9	NM_020297	2	38	5	-	22068602	22068844
332960723	chr12	22065707	22065880	22065736	22065855	ABCC9	NM_020297	2	38	6	-	22065806	22066000
332968765	chr12	22065832	22065975	22065856	22065949	ABCC9	NM_020297	2	38	6	-	22065806	22066000
332972337	chr12	22065930	22066146	22065950	22066117	ABCC9	NM_020297	2	38	6	-	22065806	22066000
332865245	chr12	22063675	22063814	22063701	22063786	ABCC9	NM_020297	2	38	7	-	22063760	22063912
332868694	chr12	22063767	22063980	22063787	22063952	ABCC9	NM_020297	2	38	7	-	22063760	22063912
333369188	chr12	22063090	22063230	22063110	22063203	ABCC9	NM_020297	2	38	8	-	22063091	22063246
333369798	chr12	22063181	22063398	22063204	22063370	ABCC9	NM_020297	2	38	8	-	22063091	22063246
333190734	chr12	22060856	22061066	22060882	22061040	ABCC9	NM_020297	2	38	9	-	22061011	22061145
333197793	chr12	22061019	22061183	22061041	22061154	ABCC9	NM_020297	2	38	9	-	22061011	22061145
332334688	chr12	22058949	22059152	22058977	22059127	ABCC9	NM_020297	2	38	10	-	22059060	22059222
332344084	chr12	22059101	22059260	22059128	22059232	ABCC9	NM_020297	2	38	10	-	22059060	22059222
332538808	chr12	22048131	22048351	22048157	22048323	ABCC9	NM_020297	2	38	11	-	22048209	22048249
332677591	chr12	22046944	22047143	22046964	22047116	ABCC9	NM_020297	2	38	12	-	22046966	22047108
333515883	chr12	22040698	22040921	22040720	22040893	ABCC9	NM_020297	2	38	13	-	22040760	22040868
332440569	chr12	22035618	22035842	22035642	22035816	ABCC9	NM_020297	2	38	14	-	22035700	22035807
333827216	chr12	22028442	22028661	22028462	22028635	ABCC9	NM_020297	2	38	15	-	22028588	22028660
332918824	chr12	22025521	22025714	22025547	22025687	ABCC9	NM_020297	2	38	16	-	22025559	22025664
333249533	chr12	22017241	22017437	22017267	22017409	ABCC9	NM_020297	2	38	17	-	22017373	22017411
333508702	chr12	22015817	22016037	22015840	22016010	ABCC9	NM_020297	2	38	18	-	22015887	22015988
332384463	chr12	22013780	22013999	22013807	22013976	ABCC9	NM_020297	2	38	19	-	22013905	22013989
333665053	chr12	22012405	22012607	22012434	22012585	ABCC9	NM_020297	2	38	20	-	22012520	22012600
333667089	chr12	22012552	22012773	22012573	22012752	ABCC9	NM_020297	2	38	20	-	22012520	22012600
332547732	chr12	22005116	22005337	22005141	22005311	ABCC9	NM_020297	2	38	21	-	22005302	22005439

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332559581	chr12	22005286	22005471	22005312	22005444	ABCC9	NM_020297	2	38	21	-	22005302	22005439
332547732	chr12	22005116	22005337	22005141	22005311	ABCC9	NM_020297	2	38	22	-	22005031	22005156
333167238	chr12	22004984	22005186	22005008	22005161	ABCC9	NM_020297	2	38	22	-	22005031	22005156
332573108	chr12	22000989	22001213	22001015	22001185	ABCC9	NM_020297	2	38	23	-	22001084	22001180
333082592	chr12	21998433	21998634	21998460	21998608	ABCC9	NM_020297	2	38	24	-	21998537	21998766
333094097	chr12	21998585	21998804	21998609	21998778	ABCC9	NM_020297	2	38	24	-	21998537	21998766
333185287	chr12	21997576	21997745	21997601	21997718	ABCC9	NM_020297	2	38	25	-	21997701	21997849
333190474	chr12	21997691	21997877	21997719	21997854	ABCC9	NM_020297	2	38	25	-	21997701	21997849
332383389	chr12	21997264	21997457	21997297	21997431	ABCC9	NM_020297	2	38	26	-	21997417	21997486
332384318	chr12	21997404	21997545	21997432	21997517	ABCC9	NM_020297	2	38	26	-	21997417	21997486
332605628	chr12	21995213	21995358	21995237	21995335	ABCC9	NM_020297	2	38	27	-	21995248	21995405
332611390	chr12	21995312	21995458	21995336	21995430	ABCC9	NM_020297	2	38	27	-	21995248	21995405
332895758	chr12	21990962	21991136	21990990	21991109	ABCC9	NM_020297	2	38	28	-	21991012	21991104
333309506	chr12	21981837	21982027	21981859	21981999	ABCC9	NM_020297	2	38	29	-	21981892	21981994
333687653	chr12	21971073	21971238	21971098	21971210	ABCC9	NM_020297	2	38	30	-	21971084	21971185
332508921	chr12	21969958	21970169	21969985	21970144	ABCC9	NM_020297	2	38	31	-	21970121	21970241
332527268	chr12	21970120	21970307	21970145	21970279	ABCC9	NM_020297	2	38	31	-	21970121	21970241
333293604	chr12	21968640	21968855	21968661	21968832	ABCC9	NM_020297	2	38	32	-	21968697	21968827
332335364	chr12	21967488	21967687	21967514	21967661	ABCC9	NM_020297	2	38	33	-	21967578	21967656
332589004	chr12	21964930	21965125	21964957	21965096	ABCC9	NM_020297	2	38	34	-	21964983	21965091
333665912	chr12	21962608	21962832	21962631	21962806	ABCC9	NM_020297	2	38	35	-	21962786	21962889
333635827	chr12	21960186	21960391	21960210	21960367	ABCC9	NM_020297	2	38	36	-	21960280	21960413
333641816	chr12	21960347	21960535	21960368	21960509	ABCC9	NM_020297	2	38	36	-	21960280	21960413
332938038	chr12	21958894	21959090	21958918	21959062	ABCC9	NM_020297	2	38	37	-	21958932	21958994
333238076	chr12	21953892	21954025	21953916	21953997	ABCC9	NM_020297	2	38	38	-	21950324	21954115
333243422	chr12	21953979	21954161	21953998	21954134	ABCC9	NM_020297	2	38	38	-	21950324	21954115
266767680	chrX	152990790	152990928	152990807	152990909	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266769400	chrX	152990806	152990947	152990826	152990928	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266769747	chrX	152990907	152991098	152990925	152991080	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266772408	chrX	152990598	152990821	152990619	152990800	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266773488	chrX	152991034	152991252	152991055	152991231	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266776507	chrX	152991338	152991537	152991357	152991519	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266780488	chrX	152991498	152991662	152991516	152991645	ABCD1	NM_000033	1	10	1	+	152990323	152991621
266782178	chrX	152991162	152991379	152991183	152991359	ABCD1	NM_000033	1	10	1	+	152990323	152991621
261360686	chrX	152994652	152994869	152994673	152994848	ABCD1	NM_000033	1	10	2	+	152994687	152994867
261410348	chrX	152994827	152995030	152994847	152995008	ABCD1	NM_000033	1	10	2	+	152994687	152994867
263648980	chrX	153001670	153001879	153001690	153001858	ABCD1	NM_000033	1	10	3	+	153001566	153001708
263654285	chrX	153001684	153001907	153001704	153001888	ABCD1	NM_000033	1	10	3	+	153001566	153001708
264555907	chrX	153001488	153001712	153001510	153001690	ABCD1	NM_000033	1	10	3	+	153001566	153001708
263648980	chrX	153001670	153001879	153001690	153001858	ABCD1	NM_000033	1	10	4	+	153001799	153001967
263654285	chrX	153001684	153001907	153001704	153001888	ABCD1	NM_000033	1	10	4	+	153001799	153001967

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263681849	chrX	153001863	153002064	153001883	153002044	ABCD1	NM_000033	1	10	4	+	153001799	153001967
256378861	chrX	153002539	153002758	153002560	153002738	ABCD1	NM_000033	1	10	5	+	153002611	153002705
257067606	chrX	153005486	153005697	153005505	153005674	ABCD1	NM_000033	1	10	6	+	153005546	153005691
257080823	chrX	153005636	153005794	153005657	153005773	ABCD1	NM_000033	1	10	6	+	153005546	153005691
255661510	chrX	153005909	153006101	153005928	153006080	ABCD1	NM_000033	1	10	7	+	153006028	153006173
255670846	chrX	153006060	153006272	153006081	153006244	ABCD1	NM_000033	1	10	7	+	153006028	153006173
266570983	chrX	153009089	153009263	153009108	153009246	ABCD1	NM_000033	1	10	10	+	153008943	153010216
256084342	chr17	7123204	7123392	7123226	7123373	ACADVL	NM_000018	1	20	1	+	7123153	7123365
256085522	chr17	7123360	7123535	7123381	7123516	ACADVL	NM_000018	1	20	2	+	7123441	7123516
260047737	chr17	7123728	7123913	7123748	7123891	ACADVL	NM_000018	1	20	3	+	7123783	7123848
260092448	chr17	7123814	7124024	7123834	7124001	ACADVL	NM_000018	1	20	3	+	7123783	7123848
260092448	chr17	7123814	7124024	7123834	7124001	ACADVL	NM_000018	1	20	4	+	7123923	7123995
259016388	chr17	7123981	7124197	7124000	7124175	ACADVL	NM_000018	1	20	5	+	7124085	7124149
257909751	chr17	7124185	7124409	7124212	7124387	ACADVL	NM_000018	1	20	6	+	7124243	7124377
256584449	chr17	7124690	7124891	7124714	7124871	ACADVL	NM_000018	1	20	7	+	7124857	7125001
256601569	chr17	7124853	7125076	7124871	7125053	ACADVL	NM_000018	1	20	7	+	7124857	7125001
263915787	chr17	7125348	7125505	7125369	7125483	ACADVL	NM_000018	1	20	8	+	7125271	7125400
264495351	chr17	7125219	7125393	7125242	7125368	ACADVL	NM_000018	1	20	8	+	7125271	7125400
263953305	chr17	7125466	7125650	7125487	7125628	ACADVL	NM_000018	1	20	9	+	7125496	7125621
265254729	chr17	7125854	7126050	7125877	7126027	ACADVL	NM_000018	1	20	10	+	7125986	7126184
265303054	chr17	7126007	7126223	7126028	7126200	ACADVL	NM_000018	1	20	10	+	7125986	7126184
262125764	chr17	7126393	7126617	7126414	7126596	ACADVL	NM_000018	1	20	11	+	7126452	7126556
263012989	chr17	7126895	7127111	7126917	7127090	ACADVL	NM_000018	1	20	12	+	7126963	7127049
253807440	chr17	7127090	7127271	7127111	7127246	ACADVL	NM_000018	1	20	13	+	7127132	7127194
264669300	chr17	7127244	7127415	7127265	7127394	ACADVL	NM_000018	1	20	14	+	7127287	7127388
255570672	chr17	7127426	7127624	7127446	7127598	ACADVL	NM_000018	1	20	15	+	7127465	7127562
254063741	chr17	7127592	7127808	7127613	7127786	ACADVL	NM_000018	1	20	16	+	7127640	7127712
258416945	chr17	7127675	7127896	7127694	7127876	ACADVL	NM_000018	1	20	16	+	7127640	7127712
258416945	chr17	7127675	7127896	7127694	7127876	ACADVL	NM_000018	1	20	17	+	7127799	7127871
256165460	chr17	7127899	7128123	7127923	7128095	ACADVL	NM_000018	1	20	18	+	7127961	7128033
256170917	chr17	7128088	7128213	7128110	7128191	ACADVL	NM_000018	1	20	19	+	7128128	7128203
258233661	chr17	7128164	7128369	7128188	7128347	ACADVL	NM_000018	1	20	19	+	7128128	7128203
258233661	chr17	7128164	7128369	7128188	7128347	ACADVL	NM_000018	1	20	20	+	7128276	7128585
258245343	chr17	7128328	7128462	7128348	7128440	ACADVL	NM_000018	1	20	20	+	7128276	7128585
256084342	chr17	7123204	7123392	7123226	7123373	ACADVL	NM_001033859	2	19	1	+	7123153	7123365
256085522	chr17	7123360	7123535	7123381	7123516	ACADVL	NM_001033859	2	19	2	+	7123441	7123516
260092448	chr17	7123814	7124024	7123834	7124001	ACADVL	NM_001033859	2	19	3	+	7123923	7123995
259016388	chr17	7123981	7124197	7124000	7124175	ACADVL	NM_001033859	2	19	4	+	7124085	7124149
257909751	chr17	7124185	7124409	7124212	7124387	ACADVL	NM_001033859	2	19	5	+	7124243	7124377
256584449	chr17	7124690	7124891	7124714	7124871	ACADVL	NM_001033859	2	19	6	+	7124857	7125001
256601569	chr17	7124853	7125076	7124871	7125053	ACADVL	NM_001033859	2	19	6	+	7124857	7125001

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263915787	chr17	7125348	7125505	7125369	7125483	ACADVL	NM_001033859	2	19	7	+	7125271	7125400
264495351	chr17	7125219	7125393	7125242	7125368	ACADVL	NM_001033859	2	19	7	+	7125271	7125400
263953305	chr17	7125466	7125650	7125487	7125628	ACADVL	NM_001033859	2	19	8	+	7125496	7125621
265254729	chr17	7125854	7126050	7125877	7126027	ACADVL	NM_001033859	2	19	9	+	7125986	7126184
265303054	chr17	7126007	7126223	7126028	7126200	ACADVL	NM_001033859	2	19	9	+	7125986	7126184
262125764	chr17	7126393	7126617	7126414	7126596	ACADVL	NM_001033859	2	19	10	+	7126452	7126556
263012989	chr17	7126895	7127111	7126917	7127090	ACADVL	NM_001033859	2	19	11	+	7126963	7127049
253807440	chr17	7127090	7127271	7127111	7127246	ACADVL	NM_001033859	2	19	12	+	7127132	7127194
264669300	chr17	7127244	7127415	7127265	7127394	ACADVL	NM_001033859	2	19	13	+	7127287	7127388
255570672	chr17	7127426	7127624	7127446	7127598	ACADVL	NM_001033859	2	19	14	+	7127465	7127562
254063741	chr17	7127592	7127808	7127613	7127786	ACADVL	NM_001033859	2	19	15	+	7127640	7127712
258416945	chr17	7127675	7127896	7127694	7127876	ACADVL	NM_001033859	2	19	15	+	7127640	7127712
258416945	chr17	7127675	7127896	7127694	7127876	ACADVL	NM_001033859	2	19	16	+	7127799	7127871
256165460	chr17	7127899	7128123	7127923	7128095	ACADVL	NM_001033859	2	19	17	+	7127961	7128033
256170917	chr17	7128088	7128213	7128110	7128191	ACADVL	NM_001033859	2	19	18	+	7128128	7128203
258233661	chr17	7128164	7128369	7128188	7128347	ACADVL	NM_001033859	2	19	18	+	7128128	7128203
258233661	chr17	7128164	7128369	7128188	7128347	ACADVL	NM_001033859	2	19	19	+	7128276	7128585
258245343	chr17	7128328	7128462	7128348	7128440	ACADVL	NM_001033859	2	19	19	+	7128276	7128585
254262711	chr10	90708493	90708717	90708520	90708692	ACTA2	NM_001141945	1	9	2	-	90708559	90708710
262401357	chr10	90706960	90707176	90706984	90707150	ACTA2	NM_001141945	1	9	3	-	90707015	90707143
264946248	chr10	90703481	90703702	90703502	90703677	ACTA2	NM_001141945	1	9	4	-	90703554	90703664
256857155	chr10	90701432	90701656	90701457	90701631	ACTA2	NM_001141945	1	9	5	-	90701542	90701626
260310754	chr10	90700957	90701175	90700978	90701152	ACTA2	NM_001141945	1	9	6	-	90700986	90701147
258062628	chr10	90699113	90699333	90699135	90699313	ACTA2	NM_001141945	1	9	7	-	90699264	90699455
258159423	chr10	90699294	90699486	90699314	90699460	ACTA2	NM_001141945	1	9	7	-	90699264	90699455
263726631	chr10	90697711	90697933	90697732	90697907	ACTA2	NM_001141945	1	9	8	-	90697818	90697999
263781039	chr10	90697887	90698048	90697908	90698023	ACTA2	NM_001141945	1	9	8	-	90697818	90697999
254259110	chr10	90694864	90695048	90694888	90695026	ACTA2	NM_001141945	1	9	9	-	90694831	90695123
254329386	chr10	90695008	90695181	90695027	90695154	ACTA2	NM_001141945	1	9	9	-	90694831	90695123
254262711	chr10	90708493	90708717	90708520	90708692	ACTA2	NM_001613	2	9	2	-	90708559	90708710
262401357	chr10	90706960	90707176	90706984	90707150	ACTA2	NM_001613	2	9	3	-	90707015	90707143
264946248	chr10	90703481	90703702	90703502	90703677	ACTA2	NM_001613	2	9	4	-	90703554	90703664
256857155	chr10	90701432	90701656	90701457	90701631	ACTA2	NM_001613	2	9	5	-	90701542	90701626
260310754	chr10	90700957	90701175	90700978	90701152	ACTA2	NM_001613	2	9	6	-	90700986	90701147
258062628	chr10	90699113	90699333	90699135	90699313	ACTA2	NM_001613	2	9	7	-	90699264	90699455
258159423	chr10	90699294	90699486	90699314	90699460	ACTA2	NM_001613	2	9	7	-	90699264	90699455
263726631	chr10	90697711	90697933	90697732	90697907	ACTA2	NM_001613	2	9	8	-	90697818	90697999
263781039	chr10	90697887	90698048	90697908	90698023	ACTA2	NM_001613	2	9	8	-	90697818	90697999
254259110	chr10	90694864	90695048	90694888	90695026	ACTA2	NM_001613	2	9	9	-	90694831	90695123
254329386	chr10	90695008	90695181	90695027	90695154	ACTA2	NM_001613	2	9	9	-	90694831	90695123
256248221	chr15	35086815	35087038	35086836	35087019	ACTC1	NM_005159	1	7	2	-	35086881	35087031

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254782913	chr15	35085294	35085517	35085322	35085495	ACTC1	NM_005159	1	7	3	-	35085446	35085770
254803496	chr15	35085458	35085681	35085481	35085657	ACTC1	NM_005159	1	7	3	-	35085446	35085770
254832354	chr15	35085635	35085813	35085657	35085788	ACTC1	NM_005159	1	7	3	-	35085446	35085770
264240190	chr15	35084466	35084652	35084491	35084630	ACTC1	NM_005159	1	7	4	-	35084609	35084770
264282955	chr15	35084609	35084813	35084631	35084786	ACTC1	NM_005159	1	7	4	-	35084609	35084770
266956318	chr15	35084160	35084381	35084181	35084358	ACTC1	NM_005159	1	7	5	-	35084291	35084482
266999529	chr15	35084334	35084540	35084359	35084512	ACTC1	NM_005159	1	7	5	-	35084291	35084482
261755655	chr15	35083194	35083407	35083222	35083383	ACTC1	NM_005159	1	7	6	-	35083315	35083496
261817414	chr15	35083360	35083576	35083384	35083553	ACTC1	NM_005159	1	7	6	-	35083315	35083496
266622534	chr15	35082573	35082795	35082596	35082767	ACTC1	NM_005159	1	7	7	-	35080297	35082756
333258046	chr1	236849895	236850027	236849913	236850005	ACTN2	NM_001103	1	21	1	+	236849770	236850099
333259206	chr1	236849989	236850208	236850006	236850190	ACTN2	NM_001103	1	21	1	+	236849770	236850099
333332488	chr1	236881092	236881313	236881115	236881285	ACTN2	NM_001103	1	21	2	+	236881158	236881272
332548322	chr1	236882141	236882360	236882164	236882338	ACTN2	NM_001103	1	21	3	+	236882194	236882313
332644279	chr1	236883251	236883449	236883271	236883426	ACTN2	NM_001103	1	21	4	+	236883405	236883491
332654447	chr1	236883402	236883580	236883427	236883552	ACTN2	NM_001103	1	21	4	+	236883405	236883491
332976877	chr1	236889145	236889363	236889168	236889337	ACTN2	NM_001103	1	21	5	+	236889233	236889320
333656301	chr1	236890914	236891137	236890935	236891114	ACTN2	NM_001103	1	21	6	+	236890978	236891056
333261819	chr1	236894433	236894647	236894453	236894619	ACTN2	NM_001103	1	21	7	+	236894533	236894614
333615671	chr1	236898850	236899073	236898872	236899045	ACTN2	NM_001103	1	21	8	+	236898935	236899020
333832134	chr1	236900385	236900548	236900406	236900527	ACTN2	NM_001103	1	21	9	+	236900422	236900514
332364906	chr1	236902564	236902756	236902589	236902734	ACTN2	NM_001103	1	21	10	+	236902602	236902832
332371517	chr1	236902683	236902907	236902704	236902886	ACTN2	NM_001103	1	21	10	+	236902602	236902832
333461704	chr1	236906153	236906377	236906176	236906349	ACTN2	NM_001103	1	21	11	+	236906196	236906343
332622254	chr1	236907750	236907968	236907771	236907949	ACTN2	NM_001103	1	21	12	+	236907926	236908076
332636808	chr1	236907928	236908139	236907950	236908116	ACTN2	NM_001103	1	21	12	+	236907926	236908076
333335858	chr1	236910900	236911109	236910927	236911081	ACTN2	NM_001103	1	21	13	+	236910967	236911075
333131036	chr1	236912279	236912478	236912305	236912456	ACTN2	NM_001103	1	21	14	+	236912424	236912564
333138106	chr1	236912429	236912603	236912457	236912576	ACTN2	NM_001103	1	21	14	+	236912424	236912564
332701115	chr1	236914654	236914876	236914678	236914853	ACTN2	NM_001103	1	21	15	+	236914770	236914952
332719411	chr1	236914833	236915011	236914854	236914988	ACTN2	NM_001103	1	21	15	+	236914770	236914952
332894145	chr1	236917209	236917426	236917230	236917404	ACTN2	NM_001103	1	21	16	+	236917247	236917381
332626306	chr1	236918261	236918428	236918282	236918400	ACTN2	NM_001103	1	21	17	+	236918319	236918498
332640927	chr1	236918377	236918573	236918401	236918551	ACTN2	NM_001103	1	21	17	+	236918319	236918498
332993605	chr1	236920747	236920968	236920774	236920940	ACTN2	NM_001103	1	21	18	+	236920786	236920932
333163390	chr1	236922952	236923176	236922977	236923151	ACTN2	NM_001103	1	21	19	+	236923024	236923089
333198645	chr1	236924191	236924414	236924219	236924389	ACTN2	NM_001103	1	21	20	+	236924315	236924473
333216294	chr1	236924369	236924523	236924390	236924499	ACTN2	NM_001103	1	21	20	+	236924315	236924473
333418107	chr1	236925728	236925952	236925750	236925927	ACTN2	NM_001103	1	21	21	+	236925761	236927558
253803467	chr20	43264824	43265007	43264845	43264981	ADA	NM_000022	1	12	2	-	43264868	43264929
264651872	chr20	43257622	43257838	43257644	43257815	ADA	NM_000022	1	12	3	-	43257688	43257810

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256478283	chr20	43255005	43255227	43255026	43255200	ADA	NM_000022	1	12	4	-	43255097	43255240
256491194	chr20	43255178	43255337	43255201	43255315	ADA	NM_000022	1	12	4	-	43255097	43255240
256802977	chr20	43254141	43254358	43254159	43254339	ADA	NM_000022	1	12	5	-	43254210	43254325
266787245	chr20	43252813	43253027	43252835	43253007	ADA	NM_000022	1	12	6	-	43252843	43252970
264267178	chr20	43251577	43251801	43251603	43251778	ADA	NM_000022	1	12	7	-	43251648	43251719
266208663	chr20	43251395	43251602	43251418	43251576	ADA	NM_000022	1	12	8	-	43251470	43251571
266852799	chr20	43251124	43251312	43251147	43251291	ADA	NM_000022	1	12	9	-	43251229	43251293
266863680	chr20	43251263	43251434	43251283	43251413	ADA	NM_000022	1	12	9	-	43251229	43251293
255669361	chr20	43249597	43249817	43249621	43249794	ADA	NM_000022	1	12	10	-	43249659	43249788
266925618	chr20	43248845	43249066	43248865	43249045	ADA	NM_000022	1	12	11	-	43248940	43249042
266972287	chr20	43249019	43249228	43249042	43249202	ADA	NM_000022	1	12	11	-	43248940	43249042
263076287	chr20	43248306	43248527	43248326	43248502	ADA	NM_000022	1	12	12	-	43248163	43248488
265584800	chr17	6338263	6338473	6338284	6338451	AIPL1	NM_001033054	1	5	1	-	6338329	6338519
255497833	chr17	6337104	6337319	6337128	6337298	AIPL1	NM_001033054	1	5	2	-	6337239	6337418
255521640	chr17	6337277	6337461	6337299	6337437	AIPL1	NM_001033054	1	5	2	-	6337239	6337418
266827502	chr17	6330084	6330295	6330104	6330273	AIPL1	NM_001033054	1	5	3	-	6330201	6330377
266838502	chr17	6330231	6330449	6330252	6330427	AIPL1	NM_001033054	1	5	3	-	6330201	6330377
257749532	chr17	6329845	6330050	6329870	6330022	AIPL1	NM_001033054	1	5	4	-	6329935	6330076
257758857	chr17	6330002	6330221	6330023	6330199	AIPL1	NM_001033054	1	5	4	-	6329935	6330076
262982703	chr17	6328944	6329158	6328962	6329139	AIPL1	NM_001033054	1	5	5	-	6327059	6329150
266982472	chr17	6329120	6329344	6329138	6329322	AIPL1	NM_001033054	1	5	5	-	6327059	6329150
265584800	chr17	6338263	6338473	6338284	6338451	AIPL1	NM_001033055	2	5	1	-	6338329	6338519
263730223	chr17	6331530	6331733	6331550	6331713	AIPL1	NM_001033055	2	5	2	-	6331638	6331826
263736629	chr17	6331685	6331905	6331704	6331883	AIPL1	NM_001033055	2	5	2	-	6331638	6331826
266827502	chr17	6330084	6330295	6330104	6330273	AIPL1	NM_001033055	2	5	3	-	6330201	6330377
266838502	chr17	6330231	6330449	6330252	6330427	AIPL1	NM_001033055	2	5	3	-	6330201	6330377
257749532	chr17	6329845	6330050	6329870	6330022	AIPL1	NM_001033055	2	5	4	-	6329935	6330076
257758857	chr17	6330002	6330221	6330023	6330199	AIPL1	NM_001033055	2	5	4	-	6329935	6330076
262982703	chr17	6328944	6329158	6328962	6329139	AIPL1	NM_001033055	2	5	5	-	6327059	6329150
266982472	chr17	6329120	6329344	6329138	6329322	AIPL1	NM_001033055	2	5	5	-	6327059	6329150
265584800	chr17	6338263	6338473	6338284	6338451	AIPL1	NM_014336	3	6	1	-	6338329	6338519
255497833	chr17	6337104	6337319	6337128	6337298	AIPL1	NM_014336	3	6	2	-	6337239	6337418
255521640	chr17	6337277	6337461	6337299	6337437	AIPL1	NM_014336	3	6	2	-	6337239	6337418
263730223	chr17	6331530	6331733	6331550	6331713	AIPL1	NM_014336	3	6	3	-	6331638	6331826
263736629	chr17	6331685	6331905	6331704	6331883	AIPL1	NM_014336	3	6	3	-	6331638	6331826
266827502	chr17	6330084	6330295	6330104	6330273	AIPL1	NM_014336	3	6	4	-	6330201	6330377
266838502	chr17	6330231	6330449	6330252	6330427	AIPL1	NM_014336	3	6	4	-	6330201	6330377
257749532	chr17	6329845	6330050	6329870	6330022	AIPL1	NM_014336	3	6	5	-	6329935	6330076
257758857	chr17	6330002	6330221	6330023	6330199	AIPL1	NM_014336	3	6	5	-	6329935	6330076
262982703	chr17	6328944	6329158	6328962	6329139	AIPL1	NM_014336	3	6	6	-	6327059	6329150
266982472	chr17	6329120	6329344	6329138	6329322	AIPL1	NM_014336	3	6	6	-	6327059	6329150

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
255983609	chr21	45705907	45706078	45705924	45706058	AIRE	NM_000383	1	14	1	+	45705763	45706021
256531256	chr21	45706358	45706578	45706382	45706556	AIRE	NM_000383	1	14	2	+	45706440	45706614
256544010	chr21	45706536	45706705	45706557	45706685	AIRE	NM_000383	1	14	2	+	45706440	45706614
263737951	chr21	45706801	45706959	45706822	45706939	AIRE	NM_000383	1	14	3	+	45706861	45707016
263742901	chr21	45706904	45707058	45706923	45707039	AIRE	NM_000383	1	14	3	+	45706861	45707016
265590953	chr21	45707346	45707539	45707363	45707521	AIRE	NM_000383	1	14	4	+	45707400	45707474
263054682	chr21	45708151	45708353	45708173	45708333	AIRE	NM_000383	1	14	5	+	45708228	45708341
263072240	chr21	45708313	45708525	45708334	45708504	AIRE	NM_000383	1	14	5	+	45708228	45708341
261275145	chr21	45709516	45709712	45709533	45709694	AIRE	NM_000383	1	14	6	+	45709540	45709685
254507263	chr21	45709844	45709979	45709862	45709960	AIRE	NM_000383	1	14	7	+	45709871	45709951
254008281	chr21	45710949	45711170	45710968	45711150	AIRE	NM_000383	1	14	8	+	45710978	45711093
260630068	chr21	45712129	45712336	45712148	45712318	AIRE	NM_000383	1	14	9	+	45712185	45712284
262748851	chr21	45712799	45712929	45712819	45712909	AIRE	NM_000383	1	14	10	+	45712876	45713058
262751263	chr21	45712888	45713108	45712905	45713089	AIRE	NM_000383	1	14	10	+	45712876	45713058
256867765	chr21	45713607	45713812	45713625	45713795	AIRE	NM_000383	1	14	11	+	45713672	45713793
264591548	chr21	45714229	45714422	45714246	45714405	AIRE	NM_000383	1	14	12	+	45714284	45714386
266999003	chr21	45716232	45716452	45716254	45716431	AIRE	NM_000383	1	14	13	+	45716266	45716328
264850810	chr21	45717425	45717647	45717447	45717624	AIRE	NM_000383	1	14	14	+	45717539	45718102
253998121	chr21	45710779	45710988	45710802	45710967	AIRE	NM_000658	2	7	1	+	45710274	45711093
254008281	chr21	45710949	45711170	45710968	45711150	AIRE	NM_000658	2	7	1	+	45710274	45711093
264470086	chr21	45710664	45710823	45710681	45710805	AIRE	NM_000658	2	7	1	+	45710274	45711093
260630068	chr21	45712129	45712336	45712148	45712318	AIRE	NM_000658	2	7	2	+	45712185	45712284
262748851	chr21	45712799	45712929	45712819	45712909	AIRE	NM_000658	2	7	3	+	45712876	45713058
262751263	chr21	45712888	45713108	45712905	45713089	AIRE	NM_000658	2	7	3	+	45712876	45713058
256867765	chr21	45713607	45713812	45713625	45713795	AIRE	NM_000658	2	7	4	+	45713672	45713793
264591548	chr21	45714229	45714422	45714246	45714405	AIRE	NM_000658	2	7	5	+	45714284	45714386
266999003	chr21	45716232	45716452	45716254	45716431	AIRE	NM_000658	2	7	6	+	45716266	45716328
264850810	chr21	45717425	45717647	45717447	45717624	AIRE	NM_000658	2	7	7	+	45717539	45718110
224037450	chr7	91570303	91570523	91570321	91570506	AKAP9	NM_005751	1	50	1	+	91570189	91570461
224091035	chr7	91602942	91603148	91602965	91603121	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224095523	chr7	91603093	91603296	91603121	91603269	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224098698	chr7	91603232	91603378	91603261	91603353	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224642519	chr7	91609489	91609637	91609522	91609613	AKAP9	NM_005751	1	50	3	+	91609603	91609647
224642543	chr7	91609612	91609739	91609636	91609711	AKAP9	NM_005751	1	50	3	+	91609603	91609647
224460601	chr7	91621366	91621517	91621394	91621490	AKAP9	NM_005751	1	50	4	+	91621472	91621525
224460718	chr7	91621468	91621622	91621493	91621594	AKAP9	NM_005751	1	50	4	+	91621472	91621525
223433634	chr7	91622240	91622405	91622260	91622377	AKAP9	NM_005751	1	50	5	+	91622199	91622369
332408412	chr7	91622062	91622286	91622088	91622259	AKAP9	NM_005751	1	50	5	+	91622199	91622369
223420515	chr7	91623937	91624062	91623965	91624031	AKAP9	NM_005751	1	50	6	+	91623935	91624090
223420540	chr7	91623982	91624107	91624007	91624074	AKAP9	NM_005751	1	50	6	+	91623935	91624090
332398095	chr7	91623764	91623988	91623790	91623964	AKAP9	NM_005751	1	50	6	+	91623935	91624090

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224413390	chr7	91624948	91625153	91624970	91625126	AKAP9	NM_005751	1	50	7	+	91624917	91625114
332757193	chr7	91624774	91624996	91624796	91624969	AKAP9	NM_005751	1	50	7	+	91624917	91625114
222654214	chr7	91632094	91632314	91632119	91632286	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222660691	chr7	91632259	91632462	91632287	91632434	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222664072	chr7	91632408	91632622	91632435	91632595	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222713662	chr7	91630426	91630644	91630447	91630620	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224460722	chr7	91630598	91630816	91630620	91630788	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224464905	chr7	91631072	91631296	91631096	91631269	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224468965	chr7	91630756	91630881	91630784	91630855	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224469905	chr7	91631252	91631448	91631279	91631420	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224470710	chr7	91631348	91631557	91631376	91631529	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224471011	chr7	91631439	91631636	91631467	91631609	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224473658	chr7	91630822	91630965	91630850	91630938	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224477058	chr7	91631578	91631777	91631606	91631748	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224478002	chr7	91630913	91631117	91630939	91631095	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224481857	chr7	91631721	91631861	91631749	91631834	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224482255	chr7	91631819	91632036	91631843	91632013	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224486019	chr7	91631836	91632058	91631864	91632030	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224486247	chr7	91632006	91632146	91632031	91632118	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222262238	chr7	91641634	91641780	91641667	91641760	AKAP9	NM_005751	1	50	9	+	91641743	91641956
222262253	chr7	91641741	91641903	91641769	91641877	AKAP9	NM_005751	1	50	9	+	91641743	91641956
222266906	chr7	91641807	91642021	91641836	91641996	AKAP9	NM_005751	1	50	9	+	91641743	91641956
222233508	chr7	91643474	91643635	91643495	91643607	AKAP9	NM_005751	1	50	10	+	91643563	91643642
222978904	chr7	91645488	91645684	91645516	91645656	AKAP9	NM_005751	1	50	11	+	91645443	91645581
333094468	chr7	91645293	91645515	91645320	91645487	AKAP9	NM_005751	1	50	11	+	91645443	91645581
222533459	chr7	91646212	91646432	91646236	91646407	AKAP9	NM_005751	1	50	12	+	91646331	91646416
222536443	chr7	91646382	91646537	91646408	91646509	AKAP9	NM_005751	1	50	12	+	91646331	91646416
223291853	chr7	91651558	91651760	91651581	91651731	AKAP9	NM_005751	1	50	13	+	91651552	91651666
332446425	chr7	91651388	91651608	91651416	91651580	AKAP9	NM_005751	1	50	13	+	91651552	91651666
223252646	chr7	91652049	91652263	91652077	91652235	AKAP9	NM_005751	1	50	14	+	91652128	91652323
223252989	chr7	91652212	91652436	91652236	91652410	AKAP9	NM_005751	1	50	14	+	91652128	91652323
223043830	chr7	91659133	91659298	91659158	91659266	AKAP9	NM_005751	1	50	15	+	91659209	91659305
223043846	chr7	91659249	91659434	91659274	91659402	AKAP9	NM_005751	1	50	15	+	91659209	91659305
222488576	chr7	91660820	91660973	91660848	91660945	AKAP9	NM_005751	1	50	16	+	91660826	91660918
222539784	chr7	91667611	91667793	91667633	91667766	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222546482	chr7	91667739	91667900	91667767	91667872	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222551477	chr7	91667830	91668048	91667857	91668021	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222555269	chr7	91667994	91668179	91668022	91668151	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222164949	chr7	91669870	91670071	91669900	91670043	AKAP9	NM_005751	1	50	18	+	91669988	91670212
222173926	chr7	91670014	91670220	91670042	91670193	AKAP9	NM_005751	1	50	18	+	91669988	91670212
332281896	chr7	91670165	91670386	91670194	91670360	AKAP9	NM_005751	1	50	18	+	91669988	91670212

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222164940	chr7	91671245	91671465	91671268	91671441	AKAP9	NM_005751	1	50	19	+	91671360	91671500
222171412	chr7	91671421	91671547	91671442	91671522	AKAP9	NM_005751	1	50	19	+	91671360	91671500
223544861	chr7	91671854	91672058	91671880	91672029	AKAP9	NM_005751	1	50	20	+	91671982	91672085
223556064	chr7	91671996	91672157	91672024	91672127	AKAP9	NM_005751	1	50	20	+	91671982	91672085
223882959	chr7	91674238	91674460	91674266	91674435	AKAP9	NM_005751	1	50	21	+	91674322	91674527
223889694	chr7	91674411	91674564	91674436	91674536	AKAP9	NM_005751	1	50	21	+	91674322	91674527
222669592	chr7	91681946	91682165	91681975	91682143	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222677239	chr7	91682123	91682340	91682144	91682312	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222892884	chr7	91690563	91690769	91690590	91690742	AKAP9	NM_005751	1	50	23	+	91690574	91690736
333800077	chr7	91690394	91690611	91690420	91690589	AKAP9	NM_005751	1	50	23	+	91690574	91690736
224115273	chr7	91691473	91691675	91691498	91691646	AKAP9	NM_005751	1	50	24	+	91691588	91691800
224118293	chr7	91691590	91691782	91691617	91691757	AKAP9	NM_005751	1	50	24	+	91691588	91691800
224124924	chr7	91691730	91691870	91691758	91691842	AKAP9	NM_005751	1	50	24	+	91691588	91691800
224492231	chr7	91694439	91694647	91694467	91694619	AKAP9	NM_005751	1	50	25	+	91694545	91694777
224492847	chr7	91694592	91694737	91694619	91694709	AKAP9	NM_005751	1	50	25	+	91694545	91694777
224494459	chr7	91694669	91694837	91694698	91694809	AKAP9	NM_005751	1	50	25	+	91694545	91694777
223782441	chr7	91695726	91695892	91695754	91695866	AKAP9	NM_005751	1	50	26	+	91695741	91695860
332953054	chr7	91695599	91695781	91695626	91695753	AKAP9	NM_005751	1	50	26	+	91695741	91695860
222446484	chr7	91699326	91699540	91699354	91699517	AKAP9	NM_005751	1	50	27	+	91699344	91699520
332564081	chr7	91699491	91699646	91699518	91699618	AKAP9	NM_005751	1	50	27	+	91699344	91699520
223209441	chr7	91700096	91700274	91700118	91700246	AKAP9	NM_005751	1	50	28	+	91700219	91700323
223211599	chr7	91700225	91700439	91700247	91700411	AKAP9	NM_005751	1	50	28	+	91700219	91700323
223931667	chr7	91706034	91706214	91706063	91706184	AKAP9	NM_005751	1	50	29	+	91706169	91706321
224425364	chr7	91706917	91707053	91706947	91707028	AKAP9	NM_005751	1	50	30	+	91707010	91707189
224425371	chr7	91707001	91707132	91707027	91707104	AKAP9	NM_005751	1	50	30	+	91707010	91707189
224430418	chr7	91707042	91707265	91707066	91707237	AKAP9	NM_005751	1	50	30	+	91707010	91707189
223483754	chr7	91708291	91708507	91708317	91708479	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223488432	chr7	91708451	91708671	91708480	91708645	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223500523	chr7	91708625	91708770	91708646	91708745	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223501147	chr7	91708802	91708996	91708826	91708970	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223510881	chr7	91708948	91709153	91708971	91709129	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223512026	chr7	91708718	91708853	91708746	91708825	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223519387	chr7	91709106	91709298	91709130	91709269	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223524897	chr7	91709239	91709389	91709267	91709360	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223529696	chr7	91709287	91709477	91709315	91709447	AKAP9	NM_005751	1	50	31	+	91708393	91709466
222336971	chr7	91711825	91711970	91711853	91711942	AKAP9	NM_005751	1	50	32	+	91711836	91711976
222337094	chr7	91711911	91712109	91711933	91712076	AKAP9	NM_005751	1	50	32	+	91711836	91711976
332432928	chr7	91711695	91711903	91711721	91711875	AKAP9	NM_005751	1	50	32	+	91711836	91711976
224044174	chr7	91712439	91712663	91712468	91712638	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224052762	chr7	91712616	91712830	91712639	91712801	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224068866	chr7	91712750	91712957	91712778	91712934	AKAP9	NM_005751	1	50	33	+	91712484	91712969

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224076414	chr7	91712908	91713072	91712935	91713047	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224318500	chr7	91713854	91714010	91713880	91713982	AKAP9	NM_005751	1	50	34	+	91713954	91714017
332299276	chr7	91713960	91714152	91713983	91714124	AKAP9	NM_005751	1	50	34	+	91713954	91714017
332303574	chr7	91713975	91714198	91714000	91714173	AKAP9	NM_005751	1	50	34	+	91713954	91714017
222167343	chr7	91714149	91714358	91714174	91714330	AKAP9	NM_005751	1	50	35	+	91714133	91714254
332303574	chr7	91713975	91714198	91714000	91714173	AKAP9	NM_005751	1	50	35	+	91714133	91714254
222333933	chr7	91714678	91714890	91714702	91714865	AKAP9	NM_005751	1	50	36	+	91714809	91715000
222353013	chr7	91714843	91715019	91714866	91714992	AKAP9	NM_005751	1	50	36	+	91714809	91715000
332386087	chr7	91714968	91715142	91714996	91715117	AKAP9	NM_005751	1	50	36	+	91714809	91715000
222609455	chr7	91715428	91715618	91715453	91715595	AKAP9	NM_005751	1	50	37	+	91715542	91715730
222612254	chr7	91715575	91715729	91715596	91715701	AKAP9	NM_005751	1	50	37	+	91715542	91715730
222613086	chr7	91715674	91715841	91715702	91715809	AKAP9	NM_005751	1	50	37	+	91715542	91715730
224695759	chr7	91718587	91718729	91718620	91718703	AKAP9	NM_005751	1	50	38	+	91718699	91718843
224701227	chr7	91718677	91718881	91718704	91718854	AKAP9	NM_005751	1	50	38	+	91718699	91718843
224419705	chr7	91722438	91722562	91722461	91722540	AKAP9	NM_005751	1	50	39	+	91722411	91722630
224432233	chr7	91722518	91722676	91722541	91722650	AKAP9	NM_005751	1	50	39	+	91722411	91722630
333621352	chr7	91722261	91722483	91722284	91722460	AKAP9	NM_005751	1	50	39	+	91722411	91722630
222469789	chr7	91724244	91724425	91724270	91724401	AKAP9	NM_005751	1	50	40	+	91724337	91724487
222474372	chr7	91724374	91724572	91724402	91724544	AKAP9	NM_005751	1	50	40	+	91724337	91724487
222164979	chr7	91726403	91726613	91726428	91726590	AKAP9	NM_005751	1	50	41	+	91726003	91726671
222174893	chr7	91726568	91726719	91726591	91726691	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224218976	chr7	91725985	91726203	91726012	91726175	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224244809	chr7	91726151	91726346	91726176	91726322	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224263135	chr7	91726300	91726449	91726323	91726427	AKAP9	NM_005751	1	50	41	+	91726003	91726671
225148020	chr7	91726826	91727018	91726855	91726990	AKAP9	NM_005751	1	50	42	+	91726900	91727108
225156563	chr7	91726963	91727164	91726990	91727143	AKAP9	NM_005751	1	50	42	+	91726900	91727108
223789797	chr7	91727296	91727516	91727323	91727487	AKAP9	NM_005751	1	50	43	+	91727423	91727528
223802796	chr7	91727427	91727606	91727455	91727578	AKAP9	NM_005751	1	50	43	+	91727423	91727528
223639004	chr7	91728909	91729068	91728931	91729041	AKAP9	NM_005751	1	50	44	+	91729001	91729183
223655430	chr7	91729017	91729241	91729042	91729213	AKAP9	NM_005751	1	50	44	+	91729001	91729183
223238062	chr7	91730178	91730401	91730202	91730375	AKAP9	NM_005751	1	50	45	+	91730170	91730370
333329500	chr7	91730025	91730224	91730049	91730201	AKAP9	NM_005751	1	50	45	+	91730170	91730370
223658806	chr7	91731848	91731981	91731875	91731956	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223662377	chr7	91731933	91732092	91731957	91732072	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223671643	chr7	91732050	91732225	91732073	91732197	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223471061	chr7	91734870	91735094	91734898	91735066	AKAP9	NM_005751	1	50	47	+	91734992	91735077
223234899	chr7	91736517	91736648	91736549	91736621	AKAP9	NM_005751	1	50	48	+	91736607	91736736
223235441	chr7	91736596	91736768	91736622	91736742	AKAP9	NM_005751	1	50	48	+	91736607	91736736
222701945	chr7	91737816	91737978	91737838	91737955	AKAP9	NM_005751	1	50	49	+	91737808	91737947
332928697	chr7	91737640	91737862	91737664	91737837	AKAP9	NM_005751	1	50	49	+	91737808	91737947
224431156	chr7	91739361	91739544	91739383	91739515	AKAP9	NM_005751	1	50	50	+	91739436	91739987

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224037450	chr7	91570303	91570523	91570321	91570506	AKAP9	NM_147185	2	50	1	+	91570189	91570461
224091035	chr7	91602942	91603148	91602965	91603121	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224095523	chr7	91603093	91603296	91603121	91603269	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224098698	chr7	91603232	91603378	91603261	91603353	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224642519	chr7	91609489	91609637	91609522	91609613	AKAP9	NM_147185	2	50	3	+	91609603	91609647
224642543	chr7	91609612	91609739	91609636	91609711	AKAP9	NM_147185	2	50	3	+	91609603	91609647
224460601	chr7	91621366	91621517	91621394	91621490	AKAP9	NM_147185	2	50	4	+	91621472	91621525
224460718	chr7	91621468	91621622	91621493	91621594	AKAP9	NM_147185	2	50	4	+	91621472	91621525
223433634	chr7	91622240	91622405	91622260	91622377	AKAP9	NM_147185	2	50	5	+	91622199	91622369
332408412	chr7	91622062	91622286	91622088	91622259	AKAP9	NM_147185	2	50	5	+	91622199	91622369
223420515	chr7	91623937	91624062	91623965	91624031	AKAP9	NM_147185	2	50	6	+	91623935	91624090
223420540	chr7	91623982	91624107	91624007	91624074	AKAP9	NM_147185	2	50	6	+	91623935	91624090
332398095	chr7	91623764	91623988	91623790	91623964	AKAP9	NM_147185	2	50	6	+	91623935	91624090
224413390	chr7	91624948	91625153	91624970	91625126	AKAP9	NM_147185	2	50	7	+	91624917	91625114
332757193	chr7	91624774	91624996	91624796	91624969	AKAP9	NM_147185	2	50	7	+	91624917	91625114
222654214	chr7	91632094	91632314	91632119	91632286	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222660691	chr7	91632259	91632462	91632287	91632434	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222664072	chr7	91632408	91632622	91632435	91632595	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222713662	chr7	91630426	91630644	91630447	91630620	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224460722	chr7	91630598	91630816	91630620	91630788	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224464905	chr7	91631072	91631296	91631096	91631269	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224468965	chr7	91630756	91630881	91630784	91630855	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224469905	chr7	91631252	91631448	91631279	91631420	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224470710	chr7	91631348	91631557	91631376	91631529	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224471011	chr7	91631439	91631636	91631467	91631609	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224473658	chr7	91630822	91630965	91630850	91630938	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224477058	chr7	91631578	91631777	91631606	91631748	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224478002	chr7	91630913	91631117	91630939	91631095	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224481857	chr7	91631721	91631861	91631749	91631834	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224482255	chr7	91631819	91632036	91631843	91632013	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224486019	chr7	91631836	91632058	91631864	91632030	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224486247	chr7	91632006	91632146	91632031	91632118	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222262238	chr7	91641634	91641780	91641667	91641760	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222262253	chr7	91641741	91641903	91641769	91641877	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222266906	chr7	91641807	91642021	91641836	91641996	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222233508	chr7	91643474	91643635	91643495	91643607	AKAP9	NM_147185	2	50	10	+	91643563	91643642
222978904	chr7	91645488	91645684	91645516	91645656	AKAP9	NM_147185	2	50	11	+	91645443	91645581
333094468	chr7	91645293	91645515	91645320	91645487	AKAP9	NM_147185	2	50	11	+	91645443	91645581
222533459	chr7	91646212	91646432	91646236	91646407	AKAP9	NM_147185	2	50	12	+	91646331	91646416
222536443	chr7	91646382	91646537	91646408	91646509	AKAP9	NM_147185	2	50	12	+	91646331	91646416
223291853	chr7	91651558	91651760	91651581	91651731	AKAP9	NM_147185	2	50	13	+	91651552	91651666

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332446425	chr7	91651388	91651608	91651416	91651580	AKAP9	NM_147185	2	50	13	+	91651552	91651666
223252646	chr7	91652049	91652263	91652077	91652235	AKAP9	NM_147185	2	50	14	+	91652128	91652323
223252989	chr7	91652212	91652436	91652236	91652410	AKAP9	NM_147185	2	50	14	+	91652128	91652323
223043830	chr7	91659133	91659298	91659158	91659266	AKAP9	NM_147185	2	50	15	+	91659209	91659305
223043846	chr7	91659249	91659434	91659274	91659402	AKAP9	NM_147185	2	50	15	+	91659209	91659305
222488576	chr7	91660820	91660973	91660848	91660945	AKAP9	NM_147185	2	50	16	+	91660826	91660918
222539784	chr7	91667611	91667793	91667633	91667766	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222546482	chr7	91667739	91667900	91667767	91667872	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222551477	chr7	91667830	91668048	91667857	91668021	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222555269	chr7	91667994	91668179	91668022	91668151	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222164949	chr7	91669870	91670071	91669900	91670043	AKAP9	NM_147185	2	50	18	+	91669988	91670212
222173926	chr7	91670014	91670220	91670042	91670193	AKAP9	NM_147185	2	50	18	+	91669988	91670212
332281896	chr7	91670165	91670386	91670194	91670360	AKAP9	NM_147185	2	50	18	+	91669988	91670212
222164940	chr7	91671245	91671465	91671268	91671441	AKAP9	NM_147185	2	50	19	+	91671360	91671500
222171412	chr7	91671421	91671547	91671442	91671522	AKAP9	NM_147185	2	50	19	+	91671360	91671500
223544861	chr7	91671854	91672058	91671880	91672029	AKAP9	NM_147185	2	50	20	+	91671982	91672085
223556064	chr7	91671996	91672157	91672024	91672127	AKAP9	NM_147185	2	50	20	+	91671982	91672085
223882959	chr7	91674238	91674460	91674266	91674435	AKAP9	NM_147185	2	50	21	+	91674322	91674527
223889694	chr7	91674411	91674564	91674436	91674536	AKAP9	NM_147185	2	50	21	+	91674322	91674527
222669592	chr7	91681946	91682165	91681975	91682143	AKAP9	NM_147185	2	50	22	+	91682040	91682272
222677239	chr7	91682123	91682340	91682144	91682312	AKAP9	NM_147185	2	50	22	+	91682040	91682272
222892884	chr7	91690563	91690769	91690590	91690742	AKAP9	NM_147185	2	50	23	+	91690574	91690736
333800077	chr7	91690394	91690611	91690420	91690589	AKAP9	NM_147185	2	50	23	+	91690574	91690736
224115273	chr7	91691473	91691675	91691498	91691646	AKAP9	NM_147185	2	50	24	+	91691588	91691800
224118293	chr7	91691590	91691782	91691617	91691757	AKAP9	NM_147185	2	50	24	+	91691588	91691800
224124924	chr7	91691730	91691870	91691758	91691842	AKAP9	NM_147185	2	50	24	+	91691588	91691800
224492231	chr7	91694439	91694647	91694467	91694619	AKAP9	NM_147185	2	50	25	+	91694545	91694777
224492847	chr7	91694592	91694737	91694619	91694709	AKAP9	NM_147185	2	50	25	+	91694545	91694777
224494459	chr7	91694669	91694837	91694698	91694809	AKAP9	NM_147185	2	50	25	+	91694545	91694777
223782441	chr7	91695726	91695892	91695754	91695866	AKAP9	NM_147185	2	50	26	+	91695741	91695860
332953054	chr7	91695599	91695781	91695626	91695753	AKAP9	NM_147185	2	50	26	+	91695741	91695860
222446484	chr7	91699326	91699540	91699354	91699517	AKAP9	NM_147185	2	50	27	+	91699344	91699496
223209441	chr7	91700096	91700274	91700118	91700246	AKAP9	NM_147185	2	50	28	+	91700219	91700323
223211599	chr7	91700225	91700439	91700247	91700411	AKAP9	NM_147185	2	50	28	+	91700219	91700323
223931667	chr7	91706034	91706214	91706063	91706184	AKAP9	NM_147185	2	50	29	+	91706169	91706321
224425364	chr7	91706917	91707053	91706947	91707028	AKAP9	NM_147185	2	50	30	+	91707010	91707189
224425371	chr7	91707001	91707132	91707027	91707104	AKAP9	NM_147185	2	50	30	+	91707010	91707189
224430418	chr7	91707042	91707265	91707066	91707237	AKAP9	NM_147185	2	50	30	+	91707010	91707189
223483754	chr7	91708291	91708507	91708317	91708479	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223488432	chr7	91708451	91708671	91708480	91708645	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223500523	chr7	91708625	91708770	91708646	91708745	AKAP9	NM_147185	2	50	31	+	91708393	91709466

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223501147	chr7	91708802	91708996	91708826	91708970	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223510881	chr7	91708948	91709153	91708971	91709129	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223512026	chr7	91708718	91708853	91708746	91708825	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223519387	chr7	91709106	91709298	91709130	91709269	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223524897	chr7	91709239	91709389	91709267	91709360	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223529696	chr7	91709287	91709477	91709315	91709447	AKAP9	NM_147185	2	50	31	+	91708393	91709466
222336971	chr7	91711825	91711970	91711853	91711942	AKAP9	NM_147185	2	50	32	+	91711836	91711976
222337094	chr7	91711911	91712109	91711933	91712076	AKAP9	NM_147185	2	50	32	+	91711836	91711976
332432928	chr7	91711695	91711903	91711721	91711875	AKAP9	NM_147185	2	50	32	+	91711836	91711976
224044174	chr7	91712439	91712663	91712468	91712638	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224052762	chr7	91712616	91712830	91712639	91712801	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224068866	chr7	91712750	91712957	91712778	91712934	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224076414	chr7	91712908	91713072	91712935	91713047	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224318500	chr7	91713854	91714010	91713880	91713982	AKAP9	NM_147185	2	50	34	+	91713954	91714017
332299276	chr7	91713960	91714152	91713983	91714124	AKAP9	NM_147185	2	50	34	+	91713954	91714017
332303574	chr7	91713975	91714198	91714000	91714173	AKAP9	NM_147185	2	50	34	+	91713954	91714017
222167343	chr7	91714149	91714358	91714174	91714330	AKAP9	NM_147185	2	50	35	+	91714133	91714254
332303574	chr7	91713975	91714198	91714000	91714173	AKAP9	NM_147185	2	50	35	+	91714133	91714254
222333933	chr7	91714678	91714890	91714702	91714865	AKAP9	NM_147185	2	50	36	+	91714809	91715000
222353013	chr7	91714843	91715019	91714866	91714992	AKAP9	NM_147185	2	50	36	+	91714809	91715000
332386087	chr7	91714968	91715142	91714996	91715117	AKAP9	NM_147185	2	50	36	+	91714809	91715000
222609455	chr7	91715428	91715618	91715453	91715595	AKAP9	NM_147185	2	50	37	+	91715542	91715730
222612254	chr7	91715575	91715729	91715596	91715701	AKAP9	NM_147185	2	50	37	+	91715542	91715730
222613086	chr7	91715674	91715841	91715702	91715809	AKAP9	NM_147185	2	50	37	+	91715542	91715730
224695759	chr7	91718587	91718729	91718620	91718703	AKAP9	NM_147185	2	50	38	+	91718699	91718843
224701227	chr7	91718677	91718881	91718704	91718854	AKAP9	NM_147185	2	50	38	+	91718699	91718843
224419705	chr7	91722438	91722562	91722461	91722540	AKAP9	NM_147185	2	50	39	+	91722411	91722630
224432233	chr7	91722518	91722676	91722541	91722650	AKAP9	NM_147185	2	50	39	+	91722411	91722630
333621352	chr7	91722261	91722483	91722284	91722460	AKAP9	NM_147185	2	50	39	+	91722411	91722630
222469789	chr7	91724244	91724425	91724270	91724401	AKAP9	NM_147185	2	50	40	+	91724337	91724487
222474372	chr7	91724374	91724572	91724402	91724544	AKAP9	NM_147185	2	50	40	+	91724337	91724487
222164979	chr7	91726403	91726613	91726428	91726590	AKAP9	NM_147185	2	50	41	+	91726003	91726671
222174893	chr7	91726568	91726719	91726591	91726691	AKAP9	NM_147185	2	50	41	+	91726003	91726671
224218976	chr7	91725985	91726203	91726012	91726175	AKAP9	NM_147185	2	50	41	+	91726003	91726671
224244809	chr7	91726151	91726346	91726176	91726322	AKAP9	NM_147185	2	50	41	+	91726003	91726671
224263135	chr7	91726300	91726449	91726323	91726427	AKAP9	NM_147185	2	50	41	+	91726003	91726671
225148020	chr7	91726826	91727018	91726855	91726990	AKAP9	NM_147185	2	50	42	+	91726900	91727108
225156563	chr7	91726963	91727164	91726990	91727143	AKAP9	NM_147185	2	50	42	+	91726900	91727108
223789797	chr7	91727296	91727516	91727323	91727487	AKAP9	NM_147185	2	50	43	+	91727423	91727528
223802796	chr7	91727427	91727606	91727455	91727578	AKAP9	NM_147185	2	50	43	+	91727423	91727528
223639004	chr7	91728909	91729068	91728931	91729041	AKAP9	NM_147185	2	50	44	+	91729001	91729183

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223655430	chr7	91729017	91729241	91729042	91729213	AKAP9	NM_147185	2	50	44	+	91729001	91729183
223238062	chr7	91730178	91730401	91730202	91730375	AKAP9	NM_147185	2	50	45	+	91730170	91730370
333329500	chr7	91730025	91730224	91730049	91730201	AKAP9	NM_147185	2	50	45	+	91730170	91730370
223658806	chr7	91731848	91731981	91731875	91731956	AKAP9	NM_147185	2	50	46	+	91731908	91732140
223662377	chr7	91731933	91732092	91731957	91732072	AKAP9	NM_147185	2	50	46	+	91731908	91732140
223671643	chr7	91732050	91732225	91732073	91732197	AKAP9	NM_147185	2	50	46	+	91731908	91732140
223471061	chr7	91734870	91735094	91734898	91735066	AKAP9	NM_147185	2	50	47	+	91734992	91735077
223234899	chr7	91736517	91736648	91736549	91736621	AKAP9	NM_147185	2	50	48	+	91736607	91736736
223235441	chr7	91736596	91736768	91736622	91736742	AKAP9	NM_147185	2	50	48	+	91736607	91736736
222701945	chr7	91737816	91737978	91737838	91737955	AKAP9	NM_147185	2	50	49	+	91737808	91737947
332928697	chr7	91737640	91737862	91737664	91737837	AKAP9	NM_147185	2	50	49	+	91737808	91737947
224431156	chr7	91739361	91739544	91739383	91739515	AKAP9	NM_147185	2	50	50	+	91739436	91739987
257387351	chr7	134143676	134143895	134143695	134143872	AKR1B1	NM_001628	1	10	1	-	134143749	134143888
263719124	chr7	134136223	134136446	134136246	134136425	AKR1B1	NM_001628	1	10	2	-	134136338	134136505
263764600	chr7	134136404	134136628	134136426	134136606	AKR1B1	NM_001628	1	10	2	-	134136338	134136505
266968374	chr7	134135471	134135686	134135493	134135664	AKR1B1	NM_001628	1	10	3	-	134135538	134135654
257524696	chr7	134134389	134134607	134134411	134134578	AKR1B1	NM_001628	1	10	4	-	134134472	134134549
254254655	chr7	134133680	134133898	134133703	134133876	AKR1B1	NM_001628	1	10	5	-	134133749	134133871
266680926	chr7	134133051	134133274	134133076	134133250	AKR1B1	NM_001628	1	10	6	-	134133139	134133245
265304540	chr7	134132619	134132843	134132642	134132818	AKR1B1	NM_001628	1	10	7	-	134132732	134132813
263590435	chr7	134131964	134132156	134131987	134132136	AKR1B1	NM_001628	1	10	8	-	134132050	134132133
262760168	chr7	134129929	134130143	134129951	134130116	AKR1B1	NM_001628	1	10	9	-	134129990	134130072
264589722	chr7	134127359	134127582	134127380	134127554	AKR1B1	NM_001628	1	10	10	-	134127107	134127522
260591757	chr1	21880519	21880671	21880539	21880649	ALPL	NM_000478	1	12	2	+	21880471	21880635
266339340	chr1	21887076	21887286	21887098	21887264	ALPL	NM_000478	1	12	3	+	21887119	21887238
258982444	chr1	21887443	21887640	21887466	21887620	ALPL	NM_000478	1	12	4	+	21887590	21887705
258995683	chr1	21887591	21887737	21887611	21887718	ALPL	NM_000478	1	12	4	+	21887590	21887705
263018004	chr1	21889571	21889785	21889590	21889767	ALPL	NM_000478	1	12	5	+	21889603	21889777
263026018	chr1	21889736	21889944	21889755	21889924	ALPL	NM_000478	1	12	5	+	21889603	21889777
262132513	chr1	21890490	21890714	21890511	21890692	ALPL	NM_000478	1	12	6	+	21890534	21890709
262159587	chr1	21890673	21890861	21890693	21890840	ALPL	NM_000478	1	12	6	+	21890534	21890709
264055185	chr1	21894478	21894674	21894498	21894650	ALPL	NM_000478	1	12	7	+	21894597	21894740
264104950	chr1	21894623	21894839	21894651	21894816	ALPL	NM_000478	1	12	7	+	21894597	21894740
254150424	chr1	21896700	21896908	21896724	21896891	ALPL	NM_000478	1	12	8	+	21896798	21896867
255096802	chr1	21900118	21900342	21900138	21900324	ALPL	NM_000478	1	12	9	+	21900158	21900292
259620070	chr1	21902173	21902396	21902194	21902374	ALPL	NM_000478	1	12	10	+	21902226	21902417
259653869	chr1	21902349	21902532	21902368	21902510	ALPL	NM_000478	1	12	10	+	21902226	21902417
256622079	chr1	21902980	21903201	21902999	21903181	ALPL	NM_000478	1	12	11	+	21903015	21903134
264890294	chr1	21903842	21904030	21903862	21904012	ALPL	NM_000478	1	12	12	+	21903876	21904905
264892401	chr1	21903986	21904192	21904007	21904171	ALPL	NM_000478	1	12	12	+	21903876	21904905
266339340	chr1	21887076	21887286	21887098	21887264	ALPL	NM_001127501	2	11	2	+	21887119	21887238

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258982444	chr1	21887443	21887640	21887466	21887620	ALPL	NM_001127501	2	11	3	+	21887590	21887705
258995683	chr1	21887591	21887737	21887611	21887718	ALPL	NM_001127501	2	11	3	+	21887590	21887705
263018004	chr1	21889571	21889785	21889590	21889767	ALPL	NM_001127501	2	11	4	+	21889603	21889777
263026018	chr1	21889736	21889944	21889755	21889924	ALPL	NM_001127501	2	11	4	+	21889603	21889777
262132513	chr1	21890490	21890714	21890511	21890692	ALPL	NM_001127501	2	11	5	+	21890534	21890709
262159587	chr1	21890673	21890861	21890693	21890840	ALPL	NM_001127501	2	11	5	+	21890534	21890709
264055185	chr1	21894478	21894674	21894498	21894650	ALPL	NM_001127501	2	11	6	+	21894597	21894740
264104950	chr1	21894623	21894839	21894651	21894816	ALPL	NM_001127501	2	11	6	+	21894597	21894740
254150424	chr1	21896700	21896908	21896724	21896891	ALPL	NM_001127501	2	11	7	+	21896798	21896867
255096802	chr1	21900118	21900342	21900138	21900324	ALPL	NM_001127501	2	11	8	+	21900158	21900292
259620070	chr1	21902173	21902396	21902194	21902374	ALPL	NM_001127501	2	11	9	+	21902226	21902417
259653869	chr1	21902349	21902532	21902368	21902510	ALPL	NM_001127501	2	11	9	+	21902226	21902417
256622079	chr1	21902980	21903201	21902999	21903181	ALPL	NM_001127501	2	11	10	+	21903015	21903134
264890294	chr1	21903842	21904030	21903862	21904012	ALPL	NM_001127501	2	11	11	+	21903876	21904905
264892401	chr1	21903986	21904192	21904007	21904171	ALPL	NM_001127501	2	11	11	+	21903876	21904905
266339340	chr1	21887076	21887286	21887098	21887264	ALPL	NM_001177520	3	10	2	+	21887119	21887238
263018004	chr1	21889571	21889785	21889590	21889767	ALPL	NM_001177520	3	10	3	+	21889603	21889777
263026018	chr1	21889736	21889944	21889755	21889924	ALPL	NM_001177520	3	10	3	+	21889603	21889777
262132513	chr1	21890490	21890714	21890511	21890692	ALPL	NM_001177520	3	10	4	+	21890534	21890709
262159587	chr1	21890673	21890861	21890693	21890840	ALPL	NM_001177520	3	10	4	+	21890534	21890709
264055185	chr1	21894478	21894674	21894498	21894650	ALPL	NM_001177520	3	10	5	+	21894597	21894740
264104950	chr1	21894623	21894839	21894651	21894816	ALPL	NM_001177520	3	10	5	+	21894597	21894740
254150424	chr1	21896700	21896908	21896724	21896891	ALPL	NM_001177520	3	10	6	+	21896798	21896867
255096802	chr1	21900118	21900342	21900138	21900324	ALPL	NM_001177520	3	10	7	+	21900158	21900292
259620070	chr1	21902173	21902396	21902194	21902374	ALPL	NM_001177520	3	10	8	+	21902226	21902417
259653869	chr1	21902349	21902532	21902368	21902510	ALPL	NM_001177520	3	10	8	+	21902226	21902417
256622079	chr1	21902980	21903201	21902999	21903181	ALPL	NM_001177520	3	10	9	+	21903015	21903134
264890294	chr1	21903842	21904030	21903862	21904012	ALPL	NM_001177520	3	10	10	+	21903876	21904905
264892401	chr1	21903986	21904192	21904007	21904171	ALPL	NM_001177520	3	10	10	+	21903876	21904905
255025870	chr3	49459766	49459963	49459788	49459942	AMT	NM_000481	1	9	1	-	49459794	49460111
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_000481	1	9	1	-	49459794	49460111
261771496	chr3	49459468	49459690	49459490	49459669	AMT	NM_000481	1	9	2	-	49459537	49459704
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_000481	1	9	2	-	49459537	49459704
263147793	chr3	49458811	49459033	49458833	49459010	AMT	NM_000481	1	9	3	-	49458925	49459005
266690177	chr3	49457499	49457716	49457520	49457694	AMT	NM_000481	1	9	4	-	49457644	49457775
266735109	chr3	49457675	49457804	49457695	49457783	AMT	NM_000481	1	9	4	-	49457644	49457775
256522995	chr3	49457030	49457251	49457054	49457228	AMT	NM_000481	1	9	5	-	49457143	49457221
264067451	chr3	49456677	49456883	49456699	49456862	AMT	NM_000481	1	9	6	-	49456693	49456838
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_000481	1	9	6	-	49456693	49456838
264769376	chr3	49456248	49456472	49456271	49456448	AMT	NM_000481	1	9	7	-	49456404	49456584
264819778	chr3	49456426	49456625	49456449	49456604	AMT	NM_000481	1	9	7	-	49456404	49456584

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_000481	1	9	7	-	49456404	49456584
261453537	chr3	49455215	49455437	49455236	49455411	AMT	NM_000481	1	9	8	-	49455251	49455406
258838454	chr3	49454676	49454875	49454699	49454851	AMT	NM_000481	1	9	9	-	49454211	49455151
262150561	chr3	49454797	49455020	49454820	49454999	AMT	NM_000481	1	9	9	-	49454211	49455151
262229167	chr3	49454971	49455180	49454999	49455160	AMT	NM_000481	1	9	9	-	49454211	49455151
255025870	chr3	49459766	49459963	49459788	49459942	AMT	NM_001164710	2	8	1	-	49459794	49460111
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_001164710	2	8	1	-	49459794	49460111
261771496	chr3	49459468	49459690	49459490	49459669	AMT	NM_001164710	2	8	2	-	49459537	49459704
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_001164710	2	8	2	-	49459537	49459704
263147793	chr3	49458811	49459033	49458833	49459010	AMT	NM_001164710	2	8	3	-	49458925	49459005
256522995	chr3	49457030	49457251	49457054	49457228	AMT	NM_001164710	2	8	4	-	49457143	49457221
264067451	chr3	49456677	49456883	49456699	49456862	AMT	NM_001164710	2	8	5	-	49456693	49456838
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164710	2	8	5	-	49456693	49456838
264769376	chr3	49456248	49456472	49456271	49456448	AMT	NM_001164710	2	8	6	-	49456404	49456584
264819778	chr3	49456426	49456625	49456449	49456604	AMT	NM_001164710	2	8	6	-	49456404	49456584
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164710	2	8	6	-	49456404	49456584
261453537	chr3	49455215	49455437	49455236	49455411	AMT	NM_001164710	2	8	7	-	49455251	49455406
258838454	chr3	49454676	49454875	49454699	49454851	AMT	NM_001164710	2	8	8	-	49454211	49455151
262150561	chr3	49454797	49455020	49454820	49454999	AMT	NM_001164710	2	8	8	-	49454211	49455151
262229167	chr3	49454971	49455180	49454999	49455160	AMT	NM_001164710	2	8	8	-	49454211	49455151
255025870	chr3	49459766	49459963	49459788	49459942	AMT	NM_001164711	3	8	1	-	49459794	49460111
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_001164711	3	8	1	-	49459794	49460111
263147793	chr3	49458811	49459033	49458833	49459010	AMT	NM_001164711	3	8	2	-	49458925	49459005
266690177	chr3	49457499	49457716	49457520	49457694	AMT	NM_001164711	3	8	3	-	49457644	49457775
266735109	chr3	49457675	49457804	49457695	49457783	AMT	NM_001164711	3	8	3	-	49457644	49457775
256522995	chr3	49457030	49457251	49457054	49457228	AMT	NM_001164711	3	8	4	-	49457143	49457221
264067451	chr3	49456677	49456883	49456699	49456862	AMT	NM_001164711	3	8	5	-	49456693	49456838
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164711	3	8	5	-	49456693	49456838
264769376	chr3	49456248	49456472	49456271	49456448	AMT	NM_001164711	3	8	6	-	49456404	49456584
264819778	chr3	49456426	49456625	49456449	49456604	AMT	NM_001164711	3	8	6	-	49456404	49456584
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164711	3	8	6	-	49456404	49456584
261453537	chr3	49455215	49455437	49455236	49455411	AMT	NM_001164711	3	8	7	-	49455251	49455406
258838454	chr3	49454676	49454875	49454699	49454851	AMT	NM_001164711	3	8	8	-	49454211	49455151
262150561	chr3	49454797	49455020	49454820	49454999	AMT	NM_001164711	3	8	8	-	49454211	49455151
262229167	chr3	49454971	49455180	49454999	49455160	AMT	NM_001164711	3	8	8	-	49454211	49455151
255025870	chr3	49459766	49459963	49459788	49459942	AMT	NM_001164712	4	10	1	-	49459794	49460111
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_001164712	4	10	1	-	49459794	49460111
261771496	chr3	49459468	49459690	49459490	49459669	AMT	NM_001164712	4	10	2	-	49459537	49459704
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NM_001164712	4	10	2	-	49459537	49459704
263147793	chr3	49458811	49459033	49458833	49459010	AMT	NM_001164712	4	10	3	-	49458925	49459005
266690177	chr3	49457499	49457716	49457520	49457694	AMT	NM_001164712	4	10	4	-	49457644	49457775

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266735109	chr3	49457675	49457804	49457695	49457783	AMT	NM_001164712	4	10	4	-	49457644	49457775
256522995	chr3	49457030	49457251	49457054	49457228	AMT	NM_001164712	4	10	5	-	49457143	49457221
264067451	chr3	49456677	49456883	49456699	49456862	AMT	NM_001164712	4	10	6	-	49456693	49456838
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164712	4	10	6	-	49456693	49456838
264769376	chr3	49456248	49456472	49456271	49456448	AMT	NM_001164712	4	10	7	-	49456404	49456584
264819778	chr3	49456426	49456625	49456449	49456604	AMT	NM_001164712	4	10	7	-	49456404	49456584
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NM_001164712	4	10	7	-	49456404	49456584
261453537	chr3	49455215	49455437	49455236	49455411	AMT	NM_001164712	4	10	8	-	49455251	49455406
262229167	chr3	49454971	49455180	49454999	49455160	AMT	NM_001164712	4	10	9	-	49455048	49455151
258838454	chr3	49454676	49454875	49454699	49454851	AMT	NM_001164712	4	10	10	-	49454211	49454800
255025870	chr3	49459766	49459963	49459788	49459942	AMT	NR_028435	5	9	1	-	49459794	49460111
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NR_028435	5	9	1	-	49459794	49460111
261771496	chr3	49459468	49459690	49459490	49459669	AMT	NR_028435	5	9	2	-	49459537	49459690
261780504	chr3	49459602	49459823	49459621	49459801	AMT	NR_028435	5	9	2	-	49459537	49459690
263147793	chr3	49458811	49459033	49458833	49459010	AMT	NR_028435	5	9	3	-	49458925	49459005
266690177	chr3	49457499	49457716	49457520	49457694	AMT	NR_028435	5	9	4	-	49457644	49457775
266735109	chr3	49457675	49457804	49457695	49457783	AMT	NR_028435	5	9	4	-	49457644	49457775
256522995	chr3	49457030	49457251	49457054	49457228	AMT	NR_028435	5	9	5	-	49457143	49457221
264067451	chr3	49456677	49456883	49456699	49456862	AMT	NR_028435	5	9	6	-	49456693	49456838
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NR_028435	5	9	6	-	49456693	49456838
264769376	chr3	49456248	49456472	49456271	49456448	AMT	NR_028435	5	9	7	-	49456404	49456584
264819778	chr3	49456426	49456625	49456449	49456604	AMT	NR_028435	5	9	7	-	49456404	49456584
264834760	chr3	49456518	49456719	49456543	49456698	AMT	NR_028435	5	9	7	-	49456404	49456584
261453537	chr3	49455215	49455437	49455236	49455411	AMT	NR_028435	5	9	8	-	49455251	49455406
258838454	chr3	49454676	49454875	49454699	49454851	AMT	NR_028435	5	9	9	-	49454211	49455151
262150561	chr3	49454797	49455020	49454820	49454999	AMT	NR_028435	5	9	9	-	49454211	49455151
262229167	chr3	49454971	49455180	49454999	49455160	AMT	NR_028435	5	9	9	-	49454211	49455151
333586457	chr4	113825495	113825675	113825517	113825652	ANK2	NM_001127493	1	47	2	+	113825611	113825670
332375804	chr4	114095475	114095699	114095504	114095679	ANK2	NM_001127493	1	47	3	+	114095572	114095673
332484014	chr4	114117430	114117635	114117456	114117606	ANK2	NM_001127493	1	47	4	+	114117524	114117622
333430694	chr4	114120084	114120292	114120109	114120264	ANK2	NM_001127493	1	47	5	+	114120167	114120265
333827433	chr4	114153225	114153441	114153252	114153420	ANK2	NM_001127493	1	47	6	+	114153317	114153415
332498539	chr4	114157985	114158171	114158018	114158149	ANK2	NM_001127493	1	47	7	+	114158143	114158328
332498646	chr4	114158127	114158284	114158150	114158263	ANK2	NM_001127493	1	47	7	+	114158143	114158328
332509342	chr4	114158243	114158368	114158264	114158341	ANK2	NM_001127493	1	47	7	+	114158143	114158328
332964764	chr4	114158633	114158850	114158657	114158823	ANK2	NM_001127493	1	47	8	+	114158755	114158778
332503337	chr4	114161601	114161825	114161625	114161797	ANK2	NM_001127493	1	47	9	+	114161641	114161739
332629268	chr4	114163213	114163428	114163233	114163400	ANK2	NM_001127493	1	47	10	+	114163267	114163365
333326438	chr4	114170835	114171056	114170860	114171029	ANK2	NM_001127493	1	47	11	+	114170920	114171018
332992835	chr4	114176741	114176961	114176770	114176940	ANK2	NM_001127493	1	47	12	+	114176891	114177088
333002295	chr4	114176921	114177115	114176941	114177093	ANK2	NM_001127493	1	47	12	+	114176891	114177088

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333327823	chr4	114179121	114179340	114179143	114179313	ANK2	NM_001127493	1	47	13	+	114179206	114179304
333373103	chr4	114179371	114179595	114179397	114179572	ANK2	NM_001127493	1	47	14	+	114179469	114179567
332652512	chr4	114186001	114186189	114186021	114186166	ANK2	NM_001127493	1	47	15	+	114186053	114186151
332948560	chr4	114195501	114195682	114195525	114195657	ANK2	NM_001127493	1	47	16	+	114195608	114195805
332963013	chr4	114195637	114195837	114195658	114195810	ANK2	NM_001127493	1	47	16	+	114195608	114195805
332618707	chr4	114198832	114199035	114198860	114199013	ANK2	NM_001127493	1	47	17	+	114198993	114199091
332620477	chr4	114198992	114199192	114199014	114199167	ANK2	NM_001127493	1	47	17	+	114198993	114199091
333114117	chr4	114199559	114199751	114199579	114199725	ANK2	NM_001127493	1	47	18	+	114199616	114199714
332881524	chr4	114203668	114203892	114203695	114203866	ANK2	NM_001127493	1	47	19	+	114203831	114204028
332884664	chr4	114203843	114204067	114203867	114204039	ANK2	NM_001127493	1	47	19	+	114203831	114204028
333207501	chr4	114208717	114208892	114208745	114208865	ANK2	NM_001127493	1	47	20	+	114208761	114208859
332945350	chr4	114209445	114209613	114209471	114209585	ANK2	NM_001127493	1	47	21	+	114209544	114209642
332948459	chr4	114209562	114209691	114209586	114209663	ANK2	NM_001127493	1	47	21	+	114209544	114209642
333774879	chr4	114213513	114213714	114213538	114213690	ANK2	NM_001127493	1	47	22	+	114213572	114213670
333275277	chr4	114214530	114214723	114214550	114214699	ANK2	NM_001127493	1	47	23	+	114214596	114214694
332408000	chr4	114223835	114224036	114223855	114224008	ANK2	NM_001127493	1	47	24	+	114223923	114223995
333364528	chr4	114232377	114232599	114232405	114232572	ANK2	NM_001127493	1	47	25	+	114232411	114232555
332716298	chr4	114238782	114238995	114238802	114238970	ANK2	NM_001127493	1	47	26	+	114238863	114238965
333343659	chr4	114239630	114239825	114239658	114239797	ANK2	NM_001127493	1	47	27	+	114239673	114239776
333557642	chr4	114244772	114244994	114244801	114244966	ANK2	NM_001127493	1	47	28	+	114244915	114244950
333140278	chr4	114251264	114251483	114251289	114251459	ANK2	NM_001127493	1	47	29	+	114251402	114251626
333151738	chr4	114251439	114251661	114251460	114251633	ANK2	NM_001127493	1	47	29	+	114251402	114251626
332331440	chr4	114253057	114253258	114253079	114253231	ANK2	NM_001127493	1	47	30	+	114253128	114253226
333365408	chr4	114254145	114254361	114254167	114254333	ANK2	NM_001127493	1	47	31	+	114254210	114254364
333376707	chr4	114254306	114254446	114254334	114254418	ANK2	NM_001127493	1	47	31	+	114254210	114254364
332580379	chr4	114256893	114257116	114256917	114257093	ANK2	NM_001127493	1	47	32	+	114257002	114257213
332604813	chr4	114257071	114257295	114257094	114257266	ANK2	NM_001127493	1	47	32	+	114257002	114257213
333396912	chr4	114257594	114257800	114257616	114257775	ANK2	NM_001127493	1	47	33	+	114257733	114257937
333404176	chr4	114257752	114257974	114257776	114257949	ANK2	NM_001127493	1	47	33	+	114257733	114257937
332583042	chr4	114260327	114260521	114260353	114260493	ANK2	NM_001127493	1	47	34	+	114260382	114260478
333702320	chr4	114262738	114262892	114262766	114262868	ANK2	NM_001127493	1	47	35	+	114262844	114263072
333702952	chr4	114262845	114263033	114262869	114263005	ANK2	NM_001127493	1	47	35	+	114262844	114263072
333721753	chr4	114262983	114263196	114263006	114263169	ANK2	NM_001127493	1	47	35	+	114262844	114263072
333072157	chr4	114263986	114264205	114264012	114264179	ANK2	NM_001127493	1	47	36	+	114264173	114264298
333079736	chr4	114264152	114264366	114264180	114264338	ANK2	NM_001127493	1	47	36	+	114264173	114264298
332763460	chr4	114267012	114267216	114267035	114267188	ANK2	NM_001127493	1	47	37	+	114267056	114267178
333632867	chr4	114269297	114269497	114269322	114269475	ANK2	NM_001127493	1	47	38	+	114269432	114269464
333116494	chr4	114271239	114271448	114271268	114271421	ANK2	NM_001127493	1	47	39	+	114271384	114271405
333083353	chr4	114281883	114282083	114281910	114282059	ANK2	NM_001127493	1	47	40	+	114281979	114282053
333191860	chr4	114284426	114284585	114284454	114284563	ANK2	NM_001127493	1	47	41	+	114284494	114284625
333197058	chr4	114284538	114284672	114284564	114284645	ANK2	NM_001127493	1	47	41	+	114284494	114284625

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333517623	chr4	114286031	114286252	114286056	114286224	ANK2	NM_001127493	1	47	42	+	114286195	114286338
333524763	chr4	114286202	114286419	114286225	114286396	ANK2	NM_001127493	1	47	42	+	114286195	114286338
333015093	chr4	114288595	114288757	114288615	114288734	ANK2	NM_001127493	1	47	43	+	114288722	114289007
333020969	chr4	114288713	114288870	114288735	114288845	ANK2	NM_001127493	1	47	43	+	114288722	114289007
333034625	chr4	114288822	114289043	114288846	114289015	ANK2	NM_001127493	1	47	43	+	114288722	114289007
332325208	chr4	114290616	114290839	114290638	114290816	ANK2	NM_001127493	1	47	44	+	114290670	114290961
332348662	chr4	114290770	114290989	114290792	114290967	ANK2	NM_001127493	1	47	44	+	114290670	114290961
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_001127493	1	47	45	+	114294246	114294329
332553329	chr4	114294164	114294371	114294191	114294343	ANK2	NM_001127493	1	47	45	+	114294246	114294329
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_001127493	1	47	46	+	114294441	114294605
332324907	chr4	114294445	114294661	114294474	114294634	ANK2	NM_001127493	1	47	46	+	114294441	114294605
333074387	chr4	114302478	114302674	114302506	114302652	ANK2	NM_001127493	1	47	47	+	114302613	114304896
333577144	chr4	113970841	113971051	113970862	113971024	ANK2	NM_001148	2	46	1	+	113970785	113970968
332375804	chr4	114095475	114095699	114095504	114095679	ANK2	NM_001148	2	46	2	+	114095572	114095673
332484014	chr4	114117430	114117635	114117456	114117606	ANK2	NM_001148	2	46	3	+	114117524	114117622
333430694	chr4	114120084	114120292	114120109	114120264	ANK2	NM_001148	2	46	4	+	114120167	114120265
333827433	chr4	114153225	114153441	114153252	114153420	ANK2	NM_001148	2	46	5	+	114153317	114153415
332498539	chr4	114157985	114158171	114158018	114158149	ANK2	NM_001148	2	46	6	+	114158143	114158328
332498646	chr4	114158127	114158284	114158150	114158263	ANK2	NM_001148	2	46	6	+	114158143	114158328
332509342	chr4	114158243	114158368	114158264	114158341	ANK2	NM_001148	2	46	6	+	114158143	114158328
332964764	chr4	114158633	114158850	114158657	114158823	ANK2	NM_001148	2	46	7	+	114158755	114158778
332503337	chr4	114161601	114161825	114161625	114161797	ANK2	NM_001148	2	46	8	+	114161641	114161739
332629268	chr4	114163213	114163428	114163233	114163400	ANK2	NM_001148	2	46	9	+	114163267	114163365
333326438	chr4	114170835	114171056	114170860	114171029	ANK2	NM_001148	2	46	10	+	114170920	114171018
332992835	chr4	114176741	114176961	114176770	114176940	ANK2	NM_001148	2	46	11	+	114176891	114177088
333002295	chr4	114176921	114177115	114176941	114177093	ANK2	NM_001148	2	46	11	+	114176891	114177088
333327823	chr4	114179121	114179340	114179143	114179313	ANK2	NM_001148	2	46	12	+	114179206	114179304
333373103	chr4	114179371	114179595	114179397	114179572	ANK2	NM_001148	2	46	13	+	114179469	114179567
332652512	chr4	114186001	114186189	114186021	114186166	ANK2	NM_001148	2	46	14	+	114186053	114186151
332948560	chr4	114195501	114195682	114195525	114195657	ANK2	NM_001148	2	46	15	+	114195608	114195805
332963013	chr4	114195637	114195837	114195658	114195810	ANK2	NM_001148	2	46	15	+	114195608	114195805
332618707	chr4	114198832	114199035	114198860	114199013	ANK2	NM_001148	2	46	16	+	114198993	114199091
332620477	chr4	114198992	114199192	114199014	114199167	ANK2	NM_001148	2	46	16	+	114198993	114199091
333114117	chr4	114199559	114199751	114199579	114199725	ANK2	NM_001148	2	46	17	+	114199616	114199714
332881524	chr4	114203668	114203892	114203695	114203866	ANK2	NM_001148	2	46	18	+	114203831	114204028
332884664	chr4	114203843	114204067	114203867	114204039	ANK2	NM_001148	2	46	18	+	114203831	114204028
333207501	chr4	114208717	114208892	114208745	114208865	ANK2	NM_001148	2	46	19	+	114208761	114208859
332945350	chr4	114209445	114209613	114209471	114209585	ANK2	NM_001148	2	46	20	+	114209544	114209642
332948459	chr4	114209562	114209691	114209586	114209663	ANK2	NM_001148	2	46	20	+	114209544	114209642
333774879	chr4	114213513	114213714	114213538	114213690	ANK2	NM_001148	2	46	21	+	114213572	114213670
333275277	chr4	114214530	114214723	114214550	114214699	ANK2	NM_001148	2	46	22	+	114214596	114214694

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332408000	chr4	114223835	114224036	114223855	114224008	ANK2	NM_001148	2	46	23	+	114223923	114223995
333364528	chr4	114232377	114232599	114232405	114232572	ANK2	NM_001148	2	46	24	+	114232411	114232555
332716298	chr4	114238782	114238995	114238802	114238970	ANK2	NM_001148	2	46	25	+	114238863	114238965
333343659	chr4	114239630	114239825	114239658	114239797	ANK2	NM_001148	2	46	26	+	114239673	114239776
333140278	chr4	114251264	114251483	114251289	114251459	ANK2	NM_001148	2	46	27	+	114251402	114251626
333151738	chr4	114251439	114251661	114251460	114251633	ANK2	NM_001148	2	46	27	+	114251402	114251626
332331440	chr4	114253057	114253258	114253079	114253231	ANK2	NM_001148	2	46	28	+	114253128	114253226
333365408	chr4	114254145	114254361	114254167	114254333	ANK2	NM_001148	2	46	29	+	114254210	114254364
333376707	chr4	114254306	114254446	114254334	114254418	ANK2	NM_001148	2	46	29	+	114254210	114254364
332580379	chr4	114256893	114257116	114256917	114257093	ANK2	NM_001148	2	46	30	+	114257002	114257213
332604813	chr4	114257071	114257295	114257094	114257266	ANK2	NM_001148	2	46	30	+	114257002	114257213
333396912	chr4	114257594	114257800	114257616	114257775	ANK2	NM_001148	2	46	31	+	114257733	114257937
333404176	chr4	114257752	114257974	114257776	114257949	ANK2	NM_001148	2	46	31	+	114257733	114257937
332583042	chr4	114260327	114260521	114260353	114260493	ANK2	NM_001148	2	46	32	+	114260382	114260478
333702320	chr4	114262738	114262892	114262766	114262868	ANK2	NM_001148	2	46	33	+	114262844	114263072
333702952	chr4	114262845	114263033	114262869	114263005	ANK2	NM_001148	2	46	33	+	114262844	114263072
333721753	chr4	114262983	114263196	114263006	114263169	ANK2	NM_001148	2	46	33	+	114262844	114263072
333072157	chr4	114263986	114264205	114264012	114264179	ANK2	NM_001148	2	46	34	+	114264173	114264298
333079736	chr4	114264152	114264366	114264180	114264338	ANK2	NM_001148	2	46	34	+	114264173	114264298
332763460	chr4	114267012	114267216	114267035	114267188	ANK2	NM_001148	2	46	35	+	114267056	114267178
333632867	chr4	114269297	114269497	114269322	114269475	ANK2	NM_001148	2	46	36	+	114269432	114269464
333116494	chr4	114271239	114271448	114271268	114271421	ANK2	NM_001148	2	46	37	+	114271384	114271405
332840130	chr4	114275244	114275441	114275271	114275416	ANK2	NM_001148	2	46	38	+	114274201	114280455
332856387	chr4	114275374	114275596	114275395	114275575	ANK2	NM_001148	2	46	38	+	114274201	114280455
332867593	chr4	114275554	114275760	114275575	114275740	ANK2	NM_001148	2	46	38	+	114274201	114280455
332888381	chr4	114279689	114279900	114279712	114279879	ANK2	NM_001148	2	46	38	+	114274201	114280455
332889625	chr4	114277142	114277366	114277165	114277345	ANK2	NM_001148	2	46	38	+	114274201	114280455
332891235	chr4	114275716	114275888	114275741	114275863	ANK2	NM_001148	2	46	38	+	114274201	114280455
332893511	chr4	114274667	114274857	114274690	114274833	ANK2	NM_001148	2	46	38	+	114274201	114280455
332916303	chr4	114274810	114274991	114274834	114274963	ANK2	NM_001148	2	46	38	+	114274201	114280455
332916320	chr4	114277324	114277521	114277346	114277498	ANK2	NM_001148	2	46	38	+	114274201	114280455
332916893	chr4	114279854	114280075	114279878	114280054	ANK2	NM_001148	2	46	38	+	114274201	114280455
332924504	chr4	114275838	114276059	114275864	114276035	ANK2	NM_001148	2	46	38	+	114274201	114280455
332930461	chr4	114274936	114275132	114274964	114275108	ANK2	NM_001148	2	46	38	+	114274201	114280455
332932500	chr4	114277476	114277696	114277499	114277671	ANK2	NM_001148	2	46	38	+	114274201	114280455
332936631	chr4	114280034	114280254	114280055	114280229	ANK2	NM_001148	2	46	38	+	114274201	114280455
332942356	chr4	114276013	114276236	114276036	114276209	ANK2	NM_001148	2	46	38	+	114274201	114280455
332942419	chr4	114278618	114278779	114278645	114278752	ANK2	NM_001148	2	46	38	+	114274201	114280455
332947719	chr4	114275089	114275295	114275109	114275270	ANK2	NM_001148	2	46	38	+	114274201	114280455
332958796	chr4	114278728	114278945	114278753	114278925	ANK2	NM_001148	2	46	38	+	114274201	114280455
332979125	chr4	114278900	114279118	114278926	114279093	ANK2	NM_001148	2	46	38	+	114274201	114280455

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332995582	chr4	114279069	114279232	114279094	114279211	ANK2	NM_001148	2	46	38	+	114274201	114280455
333679208	chr4	114274041	114274263	114274062	114274237	ANK2	NM_001148	2	46	38	+	114274201	114280455
333683550	chr4	114277649	114277870	114277672	114277847	ANK2	NM_001148	2	46	38	+	114274201	114280455
333685457	chr4	114276667	114276858	114276691	114276837	ANK2	NM_001148	2	46	38	+	114274201	114280455
333686316	chr4	114278131	114278336	114278154	114278311	ANK2	NM_001148	2	46	38	+	114274201	114280455
333689156	chr4	114274210	114274392	114274238	114274367	ANK2	NM_001148	2	46	38	+	114274201	114280455
333690688	chr4	114280204	114280338	114280230	114280310	ANK2	NM_001148	2	46	38	+	114274201	114280455
333700423	chr4	114278290	114278503	114278312	114278477	ANK2	NM_001148	2	46	38	+	114274201	114280455
333706847	chr4	114279188	114279403	114279212	114279382	ANK2	NM_001148	2	46	38	+	114274201	114280455
333708576	chr4	114280287	114280494	114280311	114280473	ANK2	NM_001148	2	46	38	+	114274201	114280455
333713656	chr4	114274344	114274558	114274368	114274529	ANK2	NM_001148	2	46	38	+	114274201	114280455
333715087	chr4	114276816	114277015	114276838	114276993	ANK2	NM_001148	2	46	38	+	114274201	114280455
333716648	chr4	114276184	114276407	114276210	114276385	ANK2	NM_001148	2	46	38	+	114274201	114280455
333725677	chr4	114277824	114278043	114277848	114278021	ANK2	NM_001148	2	46	38	+	114274201	114280455
333725714	chr4	114278449	114278672	114278478	114278644	ANK2	NM_001148	2	46	38	+	114274201	114280455
333732983	chr4	114274509	114274717	114274530	114274689	ANK2	NM_001148	2	46	38	+	114274201	114280455
333733556	chr4	114276964	114277185	114276990	114277164	ANK2	NM_001148	2	46	38	+	114274201	114280455
333738533	chr4	114279361	114279565	114279383	114279541	ANK2	NM_001148	2	46	38	+	114274201	114280455
333752416	chr4	114277999	114278175	114278022	114278153	ANK2	NM_001148	2	46	38	+	114274201	114280455
333753847	chr4	114276360	114276574	114276385	114276550	ANK2	NM_001148	2	46	38	+	114274201	114280455
333758734	chr4	114279519	114279740	114279542	114279717	ANK2	NM_001148	2	46	38	+	114274201	114280455
333763754	chr4	114276526	114276715	114276551	114276691	ANK2	NM_001148	2	46	38	+	114274201	114280455
333083353	chr4	114281883	114282083	114281910	114282059	ANK2	NM_001148	2	46	39	+	114281979	114282053
333191860	chr4	114284426	114284585	114284454	114284563	ANK2	NM_001148	2	46	40	+	114284494	114284625
333197058	chr4	114284538	114284672	114284564	114284645	ANK2	NM_001148	2	46	40	+	114284494	114284625
333517623	chr4	114286031	114286252	114286056	114286224	ANK2	NM_001148	2	46	41	+	114286195	114286338
333524763	chr4	114286202	114286419	114286225	114286396	ANK2	NM_001148	2	46	41	+	114286195	114286338
333015093	chr4	114288595	114288757	114288615	114288734	ANK2	NM_001148	2	46	42	+	114288722	114289007
333020969	chr4	114288713	114288870	114288735	114288845	ANK2	NM_001148	2	46	42	+	114288722	114289007
333034625	chr4	114288822	114289043	114288846	114289015	ANK2	NM_001148	2	46	42	+	114288722	114289007
332325208	chr4	114290616	114290839	114290638	114290816	ANK2	NM_001148	2	46	43	+	114290670	114290961
332348662	chr4	114290770	114290989	114290792	114290967	ANK2	NM_001148	2	46	43	+	114290670	114290961
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_001148	2	46	44	+	114294246	114294329
332553329	chr4	114294164	114294371	114294191	114294343	ANK2	NM_001148	2	46	44	+	114294246	114294329
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_001148	2	46	45	+	114294441	114294605
332324907	chr4	114294445	114294661	114294474	114294634	ANK2	NM_001148	2	46	45	+	114294441	114294605
333074387	chr4	114302478	114302674	114302506	114302652	ANK2	NM_001148	2	46	46	+	114302613	114304896
333577144	chr4	113970841	113971051	113970862	113971024	ANK2	NM_020977	3	45	1	+	113970785	113970968
332375804	chr4	114095475	114095699	114095504	114095679	ANK2	NM_020977	3	45	2	+	114095572	114095673
332484014	chr4	114117430	114117635	114117456	114117606	ANK2	NM_020977	3	45	3	+	114117524	114117622
333430694	chr4	114120084	114120292	114120109	114120264	ANK2	NM_020977	3	45	4	+	114120167	114120265

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333827433	chr4	114153225	114153441	114153252	114153420	ANK2	NM_020977	3	45	5	+	114153317	114153415
332498539	chr4	114157985	114158171	114158018	114158149	ANK2	NM_020977	3	45	6	+	114158143	114158328
332498646	chr4	114158127	114158284	114158150	114158263	ANK2	NM_020977	3	45	6	+	114158143	114158328
332509342	chr4	114158243	114158368	114158264	114158341	ANK2	NM_020977	3	45	6	+	114158143	114158328
332964764	chr4	114158633	114158850	114158657	114158823	ANK2	NM_020977	3	45	7	+	114158755	114158778
332503337	chr4	114161601	114161825	114161625	114161797	ANK2	NM_020977	3	45	8	+	114161641	114161739
332629268	chr4	114163213	114163428	114163233	114163400	ANK2	NM_020977	3	45	9	+	114163267	114163365
333326438	chr4	114170835	114171056	114170860	114171029	ANK2	NM_020977	3	45	10	+	114170920	114171018
332992835	chr4	114176741	114176961	114176770	114176940	ANK2	NM_020977	3	45	11	+	114176891	114177088
333002295	chr4	114176921	114177115	114176941	114177093	ANK2	NM_020977	3	45	11	+	114176891	114177088
333327823	chr4	114179121	114179340	114179143	114179313	ANK2	NM_020977	3	45	12	+	114179206	114179304
333373103	chr4	114179371	114179595	114179397	114179572	ANK2	NM_020977	3	45	13	+	114179469	114179567
332652512	chr4	114186001	114186189	114186021	114186166	ANK2	NM_020977	3	45	14	+	114186053	114186151
332948560	chr4	114195501	114195682	114195525	114195657	ANK2	NM_020977	3	45	15	+	114195608	114195805
332963013	chr4	114195637	114195837	114195658	114195810	ANK2	NM_020977	3	45	15	+	114195608	114195805
332618707	chr4	114198832	114199035	114198860	114199013	ANK2	NM_020977	3	45	16	+	114198993	114199091
332620477	chr4	114198992	114199192	114199014	114199167	ANK2	NM_020977	3	45	16	+	114198993	114199091
333114117	chr4	114199559	114199751	114199579	114199725	ANK2	NM_020977	3	45	17	+	114199616	114199714
332881524	chr4	114203668	114203892	114203695	114203866	ANK2	NM_020977	3	45	18	+	114203831	114204028
332884664	chr4	114203843	114204067	114203867	114204039	ANK2	NM_020977	3	45	18	+	114203831	114204028
333207501	chr4	114208717	114208892	114208745	114208865	ANK2	NM_020977	3	45	19	+	114208761	114208859
332945350	chr4	114209445	114209613	114209471	114209585	ANK2	NM_020977	3	45	20	+	114209544	114209642
332948459	chr4	114209562	114209691	114209586	114209663	ANK2	NM_020977	3	45	20	+	114209544	114209642
333774879	chr4	114213513	114213714	114213538	114213690	ANK2	NM_020977	3	45	21	+	114213572	114213670
333275277	chr4	114214530	114214723	114214550	114214699	ANK2	NM_020977	3	45	22	+	114214596	114214694
332408000	chr4	114223835	114224036	114223855	114224008	ANK2	NM_020977	3	45	23	+	114223923	114223995
333364528	chr4	114232377	114232599	114232405	114232572	ANK2	NM_020977	3	45	24	+	114232411	114232555
332716298	chr4	114238782	114238995	114238802	114238970	ANK2	NM_020977	3	45	25	+	114238863	114238965
333343659	chr4	114239630	114239825	114239658	114239797	ANK2	NM_020977	3	45	26	+	114239673	114239776
333140278	chr4	114251264	114251483	114251289	114251459	ANK2	NM_020977	3	45	27	+	114251402	114251626
333151738	chr4	114251439	114251661	114251460	114251633	ANK2	NM_020977	3	45	27	+	114251402	114251626
332331440	chr4	114253057	114253258	114253079	114253231	ANK2	NM_020977	3	45	28	+	114253128	114253226
333365408	chr4	114254145	114254361	114254167	114254333	ANK2	NM_020977	3	45	29	+	114254210	114254364
333376707	chr4	114254306	114254446	114254334	114254418	ANK2	NM_020977	3	45	29	+	114254210	114254364
332580379	chr4	114256893	114257116	114256917	114257093	ANK2	NM_020977	3	45	30	+	114257002	114257213
332604813	chr4	114257071	114257295	114257094	114257266	ANK2	NM_020977	3	45	30	+	114257002	114257213
333396912	chr4	114257594	114257800	114257616	114257775	ANK2	NM_020977	3	45	31	+	114257733	114257937
333404176	chr4	114257752	114257974	114257776	114257949	ANK2	NM_020977	3	45	31	+	114257733	114257937
332583042	chr4	114260327	114260521	114260353	114260493	ANK2	NM_020977	3	45	32	+	114260382	114260478
333702320	chr4	114262738	114262892	114262766	114262868	ANK2	NM_020977	3	45	33	+	114262844	114263072
333702952	chr4	114262845	114263033	114262869	114263005	ANK2	NM_020977	3	45	33	+	114262844	114263072

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333721753	chr4	114262983	114263196	114263006	114263169	ANK2	NM_020977	3	45	33	+	114262844	114263072
333072157	chr4	114263986	114264205	114264012	114264179	ANK2	NM_020977	3	45	34	+	114264173	114264298
333079736	chr4	114264152	114264366	114264180	114264338	ANK2	NM_020977	3	45	34	+	114264173	114264298
332763460	chr4	114267012	114267216	114267035	114267188	ANK2	NM_020977	3	45	35	+	114267056	114267178
333632867	chr4	114269297	114269497	114269322	114269475	ANK2	NM_020977	3	45	36	+	114269432	114269464
333116494	chr4	114271239	114271448	114271268	114271421	ANK2	NM_020977	3	45	37	+	114271384	114271405
333083353	chr4	114281883	114282083	114281910	114282059	ANK2	NM_020977	3	45	38	+	114281979	114282053
333191860	chr4	114284426	114284585	114284454	114284563	ANK2	NM_020977	3	45	39	+	114284494	114284625
333197058	chr4	114284538	114284672	114284564	114284645	ANK2	NM_020977	3	45	39	+	114284494	114284625
333517623	chr4	114286031	114286252	114286056	114286224	ANK2	NM_020977	3	45	40	+	114286195	114286338
333524763	chr4	114286202	114286419	114286225	114286396	ANK2	NM_020977	3	45	40	+	114286195	114286338
333015093	chr4	114288595	114288757	114288615	114288734	ANK2	NM_020977	3	45	41	+	114288722	114289007
333020969	chr4	114288713	114288870	114288735	114288845	ANK2	NM_020977	3	45	41	+	114288722	114289007
333034625	chr4	114288822	114289043	114288846	114289015	ANK2	NM_020977	3	45	41	+	114288722	114289007
332325208	chr4	114290616	114290839	114290638	114290816	ANK2	NM_020977	3	45	42	+	114290670	114290961
332348662	chr4	114290770	114290989	114290792	114290967	ANK2	NM_020977	3	45	42	+	114290670	114290961
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_020977	3	45	43	+	114294246	114294329
332553329	chr4	114294164	114294371	114294191	114294343	ANK2	NM_020977	3	45	43	+	114294246	114294329
332312990	chr4	114294286	114294497	114294314	114294473	ANK2	NM_020977	3	45	44	+	114294441	114294605
332324907	chr4	114294445	114294661	114294474	114294634	ANK2	NM_020977	3	45	44	+	114294441	114294605
333074387	chr4	114302478	114302674	114302506	114302652	ANK2	NM_020977	3	45	45	+	114302613	114304896
223858254	chr5	112090500	112090635	112090527	112090611	APC	NM_000038	1	16	2	+	112090570	112090722
223859952	chr5	112090589	112090792	112090612	112090764	APC	NM_000038	1	16	2	+	112090570	112090722
223303241	chr5	112101888	112102099	112101916	112102070	APC	NM_000038	1	16	3	+	112102023	112102107
329133468	chr5	112102040	112102246	112102069	112102223	APC	NM_000038	1	16	3	+	112102023	112102107
225051160	chr5	112102913	112103132	112102936	112103106	APC	NM_000038	1	16	4	+	112102886	112103087
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_000038	1	16	4	+	112102886	112103087
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_000038	1	16	5	+	112111326	112111434
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_000038	1	16	5	+	112111326	112111434
329251859	chr5	112111380	112111577	112111409	112111552	APC	NM_000038	1	16	5	+	112111326	112111434
223188131	chr5	112116363	112116545	112116385	112116518	APC	NM_000038	1	16	6	+	112116487	112116600
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_000038	1	16	6	+	112116487	112116600
222941406	chr5	112128034	112128246	112128061	112128219	APC	NM_000038	1	16	7	+	112128143	112128226
223255170	chr5	112136844	112137065	112136869	112137042	APC	NM_000038	1	16	8	+	112136976	112137080
329085597	chr5	112137021	112137224	112137043	112137197	APC	NM_000038	1	16	8	+	112136976	112137080
222616452	chr5	112151101	112151324	112151129	112151299	APC	NM_000038	1	16	9	+	112151192	112151290
222847255	chr5	112154592	112154810	112154620	112154785	APC	NM_000038	1	16	10	+	112154663	112155041
222872619	chr5	112154766	112154923	112154786	112154900	APC	NM_000038	1	16	10	+	112154663	112155041
222892108	chr5	112154881	112155075	112154901	112155047	APC	NM_000038	1	16	10	+	112154663	112155041
222509664	chr5	112157593	112157812	112157613	112157784	APC	NM_000038	1	16	11	+	112157593	112157688
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_000038	1	16	12	+	112162805	112162944

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329454935	chr5	112162854	112163077	112162879	112163049	APC	NM_000038	1	16	12	+	112162805	112162944
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_000038	1	16	13	+	112163626	112163703
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_000038	1	16	14	+	112164553	112164669
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_000038	1	16	14	+	112164553	112164669
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_000038	1	16	15	+	112170648	112170862
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_000038	1	16	15	+	112170648	112170862
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_000038	1	16	15	+	112170648	112170862
222745390	chr5	112178650	112178863	112178676	112178835	APC	NM_000038	1	16	16	+	112173250	112181936
222756111	chr5	112174708	112174906	112174736	112174879	APC	NM_000038	1	16	16	+	112173250	112181936
222774177	chr5	112174852	112175025	112174880	112175001	APC	NM_000038	1	16	16	+	112173250	112181936
222781947	chr5	112174981	112175180	112175002	112175158	APC	NM_000038	1	16	16	+	112173250	112181936
222792899	chr5	112175131	112175323	112175159	112175296	APC	NM_000038	1	16	16	+	112173250	112181936
222793015	chr5	112178812	112179018	112178836	112178990	APC	NM_000038	1	16	16	+	112173250	112181936
222796208	chr5	112176768	112176945	112176797	112176918	APC	NM_000038	1	16	16	+	112173250	112181936
222797864	chr5	112174233	112174446	112174261	112174423	APC	NM_000038	1	16	16	+	112173250	112181936
222813651	chr5	112174402	112174590	112174424	112174565	APC	NM_000038	1	16	16	+	112173250	112181936
222815524	chr5	112176891	112177093	112176918	112177067	APC	NM_000038	1	16	16	+	112173250	112181936
222817672	chr5	112178967	112179179	112178991	112179153	APC	NM_000038	1	16	16	+	112173250	112181936
222829631	chr5	112174540	112174763	112174566	112174735	APC	NM_000038	1	16	16	+	112173250	112181936
222829825	chr5	112177048	112177265	112177068	112177237	APC	NM_000038	1	16	16	+	112173250	112181936
222832849	chr5	112179111	112179327	112179139	112179301	APC	NM_000038	1	16	16	+	112173250	112181936
222834771	chr5	112175562	112175775	112175583	112175749	APC	NM_000038	1	16	16	+	112173250	112181936
224517330	chr5	112173190	112173372	112173218	112173344	APC	NM_000038	1	16	16	+	112173250	112181936
224519463	chr5	112173661	112173859	112173687	112173832	APC	NM_000038	1	16	16	+	112173250	112181936
224525490	chr5	112173319	112173538	112173345	112173515	APC	NM_000038	1	16	16	+	112173250	112181936
224532731	chr5	112177765	112177982	112177793	112177960	APC	NM_000038	1	16	16	+	112173250	112181936
224533540	chr5	112177207	112177408	112177235	112177381	APC	NM_000038	1	16	16	+	112173250	112181936
224535592	chr5	112177939	112178090	112177961	112178067	APC	NM_000038	1	16	16	+	112173250	112181936
224538823	chr5	112179737	112179961	112179759	112179933	APC	NM_000038	1	16	16	+	112173250	112181936
224538936	chr5	112178226	112178370	112178249	112178347	APC	NM_000038	1	16	16	+	112173250	112181936
224539791	chr5	112175728	112175949	112175750	112175921	APC	NM_000038	1	16	16	+	112173250	112181936
224540010	chr5	112173805	112174012	112173833	112173989	APC	NM_000038	1	16	16	+	112173250	112181936
224544462	chr5	112176228	112176450	112176256	112176423	APC	NM_000038	1	16	16	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_000038	1	16	16	+	112173250	112181936
224554830	chr5	112179276	112179482	112179302	112179460	APC	NM_000038	1	16	16	+	112173250	112181936
224555236	chr5	112178325	112178536	112178348	112178508	APC	NM_000038	1	16	16	+	112173250	112181936
224555367	chr5	112177448	112177651	112177476	112177625	APC	NM_000038	1	16	16	+	112173250	112181936
224555371	chr5	112178047	112178269	112178068	112178248	APC	NM_000038	1	16	16	+	112173250	112181936
224557361	chr5	112173493	112173713	112173516	112173686	APC	NM_000038	1	16	16	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_000038	1	16	16	+	112173250	112181936
224568800	chr5	112177599	112177820	112177626	112177792	APC	NM_000038	1	16	16	+	112173250	112181936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224568908	chr5	112175896	112176111	112175922	112176090	APC	NM_000038	1	16	16	+	112173250	112181936
224573714	chr5	112176397	112176615	112176424	112176587	APC	NM_000038	1	16	16	+	112173250	112181936
224578799	chr5	112179439	112179602	112179461	112179580	APC	NM_000038	1	16	16	+	112173250	112181936
224581599	chr5	112176556	112176773	112176579	112176744	APC	NM_000038	1	16	16	+	112173250	112181936
224582664	chr5	112174073	112174292	112174101	112174263	APC	NM_000038	1	16	16	+	112173250	112181936
224583560	chr5	112176605	112176823	112176632	112176796	APC	NM_000038	1	16	16	+	112173250	112181936
224584739	chr5	112178480	112178704	112178508	112178675	APC	NM_000038	1	16	16	+	112173250	112181936
224589069	chr5	112176071	112176284	112176091	112176255	APC	NM_000038	1	16	16	+	112173250	112181936
224604761	chr5	112179560	112179781	112179581	112179758	APC	NM_000038	1	16	16	+	112173250	112181936
326756821	chr5	112175274	112175494	112175296	112175468	APC	NM_000038	1	16	16	+	112173250	112181936
326939934	chr5	112175443	112175605	112175469	112175582	APC	NM_000038	1	16	16	+	112173250	112181936
223858254	chr5	112090500	112090635	112090527	112090611	APC	NM_001127510	2	17	3	+	112090570	112090722
223859952	chr5	112090589	112090792	112090612	112090764	APC	NM_001127510	2	17	3	+	112090570	112090722
223303241	chr5	112101888	112102099	112101916	112102070	APC	NM_001127510	2	17	4	+	112102023	112102107
329133468	chr5	112102040	112102246	112102069	112102223	APC	NM_001127510	2	17	4	+	112102023	112102107
225051160	chr5	112102913	112103132	112102936	112103106	APC	NM_001127510	2	17	5	+	112102886	112103087
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_001127510	2	17	5	+	112102886	112103087
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_001127510	2	17	6	+	112111326	112111434
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_001127510	2	17	6	+	112111326	112111434
329251859	chr5	112111380	112111577	112111409	112111552	APC	NM_001127510	2	17	6	+	112111326	112111434
223188131	chr5	112116363	112116545	112116385	112116518	APC	NM_001127510	2	17	7	+	112116487	112116600
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_001127510	2	17	7	+	112116487	112116600
222941406	chr5	112128034	112128246	112128061	112128219	APC	NM_001127510	2	17	8	+	112128143	112128226
223255170	chr5	112136844	112137065	112136869	112137042	APC	NM_001127510	2	17	9	+	112136976	112137080
329085597	chr5	112137021	112137224	112137043	112137197	APC	NM_001127510	2	17	9	+	112136976	112137080
222616452	chr5	112151101	112151324	112151129	112151299	APC	NM_001127510	2	17	10	+	112151192	112151290
222847255	chr5	112154592	112154810	112154620	112154785	APC	NM_001127510	2	17	11	+	112154663	112155041
222872619	chr5	112154766	112154923	112154786	112154900	APC	NM_001127510	2	17	11	+	112154663	112155041
222892108	chr5	112154881	112155075	112154901	112155047	APC	NM_001127510	2	17	11	+	112154663	112155041
222509664	chr5	112157593	112157812	112157613	112157784	APC	NM_001127510	2	17	12	+	112157593	112157688
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_001127510	2	17	13	+	112162805	112162944
329454935	chr5	112162854	112163077	112162879	112163049	APC	NM_001127510	2	17	13	+	112162805	112162944
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_001127510	2	17	14	+	112163626	112163703
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_001127510	2	17	15	+	112164553	112164669
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_001127510	2	17	15	+	112164553	112164669
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_001127510	2	17	16	+	112170648	112170862
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_001127510	2	17	16	+	112170648	112170862
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_001127510	2	17	16	+	112170648	112170862
222745390	chr5	112178650	112178863	112178676	112178835	APC	NM_001127510	2	17	17	+	112173250	112181936
222756111	chr5	112174708	112174906	112174736	112174879	APC	NM_001127510	2	17	17	+	112173250	112181936
222774177	chr5	112174852	112175025	112174880	112175001	APC	NM_001127510	2	17	17	+	112173250	112181936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222781947	chr5	112174981	112175180	112175002	112175158	APC	NM_001127510	2	17	17	+	112173250	112181936
222792899	chr5	112175131	112175323	112175159	112175296	APC	NM_001127510	2	17	17	+	112173250	112181936
222793015	chr5	112178812	112179018	112178836	112178990	APC	NM_001127510	2	17	17	+	112173250	112181936
222796208	chr5	112176768	112176945	112176797	112176918	APC	NM_001127510	2	17	17	+	112173250	112181936
222797864	chr5	112174233	112174446	112174261	112174423	APC	NM_001127510	2	17	17	+	112173250	112181936
222813651	chr5	112174402	112174590	112174424	112174565	APC	NM_001127510	2	17	17	+	112173250	112181936
222815524	chr5	112176891	112177093	112176918	112177067	APC	NM_001127510	2	17	17	+	112173250	112181936
222817672	chr5	112178967	112179179	112178991	112179153	APC	NM_001127510	2	17	17	+	112173250	112181936
222829631	chr5	112174540	112174763	112174566	112174735	APC	NM_001127510	2	17	17	+	112173250	112181936
222829825	chr5	112177048	112177265	112177068	112177237	APC	NM_001127510	2	17	17	+	112173250	112181936
222832849	chr5	112179111	112179327	112179139	112179301	APC	NM_001127510	2	17	17	+	112173250	112181936
222834771	chr5	112175562	112175775	112175583	112175749	APC	NM_001127510	2	17	17	+	112173250	112181936
224517330	chr5	112173190	112173372	112173218	112173344	APC	NM_001127510	2	17	17	+	112173250	112181936
224519463	chr5	112173661	112173859	112173687	112173832	APC	NM_001127510	2	17	17	+	112173250	112181936
224525490	chr5	112173319	112173538	112173345	112173515	APC	NM_001127510	2	17	17	+	112173250	112181936
224532731	chr5	112177765	112177982	112177793	112177960	APC	NM_001127510	2	17	17	+	112173250	112181936
224533540	chr5	112177207	112177408	112177235	112177381	APC	NM_001127510	2	17	17	+	112173250	112181936
224535592	chr5	112177939	112178090	112177961	112178067	APC	NM_001127510	2	17	17	+	112173250	112181936
224538823	chr5	112179737	112179961	112179759	112179933	APC	NM_001127510	2	17	17	+	112173250	112181936
224538936	chr5	112178226	112178370	112178249	112178347	APC	NM_001127510	2	17	17	+	112173250	112181936
224539791	chr5	112175728	112175949	112175750	112175921	APC	NM_001127510	2	17	17	+	112173250	112181936
224540010	chr5	112173805	112174012	112173833	112173989	APC	NM_001127510	2	17	17	+	112173250	112181936
224544462	chr5	112176228	112176450	112176256	112176423	APC	NM_001127510	2	17	17	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_001127510	2	17	17	+	112173250	112181936
224554830	chr5	112179276	112179482	112179302	112179460	APC	NM_001127510	2	17	17	+	112173250	112181936
224555236	chr5	112178325	112178536	112178348	112178508	APC	NM_001127510	2	17	17	+	112173250	112181936
224555367	chr5	112177448	112177651	112177476	112177625	APC	NM_001127510	2	17	17	+	112173250	112181936
224555371	chr5	112178047	112178269	112178068	112178248	APC	NM_001127510	2	17	17	+	112173250	112181936
224557361	chr5	112173493	112173713	112173516	112173686	APC	NM_001127510	2	17	17	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_001127510	2	17	17	+	112173250	112181936
224568800	chr5	112177599	112177820	112177626	112177792	APC	NM_001127510	2	17	17	+	112173250	112181936
224568908	chr5	112175896	112176111	112175922	112176090	APC	NM_001127510	2	17	17	+	112173250	112181936
224573714	chr5	112176397	112176615	112176424	112176587	APC	NM_001127510	2	17	17	+	112173250	112181936
224578799	chr5	112179439	112179602	112179461	112179580	APC	NM_001127510	2	17	17	+	112173250	112181936
224581599	chr5	112176556	112176773	112176579	112176744	APC	NM_001127510	2	17	17	+	112173250	112181936
224582664	chr5	112174073	112174292	112174101	112174263	APC	NM_001127510	2	17	17	+	112173250	112181936
224583560	chr5	112176605	112176823	112176632	112176796	APC	NM_001127510	2	17	17	+	112173250	112181936
224584739	chr5	112178480	112178704	112178508	112178675	APC	NM_001127510	2	17	17	+	112173250	112181936
224589069	chr5	112176071	112176284	112176091	112176255	APC	NM_001127510	2	17	17	+	112173250	112181936
224604761	chr5	112179560	112179781	112179581	112179758	APC	NM_001127510	2	17	17	+	112173250	112181936
326756821	chr5	112175274	112175494	112175296	112175468	APC	NM_001127510	2	17	17	+	112173250	112181936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326939934	chr5	112175443	112175605	112175469	112175582	APC	NM_001127510	2	17	17	+	112173250	112181936
222561014	chr5	112043333	112043480	112043355	112043457	APC	NM_001127511	3	14	1	+	112043202	112043579
222565086	chr5	112043410	112043615	112043429	112043596	APC	NM_001127511	3	14	1	+	112043202	112043579
223303241	chr5	112101888	112102099	112101916	112102070	APC	NM_001127511	3	14	2	+	112102023	112102107
329133468	chr5	112102040	112102246	112102069	112102223	APC	NM_001127511	3	14	2	+	112102023	112102107
225051160	chr5	112102913	112103132	112102936	112103106	APC	NM_001127511	3	14	3	+	112102886	112103087
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_001127511	3	14	3	+	112102886	112103087
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_001127511	3	14	4	+	112111326	112111434
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_001127511	3	14	4	+	112111326	112111434
329251859	chr5	112111380	112111577	112111409	112111552	APC	NM_001127511	3	14	4	+	112111326	112111434
223188131	chr5	112116363	112116545	112116385	112116518	APC	NM_001127511	3	14	5	+	112116487	112116600
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_001127511	3	14	5	+	112116487	112116600
223255170	chr5	112136844	112137065	112136869	112137042	APC	NM_001127511	3	14	6	+	112136976	112137080
329085597	chr5	112137021	112137224	112137043	112137197	APC	NM_001127511	3	14	6	+	112136976	112137080
222616452	chr5	112151101	112151324	112151129	112151299	APC	NM_001127511	3	14	7	+	112151192	112151290
222847255	chr5	112154592	112154810	112154620	112154785	APC	NM_001127511	3	14	8	+	112154663	112155041
222872619	chr5	112154766	112154923	112154786	112154900	APC	NM_001127511	3	14	8	+	112154663	112155041
222892108	chr5	112154881	112155075	112154901	112155047	APC	NM_001127511	3	14	8	+	112154663	112155041
222509664	chr5	112157593	112157812	112157613	112157784	APC	NM_001127511	3	14	9	+	112157593	112157688
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_001127511	3	14	10	+	112162805	112162944
329454935	chr5	112162854	112163077	112162879	112163049	APC	NM_001127511	3	14	10	+	112162805	112162944
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_001127511	3	14	11	+	112163626	112163703
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_001127511	3	14	12	+	112164553	112164669
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_001127511	3	14	12	+	112164553	112164669
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_001127511	3	14	13	+	112170648	112170862
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_001127511	3	14	13	+	112170648	112170862
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_001127511	3	14	13	+	112170648	112170862
222745390	chr5	112178650	112178863	112178676	112178835	APC	NM_001127511	3	14	14	+	112173250	112181936
222756111	chr5	112174708	112174906	112174736	112174879	APC	NM_001127511	3	14	14	+	112173250	112181936
222774177	chr5	112174852	112175025	112174880	112175001	APC	NM_001127511	3	14	14	+	112173250	112181936
222781947	chr5	112174981	112175180	112175002	112175158	APC	NM_001127511	3	14	14	+	112173250	112181936
222792899	chr5	112175131	112175323	112175159	112175296	APC	NM_001127511	3	14	14	+	112173250	112181936
222793015	chr5	112178812	112179018	112178836	112178990	APC	NM_001127511	3	14	14	+	112173250	112181936
222796208	chr5	112176768	112176945	112176797	112176918	APC	NM_001127511	3	14	14	+	112173250	112181936
222797864	chr5	112174233	112174446	112174261	112174423	APC	NM_001127511	3	14	14	+	112173250	112181936
222813651	chr5	112174402	112174590	112174424	112174565	APC	NM_001127511	3	14	14	+	112173250	112181936
222815524	chr5	112176891	112177093	112176918	112177067	APC	NM_001127511	3	14	14	+	112173250	112181936
222817672	chr5	112178967	112179179	112178991	112179153	APC	NM_001127511	3	14	14	+	112173250	112181936
222829631	chr5	112174540	112174763	112174566	112174735	APC	NM_001127511	3	14	14	+	112173250	112181936
222829825	chr5	112177048	112177265	112177068	112177237	APC	NM_001127511	3	14	14	+	112173250	112181936
222832849	chr5	112179111	112179327	112179139	112179301	APC	NM_001127511	3	14	14	+	112173250	112181936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222834771	chr5	112175562	112175775	112175583	112175749	APC	NM_001127511	3	14	14	+	112173250	112181936
224517330	chr5	112173190	112173372	112173218	112173344	APC	NM_001127511	3	14	14	+	112173250	112181936
224519463	chr5	112173661	112173859	112173687	112173832	APC	NM_001127511	3	14	14	+	112173250	112181936
224525490	chr5	112173319	112173538	112173345	112173515	APC	NM_001127511	3	14	14	+	112173250	112181936
224532731	chr5	112177765	112177982	112177793	112177960	APC	NM_001127511	3	14	14	+	112173250	112181936
224533540	chr5	112177207	112177408	112177235	112177381	APC	NM_001127511	3	14	14	+	112173250	112181936
224535592	chr5	112177939	112178090	112177961	112178067	APC	NM_001127511	3	14	14	+	112173250	112181936
224538823	chr5	112179737	112179961	112179759	112179933	APC	NM_001127511	3	14	14	+	112173250	112181936
224538936	chr5	112178226	112178370	112178249	112178347	APC	NM_001127511	3	14	14	+	112173250	112181936
224539791	chr5	112175728	112175949	112175750	112175921	APC	NM_001127511	3	14	14	+	112173250	112181936
224540010	chr5	112173805	112174012	112173833	112173989	APC	NM_001127511	3	14	14	+	112173250	112181936
224544462	chr5	112176228	112176450	112176256	112176423	APC	NM_001127511	3	14	14	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_001127511	3	14	14	+	112173250	112181936
224554830	chr5	112179276	112179482	112179302	112179460	APC	NM_001127511	3	14	14	+	112173250	112181936
224555236	chr5	112178325	112178536	112178348	112178508	APC	NM_001127511	3	14	14	+	112173250	112181936
224555367	chr5	112177448	112177651	112177476	112177625	APC	NM_001127511	3	14	14	+	112173250	112181936
224555371	chr5	112178047	112178269	112178068	112178248	APC	NM_001127511	3	14	14	+	112173250	112181936
224557361	chr5	112173493	112173713	112173516	112173686	APC	NM_001127511	3	14	14	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_001127511	3	14	14	+	112173250	112181936
224568800	chr5	112177599	112177820	112177626	112177792	APC	NM_001127511	3	14	14	+	112173250	112181936
224568908	chr5	112175896	112176111	112175922	112176090	APC	NM_001127511	3	14	14	+	112173250	112181936
224573714	chr5	112176397	112176615	112176424	112176587	APC	NM_001127511	3	14	14	+	112173250	112181936
224578799	chr5	112179439	112179602	112179461	112179580	APC	NM_001127511	3	14	14	+	112173250	112181936
224581599	chr5	112176556	112176773	112176579	112176744	APC	NM_001127511	3	14	14	+	112173250	112181936
224582664	chr5	112174073	112174292	112174101	112174263	APC	NM_001127511	3	14	14	+	112173250	112181936
224583560	chr5	112176605	112176823	112176632	112176796	APC	NM_001127511	3	14	14	+	112173250	112181936
224584739	chr5	112178480	112178704	112178508	112178675	APC	NM_001127511	3	14	14	+	112173250	112181936
224589069	chr5	112176071	112176284	112176091	112176255	APC	NM_001127511	3	14	14	+	112173250	112181936
224604761	chr5	112179560	112179781	112179581	112179758	APC	NM_001127511	3	14	14	+	112173250	112181936
326756821	chr5	112175274	112175494	112175296	112175468	APC	NM_001127511	3	14	14	+	112173250	112181936
326939934	chr5	112175443	112175605	112175469	112175582	APC	NM_001127511	3	14	14	+	112173250	112181936
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_000484	1	18	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_000484	1	18	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_000484	1	18	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_000484	1	18	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_000484	1	18	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_000484	1	18	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_000484	1	18	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_000484	1	18	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_000484	1	18	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_000484	1	18	6	-	27394156	27394358

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_000484	1	18	7	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_000484	1	18	7	-	27372330	27372497
257751478	chr21	27369568	27369789	27369595	27369761	APP	NM_000484	1	18	8	-	27369675	27369731
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_000484	1	18	9	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_000484	1	18	9	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_000484	1	18	10	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_000484	1	18	10	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_000484	1	18	11	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_000484	1	18	11	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_000484	1	18	12	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_000484	1	18	13	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_000484	1	18	14	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_000484	1	18	14	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_000484	1	18	15	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_000484	1	18	16	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_000484	1	18	17	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_000484	1	18	17	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_000484	1	18	18	-	27252861	27254082
261315252	chr21	27512339	27512543	27512363	27512522	APP	NM_001136016	2	17	1	-	27512471	27512708
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_001136016	2	17	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_001136016	2	17	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001136016	2	17	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001136016	2	17	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001136016	2	17	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001136016	2	17	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001136016	2	17	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001136016	2	17	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001136016	2	17	6	-	27394156	27394358
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_001136016	2	17	7	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_001136016	2	17	7	-	27372330	27372497
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001136016	2	17	8	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001136016	2	17	8	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001136016	2	17	9	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001136016	2	17	9	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001136016	2	17	10	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001136016	2	17	10	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001136016	2	17	11	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001136016	2	17	12	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001136016	2	17	13	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001136016	2	17	13	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_001136016	2	17	14	-	27277336	27277389

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001136016	2	17	15	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001136016	2	17	16	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001136016	2	17	16	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001136016	2	17	17	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_001136129	3	15	1	-	27542882	27543138
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001136129	3	15	2	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001136129	3	15	2	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001136129	3	15	3	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001136129	3	15	4	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001136129	3	15	4	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001136129	3	15	5	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001136129	3	15	5	-	27394156	27394358
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001136129	3	15	6	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001136129	3	15	6	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001136129	3	15	7	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001136129	3	15	7	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001136129	3	15	8	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001136129	3	15	8	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001136129	3	15	9	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001136129	3	15	10	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001136129	3	15	11	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001136129	3	15	11	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_001136129	3	15	12	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001136129	3	15	13	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001136129	3	15	14	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001136129	3	15	14	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001136129	3	15	15	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_001136130	4	17	1	-	27542882	27543138
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001136130	4	17	2	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001136130	4	17	2	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001136130	4	17	3	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001136130	4	17	4	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001136130	4	17	4	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001136130	4	17	5	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001136130	4	17	5	-	27394156	27394358
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_001136130	4	17	6	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_001136130	4	17	6	-	27372330	27372497
257751478	chr21	27369568	27369789	27369595	27369761	APP	NM_001136130	4	17	7	-	27369675	27369731
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001136130	4	17	8	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001136130	4	17	8	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001136130	4	17	9	-	27348267	27348341

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001136130	4	17	9	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001136130	4	17	10	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001136130	4	17	10	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001136130	4	17	11	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001136130	4	17	12	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001136130	4	17	13	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001136130	4	17	13	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_001136130	4	17	14	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001136130	4	17	15	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001136130	4	17	16	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001136130	4	17	16	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001136130	4	17	17	-	27252861	27254082
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_001136131	5	16	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_001136131	5	16	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001136131	5	16	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001136131	5	16	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001136131	5	16	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001136131	5	16	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001136131	5	16	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001136131	5	16	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001136131	5	16	6	-	27394156	27394358
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001136131	5	16	7	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001136131	5	16	7	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001136131	5	16	8	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001136131	5	16	8	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001136131	5	16	9	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001136131	5	16	9	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001136131	5	16	10	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001136131	5	16	11	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001136131	5	16	12	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001136131	5	16	12	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_001136131	5	16	13	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001136131	5	16	14	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001136131	5	16	15	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001136131	5	16	15	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001136131	5	16	16	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_001204301	6	17	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_001204301	6	17	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_001204301	6	17	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001204301	6	17	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001204301	6	17	3	-	27462259	27462388

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001204301	6	17	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001204301	6	17	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001204301	6	17	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001204301	6	17	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001204301	6	17	6	-	27394156	27394358
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_001204301	6	17	7	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_001204301	6	17	7	-	27372330	27372497
257751478	chr21	27369568	27369789	27369595	27369761	APP	NM_001204301	6	17	8	-	27369675	27369731
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001204301	6	17	9	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001204301	6	17	9	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001204301	6	17	10	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001204301	6	17	10	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001204301	6	17	11	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001204301	6	17	11	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001204301	6	17	12	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001204301	6	17	13	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001204301	6	17	14	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001204301	6	17	14	-	27284053	27284274
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001204301	6	17	15	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001204301	6	17	16	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001204301	6	17	16	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001204301	6	17	17	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_001204302	7	16	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_001204302	7	16	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_001204302	7	16	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001204302	7	16	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001204302	7	16	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001204302	7	16	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001204302	7	16	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001204302	7	16	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001204302	7	16	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001204302	7	16	6	-	27394156	27394358
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_001204302	7	16	7	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_001204302	7	16	7	-	27372330	27372497
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001204302	7	16	8	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001204302	7	16	8	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001204302	7	16	9	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001204302	7	16	9	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001204302	7	16	10	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001204302	7	16	10	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001204302	7	16	11	-	27327941	27328069

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001204302	7	16	12	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001204302	7	16	13	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001204302	7	16	13	-	27284053	27284274
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001204302	7	16	14	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001204302	7	16	15	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001204302	7	16	15	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001204302	7	16	16	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_001204303	8	15	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_001204303	8	15	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_001204303	8	15	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_001204303	8	15	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_001204303	8	15	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_001204303	8	15	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_001204303	8	15	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_001204303	8	15	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_001204303	8	15	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_001204303	8	15	6	-	27394156	27394358
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_001204303	8	15	7	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_001204303	8	15	7	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_001204303	8	15	8	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_001204303	8	15	8	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_001204303	8	15	9	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_001204303	8	15	9	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_001204303	8	15	10	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_001204303	8	15	11	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_001204303	8	15	12	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_001204303	8	15	12	-	27284053	27284274
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_001204303	8	15	13	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_001204303	8	15	14	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_001204303	8	15	14	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_001204303	8	15	15	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_201413	9	17	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_201413	9	17	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_201413	9	17	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_201413	9	17	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_201413	9	17	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_201413	9	17	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_201413	9	17	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_201413	9	17	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_201413	9	17	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_201413	9	17	6	-	27394156	27394358

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256142007	chr21	27372239	27372454	27372265	27372433	APP	NM_201413	9	17	7	-	27372330	27372497
256170148	chr21	27372413	27372540	27372434	27372515	APP	NM_201413	9	17	7	-	27372330	27372497
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_201413	9	17	8	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_201413	9	17	8	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_201413	9	17	9	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_201413	9	17	9	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_201413	9	17	10	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_201413	9	17	10	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_201413	9	17	11	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_201413	9	17	12	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_201413	9	17	13	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_201413	9	17	13	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_201413	9	17	14	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_201413	9	17	15	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_201413	9	17	16	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_201413	9	17	16	-	27264034	27264180
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_201413	9	17	17	-	27252861	27254082
264222831	chr21	27542784	27542985	27542803	27542967	APP	NM_201414	10	16	1	-	27542882	27543138
257296281	chr21	27484162	27484351	27484189	27484330	APP	NM_201414	10	16	2	-	27484296	27484463
257333926	chr21	27484310	27484511	27484331	27484484	APP	NM_201414	10	16	2	-	27484296	27484463
256168026	chr21	27462085	27462293	27462107	27462271	APP	NM_201414	10	16	3	-	27462259	27462388
256204367	chr21	27462253	27462433	27462272	27462408	APP	NM_201414	10	16	3	-	27462259	27462388
258450738	chr21	27425468	27425691	27425492	27425669	APP	NM_201414	10	16	4	-	27425552	27425664
255227014	chr21	27423175	27423388	27423202	27423368	APP	NM_201414	10	16	5	-	27423316	27423509
255264810	chr21	27423348	27423540	27423369	27423514	APP	NM_201414	10	16	5	-	27423316	27423509
254247057	chr21	27394015	27394181	27394041	27394160	APP	NM_201414	10	16	6	-	27394156	27394358
254291529	chr21	27394211	27394415	27394231	27394387	APP	NM_201414	10	16	6	-	27394156	27394358
264238081	chr21	27354601	27354728	27354622	27354704	APP	NM_201414	10	16	7	-	27354657	27354790
264264841	chr21	27354683	27354851	27354705	27354823	APP	NM_201414	10	16	7	-	27354657	27354790
264610976	chr21	27348137	27348342	27348161	27348319	APP	NM_201414	10	16	8	-	27348267	27348341
264623509	chr21	27348296	27348506	27348320	27348478	APP	NM_201414	10	16	8	-	27348267	27348341
263476312	chr21	27347336	27347544	27347357	27347521	APP	NM_201414	10	16	9	-	27347383	27347541
263511418	chr21	27347500	27347681	27347522	27347654	APP	NM_201414	10	16	9	-	27347383	27347541
264271763	chr21	27327899	27328120	27327923	27328095	APP	NM_201414	10	16	10	-	27327941	27328069
260303302	chr21	27326818	27327034	27326845	27327010	APP	NM_201414	10	16	11	-	27326904	27327003
261995280	chr21	27283976	27284189	27283999	27284167	APP	NM_201414	10	16	12	-	27284053	27284274
262036395	chr21	27284147	27284310	27284168	27284283	APP	NM_201414	10	16	12	-	27284053	27284274
254583300	chr21	27277232	27277436	27277257	27277409	APP	NM_201414	10	16	13	-	27277336	27277389
264024952	chr21	27269812	27270036	27269840	27270008	APP	NM_201414	10	16	14	-	27269885	27269985
254472663	chr21	27263891	27264113	27263915	27264090	APP	NM_201414	10	16	15	-	27264034	27264180
254507244	chr21	27264067	27264290	27264091	27264265	APP	NM_201414	10	16	15	-	27264034	27264180

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266887142	chr21	27253923	27254147	27253947	27254119	APP	NM_201414	10	16	16	-	27252861	27254082
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195248	1	8	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195248	1	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195248	1	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_001195248	1	8	3	-	32988077	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_001195248	1	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_001195248	1	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_001195248	1	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195248	1	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195248	1	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195248	1	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195248	1	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195248	1	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195248	1	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195248	1	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195248	1	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195248	1	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195249	2	8	1	-	33001331	33001574
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195249	2	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195249	2	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_001195249	2	8	3	-	32988077	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_001195249	2	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_001195249	2	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_001195249	2	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195249	2	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195249	2	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195249	2	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195249	2	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195249	2	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195249	2	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195249	2	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195249	2	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195249	2	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195250	3	7	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195250	3	7	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195250	3	7	2	-	32989757	32989893
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_001195250	3	7	3	-	32987542	32987729
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_001195250	3	7	3	-	32987542	32987729
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195250	3	7	4	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195250	3	7	4	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195250	3	7	5	-	32984629	32984855

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195250	3	7	5	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195250	3	7	6	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195250	3	7	6	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195250	3	7	7	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195250	3	7	7	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195250	3	7	7	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195251	4	9	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195251	4	9	3	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195251	4	9	3	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_001195251	4	9	4	-	32988077	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_001195251	4	9	5	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_001195251	4	9	5	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_001195251	4	9	5	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195251	4	9	6	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195251	4	9	6	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195251	4	9	7	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195251	4	9	7	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195251	4	9	8	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195251	4	9	8	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195251	4	9	9	-	32972604	32973686
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195251	4	9	9	-	32972604	32973686
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195251	4	9	9	-	32972604	32973686
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195252	5	8	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195252	5	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195252	5	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_001195252	5	8	3	-	32988077	32988127
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_001195252	5	8	4	-	32987758	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195252	5	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195252	5	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195252	5	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195252	5	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195252	5	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195252	5	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195252	5	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195252	5	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195252	5	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_001195254	6	7	1	-	33001514	33001610
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_001195254	6	7	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_001195254	6	7	2	-	32989757	32989893
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_001195254	6	7	3	-	32987542	32987729
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_001195254	6	7	3	-	32987542	32987729

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_001195254	6	7	4	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_001195254	6	7	4	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_001195254	6	7	5	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_001195254	6	7	5	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_001195254	6	7	6	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_001195254	6	7	6	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_001195254	6	7	7	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_001195254	6	7	7	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_001195254	6	7	7	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_175069	7	8	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_175069	7	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_175069	7	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_175069	7	8	3	-	32988077	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_175069	7	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_175069	7	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_175069	7	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_175069	7	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_175069	7	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_175069	7	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_175069	7	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_175069	7	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_175069	7	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_175069	7	8	8	-	32972604	32973686
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_175069	7	8	8	-	32972604	32973686
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_175069	7	8	8	-	32972604	32973686
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NM_175073	8	9	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NM_175073	8	9	3	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NM_175073	8	9	3	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NM_175073	8	9	4	-	32988077	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NM_175073	8	9	5	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NM_175073	8	9	5	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NM_175073	8	9	5	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NM_175073	8	9	6	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NM_175073	8	9	6	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NM_175073	8	9	7	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NM_175073	8	9	7	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NM_175073	8	9	8	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NM_175073	8	9	8	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NM_175073	8	9	9	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NM_175073	8	9	9	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NM_175073	8	9	9	-	32972604	32973650

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NR_036576	9	8	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NR_036576	9	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NR_036576	9	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NR_036576	9	8	3	-	32988077	32988122
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NR_036576	9	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NR_036576	9	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NR_036576	9	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NR_036576	9	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NR_036576	9	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NR_036576	9	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NR_036576	9	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NR_036576	9	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NR_036576	9	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NR_036576	9	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NR_036576	9	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NR_036576	9	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NR_036577	10	8	1	-	33001565	33001639
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NR_036577	10	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NR_036577	10	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NR_036577	10	8	3	-	32988081	32988127
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NR_036577	10	8	4	-	32987542	32987729
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NR_036577	10	8	4	-	32987542	32987729
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NR_036577	10	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NR_036577	10	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NR_036577	10	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NR_036577	10	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NR_036577	10	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NR_036577	10	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NR_036577	10	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NR_036577	10	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NR_036577	10	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NR_036578	11	8	1	-	33001514	33001610
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NR_036578	11	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NR_036578	11	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NR_036578	11	8	3	-	32988077	32988122
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NR_036578	11	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NR_036578	11	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NR_036578	11	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NR_036578	11	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NR_036578	11	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NR_036578	11	8	6	-	32984629	32984855

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NR_036578	11	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NR_036578	11	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NR_036578	11	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NR_036578	11	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NR_036578	11	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NR_036578	11	8	8	-	32972604	32973650
254295476	chr9	33001448	33001668	33001469	33001649	APTX	NR_036579	12	8	1	-	33001331	33001574
255417905	chr9	32989580	32989798	32989602	32989769	APTX	NR_036579	12	8	2	-	32989757	32989893
255443382	chr9	32989749	32989944	32989770	32989918	APTX	NR_036579	12	8	2	-	32989757	32989893
256650597	chr9	32987952	32988173	32987981	32988145	APTX	NR_036579	12	8	3	-	32988077	32988122
263543861	chr9	32987506	32987681	32987532	32987654	APTX	NR_036579	12	8	4	-	32987542	32987840
263568896	chr9	32987633	32987770	32987655	32987742	APTX	NR_036579	12	8	4	-	32987542	32987840
263596746	chr9	32987714	32987905	32987743	32987877	APTX	NR_036579	12	8	4	-	32987542	32987840
265337155	chr9	32985798	32986022	32985823	32986004	APTX	NR_036579	12	8	5	-	32985969	32986028
265346919	chr9	32985981	32986199	32986005	32986173	APTX	NR_036579	12	8	5	-	32985969	32986028
259520847	chr9	32984540	32984740	32984561	32984714	APTX	NR_036579	12	8	6	-	32984629	32984855
259590919	chr9	32984693	32984886	32984715	32984860	APTX	NR_036579	12	8	6	-	32984629	32984855
259429420	chr9	32974311	32974534	32974333	32974506	APTX	NR_036579	12	8	7	-	32974456	32974559
259456795	chr9	32974443	32974629	32974471	32974598	APTX	NR_036579	12	8	7	-	32974456	32974559
257958770	chr9	32973303	32973527	32973330	32973504	APTX	NR_036579	12	8	8	-	32972604	32973650
258015223	chr9	32973484	32973679	32973505	32973655	APTX	NR_036579	12	8	8	-	32972604	32973650
262380334	chr9	32973553	32973754	32973573	32973729	APTX	NR_036579	12	8	8	-	32972604	32973650
262652832	chr3	97486875	97487046	97486901	97487021	ARL6	NM_032146	1	9	3	+	97486925	97487074
262655431	chr3	97486999	97487216	97487022	97487188	ARL6	NM_032146	1	9	3	+	97486925	97487074
257496214	chr3	97498887	97499081	97498916	97499053	ARL6	NM_032146	1	9	4	+	97499003	97499064
257497511	chr3	97499021	97499217	97499049	97499189	ARL6	NM_032146	1	9	4	+	97499003	97499064
263794704	chr3	97499342	97499564	97499370	97499536	ARL6	NM_032146	1	9	5	+	97499459	97499527
254326193	chr3	97503713	97503925	97503737	97503898	ARL6	NM_032146	1	9	6	+	97503799	97503893
257757269	chr3	97506778	97506956	97506804	97506928	ARL6	NM_032146	1	9	7	+	97506834	97506963
257760371	chr3	97506904	97507079	97506929	97507052	ARL6	NM_032146	1	9	7	+	97506834	97506963
256371414	chr3	97510480	97510702	97510505	97510677	ARL6	NM_032146	1	9	8	+	97510615	97510670
267109484	chr3	97516859	97517021	97516886	97516992	ARL6	NM_032146	1	9	9	+	97516868	97517373
262652832	chr3	97486875	97487046	97486901	97487021	ARL6	NM_177976	2	9	3	+	97486925	97487074
262655431	chr3	97486999	97487216	97487022	97487188	ARL6	NM_177976	2	9	3	+	97486925	97487074
257496214	chr3	97498887	97499081	97498916	97499053	ARL6	NM_177976	2	9	4	+	97499003	97499064
257497511	chr3	97499021	97499217	97499049	97499189	ARL6	NM_177976	2	9	4	+	97499003	97499064
263794704	chr3	97499342	97499564	97499370	97499536	ARL6	NM_177976	2	9	5	+	97499459	97499527
254326193	chr3	97503713	97503925	97503737	97503898	ARL6	NM_177976	2	9	6	+	97503799	97503893
257757269	chr3	97506778	97506956	97506804	97506928	ARL6	NM_177976	2	9	7	+	97506834	97506963
257760371	chr3	97506904	97507079	97506929	97507052	ARL6	NM_177976	2	9	7	+	97506834	97506963
256371414	chr3	97510480	97510702	97510505	97510677	ARL6	NM_177976	2	9	8	+	97510615	97510670

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267109484	chr3	97516859	97517021	97516886	97516992	ARL6	NM_177976	2	9	9	+	97516868	97517373
265132142	chr22	51065917	51066141	51065939	51066119	ARSA	NM_000487	1	8	1	-	51065984	51066601
265145962	chr22	51066100	51066280	51066118	51066261	ARSA	NM_000487	1	8	1	-	51065984	51066601
257929963	chr22	51065522	51065736	51065539	51065719	ARSA	NM_000487	1	8	2	-	51065594	51065834
257944127	chr22	51065689	51065894	51065709	51065872	ARSA	NM_000487	1	8	2	-	51065594	51065834
258972504	chr22	51065193	51065393	51065214	51065375	ARSA	NM_000487	1	8	3	-	51065262	51065480
258978440	chr22	51065334	51065553	51065353	51065535	ARSA	NM_000487	1	8	3	-	51065262	51065480
264642215	chr22	51064857	51065056	51064879	51065034	ARSA	NM_000487	1	8	4	-	51065019	51065188
264657462	chr22	51065013	51065215	51065035	51065193	ARSA	NM_000487	1	8	4	-	51065019	51065188
266875858	chr22	51064511	51064705	51064532	51064684	ARSA	NM_000487	1	8	5	-	51064582	51064706
266886479	chr22	51064637	51064804	51064658	51064782	ARSA	NM_000487	1	8	5	-	51064582	51064706
255632974	chr22	51064329	51064534	51064349	51064513	ARSA	NM_000487	1	8	6	-	51064364	51064491
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_000487	1	8	7	-	51064007	51064109
264160391	chr22	51064000	51064168	51064020	51064148	ARSA	NM_000487	1	8	7	-	51064007	51064109
256007365	chr22	51063684	51063881	51063705	51063860	ARSA	NM_000487	1	8	8	-	51061182	51063892
256013029	chr22	51063825	51064024	51063847	51064002	ARSA	NM_000487	1	8	8	-	51061182	51063892
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_000487	1	8	8	-	51061182	51063892
265276853	chr22	51063531	51063730	51063551	51063708	ARSA	NM_000487	1	8	8	-	51061182	51063892
265132142	chr22	51065917	51066141	51065939	51066119	ARSA	NM_001085425	2	9	2	-	51065984	51066220
265145962	chr22	51066100	51066280	51066118	51066261	ARSA	NM_001085425	2	9	2	-	51065984	51066220
257929963	chr22	51065522	51065736	51065539	51065719	ARSA	NM_001085425	2	9	3	-	51065594	51065834
257944127	chr22	51065689	51065894	51065709	51065872	ARSA	NM_001085425	2	9	3	-	51065594	51065834
258972504	chr22	51065193	51065393	51065214	51065375	ARSA	NM_001085425	2	9	4	-	51065262	51065480
258978440	chr22	51065334	51065553	51065353	51065535	ARSA	NM_001085425	2	9	4	-	51065262	51065480
264642215	chr22	51064857	51065056	51064879	51065034	ARSA	NM_001085425	2	9	5	-	51065019	51065188
264657462	chr22	51065013	51065215	51065035	51065193	ARSA	NM_001085425	2	9	5	-	51065019	51065188
266875858	chr22	51064511	51064705	51064532	51064684	ARSA	NM_001085425	2	9	6	-	51064582	51064706
266886479	chr22	51064637	51064804	51064658	51064782	ARSA	NM_001085425	2	9	6	-	51064582	51064706
255632974	chr22	51064329	51064534	51064349	51064513	ARSA	NM_001085425	2	9	7	-	51064364	51064491
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085425	2	9	8	-	51064007	51064109
264160391	chr22	51064000	51064168	51064020	51064148	ARSA	NM_001085425	2	9	8	-	51064007	51064109
256007365	chr22	51063684	51063881	51063705	51063860	ARSA	NM_001085425	2	9	9	-	51061182	51063892
256013029	chr22	51063825	51064024	51063847	51064002	ARSA	NM_001085425	2	9	9	-	51061182	51063892
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085425	2	9	9	-	51061182	51063892
265276853	chr22	51063531	51063730	51063551	51063708	ARSA	NM_001085425	2	9	9	-	51061182	51063892
265132142	chr22	51065917	51066141	51065939	51066119	ARSA	NM_001085426	3	9	2	-	51065984	51066220
265145962	chr22	51066100	51066280	51066118	51066261	ARSA	NM_001085426	3	9	2	-	51065984	51066220
257929963	chr22	51065522	51065736	51065539	51065719	ARSA	NM_001085426	3	9	3	-	51065594	51065834
257944127	chr22	51065689	51065894	51065709	51065872	ARSA	NM_001085426	3	9	3	-	51065594	51065834
258972504	chr22	51065193	51065393	51065214	51065375	ARSA	NM_001085426	3	9	4	-	51065262	51065480
258978440	chr22	51065334	51065553	51065353	51065535	ARSA	NM_001085426	3	9	4	-	51065262	51065480

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264642215	chr22	51064857	51065056	51064879	51065034	ARSA	NM_001085426	3	9	5	-	51065019	51065188
264657462	chr22	51065013	51065215	51065035	51065193	ARSA	NM_001085426	3	9	5	-	51065019	51065188
266875858	chr22	51064511	51064705	51064532	51064684	ARSA	NM_001085426	3	9	6	-	51064582	51064706
266886479	chr22	51064637	51064804	51064658	51064782	ARSA	NM_001085426	3	9	6	-	51064582	51064706
255632974	chr22	51064329	51064534	51064349	51064513	ARSA	NM_001085426	3	9	7	-	51064364	51064491
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085426	3	9	8	-	51064007	51064109
264160391	chr22	51064000	51064168	51064020	51064148	ARSA	NM_001085426	3	9	8	-	51064007	51064109
256007365	chr22	51063684	51063881	51063705	51063860	ARSA	NM_001085426	3	9	9	-	51061182	51063892
256013029	chr22	51063825	51064024	51063847	51064002	ARSA	NM_001085426	3	9	9	-	51061182	51063892
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085426	3	9	9	-	51061182	51063892
265276853	chr22	51063531	51063730	51063551	51063708	ARSA	NM_001085426	3	9	9	-	51061182	51063892
265132142	chr22	51065917	51066141	51065939	51066119	ARSA	NM_001085427	4	9	2	-	51065984	51066220
265145962	chr22	51066100	51066280	51066118	51066261	ARSA	NM_001085427	4	9	2	-	51065984	51066220
257929963	chr22	51065522	51065736	51065539	51065719	ARSA	NM_001085427	4	9	3	-	51065594	51065834
257944127	chr22	51065689	51065894	51065709	51065872	ARSA	NM_001085427	4	9	3	-	51065594	51065834
258972504	chr22	51065193	51065393	51065214	51065375	ARSA	NM_001085427	4	9	4	-	51065262	51065480
258978440	chr22	51065334	51065553	51065353	51065535	ARSA	NM_001085427	4	9	4	-	51065262	51065480
264642215	chr22	51064857	51065056	51064879	51065034	ARSA	NM_001085427	4	9	5	-	51065019	51065188
264657462	chr22	51065013	51065215	51065035	51065193	ARSA	NM_001085427	4	9	5	-	51065019	51065188
266875858	chr22	51064511	51064705	51064532	51064684	ARSA	NM_001085427	4	9	6	-	51064582	51064706
266886479	chr22	51064637	51064804	51064658	51064782	ARSA	NM_001085427	4	9	6	-	51064582	51064706
255632974	chr22	51064329	51064534	51064349	51064513	ARSA	NM_001085427	4	9	7	-	51064364	51064491
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085427	4	9	8	-	51064007	51064109
264160391	chr22	51064000	51064168	51064020	51064148	ARSA	NM_001085427	4	9	8	-	51064007	51064109
256007365	chr22	51063684	51063881	51063705	51063860	ARSA	NM_001085427	4	9	9	-	51061182	51063892
256013029	chr22	51063825	51064024	51063847	51064002	ARSA	NM_001085427	4	9	9	-	51061182	51063892
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085427	4	9	9	-	51061182	51063892
265276853	chr22	51063531	51063730	51063551	51063708	ARSA	NM_001085427	4	9	9	-	51061182	51063892
257929963	chr22	51065522	51065736	51065539	51065719	ARSA	NM_001085428	5	8	2	-	51065594	51065834
257944127	chr22	51065689	51065894	51065709	51065872	ARSA	NM_001085428	5	8	2	-	51065594	51065834
258972504	chr22	51065193	51065393	51065214	51065375	ARSA	NM_001085428	5	8	3	-	51065262	51065480
258978440	chr22	51065334	51065553	51065353	51065535	ARSA	NM_001085428	5	8	3	-	51065262	51065480
264642215	chr22	51064857	51065056	51064879	51065034	ARSA	NM_001085428	5	8	4	-	51065019	51065188
264657462	chr22	51065013	51065215	51065035	51065193	ARSA	NM_001085428	5	8	4	-	51065019	51065188
266875858	chr22	51064511	51064705	51064532	51064684	ARSA	NM_001085428	5	8	5	-	51064582	51064706
266886479	chr22	51064637	51064804	51064658	51064782	ARSA	NM_001085428	5	8	5	-	51064582	51064706
255632974	chr22	51064329	51064534	51064349	51064513	ARSA	NM_001085428	5	8	6	-	51064364	51064491
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085428	5	8	7	-	51064007	51064109
264160391	chr22	51064000	51064168	51064020	51064148	ARSA	NM_001085428	5	8	7	-	51064007	51064109
256007365	chr22	51063684	51063881	51063705	51063860	ARSA	NM_001085428	5	8	8	-	51061182	51063892
256013029	chr22	51063825	51064024	51063847	51064002	ARSA	NM_001085428	5	8	8	-	51061182	51063892

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256014410	chr22	51063859	51064042	51063879	51064019	ARSA	NM_001085428	5	8	8	-	51061182	51063892
265276853	chr22	51063531	51063730	51063551	51063708	ARSA	NM_001085428	5	8	8	-	51061182	51063892
264423954	chr7	65541000	65541130	65541019	65541108	ASL	NM_000048	1	17	2	+	65541026	65541080
256930703	chr7	65546659	65546882	65546684	65546863	ASL	NM_000048	1	17	3	+	65546790	65546984
256963345	chr7	65546841	65547065	65546863	65547043	ASL	NM_000048	1	17	3	+	65546790	65546984
256326927	chr7	65547306	65547526	65547324	65547499	ASL	NM_000048	1	17	4	+	65547355	65547438
254085295	chr7	65547782	65547972	65547803	65547951	ASL	NM_000048	1	17	5	+	65547867	65547923
264005246	chr7	65548009	65548210	65548030	65548188	ASL	NM_000048	1	17	6	+	65548064	65548161
258846251	chr7	65551499	65551692	65551518	65551672	ASL	NM_000048	1	17	7	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_000048	1	17	7	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_000048	1	17	8	+	65551731	65551808
263423960	chr7	65551741	65551964	65551761	65551944	ASL	NM_000048	1	17	8	+	65551731	65551808
261980469	chr7	65552292	65552501	65552313	65552477	ASL	NM_000048	1	17	9	+	65552321	65552373
260642574	chr7	65552671	65552839	65552692	65552817	ASL	NM_000048	1	17	10	+	65552716	65552778
266328864	chr7	65553766	65553936	65553787	65553915	ASL	NM_000048	1	17	11	+	65553794	65553908
258664938	chr7	65553915	65554135	65553934	65554114	ASL	NM_000048	1	17	12	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_000048	1	17	12	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_000048	1	17	13	+	65554263	65554322
265621950	chr7	65554270	65554494	65554290	65554469	ASL	NM_000048	1	17	13	+	65554263	65554322
255615746	chr7	65554480	65554687	65554504	65554667	ASL	NM_000048	1	17	14	+	65554599	65554682
255619151	chr7	65554629	65554853	65554649	65554832	ASL	NM_000048	1	17	14	+	65554599	65554682
254373311	chr7	65556876	65557099	65556899	65557082	ASL	NM_000048	1	17	15	+	65556993	65557073
254719523	chr7	65557488	65557695	65557509	65557675	ASL	NM_000048	1	17	16	+	65557544	65557650
253831987	chr7	65557671	65557819	65557691	65557798	ASL	NM_000048	1	17	17	+	65557755	65558329
253834359	chr7	65557761	65557940	65557779	65557919	ASL	NM_000048	1	17	17	+	65557755	65558329
264423954	chr7	65541000	65541130	65541019	65541108	ASL	NM_001024943	2	16	1	+	65540834	65541080
256930703	chr7	65546659	65546882	65546684	65546863	ASL	NM_001024943	2	16	2	+	65546790	65546984
256963345	chr7	65546841	65547065	65546863	65547043	ASL	NM_001024943	2	16	2	+	65546790	65546984
256326927	chr7	65547306	65547526	65547324	65547499	ASL	NM_001024943	2	16	3	+	65547355	65547438
254085295	chr7	65547782	65547972	65547803	65547951	ASL	NM_001024943	2	16	4	+	65547867	65547923
264005246	chr7	65548009	65548210	65548030	65548188	ASL	NM_001024943	2	16	5	+	65548064	65548161
258846251	chr7	65551499	65551692	65551518	65551672	ASL	NM_001024943	2	16	6	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_001024943	2	16	6	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_001024943	2	16	7	+	65551731	65551808
263423960	chr7	65551741	65551964	65551761	65551944	ASL	NM_001024943	2	16	7	+	65551731	65551808
261980469	chr7	65552292	65552501	65552313	65552477	ASL	NM_001024943	2	16	8	+	65552321	65552373
260642574	chr7	65552671	65552839	65552692	65552817	ASL	NM_001024943	2	16	9	+	65552716	65552778
266328864	chr7	65553766	65553936	65553787	65553915	ASL	NM_001024943	2	16	10	+	65553794	65553908
258664938	chr7	65553915	65554135	65553934	65554114	ASL	NM_001024943	2	16	11	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_001024943	2	16	11	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_001024943	2	16	12	+	65554263	65554322

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265621950	chr7	65554270	65554494	65554290	65554469	ASL	NM_001024943	2	16	12	+	65554263	65554322
255615746	chr7	65554480	65554687	65554504	65554667	ASL	NM_001024943	2	16	13	+	65554599	65554682
255619151	chr7	65554629	65554853	65554649	65554832	ASL	NM_001024943	2	16	13	+	65554599	65554682
254373311	chr7	65556876	65557099	65556899	65557082	ASL	NM_001024943	2	16	14	+	65556993	65557073
254719523	chr7	65557488	65557695	65557509	65557675	ASL	NM_001024943	2	16	15	+	65557544	65557650
253831987	chr7	65557671	65557819	65557691	65557798	ASL	NM_001024943	2	16	16	+	65557755	65558329
253834359	chr7	65557761	65557940	65557779	65557919	ASL	NM_001024943	2	16	16	+	65557755	65558329
264423954	chr7	65541000	65541130	65541019	65541108	ASL	NM_001024944	3	15	1	+	65540834	65541080
256930703	chr7	65546659	65546882	65546684	65546863	ASL	NM_001024944	3	15	2	+	65546790	65546984
256963345	chr7	65546841	65547065	65546863	65547043	ASL	NM_001024944	3	15	2	+	65546790	65546984
256326927	chr7	65547306	65547526	65547324	65547499	ASL	NM_001024944	3	15	3	+	65547355	65547438
254085295	chr7	65547782	65547972	65547803	65547951	ASL	NM_001024944	3	15	4	+	65547867	65547923
264005246	chr7	65548009	65548210	65548030	65548188	ASL	NM_001024944	3	15	5	+	65548064	65548161
258846251	chr7	65551499	65551692	65551518	65551672	ASL	NM_001024944	3	15	6	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_001024944	3	15	6	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_001024944	3	15	7	+	65551731	65551808
263423960	chr7	65551741	65551964	65551761	65551944	ASL	NM_001024944	3	15	7	+	65551731	65551808
261980469	chr7	65552292	65552501	65552313	65552477	ASL	NM_001024944	3	15	8	+	65552321	65552373
260642574	chr7	65552671	65552839	65552692	65552817	ASL	NM_001024944	3	15	9	+	65552716	65552778
266328864	chr7	65553766	65553936	65553787	65553915	ASL	NM_001024944	3	15	10	+	65553794	65553908
258664938	chr7	65553915	65554135	65553934	65554114	ASL	NM_001024944	3	15	11	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_001024944	3	15	11	+	65554078	65554162
255615746	chr7	65554480	65554687	65554504	65554667	ASL	NM_001024944	3	15	12	+	65554599	65554682
255619151	chr7	65554629	65554853	65554649	65554832	ASL	NM_001024944	3	15	12	+	65554599	65554682
254373311	chr7	65556876	65557099	65556899	65557082	ASL	NM_001024944	3	15	13	+	65556993	65557073
254719523	chr7	65557488	65557695	65557509	65557675	ASL	NM_001024944	3	15	14	+	65557544	65557650
253831987	chr7	65557671	65557819	65557691	65557798	ASL	NM_001024944	3	15	15	+	65557755	65558329
253834359	chr7	65557761	65557940	65557779	65557919	ASL	NM_001024944	3	15	15	+	65557755	65558329
264423954	chr7	65541000	65541130	65541019	65541108	ASL	NM_001024946	4	15	1	+	65540834	65541080
256930703	chr7	65546659	65546882	65546684	65546863	ASL	NM_001024946	4	15	2	+	65546790	65546984
256963345	chr7	65546841	65547065	65546863	65547043	ASL	NM_001024946	4	15	2	+	65546790	65546984
256326927	chr7	65547306	65547526	65547324	65547499	ASL	NM_001024946	4	15	3	+	65547355	65547438
254085295	chr7	65547782	65547972	65547803	65547951	ASL	NM_001024946	4	15	4	+	65547867	65547923
264005246	chr7	65548009	65548210	65548030	65548188	ASL	NM_001024946	4	15	5	+	65548064	65548161
258846251	chr7	65551499	65551692	65551518	65551672	ASL	NM_001024946	4	15	6	+	65551572	65551649
258849605	chr7	65551562	65551784	65551582	65551767	ASL	NM_001024946	4	15	6	+	65551572	65551649
261980469	chr7	65552292	65552501	65552313	65552477	ASL	NM_001024946	4	15	7	+	65552321	65552373
260642574	chr7	65552671	65552839	65552692	65552817	ASL	NM_001024946	4	15	8	+	65552716	65552778
266328864	chr7	65553766	65553936	65553787	65553915	ASL	NM_001024946	4	15	9	+	65553794	65553908
258664938	chr7	65553915	65554135	65553934	65554114	ASL	NM_001024946	4	15	10	+	65554078	65554162
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_001024946	4	15	10	+	65554078	65554162

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258669404	chr7	65554089	65554313	65554110	65554291	ASL	NM_001024946	4	15	11	+	65554263	65554322
265621950	chr7	65554270	65554494	65554290	65554469	ASL	NM_001024946	4	15	11	+	65554263	65554322
255615746	chr7	65554480	65554687	65554504	65554667	ASL	NM_001024946	4	15	12	+	65554599	65554682
255619151	chr7	65554629	65554853	65554649	65554832	ASL	NM_001024946	4	15	12	+	65554599	65554682
254373311	chr7	65556876	65557099	65556899	65557082	ASL	NM_001024946	4	15	13	+	65556993	65557073
254719523	chr7	65557488	65557695	65557509	65557675	ASL	NM_001024946	4	15	14	+	65557544	65557650
253831987	chr7	65557671	65557819	65557691	65557798	ASL	NM_001024946	4	15	15	+	65557755	65558329
253834359	chr7	65557761	65557940	65557779	65557919	ASL	NM_001024946	4	15	15	+	65557755	65558329
262010354	chr17	3379285	3379497	3379308	3379469	ASPA	NM_000049	1	6	1	+	3379296	3379689
262023493	chr17	3379444	3379568	3379470	3379544	ASPA	NM_000049	1	6	1	+	3379296	3379689
262043335	chr17	3379520	3379744	3379545	3379717	ASPA	NM_000049	1	6	1	+	3379296	3379689
265149930	chr17	3384797	3385014	3384819	3384986	ASPA	NM_000049	1	6	2	+	3384897	3385092
265159334	chr17	3384961	3385177	3384987	3385150	ASPA	NM_000049	1	6	2	+	3384897	3385092
259175293	chr17	3386722	3386916	3386747	3386889	ASPA	NM_000049	1	6	3	+	3386793	3386886
256911404	chr17	3392357	3392575	3392379	3392551	ASPA	NM_000049	1	6	4	+	3392529	3392636
256915082	chr17	3392528	3392711	3392552	3392684	ASPA	NM_000049	1	6	4	+	3392529	3392636
255741760	chr17	3397592	3397768	3397614	3397740	ASPA	NM_000049	1	6	5	+	3397644	3397753
253876923	chr17	3402033	3402248	3402055	3402220	ASPA	NM_000049	1	6	6	+	3402185	3402700
253913493	chr17	3402192	3402413	3402213	3402389	ASPA	NM_000049	1	6	6	+	3402185	3402700
262010354	chr17	3379285	3379497	3379308	3379469	ASPA	NM_001128085	2	7	2	+	3379428	3379689
262023493	chr17	3379444	3379568	3379470	3379544	ASPA	NM_001128085	2	7	2	+	3379428	3379689
262043335	chr17	3379520	3379744	3379545	3379717	ASPA	NM_001128085	2	7	2	+	3379428	3379689
265149930	chr17	3384797	3385014	3384819	3384986	ASPA	NM_001128085	2	7	3	+	3384897	3385092
265159334	chr17	3384961	3385177	3384987	3385150	ASPA	NM_001128085	2	7	3	+	3384897	3385092
259175293	chr17	3386722	3386916	3386747	3386889	ASPA	NM_001128085	2	7	4	+	3386793	3386886
256911404	chr17	3392357	3392575	3392379	3392551	ASPA	NM_001128085	2	7	5	+	3392529	3392636
256915082	chr17	3392528	3392711	3392552	3392684	ASPA	NM_001128085	2	7	5	+	3392529	3392636
255741760	chr17	3397592	3397768	3397614	3397740	ASPA	NM_001128085	2	7	6	+	3397644	3397753
253876923	chr17	3402033	3402248	3402055	3402220	ASPA	NM_001128085	2	7	7	+	3402185	3402700
253913493	chr17	3402192	3402413	3402213	3402389	ASPA	NM_001128085	2	7	7	+	3402185	3402700
257541841	chr14	51026847	51027046	51026868	51027022	ATL1	NM_001127713	1	14	2	+	51026845	51027017
254158169	chr14	51054499	51054695	51054524	51054671	ATL1	NM_001127713	1	14	3	+	51054549	51054796
254194448	chr14	51054644	51054853	51054672	51054828	ATL1	NM_001127713	1	14	3	+	51054549	51054796
266748523	chr14	51057556	51057717	51057584	51057692	ATL1	NM_001127713	1	14	4	+	51057659	51057793
266752333	chr14	51057667	51057877	51057693	51057849	ATL1	NM_001127713	1	14	4	+	51057659	51057793
257331590	chr14	51058106	51058323	51058127	51058298	ATL1	NM_001127713	1	14	5	+	51058253	51058357
257353942	chr14	51058274	51058498	51058299	51058470	ATL1	NM_001127713	1	14	5	+	51058253	51058357
264177814	chr14	51060491	51060682	51060519	51060654	ATL1	NM_001127713	1	14	6	+	51060564	51060614
254091720	chr14	51062202	51062409	51062229	51062381	ATL1	NM_001127713	1	14	7	+	51062294	51062350
262768384	chr14	51079933	51080139	51079960	51080110	ATL1	NM_001127713	1	14	8	+	51079977	51080069
266065273	chr14	51080951	51081138	51080976	51081111	ATL1	NM_001127713	1	14	9	+	51081091	51081229

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266078111	chr14	51081091	51081308	51081112	51081279	ATL1	NM_001127713	1	14	9	+	51081091	51081229
261169242	chr14	51087250	51087474	51087274	51087449	ATL1	NM_001127713	1	14	10	+	51087317	51087444
255992871	chr14	51088517	51088652	51088547	51088625	ATL1	NM_001127713	1	14	11	+	51088561	51088617
265659447	chr14	51089799	51090023	51089823	51089994	ATL1	NM_001127713	1	14	12	+	51089895	51089966
255859547	chr14	51094632	51094853	51094661	51094829	ATL1	NM_001127713	1	14	13	+	51094749	51095180
255876328	chr14	51094803	51095026	51094830	51095003	ATL1	NM_001127713	1	14	13	+	51094749	51095180
255904171	chr14	51094975	51095164	51095004	51095142	ATL1	NM_001127713	1	14	13	+	51094749	51095180
255929020	chr14	51095121	51095326	51095142	51095304	ATL1	NM_001127713	1	14	13	+	51094749	51095180
257474353	chr14	51098768	51098992	51098795	51098971	ATL1	NM_001127713	1	14	14	+	51098947	51099784
257475281	chr14	51098952	51099094	51098975	51099066	ATL1	NM_001127713	1	14	14	+	51098947	51099784
257541841	chr14	51026847	51027046	51026868	51027022	ATL1	NM_015915	2	14	1	+	51026743	51027017
254158169	chr14	51054499	51054695	51054524	51054671	ATL1	NM_015915	2	14	2	+	51054549	51054796
254194448	chr14	51054644	51054853	51054672	51054828	ATL1	NM_015915	2	14	2	+	51054549	51054796
266748523	chr14	51057556	51057717	51057584	51057692	ATL1	NM_015915	2	14	3	+	51057659	51057793
266752333	chr14	51057667	51057877	51057693	51057849	ATL1	NM_015915	2	14	3	+	51057659	51057793
257331590	chr14	51058106	51058323	51058127	51058298	ATL1	NM_015915	2	14	4	+	51058253	51058357
257353942	chr14	51058274	51058498	51058299	51058470	ATL1	NM_015915	2	14	4	+	51058253	51058357
264177814	chr14	51060491	51060682	51060519	51060654	ATL1	NM_015915	2	14	5	+	51060564	51060614
254091720	chr14	51062202	51062409	51062229	51062381	ATL1	NM_015915	2	14	6	+	51062294	51062350
262768384	chr14	51079933	51080139	51079960	51080110	ATL1	NM_015915	2	14	7	+	51079977	51080069
266065273	chr14	51080951	51081138	51080976	51081111	ATL1	NM_015915	2	14	8	+	51081091	51081229
266078111	chr14	51081091	51081308	51081112	51081279	ATL1	NM_015915	2	14	8	+	51081091	51081229
261169242	chr14	51087250	51087474	51087274	51087449	ATL1	NM_015915	2	14	9	+	51087317	51087444
255992871	chr14	51088517	51088652	51088547	51088625	ATL1	NM_015915	2	14	10	+	51088561	51088617
265659447	chr14	51089799	51090023	51089823	51089994	ATL1	NM_015915	2	14	11	+	51089895	51089966
255859547	chr14	51094632	51094853	51094661	51094829	ATL1	NM_015915	2	14	12	+	51094749	51095189
255876328	chr14	51094803	51095026	51094830	51095003	ATL1	NM_015915	2	14	12	+	51094749	51095189
255904171	chr14	51094975	51095164	51095004	51095142	ATL1	NM_015915	2	14	12	+	51094749	51095189
255929020	chr14	51095121	51095326	51095142	51095304	ATL1	NM_015915	2	14	12	+	51094749	51095189
255929020	chr14	51095121	51095326	51095142	51095304	ATL1	NM_015915	2	14	13	+	51095224	51095227
257474353	chr14	51098768	51098992	51098795	51098971	ATL1	NM_015915	2	14	14	+	51098945	51099784
257475281	chr14	51098952	51099094	51098975	51099066	ATL1	NM_015915	2	14	14	+	51098945	51099784
257541841	chr14	51026847	51027046	51026868	51027022	ATL1	NM_181598	3	13	1	+	51026743	51027017
254158169	chr14	51054499	51054695	51054524	51054671	ATL1	NM_181598	3	13	2	+	51054549	51054796
254194448	chr14	51054644	51054853	51054672	51054828	ATL1	NM_181598	3	13	2	+	51054549	51054796
266748523	chr14	51057556	51057717	51057584	51057692	ATL1	NM_181598	3	13	3	+	51057659	51057793
266752333	chr14	51057667	51057877	51057693	51057849	ATL1	NM_181598	3	13	3	+	51057659	51057793
257331590	chr14	51058106	51058323	51058127	51058298	ATL1	NM_181598	3	13	4	+	51058253	51058357
257353942	chr14	51058274	51058498	51058299	51058470	ATL1	NM_181598	3	13	4	+	51058253	51058357
264177814	chr14	51060491	51060682	51060519	51060654	ATL1	NM_181598	3	13	5	+	51060564	51060614
254091720	chr14	51062202	51062409	51062229	51062381	ATL1	NM_181598	3	13	6	+	51062294	51062350

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262768384	chr14	51079933	51080139	51079960	51080110	ATL1	NM_181598	3	13	7	+	51079977	51080069
266065273	chr14	51080951	51081138	51080976	51081111	ATL1	NM_181598	3	13	8	+	51081091	51081229
266078111	chr14	51081091	51081308	51081112	51081279	ATL1	NM_181598	3	13	8	+	51081091	51081229
261169242	chr14	51087250	51087474	51087274	51087449	ATL1	NM_181598	3	13	9	+	51087317	51087444
255992871	chr14	51088517	51088652	51088547	51088625	ATL1	NM_181598	3	13	10	+	51088561	51088617
265659447	chr14	51089799	51090023	51089823	51089994	ATL1	NM_181598	3	13	11	+	51089895	51089966
255859547	chr14	51094632	51094853	51094661	51094829	ATL1	NM_181598	3	13	12	+	51094749	51095180
255876328	chr14	51094803	51095026	51094830	51095003	ATL1	NM_181598	3	13	12	+	51094749	51095180
255904171	chr14	51094975	51095164	51095004	51095142	ATL1	NM_181598	3	13	12	+	51094749	51095180
255929020	chr14	51095121	51095326	51095142	51095304	ATL1	NM_181598	3	13	12	+	51094749	51095180
257474353	chr14	51098768	51098992	51098795	51098971	ATL1	NM_181598	3	13	13	+	51098947	51099784
257475281	chr14	51098952	51099094	51098975	51099066	ATL1	NM_181598	3	13	13	+	51098947	51099784
223697825	chr11	108098375	108098577	108098396	108098552	ATM	NM_000051	1	63	2	+	108098322	108098423
223775985	chr11	108098314	108098527	108098341	108098500	ATM	NM_000051	1	63	2	+	108098322	108098423
223697825	chr11	108098375	108098577	108098396	108098552	ATM	NM_000051	1	63	3	+	108098503	108098615
223702876	chr11	108098525	108098740	108098553	108098710	ATM	NM_000051	1	63	3	+	108098503	108098615
225123514	chr11	108099778	108099983	108099805	108099959	ATM	NM_000051	1	63	4	+	108099905	108100050
225134000	chr11	108099933	108100100	108099960	108100072	ATM	NM_000051	1	63	4	+	108099905	108100050
222445156	chr11	108106331	108106553	108106359	108106525	ATM	NM_000051	1	63	5	+	108106397	108106561
222453945	chr11	108106478	108106644	108106506	108106618	ATM	NM_000051	1	63	5	+	108106397	108106561
222536404	chr11	108114561	108114780	108114592	108114757	ATM	NM_000051	1	63	6	+	108114680	108114845
222538257	chr11	108114720	108114858	108114748	108114831	ATM	NM_000051	1	63	6	+	108114680	108114845
328752297	chr11	108114780	108115004	108114809	108114980	ATM	NM_000051	1	63	6	+	108114680	108114845
222989777	chr11	108115427	108115599	108115455	108115574	ATM	NM_000051	1	63	7	+	108115515	108115753
222995339	chr11	108115547	108115753	108115575	108115730	ATM	NM_000051	1	63	7	+	108115515	108115753
222998755	chr11	108115705	108115866	108115734	108115838	ATM	NM_000051	1	63	7	+	108115515	108115753
224031286	chr11	108117589	108117811	108117611	108117783	ATM	NM_000051	1	63	8	+	108117691	108117854
326891326	chr11	108117736	108117869	108117766	108117845	ATM	NM_000051	1	63	8	+	108117691	108117854
329461826	chr11	108117791	108118001	108117819	108117972	ATM	NM_000051	1	63	8	+	108117691	108117854
225122927	chr11	108119668	108119793	108119696	108119765	ATM	NM_000051	1	63	9	+	108119660	108119829
225125128	chr11	108119738	108119921	108119766	108119894	ATM	NM_000051	1	63	9	+	108119660	108119829
223526382	chr11	108121294	108121493	108121327	108121468	ATM	NM_000051	1	63	10	+	108121428	108121799
223528247	chr11	108121427	108121625	108121455	108121598	ATM	NM_000051	1	63	10	+	108121428	108121799
223542933	chr11	108121573	108121736	108121599	108121709	ATM	NM_000051	1	63	10	+	108121428	108121799
223558072	chr11	108121683	108121831	108121710	108121804	ATM	NM_000051	1	63	10	+	108121428	108121799
223260051	chr11	108122510	108122733	108122532	108122704	ATM	NM_000051	1	63	11	+	108122564	108122758
223273229	chr11	108122625	108122836	108122654	108122810	ATM	NM_000051	1	63	11	+	108122564	108122758
222802821	chr11	108123502	108123722	108123528	108123694	ATM	NM_000051	1	63	12	+	108123544	108123639
223073665	chr11	108124487	108124688	108124511	108124664	ATM	NM_000051	1	63	13	+	108124541	108124766
223080829	chr11	108124637	108124832	108124665	108124804	ATM	NM_000051	1	63	13	+	108124541	108124766
222203805	chr11	108126948	108127072	108126972	108127045	ATM	NM_000051	1	63	14	+	108126942	108127067

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222204633	chr11	108127014	108127174	108127042	108127143	ATM	NM_000051	1	63	14	+	108126942	108127067
329548401	chr11	108126800	108127010	108126823	108126988	ATM	NM_000051	1	63	14	+	108126942	108127067
224417294	chr11	108128126	108128300	108128155	108128273	ATM	NM_000051	1	63	15	+	108128208	108128333
224419132	chr11	108128221	108128346	108128248	108128318	ATM	NM_000051	1	63	15	+	108128208	108128333
222204141	chr11	108129578	108129785	108129605	108129757	ATM	NM_000051	1	63	16	+	108129713	108129802
328553750	chr11	108129735	108129941	108129758	108129913	ATM	NM_000051	1	63	16	+	108129713	108129802
223736495	chr11	108137816	108137982	108137843	108137953	ATM	NM_000051	1	63	17	+	108137898	108138069
223752611	chr11	108137926	108138138	108137954	108138110	ATM	NM_000051	1	63	17	+	108137898	108138069
223647854	chr11	108139080	108139237	108139105	108139212	ATM	NM_000051	1	63	18	+	108139137	108139336
223657066	chr11	108139184	108139384	108139213	108139356	ATM	NM_000051	1	63	18	+	108139137	108139336
223395325	chr11	108141774	108141992	108141802	108141965	ATM	NM_000051	1	63	19	+	108141791	108141873
329146211	chr11	108141798	108142020	108141822	108141993	ATM	NM_000051	1	63	19	+	108141791	108141873
223505899	chr11	108141968	108142190	108141994	108142162	ATM	NM_000051	1	63	20	+	108141978	108142133
329146211	chr11	108141798	108142020	108141822	108141993	ATM	NM_000051	1	63	20	+	108141978	108142133
223582379	chr11	108143147	108143336	108143176	108143309	ATM	NM_000051	1	63	21	+	108143259	108143334
329186382	chr11	108143256	108143476	108143281	108143449	ATM	NM_000051	1	63	21	+	108143259	108143334
223779456	chr11	108143428	108143624	108143450	108143600	ATM	NM_000051	1	63	22	+	108143449	108143579
329186382	chr11	108143256	108143476	108143281	108143449	ATM	NM_000051	1	63	22	+	108143449	108143579
222421677	chr11	108150132	108150327	108150160	108150300	ATM	NM_000051	1	63	23	+	108150218	108150335
222424844	chr11	108150275	108150468	108150301	108150440	ATM	NM_000051	1	63	23	+	108150218	108150335
222171888	chr11	108151606	108151824	108151634	108151799	ATM	NM_000051	1	63	24	+	108151722	108151895
222179771	chr11	108151774	108151985	108151800	108151957	ATM	NM_000051	1	63	24	+	108151722	108151895
223202554	chr11	108153472	108153695	108153500	108153674	ATM	NM_000051	1	63	25	+	108153437	108153606
224357617	chr11	108154856	108155022	108154888	108154996	ATM	NM_000051	1	63	26	+	108154954	108155200
224359488	chr11	108154966	108155115	108154994	108155086	ATM	NM_000051	1	63	26	+	108154954	108155200
224367400	chr11	108155057	108155207	108155084	108155179	ATM	NM_000051	1	63	26	+	108154954	108155200
328741172	chr11	108155148	108155343	108155177	108155315	ATM	NM_000051	1	63	26	+	108154954	108155200
223777262	chr11	108158248	108158409	108158277	108158385	ATM	NM_000051	1	63	27	+	108158327	108158442
223782500	chr11	108158361	108158524	108158386	108158496	ATM	NM_000051	1	63	27	+	108158327	108158442
224114330	chr11	108159628	108159847	108159656	108159819	ATM	NM_000051	1	63	28	+	108159704	108159830
222737398	chr11	108160340	108160471	108160367	108160443	ATM	NM_000051	1	63	29	+	108160329	108160528
222740341	chr11	108160363	108160586	108160389	108160558	ATM	NM_000051	1	63	29	+	108160329	108160528
222320255	chr11	108163252	108163464	108163277	108163437	ATM	NM_000051	1	63	30	+	108163346	108163520
222325241	chr11	108163415	108163597	108163435	108163564	ATM	NM_000051	1	63	30	+	108163346	108163520
224735732	chr11	108165602	108165824	108165626	108165797	ATM	NM_000051	1	63	32	+	108165654	108165786
223690725	chr11	108170319	108170480	108170347	108170456	ATM	NM_000051	1	63	34	+	108170441	108170612
326780255	chr11	108170431	108170619	108170457	108170595	ATM	NM_000051	1	63	34	+	108170441	108170612
223705993	chr11	108172301	108172436	108172330	108172409	ATM	NM_000051	1	63	35	+	108172375	108172516
223708537	chr11	108172387	108172580	108172410	108172555	ATM	NM_000051	1	63	35	+	108172375	108172516
224426408	chr11	108173609	108173830	108173631	108173802	ATM	NM_000051	1	63	36	+	108173580	108173756
328813149	chr11	108173434	108173644	108173462	108173617	ATM	NM_000051	1	63	36	+	108173580	108173756

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223037706	chr11	108175355	108175508	108175385	108175481	ATM	NM_000051	1	63	37	+	108175402	108175579
223038506	chr11	108175418	108175560	108175447	108175540	ATM	NM_000051	1	63	37	+	108175402	108175579
223039345	chr11	108175517	108175673	108175539	108175646	ATM	NM_000051	1	63	37	+	108175402	108175579
222211833	chr11	108178559	108178746	108178584	108178717	ATM	NM_000051	1	63	38	+	108178624	108178711
222602733	chr11	108180784	108180985	108180811	108180962	ATM	NM_000051	1	63	39	+	108180887	108181042
222602923	chr11	108180939	108181102	108180963	108181074	ATM	NM_000051	1	63	39	+	108180887	108181042
223583332	chr11	108183016	108183163	108183044	108183139	ATM	NM_000051	1	63	40	+	108183138	108183225
223584970	chr11	108183115	108183310	108183140	108183282	ATM	NM_000051	1	63	40	+	108183138	108183225
224716834	chr11	108186514	108186708	108186544	108186680	ATM	NM_000051	1	63	41	+	108186550	108186638
224007776	chr11	108186682	108186883	108186709	108186855	ATM	NM_000051	1	63	42	+	108186738	108186840
222233512	chr11	108188088	108188302	108188109	108188275	ATM	NM_000051	1	63	43	+	108188100	108188248
222547018	chr11	108190663	108190852	108190693	108190824	ATM	NM_000051	1	63	44	+	108190681	108190785
223107583	chr11	108192045	108192194	108192065	108192167	ATM	NM_000051	1	63	45	+	108192028	108192147
329002576	chr11	108191878	108192088	108191905	108192064	ATM	NM_000051	1	63	45	+	108192028	108192147
223462800	chr11	108196001	108196192	108196028	108196166	ATM	NM_000051	1	63	46	+	108196037	108196271
223491844	chr11	108196144	108196354	108196167	108196330	ATM	NM_000051	1	63	46	+	108196037	108196271
223557787	chr11	108196763	108196914	108196791	108196890	ATM	NM_000051	1	63	47	+	108196785	108196952
223561270	chr11	108196860	108196997	108196884	108196964	ATM	NM_000051	1	63	47	+	108196785	108196952
223676930	chr11	108198378	108198523	108198406	108198495	ATM	NM_000051	1	63	48	+	108198372	108198485
329279178	chr11	108198222	108198426	108198246	108198405	ATM	NM_000051	1	63	48	+	108198372	108198485
222347510	chr11	108199723	108199932	108199751	108199906	ATM	NM_000051	1	63	49	+	108199748	108199965
222358249	chr11	108199881	108200047	108199907	108200019	ATM	NM_000051	1	63	49	+	108199748	108199965
222167249	chr11	108200888	108201017	108200916	108200993	ATM	NM_000051	1	63	50	+	108200941	108201148
222179007	chr11	108200972	108201181	108200993	108201157	ATM	NM_000051	1	63	50	+	108200941	108201148
224644666	chr11	108202048	108202271	108202075	108202249	ATM	NM_000051	1	63	51	+	108202171	108202284
328931168	chr11	108202243	108202451	108202264	108202421	ATM	NM_000051	1	63	51	+	108202171	108202284
222587273	chr11	108202488	108202709	108202508	108202681	ATM	NM_000051	1	63	52	+	108202606	108202764
222591174	chr11	108202659	108202875	108202682	108202847	ATM	NM_000051	1	63	52	+	108202606	108202764
222306847	chr11	108203430	108203613	108203459	108203585	ATM	NM_000051	1	63	53	+	108203489	108203627
329137616	chr11	108203558	108203776	108203585	108203754	ATM	NM_000051	1	63	53	+	108203489	108203627
223221577	chr11	108204568	108204704	108204596	108204673	ATM	NM_000051	1	63	54	+	108204613	108204695
329033073	chr11	108204663	108204857	108204690	108204828	ATM	NM_000051	1	63	54	+	108204613	108204695
222974856	chr11	108205705	108205878	108205733	108205853	ATM	NM_000051	1	63	55	+	108205696	108205836
328878062	chr11	108205548	108205763	108205570	108205735	ATM	NM_000051	1	63	55	+	108205696	108205836
224361111	chr11	108206459	108206601	108206481	108206579	ATM	NM_000051	1	63	56	+	108206572	108206688
224369561	chr11	108206555	108206748	108206580	108206720	ATM	NM_000051	1	63	56	+	108206572	108206688
224106118	chr11	108213952	108214165	108213972	108214138	ATM	NM_000051	1	63	57	+	108213949	108214098
329506452	chr11	108213802	108213993	108213825	108213971	ATM	NM_000051	1	63	57	+	108213949	108214098
223800280	chr11	108216502	108216626	108216526	108216602	ATM	NM_000051	1	63	58	+	108216470	108216635
223808104	chr11	108216578	108216732	108216603	108216705	ATM	NM_000051	1	63	58	+	108216470	108216635
223621257	chr11	108218020	108218159	108218047	108218131	ATM	NM_000051	1	63	59	+	108218006	108218092

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329887079	chr11	108217852	108218073	108217872	108218046	ATM	NM_000051	1	63	59	+	108218006	108218092
223533360	chr11	108224453	108224666	108224477	108224641	ATM	NM_000051	1	63	60	+	108224493	108224607
223100547	chr11	108225438	108225661	108225461	108225632	ATM	NM_000051	1	63	61	+	108225538	108225601
223017608	chr11	108235827	108235985	108235851	108235957	ATM	NM_000051	1	63	62	+	108235809	108235945
328931865	chr11	108235657	108235877	108235681	108235850	ATM	NM_000051	1	63	62	+	108235809	108235945
224447475	chr11	108235961	108236180	108235986	108236158	ATM	NM_000051	1	63	63	+	108236052	108239826
224477897	chr11	108236138	108236324	108236159	108236296	ATM	NM_000051	1	63	63	+	108236052	108239826
264753303	chr12	110719625	110719779	110719642	110719761	ATP2A2	NM_001681	1	21	1	+	110719032	110719712
265639097	chr12	110720325	110720484	110720353	110720461	ATP2A2	NM_001681	1	21	2	+	110720409	110720426
264122812	chr12	110720462	110720686	110720485	110720658	ATP2A2	NM_001681	1	21	3	+	110720518	110720600
264461666	chr12	110729748	110729878	110729770	110729850	ATP2A2	NM_001681	1	21	4	+	110729825	110729929
264475935	chr12	110729829	110730045	110729851	110730017	ATP2A2	NM_001681	1	21	4	+	110729825	110729929
266764781	chr12	110734244	110734452	110734268	110734427	ATP2A2	NM_001681	1	21	5	+	110734404	110734542
266804091	chr12	110734402	110734610	110734428	110734582	ATP2A2	NM_001681	1	21	5	+	110734404	110734542
261890485	chr12	110760762	110760920	110760783	110760893	ATP2A2	NM_001681	1	21	6	+	110760797	110760877
261087687	chr12	110764151	110764359	110764171	110764331	ATP2A2	NM_001681	1	21	7	+	110764195	110764280
263296815	chr12	110765324	110765543	110765351	110765519	ATP2A2	NM_001681	1	21	8	+	110765358	110765822
263367748	chr12	110765497	110765706	110765519	110765685	ATP2A2	NM_001681	1	21	8	+	110765358	110765822
263415174	chr12	110765637	110765859	110765658	110765830	ATP2A2	NM_001681	1	21	8	+	110765358	110765822
263724722	chr12	110770300	110770522	110770324	110770496	ATP2A2	NM_001681	1	21	9	+	110770402	110770490
254848812	chr12	110770924	110771134	110770944	110771109	ATP2A2	NM_001681	1	21	10	+	110770986	110771088
260491702	chr12	110771669	110771859	110771690	110771835	ATP2A2	NM_001681	1	21	11	+	110771817	110771948
260514877	chr12	110771813	110771974	110771836	110771945	ATP2A2	NM_001681	1	21	11	+	110771817	110771948
254939221	chr12	110777038	110777240	110777060	110777213	ATP2A2	NM_001681	1	21	12	+	110777086	110777208
254975735	chr12	110777162	110777385	110777187	110777362	ATP2A2	NM_001681	1	21	12	+	110777086	110777208
254975735	chr12	110777162	110777385	110777187	110777362	ATP2A2	NM_001681	1	21	13	+	110777308	110777526
262332830	chr12	110777338	110777562	110777363	110777539	ATP2A2	NM_001681	1	21	13	+	110777308	110777526
263522986	chr12	110778366	110778570	110778393	110778550	ATP2A2	NM_001681	1	21	14	+	110778464	110778799
263531509	chr12	110778493	110778663	110778514	110778640	ATP2A2	NM_001681	1	21	14	+	110778464	110778799
263546919	chr12	110778618	110778840	110778638	110778818	ATP2A2	NM_001681	1	21	14	+	110778464	110778799
263970846	chr12	110780004	110780225	110780025	110780202	ATP2A2	NM_001681	1	21	15	+	110780033	110780253
264016644	chr12	110780182	110780306	110780203	110780279	ATP2A2	NM_001681	1	21	15	+	110780033	110780253
264590014	chr12	110780990	110781205	110781014	110781183	ATP2A2	NM_001681	1	21	16	+	110781037	110781239
264618117	chr12	110781160	110781367	110781184	110781340	ATP2A2	NM_001681	1	21	16	+	110781037	110781239
262836401	chr12	110782587	110782810	110782610	110782782	ATP2A2	NM_001681	1	21	17	+	110782691	110782776
266329898	chr12	110782912	110783086	110782933	110783064	ATP2A2	NM_001681	1	21	18	+	110783054	110783187
266342306	chr12	110783039	110783263	110783065	110783241	ATP2A2	NM_001681	1	21	18	+	110783054	110783187
257353991	chr12	110783866	110784019	110783887	110783996	ATP2A2	NM_001681	1	21	19	+	110783806	110783923
266025745	chr12	110783697	110783911	110783718	110783886	ATP2A2	NM_001681	1	21	19	+	110783806	110783923
257378730	chr12	110783976	110784192	110783994	110784172	ATP2A2	NM_001681	1	21	20	+	110784006	110784126
259203830	chr12	110787929	110788146	110787950	110788120	ATP2A2	NM_001681	1	21	21	+	110788097	110788897

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264753303	chr12	110719625	110719779	110719642	110719761	ATP2A2	NM_170665	2	20	1	+	110719032	110719712
265639097	chr12	110720325	110720484	110720353	110720461	ATP2A2	NM_170665	2	20	2	+	110720409	110720426
264122812	chr12	110720462	110720686	110720485	110720658	ATP2A2	NM_170665	2	20	3	+	110720518	110720600
264461666	chr12	110729748	110729878	110729770	110729850	ATP2A2	NM_170665	2	20	4	+	110729825	110729929
264475935	chr12	110729829	110730045	110729851	110730017	ATP2A2	NM_170665	2	20	4	+	110729825	110729929
266764781	chr12	110734244	110734452	110734268	110734427	ATP2A2	NM_170665	2	20	5	+	110734404	110734542
266804091	chr12	110734402	110734610	110734428	110734582	ATP2A2	NM_170665	2	20	5	+	110734404	110734542
261890485	chr12	110760762	110760920	110760783	110760893	ATP2A2	NM_170665	2	20	6	+	110760797	110760877
261087687	chr12	110764151	110764359	110764171	110764331	ATP2A2	NM_170665	2	20	7	+	110764195	110764280
263296815	chr12	110765324	110765543	110765351	110765519	ATP2A2	NM_170665	2	20	8	+	110765358	110765822
263367748	chr12	110765497	110765706	110765519	110765685	ATP2A2	NM_170665	2	20	8	+	110765358	110765822
263415174	chr12	110765637	110765859	110765658	110765830	ATP2A2	NM_170665	2	20	8	+	110765358	110765822
263724722	chr12	110770300	110770522	110770324	110770496	ATP2A2	NM_170665	2	20	9	+	110770402	110770490
254848812	chr12	110770924	110771134	110770944	110771109	ATP2A2	NM_170665	2	20	10	+	110770986	110771088
260491702	chr12	110771669	110771859	110771690	110771835	ATP2A2	NM_170665	2	20	11	+	110771817	110771948
260514877	chr12	110771813	110771974	110771836	110771945	ATP2A2	NM_170665	2	20	11	+	110771817	110771948
254939221	chr12	110777038	110777240	110777060	110777213	ATP2A2	NM_170665	2	20	12	+	110777086	110777208
254975735	chr12	110777162	110777385	110777187	110777362	ATP2A2	NM_170665	2	20	12	+	110777086	110777208
254975735	chr12	110777162	110777385	110777187	110777362	ATP2A2	NM_170665	2	20	13	+	110777308	110777526
262332830	chr12	110777338	110777562	110777363	110777539	ATP2A2	NM_170665	2	20	13	+	110777308	110777526
263522986	chr12	110778366	110778570	110778393	110778550	ATP2A2	NM_170665	2	20	14	+	110778464	110778799
263531509	chr12	110778493	110778663	110778514	110778640	ATP2A2	NM_170665	2	20	14	+	110778464	110778799
263546919	chr12	110778618	110778840	110778638	110778818	ATP2A2	NM_170665	2	20	14	+	110778464	110778799
263970846	chr12	110780004	110780225	110780025	110780202	ATP2A2	NM_170665	2	20	15	+	110780033	110780253
264016644	chr12	110780182	110780306	110780203	110780279	ATP2A2	NM_170665	2	20	15	+	110780033	110780253
264590014	chr12	110780990	110781205	110781014	110781183	ATP2A2	NM_170665	2	20	16	+	110781037	110781239
264618117	chr12	110781160	110781367	110781184	110781340	ATP2A2	NM_170665	2	20	16	+	110781037	110781239
262836401	chr12	110782587	110782810	110782610	110782782	ATP2A2	NM_170665	2	20	17	+	110782691	110782776
266329898	chr12	110782912	110783086	110782933	110783064	ATP2A2	NM_170665	2	20	18	+	110783054	110783187
266342306	chr12	110783039	110783263	110783065	110783241	ATP2A2	NM_170665	2	20	18	+	110783054	110783187
257353991	chr12	110783866	110784019	110783887	110783996	ATP2A2	NM_170665	2	20	19	+	110783806	110783923
266025745	chr12	110783697	110783911	110783718	110783886	ATP2A2	NM_170665	2	20	19	+	110783806	110783923
257378730	chr12	110783976	110784192	110783994	110784172	ATP2A2	NM_170665	2	20	20	+	110784006	110788897
258809333	chr12	110784148	110784362	110784168	110784334	ATP2A2	NM_170665	2	20	20	+	110784006	110788897
259203830	chr12	110787929	110788146	110787950	110788120	ATP2A2	NM_170665	2	20	20	+	110784006	110788897
266846867	chrX	77227065	77227189	77227092	77227161	ATP7A	NM_000052	1	23	2	+	77227118	77227258
266851949	chrX	77227136	77227291	77227162	77227263	ATP7A	NM_000052	1	23	2	+	77227118	77227258
259808855	chrX	77243635	77243824	77243663	77243798	ATP7A	NM_000052	1	23	3	+	77243738	77244227
259828876	chrX	77243773	77243908	77243799	77243888	ATP7A	NM_000052	1	23	3	+	77243738	77244227
259922178	chrX	77243862	77244086	77243889	77244059	ATP7A	NM_000052	1	23	3	+	77243738	77244227
260061549	chrX	77244038	77244259	77244060	77244232	ATP7A	NM_000052	1	23	3	+	77243738	77244227

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257399551	chrX	77244668	77244851	77244693	77244829	ATP7A	NM_000052	1	23	4	+	77244729	77245454
257419549	chrX	77244808	77244940	77244830	77244914	ATP7A	NM_000052	1	23	4	+	77244729	77245454
257439361	chrX	77244891	77245101	77244915	77245076	ATP7A	NM_000052	1	23	4	+	77244729	77245454
257488386	chrX	77245050	77245203	77245077	77245181	ATP7A	NM_000052	1	23	4	+	77244729	77245454
265853418	chrX	77245154	77245344	77245182	77245318	ATP7A	NM_000052	1	23	4	+	77244729	77245454
265876667	chrX	77245293	77245512	77245319	77245484	ATP7A	NM_000052	1	23	4	+	77244729	77245454
254553901	chrX	77253884	77254107	77253906	77254078	ATP7A	NM_000052	1	23	5	+	77253975	77254181
254615933	chrX	77254056	77254228	77254079	77254199	ATP7A	NM_000052	1	23	5	+	77253975	77254181
254019737	chrX	77258584	77258717	77258602	77258689	ATP7A	NM_000052	1	23	6	+	77258570	77258733
254033845	chrX	77258608	77258738	77258636	77258711	ATP7A	NM_000052	1	23	6	+	77258570	77258733
257075441	chrX	77264531	77264663	77264559	77264635	ATP7A	NM_000052	1	23	7	+	77264599	77264760
257080038	chrX	77264614	77264814	77264636	77264786	ATP7A	NM_000052	1	23	7	+	77264599	77264760
256225706	chrX	77266555	77266770	77266578	77266743	ATP7A	NM_000052	1	23	8	+	77266673	77266749
256231560	chrX	77266711	77266923	77266739	77266891	ATP7A	NM_000052	1	23	8	+	77266673	77266749
255881169	chrX	77266834	77267000	77266863	77266974	ATP7A	NM_000052	1	23	9	+	77266946	77267171
255883354	chrX	77266951	77267164	77266975	77267136	ATP7A	NM_000052	1	23	9	+	77266946	77267171
255892050	chrX	77267109	77267235	77267137	77267208	ATP7A	NM_000052	1	23	9	+	77266946	77267171
257483443	chrX	77268224	77268435	77268252	77268410	ATP7A	NM_000052	1	23	10	+	77268376	77268609
257501403	chrX	77268386	77268521	77268411	77268493	ATP7A	NM_000052	1	23	10	+	77268376	77268609
257519270	chrX	77268467	77268661	77268494	77268632	ATP7A	NM_000052	1	23	10	+	77268376	77268609
266794344	chrX	77271125	77271319	77271147	77271291	ATP7A	NM_000052	1	23	12	+	77271251	77271378
266821176	chrX	77271267	77271454	77271292	77271426	ATP7A	NM_000052	1	23	12	+	77271251	77271378
259096597	chrX	77275607	77275821	77275631	77275799	ATP7A	NM_000052	1	23	13	+	77275741	77275895
259124183	chrX	77275775	77275925	77275799	77275898	ATP7A	NM_000052	1	23	13	+	77275741	77275895
260715804	chrX	77276311	77276528	77276336	77276506	ATP7A	NM_000052	1	23	14	+	77276442	77276576
260717901	chrX	77276469	77276691	77276498	77276664	ATP7A	NM_000052	1	23	14	+	77276442	77276576
263830251	chrX	77284621	77284806	77284649	77284780	ATP7A	NM_000052	1	23	15	+	77284747	77284941
263831731	chrX	77284757	77284978	77284781	77284953	ATP7A	NM_000052	1	23	15	+	77284747	77284941
254096493	chrX	77286843	77287040	77286866	77287016	ATP7A	NM_000052	1	23	16	+	77286898	77287080
254116541	chrX	77286992	77287133	77287017	77287109	ATP7A	NM_000052	1	23	16	+	77286898	77287080
254837958	chrX	77289046	77289196	77289073	77289171	ATP7A	NM_000052	1	23	17	+	77289103	77289319
254855545	chrX	77289151	77289356	77289172	77289328	ATP7A	NM_000052	1	23	17	+	77289103	77289319
263909434	chrX	77294219	77294396	77294247	77294371	ATP7A	NM_000052	1	23	18	+	77294334	77294480
263929249	chrX	77294346	77294570	77294372	77294543	ATP7A	NM_000052	1	23	18	+	77294334	77294480
256710858	chrX	77296057	77296232	77296083	77296204	ATP7A	NM_000052	1	23	19	+	77296089	77296231
256720720	chrX	77296181	77296355	77296205	77296327	ATP7A	NM_000052	1	23	19	+	77296089	77296231
256025597	chrX	77298018	77298145	77298045	77298121	ATP7A	NM_000052	1	23	20	+	77298083	77298286
256038667	chrX	77298097	77298319	77298122	77298295	ATP7A	NM_000052	1	23	20	+	77298083	77298286
260173884	chrX	77298650	77298872	77298672	77298844	ATP7A	NM_000052	1	23	21	+	77298815	77298932
260188843	chrX	77298818	77299002	77298845	77298975	ATP7A	NM_000052	1	23	21	+	77298815	77298932
259080084	chrX	77300988	77301203	77301007	77301175	ATP7A	NM_000052	1	23	22	+	77300967	77301069

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262308310	chrX	77301721	77301943	77301743	77301915	ATP7A	NM_000052	1	23	23	+	77301791	77305892
262374184	chrX	77301888	77302100	77301916	77302077	ATP7A	NM_000052	1	23	23	+	77301791	77305892
266927653	chr13	52585366	52585534	52585387	52585514	ATP7B	NM_000053	1	21	1	-	52585423	52585630
256342315	chr13	52548037	52548229	52548058	52548207	ATP7B	NM_000053	1	21	2	-	52548071	52549304
256392516	chr13	52548184	52548408	52548205	52548388	ATP7B	NM_000053	1	21	2	-	52548071	52549304
256436741	chr13	52548363	52548587	52548389	52548562	ATP7B	NM_000053	1	21	2	-	52548071	52549304
258720958	chr13	52549005	52549229	52549028	52549207	ATP7B	NM_000053	1	21	2	-	52548071	52549304
258764375	chr13	52549156	52549375	52549177	52549352	ATP7B	NM_000053	1	21	2	-	52548071	52549304
265315339	chr13	52548538	52548735	52548563	52548714	ATP7B	NM_000053	1	21	2	-	52548071	52549304
265358606	chr13	52548681	52548881	52548708	52548860	ATP7B	NM_000053	1	21	2	-	52548071	52549304
265387225	chr13	52548836	52549057	52548860	52549033	ATP7B	NM_000053	1	21	2	-	52548071	52549304
254845504	chr13	52544544	52544672	52544568	52544645	ATP7B	NM_000053	1	21	3	-	52544628	52544885
254873980	chr13	52544621	52544837	52544646	52544813	ATP7B	NM_000053	1	21	3	-	52544628	52544885
254898885	chr13	52544792	52544958	52544814	52544931	ATP7B	NM_000053	1	21	3	-	52544628	52544885
265779537	chr13	52542547	52542770	52542566	52542748	ATP7B	NM_000053	1	21	4	-	52542580	52542743
255317963	chr13	52538881	52539073	52538909	52539049	ATP7B	NM_000053	1	21	5	-	52539008	52539169
255318384	chr13	52539020	52539229	52539048	52539207	ATP7B	NM_000053	1	21	5	-	52539008	52539169
254503647	chr13	52535914	52536097	52535935	52536073	ATP7B	NM_000053	1	21	6	-	52535973	52536049
266321807	chr13	52534160	52534336	52534183	52534308	ATP7B	NM_000053	1	21	7	-	52534284	52534458
266327620	chr13	52534282	52534495	52534309	52534467	ATP7B	NM_000053	1	21	7	-	52534284	52534458
257864635	chr13	52532375	52532597	52532398	52532575	ATP7B	NM_000053	1	21	8	-	52532447	52532680
257948552	chr13	52532553	52532730	52532576	52532708	ATP7B	NM_000053	1	21	8	-	52532447	52532680
265257730	chr13	52531566	52531779	52531591	52531751	ATP7B	NM_000053	1	21	9	-	52531652	52531743
258133849	chr13	52524348	52524566	52524369	52524542	ATP7B	NM_000053	1	21	10	-	52524408	52524535
260685539	chr13	52523976	52524183	52524003	52524159	ATP7B	NM_000053	1	21	11	-	52524143	52524297
260697217	chr13	52524134	52524332	52524160	52524308	ATP7B	NM_000053	1	21	11	-	52524143	52524297
264105146	chr13	52523760	52523972	52523784	52523947	ATP7B	NM_000053	1	21	12	-	52523798	52523932
262253781	chr13	52520370	52520586	52520398	52520564	ATP7B	NM_000053	1	21	13	-	52520420	52520614
262284623	chr13	52520536	52520760	52520556	52520737	ATP7B	NM_000053	1	21	13	-	52520420	52520614
263256119	chr13	52518111	52518272	52518131	52518250	ATP7B	NM_000053	1	21	14	-	52518245	52518427
263269505	chr13	52518230	52518449	52518251	52518424	ATP7B	NM_000053	1	21	14	-	52518245	52518427
263303598	chr13	52518399	52518531	52518425	52518510	ATP7B	NM_000053	1	21	14	-	52518245	52518427
254006626	chr13	52516467	52516689	52516489	52516667	ATP7B	NM_000053	1	21	15	-	52516522	52516690
254078606	chr13	52516648	52516822	52516668	52516799	ATP7B	NM_000053	1	21	15	-	52516522	52516690
255712361	chr13	52515173	52515395	52515197	52515368	ATP7B	NM_000053	1	21	16	-	52515217	52515360
266180360	chr13	52513145	52513367	52513173	52513345	ATP7B	NM_000053	1	21	17	-	52513187	52513329
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_000053	1	21	18	-	52511612	52511815
265643103	chr13	52511529	52511748	52511550	52511723	ATP7B	NM_000053	1	21	18	-	52511612	52511815
265652469	chr13	52511698	52511893	52511718	52511871	ATP7B	NM_000053	1	21	18	-	52511612	52511815
264919889	chr13	52511290	52511458	52511312	52511434	ATP7B	NM_000053	1	21	19	-	52511412	52511529
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_000053	1	21	19	-	52511412	52511529

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265859053	chr13	52509636	52509859	52509658	52509836	ATP7B	NM_000053	1	21	20	-	52509729	52509831
254703758	chr13	52508751	52508939	52508773	52508917	ATP7B	NM_000053	1	21	21	-	52506806	52509165
254718370	chr13	52508887	52509082	52508912	52509060	ATP7B	NM_000053	1	21	21	-	52506806	52509165
254732927	chr13	52509016	52509213	52509037	52509189	ATP7B	NM_000053	1	21	21	-	52506806	52509165
266927653	chr13	52585366	52585534	52585387	52585514	ATP7B	NM_001005918	2	17	1	-	52585423	52585630
256342315	chr13	52548037	52548229	52548058	52548207	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
256392516	chr13	52548184	52548408	52548205	52548388	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
256436741	chr13	52548363	52548587	52548389	52548562	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
258720958	chr13	52549005	52549229	52549028	52549207	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
258764375	chr13	52549156	52549375	52549177	52549352	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
265315339	chr13	52548538	52548735	52548563	52548714	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
265358606	chr13	52548681	52548881	52548708	52548860	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
265387225	chr13	52548836	52549057	52548860	52549033	ATP7B	NM_001005918	2	17	2	-	52548071	52549304
254845504	chr13	52544544	52544672	52544568	52544645	ATP7B	NM_001005918	2	17	3	-	52544628	52544885
254873980	chr13	52544621	52544837	52544646	52544813	ATP7B	NM_001005918	2	17	3	-	52544628	52544885
254898885	chr13	52544792	52544958	52544814	52544931	ATP7B	NM_001005918	2	17	3	-	52544628	52544885
265779537	chr13	52542547	52542770	52542566	52542748	ATP7B	NM_001005918	2	17	4	-	52542580	52542743
255317963	chr13	52538881	52539073	52538909	52539049	ATP7B	NM_001005918	2	17	5	-	52539008	52539169
255318384	chr13	52539020	52539229	52539048	52539207	ATP7B	NM_001005918	2	17	5	-	52539008	52539169
265257730	chr13	52531566	52531779	52531591	52531751	ATP7B	NM_001005918	2	17	6	-	52531652	52531743
258133849	chr13	52524348	52524566	52524369	52524542	ATP7B	NM_001005918	2	17	7	-	52524408	52524535
260685539	chr13	52523976	52524183	52524003	52524159	ATP7B	NM_001005918	2	17	8	-	52524143	52524297
260697217	chr13	52524134	52524332	52524160	52524308	ATP7B	NM_001005918	2	17	8	-	52524143	52524297
262253781	chr13	52520370	52520586	52520398	52520564	ATP7B	NM_001005918	2	17	9	-	52520420	52520614
262284623	chr13	52520536	52520760	52520556	52520737	ATP7B	NM_001005918	2	17	9	-	52520420	52520614
263256119	chr13	52518111	52518272	52518131	52518250	ATP7B	NM_001005918	2	17	10	-	52518245	52518427
263269505	chr13	52518230	52518449	52518251	52518424	ATP7B	NM_001005918	2	17	10	-	52518245	52518427
263303598	chr13	52518399	52518531	52518425	52518510	ATP7B	NM_001005918	2	17	10	-	52518245	52518427
254006626	chr13	52516467	52516689	52516489	52516667	ATP7B	NM_001005918	2	17	11	-	52516522	52516690
254078606	chr13	52516648	52516822	52516668	52516799	ATP7B	NM_001005918	2	17	11	-	52516522	52516690
255712361	chr13	52515173	52515395	52515197	52515368	ATP7B	NM_001005918	2	17	12	-	52515217	52515360
266180360	chr13	52513145	52513367	52513173	52513345	ATP7B	NM_001005918	2	17	13	-	52513187	52513329
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_001005918	2	17	14	-	52511612	52511815
265643103	chr13	52511529	52511748	52511550	52511723	ATP7B	NM_001005918	2	17	14	-	52511612	52511815
265652469	chr13	52511698	52511893	52511718	52511871	ATP7B	NM_001005918	2	17	14	-	52511612	52511815
264919889	chr13	52511290	52511458	52511312	52511434	ATP7B	NM_001005918	2	17	15	-	52511412	52511529
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_001005918	2	17	15	-	52511412	52511529
265859053	chr13	52509636	52509859	52509658	52509836	ATP7B	NM_001005918	2	17	16	-	52509729	52509831
254703758	chr13	52508751	52508939	52508773	52508917	ATP7B	NM_001005918	2	17	17	-	52506806	52509165
254718370	chr13	52508887	52509082	52508912	52509060	ATP7B	NM_001005918	2	17	17	-	52506806	52509165
254732927	chr13	52509016	52509213	52509037	52509189	ATP7B	NM_001005918	2	17	17	-	52506806	52509165

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266927653	chr13	52585366	52585534	52585387	52585514	ATP7B	NM_001243182	3	22	1	-	52585423	52585630
256436741	chr13	52548363	52548587	52548389	52548562	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
258720958	chr13	52549005	52549229	52549028	52549207	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
258764375	chr13	52549156	52549375	52549177	52549352	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
265315339	chr13	52548538	52548735	52548563	52548714	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
265358606	chr13	52548681	52548881	52548708	52548860	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
265387225	chr13	52548836	52549057	52548860	52549033	ATP7B	NM_001243182	3	22	2	-	52548554	52549304
256342315	chr13	52548037	52548229	52548058	52548207	ATP7B	NM_001243182	3	22	3	-	52548071	52548220
256392516	chr13	52548184	52548408	52548205	52548388	ATP7B	NM_001243182	3	22	3	-	52548071	52548220
254845504	chr13	52544544	52544672	52544568	52544645	ATP7B	NM_001243182	3	22	4	-	52544628	52544885
254873980	chr13	52544621	52544837	52544646	52544813	ATP7B	NM_001243182	3	22	4	-	52544628	52544885
254898885	chr13	52544792	52544958	52544814	52544931	ATP7B	NM_001243182	3	22	4	-	52544628	52544885
265779537	chr13	52542547	52542770	52542566	52542748	ATP7B	NM_001243182	3	22	5	-	52542580	52542743
255317963	chr13	52538881	52539073	52538909	52539049	ATP7B	NM_001243182	3	22	6	-	52539008	52539169
255318384	chr13	52539020	52539229	52539048	52539207	ATP7B	NM_001243182	3	22	6	-	52539008	52539169
254503647	chr13	52535914	52536097	52535935	52536073	ATP7B	NM_001243182	3	22	7	-	52535973	52536049
266321807	chr13	52534160	52534336	52534183	52534308	ATP7B	NM_001243182	3	22	8	-	52534284	52534458
266327620	chr13	52534282	52534495	52534309	52534467	ATP7B	NM_001243182	3	22	8	-	52534284	52534458
257864635	chr13	52532375	52532597	52532398	52532575	ATP7B	NM_001243182	3	22	9	-	52532447	52532680
257948552	chr13	52532553	52532730	52532576	52532708	ATP7B	NM_001243182	3	22	9	-	52532447	52532680
265257730	chr13	52531566	52531779	52531591	52531751	ATP7B	NM_001243182	3	22	10	-	52531652	52531743
258133849	chr13	52524348	52524566	52524369	52524542	ATP7B	NM_001243182	3	22	11	-	52524408	52524535
260685539	chr13	52523976	52524183	52524003	52524159	ATP7B	NM_001243182	3	22	12	-	52524143	52524297
260697217	chr13	52524134	52524332	52524160	52524308	ATP7B	NM_001243182	3	22	12	-	52524143	52524297
264105146	chr13	52523760	52523972	52523784	52523947	ATP7B	NM_001243182	3	22	13	-	52523798	52523932
262253781	chr13	52520370	52520586	52520398	52520564	ATP7B	NM_001243182	3	22	14	-	52520420	52520614
262284623	chr13	52520536	52520760	52520556	52520737	ATP7B	NM_001243182	3	22	14	-	52520420	52520614
263256119	chr13	52518111	52518272	52518131	52518250	ATP7B	NM_001243182	3	22	15	-	52518245	52518427
263269505	chr13	52518230	52518449	52518251	52518424	ATP7B	NM_001243182	3	22	15	-	52518245	52518427
263303598	chr13	52518399	52518531	52518425	52518510	ATP7B	NM_001243182	3	22	15	-	52518245	52518427
254006626	chr13	52516467	52516689	52516489	52516667	ATP7B	NM_001243182	3	22	16	-	52516522	52516690
254078606	chr13	52516648	52516822	52516668	52516799	ATP7B	NM_001243182	3	22	16	-	52516522	52516690
255712361	chr13	52515173	52515395	52515197	52515368	ATP7B	NM_001243182	3	22	17	-	52515217	52515360
266180360	chr13	52513145	52513367	52513173	52513345	ATP7B	NM_001243182	3	22	18	-	52513187	52513329
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_001243182	3	22	19	-	52511612	52511815
265643103	chr13	52511529	52511748	52511550	52511723	ATP7B	NM_001243182	3	22	19	-	52511612	52511815
265652469	chr13	52511698	52511893	52511718	52511871	ATP7B	NM_001243182	3	22	19	-	52511612	52511815
264919889	chr13	52511290	52511458	52511312	52511434	ATP7B	NM_001243182	3	22	20	-	52511412	52511529
264945513	chr13	52511415	52511632	52511435	52511613	ATP7B	NM_001243182	3	22	20	-	52511412	52511529
265859053	chr13	52509636	52509859	52509658	52509836	ATP7B	NM_001243182	3	22	21	-	52509729	52509831
254703758	chr13	52508751	52508939	52508773	52508917	ATP7B	NM_001243182	3	22	22	-	52506806	52509165

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254718370	chr13	52508887	52509082	52508912	52509060	ATP7B	NM_001243182	3	22	22	-	52506806	52509165
254732927	chr13	52509016	52509213	52509037	52509189	ATP7B	NM_001243182	3	22	22	-	52506806	52509165
256783530	chr6	16328127	16328348	16328149	16328327	ATXN1	NM_000332	1	9	8	-	16326625	16328701
256788296	chr6	16328302	16328520	16328328	16328502	ATXN1	NM_000332	1	9	8	-	16326625	16328701
256792428	chr6	16328483	16328649	16328502	16328629	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265482330	chr6	16326520	16326744	16326541	16326721	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265516853	chr6	16326701	16326834	16326722	16326811	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265523436	chr6	16326791	16327006	16326811	16326988	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265528530	chr6	16326967	16327186	16326986	16327165	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265547275	chr6	16327145	16327326	16327165	16327306	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265548304	chr6	16327284	16327488	16327306	16327468	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265548852	chr6	16327445	16327659	16327462	16327642	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265550869	chr6	16327606	16327817	16327627	16327797	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265551545	chr6	16327779	16327998	16327800	16327979	ATXN1	NM_000332	1	9	8	-	16326625	16328701
265552678	chr6	16327960	16328171	16327977	16328150	ATXN1	NM_000332	1	9	8	-	16326625	16328701
261160333	chr6	16306749	16306959	16306772	16306937	ATXN1	NM_000332	1	9	9	-	16299343	16307090
261235055	chr6	16306915	16307138	16306938	16307113	ATXN1	NM_000332	1	9	9	-	16299343	16307090
263201183	chr6	16306407	16306622	16306429	16306595	ATXN1	NM_000332	1	9	9	-	16299343	16307090
263238079	chr6	16306576	16306794	16306596	16306771	ATXN1	NM_000332	1	9	9	-	16299343	16307090
256783530	chr6	16328127	16328348	16328149	16328327	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
256788296	chr6	16328302	16328520	16328328	16328502	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
256792428	chr6	16328483	16328649	16328502	16328629	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265482330	chr6	16326520	16326744	16326541	16326721	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265516853	chr6	16326701	16326834	16326722	16326811	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265523436	chr6	16326791	16327006	16326811	16326988	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265528530	chr6	16326967	16327186	16326986	16327165	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265547275	chr6	16327145	16327326	16327165	16327306	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265548304	chr6	16327284	16327488	16327306	16327468	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265548852	chr6	16327445	16327659	16327462	16327642	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265550869	chr6	16327606	16327817	16327627	16327797	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265551545	chr6	16327779	16327998	16327800	16327979	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
265552678	chr6	16327960	16328171	16327977	16328150	ATXN1	NM_001128164	2	8	7	-	16326625	16328701
261160333	chr6	16306749	16306959	16306772	16306937	ATXN1	NM_001128164	2	8	8	-	16299343	16307090
261235055	chr6	16306915	16307138	16306938	16307113	ATXN1	NM_001128164	2	8	8	-	16299343	16307090
263201183	chr6	16306407	16306622	16306429	16306595	ATXN1	NM_001128164	2	8	8	-	16299343	16307090
263238079	chr6	16306576	16306794	16306596	16306771	ATXN1	NM_001128164	2	8	8	-	16299343	16307090
263006586	chr12	112037071	112037275	112037089	112037258	ATXN2	NM_002973	1	25	1	-	112036588	112037480
267026029	chr12	112036720	112036865	112036737	112036848	ATXN2	NM_002973	1	25	1	-	112036588	112037480
267026918	chr12	112036824	112037044	112036842	112037027	ATXN2	NM_002973	1	25	1	-	112036588	112037480
264913863	chr12	111993609	111993830	111993630	111993802	ATXN2	NM_002973	1	25	2	-	111993687	111993723
264797954	chr12	111991841	111992009	111991870	111991980	ATXN2	NM_002973	1	25	3	-	111991962	111992021

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257775957	chr12	111990559	111990783	111990583	111990759	ATXN2	NM_002973	1	25	4	-	111990710	111990781
257777330	chr12	111990746	111990969	111990773	111990943	ATXN2	NM_002973	1	25	4	-	111990710	111990781
265645147	chr12	111990075	111990222	111990101	111990201	ATXN2	NM_002973	1	25	5	-	111990084	111990234
265648399	chr12	111990181	111990315	111990202	111990286	ATXN2	NM_002973	1	25	5	-	111990084	111990234
266915030	chr12	111962860	111963037	111962888	111963014	ATXN2	NM_002973	1	25	6	-	111962996	111963120
266924528	chr12	111962987	111963178	111963015	111963151	ATXN2	NM_002973	1	25	6	-	111962996	111963120
264127655	chr12	111958618	111958767	111958651	111958743	ATXN2	NM_002973	1	25	7	-	111958686	111958777
264127876	chr12	111958702	111958850	111958730	111958820	ATXN2	NM_002973	1	25	7	-	111958686	111958777
257721727	chr12	111957622	111957748	111957644	111957720	ATXN2	NM_002973	1	25	8	-	111957683	111957880
257730690	chr12	111957700	111957914	111957721	111957885	ATXN2	NM_002973	1	25	8	-	111957683	111957880
260059731	chr12	111955921	111956116	111955945	111956089	ATXN2	NM_002973	1	25	9	-	111956053	111956231
260083191	chr12	111956066	111956290	111956090	111956262	ATXN2	NM_002973	1	25	9	-	111956053	111956231
265170506	chr12	111953893	111954019	111953926	111953999	ATXN2	NM_002973	1	25	10	-	111953958	111954167
265178670	chr12	111953968	111954126	111953993	111954106	ATXN2	NM_002973	1	25	10	-	111953958	111954167
265183192	chr12	111954086	111954291	111954107	111954263	ATXN2	NM_002973	1	25	10	-	111953958	111954167
256737476	chr12	111951085	111951304	111951107	111951280	ATXN2	NM_002973	1	25	11	-	111951161	111951343
256770982	chr12	111951246	111951467	111951274	111951441	ATXN2	NM_002973	1	25	11	-	111951161	111951343
265802459	chr12	111948148	111948287	111948173	111948261	ATXN2	NM_002973	1	25	12	-	111948189	111948386
265814411	chr12	111948240	111948455	111948262	111948427	ATXN2	NM_002973	1	25	12	-	111948189	111948386
264207230	chr12	111947627	111947770	111947655	111947743	ATXN2	NM_002973	1	25	13	-	111947695	111947802
264207896	chr12	111947716	111947868	111947744	111947839	ATXN2	NM_002973	1	25	13	-	111947695	111947802
266817680	chr12	111926120	111926329	111926147	111926300	ATXN2	NM_002973	1	25	15	-	111926280	111926584
266847909	chr12	111926279	111926489	111926301	111926462	ATXN2	NM_002973	1	25	15	-	111926280	111926584
266867811	chr12	111926440	111926656	111926463	111926628	ATXN2	NM_002973	1	25	15	-	111926280	111926584
266729073	chr12	111924443	111924666	111924466	111924638	ATXN2	NM_002973	1	25	16	-	111924565	111924628
263080990	chr12	111923482	111923682	111923505	111923657	ATXN2	NM_002973	1	25	17	-	111923517	111923669
266256511	chr12	111923011	111923235	111923036	111923209	ATXN2	NM_002973	1	25	18	-	111923075	111923135
255945408	chr12	111908231	111908439	111908253	111908416	ATXN2	NM_002973	1	25	19	-	111908362	111908546
255964901	chr12	111908396	111908604	111908417	111908576	ATXN2	NM_002973	1	25	19	-	111908362	111908546
265315350	chr12	111907870	111908094	111907893	111908067	ATXN2	NM_002973	1	25	20	-	111907912	111908044
263621066	chr12	111902346	111902568	111902373	111902540	ATXN2	NM_002973	1	25	21	-	111902466	111902519
264617377	chr12	111894976	111895199	111894999	111895175	ATXN2	NM_002973	1	25	22	-	111895018	111895163
261022545	chr12	111893729	111893917	111893750	111893894	ATXN2	NM_002973	1	25	23	-	111893833	111894060
261096698	chr12	111893874	111894089	111893895	111894066	ATXN2	NM_002973	1	25	23	-	111893833	111894060
265870858	chr12	111891316	111891517	111891337	111891496	ATXN2	NM_002973	1	25	24	-	111891481	111891649
265881487	chr12	111891478	111891679	111891497	111891654	ATXN2	NM_002973	1	25	24	-	111891481	111891649
260312948	chr12	111890457	111890680	111890481	111890651	ATXN2	NM_002973	1	25	25	-	111890018	111890644
264529884	chr3	63898517	63898724	63898534	63898702	ATXN7	NM_000333	1	13	3	+	63898264	63898599
266896014	chr3	63898803	63898966	63898825	63898941	ATXN7	NM_000333	1	13	4	+	63898833	63898901
255569944	chr3	63938015	63938236	63938038	63938207	ATXN7	NM_000333	1	13	5	+	63938055	63938159
264456900	chr3	63965540	63965732	63965567	63965711	ATXN7	NM_000333	1	13	6	+	63965591	63965843

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264523048	chr3	63965690	63965892	63965712	63965867	ATXN7	NM_000333	1	13	6	+	63965591	63965843
258658571	chr3	63967824	63968026	63967846	63968005	ATXN7	NM_000333	1	13	7	+	63967862	63968121
258712625	chr3	63967985	63968183	63968006	63968159	ATXN7	NM_000333	1	13	7	+	63967862	63968121
260874475	chr3	63968558	63968751	63968585	63968727	ATXN7	NM_000333	1	13	8	+	63968615	63968697
260755651	chr3	63973593	63973803	63973621	63973777	ATXN7	NM_000333	1	13	9	+	63973735	63974000
260797179	chr3	63973757	63973961	63973778	63973937	ATXN7	NM_000333	1	13	9	+	63973735	63974000
260828456	chr3	63973917	63974041	63973938	63974017	ATXN7	NM_000333	1	13	9	+	63973735	63974000
256553931	chr3	63975819	63976029	63975839	63976001	ATXN7	NM_000333	1	13	10	+	63975852	63976050
256582055	chr3	63975979	63976146	63976002	63976126	ATXN7	NM_000333	1	13	10	+	63975852	63976050
260634237	chr3	63976347	63976565	63976368	63976543	ATXN7	NM_000333	1	13	11	+	63976414	63976535
261918436	chr3	63981059	63981281	63981084	63981258	ATXN7	NM_000333	1	13	12	+	63981181	63982159
261968668	chr3	63981238	63981455	63981259	63981432	ATXN7	NM_000333	1	13	12	+	63981181	63982159
262001994	chr3	63981411	63981592	63981433	63981568	ATXN7	NM_000333	1	13	12	+	63981181	63982159
262043514	chr3	63981546	63981770	63981569	63981749	ATXN7	NM_000333	1	13	12	+	63981181	63982159
262119871	chr3	63981729	63981953	63981749	63981933	ATXN7	NM_000333	1	13	12	+	63981181	63982159
262270788	chr3	63981912	63982118	63981934	63982097	ATXN7	NM_000333	1	13	12	+	63981181	63982159
262320402	chr3	63982076	63982290	63982096	63982262	ATXN7	NM_000333	1	13	12	+	63981181	63982159
267169728	chr3	63985059	63985283	63985085	63985263	ATXN7	NM_000333	1	13	13	+	63985126	63989136
253987860	chr3	63953471	63953683	63953498	63953661	ATXN7	NM_001128149	2	9	1	+	63953420	63953651
264456900	chr3	63965540	63965732	63965567	63965711	ATXN7	NM_001128149	2	9	2	+	63965591	63965843
264523048	chr3	63965690	63965892	63965712	63965867	ATXN7	NM_001128149	2	9	2	+	63965591	63965843
258658571	chr3	63967824	63968026	63967846	63968005	ATXN7	NM_001128149	2	9	3	+	63967862	63968121
258712625	chr3	63967985	63968183	63968006	63968159	ATXN7	NM_001128149	2	9	3	+	63967862	63968121
260874475	chr3	63968558	63968751	63968585	63968727	ATXN7	NM_001128149	2	9	4	+	63968615	63968697
260755651	chr3	63973593	63973803	63973621	63973777	ATXN7	NM_001128149	2	9	5	+	63973735	63974000
260797179	chr3	63973757	63973961	63973778	63973937	ATXN7	NM_001128149	2	9	5	+	63973735	63974000
260828456	chr3	63973917	63974041	63973938	63974017	ATXN7	NM_001128149	2	9	5	+	63973735	63974000
256553931	chr3	63975819	63976029	63975839	63976001	ATXN7	NM_001128149	2	9	6	+	63975852	63976050
256582055	chr3	63975979	63976146	63976002	63976126	ATXN7	NM_001128149	2	9	6	+	63975852	63976050
260634237	chr3	63976347	63976565	63976368	63976543	ATXN7	NM_001128149	2	9	7	+	63976414	63976535
261918436	chr3	63981059	63981281	63981084	63981258	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
261968668	chr3	63981238	63981455	63981259	63981432	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
262001994	chr3	63981411	63981592	63981433	63981568	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
262043514	chr3	63981546	63981770	63981569	63981749	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
262119871	chr3	63981729	63981953	63981749	63981933	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
262270788	chr3	63981912	63982118	63981934	63982097	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
262320402	chr3	63982076	63982290	63982096	63982262	ATXN7	NM_001128149	2	9	8	+	63981181	63982159
267169728	chr3	63985059	63985283	63985085	63985263	ATXN7	NM_001128149	2	9	9	+	63985126	63989136
264529884	chr3	63898517	63898724	63898534	63898702	ATXN7	NM_001177387	3	13	2	+	63898264	63898599
266896014	chr3	63898803	63898966	63898825	63898941	ATXN7	NM_001177387	3	13	3	+	63898833	63898901
255569944	chr3	63938015	63938236	63938038	63938207	ATXN7	NM_001177387	3	13	4	+	63938055	63938159

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264456900	chr3	63965540	63965732	63965567	63965711	ATXN7	NM_001177387	3	13	5	+	63965591	63965843
264523048	chr3	63965690	63965892	63965712	63965867	ATXN7	NM_001177387	3	13	5	+	63965591	63965843
258658571	chr3	63967824	63968026	63967846	63968005	ATXN7	NM_001177387	3	13	6	+	63967862	63968121
258712625	chr3	63967985	63968183	63968006	63968159	ATXN7	NM_001177387	3	13	6	+	63967862	63968121
260874475	chr3	63968558	63968751	63968585	63968727	ATXN7	NM_001177387	3	13	7	+	63968615	63968697
260755651	chr3	63973593	63973803	63973621	63973777	ATXN7	NM_001177387	3	13	8	+	63973735	63974000
260797179	chr3	63973757	63973961	63973778	63973937	ATXN7	NM_001177387	3	13	8	+	63973735	63974000
260828456	chr3	63973917	63974041	63973938	63974017	ATXN7	NM_001177387	3	13	8	+	63973735	63974000
256553931	chr3	63975819	63976029	63975839	63976001	ATXN7	NM_001177387	3	13	9	+	63975852	63976050
256582055	chr3	63975979	63976146	63976002	63976126	ATXN7	NM_001177387	3	13	9	+	63975852	63976050
260634237	chr3	63976347	63976565	63976368	63976543	ATXN7	NM_001177387	3	13	10	+	63976414	63976535
261918436	chr3	63981059	63981281	63981084	63981258	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
261968668	chr3	63981238	63981455	63981259	63981432	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
262001994	chr3	63981411	63981592	63981433	63981568	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
262043514	chr3	63981546	63981770	63981569	63981749	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
262119871	chr3	63981729	63981953	63981749	63981933	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
262270788	chr3	63981912	63982118	63981934	63982097	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
262320402	chr3	63982076	63982290	63982096	63982262	ATXN7	NM_001177387	3	13	11	+	63981181	63982159
254149116	chr3	63983204	63983428	63983225	63983401	ATXN7	NM_001177387	3	13	12	+	63983297	63983363
267169728	chr3	63985059	63985283	63985085	63985263	ATXN7	NM_001177387	3	13	13	+	63985126	63989136
333229016	chr10	121411033	121411253	121411050	121411236	BAG3	NM_004281	1	4	1	+	121410882	121411367
333230022	chr10	121411199	121411344	121411217	121411327	BAG3	NM_004281	1	4	1	+	121410882	121411367
333518147	chr10	121429332	121429555	121429354	121429535	BAG3	NM_004281	1	4	2	+	121429363	121429689
333530329	chr10	121429503	121429699	121429525	121429678	BAG3	NM_004281	1	4	2	+	121429363	121429689
333535178	chr10	121429620	121429844	121429643	121429823	BAG3	NM_004281	1	4	2	+	121429363	121429689
332432857	chr10	121431692	121431911	121431711	121431891	BAG3	NM_004281	1	4	3	+	121431767	121432168
332441250	chr10	121431870	121432021	121431892	121432000	BAG3	NM_004281	1	4	3	+	121431767	121432168
332444179	chr10	121431981	121432203	121432000	121432182	BAG3	NM_004281	1	4	3	+	121431767	121432168
333588647	chr10	121435911	121436123	121435939	121436099	BAG3	NM_004281	1	4	4	+	121435976	121437329
333595737	chr10	121436077	121436296	121436100	121436273	BAG3	NM_004281	1	4	4	+	121435976	121437329
333596218	chr10	121436390	121436564	121436417	121436537	BAG3	NM_004281	1	4	4	+	121435976	121437329
333608318	chr10	121436227	121436444	121436251	121436416	BAG3	NM_004281	1	4	4	+	121435976	121437329
333609076	chr10	121436515	121436654	121436538	121436633	BAG3	NM_004281	1	4	4	+	121435976	121437329
333621038	chr10	121436608	121436831	121436629	121436809	BAG3	NM_004281	1	4	4	+	121435976	121437329
255046582	chr19	41903681	41903903	41903702	41903875	BCKDHA	NM_000709	1	9	1	+	41903694	41903840
256367365	chr19	41916515	41916662	41916536	41916640	BCKDHA	NM_000709	1	9	2	+	41916542	41916721
256369596	chr19	41916606	41916821	41916634	41916800	BCKDHA	NM_000709	1	9	2	+	41916542	41916721
265765561	chr19	41916777	41916986	41916798	41916965	BCKDHA	NM_000709	1	9	3	+	41916828	41916914
256221541	chr19	41919780	41919994	41919801	41919971	BCKDHA	NM_000709	1	9	4	+	41919954	41920062
256244881	chr19	41919952	41920138	41919972	41920110	BCKDHA	NM_000709	1	9	4	+	41919954	41920062
266957518	chr19	41925004	41925226	41925023	41925206	BCKDHA	NM_000709	1	9	5	+	41925040	41925201

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259136056	chr19	41928004	41928225	41928027	41928203	BCKDHA	NM_000709	1	9	6	+	41928069	41928275
259150188	chr19	41928184	41928329	41928204	41928308	BCKDHA	NM_000709	1	9	6	+	41928069	41928275
256112718	chr19	41928473	41928605	41928493	41928578	BCKDHA	NM_000709	1	9	7	+	41928534	41928675
256123264	chr19	41928559	41928751	41928579	41928724	BCKDHA	NM_000709	1	9	7	+	41928534	41928675
257530320	chr19	41928764	41928986	41928788	41928963	BCKDHA	NM_000709	1	9	8	+	41928903	41929074
257559254	chr19	41928944	41929144	41928964	41929122	BCKDHA	NM_000709	1	9	8	+	41928903	41929074
259219568	chr19	41930186	41930409	41930213	41930387	BCKDHA	NM_000709	1	9	9	+	41930343	41930910
259250376	chr19	41930340	41930524	41930361	41930501	BCKDHA	NM_000709	1	9	9	+	41930343	41930910
259261453	chr19	41930481	41930638	41930502	41930612	BCKDHA	NM_000709	1	9	9	+	41930343	41930910
255046582	chr19	41903681	41903903	41903702	41903875	BCKDHA	NM_001164783	2	9	1	+	41903694	41903840
256367365	chr19	41916515	41916662	41916536	41916640	BCKDHA	NM_001164783	2	9	2	+	41916542	41916721
256369596	chr19	41916606	41916821	41916634	41916800	BCKDHA	NM_001164783	2	9	2	+	41916542	41916721
265765561	chr19	41916777	41916986	41916798	41916965	BCKDHA	NM_001164783	2	9	3	+	41916828	41916914
256221541	chr19	41919780	41919994	41919801	41919971	BCKDHA	NM_001164783	2	9	4	+	41919954	41920062
256244881	chr19	41919952	41920138	41919972	41920110	BCKDHA	NM_001164783	2	9	4	+	41919954	41920062
266957518	chr19	41925004	41925226	41925023	41925206	BCKDHA	NM_001164783	2	9	5	+	41925040	41925201
259136056	chr19	41928004	41928225	41928027	41928203	BCKDHA	NM_001164783	2	9	6	+	41928069	41928275
259150188	chr19	41928184	41928329	41928204	41928308	BCKDHA	NM_001164783	2	9	6	+	41928069	41928275
256112718	chr19	41928473	41928605	41928493	41928578	BCKDHA	NM_001164783	2	9	7	+	41928537	41928675
256123264	chr19	41928559	41928751	41928579	41928724	BCKDHA	NM_001164783	2	9	7	+	41928537	41928675
257530320	chr19	41928764	41928986	41928788	41928963	BCKDHA	NM_001164783	2	9	8	+	41928903	41929074
257559254	chr19	41928944	41929144	41928964	41929122	BCKDHA	NM_001164783	2	9	8	+	41928903	41929074
259219568	chr19	41930186	41930409	41930213	41930387	BCKDHA	NM_001164783	2	9	9	+	41930343	41930910
259250376	chr19	41930340	41930524	41930361	41930501	BCKDHA	NM_001164783	2	9	9	+	41930343	41930910
259261453	chr19	41930481	41930638	41930502	41930612	BCKDHA	NM_001164783	2	9	9	+	41930343	41930910
256933022	chr6	80816374	80816582	80816395	80816558	BCKDHB	NM_000056	1	11	1	+	80816344	80816606
256934683	chr6	80816526	80816740	80816543	80816718	BCKDHB	NM_000056	1	11	1	+	80816344	80816606
264158992	chr6	80837139	80837308	80837171	80837284	BCKDHB	NM_000056	1	11	2	+	80837264	80837341
264162624	chr6	80837259	80837389	80837285	80837362	BCKDHB	NM_000056	1	11	2	+	80837264	80837341
266784645	chr6	80838874	80839080	80838902	80839055	BCKDHB	NM_000056	1	11	3	+	80838878	80838946
262538731	chr6	80877251	80877461	80877278	80877435	BCKDHB	NM_000056	1	11	4	+	80877395	80877528
262544760	chr6	80877409	80877591	80877436	80877564	BCKDHB	NM_000056	1	11	4	+	80877395	80877528
263925859	chr6	80878563	80878753	80878584	80878729	BCKDHB	NM_000056	1	11	5	+	80878592	80878747
263933050	chr6	80878699	80878905	80878726	80878883	BCKDHB	NM_000056	1	11	5	+	80878592	80878747
256865980	chr6	80880928	80881117	80880948	80881095	BCKDHB	NM_000056	1	11	6	+	80880999	80881107
263218672	chr6	80910559	80910780	80910582	80910753	BCKDHB	NM_000056	1	11	7	+	80910651	80910748
254417419	chr6	80912751	80912968	80912779	80912940	BCKDHB	NM_000056	1	11	8	+	80912819	80912929
261164349	chr6	80982672	80982896	80982698	80982875	BCKDHB	NM_000056	1	11	9	+	80982852	80982938
261182394	chr6	80982855	80982990	80982876	80982968	BCKDHB	NM_000056	1	11	9	+	80982852	80982938
255513017	chr6	81053349	81053553	81053375	81053526	BCKDHB	NM_000056	1	11	10	+	81053381	81053529
256933022	chr6	80816374	80816582	80816395	80816558	BCKDHB	NM_183050	2	10	1	+	80816344	80816606

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256934683	chr6	80816526	80816740	80816543	80816718	BCKDHB	NM_183050	2	10	1	+	80816344	80816606
264158992	chr6	80837139	80837308	80837171	80837284	BCKDHB	NM_183050	2	10	2	+	80837264	80837341
264162624	chr6	80837259	80837389	80837285	80837362	BCKDHB	NM_183050	2	10	2	+	80837264	80837341
266784645	chr6	80838874	80839080	80838902	80839055	BCKDHB	NM_183050	2	10	3	+	80838878	80838946
262538731	chr6	80877251	80877461	80877278	80877435	BCKDHB	NM_183050	2	10	4	+	80877395	80877528
262544760	chr6	80877409	80877591	80877436	80877564	BCKDHB	NM_183050	2	10	4	+	80877395	80877528
263925859	chr6	80878563	80878753	80878584	80878729	BCKDHB	NM_183050	2	10	5	+	80878592	80878747
263933050	chr6	80878699	80878905	80878726	80878883	BCKDHB	NM_183050	2	10	5	+	80878592	80878747
256865980	chr6	80880928	80881117	80880948	80881095	BCKDHB	NM_183050	2	10	6	+	80880999	80881107
263218672	chr6	80910559	80910780	80910582	80910753	BCKDHB	NM_183050	2	10	7	+	80910651	80910748
254417419	chr6	80912751	80912968	80912779	80912940	BCKDHB	NM_183050	2	10	8	+	80912819	80912929
261164349	chr6	80982672	80982896	80982698	80982875	BCKDHB	NM_183050	2	10	9	+	80982852	80982938
261182394	chr6	80982855	80982990	80982876	80982968	BCKDHB	NM_183050	2	10	9	+	80982852	80982938
255513017	chr6	81053349	81053553	81053375	81053526	BCKDHB	NM_183050	2	10	10	+	81053381	81055987
265747724	chr11	61722539	61722755	61722557	61722736	BEST1	NM_001139443	1	9	2	+	61722579	61722673
266805161	chr11	61723084	61723248	61723102	61723230	BEST1	NM_001139443	1	9	3	+	61723190	61723423
266806574	chr11	61723210	61723362	61723227	61723344	BEST1	NM_001139443	1	9	3	+	61723190	61723423
266808198	chr11	61723324	61723514	61723342	61723494	BEST1	NM_001139443	1	9	3	+	61723190	61723423
264132004	chr11	61724223	61724441	61724245	61724422	BEST1	NM_001139443	1	9	4	+	61724316	61724470
264170219	chr11	61724394	61724618	61724416	61724592	BEST1	NM_001139443	1	9	4	+	61724316	61724470
262581321	chr11	61724772	61724985	61724793	61724961	BEST1	NM_001139443	1	9	5	+	61724859	61724936
261380877	chr11	61725554	61725769	61725575	61725746	BEST1	NM_001139443	1	9	6	+	61725618	61725770
261441195	chr11	61725726	61725872	61725747	61725849	BEST1	NM_001139443	1	9	6	+	61725618	61725770
264409284	chr11	61726880	61727089	61726901	61727066	BEST1	NM_001139443	1	9	7	+	61726970	61727050
264865610	chr11	61727319	61727525	61727341	61727505	BEST1	NM_001139443	1	9	8	+	61727364	61727515
264886455	chr11	61727485	61727611	61727506	61727583	BEST1	NM_001139443	1	9	8	+	61727364	61727515
259716484	chr11	61730252	61730474	61730274	61730453	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265394242	chr11	61729659	61729867	61729681	61729842	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265446477	chr11	61729812	61729991	61729833	61729971	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265463382	chr11	61729951	61730141	61729972	61730114	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265504675	chr11	61730092	61730299	61730115	61730273	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265525032	chr11	61730433	61730651	61730454	61730630	BEST1	NM_001139443	1	9	9	+	61729727	61731066
265754114	chr11	61719195	61719416	61719216	61719391	BEST1	NM_004183	2	11	2	+	61719243	61719430
265768143	chr11	61719366	61719542	61719392	61719517	BEST1	NM_004183	2	11	2	+	61719243	61719430
265747724	chr11	61722539	61722755	61722557	61722736	BEST1	NM_004183	2	11	3	+	61722579	61722673
266805161	chr11	61723084	61723248	61723102	61723230	BEST1	NM_004183	2	11	4	+	61723190	61723423
266806574	chr11	61723210	61723362	61723227	61723344	BEST1	NM_004183	2	11	4	+	61723190	61723423
266808198	chr11	61723324	61723514	61723342	61723494	BEST1	NM_004183	2	11	4	+	61723190	61723423
264132004	chr11	61724223	61724441	61724245	61724422	BEST1	NM_004183	2	11	5	+	61724316	61724470
264170219	chr11	61724394	61724618	61724416	61724592	BEST1	NM_004183	2	11	5	+	61724316	61724470
262581321	chr11	61724772	61724985	61724793	61724961	BEST1	NM_004183	2	11	6	+	61724859	61724936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261380877	chr11	61725554	61725769	61725575	61725746	BEST1	NM_004183	2	11	7	+	61725618	61725770
261441195	chr11	61725726	61725872	61725747	61725849	BEST1	NM_004183	2	11	7	+	61725618	61725770
264409284	chr11	61726880	61727089	61726901	61727066	BEST1	NM_004183	2	11	8	+	61726970	61727050
264865610	chr11	61727319	61727525	61727341	61727505	BEST1	NM_004183	2	11	9	+	61727364	61727515
264886455	chr11	61727485	61727611	61727506	61727583	BEST1	NM_004183	2	11	9	+	61727364	61727515
259716484	chr11	61730252	61730474	61730274	61730453	BEST1	NM_004183	2	11	10	+	61729727	61730365
265394242	chr11	61729659	61729867	61729681	61729842	BEST1	NM_004183	2	11	10	+	61729727	61730365
265446477	chr11	61729812	61729991	61729833	61729971	BEST1	NM_004183	2	11	10	+	61729727	61730365
265463382	chr11	61729951	61730141	61729972	61730114	BEST1	NM_004183	2	11	10	+	61729727	61730365
265504675	chr11	61730092	61730299	61730115	61730273	BEST1	NM_004183	2	11	10	+	61729727	61730365
260112541	chr11	61731478	61731698	61731499	61731674	BEST1	NM_004183	2	11	11	+	61731576	61731935
223430134	chr10	88635723	88635921	88635751	88635895	BMPR1A	NM_004329	1	13	3	+	88635624	88635842
223123572	chr10	88649751	88649877	88649778	88649852	BMPR1A	NM_004329	1	13	4	+	88649819	88649981
223128731	chr10	88649829	88650016	88649853	88649988	BMPR1A	NM_004329	1	13	4	+	88649819	88649981
222176902	chr10	88651797	88652021	88651824	88651998	BMPR1A	NM_004329	1	13	5	+	88651884	88651986
223979161	chr10	88659444	88659611	88659466	88659583	BMPR1A	NM_004329	1	13	6	+	88659551	88659647
223980312	chr10	88659565	88659691	88659584	88659666	BMPR1A	NM_004329	1	13	6	+	88659551	88659647
222908297	chr10	88659790	88659943	88659813	88659916	BMPR1A	NM_004329	1	13	7	+	88659784	88659883
328895758	chr10	88659633	88659837	88659657	88659812	BMPR1A	NM_004329	1	13	7	+	88659784	88659883
222389872	chr10	88671886	88672051	88671912	88672025	BMPR1A	NM_004329	1	13	8	+	88671997	88672141
222393209	chr10	88672005	88672195	88672026	88672167	BMPR1A	NM_004329	1	13	8	+	88671997	88672141
223140586	chr10	88676792	88676956	88676816	88676932	BMPR1A	NM_004329	1	13	9	+	88676891	88677083
223164219	chr10	88676912	88677134	88676933	88677106	BMPR1A	NM_004329	1	13	9	+	88676891	88677083
223038391	chr10	88678856	88679080	88678881	88679058	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
223057641	chr10	88679039	88679243	88679059	88679223	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
223061587	chr10	88679201	88679333	88679224	88679302	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
222658484	chr10	88681229	88681388	88681256	88681366	BMPR1A	NM_004329	1	13	11	+	88681277	88681452
222673095	chr10	88681346	88681474	88681367	88681450	BMPR1A	NM_004329	1	13	11	+	88681277	88681452
223003751	chr10	88683091	88683309	88683113	88683284	BMPR1A	NM_004329	1	13	12	+	88683133	88683263
224580728	chr10	88683282	88683506	88683307	88683481	BMPR1A	NM_004329	1	13	13	+	88683351	88684945
255942624	chr3	15643273	15643493	15643294	15643475	BTD	NM_000060	1	4	1	+	15643255	15643401
266535608	chr3	15676855	15677077	15676882	15677055	BTD	NM_000060	1	4	2	+	15676931	15677195
266570607	chr3	15677035	15677226	15677056	15677204	BTD	NM_000060	1	4	2	+	15676931	15677195
257518398	chr3	15683362	15683576	15683385	15683555	BTD	NM_000060	1	4	3	+	15683415	15683564
257545338	chr3	15683537	15683674	15683556	15683646	BTD	NM_000060	1	4	3	+	15683415	15683564
263373697	chr3	15686310	15686533	15686333	15686512	BTD	NM_000060	1	4	4	+	15685823	15687325
263378654	chr3	15686824	15687048	15686852	15687027	BTD	NM_000060	1	4	4	+	15685823	15687325
263469851	chr3	15686487	15686708	15686509	15686686	BTD	NM_000060	1	4	4	+	15685823	15687325
263507800	chr3	15685825	15686021	15685842	15685997	BTD	NM_000060	1	4	4	+	15685823	15687325
263557252	chr3	15686657	15686877	15686681	15686853	BTD	NM_000060	1	4	4	+	15685823	15687325
263574210	chr3	15685978	15686181	15685998	15686161	BTD	NM_000060	1	4	4	+	15685823	15687325

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263683168	chr3	15686137	15686357	15686162	15686332	BTD	NM_000060	1	4	4	+	15685823	15687325
253815806	chrX	100630077	100630301	100630104	100630277	BTK	NM_000061	1	19	2	-	100630132	100630302
299083532	chrX	100629467	100629683	100629495	100629658	BTK	NM_000061	1	19	3	-	100629524	100629622
299078680	chrX	100626509	100626733	100626533	100626706	BTK	NM_000061	1	19	4	-	100626621	100626689
257231228	chrX	100624983	100625108	100625005	100625083	BTK	NM_000061	1	19	5	-	100624986	100625067
254470396	chrX	100617487	100617711	100617509	100617684	BTK	NM_000061	1	19	6	-	100617549	100617677
264478250	chrX	100617042	100617263	100617068	100617238	BTK	NM_000061	1	19	7	-	100617161	100617228
265950916	chrX	100615408	100615599	100615431	100615576	BTK	NM_000061	1	19	8	-	100615556	100615743
265956596	chrX	100615552	100615775	100615577	100615748	BTK	NM_000061	1	19	8	-	100615556	100615743
256744738	chrX	100615025	100615167	100615048	100615144	BTK	NM_000061	1	19	9	-	100615076	100615138
266705515	chrX	100614209	100614377	100614230	100614354	BTK	NM_000061	1	19	10	-	100614281	100614335
257994097	chrX	100613491	100613715	100613519	100613689	BTK	NM_000061	1	19	11	-	100613605	100613684
263845256	chrX	100613234	100613458	100613257	100613434	BTK	NM_000061	1	19	12	-	100613298	100613425
262464258	chrX	100612392	100612600	100612413	100612577	BTK	NM_000061	1	19	13	-	100612497	100612571
259081402	chrX	100611622	100611820	100611642	100611795	BTK	NM_000061	1	19	14	-	100611772	100611943
259162471	chrX	100611769	100611976	100611796	100611948	BTK	NM_000061	1	19	14	-	100611772	100611943
265671886	chrX	100610893	100611109	100610913	100611086	BTK	NM_000061	1	19	15	-	100611040	100611256
265688557	chrX	100611065	100611287	100611087	100611262	BTK	NM_000061	1	19	15	-	100611040	100611256
263776537	chrX	100609490	100609709	100609513	100609687	BTK	NM_000061	1	19	16	-	100609618	100609682
254227094	chrX	100608782	100609006	100608808	100608981	BTK	NM_000061	1	19	17	-	100608858	100608976
253937392	chrX	100608084	100608235	100608109	100608208	BTK	NM_000061	1	19	18	-	100608182	100608339
253964373	chrX	100608187	100608389	100608209	100608361	BTK	NM_000061	1	19	18	-	100608182	100608339
264888396	chrX	100604786	100604987	100604807	100604959	BTK	NM_000061	1	19	19	-	100604435	100604944
262170042	chr17	58227294	58227463	58227313	58227446	CA4	NM_000717	1	8	1	+	58227302	58227453
264935758	chr17	58232604	58232795	58232626	58232776	CA4	NM_000717	1	8	2	+	58232675	58232728
254012826	chr17	58233891	58234058	58233912	58234035	CA4	NM_000717	1	8	3	+	58233921	58234076
254032137	chr17	58234014	58234205	58234036	58234184	CA4	NM_000717	1	8	3	+	58233921	58234076
266201199	chr17	58234697	58234891	58234719	58234868	CA4	NM_000717	1	8	4	+	58234788	58234933
266205722	chr17	58234841	58235023	58234862	58235001	CA4	NM_000717	1	8	4	+	58234788	58234933
256502507	chr17	58234999	58235215	58235020	58235188	CA4	NM_000717	1	8	5	+	58235051	58235149
266725963	chr17	58235345	58235551	58235366	58235529	CA4	NM_000717	1	8	6	+	58235422	58235488
266393561	chr17	58235600	58235808	58235620	58235784	CA4	NM_000717	1	8	7	+	58235644	58235807
266447687	chr17	58235756	58235969	58235777	58235947	CA4	NM_000717	1	8	7	+	58235644	58235807
257428598	chr17	58236563	58236705	58236581	58236686	CA4	NM_000717	1	8	8	+	58236591	58236906
257443689	chr17	58236635	58236843	58236658	58236822	CA4	NM_000717	1	8	8	+	58236591	58236906
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_000719	1	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_000719	1	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_000719	1	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_000719	1	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_000719	1	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_000719	1	47	4	+	2558142	2558281

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_000719	1	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_000719	1	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_000719	1	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_000719	1	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_000719	1	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_000719	1	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_000719	1	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_000719	1	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_000719	1	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_000719	1	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_000719	1	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_000719	1	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_000719	1	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_000719	1	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_000719	1	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_000719	1	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_000719	1	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_000719	1	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_000719	1	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_000719	1	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_000719	1	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_000719	1	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_000719	1	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_000719	1	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_000719	1	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_000719	1	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_000719	1	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_000719	1	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_000719	1	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_000719	1	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_000719	1	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_000719	1	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_000719	1	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_000719	1	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_000719	1	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_000719	1	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_000719	1	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_000719	1	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_000719	1	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_000719	1	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_000719	1	47	31	+	2757641	2757673

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_000719	1	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_000719	1	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_000719	1	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_000719	1	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_000719	1	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_000719	1	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_000719	1	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_000719	1	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_000719	1	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_000719	1	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_000719	1	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_000719	1	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_000719	1	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_000719	1	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_000719	1	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_000719	1	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_000719	1	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_000719	1	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_000719	1	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_000719	1	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_000719	1	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_000719	1	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_000719	1	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_000719	1	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_000719	1	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_000719	1	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129827	2	49	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129827	2	49	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129827	2	49	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129827	2	49	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129827	2	49	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129827	2	49	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129827	2	49	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129827	2	49	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129827	2	49	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129827	2	49	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129827	2	49	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129827	2	49	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129827	2	49	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129827	2	49	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129827	2	49	9	+	2621978	2622150

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129827	2	49	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129827	2	49	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129827	2	49	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129827	2	49	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129827	2	49	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129827	2	49	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129827	2	49	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129827	2	49	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129827	2	49	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129827	2	49	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129827	2	49	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129827	2	49	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129827	2	49	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129827	2	49	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129827	2	49	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129827	2	49	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129827	2	49	21	+	2706396	2706455
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129827	2	49	22	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129827	2	49	23	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129827	2	49	24	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129827	2	49	25	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129827	2	49	26	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129827	2	49	27	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129827	2	49	27	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129827	2	49	28	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129827	2	49	28	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129827	2	49	28	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129827	2	49	29	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129827	2	49	29	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129827	2	49	30	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129827	2	49	30	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129827	2	49	31	+	2742795	2742878
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129827	2	49	32	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129827	2	49	33	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129827	2	49	34	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129827	2	49	34	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129827	2	49	35	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129827	2	49	36	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129827	2	49	37	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129827	2	49	37	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129827	2	49	38	+	2774747	2774874

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129827	2	49	39	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129827	2	49	40	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129827	2	49	41	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129827	2	49	41	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129827	2	49	42	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129827	2	49	42	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129827	2	49	43	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129827	2	49	43	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129827	2	49	44	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129827	2	49	44	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129827	2	49	44	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129827	2	49	45	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129827	2	49	46	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129827	2	49	46	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129827	2	49	47	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129827	2	49	48	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129827	2	49	48	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129827	2	49	49	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129827	2	49	49	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129829	3	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129829	3	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129829	3	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129829	3	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129829	3	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129829	3	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129829	3	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129829	3	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129829	3	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129829	3	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129829	3	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129829	3	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129829	3	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129829	3	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129829	3	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129829	3	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129829	3	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129829	3	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129829	3	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129829	3	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129829	3	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129829	3	47	14	+	2690756	2690963

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129829	3	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129829	3	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129829	3	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129829	3	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129829	3	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129829	3	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129829	3	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129829	3	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129829	3	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129829	3	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129829	3	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129829	3	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129829	3	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129829	3	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129829	3	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129829	3	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129829	3	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129829	3	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129829	3	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129829	3	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129829	3	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129829	3	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129829	3	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129829	3	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129829	3	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129829	3	47	32	+	2760740	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129829	3	47	32	+	2760740	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129829	3	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129829	3	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129829	3	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129829	3	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129829	3	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129829	3	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129829	3	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129829	3	47	39	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129829	3	47	39	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129829	3	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129829	3	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129829	3	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129829	3	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129829	3	47	42	+	2788610	2788962

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129829	3	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129829	3	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129829	3	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129829	3	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129829	3	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129829	3	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129829	3	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129829	3	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129829	3	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129829	3	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129830	4	48	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129830	4	48	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129830	4	48	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129830	4	48	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129830	4	48	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129830	4	48	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129830	4	48	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129830	4	48	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129830	4	48	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129830	4	48	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129830	4	48	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129830	4	48	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129830	4	48	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129830	4	48	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129830	4	48	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129830	4	48	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129830	4	48	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129830	4	48	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129830	4	48	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129830	4	48	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129830	4	48	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129830	4	48	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129830	4	48	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129830	4	48	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129830	4	48	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129830	4	48	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129830	4	48	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129830	4	48	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129830	4	48	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129830	4	48	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129830	4	48	20	+	2705040	2705169

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129830	4	48	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129830	4	48	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129830	4	48	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129830	4	48	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129830	4	48	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129830	4	48	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129830	4	48	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129830	4	48	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129830	4	48	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129830	4	48	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129830	4	48	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129830	4	48	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129830	4	48	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129830	4	48	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129830	4	48	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129830	4	48	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129830	4	48	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129830	4	48	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129830	4	48	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129830	4	48	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129830	4	48	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129830	4	48	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129830	4	48	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129830	4	48	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129830	4	48	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129830	4	48	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129830	4	48	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129830	4	48	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129830	4	48	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129830	4	48	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129830	4	48	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129830	4	48	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129830	4	48	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129830	4	48	42	+	2788610	2788962
333562690	chr12	2791072	2791274	2791093	2791253	CACNA1C	NM_001129830	4	48	43	+	2791116	2791220
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129830	4	48	44	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129830	4	48	45	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129830	4	48	45	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129830	4	48	46	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129830	4	48	47	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129830	4	48	47	+	2797613	2797945

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129830	4	48	48	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129830	4	48	48	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129831	5	48	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129831	5	48	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129831	5	48	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129831	5	48	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129831	5	48	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129831	5	48	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129831	5	48	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129831	5	48	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129831	5	48	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129831	5	48	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129831	5	48	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129831	5	48	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129831	5	48	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129831	5	48	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129831	5	48	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129831	5	48	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129831	5	48	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129831	5	48	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129831	5	48	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129831	5	48	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129831	5	48	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129831	5	48	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129831	5	48	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129831	5	48	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129831	5	48	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129831	5	48	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129831	5	48	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129831	5	48	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129831	5	48	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129831	5	48	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129831	5	48	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129831	5	48	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129831	5	48	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129831	5	48	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129831	5	48	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129831	5	48	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129831	5	48	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129831	5	48	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129831	5	48	27	+	2717677	2717878

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129831	5	48	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129831	5	48	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129831	5	48	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129831	5	48	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129831	5	48	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129831	5	48	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129831	5	48	30	+	2742795	2742878
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129831	5	48	31	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129831	5	48	32	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129831	5	48	33	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129831	5	48	33	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129831	5	48	34	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129831	5	48	35	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129831	5	48	36	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129831	5	48	36	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129831	5	48	37	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129831	5	48	38	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129831	5	48	39	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129831	5	48	40	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129831	5	48	40	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129831	5	48	41	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129831	5	48	41	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129831	5	48	42	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129831	5	48	42	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129831	5	48	43	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129831	5	48	43	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129831	5	48	43	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129831	5	48	44	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129831	5	48	45	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129831	5	48	45	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129831	5	48	46	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129831	5	48	47	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129831	5	48	47	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129831	5	48	48	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129831	5	48	48	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129832	6	48	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129832	6	48	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129832	6	48	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129832	6	48	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129832	6	48	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129832	6	48	4	+	2558142	2558281

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129832	6	48	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129832	6	48	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129832	6	48	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129832	6	48	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129832	6	48	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129832	6	48	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129832	6	48	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129832	6	48	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129832	6	48	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129832	6	48	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129832	6	48	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129832	6	48	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129832	6	48	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129832	6	48	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129832	6	48	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129832	6	48	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129832	6	48	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129832	6	48	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129832	6	48	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129832	6	48	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129832	6	48	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129832	6	48	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129832	6	48	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129832	6	48	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129832	6	48	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129832	6	48	21	+	2706396	2706455
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129832	6	48	22	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129832	6	48	23	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129832	6	48	24	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129832	6	48	25	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129832	6	48	26	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129832	6	48	27	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129832	6	48	27	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129832	6	48	28	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129832	6	48	28	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129832	6	48	28	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129832	6	48	29	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129832	6	48	29	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129832	6	48	30	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129832	6	48	30	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129832	6	48	31	+	2743463	2743546

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129832	6	48	32	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129832	6	48	33	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129832	6	48	33	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129832	6	48	34	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129832	6	48	35	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129832	6	48	36	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129832	6	48	36	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129832	6	48	37	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129832	6	48	38	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129832	6	48	39	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129832	6	48	40	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129832	6	48	40	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129832	6	48	41	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129832	6	48	41	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129832	6	48	42	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129832	6	48	42	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129832	6	48	43	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129832	6	48	43	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129832	6	48	43	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129832	6	48	44	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129832	6	48	45	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129832	6	48	45	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129832	6	48	46	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129832	6	48	47	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129832	6	48	47	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129832	6	48	48	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129832	6	48	48	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129833	7	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129833	7	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129833	7	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129833	7	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129833	7	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129833	7	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129833	7	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129833	7	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129833	7	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129833	7	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129833	7	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129833	7	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129833	7	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129833	7	47	9	+	2621978	2622150

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129833	7	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129833	7	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129833	7	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129833	7	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129833	7	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129833	7	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129833	7	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129833	7	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129833	7	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129833	7	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129833	7	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129833	7	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129833	7	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129833	7	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129833	7	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129833	7	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129833	7	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129833	7	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129833	7	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129833	7	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129833	7	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129833	7	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129833	7	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129833	7	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129833	7	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129833	7	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129833	7	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129833	7	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129833	7	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129833	7	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129833	7	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129833	7	47	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129833	7	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129833	7	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129833	7	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129833	7	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129833	7	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129833	7	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129833	7	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129833	7	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129833	7	47	37	+	2775852	2775948

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129833	7	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129833	7	47	39	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129833	7	47	39	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129833	7	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129833	7	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129833	7	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129833	7	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129833	7	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129833	7	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129833	7	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129833	7	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129833	7	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129833	7	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129833	7	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129833	7	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129833	7	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129833	7	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129833	7	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129834	8	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129834	8	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129834	8	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129834	8	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129834	8	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129834	8	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129834	8	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129834	8	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129834	8	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129834	8	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129834	8	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129834	8	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129834	8	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129834	8	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129834	8	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129834	8	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129834	8	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129834	8	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129834	8	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129834	8	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129834	8	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129834	8	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129834	8	47	14	+	2690756	2690963

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129834	8	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129834	8	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129834	8	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129834	8	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129834	8	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129834	8	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129834	8	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129834	8	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129834	8	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129834	8	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129834	8	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129834	8	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129834	8	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129834	8	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129834	8	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129834	8	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129834	8	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129834	8	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129834	8	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129834	8	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129834	8	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129834	8	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129834	8	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129834	8	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129834	8	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129834	8	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129834	8	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129834	8	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129834	8	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129834	8	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129834	8	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129834	8	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129834	8	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129834	8	47	39	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129834	8	47	39	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129834	8	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129834	8	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129834	8	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129834	8	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129834	8	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129834	8	47	42	+	2788610	2788962

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129834	8	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129834	8	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129834	8	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129834	8	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129834	8	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129834	8	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129834	8	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129834	8	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129834	8	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129835	9	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129835	9	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129835	9	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129835	9	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129835	9	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129835	9	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129835	9	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129835	9	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129835	9	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129835	9	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129835	9	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129835	9	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129835	9	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129835	9	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129835	9	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129835	9	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129835	9	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129835	9	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129835	9	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129835	9	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129835	9	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129835	9	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129835	9	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129835	9	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129835	9	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129835	9	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129835	9	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129835	9	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129835	9	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129835	9	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129835	9	47	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129835	9	47	21	+	2706603	2706662

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129835	9	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129835	9	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129835	9	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129835	9	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129835	9	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129835	9	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129835	9	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129835	9	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129835	9	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129835	9	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129835	9	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129835	9	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129835	9	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129835	9	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129835	9	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129835	9	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129835	9	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129835	9	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129835	9	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129835	9	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129835	9	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129835	9	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129835	9	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129835	9	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129835	9	47	39	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129835	9	47	39	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129835	9	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129835	9	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129835	9	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129835	9	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129835	9	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129835	9	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129835	9	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129835	9	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129835	9	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129835	9	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129835	9	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129835	9	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129835	9	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129835	9	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129835	9	47	47	+	2800066	2807115

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129836	10	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129836	10	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129836	10	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129836	10	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129836	10	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129836	10	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129836	10	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129836	10	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129836	10	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129836	10	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129836	10	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129836	10	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129836	10	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129836	10	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129836	10	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129836	10	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129836	10	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129836	10	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129836	10	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129836	10	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129836	10	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129836	10	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129836	10	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129836	10	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129836	10	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129836	10	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129836	10	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129836	10	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129836	10	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129836	10	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129836	10	47	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129836	10	47	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129836	10	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129836	10	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129836	10	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129836	10	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129836	10	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129836	10	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129836	10	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129836	10	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129836	10	47	27	+	2717677	2717878

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129836	10	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129836	10	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129836	10	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129836	10	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129836	10	47	30	+	2742795	2742878
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129836	10	47	31	+	2743463	2743546
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129836	10	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129836	10	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129836	10	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129836	10	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129836	10	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129836	10	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129836	10	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129836	10	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129836	10	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129836	10	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129836	10	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129836	10	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129836	10	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129836	10	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129836	10	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129836	10	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129836	10	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129836	10	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129836	10	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129836	10	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129836	10	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129836	10	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129836	10	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129836	10	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129836	10	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129836	10	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129837	11	46	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129837	11	46	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129837	11	46	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129837	11	46	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129837	11	46	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129837	11	46	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129837	11	46	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129837	11	46	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129837	11	46	6	+	2595270	2595428

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129837	11	46	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129837	11	46	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129837	11	46	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129837	11	46	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129837	11	46	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129837	11	46	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129837	11	46	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129837	11	46	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129837	11	46	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129837	11	46	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129837	11	46	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129837	11	46	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129837	11	46	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129837	11	46	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129837	11	46	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129837	11	46	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129837	11	46	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129837	11	46	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129837	11	46	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129837	11	46	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129837	11	46	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129837	11	46	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129837	11	46	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129837	11	46	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129837	11	46	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129837	11	46	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129837	11	46	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129837	11	46	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129837	11	46	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129837	11	46	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129837	11	46	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129837	11	46	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129837	11	46	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129837	11	46	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129837	11	46	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129837	11	46	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129837	11	46	30	+	2743463	2743546
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129837	11	46	31	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129837	11	46	31	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129837	11	46	32	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129837	11	46	33	+	2764313	2764404

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129837	11	46	34	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129837	11	46	34	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129837	11	46	35	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129837	11	46	36	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129837	11	46	37	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129837	11	46	38	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129837	11	46	38	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129837	11	46	39	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129837	11	46	39	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129837	11	46	40	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129837	11	46	40	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129837	11	46	41	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129837	11	46	41	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129837	11	46	41	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129837	11	46	42	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129837	11	46	43	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129837	11	46	43	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129837	11	46	44	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129837	11	46	45	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129837	11	46	45	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129837	11	46	46	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129837	11	46	46	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129838	12	46	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129838	12	46	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129838	12	46	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129838	12	46	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129838	12	46	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129838	12	46	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129838	12	46	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129838	12	46	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129838	12	46	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129838	12	46	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129838	12	46	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129838	12	46	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129838	12	46	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129838	12	46	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129838	12	46	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129838	12	46	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129838	12	46	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129838	12	46	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129838	12	46	12	+	2675588	2675748

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129838	12	46	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129838	12	46	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129838	12	46	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129838	12	46	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129838	12	46	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129838	12	46	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129838	12	46	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129838	12	46	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129838	12	46	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129838	12	46	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129838	12	46	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129838	12	46	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129838	12	46	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129838	12	46	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129838	12	46	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129838	12	46	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129838	12	46	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129838	12	46	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129838	12	46	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129838	12	46	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129838	12	46	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129838	12	46	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129838	12	46	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129838	12	46	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129838	12	46	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129838	12	46	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129838	12	46	30	+	2743463	2743546
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129838	12	46	31	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129838	12	46	31	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129838	12	46	32	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129838	12	46	33	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129838	12	46	34	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129838	12	46	34	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129838	12	46	35	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129838	12	46	36	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129838	12	46	37	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129838	12	46	38	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129838	12	46	38	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129838	12	46	39	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129838	12	46	39	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129838	12	46	40	+	2786899	2787033

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129838	12	46	40	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129838	12	46	41	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129838	12	46	41	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129838	12	46	41	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129838	12	46	42	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129838	12	46	43	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129838	12	46	43	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129838	12	46	44	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129838	12	46	45	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129838	12	46	45	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129838	12	46	46	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129838	12	46	46	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129839	13	46	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129839	13	46	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129839	13	46	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129839	13	46	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129839	13	46	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129839	13	46	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129839	13	46	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129839	13	46	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129839	13	46	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129839	13	46	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129839	13	46	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129839	13	46	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129839	13	46	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129839	13	46	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129839	13	46	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129839	13	46	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129839	13	46	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129839	13	46	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129839	13	46	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129839	13	46	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129839	13	46	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129839	13	46	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129839	13	46	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129839	13	46	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129839	13	46	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129839	13	46	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129839	13	46	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129839	13	46	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129839	13	46	19	+	2702379	2702511

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129839	13	46	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129839	13	46	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129839	13	46	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129839	13	46	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129839	13	46	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129839	13	46	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129839	13	46	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129839	13	46	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129839	13	46	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129839	13	46	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129839	13	46	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129839	13	46	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129839	13	46	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129839	13	46	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129839	13	46	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129839	13	46	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129839	13	46	30	+	2743463	2743540
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129839	13	46	31	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129839	13	46	31	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129839	13	46	32	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129839	13	46	33	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129839	13	46	34	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129839	13	46	34	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129839	13	46	35	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129839	13	46	36	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129839	13	46	37	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129839	13	46	38	+	2783650	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129839	13	46	38	+	2783650	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129839	13	46	39	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129839	13	46	39	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129839	13	46	40	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129839	13	46	40	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129839	13	46	41	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129839	13	46	41	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129839	13	46	41	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129839	13	46	42	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129839	13	46	43	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129839	13	46	43	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129839	13	46	44	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129839	13	46	45	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129839	13	46	45	+	2797613	2797945

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129839	13	46	46	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129839	13	46	46	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129840	14	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129840	14	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129840	14	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129840	14	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129840	14	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129840	14	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129840	14	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129840	14	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129840	14	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129840	14	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129840	14	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129840	14	47	7	+	2602356	2602552
332304660	chr12	2613541	2613740	2613562	2613716	CACNA1C	NM_001129840	14	47	8	+	2613602	2613705
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129840	14	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129840	14	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129840	14	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129840	14	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129840	14	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129840	14	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129840	14	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129840	14	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129840	14	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129840	14	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129840	14	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129840	14	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129840	14	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129840	14	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129840	14	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129840	14	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129840	14	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129840	14	47	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129840	14	47	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129840	14	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129840	14	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129840	14	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129840	14	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129840	14	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129840	14	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129840	14	47	27	+	2717677	2717878

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129840	14	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129840	14	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129840	14	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129840	14	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129840	14	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129840	14	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129840	14	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129840	14	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129840	14	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129840	14	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129840	14	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129840	14	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129840	14	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129840	14	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129840	14	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129840	14	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129840	14	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129840	14	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129840	14	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129840	14	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129840	14	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129840	14	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129840	14	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129840	14	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129840	14	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129840	14	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129840	14	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129840	14	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129840	14	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129840	14	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129840	14	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129840	14	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129840	14	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129840	14	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129841	15	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129841	15	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129841	15	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129841	15	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129841	15	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129841	15	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129841	15	47	4	+	2558142	2558281

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129841	15	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129841	15	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129841	15	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129841	15	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129841	15	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129841	15	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129841	15	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129841	15	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129841	15	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129841	15	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129841	15	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129841	15	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129841	15	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129841	15	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129841	15	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129841	15	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129841	15	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129841	15	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129841	15	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129841	15	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129841	15	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129841	15	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129841	15	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129841	15	47	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129841	15	47	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129841	15	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129841	15	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129841	15	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129841	15	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129841	15	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129841	15	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129841	15	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129841	15	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129841	15	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129841	15	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129841	15	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129841	15	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129841	15	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129841	15	47	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129841	15	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129841	15	47	32	+	2760806	2760934

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129841	15	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129841	15	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129841	15	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129841	15	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129841	15	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129841	15	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129841	15	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129841	15	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129841	15	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129841	15	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129841	15	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129841	15	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129841	15	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129841	15	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129841	15	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129841	15	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129841	15	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129841	15	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129841	15	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129841	15	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129841	15	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129841	15	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129841	15	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129841	15	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129841	15	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129842	16	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129842	16	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129842	16	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129842	16	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129842	16	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129842	16	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129842	16	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129842	16	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129842	16	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129842	16	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129842	16	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129842	16	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129842	16	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129842	16	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129842	16	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129842	16	47	10	+	2659109	2659199

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129842	16	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129842	16	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129842	16	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129842	16	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129842	16	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129842	16	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129842	16	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129842	16	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129842	16	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129842	16	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129842	16	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129842	16	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129842	16	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129842	16	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129842	16	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129842	16	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129842	16	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129842	16	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129842	16	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129842	16	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129842	16	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129842	16	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129842	16	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129842	16	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129842	16	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129842	16	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129842	16	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129842	16	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129842	16	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129842	16	47	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129842	16	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129842	16	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129842	16	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129842	16	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129842	16	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129842	16	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129842	16	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129842	16	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129842	16	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129842	16	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129842	16	47	39	+	2783707	2783808

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129842	16	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129842	16	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129842	16	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129842	16	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129842	16	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129842	16	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129842	16	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129842	16	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129842	16	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129842	16	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129842	16	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129842	16	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129842	16	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129842	16	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129842	16	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129842	16	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129843	17	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129843	17	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129843	17	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129843	17	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129843	17	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129843	17	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129843	17	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129843	17	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129843	17	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129843	17	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129843	17	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129843	17	47	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129843	17	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129843	17	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129843	17	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129843	17	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129843	17	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129843	17	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129843	17	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129843	17	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129843	17	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129843	17	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129843	17	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129843	17	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129843	17	47	15	+	2691988	2692108

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129843	17	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129843	17	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129843	17	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129843	17	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129843	17	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129843	17	47	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129843	17	47	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129843	17	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129843	17	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129843	17	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129843	17	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129843	17	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129843	17	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129843	17	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129843	17	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129843	17	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129843	17	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129843	17	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129843	17	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129843	17	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129843	17	47	30	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129843	17	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129843	17	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129843	17	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129843	17	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129843	17	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129843	17	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129843	17	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129843	17	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129843	17	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129843	17	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129843	17	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129843	17	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129843	17	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129843	17	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129843	17	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129843	17	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129843	17	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129843	17	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129843	17	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129843	17	47	43	+	2791716	2791844

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129843	17	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129843	17	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129843	17	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129843	17	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129843	17	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129843	17	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129843	17	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129844	18	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129844	18	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129844	18	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129844	18	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129844	18	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129844	18	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129844	18	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129844	18	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129844	18	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129844	18	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129844	18	47	7	+	2602365	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129844	18	47	7	+	2602365	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129844	18	47	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129844	18	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129844	18	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129844	18	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129844	18	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129844	18	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129844	18	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129844	18	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129844	18	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129844	18	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129844	18	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129844	18	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129844	18	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129844	18	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129844	18	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129844	18	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129844	18	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129844	18	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129844	18	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001129844	18	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129844	18	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129844	18	47	23	+	2714247	2714334

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129844	18	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129844	18	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129844	18	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129844	18	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129844	18	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129844	18	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129844	18	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129844	18	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129844	18	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129844	18	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129844	18	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001129844	18	47	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001129844	18	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129844	18	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129844	18	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129844	18	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129844	18	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129844	18	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129844	18	47	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129844	18	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129844	18	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129844	18	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129844	18	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129844	18	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129844	18	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129844	18	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129844	18	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129844	18	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129844	18	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129844	18	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129844	18	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129844	18	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129844	18	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129844	18	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129844	18	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129844	18	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129844	18	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129844	18	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129844	18	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001129846	19	46	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001129846	19	46	2	+	2224390	2224711

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001129846	19	46	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001129846	19	46	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001129846	19	46	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001129846	19	46	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001129846	19	46	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001129846	19	46	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001129846	19	46	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001129846	19	46	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001129846	19	46	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001129846	19	46	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_001129846	19	46	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001129846	19	46	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001129846	19	46	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001129846	19	46	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001129846	19	46	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001129846	19	46	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001129846	19	46	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001129846	19	46	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001129846	19	46	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001129846	19	46	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001129846	19	46	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001129846	19	46	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001129846	19	46	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001129846	19	46	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001129846	19	46	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001129846	19	46	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001129846	19	46	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001129846	19	46	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001129846	19	46	20	+	2705040	2705169
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_001129846	19	46	21	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001129846	19	46	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001129846	19	46	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001129846	19	46	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001129846	19	46	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001129846	19	46	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001129846	19	46	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001129846	19	46	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001129846	19	46	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001129846	19	46	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001129846	19	46	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001129846	19	46	28	+	2719707	2719865

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001129846	19	46	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001129846	19	46	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001129846	19	46	30	+	2743463	2743546
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001129846	19	46	31	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001129846	19	46	31	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001129846	19	46	32	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001129846	19	46	33	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001129846	19	46	34	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001129846	19	46	34	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001129846	19	46	35	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001129846	19	46	36	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001129846	19	46	37	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001129846	19	46	38	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001129846	19	46	38	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001129846	19	46	39	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001129846	19	46	39	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001129846	19	46	40	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001129846	19	46	40	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001129846	19	46	41	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001129846	19	46	41	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001129846	19	46	41	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001129846	19	46	42	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001129846	19	46	43	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001129846	19	46	43	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001129846	19	46	44	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001129846	19	46	45	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001129846	19	46	45	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001129846	19	46	46	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001129846	19	46	46	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001167623	20	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001167623	20	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001167623	20	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001167623	20	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001167623	20	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001167623	20	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001167623	20	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001167623	20	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001167623	20	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001167623	20	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001167623	20	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001167623	20	47	7	+	2602356	2602552

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332304660	chr12	2613541	2613740	2613562	2613716	CACNA1C	NM_001167623	20	47	8	+	2613602	2613705
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001167623	20	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001167623	20	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001167623	20	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001167623	20	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001167623	20	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001167623	20	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001167623	20	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001167623	20	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001167623	20	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001167623	20	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001167623	20	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001167623	20	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001167623	20	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001167623	20	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001167623	20	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001167623	20	47	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001167623	20	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001167623	20	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001167623	20	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001167623	20	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001167623	20	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001167623	20	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001167623	20	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001167623	20	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001167623	20	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001167623	20	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001167623	20	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001167623	20	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001167623	20	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001167623	20	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001167623	20	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001167623	20	47	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001167623	20	47	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001167623	20	47	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001167623	20	47	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001167623	20	47	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001167623	20	47	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001167623	20	47	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001167623	20	47	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001167623	20	47	35	+	2773991	2774156

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001167623	20	47	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001167623	20	47	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001167623	20	47	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001167623	20	47	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001167623	20	47	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001167623	20	47	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001167623	20	47	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001167623	20	47	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001167623	20	47	41	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001167623	20	47	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001167623	20	47	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001167623	20	47	42	+	2788610	2788962
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001167623	20	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001167623	20	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001167623	20	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001167623	20	47	45	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001167623	20	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001167623	20	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001167623	20	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001167623	20	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001167624	21	48	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001167624	21	48	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001167624	21	48	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001167624	21	48	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001167624	21	48	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001167624	21	48	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001167624	21	48	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001167624	21	48	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001167624	21	48	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001167624	21	48	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001167624	21	48	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001167624	21	48	7	+	2602356	2602552
332304660	chr12	2613541	2613740	2613562	2613716	CACNA1C	NM_001167624	21	48	8	+	2613602	2613705
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001167624	21	48	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001167624	21	48	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001167624	21	48	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001167624	21	48	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001167624	21	48	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001167624	21	48	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001167624	21	48	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001167624	21	48	13	+	2676735	2676960

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001167624	21	48	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001167624	21	48	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001167624	21	48	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001167624	21	48	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001167624	21	48	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001167624	21	48	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001167624	21	48	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001167624	21	48	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001167624	21	48	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001167624	21	48	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001167624	21	48	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001167624	21	48	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001167624	21	48	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001167624	21	48	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001167624	21	48	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001167624	21	48	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001167624	21	48	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001167624	21	48	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001167624	21	48	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001167624	21	48	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001167624	21	48	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001167624	21	48	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001167624	21	48	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001167624	21	48	29	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_001167624	21	48	30	+	2742795	2742878
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_001167624	21	48	31	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001167624	21	48	32	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001167624	21	48	32	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001167624	21	48	33	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001167624	21	48	34	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001167624	21	48	35	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001167624	21	48	35	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001167624	21	48	36	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001167624	21	48	37	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001167624	21	48	38	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001167624	21	48	39	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001167624	21	48	39	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001167624	21	48	40	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001167624	21	48	40	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001167624	21	48	41	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001167624	21	48	41	+	2786899	2787033

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001167624	21	48	42	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001167624	21	48	42	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001167624	21	48	42	+	2788610	2788962
333562690	chr12	2791072	2791274	2791093	2791253	CACNA1C	NM_001167624	21	48	43	+	2791116	2791220
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001167624	21	48	44	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001167624	21	48	45	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001167624	21	48	45	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001167624	21	48	46	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001167624	21	48	47	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001167624	21	48	47	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001167624	21	48	48	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001167624	21	48	48	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_001167625	22	47	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_001167625	22	47	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_001167625	22	47	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_001167625	22	47	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_001167625	22	47	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_001167625	22	47	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_001167625	22	47	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_001167625	22	47	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_001167625	22	47	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_001167625	22	47	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_001167625	22	47	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_001167625	22	47	7	+	2602356	2602552
332304660	chr12	2613541	2613740	2613562	2613716	CACNA1C	NM_001167625	22	47	8	+	2613602	2613705
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_001167625	22	47	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_001167625	22	47	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_001167625	22	47	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_001167625	22	47	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_001167625	22	47	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_001167625	22	47	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_001167625	22	47	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_001167625	22	47	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_001167625	22	47	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_001167625	22	47	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_001167625	22	47	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_001167625	22	47	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_001167625	22	47	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_001167625	22	47	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_001167625	22	47	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_001167625	22	47	19	+	2702379	2702511

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_001167625	22	47	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_001167625	22	47	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_001167625	22	47	21	+	2706396	2706455
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_001167625	22	47	22	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_001167625	22	47	23	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_001167625	22	47	24	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_001167625	22	47	25	+	2715777	2715829
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_001167625	22	47	26	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_001167625	22	47	26	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_001167625	22	47	27	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_001167625	22	47	27	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_001167625	22	47	27	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_001167625	22	47	28	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_001167625	22	47	28	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_001167625	22	47	29	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_001167625	22	47	29	+	2721069	2721179
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_001167625	22	47	30	+	2743463	2743546
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_001167625	22	47	31	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_001167625	22	47	31	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_001167625	22	47	32	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_001167625	22	47	33	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_001167625	22	47	34	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_001167625	22	47	34	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_001167625	22	47	35	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_001167625	22	47	36	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_001167625	22	47	37	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_001167625	22	47	38	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_001167625	22	47	38	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_001167625	22	47	39	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_001167625	22	47	39	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_001167625	22	47	40	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_001167625	22	47	40	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_001167625	22	47	41	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_001167625	22	47	41	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_001167625	22	47	41	+	2788610	2788962
332271953	chr12	2789490	2789711	2789516	2789690	CACNA1C	NM_001167625	22	47	42	+	2789529	2789741
332280914	chr12	2789671	2789894	2789691	2789873	CACNA1C	NM_001167625	22	47	42	+	2789529	2789741
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_001167625	22	47	43	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_001167625	22	47	44	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_001167625	22	47	44	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_001167625	22	47	45	+	2795332	2795435

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_001167625	22	47	46	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_001167625	22	47	46	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_001167625	22	47	47	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_001167625	22	47	47	+	2800066	2807115
333180443	chr12	2162597	2162790	2162616	2162770	CACNA1C	NM_199460	23	50	1	+	2162416	2162777
332434284	chr12	2224269	2224441	2224290	2224419	CACNA1C	NM_199460	23	50	2	+	2224390	2224711
332442117	chr12	2224377	2224600	2224401	2224581	CACNA1C	NM_199460	23	50	2	+	2224390	2224711
332445867	chr12	2224547	2224750	2224568	2224733	CACNA1C	NM_199460	23	50	2	+	2224390	2224711
333404929	chr12	2229440	2229628	2229465	2229604	CACNA1C	NM_199460	23	50	3	+	2229491	2229596
332731929	chr12	2557973	2558186	2557993	2558159	CACNA1C	NM_199460	23	50	4	+	2558142	2558281
332745996	chr12	2558136	2558328	2558160	2558302	CACNA1C	NM_199460	23	50	4	+	2558142	2558281
333466182	chr12	2566683	2566898	2566707	2566877	CACNA1C	NM_199460	23	50	5	+	2566733	2566872
332758510	chr12	2595232	2595370	2595254	2595348	CACNA1C	NM_199460	23	50	6	+	2595270	2595428
332767751	chr12	2595328	2595522	2595349	2595500	CACNA1C	NM_199460	23	50	6	+	2595270	2595428
332347609	chr12	2602284	2602499	2602307	2602480	CACNA1C	NM_199460	23	50	7	+	2602356	2602552
332362864	chr12	2602460	2602657	2602481	2602636	CACNA1C	NM_199460	23	50	7	+	2602356	2602552
333546598	chr12	2613966	2614189	2613987	2614161	CACNA1C	NM_199460	23	50	8	+	2614008	2614111
333325087	chr12	2621870	2622084	2621898	2622061	CACNA1C	NM_199460	23	50	9	+	2621978	2622150
333338723	chr12	2622040	2622232	2622062	2622211	CACNA1C	NM_199460	23	50	9	+	2621978	2622150
332516113	chr12	2659031	2659253	2659055	2659231	CACNA1C	NM_199460	23	50	10	+	2659109	2659199
333614007	chr12	2666037	2666252	2666059	2666230	CACNA1C	NM_199460	23	50	11	+	2666117	2666143
332896818	chr12	2675459	2675675	2675479	2675650	CACNA1C	NM_199460	23	50	12	+	2675588	2675748
332916288	chr12	2675632	2675795	2675651	2675773	CACNA1C	NM_199460	23	50	12	+	2675588	2675748
332538899	chr12	2676697	2676902	2676716	2676880	CACNA1C	NM_199460	23	50	13	+	2676735	2676960
332545429	chr12	2676837	2677024	2676857	2677003	CACNA1C	NM_199460	23	50	13	+	2676735	2676960
333771000	chr12	2690675	2690886	2690697	2690865	CACNA1C	NM_199460	23	50	14	+	2690756	2690963
333778219	chr12	2690793	2690990	2690813	2690968	CACNA1C	NM_199460	23	50	14	+	2690756	2690963
332851426	chr12	2691927	2692125	2691949	2692104	CACNA1C	NM_199460	23	50	15	+	2691988	2692108
332860700	chr12	2692079	2692292	2692105	2692271	CACNA1C	NM_199460	23	50	15	+	2691988	2692108
333013033	chr12	2693632	2693848	2693660	2693825	CACNA1C	NM_199460	23	50	16	+	2693669	2693783
333168775	chr12	2694471	2694695	2694494	2694675	CACNA1C	NM_199460	23	50	17	+	2694542	2694662
332382194	chr12	2694897	2695109	2694924	2695086	CACNA1C	NM_199460	23	50	18	+	2695001	2695070
332970686	chr12	2702337	2702561	2702363	2702539	CACNA1C	NM_199460	23	50	19	+	2702379	2702511
333495105	chr12	2704877	2705101	2704900	2705077	CACNA1C	NM_199460	23	50	20	+	2705040	2705169
333504229	chr12	2705057	2705254	2705078	2705227	CACNA1C	NM_199460	23	50	20	+	2705040	2705169
332272910	chr12	2706367	2706545	2706388	2706524	CACNA1C	NM_199460	23	50	21	+	2706396	2706455
332754072	chr12	2706524	2706700	2706545	2706678	CACNA1C	NM_199460	23	50	22	+	2706603	2706662
333023534	chr12	2710984	2711184	2711006	2711165	CACNA1C	NM_199460	23	50	23	+	2711020	2711126
333114222	chr12	2714153	2714367	2714176	2714347	CACNA1C	NM_199460	23	50	24	+	2714247	2714334
333650700	chr12	2714792	2715014	2714812	2714993	CACNA1C	NM_199460	23	50	25	+	2714845	2714952
332929696	chr12	2715692	2715910	2715713	2715889	CACNA1C	NM_199460	23	50	26	+	2715777	2715829

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333099715	chr12	2715965	2716174	2715987	2716150	CACNA1C	NM_199460	23	50	27	+	2716150	2716296
333112449	chr12	2716129	2716349	2716151	2716327	CACNA1C	NM_199460	23	50	27	+	2716150	2716296
332760232	chr12	2717603	2717748	2717621	2717725	CACNA1C	NM_199460	23	50	28	+	2717677	2717878
332765724	chr12	2717680	2717892	2717699	2717870	CACNA1C	NM_199460	23	50	28	+	2717677	2717878
332772831	chr12	2717848	2718007	2717871	2717981	CACNA1C	NM_199460	23	50	28	+	2717677	2717878
332660172	chr12	2719566	2719788	2719587	2719766	CACNA1C	NM_199460	23	50	29	+	2719707	2719865
332672668	chr12	2719746	2719939	2719767	2719917	CACNA1C	NM_199460	23	50	29	+	2719707	2719865
333703368	chr12	2720952	2721129	2720975	2721105	CACNA1C	NM_199460	23	50	30	+	2721069	2721179
333717075	chr12	2721085	2721211	2721106	2721186	CACNA1C	NM_199460	23	50	30	+	2721069	2721179
333320632	chr12	2742702	2742926	2742724	2742904	CACNA1C	NM_199460	23	50	31	+	2742795	2742878
332479183	chr12	2743401	2743572	2743429	2743552	CACNA1C	NM_199460	23	50	32	+	2743463	2743546
333532359	chr12	2757561	2757765	2757581	2757745	CACNA1C	NM_199460	23	50	33	+	2757641	2757673
332418432	chr12	2760710	2760927	2760733	2760905	CACNA1C	NM_199460	23	50	34	+	2760806	2760934
332423203	chr12	2760855	2761010	2760875	2760988	CACNA1C	NM_199460	23	50	34	+	2760806	2760934
332713113	chr12	2762973	2763187	2762994	2763164	CACNA1C	NM_199460	23	50	35	+	2763001	2763066
332957077	chr12	2764219	2764440	2764240	2764415	CACNA1C	NM_199460	23	50	36	+	2764313	2764404
332527749	chr12	2773935	2774133	2773956	2774107	CACNA1C	NM_199460	23	50	37	+	2773991	2774156
332538773	chr12	2774087	2774244	2774108	2774223	CACNA1C	NM_199460	23	50	37	+	2773991	2774156
332825411	chr12	2774709	2774926	2774731	2774903	CACNA1C	NM_199460	23	50	38	+	2774747	2774874
332697842	chr12	2775803	2775975	2775823	2775955	CACNA1C	NM_199460	23	50	39	+	2775852	2775948
332607328	chr12	2778060	2778240	2778081	2778218	CACNA1C	NM_199460	23	50	40	+	2778099	2778201
332390528	chr12	2783623	2783765	2783644	2783741	CACNA1C	NM_199460	23	50	41	+	2783707	2783808
332391804	chr12	2783706	2783901	2783730	2783881	CACNA1C	NM_199460	23	50	41	+	2783707	2783808
333734731	chr12	2786211	2786339	2786232	2786316	CACNA1C	NM_199460	23	50	42	+	2786260	2786387
333739746	chr12	2786282	2786443	2786303	2786422	CACNA1C	NM_199460	23	50	42	+	2786260	2786387
332790867	chr12	2786745	2786937	2786768	2786917	CACNA1C	NM_199460	23	50	43	+	2786899	2787033
332795564	chr12	2786874	2787094	2786895	2787072	CACNA1C	NM_199460	23	50	43	+	2786899	2787033
333424593	chr12	2788437	2788661	2788459	2788641	CACNA1C	NM_199460	23	50	44	+	2788610	2788962
333431169	chr12	2788624	2788845	2788642	2788828	CACNA1C	NM_199460	23	50	44	+	2788610	2788962
333434672	chr12	2788804	2789028	2788825	2789008	CACNA1C	NM_199460	23	50	44	+	2788610	2788962
333562690	chr12	2791072	2791274	2791093	2791253	CACNA1C	NM_199460	23	50	45	+	2791116	2791220
333227945	chr12	2791669	2791893	2791692	2791871	CACNA1C	NM_199460	23	50	46	+	2791716	2791844
333641714	chr12	2794753	2794952	2794772	2794935	CACNA1C	NM_199460	23	50	47	+	2794902	2795008
333654826	chr12	2794913	2795136	2794935	2795116	CACNA1C	NM_199460	23	50	47	+	2794902	2795008
332912649	chr12	2795287	2795511	2795308	2795491	CACNA1C	NM_199460	23	50	48	+	2795332	2795435
332876097	chr12	2797577	2797795	2797603	2797774	CACNA1C	NM_199460	23	50	49	+	2797613	2797945
332878353	chr12	2797755	2797968	2797775	2797950	CACNA1C	NM_199460	23	50	49	+	2797613	2797945
332409110	chr12	2800031	2800254	2800052	2800234	CACNA1C	NM_199460	23	50	50	+	2800066	2807115
332416109	chr12	2800216	2800422	2800235	2800394	CACNA1C	NM_199460	23	50	50	+	2800066	2807115
332569971	chr10	18550055	18550278	18550079	18550253	CACNB2	NM_000724	1	13	1	+	18549584	18550246
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_000724	1	13	2	+	18690853	18690972

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_000724	1	13	3	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_000724	1	13	4	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_000724	1	13	5	+	18795400	18795476
332262640	chr10	18803117	18803328	18803141	18803303	CACNB2	NM_000724	1	13	6	+	18803165	18803298
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_000724	1	13	7	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_000724	1	13	8	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_000724	1	13	9	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_000724	1	13	10	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_000724	1	13	10	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_000724	1	13	11	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_000724	1	13	12	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_000724	1	13	12	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_000724	1	13	13	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_000724	1	13	13	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_000724	1	13	13	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_000724	1	13	13	+	18828159	18830688
332728911	chr10	18429987	18430207	18430008	18430185	CACNB2	NM_001167945	2	14	1	+	18429742	18430144
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_001167945	2	14	1	+	18429742	18430144
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_001167945	2	14	1	+	18429742	18430144
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_001167945	2	14	2	+	18439812	18439904
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_001167945	2	14	2	+	18439812	18439904
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_001167945	2	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_001167945	2	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_001167945	2	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_001167945	2	14	6	+	18795400	18795476
333577113	chr10	18803298	18803496	18803323	18803470	CACNB2	NM_001167945	2	14	7	+	18803440	18803459
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_001167945	2	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_001167945	2	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_001167945	2	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_001167945	2	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_001167945	2	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_001167945	2	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_001167945	2	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_001167945	2	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_001167945	2	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_001167945	2	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_001167945	2	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_001167945	2	14	14	+	18828159	18830688
332434464	chr10	18689850	18690063	18689871	18690042	CACNB2	NM_201570	3	13	1	+	18689513	18690029
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201570	3	13	2	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201570	3	13	3	+	18787284	18787406

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201570	3	13	4	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201570	3	13	5	+	18795400	18795476
332262640	chr10	18803117	18803328	18803141	18803303	CACNB2	NM_201570	3	13	6	+	18803165	18803298
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201570	3	13	7	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201570	3	13	8	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201570	3	13	9	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201570	3	13	10	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201570	3	13	10	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201570	3	13	11	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201570	3	13	12	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201570	3	13	12	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201570	3	13	13	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201570	3	13	13	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201570	3	13	13	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201570	3	13	13	+	18828159	18830688
332728911	chr10	18429987	18430207	18430008	18430185	CACNB2	NM_201571	4	14	1	+	18429742	18430144
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_201571	4	14	1	+	18429742	18430144
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_201571	4	14	1	+	18429742	18430144
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_201571	4	14	2	+	18439812	18439904
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_201571	4	14	2	+	18439812	18439904
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201571	4	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201571	4	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201571	4	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201571	4	14	6	+	18795400	18795476
332262640	chr10	18803117	18803328	18803141	18803303	CACNB2	NM_201571	4	14	7	+	18803165	18803298
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201571	4	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201571	4	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201571	4	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201571	4	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201571	4	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201571	4	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201571	4	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201571	4	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201571	4	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201571	4	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201571	4	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201571	4	14	14	+	18828159	18830688
332728911	chr10	18429987	18430207	18430008	18430185	CACNB2	NM_201572	5	14	1	+	18429742	18430144
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_201572	5	14	1	+	18429742	18430144
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_201572	5	14	1	+	18429742	18430144
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_201572	5	14	2	+	18439812	18439904

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_201572	5	14	2	+	18439812	18439904
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201572	5	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201572	5	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201572	5	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201572	5	14	6	+	18795400	18795476
333760617	chr10	18803730	18803945	18803756	18803920	CACNB2	NM_201572	5	14	7	+	18803909	18803970
333760947	chr10	18803893	18804021	18803921	18803993	CACNB2	NM_201572	5	14	7	+	18803909	18803970
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201572	5	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201572	5	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201572	5	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201572	5	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201572	5	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201572	5	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201572	5	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201572	5	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201572	5	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201572	5	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201572	5	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201572	5	14	14	+	18828159	18830688
332847259	chr10	18629739	18629954	18629762	18629934	CACNB2	NM_201590	6	13	1	+	18629614	18629906
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201590	6	13	2	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201590	6	13	3	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201590	6	13	4	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201590	6	13	5	+	18795400	18795476
332262640	chr10	18803117	18803328	18803141	18803303	CACNB2	NM_201590	6	13	6	+	18803165	18803298
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201590	6	13	7	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201590	6	13	8	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201590	6	13	9	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201590	6	13	10	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201590	6	13	10	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201590	6	13	11	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201590	6	13	12	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201590	6	13	12	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201590	6	13	13	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201590	6	13	13	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201590	6	13	13	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201590	6	13	13	+	18828159	18830688
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_201593	7	14	1	+	18429606	18429785
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_201593	7	14	1	+	18429606	18429785
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_201593	7	14	2	+	18439812	18439904
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_201593	7	14	2	+	18439812	18439904

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201593	7	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201593	7	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201593	7	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201593	7	14	6	+	18795400	18795476
333577113	chr10	18803298	18803496	18803323	18803470	CACNB2	NM_201593	7	14	7	+	18803440	18803459
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201593	7	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201593	7	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201593	7	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201593	7	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201593	7	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201593	7	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201593	7	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201593	7	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201593	7	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201593	7	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201593	7	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201593	7	14	14	+	18828159	18830688
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_201596	8	14	1	+	18429606	18429785
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_201596	8	14	1	+	18429606	18429785
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_201596	8	14	2	+	18439812	18439904
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_201596	8	14	2	+	18439812	18439904
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201596	8	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201596	8	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201596	8	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201596	8	14	6	+	18795400	18795476
332262640	chr10	18803117	18803328	18803141	18803303	CACNB2	NM_201596	8	14	7	+	18803165	18803298
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201596	8	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201596	8	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201596	8	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201596	8	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201596	8	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201596	8	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201596	8	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201596	8	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201596	8	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201596	8	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201596	8	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201596	8	14	14	+	18828159	18830688
333208875	chr10	18429643	18429798	18429660	18429780	CACNB2	NM_201597	9	14	1	+	18429606	18429785
333209788	chr10	18429724	18429881	18429749	18429860	CACNB2	NM_201597	9	14	1	+	18429606	18429785
332436229	chr10	18439710	18439903	18439738	18439875	CACNB2	NM_201597	9	14	2	+	18439812	18439904

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332444318	chr10	18439854	18439987	18439876	18439961	CACNB2	NM_201597	9	14	2	+	18439812	18439904
332528706	chr10	18690782	18691004	18690807	18690982	CACNB2	NM_201597	9	14	3	+	18690853	18690972
333370253	chr10	18787230	18787453	18787253	18787427	CACNB2	NM_201597	9	14	4	+	18787284	18787406
333244907	chr10	18789690	18789910	18789714	18789882	CACNB2	NM_201597	9	14	5	+	18789741	18789877
333047459	chr10	18795344	18795527	18795370	18795499	CACNB2	NM_201597	9	14	6	+	18795400	18795476
333760617	chr10	18803730	18803945	18803756	18803920	CACNB2	NM_201597	9	14	7	+	18803909	18803970
333760947	chr10	18803893	18804021	18803921	18803993	CACNB2	NM_201597	9	14	7	+	18803909	18803970
332454542	chr10	18807157	18807381	18807182	18807358	CACNB2	NM_201597	9	14	8	+	18807265	18807345
333408955	chr10	18807707	18807929	18807731	18807905	CACNB2	NM_201597	9	14	9	+	18807839	18807897
332552332	chr10	18816448	18816672	18816476	18816645	CACNB2	NM_201597	9	14	10	+	18816517	18816626
332848309	chr10	18822826	18823049	18822847	18823021	CACNB2	NM_201597	9	14	11	+	18823005	18823156
332855623	chr10	18822998	18823189	18823022	18823162	CACNB2	NM_201597	9	14	11	+	18823005	18823156
332867131	chr10	18824946	18825170	18824971	18825141	CACNB2	NM_201597	9	14	12	+	18825030	18825125
332688628	chr10	18827061	18827260	18827082	18827236	CACNB2	NM_201597	9	14	13	+	18827109	18827294
332701987	chr10	18827216	18827363	18827237	18827340	CACNB2	NM_201597	9	14	13	+	18827109	18827294
333366118	chr10	18828031	18828248	18828059	18828224	CACNB2	NM_201597	9	14	14	+	18828159	18830688
333386847	chr10	18828203	18828409	18828225	18828386	CACNB2	NM_201597	9	14	14	+	18828159	18830688
333402915	chr10	18828366	18828583	18828387	18828559	CACNB2	NM_201597	9	14	14	+	18828159	18830688
333409552	chr10	18828540	18828744	18828560	18828721	CACNB2	NM_201597	9	14	14	+	18828159	18830688
257234322	chr19	16606676	16606886	16606702	16606861	CALR3	NM_145046	1	9	1	-	16606850	16607003
257241741	chr19	16606841	16607041	16606862	16607019	CALR3	NM_145046	1	9	1	-	16606850	16607003
259078007	chr19	16606517	16606705	16606545	16606681	CALR3	NM_145046	1	9	2	-	16606562	16606663
255820178	chr19	16601035	16601243	16601063	16601220	CALR3	NM_145046	1	9	3	-	16601178	16601381
255857305	chr19	16601196	16601420	16601221	16601392	CALR3	NM_145046	1	9	3	-	16601178	16601381
255340014	chr19	16595918	16596104	16595945	16596076	CALR3	NM_145046	1	9	4	-	16595974	16596068
261750079	chr19	16594566	16594784	16594593	16594761	CALR3	NM_145046	1	9	5	-	16594741	16594926
261776694	chr19	16594739	16594963	16594762	16594935	CALR3	NM_145046	1	9	5	-	16594741	16594926
263935021	chr19	16593455	16593613	16593475	16593588	CALR3	NM_145046	1	9	6	-	16593489	16593596
259942415	chr19	16593240	16593439	16593267	16593419	CALR3	NM_145046	1	9	7	-	16593261	16593392
257590045	chr19	16591393	16591615	16591419	16591588	CALR3	NM_145046	1	9	8	-	16591425	16591517
259628303	chr19	16589817	16589989	16589839	16589961	CALR3	NM_145046	1	9	9	-	16589868	16590085
259658143	chr19	16589935	16590100	16589962	16590077	CALR3	NM_145046	1	9	9	-	16589868	16590085
265611361	chr15	42652112	42652314	42652136	42652294	CAPN3	NM_000070	1	24	1	+	42651698	42652312
265624404	chr15	42652273	42652465	42652295	42652441	CAPN3	NM_000070	1	24	1	+	42651698	42652312
265645493	chr15	42651938	42652158	42651964	42652136	CAPN3	NM_000070	1	24	1	+	42651698	42652312
258897396	chr15	42676650	42676777	42676678	42676756	CAPN3	NM_000070	1	24	2	+	42676681	42676750
266541774	chr15	42678306	42678514	42678328	42678488	CAPN3	NM_000070	1	24	3	+	42678365	42678483
261381088	chr15	42679911	42680114	42679936	42680090	CAPN3	NM_000070	1	24	4	+	42679951	42680084
266800430	chr15	42681023	42681170	42681047	42681149	CAPN3	NM_000070	1	24	5	+	42681126	42681294
266841526	chr15	42681128	42681352	42681150	42681328	CAPN3	NM_000070	1	24	5	+	42681126	42681294
253849454	chr15	42682112	42682326	42682133	42682302	CAPN3	NM_000070	1	24	6	+	42682151	42682294

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254787445	chr15	42684759	42684979	42684784	42684955	CAPN3	NM_000070	1	24	7	+	42684837	42684920
255886149	chr15	42686419	42686632	42686440	42686605	CAPN3	NM_000070	1	24	8	+	42686454	42686539
264545504	chr15	42688894	42689111	42688915	42689089	CAPN3	NM_000070	1	24	9	+	42688998	42689075
264845461	chr15	42691526	42691737	42691547	42691709	CAPN3	NM_000070	1	24	10	+	42691690	42691850
264870979	chr15	42691684	42691900	42691710	42691877	CAPN3	NM_000070	1	24	10	+	42691690	42691850
260954433	chr15	42693702	42693923	42693725	42693903	CAPN3	NM_000070	1	24	11	+	42693839	42694008
261030440	chr15	42693883	42694061	42693904	42694039	CAPN3	NM_000070	1	24	11	+	42693839	42694008
266733487	chr15	42694269	42694457	42694292	42694436	CAPN3	NM_000070	1	24	12	+	42694322	42694333
254429271	chr15	42694856	42695075	42694877	42695050	CAPN3	NM_000070	1	24	13	+	42694992	42695200
254454776	chr15	42695028	42695251	42695049	42695229	CAPN3	NM_000070	1	24	13	+	42694992	42695200
256230877	chr15	42695817	42696008	42695839	42695982	CAPN3	NM_000070	1	24	14	+	42695939	42695975
266345702	chr15	42697974	42698168	42697996	42698146	CAPN3	NM_000070	1	24	15	+	42698124	42698141
262245463	chr15	42700359	42700580	42700384	42700561	CAPN3	NM_000070	1	24	16	+	42700409	42700522
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_000070	1	24	17	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_000070	1	24	18	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_000070	1	24	19	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_000070	1	24	20	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_000070	1	24	21	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_000070	1	24	22	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_000070	1	24	23	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_000070	1	24	24	+	42703945	42704515
265611361	chr15	42652112	42652314	42652136	42652294	CAPN3	NM_024344	2	23	1	+	42651698	42652312
265624404	chr15	42652273	42652465	42652295	42652441	CAPN3	NM_024344	2	23	1	+	42651698	42652312
265645493	chr15	42651938	42652158	42651964	42652136	CAPN3	NM_024344	2	23	1	+	42651698	42652312
258897396	chr15	42676650	42676777	42676678	42676756	CAPN3	NM_024344	2	23	2	+	42676681	42676750
266541774	chr15	42678306	42678514	42678328	42678488	CAPN3	NM_024344	2	23	3	+	42678365	42678483
261381088	chr15	42679911	42680114	42679936	42680090	CAPN3	NM_024344	2	23	4	+	42679951	42680084
266800430	chr15	42681023	42681170	42681047	42681149	CAPN3	NM_024344	2	23	5	+	42681126	42681294
266841526	chr15	42681128	42681352	42681150	42681328	CAPN3	NM_024344	2	23	5	+	42681126	42681294
253849454	chr15	42682112	42682326	42682133	42682302	CAPN3	NM_024344	2	23	6	+	42682151	42682294
254787445	chr15	42684759	42684979	42684784	42684955	CAPN3	NM_024344	2	23	7	+	42684837	42684920
255886149	chr15	42686419	42686632	42686440	42686605	CAPN3	NM_024344	2	23	8	+	42686454	42686539
264545504	chr15	42688894	42689111	42688915	42689089	CAPN3	NM_024344	2	23	9	+	42688998	42689075
264845461	chr15	42691526	42691737	42691547	42691709	CAPN3	NM_024344	2	23	10	+	42691690	42691850
264870979	chr15	42691684	42691900	42691710	42691877	CAPN3	NM_024344	2	23	10	+	42691690	42691850
260954433	chr15	42693702	42693923	42693725	42693903	CAPN3	NM_024344	2	23	11	+	42693839	42694008
261030440	chr15	42693883	42694061	42693904	42694039	CAPN3	NM_024344	2	23	11	+	42693839	42694008
266733487	chr15	42694269	42694457	42694292	42694436	CAPN3	NM_024344	2	23	12	+	42694322	42694333
254429271	chr15	42694856	42695075	42694877	42695050	CAPN3	NM_024344	2	23	13	+	42694992	42695200
254454776	chr15	42695028	42695251	42695049	42695229	CAPN3	NM_024344	2	23	13	+	42694992	42695200
256230877	chr15	42695817	42696008	42695839	42695982	CAPN3	NM_024344	2	23	14	+	42695939	42695975

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262245463	chr15	42700359	42700580	42700384	42700561	CAPN3	NM_024344	2	23	15	+	42700409	42700522
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_024344	2	23	16	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_024344	2	23	17	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_024344	2	23	18	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_024344	2	23	19	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_024344	2	23	20	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_024344	2	23	21	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_024344	2	23	22	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_024344	2	23	23	+	42703945	42704515
265611361	chr15	42652112	42652314	42652136	42652294	CAPN3	NM_173087	3	21	1	+	42651698	42652312
265624404	chr15	42652273	42652465	42652295	42652441	CAPN3	NM_173087	3	21	1	+	42651698	42652312
265645493	chr15	42651938	42652158	42651964	42652136	CAPN3	NM_173087	3	21	1	+	42651698	42652312
258897396	chr15	42676650	42676777	42676678	42676756	CAPN3	NM_173087	3	21	2	+	42676681	42676750
266541774	chr15	42678306	42678514	42678328	42678488	CAPN3	NM_173087	3	21	3	+	42678365	42678483
261381088	chr15	42679911	42680114	42679936	42680090	CAPN3	NM_173087	3	21	4	+	42679951	42680084
266800430	chr15	42681023	42681170	42681047	42681149	CAPN3	NM_173087	3	21	5	+	42681126	42681294
266841526	chr15	42681128	42681352	42681150	42681328	CAPN3	NM_173087	3	21	5	+	42681126	42681294
254787445	chr15	42684759	42684979	42684784	42684955	CAPN3	NM_173087	3	21	6	+	42684837	42684920
255886149	chr15	42686419	42686632	42686440	42686605	CAPN3	NM_173087	3	21	7	+	42686454	42686539
264545504	chr15	42688894	42689111	42688915	42689089	CAPN3	NM_173087	3	21	8	+	42688998	42689075
264845461	chr15	42691526	42691737	42691547	42691709	CAPN3	NM_173087	3	21	9	+	42691690	42691850
264870979	chr15	42691684	42691900	42691710	42691877	CAPN3	NM_173087	3	21	9	+	42691690	42691850
260954433	chr15	42693702	42693923	42693725	42693903	CAPN3	NM_173087	3	21	10	+	42693839	42694008
261030440	chr15	42693883	42694061	42693904	42694039	CAPN3	NM_173087	3	21	10	+	42693839	42694008
266733487	chr15	42694269	42694457	42694292	42694436	CAPN3	NM_173087	3	21	11	+	42694322	42694333
254429271	chr15	42694856	42695075	42694877	42695050	CAPN3	NM_173087	3	21	12	+	42694992	42695200
254454776	chr15	42695028	42695251	42695049	42695229	CAPN3	NM_173087	3	21	12	+	42694992	42695200
256230877	chr15	42695817	42696008	42695839	42695982	CAPN3	NM_173087	3	21	13	+	42695939	42695975
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_173087	3	21	14	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_173087	3	21	15	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_173087	3	21	16	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_173087	3	21	17	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_173087	3	21	18	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_173087	3	21	19	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_173087	3	21	20	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_173087	3	21	21	+	42703945	42704515
254429271	chr15	42694856	42695075	42694877	42695050	CAPN3	NM_173088	4	13	2	+	42694992	42695200
254454776	chr15	42695028	42695251	42695049	42695229	CAPN3	NM_173088	4	13	2	+	42694992	42695200
256230877	chr15	42695817	42696008	42695839	42695982	CAPN3	NM_173088	4	13	3	+	42695939	42695975
266345702	chr15	42697974	42698168	42697996	42698146	CAPN3	NM_173088	4	13	4	+	42698124	42698141
262245463	chr15	42700359	42700580	42700384	42700561	CAPN3	NM_173088	4	13	5	+	42700409	42700522

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_173088	4	13	6	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_173088	4	13	7	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_173088	4	13	8	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_173088	4	13	9	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_173088	4	13	10	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_173088	4	13	11	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_173088	4	13	12	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_173088	4	13	13	+	42703945	42704515
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_173089	5	9	2	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_173089	5	9	3	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_173089	5	9	4	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_173089	5	9	5	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_173089	5	9	6	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_173089	5	9	7	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_173089	5	9	8	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_173089	5	9	9	+	42703945	42704515
266345702	chr15	42697974	42698168	42697996	42698146	CAPN3	NM_173090	6	10	2	+	42698124	42698141
256873304	chr15	42701462	42701638	42701482	42701614	CAPN3	NM_173090	6	10	3	+	42701501	42701578
257325658	chr15	42701888	42702109	42701910	42702087	CAPN3	NM_173090	6	10	4	+	42701985	42702042
261655982	chr15	42702079	42702269	42702100	42702249	CAPN3	NM_173090	6	10	5	+	42702129	42702193
267004947	chr15	42702511	42702722	42702536	42702699	CAPN3	NM_173090	6	10	6	+	42702626	42702694
266823593	chr15	42702731	42702938	42702754	42702917	CAPN3	NM_173090	6	10	7	+	42702786	42702864
266477808	chr15	42703050	42703274	42703071	42703249	CAPN3	NM_173090	6	10	8	+	42703082	42703198
257471946	chr15	42703356	42703569	42703379	42703549	CAPN3	NM_173090	6	10	9	+	42703485	42703543
265374131	chr15	42703791	42704004	42703814	42703983	CAPN3	NM_173090	6	10	10	+	42703945	42704515
333330228	chr1	116310903	116311073	116310923	116311051	CASQ2	NM_001232	1	11	1	-	116310929	116311426
333345380	chr1	116311030	116311199	116311052	116311174	CASQ2	NM_001232	1	11	1	-	116310929	116311426
332836709	chr1	116287356	116287568	116287382	116287541	CASQ2	NM_001232	1	11	2	-	116287449	116287533
332805051	chr1	116283254	116283476	116283276	116283454	CASQ2	NM_001232	1	11	3	-	116283349	116283449
332280930	chr1	116280782	116281003	116280810	116280976	CASQ2	NM_001232	1	11	4	-	116280845	116280956
333092002	chr1	116275415	116275639	116275443	116275611	CASQ2	NM_001232	1	11	5	-	116275522	116275595
332732847	chr1	116269433	116269645	116269461	116269623	CASQ2	NM_001232	1	11	6	-	116269613	116269743
332746718	chr1	116269603	116269809	116269624	116269782	CASQ2	NM_001232	1	11	6	-	116269613	116269743
333547711	chr1	116268008	116268227	116268030	116268202	CASQ2	NM_001232	1	11	7	-	116268129	116268174
332790540	chr1	116260337	116260554	116260359	116260527	CASQ2	NM_001232	1	11	8	-	116260461	116260515
333757349	chr1	116247727	116247944	116247750	116247918	CASQ2	NM_001232	1	11	9	-	116247813	116247913
333294606	chr1	116245435	116245656	116245457	116245628	CASQ2	NM_001232	1	11	10	-	116245542	116245616
332592878	chr1	116243794	116243990	116243816	116243968	CASQ2	NM_001232	1	11	11	-	116242626	116244047
332614601	chr1	116243941	116244076	116243969	116244052	CASQ2	NM_001232	1	11	11	-	116242626	116244047
259395990	chr3	8775527	8775727	8775548	8775706	CAV3	NM_001234	1	3	1	+	8775486	8775676
257992768	chr3	8787173	8787323	8787195	8787301	CAV3	NM_001234	1	3	2	+	8787212	8787559

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258026832	chr3	8787279	8787462	8787300	8787440	CAV3	NM_001234	1	3	2	+	8787212	8787559
258063012	chr3	8787415	8787634	8787441	8787614	CAV3	NM_001234	1	3	2	+	8787212	8787559
259395990	chr3	8775527	8775727	8775548	8775706	CAV3	NM_033337	2	2	1	+	8775486	8775676
257992768	chr3	8787173	8787323	8787195	8787301	CAV3	NM_033337	2	2	2	+	8787212	8788451
258026832	chr3	8787279	8787462	8787300	8787440	CAV3	NM_033337	2	2	2	+	8787212	8788451
258063012	chr3	8787415	8787634	8787441	8787614	CAV3	NM_033337	2	2	2	+	8787212	8788451
260884572	chr3	180397004	180397201	180397025	180397173	CCDC39	NM_181426	1	20	1	-	180397079	180397283
266799779	chr3	180381598	180381780	180381625	180381754	CCDC39	NM_181426	1	20	2	-	180381655	180381774
255751778	chr3	180379579	180379783	180379604	180379764	CCDC39	NM_181426	1	20	3	-	180379649	180379795
255763678	chr3	180379768	180379975	180379788	180379944	CCDC39	NM_181426	1	20	3	-	180379649	180379795
262508879	chr3	180378371	180378553	180378397	180378525	CCDC39	NM_181426	1	20	4	-	180378358	180378516
262044193	chr3	180377343	180377565	180377371	180377542	CCDC39	NM_181426	1	20	5	-	180377465	180377557
262013437	chr3	180377206	180377429	180377231	180377401	CCDC39	NM_181426	1	20	6	-	180377240	180377368
260816907	chr3	180372509	180372667	180372531	180372639	CCDC39	NM_181426	1	20	7	-	180372550	180372741
260826892	chr3	180372612	180372746	180372640	180372719	CCDC39	NM_181426	1	20	7	-	180372550	180372741
266364930	chr3	180369945	180370163	180369973	180370135	CCDC39	NM_181426	1	20	8	-	180369951	180370054
265571134	chr3	180369034	180369257	180369058	180369229	CCDC39	NM_181426	1	20	9	-	180369189	180369321
265573086	chr3	180369203	180369375	180369230	180369347	CCDC39	NM_181426	1	20	9	-	180369189	180369321
255423765	chr3	180365806	180366028	180365833	180366000	CCDC39	NM_181426	1	20	10	-	180365953	180366147
255446399	chr3	180365974	180366113	180366001	180366086	CCDC39	NM_181426	1	20	10	-	180365953	180366147
255448141	chr3	180366059	180366261	180366087	180366238	CCDC39	NM_181426	1	20	10	-	180365953	180366147
253895190	chr3	180364770	180364904	180364791	180364881	CCDC39	NM_181426	1	20	11	-	180364867	180365031
253907061	chr3	180364854	180365040	180364882	180365011	CCDC39	NM_181426	1	20	11	-	180364867	180365031
253915732	chr3	180364993	180365131	180365013	180365101	CCDC39	NM_181426	1	20	11	-	180364867	180365031
259456459	chr3	180361889	180362026	180361913	180361998	CCDC39	NM_181426	1	20	12	-	180361908	180362045
259457383	chr3	180361898	180362029	180361924	180362001	CCDC39	NM_181426	1	20	12	-	180361908	180362045
261165028	chr3	180359670	180359862	180359698	180359835	CCDC39	NM_181426	1	20	13	-	180359781	180359989
261194463	chr3	180359809	180359953	180359836	180359928	CCDC39	NM_181426	1	20	13	-	180359781	180359989
261200248	chr3	180359903	180360127	180359929	180360099	CCDC39	NM_181426	1	20	13	-	180359781	180359989
257038973	chr3	180349146	180349370	180349171	180349348	CCDC39	NM_181426	1	20	14	-	180349257	180349380
258979370	chr3	180337504	180337710	180337530	180337682	CCDC39	NM_181426	1	20	15	-	180337599	180337758
258999683	chr3	180337655	180337823	180337683	180337797	CCDC39	NM_181426	1	20	15	-	180337599	180337758
256789054	chr3	180336959	180337165	180336985	180337136	CCDC39	NM_181426	1	20	16	-	180337047	180337153
264232568	chr3	180334470	180334694	180334494	180334667	CCDC39	NM_181426	1	20	17	-	180334614	180334754
254178805	chr3	180334291	180334446	180334319	180334417	CCDC39	NM_181426	1	20	18	-	180334304	180334483
254179374	chr3	180334390	180334577	180334418	180334550	CCDC39	NM_181426	1	20	18	-	180334304	180334483
261983747	chr3	180334147	180334348	180334175	180334318	CCDC39	NM_181426	1	20	18	-	180334304	180334483
261960356	chr3	180333917	180334136	180333942	180334114	CCDC39	NM_181426	1	20	19	-	180334069	180334151
261982492	chr3	180334092	180334316	180334115	180334288	CCDC39	NM_181426	1	20	19	-	180334069	180334151
263105387	chr3	180332620	180332791	180332647	180332769	CCDC39	NM_181426	1	20	20	-	180331796	180332865
267040918	chr3	180332745	180332942	180332770	180332915	CCDC39	NM_181426	1	20	20	-	180331796	180332865

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258636120	chr17	78010433	78010560	78010452	78010542	CCDC40	NM_001243342	1	18	1	+	78010431	78010490
263575014	chr17	78011808	78012013	78011830	78011990	CCDC40	NM_001243342	1	18	2	+	78011922	78011985
262778540	chr17	78013493	78013712	78013519	78013691	CCDC40	NM_001243342	1	18	3	+	78013611	78014069
262814213	chr17	78013670	78013879	78013692	78013855	CCDC40	NM_001243342	1	18	3	+	78013611	78014069
262854776	chr17	78013832	78014017	78013855	78013997	CCDC40	NM_001243342	1	18	3	+	78013611	78014069
262882764	chr17	78013956	78014147	78013979	78014125	CCDC40	NM_001243342	1	18	3	+	78013611	78014069
255740643	chr17	78021031	78021255	78021053	78021236	CCDC40	NM_001243342	1	18	4	+	78021078	78021201
257447369	chr17	78022303	78022525	78022324	78022504	CCDC40	NM_001243342	1	18	5	+	78022382	78022560
257473907	chr17	78022476	78022688	78022497	78022666	CCDC40	NM_001243342	1	18	5	+	78022382	78022560
253799342	chr17	78023655	78023873	78023678	78023852	CCDC40	NM_001243342	1	18	6	+	78023705	78023788
255059427	chr17	78023833	78024056	78023855	78024036	CCDC40	NM_001243342	1	18	7	+	78023863	78024082
255070403	chr17	78023953	78024168	78023973	78024147	CCDC40	NM_001243342	1	18	7	+	78023863	78024082
264133648	chr17	78032159	78032342	78032183	78032320	CCDC40	NM_001243342	1	18	8	+	78032293	78032450
264171067	chr17	78032299	78032486	78032321	78032458	CCDC40	NM_001243342	1	18	8	+	78032293	78032450
262898015	chr17	78032565	78032737	78032587	78032717	CCDC40	NM_001243342	1	18	9	+	78032657	78032779
262914177	chr17	78032696	78032823	78032718	78032803	CCDC40	NM_001243342	1	18	9	+	78032657	78032779
261622465	chr17	78039211	78039435	78039232	78039417	CCDC40	NM_001243342	1	18	10	+	78039284	78039405
262622786	chr17	78055217	78055423	78055245	78055394	CCDC40	NM_001243342	1	18	11	+	78055345	78055588
262676061	chr17	78055374	78055575	78055395	78055555	CCDC40	NM_001243342	1	18	11	+	78055345	78055588
262698943	chr17	78055517	78055704	78055540	78055683	CCDC40	NM_001243342	1	18	11	+	78055345	78055588
262698943	chr17	78055517	78055704	78055540	78055683	CCDC40	NM_001243342	1	18	12	+	78055675	78055857
266622635	chr17	78055660	78055832	78055684	78055806	CCDC40	NM_001243342	1	18	12	+	78055675	78055857
266632546	chr17	78055784	78055927	78055806	78055908	CCDC40	NM_001243342	1	18	12	+	78055675	78055857
262618256	chr17	78058354	78058578	78058376	78058557	CCDC40	NM_001243342	1	18	13	+	78058542	78058787
262663311	chr17	78058530	78058749	78058558	78058728	CCDC40	NM_001243342	1	18	13	+	78058542	78058787
262688458	chr17	78058708	78058889	78058729	78058867	CCDC40	NM_001243342	1	18	13	+	78058542	78058787
256783873	chr17	78059763	78059981	78059790	78059961	CCDC40	NM_001243342	1	18	14	+	78059802	78060015
256801008	chr17	78059915	78060135	78059936	78060115	CCDC40	NM_001243342	1	18	14	+	78059802	78060015
259827660	chr17	78061306	78061514	78061327	78061488	CCDC40	NM_001243342	1	18	15	+	78061406	78061575
259872738	chr17	78061467	78061669	78061489	78061645	CCDC40	NM_001243342	1	18	15	+	78061406	78061575
264140263	chr17	78061646	78061852	78061671	78061830	CCDC40	NM_001243342	1	18	16	+	78061810	78061901
264153229	chr17	78061810	78061986	78061831	78061964	CCDC40	NM_001243342	1	18	16	+	78061810	78061901
257105290	chr17	78063527	78063747	78063554	78063728	CCDC40	NM_001243342	1	18	17	+	78063563	78063683
266861544	chr17	78063807	78063965	78063827	78063945	CCDC40	NM_001243342	1	18	18	+	78063938	78064620
258636120	chr17	78010433	78010560	78010452	78010542	CCDC40	NM_017950	2	20	1	+	78010431	78010490
263575014	chr17	78011808	78012013	78011830	78011990	CCDC40	NM_017950	2	20	2	+	78011922	78011985
262778540	chr17	78013493	78013712	78013519	78013691	CCDC40	NM_017950	2	20	3	+	78013611	78014069
262814213	chr17	78013670	78013879	78013692	78013855	CCDC40	NM_017950	2	20	3	+	78013611	78014069
262854776	chr17	78013832	78014017	78013855	78013997	CCDC40	NM_017950	2	20	3	+	78013611	78014069
262882764	chr17	78013956	78014147	78013979	78014125	CCDC40	NM_017950	2	20	3	+	78013611	78014069
255740643	chr17	78021031	78021255	78021053	78021236	CCDC40	NM_017950	2	20	4	+	78021078	78021201

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257447369	chr17	78022303	78022525	78022324	78022504	CCDC40	NM_017950	2	20	5	+	78022382	78022560
257473907	chr17	78022476	78022688	78022497	78022666	CCDC40	NM_017950	2	20	5	+	78022382	78022560
253799342	chr17	78023655	78023873	78023678	78023852	CCDC40	NM_017950	2	20	6	+	78023705	78023788
255059427	chr17	78023833	78024056	78023855	78024036	CCDC40	NM_017950	2	20	7	+	78023863	78024082
255070403	chr17	78023953	78024168	78023973	78024147	CCDC40	NM_017950	2	20	7	+	78023863	78024082
264133648	chr17	78032159	78032342	78032183	78032320	CCDC40	NM_017950	2	20	8	+	78032293	78032450
264171067	chr17	78032299	78032486	78032321	78032458	CCDC40	NM_017950	2	20	8	+	78032293	78032450
262898015	chr17	78032565	78032737	78032587	78032717	CCDC40	NM_017950	2	20	9	+	78032657	78032779
262914177	chr17	78032696	78032823	78032718	78032803	CCDC40	NM_017950	2	20	9	+	78032657	78032779
261622465	chr17	78039211	78039435	78039232	78039417	CCDC40	NM_017950	2	20	10	+	78039284	78039405
262622786	chr17	78055217	78055423	78055245	78055394	CCDC40	NM_017950	2	20	11	+	78055345	78055588
262676061	chr17	78055374	78055575	78055395	78055555	CCDC40	NM_017950	2	20	11	+	78055345	78055588
262698943	chr17	78055517	78055704	78055540	78055683	CCDC40	NM_017950	2	20	11	+	78055345	78055588
262698943	chr17	78055517	78055704	78055540	78055683	CCDC40	NM_017950	2	20	12	+	78055675	78055857
266622635	chr17	78055660	78055832	78055684	78055806	CCDC40	NM_017950	2	20	12	+	78055675	78055857
266632546	chr17	78055784	78055927	78055806	78055908	CCDC40	NM_017950	2	20	12	+	78055675	78055857
262618256	chr17	78058354	78058578	78058376	78058557	CCDC40	NM_017950	2	20	13	+	78058542	78058787
262663311	chr17	78058530	78058749	78058558	78058728	CCDC40	NM_017950	2	20	13	+	78058542	78058787
262688458	chr17	78058708	78058889	78058729	78058867	CCDC40	NM_017950	2	20	13	+	78058542	78058787
256783873	chr17	78059763	78059981	78059790	78059961	CCDC40	NM_017950	2	20	14	+	78059802	78060015
256801008	chr17	78059915	78060135	78059936	78060115	CCDC40	NM_017950	2	20	14	+	78059802	78060015
259827660	chr17	78061306	78061514	78061327	78061488	CCDC40	NM_017950	2	20	15	+	78061406	78061575
259872738	chr17	78061467	78061669	78061489	78061645	CCDC40	NM_017950	2	20	15	+	78061406	78061575
264140263	chr17	78061646	78061852	78061671	78061830	CCDC40	NM_017950	2	20	16	+	78061810	78061901
264153229	chr17	78061810	78061986	78061831	78061964	CCDC40	NM_017950	2	20	16	+	78061810	78061901
257105290	chr17	78063527	78063747	78063554	78063728	CCDC40	NM_017950	2	20	17	+	78063563	78063683
263131954	chr17	78068961	78069139	78068978	78069121	CCDC40	NM_017950	2	20	18	+	78069062	78069250
263141949	chr17	78069097	78069321	78069118	78069300	CCDC40	NM_017950	2	20	18	+	78069062	78069250
262731891	chr17	78070982	78071106	78071002	78071079	CCDC40	NM_017950	2	20	19	+	78071044	78071202
262757257	chr17	78071059	78071260	78071080	78071239	CCDC40	NM_017950	2	20	19	+	78071044	78071202
262086822	chr17	78073267	78073466	78073290	78073446	CCDC40	NM_017950	2	20	20	+	78073326	78074412
262137042	chr17	78073410	78073634	78073430	78073609	CCDC40	NM_017950	2	20	20	+	78073326	78074412
255487045	chr10	73199546	73199696	73199569	73199677	CDH23	NM_001171930	1	31	2	+	73199584	73199655
256421425	chr10	73205992	73206198	73206009	73206181	CDH23	NM_001171930	1	31	3	+	73206075	73206152
256979565	chr10	73269813	73270026	73269833	73270005	CDH23	NM_001171930	1	31	4	+	73269839	73269981
264057394	chr10	73270662	73270885	73270680	73270863	CDH23	NM_001171930	1	31	5	+	73270711	73270758
267043519	chr10	73270798	73271018	73270820	73270997	CDH23	NM_001171930	1	31	6	+	73270877	73270969
261833522	chr10	73326469	73326688	73326493	73326668	CDH23	NM_001171930	1	31	7	+	73326499	73326693
261848789	chr10	73326646	73326843	73326667	73326815	CDH23	NM_001171930	1	31	7	+	73326499	73326693
254491316	chr10	73330510	73330712	73330533	73330689	CDH23	NM_001171930	1	31	8	+	73330547	73330675
265278632	chr10	73337640	73337830	73337663	73337809	CDH23	NM_001171930	1	31	9	+	73337671	73337749

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265718574	chr10	73375228	73375439	73375249	73375419	CDH23	NM_001171930	1	31	10	+	73375261	73375373
255251436	chr10	73376910	73377130	73376931	73377108	CDH23	NM_001171930	1	31	11	+	73376962	73377150
255279173	chr10	73377055	73377261	73377078	73377239	CDH23	NM_001171930	1	31	11	+	73376962	73377150
258039902	chr10	73405552	73405769	73405574	73405747	CDH23	NM_001171930	1	31	12	+	73405582	73405737
266613275	chr10	73406172	73406372	73406192	73406352	CDH23	NM_001171930	1	31	13	+	73406216	73406374
266640988	chr10	73406326	73406547	73406346	73406525	CDH23	NM_001171930	1	31	13	+	73406216	73406374
262934793	chr10	73434801	73435017	73434822	73434991	CDH23	NM_001171930	1	31	14	+	73434869	73434933
254942131	chr10	73437161	73437373	73437183	73437353	CDH23	NM_001171930	1	31	15	+	73437213	73437450
254965183	chr10	73437333	73437493	73437354	73437468	CDH23	NM_001171930	1	31	15	+	73437213	73437450
256266088	chr10	73439111	73439325	73439129	73439306	CDH23	NM_001171930	1	31	16	+	73439144	73439249
257002196	chr10	73442157	73442381	73442181	73442358	CDH23	NM_001171930	1	31	17	+	73442202	73442329
260977353	chr10	73447375	73447584	73447396	73447562	CDH23	NM_001171930	1	31	18	+	73447404	73447476
266161995	chr10	73450197	73450380	73450216	73450361	CDH23	NM_001171930	1	31	19	+	73450225	73450341
259519994	chr10	73453768	73453962	73453791	73453935	CDH23	NM_001171930	1	31	20	+	73453904	73454016
259569694	chr10	73453917	73454132	73453936	73454109	CDH23	NM_001171930	1	31	20	+	73453904	73454016
254532634	chr10	73455049	73455258	73455071	73455237	CDH23	NM_001171930	1	31	21	+	73455175	73455282
254553900	chr10	73455218	73455417	73455238	73455395	CDH23	NM_001171930	1	31	21	+	73455175	73455282
265235156	chr10	73461683	73461864	73461702	73461840	CDH23	NM_001171930	1	31	22	+	73461779	73461968
265237712	chr10	73461809	73461978	73461829	73461955	CDH23	NM_001171930	1	31	22	+	73461779	73461968
265244538	chr10	73461936	73462102	73461956	73462077	CDH23	NM_001171930	1	31	22	+	73461779	73461968
254013268	chr10	73462258	73462482	73462279	73462457	CDH23	NM_001171930	1	31	23	+	73462306	73462451
254712605	chr10	73464632	73464844	73464650	73464826	CDH23	NM_001171930	1	31	24	+	73464668	73464887
254718634	chr10	73464800	73465024	73464817	73465002	CDH23	NM_001171930	1	31	24	+	73464668	73464887
254585098	chr10	73466551	73466768	73466576	73466749	CDH23	NM_001171930	1	31	25	+	73466654	73466806
254598616	chr10	73466706	73466930	73466725	73466908	CDH23	NM_001171930	1	31	25	+	73466654	73466806
263235152	chr10	73468806	73469013	73468824	73468992	CDH23	NM_001171930	1	31	26	+	73468855	73468968
264781125	chr10	73472277	73472497	73472298	73472474	CDH23	NM_001171930	1	31	27	+	73472422	73472570
264821184	chr10	73472457	73472661	73472475	73472642	CDH23	NM_001171930	1	31	27	+	73472422	73472570
266897879	chr10	73483721	73483941	73483749	73483920	CDH23	NM_001171930	1	31	28	+	73483802	73483862
265706452	chr10	73484972	73485176	73484994	73485157	CDH23	NM_001171930	1	31	29	+	73485129	73485277
265713923	chr10	73485137	73485341	73485158	73485320	CDH23	NM_001171930	1	31	29	+	73485129	73485277
259402335	chr10	73490185	73490392	73490202	73490375	CDH23	NM_001171930	1	31	30	+	73490226	73490361
263064377	chr10	73491691	73491849	73491711	73491826	CDH23	NM_001171930	1	31	31	+	73491744	73492481
263082470	chr10	73491805	73491979	73491827	73491958	CDH23	NM_001171930	1	31	31	+	73491744	73492481
263128703	chr10	73491934	73492083	73491953	73492063	CDH23	NM_001171930	1	31	31	+	73491744	73492481
263174198	chr10	73492042	73492244	73492064	73492216	CDH23	NM_001171930	1	31	31	+	73491744	73492481
255487045	chr10	73199546	73199696	73199569	73199677	CDH23	NM_001171931	2	25	2	+	73199584	73199655
256421425	chr10	73205992	73206198	73206009	73206181	CDH23	NM_001171931	2	25	3	+	73206075	73206152
256979565	chr10	73269813	73270026	73269833	73270005	CDH23	NM_001171931	2	25	4	+	73269839	73269981
264057394	chr10	73270662	73270885	73270680	73270863	CDH23	NM_001171931	2	25	5	+	73270711	73270758
267043519	chr10	73270798	73271018	73270820	73270997	CDH23	NM_001171931	2	25	6	+	73270877	73270969

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261833522	chr10	73326469	73326688	73326493	73326668	CDH23	NM_001171931	2	25	7	+	73326499	73326693
261848789	chr10	73326646	73326843	73326667	73326815	CDH23	NM_001171931	2	25	7	+	73326499	73326693
254491316	chr10	73330510	73330712	73330533	73330689	CDH23	NM_001171931	2	25	8	+	73330547	73330675
265278632	chr10	73337640	73337830	73337663	73337809	CDH23	NM_001171931	2	25	9	+	73337671	73337749
265718574	chr10	73375228	73375439	73375249	73375419	CDH23	NM_001171931	2	25	10	+	73375261	73375373
255251436	chr10	73376910	73377130	73376931	73377108	CDH23	NM_001171931	2	25	11	+	73376962	73377150
255279173	chr10	73377055	73377261	73377078	73377239	CDH23	NM_001171931	2	25	11	+	73376962	73377150
258039902	chr10	73405552	73405769	73405574	73405747	CDH23	NM_001171931	2	25	12	+	73405582	73405737
266613275	chr10	73406172	73406372	73406192	73406352	CDH23	NM_001171931	2	25	13	+	73406216	73406374
266640988	chr10	73406326	73406547	73406346	73406525	CDH23	NM_001171931	2	25	13	+	73406216	73406374
262934793	chr10	73434801	73435017	73434822	73434991	CDH23	NM_001171931	2	25	14	+	73434869	73434933
254942131	chr10	73437161	73437373	73437183	73437353	CDH23	NM_001171931	2	25	15	+	73437213	73437450
254965183	chr10	73437333	73437493	73437354	73437468	CDH23	NM_001171931	2	25	15	+	73437213	73437450
256266088	chr10	73439111	73439325	73439129	73439306	CDH23	NM_001171931	2	25	16	+	73439144	73439249
257002196	chr10	73442157	73442381	73442181	73442358	CDH23	NM_001171931	2	25	17	+	73442202	73442329
260977353	chr10	73447375	73447584	73447396	73447562	CDH23	NM_001171931	2	25	18	+	73447404	73447476
266161995	chr10	73450197	73450380	73450216	73450361	CDH23	NM_001171931	2	25	19	+	73450225	73450341
259519994	chr10	73453768	73453962	73453791	73453935	CDH23	NM_001171931	2	25	20	+	73453904	73454016
259569694	chr10	73453917	73454132	73453936	73454109	CDH23	NM_001171931	2	25	20	+	73453904	73454016
254532634	chr10	73455049	73455258	73455071	73455237	CDH23	NM_001171931	2	25	21	+	73455175	73455282
254553900	chr10	73455218	73455417	73455238	73455395	CDH23	NM_001171931	2	25	21	+	73455175	73455282
265235156	chr10	73461683	73461864	73461702	73461840	CDH23	NM_001171931	2	25	22	+	73461779	73461968
265237712	chr10	73461809	73461978	73461829	73461955	CDH23	NM_001171931	2	25	22	+	73461779	73461968
265244538	chr10	73461936	73462102	73461956	73462077	CDH23	NM_001171931	2	25	22	+	73461779	73461968
254013268	chr10	73462258	73462482	73462279	73462457	CDH23	NM_001171931	2	25	23	+	73462306	73462451
254712605	chr10	73464632	73464844	73464650	73464826	CDH23	NM_001171931	2	25	24	+	73464668	73464887
254718634	chr10	73464800	73465024	73464817	73465002	CDH23	NM_001171931	2	25	24	+	73464668	73464887
254585098	chr10	73466551	73466768	73466576	73466749	CDH23	NM_001171931	2	25	25	+	73466654	73467264
254598616	chr10	73466706	73466930	73466725	73466908	CDH23	NM_001171931	2	25	25	+	73466654	73467264
255487045	chr10	73199546	73199696	73199569	73199677	CDH23	NM_001171932	3	11	2	+	73199584	73199655
256421425	chr10	73205992	73206198	73206009	73206181	CDH23	NM_001171932	3	11	3	+	73206075	73206152
256979565	chr10	73269813	73270026	73269833	73270005	CDH23	NM_001171932	3	11	4	+	73269839	73269981
264057394	chr10	73270662	73270885	73270680	73270863	CDH23	NM_001171932	3	11	5	+	73270711	73270758
267043519	chr10	73270798	73271018	73270820	73270997	CDH23	NM_001171932	3	11	6	+	73270877	73270969
261833522	chr10	73326469	73326688	73326493	73326668	CDH23	NM_001171932	3	11	7	+	73326499	73326693
261848789	chr10	73326646	73326843	73326667	73326815	CDH23	NM_001171932	3	11	7	+	73326499	73326693
254491316	chr10	73330510	73330712	73330533	73330689	CDH23	NM_001171932	3	11	8	+	73330547	73330675
265278632	chr10	73337640	73337830	73337663	73337809	CDH23	NM_001171932	3	11	9	+	73337671	73337749
265718574	chr10	73375228	73375439	73375249	73375419	CDH23	NM_001171932	3	11	10	+	73375261	73375373
255251436	chr10	73376910	73377130	73376931	73377108	CDH23	NM_001171932	3	11	11	+	73376962	73377362
255279173	chr10	73377055	73377261	73377078	73377239	CDH23	NM_001171932	3	11	11	+	73376962	73377362

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257665455	chr10	73556798	73557006	73556820	73556983	CDH23	NM_001171933	4	23	2	+	73556861	73556977
261842911	chr10	73557964	73558188	73557984	73558164	CDH23	NM_001171933	4	23	3	+	73558111	73558335
261853939	chr10	73558142	73558366	73558164	73558345	CDH23	NM_001171933	4	23	3	+	73558111	73558335
255396070	chr10	73558788	73559010	73558813	73558986	CDH23	NM_001171933	4	23	4	+	73558868	73559037
255417512	chr10	73558964	73559180	73558987	73559158	CDH23	NM_001171933	4	23	4	+	73558868	73559037
256716997	chr10	73559205	73559429	73559226	73559406	CDH23	NM_001171933	4	23	5	+	73559249	73559386
264440524	chr10	73560371	73560557	73560389	73560537	CDH23	NM_001171933	4	23	6	+	73560393	73560512
255612856	chr10	73562611	73562799	73562632	73562777	CDH23	NM_001171933	4	23	7	+	73562655	73562832
255634797	chr10	73562758	73562946	73562778	73562922	CDH23	NM_001171933	4	23	7	+	73562655	73562832
257235485	chr10	73562833	73563052	73562854	73563032	CDH23	NM_001171933	4	23	8	+	73562966	73563177
257248905	chr10	73563013	73563228	73563033	73563204	CDH23	NM_001171933	4	23	8	+	73562966	73563177
254466324	chr10	73565499	73565703	73565522	73565685	CDH23	NM_001171933	4	23	9	+	73565563	73565754
254482130	chr10	73565665	73565853	73565686	73565832	CDH23	NM_001171933	4	23	9	+	73565563	73565754
266858170	chr10	73565891	73566110	73565915	73566090	CDH23	NM_001171933	4	23	10	+	73565925	73566038
263562091	chr10	73567000	73567195	73567020	73567173	CDH23	NM_001171933	4	23	11	+	73567034	73567163
261560933	chr10	73567200	73567403	73567221	73567384	CDH23	NM_001171933	4	23	12	+	73567273	73567524
261571512	chr10	73567353	73567521	73567377	73567499	CDH23	NM_001171933	4	23	12	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_001171933	4	23	12	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_001171933	4	23	13	+	73567603	73567764
262619695	chr10	73567575	73567799	73567596	73567779	CDH23	NM_001171933	4	23	13	+	73567603	73567764
266615060	chr10	73569533	73569748	73569554	73569722	CDH23	NM_001171933	4	23	14	+	73569577	73569833
266635668	chr10	73569694	73569917	73569716	73569896	CDH23	NM_001171933	4	23	14	+	73569577	73569833
256254262	chr10	73570199	73570421	73570220	73570399	CDH23	NM_001171933	4	23	15	+	73570229	73570326
257421579	chr10	73570908	73571117	73570934	73571095	CDH23	NM_001171933	4	23	16	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_001171933	4	23	16	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_001171933	4	23	17	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_001171933	4	23	17	+	73571268	73571347
265738461	chr10	73571232	73571437	73571249	73571419	CDH23	NM_001171933	4	23	17	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_001171933	4	23	18	+	73571470	73571510
257757036	chr10	73571656	73571852	73571675	73571834	CDH23	NM_001171933	4	23	19	+	73571712	73571772
266901503	chr10	73572111	73572320	73572132	73572298	CDH23	NM_001171933	4	23	20	+	73572237	73572366
266915789	chr10	73572255	73572460	73572276	73572438	CDH23	NM_001171933	4	23	20	+	73572237	73572366
261824085	chr10	73572432	73572640	73572455	73572620	CDH23	NM_001171933	4	23	21	+	73572525	73572647
261845800	chr10	73572594	73572730	73572618	73572710	CDH23	NM_001171933	4	23	21	+	73572525	73572647
254075625	chr10	73572896	73573075	73572918	73573055	CDH23	NM_001171933	4	23	22	+	73573001	73573105
254094374	chr10	73573034	73573236	73573055	73573215	CDH23	NM_001171933	4	23	22	+	73573001	73573105
263897028	chr10	73574609	73574824	73574629	73574805	CDH23	NM_001171933	4	23	23	+	73574709	73575704
263903339	chr10	73574785	73575006	73574804	73574986	CDH23	NM_001171933	4	23	23	+	73574709	73575704
263906427	chr10	73574967	73575160	73574987	73575141	CDH23	NM_001171933	4	23	23	+	73574709	73575704
257665455	chr10	73556798	73557006	73556820	73556983	CDH23	NM_001171934	5	22	2	+	73556861	73556977
261842911	chr10	73557964	73558188	73557984	73558164	CDH23	NM_001171934	5	22	3	+	73558111	73558335

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261853939	chr10	73558142	73558366	73558164	73558345	CDH23	NM_001171934	5	22	3	+	73558111	73558335
255396070	chr10	73558788	73559010	73558813	73558986	CDH23	NM_001171934	5	22	4	+	73558868	73559037
255417512	chr10	73558964	73559180	73558987	73559158	CDH23	NM_001171934	5	22	4	+	73558868	73559037
256716997	chr10	73559205	73559429	73559226	73559406	CDH23	NM_001171934	5	22	5	+	73559249	73559386
264440524	chr10	73560371	73560557	73560389	73560537	CDH23	NM_001171934	5	22	6	+	73560393	73560512
255612856	chr10	73562611	73562799	73562632	73562777	CDH23	NM_001171934	5	22	7	+	73562655	73562832
255634797	chr10	73562758	73562946	73562778	73562922	CDH23	NM_001171934	5	22	7	+	73562655	73562832
257235485	chr10	73562833	73563052	73562854	73563032	CDH23	NM_001171934	5	22	8	+	73562966	73563177
257248905	chr10	73563013	73563228	73563033	73563204	CDH23	NM_001171934	5	22	8	+	73562966	73563177
254466324	chr10	73565499	73565703	73565522	73565685	CDH23	NM_001171934	5	22	9	+	73565563	73565754
254482130	chr10	73565665	73565853	73565686	73565832	CDH23	NM_001171934	5	22	9	+	73565563	73565754
266858170	chr10	73565891	73566110	73565915	73566090	CDH23	NM_001171934	5	22	10	+	73565925	73566038
263562091	chr10	73567000	73567195	73567020	73567173	CDH23	NM_001171934	5	22	11	+	73567034	73567163
261560933	chr10	73567200	73567403	73567221	73567384	CDH23	NM_001171934	5	22	12	+	73567273	73567524
261571512	chr10	73567353	73567521	73567377	73567499	CDH23	NM_001171934	5	22	12	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_001171934	5	22	12	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_001171934	5	22	13	+	73567603	73567764
262619695	chr10	73567575	73567799	73567596	73567779	CDH23	NM_001171934	5	22	13	+	73567603	73567764
266615060	chr10	73569533	73569748	73569554	73569722	CDH23	NM_001171934	5	22	14	+	73569577	73569833
266635668	chr10	73569694	73569917	73569716	73569896	CDH23	NM_001171934	5	22	14	+	73569577	73569833
256254262	chr10	73570199	73570421	73570220	73570399	CDH23	NM_001171934	5	22	15	+	73570229	73570326
257421579	chr10	73570908	73571117	73570934	73571095	CDH23	NM_001171934	5	22	16	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_001171934	5	22	16	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_001171934	5	22	17	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_001171934	5	22	17	+	73571268	73571347
265738461	chr10	73571232	73571437	73571249	73571419	CDH23	NM_001171934	5	22	17	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_001171934	5	22	18	+	73571470	73571510
257757036	chr10	73571656	73571852	73571675	73571834	CDH23	NM_001171934	5	22	19	+	73571712	73571772
266901503	chr10	73572111	73572320	73572132	73572298	CDH23	NM_001171934	5	22	20	+	73572237	73572366
266915789	chr10	73572255	73572460	73572276	73572438	CDH23	NM_001171934	5	22	20	+	73572237	73572366
261824085	chr10	73572432	73572640	73572455	73572620	CDH23	NM_001171934	5	22	21	+	73572525	73572647
261845800	chr10	73572594	73572730	73572618	73572710	CDH23	NM_001171934	5	22	21	+	73572525	73572647
263897028	chr10	73574609	73574824	73574629	73574805	CDH23	NM_001171934	5	22	22	+	73574709	73575704
263903339	chr10	73574785	73575006	73574804	73574986	CDH23	NM_001171934	5	22	22	+	73574709	73575704
263906427	chr10	73574967	73575160	73574987	73575141	CDH23	NM_001171934	5	22	22	+	73574709	73575704
257757036	chr10	73571656	73571852	73571675	73571834	CDH23	NM_001171935	6	5	1	+	73571640	73572119
264171790	chr10	73572020	73572146	73572040	73572124	CDH23	NM_001171935	6	5	1	+	73571640	73572119
266901503	chr10	73572111	73572320	73572132	73572298	CDH23	NM_001171935	6	5	2	+	73572237	73572366
266915789	chr10	73572255	73572460	73572276	73572438	CDH23	NM_001171935	6	5	2	+	73572237	73572366
261824085	chr10	73572432	73572640	73572455	73572620	CDH23	NM_001171935	6	5	3	+	73572525	73572647
261845800	chr10	73572594	73572730	73572618	73572710	CDH23	NM_001171935	6	5	3	+	73572525	73572647

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254075625	chr10	73572896	73573075	73572918	73573055	CDH23	NM_001171935	6	5	4	+	73573001	73573105
254094374	chr10	73573034	73573236	73573055	73573215	CDH23	NM_001171935	6	5	4	+	73573001	73573105
263897028	chr10	73574609	73574824	73574629	73574805	CDH23	NM_001171935	6	5	5	+	73574709	73575704
263903339	chr10	73574785	73575006	73574804	73574986	CDH23	NM_001171935	6	5	5	+	73574709	73575704
263906427	chr10	73574967	73575160	73574987	73575141	CDH23	NM_001171935	6	5	5	+	73574709	73575704
257757036	chr10	73571656	73571852	73571675	73571834	CDH23	NM_001171936	7	4	1	+	73571640	73572119
264171790	chr10	73572020	73572146	73572040	73572124	CDH23	NM_001171936	7	4	1	+	73571640	73572119
266901503	chr10	73572111	73572320	73572132	73572298	CDH23	NM_001171936	7	4	2	+	73572237	73572366
266915789	chr10	73572255	73572460	73572276	73572438	CDH23	NM_001171936	7	4	2	+	73572237	73572366
261824085	chr10	73572432	73572640	73572455	73572620	CDH23	NM_001171936	7	4	3	+	73572525	73572647
261845800	chr10	73572594	73572730	73572618	73572710	CDH23	NM_001171936	7	4	3	+	73572525	73572647
263897028	chr10	73574609	73574824	73574629	73574805	CDH23	NM_001171936	7	4	4	+	73574709	73575704
263903339	chr10	73574785	73575006	73574804	73574986	CDH23	NM_001171936	7	4	4	+	73574709	73575704
263906427	chr10	73574967	73575160	73574987	73575141	CDH23	NM_001171936	7	4	4	+	73574709	73575704
255487045	chr10	73199546	73199696	73199569	73199677	CDH23	NM_022124	8	68	2	+	73199584	73199655
256421425	chr10	73205992	73206198	73206009	73206181	CDH23	NM_022124	8	68	3	+	73206075	73206152
256979565	chr10	73269813	73270026	73269833	73270005	CDH23	NM_022124	8	68	4	+	73269839	73269981
264057394	chr10	73270662	73270885	73270680	73270863	CDH23	NM_022124	8	68	5	+	73270711	73270758
267043519	chr10	73270798	73271018	73270820	73270997	CDH23	NM_022124	8	68	6	+	73270877	73270969
261833522	chr10	73326469	73326688	73326493	73326668	CDH23	NM_022124	8	68	7	+	73326499	73326693
261848789	chr10	73326646	73326843	73326667	73326815	CDH23	NM_022124	8	68	7	+	73326499	73326693
254491316	chr10	73330510	73330712	73330533	73330689	CDH23	NM_022124	8	68	8	+	73330547	73330675
265278632	chr10	73337640	73337830	73337663	73337809	CDH23	NM_022124	8	68	9	+	73337671	73337749
265718574	chr10	73375228	73375439	73375249	73375419	CDH23	NM_022124	8	68	10	+	73375261	73375373
255251436	chr10	73376910	73377130	73376931	73377108	CDH23	NM_022124	8	68	11	+	73376962	73377150
255279173	chr10	73377055	73377261	73377078	73377239	CDH23	NM_022124	8	68	11	+	73376962	73377150
258039902	chr10	73405552	73405769	73405574	73405747	CDH23	NM_022124	8	68	12	+	73405582	73405737
266613275	chr10	73406172	73406372	73406192	73406352	CDH23	NM_022124	8	68	13	+	73406216	73406374
266640988	chr10	73406326	73406547	73406346	73406525	CDH23	NM_022124	8	68	13	+	73406216	73406374
262934793	chr10	73434801	73435017	73434822	73434991	CDH23	NM_022124	8	68	14	+	73434869	73434933
254942131	chr10	73437161	73437373	73437183	73437353	CDH23	NM_022124	8	68	15	+	73437213	73437450
254965183	chr10	73437333	73437493	73437354	73437468	CDH23	NM_022124	8	68	15	+	73437213	73437450
256266088	chr10	73439111	73439325	73439129	73439306	CDH23	NM_022124	8	68	16	+	73439144	73439249
257002196	chr10	73442157	73442381	73442181	73442358	CDH23	NM_022124	8	68	17	+	73442202	73442329
260977353	chr10	73447375	73447584	73447396	73447562	CDH23	NM_022124	8	68	18	+	73447404	73447476
266161995	chr10	73450197	73450380	73450216	73450361	CDH23	NM_022124	8	68	19	+	73450225	73450341
259519994	chr10	73453768	73453962	73453791	73453935	CDH23	NM_022124	8	68	20	+	73453904	73454016
259569694	chr10	73453917	73454132	73453936	73454109	CDH23	NM_022124	8	68	20	+	73453904	73454016
254532634	chr10	73455049	73455258	73455071	73455237	CDH23	NM_022124	8	68	21	+	73455175	73455282
254553900	chr10	73455218	73455417	73455238	73455395	CDH23	NM_022124	8	68	21	+	73455175	73455282
265235156	chr10	73461683	73461864	73461702	73461840	CDH23	NM_022124	8	68	22	+	73461779	73461968

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265237712	chr10	73461809	73461978	73461829	73461955	CDH23	NM_022124	8	68	22	+	73461779	73461968
265244538	chr10	73461936	73462102	73461956	73462077	CDH23	NM_022124	8	68	22	+	73461779	73461968
254013268	chr10	73462258	73462482	73462279	73462457	CDH23	NM_022124	8	68	23	+	73462306	73462451
254712605	chr10	73464632	73464844	73464650	73464826	CDH23	NM_022124	8	68	24	+	73464668	73464887
254718634	chr10	73464800	73465024	73464817	73465002	CDH23	NM_022124	8	68	24	+	73464668	73464887
254585098	chr10	73466551	73466768	73466576	73466749	CDH23	NM_022124	8	68	25	+	73466654	73466806
254598616	chr10	73466706	73466930	73466725	73466908	CDH23	NM_022124	8	68	25	+	73466654	73466806
263235152	chr10	73468806	73469013	73468824	73468992	CDH23	NM_022124	8	68	26	+	73468855	73468968
264781125	chr10	73472277	73472497	73472298	73472474	CDH23	NM_022124	8	68	27	+	73472422	73472570
264821184	chr10	73472457	73472661	73472475	73472642	CDH23	NM_022124	8	68	27	+	73472422	73472570
266897879	chr10	73483721	73483941	73483749	73483920	CDH23	NM_022124	8	68	28	+	73483802	73483862
265706452	chr10	73484972	73485176	73484994	73485157	CDH23	NM_022124	8	68	29	+	73485129	73485277
265713923	chr10	73485137	73485341	73485158	73485320	CDH23	NM_022124	8	68	29	+	73485129	73485277
259402335	chr10	73490185	73490392	73490202	73490375	CDH23	NM_022124	8	68	30	+	73490226	73490361
263064377	chr10	73491691	73491849	73491711	73491826	CDH23	NM_022124	8	68	31	+	73491744	73492132
263082470	chr10	73491805	73491979	73491827	73491958	CDH23	NM_022124	8	68	31	+	73491744	73492132
263128703	chr10	73491934	73492083	73491953	73492063	CDH23	NM_022124	8	68	31	+	73491744	73492132
263174198	chr10	73492042	73492244	73492064	73492216	CDH23	NM_022124	8	68	31	+	73491744	73492132
257126739	chr10	73493946	73494170	73493968	73494147	CDH23	NM_022124	8	68	32	+	73493997	73494098
255602964	chr10	73498225	73498436	73498246	73498415	CDH23	NM_022124	8	68	33	+	73498252	73498404
265818352	chr10	73499259	73499480	73499282	73499458	CDH23	NM_022124	8	68	34	+	73499401	73499529
265834224	chr10	73499438	73499572	73499459	73499550	CDH23	NM_022124	8	68	34	+	73499401	73499529
266378837	chr10	73500542	73500749	73500563	73500727	CDH23	NM_022124	8	68	35	+	73500579	73500707
264826015	chr10	73501384	73501567	73501402	73501549	CDH23	NM_022124	8	68	36	+	73501451	73501678
264843440	chr10	73501528	73501752	73501548	73501732	CDH23	NM_022124	8	68	36	+	73501451	73501678
255919079	chr10	73537311	73537523	73537334	73537502	CDH23	NM_022124	8	68	37	+	73537437	73537658
255954549	chr10	73537469	73537689	73537490	73537667	CDH23	NM_022124	8	68	37	+	73537437	73537658
261334792	chr10	73537893	73538117	73537913	73538097	CDH23	NM_022124	8	68	38	+	73537946	73538065
253813553	chr10	73538991	73539190	73539012	73539168	CDH23	NM_022124	8	68	39	+	73539024	73539204
253841374	chr10	73539140	73539309	73539160	73539287	CDH23	NM_022124	8	68	39	+	73539024	73539204
258305147	chr10	73543874	73544091	73543896	73544072	CDH23	NM_022124	8	68	40	+	73544044	73544177
258320736	chr10	73544045	73544249	73544068	73544223	CDH23	NM_022124	8	68	40	+	73544044	73544177
259927399	chr10	73544593	73544739	73544614	73544720	CDH23	NM_022124	8	68	41	+	73544648	73544857
259971025	chr10	73544700	73544914	73544721	73544891	CDH23	NM_022124	8	68	41	+	73544648	73544857
260307652	chr10	73545339	73545553	73545362	73545533	CDH23	NM_022124	8	68	42	+	73545388	73545495
259153727	chr10	73548665	73548882	73548684	73548861	CDH23	NM_022124	8	68	43	+	73548697	73548799
265707346	chr10	73549943	73550160	73549964	73550137	CDH23	NM_022124	8	68	44	+	73550045	73550170
265715738	chr10	73550103	73550308	73550122	73550286	CDH23	NM_022124	8	68	44	+	73550045	73550170
267003137	chr10	73550842	73551048	73550864	73551029	CDH23	NM_022124	8	68	45	+	73550889	73551092
267020269	chr10	73551005	73551182	73551028	73551162	CDH23	NM_022124	8	68	45	+	73550889	73551092
266679991	chr10	73552907	73553112	73552927	73553091	CDH23	NM_022124	8	68	46	+	73552939	73553397

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266706191	chr10	73553068	73553289	73553091	73553270	CDH23	NM_022124	8	68	46	+	73552939	73553397
266728853	chr10	73553251	73553410	73553271	73553390	CDH23	NM_022124	8	68	46	+	73552939	73553397
266734686	chr10	73553368	73553559	73553390	73553536	CDH23	NM_022124	8	68	46	+	73552939	73553397
257665455	chr10	73556798	73557006	73556820	73556983	CDH23	NM_022124	8	68	47	+	73556861	73556977
261842911	chr10	73557964	73558188	73557984	73558164	CDH23	NM_022124	8	68	48	+	73558111	73558335
261853939	chr10	73558142	73558366	73558164	73558345	CDH23	NM_022124	8	68	48	+	73558111	73558335
255396070	chr10	73558788	73559010	73558813	73558986	CDH23	NM_022124	8	68	49	+	73558868	73559037
255417512	chr10	73558964	73559180	73558987	73559158	CDH23	NM_022124	8	68	49	+	73558868	73559037
256716997	chr10	73559205	73559429	73559226	73559406	CDH23	NM_022124	8	68	50	+	73559249	73559386
264440524	chr10	73560371	73560557	73560389	73560537	CDH23	NM_022124	8	68	51	+	73560393	73560512
255612856	chr10	73562611	73562799	73562632	73562777	CDH23	NM_022124	8	68	52	+	73562655	73562832
255634797	chr10	73562758	73562946	73562778	73562922	CDH23	NM_022124	8	68	52	+	73562655	73562832
257235485	chr10	73562833	73563052	73562854	73563032	CDH23	NM_022124	8	68	53	+	73562966	73563177
257248905	chr10	73563013	73563228	73563033	73563204	CDH23	NM_022124	8	68	53	+	73562966	73563177
254466324	chr10	73565499	73565703	73565522	73565685	CDH23	NM_022124	8	68	54	+	73565563	73565754
254482130	chr10	73565665	73565853	73565686	73565832	CDH23	NM_022124	8	68	54	+	73565563	73565754
266858170	chr10	73565891	73566110	73565915	73566090	CDH23	NM_022124	8	68	55	+	73565925	73566038
263562091	chr10	73567000	73567195	73567020	73567173	CDH23	NM_022124	8	68	56	+	73567034	73567163
261560933	chr10	73567200	73567403	73567221	73567384	CDH23	NM_022124	8	68	57	+	73567273	73567524
261571512	chr10	73567353	73567521	73567377	73567499	CDH23	NM_022124	8	68	57	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_022124	8	68	57	+	73567273	73567524
261588530	chr10	73567469	73567678	73567491	73567656	CDH23	NM_022124	8	68	58	+	73567603	73567764
262619695	chr10	73567575	73567799	73567596	73567779	CDH23	NM_022124	8	68	58	+	73567603	73567764
266615060	chr10	73569533	73569748	73569554	73569722	CDH23	NM_022124	8	68	59	+	73569577	73569833
266635668	chr10	73569694	73569917	73569716	73569896	CDH23	NM_022124	8	68	59	+	73569577	73569833
256254262	chr10	73570199	73570421	73570220	73570399	CDH23	NM_022124	8	68	60	+	73570229	73570326
257421579	chr10	73570908	73571117	73570934	73571095	CDH23	NM_022124	8	68	61	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_022124	8	68	61	+	73571072	73571192
257430105	chr10	73571072	73571295	73571096	73571273	CDH23	NM_022124	8	68	62	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_022124	8	68	62	+	73571268	73571347
265738461	chr10	73571232	73571437	73571249	73571419	CDH23	NM_022124	8	68	62	+	73571268	73571347
259538495	chr10	73571321	73571545	73571346	73571523	CDH23	NM_022124	8	68	63	+	73571470	73571510
257757036	chr10	73571656	73571852	73571675	73571834	CDH23	NM_022124	8	68	64	+	73571712	73571772
266901503	chr10	73572111	73572320	73572132	73572298	CDH23	NM_022124	8	68	65	+	73572237	73572366
266915789	chr10	73572255	73572460	73572276	73572438	CDH23	NM_022124	8	68	65	+	73572237	73572366
261824085	chr10	73572432	73572640	73572455	73572620	CDH23	NM_022124	8	68	66	+	73572525	73572647
261845800	chr10	73572594	73572730	73572618	73572710	CDH23	NM_022124	8	68	66	+	73572525	73572647
254075625	chr10	73572896	73573075	73572918	73573055	CDH23	NM_022124	8	68	67	+	73573001	73573105
254094374	chr10	73573034	73573236	73573055	73573215	CDH23	NM_022124	8	68	67	+	73573001	73573105
263897028	chr10	73574609	73574824	73574629	73574805	CDH23	NM_022124	8	68	68	+	73574709	73575704
263903339	chr10	73574785	73575006	73574804	73574986	CDH23	NM_022124	8	68	68	+	73574709	73575704

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263906427	chr10	73574967	73575160	73574987	73575141	CDH23	NM_022124	8	68	68	+	73574709	73575704
255487045	chr10	73199546	73199696	73199569	73199677	CDH23	NM_052836	9	13	2	+	73199584	73199655
256421425	chr10	73205992	73206198	73206009	73206181	CDH23	NM_052836	9	13	3	+	73206075	73206152
256979565	chr10	73269813	73270026	73269833	73270005	CDH23	NM_052836	9	13	4	+	73269839	73269981
264057394	chr10	73270662	73270885	73270680	73270863	CDH23	NM_052836	9	13	5	+	73270711	73270758
267043519	chr10	73270798	73271018	73270820	73270997	CDH23	NM_052836	9	13	6	+	73270877	73270969
261833522	chr10	73326469	73326688	73326493	73326668	CDH23	NM_052836	9	13	7	+	73326499	73326693
261848789	chr10	73326646	73326843	73326667	73326815	CDH23	NM_052836	9	13	7	+	73326499	73326693
254491316	chr10	73330510	73330712	73330533	73330689	CDH23	NM_052836	9	13	8	+	73330547	73330675
265278632	chr10	73337640	73337830	73337663	73337809	CDH23	NM_052836	9	13	9	+	73337671	73337749
265718574	chr10	73375228	73375439	73375249	73375419	CDH23	NM_052836	9	13	10	+	73375261	73375373
255251436	chr10	73376910	73377130	73376931	73377108	CDH23	NM_052836	9	13	11	+	73376962	73377150
255279173	chr10	73377055	73377261	73377078	73377239	CDH23	NM_052836	9	13	11	+	73376962	73377150
258039902	chr10	73405552	73405769	73405574	73405747	CDH23	NM_052836	9	13	12	+	73405582	73405737
266613275	chr10	73406172	73406372	73406192	73406352	CDH23	NM_052836	9	13	13	+	73406216	73407219
266640988	chr10	73406326	73406547	73406346	73406525	CDH23	NM_052836	9	13	13	+	73406216	73407219
264155120	chr12	88534848	88535028	88534878	88535001	CEP290	NM_025114	1	54	2	-	88534983	88535111
264156791	chr12	88534971	88535124	88534999	88535101	CEP290	NM_025114	1	54	2	-	88534983	88535111
254923382	chr12	88534623	88534832	88534654	88534804	CEP290	NM_025114	1	54	3	-	88534733	88534810
260610601	chr12	88533104	88533322	88533133	88533297	CEP290	NM_025114	1	54	4	-	88533272	88533341
266325855	chr12	88532915	88533131	88532942	88533102	CEP290	NM_025114	1	54	5	-	88532922	88532968
257010803	chr12	88530368	88530552	88530392	88530531	CEP290	NM_025114	1	54	6	-	88530420	88530563
257014785	chr12	88530504	88530634	88530532	88530609	CEP290	NM_025114	1	54	6	-	88530420	88530563
255104064	chr12	88524784	88525001	88524812	88524975	CEP290	NM_025114	1	54	7	-	88524942	88524995
264865511	chr12	88524143	88524367	88524172	88524344	CEP290	NM_025114	1	54	8	-	88524322	88524342
264868488	chr12	88524193	88524379	88524220	88524350	CEP290	NM_025114	1	54	8	-	88524322	88524342
254009311	chr12	88524004	88524204	88524031	88524176	CEP290	NM_025114	1	54	9	-	88524045	88524197
264865511	chr12	88524143	88524367	88524172	88524344	CEP290	NM_025114	1	54	9	-	88524045	88524197
261993725	chr12	88523363	88523581	88523394	88523554	CEP290	NM_025114	1	54	10	-	88523471	88523653
261994943	chr12	88523522	88523745	88523550	88523722	CEP290	NM_025114	1	54	10	-	88523471	88523653
255990770	chr12	88522558	88522776	88522586	88522747	CEP290	NM_025114	1	54	11	-	88522723	88522812
255990823	chr12	88522721	88522857	88522749	88522829	CEP290	NM_025114	1	54	11	-	88522723	88522812
261110657	chr12	88519935	88520159	88519958	88520132	CEP290	NM_025114	1	54	12	-	88520093	88520215
253786203	chr12	88519093	88519280	88519117	88519254	CEP290	NM_025114	1	54	13	-	88519023	88519146
255415664	chr12	88514708	88514839	88514734	88514811	CEP290	NM_025114	1	54	14	-	88514774	88514943
255417541	chr12	88514785	88515009	88514812	88514981	CEP290	NM_025114	1	54	14	-	88514774	88514943
266925051	chr12	88513842	88514045	88513866	88514017	CEP290	NM_025114	1	54	15	-	88513891	88514053
266929838	chr12	88513901	88514074	88513928	88514041	CEP290	NM_025114	1	54	15	-	88513891	88514053
266929850	chr12	88514021	88514163	88514046	88514131	CEP290	NM_025114	1	54	15	-	88513891	88514053
266752353	chr12	88512244	88512454	88512274	88512427	CEP290	NM_025114	1	54	16	-	88512420	88512520
266766107	chr12	88512402	88512602	88512424	88512574	CEP290	NM_025114	1	54	16	-	88512420	88512520

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
255474517	chr12	88512081	88512301	88512104	88512273	CEP290	NM_025114	1	54	17	-	88512260	88512347
266752353	chr12	88512244	88512454	88512274	88512427	CEP290	NM_025114	1	54	17	-	88512260	88512347
258798047	chr12	88510876	88511065	88510905	88511037	CEP290	NM_025114	1	54	18	-	88510810	88510922
263717271	chr12	88508716	88508924	88508742	88508895	CEP290	NM_025114	1	54	19	-	88508875	88508959
263718970	chr12	88508882	88509096	88508909	88509070	CEP290	NM_025114	1	54	19	-	88508875	88508959
265566086	chr12	88508249	88508375	88508275	88508347	CEP290	NM_025114	1	54	20	-	88508197	88508339
263868400	chr12	88505466	88505597	88505494	88505575	CEP290	NM_025114	1	54	21	-	88505471	88505635
263871094	chr12	88505551	88505753	88505576	88505725	CEP290	NM_025114	1	54	21	-	88505471	88505635
256688832	chr12	88504837	88505061	88504864	88505035	CEP290	NM_025114	1	54	22	-	88504979	88505128
256690543	chr12	88505008	88505164	88505037	88505137	CEP290	NM_025114	1	54	22	-	88504979	88505128
261270235	chr12	88502863	88503087	88502891	88503059	CEP290	NM_025114	1	54	23	-	88502843	88502958
253977956	chr12	88500649	88500869	88500673	88500840	CEP290	NM_025114	1	54	24	-	88500773	88500875
253988776	chr12	88500795	88500991	88500819	88500962	CEP290	NM_025114	1	54	24	-	88500773	88500875
253977956	chr12	88500649	88500869	88500673	88500840	CEP290	NM_025114	1	54	25	-	88500452	88500682
258544841	chr12	88500476	88500669	88500502	88500641	CEP290	NM_025114	1	54	25	-	88500452	88500682
258559163	chr12	88500544	88500708	88500573	88500680	CEP290	NM_025114	1	54	25	-	88500452	88500682
262012757	chr12	88496576	88496768	88496604	88496740	CEP290	NM_025114	1	54	26	-	88496615	88496788
262028671	chr12	88496713	88496850	88496741	88496827	CEP290	NM_025114	1	54	26	-	88496615	88496788
255323413	chr12	88490495	88490718	88490523	88490690	CEP290	NM_025114	1	54	27	-	88490665	88490776
255323449	chr12	88490674	88490844	88490694	88490816	CEP290	NM_025114	1	54	27	-	88490665	88490776
259342823	chr12	88487446	88487644	88487474	88487624	CEP290	NM_025114	1	54	28	-	88487547	88487752
259357418	chr12	88487597	88487761	88487624	88487734	CEP290	NM_025114	1	54	28	-	88487547	88487752
260179072	chr12	88486370	88486525	88486399	88486501	CEP290	NM_025114	1	54	29	-	88486458	88486609
260179443	chr12	88486441	88486588	88486470	88486566	CEP290	NM_025114	1	54	29	-	88486458	88486609
260189127	chr12	88486538	88486716	88486567	88486689	CEP290	NM_025114	1	54	29	-	88486458	88486609
264942688	chr12	88484427	88484561	88484453	88484534	CEP290	NM_025114	1	54	30	-	88484505	88484616
264945352	chr12	88484513	88484734	88484535	88484706	CEP290	NM_025114	1	54	30	-	88484505	88484616
262084306	chr12	88482807	88483027	88482830	88483002	CEP290	NM_025114	1	54	31	-	88482809	88483264
262129826	chr12	88482980	88483201	88483003	88483179	CEP290	NM_025114	1	54	31	-	88482809	88483264
262251391	chr12	88483152	88483372	88483180	88483344	CEP290	NM_025114	1	54	31	-	88482809	88483264
266666741	chr12	88481557	88481714	88481585	88481685	CEP290	NM_025114	1	54	32	-	88481557	88481721
266666952	chr12	88481584	88481738	88481612	88481705	CEP290	NM_025114	1	54	32	-	88481557	88481721
257157294	chr12	88480108	88480322	88480136	88480297	CEP290	NM_025114	1	54	33	-	88480168	88480275
265283692	chr12	88479715	88479917	88479740	88479894	CEP290	NM_025114	1	54	34	-	88479816	88479950
265291961	chr12	88479867	88479999	88479895	88479975	CEP290	NM_025114	1	54	34	-	88479816	88479950
256200857	chr12	88478216	88478436	88478244	88478408	CEP290	NM_025114	1	54	35	-	88478363	88478629
256204296	chr12	88478368	88478513	88478396	88478488	CEP290	NM_025114	1	54	35	-	88478363	88478629
256206651	chr12	88478465	88478634	88478489	88478605	CEP290	NM_025114	1	54	35	-	88478363	88478629
256206705	chr12	88478593	88478816	88478622	88478788	CEP290	NM_025114	1	54	35	-	88478363	88478629
263797526	chr12	88477465	88477681	88477487	88477653	CEP290	NM_025114	1	54	36	-	88477624	88477731
263800070	chr12	88477619	88477749	88477644	88477722	CEP290	NM_025114	1	54	36	-	88477624	88477731

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263800397	chr12	88477695	88477891	88477723	88477862	CEP290	NM_025114	1	54	36	-	88477624	88477731
336400623	chr12	88476767	88476913	88476800	88476885	CEP290	NM_025114	1	54	37	-	88476808	88477007
336400667	chr12	88476773	88476914	88476806	88476887	CEP290	NM_025114	1	54	37	-	88476808	88477007
336401109	chr12	88476938	88477081	88476961	88477048	CEP290	NM_025114	1	54	37	-	88476808	88477007
253786129	chr12	88473889	88474034	88473920	88474007	CEP290	NM_025114	1	54	38	-	88473959	88474172
253789588	chr12	88473982	88474179	88474008	88474154	CEP290	NM_025114	1	54	38	-	88473959	88474172
257348984	chr12	88472716	88472899	88472742	88472871	CEP290	NM_025114	1	54	39	-	88472869	88473006
257364253	chr12	88472851	88473007	88472872	88472989	CEP290	NM_025114	1	54	39	-	88472869	88473006
257373173	chr12	88472972	88473164	88472994	88473131	CEP290	NM_025114	1	54	39	-	88472869	88473006
258522617	chr12	88471301	88471506	88471334	88471478	CEP290	NM_025114	1	54	40	-	88471474	88471695
258522853	chr12	88471563	88471750	88471589	88471718	CEP290	NM_025114	1	54	40	-	88471474	88471695
254310757	chr12	88470880	88471059	88470909	88471032	CEP290	NM_025114	1	54	41	-	88470999	88471121
254314838	chr12	88471006	88471226	88471034	88471199	CEP290	NM_025114	1	54	41	-	88470999	88471121
264091007	chr12	88465485	88465655	88465518	88465627	CEP290	NM_025114	1	54	42	-	88465558	88465703
264092387	chr12	88465603	88465739	88465626	88465714	CEP290	NM_025114	1	54	42	-	88465558	88465703
258857436	chr12	88465017	88465177	88465044	88465152	CEP290	NM_025114	1	54	43	-	88465071	88465226
258870436	chr12	88465126	88465283	88465153	88465257	CEP290	NM_025114	1	54	43	-	88465071	88465226
265735203	chr12	88462210	88462433	88462238	88462413	CEP290	NM_025114	1	54	44	-	88462299	88462422
262698536	chr12	88457700	88457880	88457728	88457852	CEP290	NM_025114	1	54	45	-	88457758	88457892
262699129	chr12	88457828	88458034	88457853	88458010	CEP290	NM_025114	1	54	45	-	88457758	88457892
262082955	chr12	88456406	88456617	88456433	88456590	CEP290	NM_025114	1	54	46	-	88456469	88456555
263532772	chr12	88454673	88454846	88454701	88454818	CEP290	NM_025114	1	54	47	-	88454607	88454771
253794539	chr12	88453577	88453788	88453604	88453761	CEP290	NM_025114	1	54	48	-	88453675	88453797
254412240	chr12	88452509	88452733	88452536	88452705	CEP290	NM_025114	1	54	49	-	88452625	88452797
254434273	chr12	88452683	88452907	88452706	88452880	CEP290	NM_025114	1	54	49	-	88452625	88452797
265321852	chr12	88449291	88449442	88449319	88449415	CEP290	NM_025114	1	54	50	-	88449353	88449494
265322073	chr12	88449451	88449674	88449483	88449648	CEP290	NM_025114	1	54	50	-	88449353	88449494
263014058	chr12	88448011	88448233	88448038	88448205	CEP290	NM_025114	1	54	51	-	88448117	88448190
261987923	chr12	88447291	88447469	88447317	88447446	CEP290	NM_025114	1	54	52	-	88447429	88447523
261994469	chr12	88447422	88447640	88447447	88447613	CEP290	NM_025114	1	54	52	-	88447429	88447523
257046750	chr12	88444086	88444217	88444111	88444189	CEP290	NM_025114	1	54	53	-	88444131	88444210
257052846	chr12	88444156	88444380	88444184	88444355	CEP290	NM_025114	1	54	53	-	88444131	88444210
266197333	chr12	88442878	88443045	88442905	88443020	CEP290	NM_025114	1	54	54	-	88442790	88443191
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NM_001030311	1	14	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NM_001030311	1	14	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NM_001030311	1	14	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NM_001030311	1	14	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NM_001030311	1	14	2	-	182468564	182468806
255490446	chr2	182438337	182438549	182438359	182438521	CERKL	NM_001030311	1	14	3	-	182438480	182438611
255499283	chr2	182438500	182438694	182438522	182438667	CERKL	NM_001030311	1	14	3	-	182438480	182438611
263795899	chr2	182430654	182430832	182430683	182430811	CERKL	NM_001030311	1	14	4	-	182430785	182430848

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263795998	chr2	182430786	182430922	182430811	182430894	CERKL	NM_001030311	1	14	4	-	182430785	182430848
266767271	chr2	182430086	182430215	182430112	182430187	CERKL	NM_001030311	1	14	5	-	182430160	182430237
266771220	chr2	182430166	182430370	182430188	182430341	CERKL	NM_001030311	1	14	5	-	182430160	182430237
253819444	chr2	182423248	182423471	182423273	182423442	CERKL	NM_001030311	1	14	6	-	182423293	182423435
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NM_001030311	1	14	7	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NM_001030311	1	14	7	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030311	1	14	8	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030311	1	14	8	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NM_001030311	1	14	8	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NM_001030311	1	14	9	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030311	1	14	9	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030311	1	14	9	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030311	1	14	10	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NM_001030311	1	14	11	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030311	1	14	11	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NM_001030311	1	14	12	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NM_001030311	1	14	13	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NM_001030311	1	14	13	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NM_001030311	1	14	14	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NM_001030312	2	10	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NM_001030312	2	10	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NM_001030312	2	10	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NM_001030312	2	10	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NM_001030312	2	10	2	-	182468564	182468806
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NM_001030312	2	10	3	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NM_001030312	2	10	3	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030312	2	10	4	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030312	2	10	4	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NM_001030312	2	10	4	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NM_001030312	2	10	5	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030312	2	10	5	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030312	2	10	5	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030312	2	10	6	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NM_001030312	2	10	7	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030312	2	10	7	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NM_001030312	2	10	8	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NM_001030312	2	10	9	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NM_001030312	2	10	9	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NM_001030312	2	10	10	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NM_001030313	3	11	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NM_001030313	3	11	1	-	182521496	182521834

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NM_001030313	3	11	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NM_001030313	3	11	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NM_001030313	3	11	2	-	182468564	182468806
255490446	chr2	182438337	182438549	182438359	182438521	CERKL	NM_001030313	3	11	3	-	182438480	182438611
255499283	chr2	182438500	182438694	182438522	182438667	CERKL	NM_001030313	3	11	3	-	182438480	182438611
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NM_001030313	3	11	4	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NM_001030313	3	11	4	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030313	3	11	5	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030313	3	11	5	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NM_001030313	3	11	5	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NM_001030313	3	11	6	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001030313	3	11	6	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001030313	3	11	6	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030313	3	11	7	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NM_001030313	3	11	8	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001030313	3	11	8	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NM_001030313	3	11	9	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NM_001030313	3	11	10	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NM_001030313	3	11	10	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NM_001030313	3	11	11	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NM_001160277	4	13	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NM_001160277	4	13	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NM_001160277	4	13	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NM_001160277	4	13	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NM_001160277	4	13	2	-	182468564	182468806
263795899	chr2	182430654	182430832	182430683	182430811	CERKL	NM_001160277	4	13	3	-	182430785	182430848
263795998	chr2	182430786	182430922	182430811	182430894	CERKL	NM_001160277	4	13	3	-	182430785	182430848
266767271	chr2	182430086	182430215	182430112	182430187	CERKL	NM_001160277	4	13	4	-	182430160	182430237
266771220	chr2	182430166	182430370	182430188	182430341	CERKL	NM_001160277	4	13	4	-	182430160	182430237
253819444	chr2	182423248	182423471	182423273	182423442	CERKL	NM_001160277	4	13	5	-	182423293	182423435
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NM_001160277	4	13	6	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NM_001160277	4	13	6	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001160277	4	13	7	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001160277	4	13	7	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NM_001160277	4	13	7	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NM_001160277	4	13	8	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_001160277	4	13	8	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_001160277	4	13	8	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001160277	4	13	9	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NM_001160277	4	13	10	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_001160277	4	13	10	-	182412345	182412453

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NM_001160277	4	13	11	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NM_001160277	4	13	12	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NM_001160277	4	13	12	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NM_001160277	4	13	13	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NM_201548	5	13	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NM_201548	5	13	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NM_201548	5	13	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NM_201548	5	13	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NM_201548	5	13	2	-	182468564	182468806
255490446	chr2	182438337	182438549	182438359	182438521	CERKL	NM_201548	5	13	3	-	182438480	182438611
255499283	chr2	182438500	182438694	182438522	182438667	CERKL	NM_201548	5	13	3	-	182438480	182438611
263795899	chr2	182430654	182430832	182430683	182430811	CERKL	NM_201548	5	13	4	-	182430785	182430848
263795998	chr2	182430786	182430922	182430811	182430894	CERKL	NM_201548	5	13	4	-	182430785	182430848
253819444	chr2	182423248	182423471	182423273	182423442	CERKL	NM_201548	5	13	5	-	182423293	182423435
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NM_201548	5	13	6	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NM_201548	5	13	6	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_201548	5	13	7	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_201548	5	13	7	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NM_201548	5	13	7	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NM_201548	5	13	8	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NM_201548	5	13	8	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NM_201548	5	13	8	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_201548	5	13	9	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NM_201548	5	13	10	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NM_201548	5	13	10	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NM_201548	5	13	11	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NM_201548	5	13	12	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NM_201548	5	13	12	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NM_201548	5	13	13	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NR_027689	6	11	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NR_027689	6	11	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NR_027689	6	11	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NR_027689	6	11	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NR_027689	6	11	2	-	182468564	182468806
253819444	chr2	182423248	182423471	182423273	182423442	CERKL	NR_027689	6	11	3	-	182423293	182423435
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NR_027689	6	11	4	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NR_027689	6	11	4	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NR_027689	6	11	5	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NR_027689	6	11	5	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NR_027689	6	11	5	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NR_027689	6	11	6	-	182413272	182413331

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NR_027689	6	11	6	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NR_027689	6	11	6	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NR_027689	6	11	7	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NR_027689	6	11	8	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NR_027689	6	11	8	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NR_027689	6	11	9	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NR_027689	6	11	10	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NR_027689	6	11	10	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NR_027689	6	11	11	-	182401401	182402971
253978663	chr2	182521410	182521583	182521430	182521563	CERKL	NR_027690	7	12	1	-	182521496	182521834
253979701	chr2	182521542	182521717	182521561	182521699	CERKL	NR_027690	7	12	1	-	182521496	182521834
253980985	chr2	182521582	182521798	182521600	182521777	CERKL	NR_027690	7	12	1	-	182521496	182521834
264451323	chr2	182468511	182468689	182468538	182468661	CERKL	NR_027690	7	12	2	-	182468564	182468806
264462988	chr2	182468592	182468757	182468620	182468729	CERKL	NR_027690	7	12	2	-	182468564	182468806
255490446	chr2	182438337	182438549	182438359	182438521	CERKL	NR_027690	7	12	3	-	182438480	182438611
255499283	chr2	182438500	182438694	182438522	182438667	CERKL	NR_027690	7	12	3	-	182438480	182438611
253819444	chr2	182423248	182423471	182423273	182423442	CERKL	NR_027690	7	12	4	-	182423293	182423435
263724826	chr2	182414249	182414458	182414276	182414430	CERKL	NR_027690	7	12	5	-	182414361	182414435
263726078	chr2	182414401	182414540	182414426	182414507	CERKL	NR_027690	7	12	5	-	182414361	182414435
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NR_027690	7	12	6	-	182413407	182413584
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NR_027690	7	12	6	-	182413407	182413584
256119708	chr2	182413412	182413636	182413435	182413608	CERKL	NR_027690	7	12	6	-	182413407	182413584
255049220	chr2	182413100	182413302	182413125	182413275	CERKL	NR_027690	7	12	7	-	182413272	182413331
255053265	chr2	182413257	182413458	182413285	182413434	CERKL	NR_027690	7	12	7	-	182413272	182413331
256093790	chr2	182413244	182413432	182413276	182413408	CERKL	NR_027690	7	12	7	-	182413272	182413331
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NR_027690	7	12	8	-	182412549	182412574
263178331	chr2	182412266	182412490	182412292	182412462	CERKL	NR_027690	7	12	9	-	182412345	182412453
263221028	chr2	182412395	182412619	182412421	182412591	CERKL	NR_027690	7	12	9	-	182412345	182412453
260865767	chr2	182409330	182409512	182409354	182409485	CERKL	NR_027690	7	12	10	-	182409427	182409523
255173443	chr2	182403782	182403946	182403805	182403919	CERKL	NR_027690	7	12	11	-	182403819	182403991
255191386	chr2	182403894	182404045	182403920	182404018	CERKL	NR_027690	7	12	11	-	182403819	182403991
253786883	chr2	182402836	182403054	182402858	182403027	CERKL	NR_027690	7	12	12	-	182401401	182402971
262275112	chr7	117120014	117120233	117120038	117120213	CFTR	NM_000492	1	27	1	+	117120017	117120201
254869759	chr7	117144248	117144405	117144276	117144377	CFTR	NM_000492	1	27	2	+	117144307	117144417
259672034	chr7	117148895	117149112	117148920	117149089	CFTR	NM_000492	1	27	3	+	117149088	117149196
259708645	chr7	117149063	117149287	117149090	117149260	CFTR	NM_000492	1	27	3	+	117149088	117149196
263043229	chr7	117170875	117171046	117170901	117171022	CFTR	NM_000492	1	27	4	+	117170953	117171168
263060752	chr7	117170998	117171217	117171021	117171189	CFTR	NM_000492	1	27	4	+	117170953	117171168
256885320	chr7	117174330	117174487	117174353	117174459	CFTR	NM_000492	1	27	5	+	117174330	117174419
266080801	chr7	117175169	117175376	117175192	117175355	CFTR	NM_000492	1	27	6	+	117175302	117175465
266091526	chr7	117175336	117175550	117175356	117175523	CFTR	NM_000492	1	27	6	+	117175302	117175465

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256851407	chr7	117176594	117176814	117176619	117176787	CFTR	NM_000492	1	27	7	+	117176602	117176727
255257887	chr7	117180153	117180316	117180177	117180289	CFTR	NM_000492	1	27	8	+	117180154	117180400
255286312	chr7	117180263	117180487	117180290	117180459	CFTR	NM_000492	1	27	8	+	117180154	117180400
259606595	chr7	117181981	117182160	117182014	117182137	CFTR	NM_000492	1	27	9	+	117182070	117182162
259606613	chr7	117182110	117182286	117182138	117182258	CFTR	NM_000492	1	27	9	+	117182070	117182162
258162971	chr7	117188581	117188805	117188607	117188779	CFTR	NM_000492	1	27	10	+	117188695	117188877
258176514	chr7	117188756	117188897	117188780	117188871	CFTR	NM_000492	1	27	10	+	117188695	117188877
255995424	chr7	117199437	117199614	117199462	117199586	CFTR	NM_000492	1	27	11	+	117199518	117199709
256018109	chr7	117199560	117199763	117199587	117199735	CFTR	NM_000492	1	27	11	+	117199518	117199709
263693016	chr7	117227720	117227922	117227746	117227894	CFTR	NM_000492	1	27	12	+	117227793	117227887
258929852	chr7	117230350	117230568	117230378	117230543	CFTR	NM_000492	1	27	13	+	117230407	117230493
266684436	chr7	117231802	117232022	117231829	117231993	CFTR	NM_000492	1	27	14	+	117231988	117232711
266684983	chr7	117231980	117232166	117232008	117232139	CFTR	NM_000492	1	27	14	+	117231988	117232711
266693851	chr7	117232115	117232251	117232140	117232225	CFTR	NM_000492	1	27	14	+	117231988	117232711
266705493	chr7	117232203	117232405	117232226	117232379	CFTR	NM_000492	1	27	14	+	117231988	117232711
266711528	chr7	117232519	117232741	117232540	117232718	CFTR	NM_000492	1	27	14	+	117231988	117232711
266715297	chr7	117232356	117232563	117232380	117232539	CFTR	NM_000492	1	27	14	+	117231988	117232711
266983730	chr7	117234915	117235110	117234942	117235082	CFTR	NM_000492	1	27	15	+	117234984	117235112
266986426	chr7	117235021	117235181	117235049	117235148	CFTR	NM_000492	1	27	15	+	117234984	117235112
258624818	chr7	117242812	117242953	117242833	117242924	CFTR	NM_000492	1	27	16	+	117242880	117242917
260068498	chr7	117243536	117243698	117243562	117243674	CFTR	NM_000492	1	27	17	+	117243586	117243836
260127814	chr7	117243651	117243872	117243675	117243843	CFTR	NM_000492	1	27	17	+	117243586	117243836
263115945	chr7	117246617	117246808	117246643	117246780	CFTR	NM_000492	1	27	18	+	117246728	117246807
263124388	chr7	117246761	117246917	117246784	117246889	CFTR	NM_000492	1	27	18	+	117246728	117246807
263206634	chr7	117250506	117250640	117250530	117250614	CFTR	NM_000492	1	27	19	+	117250573	117250723
263227514	chr7	117250593	117250753	117250615	117250728	CFTR	NM_000492	1	27	19	+	117250573	117250723
264223416	chr7	117251482	117251687	117251504	117251658	CFTR	NM_000492	1	27	20	+	117251635	117251862
264239055	chr7	117251635	117251769	117251659	117251742	CFTR	NM_000492	1	27	20	+	117251635	117251862
264249771	chr7	117251719	117251864	117251743	117251836	CFTR	NM_000492	1	27	20	+	117251635	117251862
264254203	chr7	117251815	117252026	117251842	117251997	CFTR	NM_000492	1	27	20	+	117251635	117251862
254197381	chr7	117254575	117254772	117254599	117254746	CFTR	NM_000492	1	27	21	+	117254667	117254767
265796082	chr7	117267437	117267624	117267463	117267600	CFTR	NM_000492	1	27	22	+	117267576	117267824
265804838	chr7	117267579	117267712	117267601	117267684	CFTR	NM_000492	1	27	22	+	117267576	117267824
265835401	chr7	117267657	117267856	117267685	117267829	CFTR	NM_000492	1	27	22	+	117267576	117267824
265591648	chr7	117282435	117282622	117282463	117282595	CFTR	NM_000492	1	27	23	+	117282492	117282647
265597349	chr7	117282573	117282796	117282596	117282768	CFTR	NM_000492	1	27	23	+	117282492	117282647
257686010	chr7	117292762	117292981	117292789	117292952	CFTR	NM_000492	1	27	24	+	117292896	117292985
257686509	chr7	117292928	117293149	117292953	117293126	CFTR	NM_000492	1	27	24	+	117292896	117292985
259433108	chr7	117304566	117304784	117304594	117304761	CFTR	NM_000492	1	27	25	+	117304742	117304914
259465766	chr7	117304741	117304955	117304762	117304927	CFTR	NM_000492	1	27	25	+	117304742	117304914
266819342	chr7	117305356	117305576	117305379	117305551	CFTR	NM_000492	1	27	26	+	117305513	117305618

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266822086	chr7	117305530	117305706	117305558	117305680	CFTR	NM_000492	1	27	26	+	117305513	117305618
265397991	chr7	117306795	117307017	117306821	117306995	CFTR	NM_000492	1	27	27	+	117306962	117308718
265471177	chr7	117306975	117307198	117306996	117307175	CFTR	NM_000492	1	27	27	+	117306962	117308718
258800042	chr10	50822322	50822543	50822339	50822526	CHAT	NM_001142929	1	15	1	+	50822083	50822521
262613924	chr10	50822128	50822352	50822149	50822332	CHAT	NM_001142929	1	15	1	+	50822083	50822521
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_001142929	1	15	2	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_001142929	1	15	3	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_001142929	1	15	3	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_001142929	1	15	4	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_001142929	1	15	5	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_001142929	1	15	6	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_001142929	1	15	6	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_001142929	1	15	7	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_001142929	1	15	7	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_001142929	1	15	8	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_001142929	1	15	8	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_001142929	1	15	9	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_001142929	1	15	10	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_001142929	1	15	10	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_001142929	1	15	11	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_001142929	1	15	11	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_001142929	1	15	12	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_001142929	1	15	13	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_001142929	1	15	14	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_001142929	1	15	15	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_001142929	1	15	15	+	50872823	50873150
258800042	chr10	50822322	50822543	50822339	50822526	CHAT	NM_001142933	2	16	1	+	50822083	50822521
262613924	chr10	50822128	50822352	50822149	50822332	CHAT	NM_001142933	2	16	1	+	50822083	50822521
263710523	chr10	50823977	50824168	50823998	50824144	CHAT	NM_001142933	2	16	2	+	50824069	50824138
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_001142933	2	16	3	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_001142933	2	16	4	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_001142933	2	16	4	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_001142933	2	16	5	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_001142933	2	16	6	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_001142933	2	16	7	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_001142933	2	16	7	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_001142933	2	16	8	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_001142933	2	16	8	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_001142933	2	16	9	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_001142933	2	16	9	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_001142933	2	16	10	+	50856553	50856653

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_001142933	2	16	11	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_001142933	2	16	11	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_001142933	2	16	12	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_001142933	2	16	12	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_001142933	2	16	13	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_001142933	2	16	14	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_001142933	2	16	15	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_001142933	2	16	16	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_001142933	2	16	16	+	50872823	50873150
258800042	chr10	50822322	50822543	50822339	50822526	CHAT	NM_001142934	3	16	1	+	50822083	50822521
262613924	chr10	50822128	50822352	50822149	50822332	CHAT	NM_001142934	3	16	1	+	50822083	50822521
263710523	chr10	50823977	50824168	50823998	50824144	CHAT	NM_001142934	3	16	2	+	50824069	50824138
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_001142934	3	16	3	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_001142934	3	16	4	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_001142934	3	16	4	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_001142934	3	16	5	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_001142934	3	16	6	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_001142934	3	16	7	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_001142934	3	16	7	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_001142934	3	16	8	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_001142934	3	16	8	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_001142934	3	16	9	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_001142934	3	16	9	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_001142934	3	16	10	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_001142934	3	16	11	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_001142934	3	16	11	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_001142934	3	16	12	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_001142934	3	16	12	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_001142934	3	16	13	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_001142934	3	16	14	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_001142934	3	16	15	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_001142934	3	16	16	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_001142934	3	16	16	+	50872823	50873150
258800042	chr10	50822322	50822543	50822339	50822526	CHAT	NM_020549	4	15	1	+	50822083	50822521
262613924	chr10	50822128	50822352	50822149	50822332	CHAT	NM_020549	4	15	1	+	50822083	50822521
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_020549	4	15	2	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_020549	4	15	3	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_020549	4	15	3	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_020549	4	15	4	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_020549	4	15	5	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_020549	4	15	6	+	50833519	50833699

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_020549	4	15	6	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_020549	4	15	7	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_020549	4	15	7	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_020549	4	15	8	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_020549	4	15	8	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_020549	4	15	9	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_020549	4	15	10	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_020549	4	15	10	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_020549	4	15	11	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_020549	4	15	11	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_020549	4	15	12	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_020549	4	15	13	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_020549	4	15	14	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_020549	4	15	15	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_020549	4	15	15	+	50872823	50873150
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_020984	5	15	2	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_020984	5	15	3	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_020984	5	15	3	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_020984	5	15	4	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_020984	5	15	5	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_020984	5	15	6	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_020984	5	15	6	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_020984	5	15	7	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_020984	5	15	7	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_020984	5	15	8	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_020984	5	15	8	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_020984	5	15	9	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_020984	5	15	10	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_020984	5	15	10	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_020984	5	15	11	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_020984	5	15	11	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_020984	5	15	12	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_020984	5	15	13	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_020984	5	15	14	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_020984	5	15	15	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_020984	5	15	15	+	50872823	50873150
258800042	chr10	50822322	50822543	50822339	50822526	CHAT	NM_020985	6	16	2	+	50822350	50822521
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_020985	6	16	3	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_020985	6	16	4	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_020985	6	16	4	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_020985	6	16	5	+	50828541	50828659

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_020985	6	16	6	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_020985	6	16	7	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_020985	6	16	7	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_020985	6	16	8	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_020985	6	16	8	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_020985	6	16	9	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_020985	6	16	9	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_020985	6	16	10	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_020985	6	16	11	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_020985	6	16	11	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_020985	6	16	12	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_020985	6	16	12	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_020985	6	16	13	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_020985	6	16	14	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_020985	6	16	15	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_020985	6	16	16	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_020985	6	16	16	+	50872823	50873150
258105607	chr10	50824487	50824675	50824507	50824653	CHAT	NM_020986	7	15	2	+	50824548	50824648
260776656	chr10	50827654	50827868	50827676	50827847	CHAT	NM_020986	7	15	3	+	50827771	50827962
260800401	chr10	50827824	50827998	50827843	50827975	CHAT	NM_020986	7	15	3	+	50827771	50827962
257731247	chr10	50828483	50828698	50828505	50828677	CHAT	NM_020986	7	15	4	+	50828541	50828659
260554039	chr10	50830117	50830242	50830135	50830221	CHAT	NM_020986	7	15	5	+	50830143	50830196
254945293	chr10	50833416	50833637	50833437	50833618	CHAT	NM_020986	7	15	6	+	50833519	50833699
254974328	chr10	50833581	50833783	50833607	50833763	CHAT	NM_020986	7	15	6	+	50833519	50833699
264857009	chr10	50835496	50835697	50835517	50835677	CHAT	NM_020986	7	15	7	+	50835654	50835831
264907981	chr10	50835651	50835872	50835678	50835850	CHAT	NM_020986	7	15	7	+	50835654	50835831
264232239	chr10	50854437	50854608	50854459	50854587	CHAT	NM_020986	7	15	8	+	50854551	50854720
264247313	chr10	50854564	50854787	50854585	50854767	CHAT	NM_020986	7	15	8	+	50854551	50854720
254186843	chr10	50856517	50856736	50856536	50856715	CHAT	NM_020986	7	15	9	+	50856553	50856653
253792759	chr10	50857452	50857663	50857474	50857643	CHAT	NM_020986	7	15	10	+	50857554	50857682
253804655	chr10	50857624	50857753	50857644	50857732	CHAT	NM_020986	7	15	10	+	50857554	50857682
267033688	chr10	50859817	50860035	50859836	50860016	CHAT	NM_020986	7	15	11	+	50859930	50860052
267035884	chr10	50859995	50860219	50860015	50860196	CHAT	NM_020986	7	15	11	+	50859930	50860052
261408848	chr10	50863109	50863328	50863132	50863308	CHAT	NM_020986	7	15	12	+	50863141	50863282
259299795	chr10	50863360	50863532	50863382	50863511	CHAT	NM_020986	7	15	13	+	50863432	50863494
257802553	chr10	50870650	50870869	50870671	50870844	CHAT	NM_020986	7	15	14	+	50870691	50870828
265572299	chr10	50872786	50872955	50872807	50872932	CHAT	NM_020986	7	15	15	+	50872823	50873150
265578912	chr10	50872908	50873122	50872933	50873100	CHAT	NM_020986	7	15	15	+	50872823	50873150
259072591	chr8	61655353	61655519	61655373	61655497	CHD7	NM_017780	1	38	2	+	61653818	61655656
259125762	chr8	61655472	61655687	61655495	61655666	CHD7	NM_017780	1	38	2	+	61653818	61655656
266353615	chr8	61654245	61654408	61654267	61654388	CHD7	NM_017780	1	38	2	+	61653818	61655656

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266369765	chr8	61654364	61654580	61654385	61654560	CHD7	NM_017780	1	38	2	+	61653818	61655656
266380871	chr8	61654843	61655054	61654863	61655032	CHD7	NM_017780	1	38	2	+	61653818	61655656
266396398	chr8	61654538	61654747	61654558	61654727	CHD7	NM_017780	1	38	2	+	61653818	61655656
266423713	chr8	61654660	61654884	61654685	61654862	CHD7	NM_017780	1	38	2	+	61653818	61655656
266452254	chr8	61653899	61654116	61653924	61654093	CHD7	NM_017780	1	38	2	+	61653818	61655656
266467136	chr8	61655006	61655216	61655033	61655194	CHD7	NM_017780	1	38	2	+	61653818	61655656
266522177	chr8	61654071	61654293	61654094	61654275	CHD7	NM_017780	1	38	2	+	61653818	61655656
266541284	chr8	61655174	61655393	61655195	61655372	CHD7	NM_017780	1	38	2	+	61653818	61655656
266874849	chr8	61693469	61693631	61693495	61693609	CHD7	NM_017780	1	38	3	+	61693559	61693989
266903266	chr8	61693589	61693796	61693610	61693768	CHD7	NM_017780	1	38	3	+	61693559	61693989
266933831	chr8	61693736	61693960	61693761	61693937	CHD7	NM_017780	1	38	3	+	61693559	61693989
266946463	chr8	61693912	61694081	61693935	61694059	CHD7	NM_017780	1	38	3	+	61693559	61693989
262458333	chr8	61707503	61707724	61707531	61707701	CHD7	NM_017780	1	38	4	+	61707545	61707686
264124925	chr8	61712920	61713115	61712941	61713089	CHD7	NM_017780	1	38	5	+	61712947	61713084
264219588	chr8	61713969	61714186	61713995	61714160	CHD7	NM_017780	1	38	6	+	61714087	61714152
254139219	chr8	61720749	61720956	61720776	61720931	CHD7	NM_017780	1	38	7	+	61720776	61720831
256131247	chr8	61728814	61729038	61728835	61729017	CHD7	NM_017780	1	38	8	+	61728946	61729060
256139322	chr8	61728965	61729185	61728993	61729161	CHD7	NM_017780	1	38	8	+	61728946	61729060
258526395	chr8	61732471	61732693	61732499	61732668	CHD7	NM_017780	1	38	9	+	61732566	61732649
266720818	chr8	61734328	61734543	61734356	61734515	CHD7	NM_017780	1	38	10	+	61734349	61734486
263395354	chr8	61734528	61734705	61734552	61734678	CHD7	NM_017780	1	38	11	+	61734583	61734704
256908810	chr8	61735005	61735215	61735030	61735194	CHD7	NM_017780	1	38	12	+	61735062	61735305
256928921	chr8	61735174	61735395	61735195	61735374	CHD7	NM_017780	1	38	12	+	61735062	61735305
254555250	chr8	61736381	61736506	61736407	61736486	CHD7	NM_017780	1	38	13	+	61736399	61736575
254572831	chr8	61736465	61736604	61736487	61736580	CHD7	NM_017780	1	38	13	+	61736399	61736575
257123957	chr8	61741080	61741297	61741105	61741272	CHD7	NM_017780	1	38	14	+	61741222	61741365
257156928	chr8	61741250	61741427	61741273	61741401	CHD7	NM_017780	1	38	14	+	61741222	61741365
255784858	chr8	61742827	61743031	61742855	61743005	CHD7	NM_017780	1	38	15	+	61742881	61743136
255793184	chr8	61742977	61743188	61743006	61743163	CHD7	NM_017780	1	38	15	+	61742881	61743136
261459434	chr8	61748546	61748762	61748570	61748741	CHD7	NM_017780	1	38	16	+	61748632	61748842
261546845	chr8	61748721	61748901	61748742	61748875	CHD7	NM_017780	1	38	16	+	61748632	61748842
266506040	chr8	61749347	61749475	61749369	61749447	CHD7	NM_017780	1	38	17	+	61749376	61749571
266523287	chr8	61749425	61749606	61749448	61749578	CHD7	NM_017780	1	38	17	+	61749376	61749571
263764419	chr8	61750214	61750388	61750236	61750360	CHD7	NM_017780	1	38	18	+	61750227	61750394
263776241	chr8	61750339	61750492	61750361	61750464	CHD7	NM_017780	1	38	18	+	61750227	61750394
262396835	chr8	61750469	61750683	61750496	61750655	CHD7	NM_017780	1	38	19	+	61750635	61750814
262411707	chr8	61750631	61750850	61750656	61750824	CHD7	NM_017780	1	38	19	+	61750635	61750814
261271166	chr8	61754270	61754494	61754293	61754470	CHD7	NM_017780	1	38	20	+	61754203	61754313
262200502	chr8	61754132	61754345	61754158	61754318	CHD7	NM_017780	1	38	20	+	61754203	61754313
261271166	chr8	61754270	61754494	61754293	61754470	CHD7	NM_017780	1	38	21	+	61754406	61754611
261376550	chr8	61754450	61754674	61754471	61754646	CHD7	NM_017780	1	38	21	+	61754406	61754611

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256803310	chr8	61757266	61757482	61757290	61757461	CHD7	NM_017780	1	38	22	+	61757423	61757622
256860797	chr8	61757441	61757656	61757462	61757635	CHD7	NM_017780	1	38	22	+	61757423	61757622
258822682	chr8	61757666	61757855	61757689	61757831	CHD7	NM_017780	1	38	23	+	61757809	61757968
258857273	chr8	61757802	61757997	61757826	61757976	CHD7	NM_017780	1	38	23	+	61757809	61757968
254782445	chr8	61761016	61761212	61761038	61761187	CHD7	NM_017780	1	38	24	+	61761074	61761163
257342502	chr8	61761455	61761641	61761477	61761620	CHD7	NM_017780	1	38	25	+	61761610	61761713
257395145	chr8	61761598	61761761	61761621	61761737	CHD7	NM_017780	1	38	25	+	61761610	61761713
262957060	chr8	61763018	61763241	61763039	61763213	CHD7	NM_017780	1	38	26	+	61763052	61763181
263706276	chr8	61763482	61763656	61763510	61763633	CHD7	NM_017780	1	38	27	+	61763591	61763663
266323371	chr8	61763632	61763827	61763656	61763801	CHD7	NM_017780	1	38	27	+	61763591	61763663
266323618	chr8	61763797	61763947	61763822	61763925	CHD7	NM_017780	1	38	28	+	61763821	61763878
261167267	chr8	61764490	61764707	61764519	61764684	CHD7	NM_017780	1	38	29	+	61764578	61764806
261269615	chr8	61764665	61764835	61764685	61764811	CHD7	NM_017780	1	38	29	+	61764578	61764806
256975436	chr8	61764946	61765169	61764969	61765147	CHD7	NM_017780	1	38	30	+	61765057	61765265
256987892	chr8	61765123	61765347	61765148	61765320	CHD7	NM_017780	1	38	30	+	61765057	61765265
258002990	chr8	61765256	61765478	61765282	61765458	CHD7	NM_017780	1	38	31	+	61765388	61766059
258055203	chr8	61765437	61765654	61765459	61765629	CHD7	NM_017780	1	38	31	+	61765388	61766059
258142843	chr8	61765608	61765793	61765630	61765766	CHD7	NM_017780	1	38	31	+	61765388	61766059
258234182	chr8	61765744	61765956	61765767	61765935	CHD7	NM_017780	1	38	31	+	61765388	61766059
266144862	chr8	61765913	61766123	61765936	61766102	CHD7	NM_017780	1	38	31	+	61765388	61766059
257247459	chr8	61766875	61767010	61766900	61766984	CHD7	NM_017780	1	38	32	+	61766922	61767082
257258525	chr8	61766963	61767120	61766985	61767097	CHD7	NM_017780	1	38	32	+	61766922	61767082
265340451	chr8	61768404	61768623	61768432	61768599	CHD7	NM_017780	1	38	33	+	61768534	61768761
265362577	chr8	61768578	61768794	61768600	61768769	CHD7	NM_017780	1	38	33	+	61768534	61768761
255114864	chr8	61768966	61769189	61768989	61769161	CHD7	NM_017780	1	38	34	+	61769004	61769447
255144214	chr8	61769133	61769337	61769159	61769314	CHD7	NM_017780	1	38	34	+	61769004	61769447
255170272	chr8	61769275	61769495	61769299	61769475	CHD7	NM_017780	1	38	34	+	61769004	61769447
254141710	chr8	61773314	61773537	61773339	61773514	CHD7	NM_017780	1	38	35	+	61773463	61773684
254190152	chr8	61773488	61773683	61773515	61773655	CHD7	NM_017780	1	38	35	+	61773463	61773684
254226882	chr8	61773636	61773823	61773656	61773800	CHD7	NM_017780	1	38	35	+	61773463	61773684
264011624	chr8	61774668	61774800	61774693	61774774	CHD7	NM_017780	1	38	36	+	61774755	61774895
264016701	chr8	61774752	61774928	61774775	61774903	CHD7	NM_017780	1	38	36	+	61774755	61774895
261837813	chr8	61774946	61775166	61774972	61775144	CHD7	NM_017780	1	38	37	+	61775107	61775211
261854525	chr8	61775122	61775291	61775144	61775262	CHD7	NM_017780	1	38	37	+	61775107	61775211
263089665	chr8	61778034	61778226	61778062	61778200	CHD7	NM_017780	1	38	38	+	61777575	61780586
263145003	chr8	61778171	61778394	61778192	61778372	CHD7	NM_017780	1	38	38	+	61777575	61780586
263212525	chr8	61778335	61778559	61778361	61778533	CHD7	NM_017780	1	38	38	+	61777575	61780586
267053487	chr8	61777434	61777614	61777461	61777594	CHD7	NM_017780	1	38	38	+	61777575	61780586
267079227	chr8	61777572	61777796	61777595	61777771	CHD7	NM_017780	1	38	38	+	61777575	61780586
267089049	chr8	61777753	61777976	61777772	61777954	CHD7	NM_017780	1	38	38	+	61777575	61780586
267117026	chr8	61777934	61778086	61777953	61778061	CHD7	NM_017780	1	38	38	+	61777575	61780586

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226152245	chr22	29130379	29130603	29130402	29130581	CHEK2	NM_001005735	1	16	2	-	29130391	29130715
226173874	chr22	29130550	29130763	29130571	29130741	CHEK2	NM_001005735	1	16	2	-	29130391	29130715
226111566	chr22	29121180	29121399	29121205	29121374	CHEK2	NM_001005735	1	16	4	-	29121231	29121355
253752693	chr22	29120846	29121049	29120871	29121021	CHEK2	NM_001005735	1	16	5	-	29120965	29121112
253754549	chr22	29120997	29121203	29121022	29121176	CHEK2	NM_001005735	1	16	5	-	29120965	29121112
226235955	chr22	29115310	29115534	29115337	29115507	CHEK2	NM_001005735	1	16	6	-	29115383	29115473
225437160	chr22	29107870	29108071	29107899	29108043	CHEK2	NM_001005735	1	16	7	-	29107897	29108005
328640719	chr22	29107742	29107921	29107767	29107898	CHEK2	NM_001005735	1	16	7	-	29107897	29108005
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_001005735	1	16	8	-	29105994	29106047
225434981	chr22	29099400	29099603	29099422	29099577	CHEK2	NM_001005735	1	16	9	-	29099493	29099554
226242301	chr22	29095740	29095961	29095760	29095940	CHEK2	NM_001005735	1	16	10	-	29095826	29095925
226443845	chr22	29092794	29093018	29092819	29092994	CHEK2	NM_001005735	1	16	11	-	29092889	29092975
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_001005735	1	16	12	-	29091698	29091861
226431231	chr22	29091769	29091949	29091790	29091927	CHEK2	NM_001005735	1	16	12	-	29091698	29091861
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_001005735	1	16	13	-	29091115	29091230
225795695	chr22	29089969	29090183	29089988	29090159	CHEK2	NM_001005735	1	16	14	-	29090020	29090105
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_001005735	1	16	15	-	29085123	29085203
329659848	chr22	29084965	29085188	29084987	29085160	CHEK2	NM_001005735	1	16	15	-	29085123	29085203
225923247	chr22	29083865	29084070	29083886	29084047	CHEK2	NM_001005735	1	16	16	-	29083731	29083974
226152245	chr22	29130379	29130603	29130402	29130581	CHEK2	NM_007194	2	15	2	-	29130391	29130715
226173874	chr22	29130550	29130763	29130571	29130741	CHEK2	NM_007194	2	15	2	-	29130391	29130715
226111566	chr22	29121180	29121399	29121205	29121374	CHEK2	NM_007194	2	15	3	-	29121231	29121355
253752693	chr22	29120846	29121049	29120871	29121021	CHEK2	NM_007194	2	15	4	-	29120965	29121112
253754549	chr22	29120997	29121203	29121022	29121176	CHEK2	NM_007194	2	15	4	-	29120965	29121112
226235955	chr22	29115310	29115534	29115337	29115507	CHEK2	NM_007194	2	15	5	-	29115383	29115473
225437160	chr22	29107870	29108071	29107899	29108043	CHEK2	NM_007194	2	15	6	-	29107897	29108005
328640719	chr22	29107742	29107921	29107767	29107898	CHEK2	NM_007194	2	15	6	-	29107897	29108005
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_007194	2	15	7	-	29105994	29106047
225434981	chr22	29099400	29099603	29099422	29099577	CHEK2	NM_007194	2	15	8	-	29099493	29099554
226242301	chr22	29095740	29095961	29095760	29095940	CHEK2	NM_007194	2	15	9	-	29095826	29095925
226443845	chr22	29092794	29093018	29092819	29092994	CHEK2	NM_007194	2	15	10	-	29092889	29092975
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_007194	2	15	11	-	29091698	29091861
226431231	chr22	29091769	29091949	29091790	29091927	CHEK2	NM_007194	2	15	11	-	29091698	29091861
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_007194	2	15	12	-	29091115	29091230
225795695	chr22	29089969	29090183	29089988	29090159	CHEK2	NM_007194	2	15	13	-	29090020	29090105
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_007194	2	15	14	-	29085123	29085203
329659848	chr22	29084965	29085188	29084987	29085160	CHEK2	NM_007194	2	15	14	-	29085123	29085203
225923247	chr22	29083865	29084070	29083886	29084047	CHEK2	NM_007194	2	15	15	-	29083731	29083974
226152245	chr22	29130379	29130603	29130402	29130581	CHEK2	NM_145862	3	14	2	-	29130391	29130715
226173874	chr22	29130550	29130763	29130571	29130741	CHEK2	NM_145862	3	14	2	-	29130391	29130715
226111566	chr22	29121180	29121399	29121205	29121374	CHEK2	NM_145862	3	14	3	-	29121231	29121355

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253752693	chr22	29120846	29121049	29120871	29121021	CHEK2	NM_145862	3	14	4	-	29120965	29121112
253754549	chr22	29120997	29121203	29121022	29121176	CHEK2	NM_145862	3	14	4	-	29120965	29121112
226235955	chr22	29115310	29115534	29115337	29115507	CHEK2	NM_145862	3	14	5	-	29115383	29115473
225437160	chr22	29107870	29108071	29107899	29108043	CHEK2	NM_145862	3	14	6	-	29107897	29108005
328640719	chr22	29107742	29107921	29107767	29107898	CHEK2	NM_145862	3	14	6	-	29107897	29108005
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_145862	3	14	7	-	29105994	29106047
225434981	chr22	29099400	29099603	29099422	29099577	CHEK2	NM_145862	3	14	8	-	29099493	29099554
226242301	chr22	29095740	29095961	29095760	29095940	CHEK2	NM_145862	3	14	9	-	29095826	29095925
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_145862	3	14	10	-	29091698	29091861
226431231	chr22	29091769	29091949	29091790	29091927	CHEK2	NM_145862	3	14	10	-	29091698	29091861
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_145862	3	14	11	-	29091115	29091230
225795695	chr22	29089969	29090183	29089988	29090159	CHEK2	NM_145862	3	14	12	-	29090020	29090105
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_145862	3	14	13	-	29085123	29085203
329659848	chr22	29084965	29085188	29084987	29085160	CHEK2	NM_145862	3	14	13	-	29085123	29085203
225923247	chr22	29083865	29084070	29083886	29084047	CHEK2	NM_145862	3	14	14	-	29083731	29083974
256020848	chrX	85302344	85302568	85302365	85302542	CHM	NM_000390	1	15	1	-	85302488	85302566
264816293	chrX	85282336	85282541	85282367	85282519	CHM	NM_000390	1	15	2	-	85282495	85282561
264817582	chrX	85282493	85282680	85282517	85282659	CHM	NM_000390	1	15	2	-	85282495	85282561
255826748	chrX	85236631	85236789	85236659	85236763	CHM	NM_000390	1	15	3	-	85236741	85236813
255832155	chrX	85236741	85236901	85236764	85236873	CHM	NM_000390	1	15	3	-	85236741	85236813
259671123	chrX	85233646	85233835	85233671	85233813	CHM	NM_000390	1	15	4	-	85233771	85233895
259703450	chrX	85233786	85233939	85233814	85233912	CHM	NM_000390	1	15	4	-	85233771	85233895
255728133	chrX	85218623	85218845	85218648	85218817	CHM	NM_000390	1	15	5	-	85218670	85219057
255757818	chrX	85218795	85219019	85218818	85218994	CHM	NM_000390	1	15	5	-	85218670	85219057
255787543	chrX	85218973	85219144	85218995	85219117	CHM	NM_000390	1	15	5	-	85218670	85219057
258704479	chrX	85213815	85213983	85213842	85213955	CHM	NM_000390	1	15	6	-	85213866	85213982
258710392	chrX	85213873	85214001	85213895	85213971	CHM	NM_000390	1	15	6	-	85213866	85213982
257107914	chrX	85212776	85212972	85212800	85212944	CHM	NM_000390	1	15	7	-	85212860	85212980
257109859	chrX	85212917	85213095	85212945	85213071	CHM	NM_000390	1	15	7	-	85212860	85212980
261232120	chrX	85211126	85211346	85211151	85211320	CHM	NM_000390	1	15	8	-	85211158	85211383
261266070	chrX	85211293	85211492	85211317	85211467	CHM	NM_000390	1	15	8	-	85211158	85211383
253990020	chrX	85166294	85166508	85166320	85166478	CHM	NM_000390	1	15	9	-	85166266	85166343
254926060	chrX	85156058	85156269	85156078	85156241	CHM	NM_000390	1	15	10	-	85156089	85156193
253786879	chrX	85155640	85155800	85155669	85155776	CHM	NM_000390	1	15	11	-	85155651	85155714
263541303	chrX	85149120	85149338	85149144	85149310	CHM	NM_000390	1	15	12	-	85149193	85149289
256876968	chrX	85133871	85134051	85133895	85134024	CHM	NM_000390	1	15	13	-	85133970	85134068
256880939	chrX	85133992	85134186	85134020	85134163	CHM	NM_000390	1	15	13	-	85133970	85134068
265912573	chrX	85127948	85128146	85127977	85128118	CHM	NM_000390	1	15	14	-	85128057	85128217
265914980	chrX	85128097	85128307	85128119	85128281	CHM	NM_000390	1	15	14	-	85128057	85128217
256635386	chrX	85119479	85119703	85119507	85119681	CHM	NM_000390	1	15	15	-	85116185	85119826
265488851	chrX	85119659	85119883	85119682	85119856	CHM	NM_000390	1	15	15	-	85116185	85119826

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
256020848	chrX	85302344	85302568	85302365	85302542	CHM	NM_001145414	2	5	1	-	85302488	85302566
264816293	chrX	85282336	85282541	85282367	85282519	CHM	NM_001145414	2	5	2	-	85282495	85282561
264817582	chrX	85282493	85282680	85282517	85282659	CHM	NM_001145414	2	5	2	-	85282495	85282561
255826748	chrX	85236631	85236789	85236659	85236763	CHM	NM_001145414	2	5	3	-	85236741	85236813
255832155	chrX	85236741	85236901	85236764	85236873	CHM	NM_001145414	2	5	3	-	85236741	85236813
259671123	chrX	85233646	85233835	85233671	85233813	CHM	NM_001145414	2	5	4	-	85233771	85233895
259703450	chrX	85233786	85233939	85233814	85233912	CHM	NM_001145414	2	5	4	-	85233771	85233895
268202652	chr2	175629021	175629232	175629042	175629213	CHRNA1	NM_000079	1	9	1	-	175629080	175629200
265612886	chr2	175624029	175624243	175624054	175624221	CHRNA1	NM_000079	1	9	2	-	175624216	175624361
269232777	chr2	175624200	175624387	175624222	175624366	CHRNA1	NM_000079	1	9	2	-	175624216	175624361
265609488	chr2	175623970	175624144	175623997	175624116	CHRNA1	NM_000079	1	9	3	-	175624059	175624103
265612886	chr2	175624029	175624243	175624054	175624221	CHRNA1	NM_000079	1	9	3	-	175624059	175624103
260651291	chr2	175622168	175622319	175622190	175622295	CHRNA1	NM_000079	1	9	4	-	175622294	175622403
260674009	chr2	175622275	175622479	175622296	175622451	CHRNA1	NM_000079	1	9	4	-	175622294	175622403
267597478	chr2	175618859	175619037	175618883	175619016	CHRNA1	NM_000079	1	9	5	-	175618947	175619142
267616927	chr2	175618994	175619174	175619017	175619147	CHRNA1	NM_000079	1	9	5	-	175618947	175619142
268420839	chr2	175618125	175618345	175618146	175618324	CHRNA1	NM_000079	1	9	6	-	175618231	175618468
268438419	chr2	175618289	175618506	175618315	175618485	CHRNA1	NM_000079	1	9	6	-	175618231	175618468
263759862	chr2	175614563	175614768	175614590	175614745	CHRNA1	NM_000079	1	9	7	-	175614674	175614897
263785186	chr2	175614722	175614945	175614746	175614920	CHRNA1	NM_000079	1	9	7	-	175614674	175614897
267149356	chr2	175613174	175613333	175613194	175613309	CHRNA1	NM_000079	1	9	8	-	175613308	175613547
267193435	chr2	175613285	175613509	175613310	175613481	CHRNA1	NM_000079	1	9	8	-	175613308	175613547
267200652	chr2	175613426	175613603	175613455	175613581	CHRNA1	NM_000079	1	9	8	-	175613308	175613547
268945734	chr2	175612797	175613016	175612819	175612988	CHRNA1	NM_000079	1	9	9	-	175612323	175612983
268202652	chr2	175629021	175629232	175629042	175629213	CHRNA1	NM_001039523	2	10	1	-	175629080	175629200
265612886	chr2	175624029	175624243	175624054	175624221	CHRNA1	NM_001039523	2	10	2	-	175624216	175624361
269232777	chr2	175624200	175624387	175624222	175624366	CHRNA1	NM_001039523	2	10	2	-	175624216	175624361
265609488	chr2	175623970	175624144	175623997	175624116	CHRNA1	NM_001039523	2	10	3	-	175624059	175624103
265612886	chr2	175624029	175624243	175624054	175624221	CHRNA1	NM_001039523	2	10	3	-	175624059	175624103
260651291	chr2	175622168	175622319	175622190	175622295	CHRNA1	NM_001039523	2	10	5	-	175622294	175622403
260674009	chr2	175622275	175622479	175622296	175622451	CHRNA1	NM_001039523	2	10	5	-	175622294	175622403
267597478	chr2	175618859	175619037	175618883	175619016	CHRNA1	NM_001039523	2	10	6	-	175618947	175619142
267616927	chr2	175618994	175619174	175619017	175619147	CHRNA1	NM_001039523	2	10	6	-	175618947	175619142
268420839	chr2	175618125	175618345	175618146	175618324	CHRNA1	NM_001039523	2	10	7	-	175618231	175618468
268438419	chr2	175618289	175618506	175618315	175618485	CHRNA1	NM_001039523	2	10	7	-	175618231	175618468
263759862	chr2	175614563	175614768	175614590	175614745	CHRNA1	NM_001039523	2	10	8	-	175614674	175614897
263785186	chr2	175614722	175614945	175614746	175614920	CHRNA1	NM_001039523	2	10	8	-	175614674	175614897
267149356	chr2	175613174	175613333	175613194	175613309	CHRNA1	NM_001039523	2	10	9	-	175613308	175613547
267193435	chr2	175613285	175613509	175613310	175613481	CHRNA1	NM_001039523	2	10	9	-	175613308	175613547
267200652	chr2	175613426	175613603	175613455	175613581	CHRNA1	NM_001039523	2	10	9	-	175613308	175613547
268945734	chr2	175612797	175613016	175612819	175612988	CHRNA1	NM_001039523	2	10	10	-	175612323	175612983

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263994656	chr17	7348410	7348577	7348430	7348556	CHRNB1	NM_000747	1	11	1	+	7348406	7348504
265080639	chr17	7348555	7348734	7348575	7348713	CHRNB1	NM_000747	1	11	2	+	7348589	7348728
265091309	chr17	7348690	7348900	7348710	7348879	CHRNB1	NM_000747	1	11	2	+	7348589	7348728
267810877	chr17	7349333	7349495	7349357	7349467	CHRNB1	NM_000747	1	11	3	+	7349388	7349432
268302995	chr17	7350074	7350287	7350096	7350268	CHRNB1	NM_000747	1	11	4	+	7350152	7350261
259869390	chr17	7350328	7350506	7350349	7350484	CHRNB1	NM_000747	1	11	5	+	7350362	7350470
263984359	chr17	7350786	7351009	7350807	7350984	CHRNB1	NM_000747	1	11	6	+	7350822	7350969
268330893	chr17	7351853	7352076	7351874	7352054	CHRNB1	NM_000747	1	11	7	+	7351898	7352107
268352590	chr17	7352034	7352222	7352054	7352199	CHRNB1	NM_000747	1	11	7	+	7351898	7352107
267547038	chr17	7357528	7357746	7357549	7357718	CHRNB1	NM_000747	1	11	8	+	7357616	7357839
267578164	chr17	7357691	7357865	7357719	7357844	CHRNB1	NM_000747	1	11	8	+	7357616	7357839
260994314	chr17	7358574	7358798	7358594	7358780	CHRNB1	NM_000747	1	11	9	+	7358603	7358775
268167175	chr17	7359066	7359286	7359086	7359267	CHRNB1	NM_000747	1	11	10	+	7359113	7359260
267252003	chr17	7359798	7360000	7359820	7359978	CHRNB1	NM_000747	1	11	11	+	7359902	7360932
267272880	chr17	7359956	7360100	7359979	7360073	CHRNB1	NM_000747	1	11	11	+	7359902	7360932
260734496	chr2	233390866	233391065	233390886	233391044	CHRND	NM_000751	1	12	1	+	233390922	233390977
268638293	chr2	233391139	233391310	233391160	233391288	CHRND	NM_000751	1	12	2	+	233391239	233391384
268641959	chr2	233391269	233391448	233391289	233391424	CHRND	NM_000751	1	12	2	+	233391239	233391384
267256189	chr2	233392826	233393032	233392847	233393009	CHRND	NM_000751	1	12	4	+	233392972	233393081
267279549	chr2	233392988	233393199	233393010	233393175	CHRND	NM_000751	1	12	4	+	233392972	233393081
261694880	chr2	233393061	233393274	233393085	233393253	CHRND	NM_000751	1	12	5	+	233393211	233393366
261715605	chr2	233393234	233393438	233393254	233393416	CHRND	NM_000751	1	12	5	+	233393211	233393366
261470555	chr2	233393477	233393696	233393494	233393679	CHRND	NM_000751	1	12	6	+	233393572	233393681
267236161	chr2	233394610	233394823	233394630	233394800	CHRND	NM_000751	1	12	7	+	233394649	233394849
267240056	chr2	233394768	233394974	233394794	233394955	CHRND	NM_000751	1	12	7	+	233394649	233394849
262983084	chr2	233396031	233396254	233396053	233396234	CHRND	NM_000751	1	12	8	+	233396062	233396173
269352973	chr2	233396169	233396382	233396189	233396362	CHRND	NM_000751	1	12	9	+	233396252	233396366
269359408	chr2	233398612	233398803	233398632	233398781	CHRND	NM_000751	1	12	10	+	233398641	233398845
269362952	chr2	233398757	233398882	233398779	233398860	CHRND	NM_000751	1	12	10	+	233398641	233398845
267675837	chr2	233398859	233399080	233398881	233399058	CHRND	NM_000751	1	12	11	+	233398934	233399052
264860996	chr2	233399805	233400023	233399826	233400001	CHRND	NM_000751	1	12	12	+	233399840	233400205
264883903	chr2	233399981	233400139	233400002	233400118	CHRND	NM_000751	1	12	12	+	233399840	233400205
267866970	chr17	4806184	4806399	4806206	4806377	CHRNE	NM_000080	1	12	1	-	4806313	4806369
263327971	chr17	4805870	4806091	4805894	4806068	CHRNE	NM_000080	1	12	2	-	4805916	4806058
267473709	chr17	4805598	4805818	4805621	4805794	CHRNE	NM_000080	1	12	3	-	4805745	4805789
267473709	chr17	4805598	4805818	4805621	4805794	CHRNE	NM_000080	1	12	4	-	4805512	4805621
268124648	chr17	4805361	4805576	4805382	4805554	CHRNE	NM_000080	1	12	4	-	4805512	4805621
268133781	chr17	4805534	4805758	4805554	4805733	CHRNE	NM_000080	1	12	4	-	4805512	4805621
266823400	chr17	4805053	4805256	4805075	4805233	CHRNE	NM_000080	1	12	5	-	4805227	4805382
266828308	chr17	4805213	4805417	4805234	4805395	CHRNE	NM_000080	1	12	5	-	4805227	4805382
268124648	chr17	4805361	4805576	4805382	4805554	CHRNE	NM_000080	1	12	5	-	4805227	4805382

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259187102	chr17	4804700	4804907	4804724	4804886	CHRNE	NM_000080	1	12	6	-	4804820	4804920
259220732	chr17	4804866	4805075	4804887	4805053	CHRNE	NM_000080	1	12	6	-	4804820	4804920
268896821	chr17	4804129	4804351	4804152	4804331	CHRNE	NM_000080	1	12	7	-	4804285	4804485
268898230	chr17	4804170	4804373	4804190	4804350	CHRNE	NM_000080	1	12	7	-	4804285	4804485
268900932	chr17	4804332	4804556	4804351	4804538	CHRNE	NM_000080	1	12	7	-	4804285	4804485
267658374	chr17	4803962	4804182	4803981	4804161	CHRNE	NM_000080	1	12	8	-	4804088	4804202
268896821	chr17	4804129	4804351	4804152	4804331	CHRNE	NM_000080	1	12	8	-	4804088	4804202
268898230	chr17	4804170	4804373	4804190	4804350	CHRNE	NM_000080	1	12	8	-	4804088	4804202
264495586	chr17	4802703	4802916	4802724	4802895	CHRNE	NM_000080	1	12	9	-	4802763	4802877
257665792	chr17	4802545	4802720	4802569	4802697	CHRNE	NM_000080	1	12	10	-	4802493	4802679
264688660	chr17	4802381	4802589	4802398	4802571	CHRNE	NM_000080	1	12	10	-	4802493	4802679
264683586	chr17	4802244	4802427	4802262	4802409	CHRNE	NM_000080	1	12	11	-	4802296	4802402
264688660	chr17	4802381	4802589	4802398	4802571	CHRNE	NM_000080	1	12	11	-	4802296	4802402
265442567	chr17	4801999	4802223	4802022	4802201	CHRNE	NM_000080	1	12	12	-	4801064	4802186
263707074	chr7	143013225	143013421	143013247	143013401	CLCN1	NM_000083	1	23	1	+	143013219	143013485
263718770	chr7	143013374	143013592	143013398	143013566	CLCN1	NM_000083	1	23	1	+	143013219	143013485
268710443	chr7	143016800	143017016	143016825	143016988	CLCN1	NM_000083	1	23	2	+	143016848	143016968
259820389	chr7	143017605	143017817	143017632	143017794	CLCN1	NM_000083	1	23	3	+	143017757	143017888
259892710	chr7	143017773	143017915	143017795	143017894	CLCN1	NM_000083	1	23	3	+	143017757	143017888
268598630	chr7	143018415	143018575	143018436	143018553	CLCN1	NM_000083	1	23	4	+	143018458	143018586
268602374	chr7	143018525	143018748	143018549	143018723	CLCN1	NM_000083	1	23	4	+	143018458	143018586
257656676	chr7	143018748	143018972	143018774	143018952	CLCN1	NM_000083	1	23	5	+	143018808	143018941
262605305	chr7	143020335	143020508	143020354	143020485	CLCN1	NM_000083	1	23	6	+	143020402	143020479
269335807	chr7	143021401	143021625	143021426	143021606	CLCN1	NM_000083	1	23	7	+	143021507	143021585
268074220	chr7	143027704	143027906	143027726	143027884	CLCN1	NM_000083	1	23	8	+	143027865	143027990
268092868	chr7	143027861	143028048	143027885	143028024	CLCN1	NM_000083	1	23	8	+	143027865	143027990
266957036	chr7	143028248	143028469	143028270	143028446	CLCN1	NM_000083	1	23	9	+	143028325	143028409
267792121	chr7	143028587	143028804	143028613	143028776	CLCN1	NM_000083	1	23	10	+	143028644	143028745
267170040	chr7	143029416	143029638	143029440	143029614	CLCN1	NM_000083	1	23	11	+	143029512	143029596
268968223	chr7	143029783	143029994	143029804	143029973	CLCN1	NM_000083	1	23	12	+	143029817	143029966
268236336	chr7	143036256	143036465	143036279	143036440	CLCN1	NM_000083	1	23	13	+	143036346	143036415
267843763	chr7	143036521	143036745	143036543	143036719	CLCN1	NM_000083	1	23	14	+	143036604	143036714
268613228	chr7	143038886	143039107	143038914	143039084	CLCN1	NM_000083	1	23	15	+	143039022	143039235
268633776	chr7	143039063	143039269	143039085	143039243	CLCN1	NM_000083	1	23	15	+	143039022	143039235
261061318	chr7	143039433	143039630	143039453	143039608	CLCN1	NM_000083	1	23	16	+	143039465	143039598
264629187	chr7	143042525	143042744	143042545	143042726	CLCN1	NM_000083	1	23	17	+	143042614	143042855
264641018	chr7	143042707	143042920	143042726	143042900	CLCN1	NM_000083	1	23	17	+	143042614	143042855
267707764	chr7	143043198	143043409	143043220	143043386	CLCN1	NM_000083	1	23	18	+	143043233	143043344
264811166	chr7	143043577	143043781	143043599	143043758	CLCN1	NM_000083	1	23	19	+	143043672	143043751
263152647	chr7	143043852	143044075	143043879	143044053	CLCN1	NM_000083	1	23	20	+	143044004	143044042
267592437	chr7	143047423	143047645	143047446	143047623	CLCN1	NM_000083	1	23	21	+	143047465	143047569

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268775415	chr7	143047559	143047776	143047580	143047755	CLCN1	NM_000083	1	23	22	+	143047661	143047747
263136299	chr7	143048665	143048861	143048687	143048839	CLCN1	NM_000083	1	23	23	+	143048687	143049097
263161412	chr7	143048810	143048982	143048829	143048963	CLCN1	NM_000083	1	23	23	+	143048687	143049097
263170172	chr7	143048925	143049097	143048945	143049076	CLCN1	NM_000083	1	23	23	+	143048687	143049097
263606258	chr16	58000854	58001076	58000875	58001055	CNGB1	NM_001135639	1	13	2	-	58001032	58001198
263640207	chr16	58001018	58001223	58001041	58001201	CNGB1	NM_001135639	1	13	2	-	58001032	58001198
269205569	chr16	57998365	57998491	57998383	57998466	CNGB1	NM_001135639	1	13	3	-	57998391	57998448
266412977	chr16	57997970	57998140	57997990	57998112	CNGB1	NM_001135639	1	13	4	-	57998034	57998106
260636875	chr16	57996724	57996939	57996745	57996917	CNGB1	NM_001135639	1	13	5	-	57996878	57996968
260655214	chr16	57996888	57997111	57996908	57997085	CNGB1	NM_001135639	1	13	5	-	57996878	57996968
260636875	chr16	57996724	57996939	57996745	57996917	CNGB1	NM_001135639	1	13	6	-	57996746	57996776
265623669	chr16	57996613	57996804	57996634	57996783	CNGB1	NM_001135639	1	13	6	-	57996746	57996776
258969497	chr16	57996419	57996548	57996440	57996522	CNGB1	NM_001135639	1	13	7	-	57996469	57996514
266996756	chr16	57994705	57994852	57994729	57994833	CNGB1	NM_001135639	1	13	8	-	57994744	57994819
268042500	chr16	57994259	57994475	57994278	57994454	CNGB1	NM_001135639	1	13	9	-	57994386	57994434
269276371	chr16	57993768	57993988	57993785	57993969	CNGB1	NM_001135639	1	13	10	-	57993792	57993969
269280346	chr16	57993932	57994067	57993950	57994045	CNGB1	NM_001135639	1	13	10	-	57993792	57993969
268136181	chr16	57992230	57992446	57992251	57992423	CNGB1	NM_001135639	1	13	11	-	57992314	57992389
269336554	chr16	57991167	57991318	57991189	57991296	CNGB1	NM_001135639	1	13	12	-	57991245	57991281
267802419	chr16	57989160	57989378	57989181	57989356	CNGB1	NM_001135639	1	13	13	-	57988580	57989272
263606258	chr16	58000854	58001076	58000875	58001055	CNGB1	NM_001297	2	33	2	-	58001032	58001198
263640207	chr16	58001018	58001223	58001041	58001201	CNGB1	NM_001297	2	33	2	-	58001032	58001198
269205569	chr16	57998365	57998491	57998383	57998466	CNGB1	NM_001297	2	33	3	-	57998391	57998448
266412977	chr16	57997970	57998140	57997990	57998112	CNGB1	NM_001297	2	33	4	-	57998034	57998106
260636875	chr16	57996724	57996939	57996745	57996917	CNGB1	NM_001297	2	33	5	-	57996878	57996968
260655214	chr16	57996888	57997111	57996908	57997085	CNGB1	NM_001297	2	33	5	-	57996878	57996968
260636875	chr16	57996724	57996939	57996745	57996917	CNGB1	NM_001297	2	33	6	-	57996746	57996776
265623669	chr16	57996613	57996804	57996634	57996783	CNGB1	NM_001297	2	33	6	-	57996746	57996776
258969497	chr16	57996419	57996548	57996440	57996522	CNGB1	NM_001297	2	33	7	-	57996469	57996514
266996756	chr16	57994705	57994852	57994729	57994833	CNGB1	NM_001297	2	33	8	-	57994744	57994819
268042500	chr16	57994259	57994475	57994278	57994454	CNGB1	NM_001297	2	33	9	-	57994386	57994434
269276371	chr16	57993768	57993988	57993785	57993969	CNGB1	NM_001297	2	33	10	-	57993792	57993969
269280346	chr16	57993932	57994067	57993950	57994045	CNGB1	NM_001297	2	33	10	-	57993792	57993969
268136181	chr16	57992230	57992446	57992251	57992423	CNGB1	NM_001297	2	33	11	-	57992314	57992389
269336554	chr16	57991167	57991318	57991189	57991296	CNGB1	NM_001297	2	33	12	-	57991245	57991281
262804669	chr16	57984110	57984334	57984132	57984309	CNGB1	NM_001297	2	33	13	-	57984285	57984444
262881844	chr16	57984288	57984474	57984310	57984450	CNGB1	NM_001297	2	33	13	-	57984285	57984444
258974210	chr16	57983228	57983415	57983250	57983391	CNGB1	NM_001297	2	33	14	-	57983257	57983343
268765807	chr16	57974050	57974272	57974072	57974248	CNGB1	NM_001297	2	33	15	-	57974138	57974225
262245596	chr16	57973148	57973354	57973169	57973336	CNGB1	NM_001297	2	33	16	-	57973334	57973496
262268930	chr16	57973318	57973537	57973337	57973512	CNGB1	NM_001297	2	33	16	-	57973334	57973496

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268744903	chr16	57965593	57965750	57965619	57965724	CNGB1	NM_001297	2	33	17	-	57965620	57965782
268756646	chr16	57965697	57965914	57965718	57965890	CNGB1	NM_001297	2	33	17	-	57965620	57965782
268063545	chr16	57957131	57957310	57957151	57957289	CNGB1	NM_001297	2	33	18	-	57957177	57957284
267431370	chr16	57954172	57954359	57954194	57954333	CNGB1	NM_001297	2	33	19	-	57954291	57954448
267440413	chr16	57954314	57954475	57954334	57954454	CNGB1	NM_001297	2	33	19	-	57954291	57954448
258881167	chr16	57952967	57953189	57952989	57953166	CNGB1	NM_001297	2	33	20	-	57953003	57953158
261728381	chr16	57951044	57951268	57951070	57951247	CNGB1	NM_001297	2	33	21	-	57951172	57951380
261759123	chr16	57951226	57951450	57951248	57951426	CNGB1	NM_001297	2	33	21	-	57951172	57951380
267686859	chr16	57949928	57950116	57949950	57950089	CNGB1	NM_001297	2	33	22	-	57950033	57950083
264638343	chr16	57949077	57949289	57949097	57949267	CNGB1	NM_001297	2	33	23	-	57949153	57949239
264481292	chr16	57946823	57947026	57946845	57947005	CNGB1	NM_001297	2	33	24	-	57946834	57946898
260869098	chr16	57945581	57945805	57945602	57945785	CNGB1	NM_001297	2	33	25	-	57945657	57945779
269183297	chr16	57938530	57938669	57938553	57938645	CNGB1	NM_001297	2	33	26	-	57938638	57938779
269187440	chr16	57938628	57938815	57938646	57938792	CNGB1	NM_001297	2	33	26	-	57938638	57938779
259573079	chr16	57937563	57937767	57937584	57937745	CNGB1	NM_001297	2	33	27	-	57937726	57937885
259597269	chr16	57937717	57937918	57937738	57937896	CNGB1	NM_001297	2	33	27	-	57937726	57937885
257560335	chr16	57935249	57935457	57935270	57935435	CNGB1	NM_001297	2	33	28	-	57935432	57935529
265881533	chr16	57935415	57935600	57935436	57935578	CNGB1	NM_001297	2	33	28	-	57935432	57935529
257545939	chr16	57935182	57935369	57935203	57935346	CNGB1	NM_001297	2	33	29	-	57935256	57935339
257560335	chr16	57935249	57935457	57935270	57935435	CNGB1	NM_001297	2	33	29	-	57935256	57935339
265068064	chr16	57931644	57931847	57931664	57931823	CNGB1	NM_001297	2	33	30	-	57931700	57931818
267364687	chr16	57931281	57931500	57931307	57931481	CNGB1	NM_001297	2	33	31	-	57931301	57931447
262477371	chr16	57921700	57921875	57921722	57921854	CNGB1	NM_001297	2	33	32	-	57921759	57921978
262513284	chr16	57921831	57922013	57921851	57921990	CNGB1	NM_001297	2	33	32	-	57921759	57921978
266199553	chr16	57918022	57918240	57918040	57918222	CNGB1	NM_001297	2	33	33	-	57916244	57918361
268963268	chr16	57918148	57918353	57918169	57918334	CNGB1	NM_001297	2	33	33	-	57916244	57918361
268964752	chr16	57918293	57918507	57918311	57918487	CNGB1	NM_001297	2	33	33	-	57916244	57918361
267640154	chr1	103573579	103573770	103573599	103573747	COL11A1	NM_001190709	1	66	1	-	103573629	103574052
268808660	chr1	103548177	103548395	103548201	103548376	COL11A1	NM_001190709	1	66	2	-	103548361	103548528
268813538	chr1	103548477	103548655	103548505	103548629	COL11A1	NM_001190709	1	66	2	-	103548361	103548528
288659903	chr1	103548347	103548530	103548380	103548504	COL11A1	NM_001190709	1	66	2	-	103548361	103548528
268922081	chr1	103544205	103544338	103544227	103544311	COL11A1	NM_001190709	1	66	3	-	103544214	103544427
268926269	chr1	103544287	103544456	103544312	103544428	COL11A1	NM_001190709	1	66	3	-	103544214	103544427
268929249	chr1	103544401	103544592	103544427	103544567	COL11A1	NM_001190709	1	66	3	-	103544214	103544427
266350613	chr1	103540019	103540233	103540046	103540207	COL11A1	NM_001190709	1	66	4	-	103540174	103540336
266372753	chr1	103540181	103540383	103540208	103540355	COL11A1	NM_001190709	1	66	4	-	103540174	103540336
264825721	chr1	103496625	103496848	103496653	103496821	COL11A1	NM_001190709	1	66	5	-	103496672	103496800
285261469	chr1	103491034	103491183	103491066	103491155	COL11A1	NM_001190709	1	66	6	-	103491077	103491169
285264859	chr1	103491110	103491286	103491136	103491256	COL11A1	NM_001190709	1	66	6	-	103491077	103491169
267355855	chr1	103488153	103488354	103488178	103488328	COL11A1	NM_001190709	1	66	7	-	103488298	103488552
267357916	chr1	103488301	103488447	103488329	103488426	COL11A1	NM_001190709	1	66	7	-	103488298	103488552

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267358940	chr1	103488399	103488590	103488427	103488562	COL11A1	NM_001190709	1	66	7	-	103488298	103488552
263920654	chr1	103487207	103487370	103487232	103487343	COL11A1	NM_001190709	1	66	8	-	103487263	103487325
266363885	chr1	103484235	103484459	103484257	103484432	COL11A1	NM_001190709	1	66	9	-	103484374	103484415
262530519	chr1	103483225	103483430	103483252	103483409	COL11A1	NM_001190709	1	66	10	-	103483376	103483438
286215364	chr1	103483351	103483568	103483379	103483544	COL11A1	NM_001190709	1	66	10	-	103483376	103483438
261443928	chr1	103481074	103481267	103481097	103481246	COL11A1	NM_001190709	1	66	11	-	103481224	103481298
261449980	chr1	103481219	103481413	103481246	103481393	COL11A1	NM_001190709	1	66	11	-	103481224	103481298
266666016	chr1	103480016	103480213	103480043	103480186	COL11A1	NM_001190709	1	66	12	-	103480067	103480150
259414300	chr1	103477850	103478074	103477878	103478046	COL11A1	NM_001190709	1	66	13	-	103477969	103478025
268594158	chr1	103473833	103474053	103473861	103474034	COL11A1	NM_001190709	1	66	14	-	103474019	103474072
268595288	chr1	103474017	103474142	103474037	103474114	COL11A1	NM_001190709	1	66	14	-	103474019	103474072
258136770	chr1	103471764	103471956	103471789	103471928	COL11A1	NM_001190709	1	66	15	-	103471818	103471871
267389279	chr1	103471570	103471705	103471593	103471682	COL11A1	NM_001190709	1	66	16	-	103471624	103471677
263904662	chr1	103471210	103471421	103471238	103471403	COL11A1	NM_001190709	1	66	17	-	103471394	103471447
263904850	chr1	103471376	103471597	103471404	103471574	COL11A1	NM_001190709	1	66	17	-	103471394	103471447
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_001190709	1	66	18	-	103470164	103470217
269277244	chr1	103470166	103470322	103470189	103470301	COL11A1	NM_001190709	1	66	18	-	103470164	103470217
264578556	chr1	103469863	103470033	103469889	103470009	COL11A1	NM_001190709	1	66	19	-	103470000	103470044
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_001190709	1	66	19	-	103470000	103470044
269266422	chr1	103469984	103470181	103470010	103470153	COL11A1	NM_001190709	1	66	19	-	103470000	103470044
267677208	chr1	103468684	103468903	103468705	103468876	COL11A1	NM_001190709	1	66	20	-	103468771	103468824
268583156	chr1	103468126	103468350	103468151	103468328	COL11A1	NM_001190709	1	66	21	-	103468303	103468347
268583898	chr1	103468298	103468502	103468322	103468474	COL11A1	NM_001190709	1	66	21	-	103468303	103468347
263208014	chr1	103467947	103468123	103467971	103468095	COL11A1	NM_001190709	1	66	22	-	103467984	103468037
266940616	chr1	103467310	103467524	103467334	103467503	COL11A1	NM_001190709	1	66	23	-	103467481	103467525
266956643	chr1	103467477	103467696	103467503	103467672	COL11A1	NM_001190709	1	66	23	-	103467481	103467525
285850381	chr1	103463828	103464019	103463859	103463992	COL11A1	NM_001190709	1	66	24	-	103463866	103463919
287545341	chr1	103462567	103462692	103462595	103462666	COL11A1	NM_001190709	1	66	25	-	103462636	103462680
287545346	chr1	103462645	103462816	103462667	103462788	COL11A1	NM_001190709	1	66	25	-	103462636	103462680
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_001190709	1	66	26	-	103461545	103461598
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_001190709	1	66	26	-	103461545	103461598
267993173	chr1	103461303	103461463	103461331	103461442	COL11A1	NM_001190709	1	66	27	-	103461420	103461464
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_001190709	1	66	27	-	103461420	103461464
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_001190709	1	66	27	-	103461420	103461464
268611523	chr1	103454944	103455105	103454976	103455080	COL11A1	NM_001190709	1	66	28	-	103455074	103455127
268611531	chr1	103455047	103455257	103455079	103455230	COL11A1	NM_001190709	1	66	28	-	103455074	103455127
267832844	chr1	103453142	103453316	103453165	103453293	COL11A1	NM_001190709	1	66	29	-	103453189	103453296
267436171	chr1	103449546	103449729	103449568	103449703	COL11A1	NM_001190709	1	66	30	-	103449694	103449747
267438589	chr1	103449679	103449869	103449704	103449841	COL11A1	NM_001190709	1	66	30	-	103449694	103449747
263550626	chr1	103444931	103445087	103444953	103445062	COL11A1	NM_001190709	1	66	31	-	103444938	103444991
266868808	chr1	103444496	103444720	103444523	103444691	COL11A1	NM_001190709	1	66	32	-	103444616	103444660

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267061252	chr1	103444340	103444506	103444367	103444478	COL11A1	NM_001190709	1	66	33	-	103444416	103444469
268666431	chr1	103444158	103444364	103444186	103444336	COL11A1	NM_001190709	1	66	34	-	103444264	103444308
267475919	chr1	103440357	103440561	103440383	103440534	COL11A1	NM_001190709	1	66	35	-	103440386	103440439
265725259	chr1	103435768	103435957	103435789	103435926	COL11A1	NM_001190709	1	66	36	-	103435775	103435828
267916351	chr1	103430880	103431103	103430907	103431079	COL11A1	NM_001190709	1	66	37	-	103431043	103431096
267916479	chr1	103431030	103431204	103431054	103431174	COL11A1	NM_001190709	1	66	37	-	103431043	103431096
269193904	chr1	103428056	103428258	103428084	103428237	COL11A1	NM_001190709	1	66	38	-	103428209	103428316
269196827	chr1	103428204	103428388	103428228	103428360	COL11A1	NM_001190709	1	66	38	-	103428209	103428316
268158870	chr1	103427768	103427957	103427789	103427929	COL11A1	NM_001190709	1	66	39	-	103427732	103427821
285945377	chr1	103427677	103427812	103427707	103427788	COL11A1	NM_001190709	1	66	39	-	103427732	103427821
257321149	chr1	103427344	103427545	103427372	103427513	COL11A1	NM_001190709	1	66	40	-	103427422	103427475
264439090	chr1	103412300	103412517	103412323	103412496	COL11A1	NM_001190709	1	66	41	-	103412405	103412512
264452778	chr1	103412464	103412672	103412484	103412647	COL11A1	NM_001190709	1	66	41	-	103412405	103412512
266869427	chr1	103405841	103406045	103405869	103406017	COL11A1	NM_001190709	1	66	42	-	103405883	103405990
269340143	chr1	103404589	103404793	103404613	103404770	COL11A1	NM_001190709	1	66	43	-	103404591	103404644
287501982	chr1	103404456	103404639	103404481	103404620	COL11A1	NM_001190709	1	66	43	-	103404591	103404644
267638150	chr1	103400517	103400718	103400544	103400691	COL11A1	NM_001190709	1	66	44	-	103400616	103400669
264502914	chr1	103399944	103400122	103399968	103400099	COL11A1	NM_001190709	1	66	45	-	103400005	103400112
264521869	chr1	103400079	103400249	103400100	103400221	COL11A1	NM_001190709	1	66	45	-	103400005	103400112
258812152	chr1	103388905	103389129	103388929	103389101	COL11A1	NM_001190709	1	66	46	-	103388892	103388945
284987101	chr1	103388837	103388966	103388863	103388934	COL11A1	NM_001190709	1	66	46	-	103388892	103388945
257911326	chr1	103386930	103387106	103386954	103387087	COL11A1	NM_001190709	1	66	47	-	103387074	103387127
257915763	chr1	103387060	103387275	103387087	103387247	COL11A1	NM_001190709	1	66	47	-	103387074	103387127
265677225	chr1	103385722	103385931	103385751	103385911	COL11A1	NM_001190709	1	66	48	-	103385867	103385920
265677618	chr1	103385871	103386093	103385893	103386066	COL11A1	NM_001190709	1	66	48	-	103385867	103385920
266371875	chr1	103381060	103381256	103381085	103381228	COL11A1	NM_001190709	1	66	49	-	103381187	103381240
266382837	chr1	103381211	103381413	103381229	103381385	COL11A1	NM_001190709	1	66	49	-	103381187	103381240
263154089	chr1	103380159	103380339	103380185	103380322	COL11A1	NM_001190709	1	66	50	-	103380260	103380367
261551842	chr1	103379751	103379971	103379779	103379949	COL11A1	NM_001190709	1	66	51	-	103379908	103379961
261556488	chr1	103379929	103380056	103379950	103380029	COL11A1	NM_001190709	1	66	51	-	103379908	103379961
260147361	chr1	103379098	103379227	103379127	103379204	COL11A1	NM_001190709	1	66	52	-	103379193	103379246
260151355	chr1	103379195	103379419	103379218	103379391	COL11A1	NM_001190709	1	66	52	-	103379193	103379246
267830700	chr1	103377631	103377855	103377653	103377828	COL11A1	NM_001190709	1	66	53	-	103377715	103377768
268784639	chr1	103364349	103364552	103364377	103364534	COL11A1	NM_001190709	1	66	54	-	103364497	103364550
268786914	chr1	103364233	103364375	103364251	103364347	COL11A1	NM_001190709	1	66	55	-	103364222	103364329
260581473	chr1	103363515	103363713	103363547	103363695	COL11A1	NM_001190709	1	66	56	-	103363681	103363734
260581810	chr1	103363664	103363872	103363692	103363847	COL11A1	NM_001190709	1	66	56	-	103363681	103363734
266630393	chr1	103355848	103356072	103355875	103356044	COL11A1	NM_001190709	1	66	57	-	103356007	103356060
266634864	chr1	103356022	103356163	103356041	103356133	COL11A1	NM_001190709	1	66	57	-	103356007	103356060
268213011	chr1	103354900	103355039	103354932	103355017	COL11A1	NM_001190709	1	66	58	-	103355011	103355118
268216218	chr1	103355008	103355134	103355027	103355111	COL11A1	NM_001190709	1	66	58	-	103355011	103355118

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268216720	chr1	103355088	103355302	103355112	103355276	COL11A1	NM_001190709	1	66	58	-	103355011	103355118
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_001190709	1	66	59	-	103354422	103354475
263436532	chr1	103354432	103354626	103354453	103354598	COL11A1	NM_001190709	1	66	59	-	103354422	103354475
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_001190709	1	66	60	-	103354279	103354314
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_001190709	1	66	60	-	103354279	103354314
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_001190709	1	66	61	-	103354133	103354186
268814516	chr1	103354069	103354287	103354092	103354260	COL11A1	NM_001190709	1	66	61	-	103354133	103354186
260880134	chr1	103352299	103352504	103352320	103352477	COL11A1	NM_001190709	1	66	62	-	103352363	103352612
260938554	chr1	103352454	103352654	103352478	103352626	COL11A1	NM_001190709	1	66	62	-	103352363	103352612
260975454	chr1	103348693	103348841	103348719	103348818	COL11A1	NM_001190709	1	66	63	-	103348755	103348867
285945847	chr1	103348791	103348932	103348819	103348901	COL11A1	NM_001190709	1	66	63	-	103348755	103348867
268004777	chr1	103347133	103347357	103347156	103347329	COL11A1	NM_001190709	1	66	64	-	103347253	103347321
264528733	chr1	103345172	103345392	103345192	103345366	COL11A1	NM_001190709	1	66	65	-	103345239	103345472
264566488	chr1	103345346	103345549	103345367	103345521	COL11A1	NM_001190709	1	66	65	-	103345239	103345472
267664076	chr1	103343423	103343640	103343445	103343612	COL11A1	NM_001190709	1	66	66	-	103342023	103343721
267668071	chr1	103343590	103343807	103343613	103343784	COL11A1	NM_001190709	1	66	66	-	103342023	103343721
267640154	chr1	103573579	103573770	103573599	103573747	COL11A1	NM_001854	2	67	1	-	103573629	103574052
268808660	chr1	103548177	103548395	103548201	103548376	COL11A1	NM_001854	2	67	2	-	103548361	103548528
268813538	chr1	103548477	103548655	103548505	103548629	COL11A1	NM_001854	2	67	2	-	103548361	103548528
288659903	chr1	103548347	103548530	103548380	103548504	COL11A1	NM_001854	2	67	2	-	103548361	103548528
268922081	chr1	103544205	103544338	103544227	103544311	COL11A1	NM_001854	2	67	3	-	103544214	103544427
268926269	chr1	103544287	103544456	103544312	103544428	COL11A1	NM_001854	2	67	3	-	103544214	103544427
268929249	chr1	103544401	103544592	103544427	103544567	COL11A1	NM_001854	2	67	3	-	103544214	103544427
266350613	chr1	103540019	103540233	103540046	103540207	COL11A1	NM_001854	2	67	4	-	103540174	103540336
266372753	chr1	103540181	103540383	103540208	103540355	COL11A1	NM_001854	2	67	4	-	103540174	103540336
264825721	chr1	103496625	103496848	103496653	103496821	COL11A1	NM_001854	2	67	5	-	103496672	103496800
268283839	chr1	103491708	103491931	103491731	103491903	COL11A1	NM_001854	2	67	6	-	103491772	103491888
285261469	chr1	103491034	103491183	103491066	103491155	COL11A1	NM_001854	2	67	7	-	103491077	103491169
285264859	chr1	103491110	103491286	103491136	103491256	COL11A1	NM_001854	2	67	7	-	103491077	103491169
267355855	chr1	103488153	103488354	103488178	103488328	COL11A1	NM_001854	2	67	8	-	103488298	103488552
267357916	chr1	103488301	103488447	103488329	103488426	COL11A1	NM_001854	2	67	8	-	103488298	103488552
267358940	chr1	103488399	103488590	103488427	103488562	COL11A1	NM_001854	2	67	8	-	103488298	103488552
263920654	chr1	103487207	103487370	103487232	103487343	COL11A1	NM_001854	2	67	9	-	103487263	103487325
266363885	chr1	103484235	103484459	103484257	103484432	COL11A1	NM_001854	2	67	10	-	103484374	103484415
262530519	chr1	103483225	103483430	103483252	103483409	COL11A1	NM_001854	2	67	11	-	103483376	103483438
286215364	chr1	103483351	103483568	103483379	103483544	COL11A1	NM_001854	2	67	11	-	103483376	103483438
261443928	chr1	103481074	103481267	103481097	103481246	COL11A1	NM_001854	2	67	12	-	103481224	103481298
261449980	chr1	103481219	103481413	103481246	103481393	COL11A1	NM_001854	2	67	12	-	103481224	103481298
266666016	chr1	103480016	103480213	103480043	103480186	COL11A1	NM_001854	2	67	13	-	103480067	103480150
259414300	chr1	103477850	103478074	103477878	103478046	COL11A1	NM_001854	2	67	14	-	103477969	103478025
268594158	chr1	103473833	103474053	103473861	103474034	COL11A1	NM_001854	2	67	15	-	103474019	103474072

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268595288	chr1	103474017	103474142	103474037	103474114	COL11A1	NM_001854	2	67	15	-	103474019	103474072
258136770	chr1	103471764	103471956	103471789	103471928	COL11A1	NM_001854	2	67	16	-	103471818	103471871
267389279	chr1	103471570	103471705	103471593	103471682	COL11A1	NM_001854	2	67	17	-	103471624	103471677
263904662	chr1	103471210	103471421	103471238	103471403	COL11A1	NM_001854	2	67	18	-	103471394	103471447
263904850	chr1	103471376	103471597	103471404	103471574	COL11A1	NM_001854	2	67	18	-	103471394	103471447
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_001854	2	67	19	-	103470164	103470217
269277244	chr1	103470166	103470322	103470189	103470301	COL11A1	NM_001854	2	67	19	-	103470164	103470217
264578556	chr1	103469863	103470033	103469889	103470009	COL11A1	NM_001854	2	67	20	-	103470000	103470044
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_001854	2	67	20	-	103470000	103470044
269266422	chr1	103469984	103470181	103470010	103470153	COL11A1	NM_001854	2	67	20	-	103470000	103470044
267677208	chr1	103468684	103468903	103468705	103468876	COL11A1	NM_001854	2	67	21	-	103468771	103468824
268583156	chr1	103468126	103468350	103468151	103468328	COL11A1	NM_001854	2	67	22	-	103468303	103468347
268583898	chr1	103468298	103468502	103468322	103468474	COL11A1	NM_001854	2	67	22	-	103468303	103468347
263208014	chr1	103467947	103468123	103467971	103468095	COL11A1	NM_001854	2	67	23	-	103467984	103468037
266940616	chr1	103467310	103467524	103467334	103467503	COL11A1	NM_001854	2	67	24	-	103467481	103467525
266956643	chr1	103467477	103467696	103467503	103467672	COL11A1	NM_001854	2	67	24	-	103467481	103467525
285850381	chr1	103463828	103464019	103463859	103463992	COL11A1	NM_001854	2	67	25	-	103463866	103463919
287545341	chr1	103462567	103462692	103462595	103462666	COL11A1	NM_001854	2	67	26	-	103462636	103462680
287545346	chr1	103462645	103462816	103462667	103462788	COL11A1	NM_001854	2	67	26	-	103462636	103462680
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_001854	2	67	27	-	103461545	103461598
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_001854	2	67	27	-	103461545	103461598
267993173	chr1	103461303	103461463	103461331	103461442	COL11A1	NM_001854	2	67	28	-	103461420	103461464
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_001854	2	67	28	-	103461420	103461464
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_001854	2	67	28	-	103461420	103461464
268611523	chr1	103454944	103455105	103454976	103455080	COL11A1	NM_001854	2	67	29	-	103455074	103455127
268611531	chr1	103455047	103455257	103455079	103455230	COL11A1	NM_001854	2	67	29	-	103455074	103455127
267832844	chr1	103453142	103453316	103453165	103453293	COL11A1	NM_001854	2	67	30	-	103453189	103453296
267436171	chr1	103449546	103449729	103449568	103449703	COL11A1	NM_001854	2	67	31	-	103449694	103449747
267438589	chr1	103449679	103449869	103449704	103449841	COL11A1	NM_001854	2	67	31	-	103449694	103449747
263550626	chr1	103444931	103445087	103444953	103445062	COL11A1	NM_001854	2	67	32	-	103444938	103444991
266868808	chr1	103444496	103444720	103444523	103444691	COL11A1	NM_001854	2	67	33	-	103444616	103444660
267061252	chr1	103444340	103444506	103444367	103444478	COL11A1	NM_001854	2	67	34	-	103444416	103444469
268666431	chr1	103444158	103444364	103444186	103444336	COL11A1	NM_001854	2	67	35	-	103444264	103444308
267475919	chr1	103440357	103440561	103440383	103440534	COL11A1	NM_001854	2	67	36	-	103440386	103440439
265725259	chr1	103435768	103435957	103435789	103435926	COL11A1	NM_001854	2	67	37	-	103435775	103435828
267916351	chr1	103430880	103431103	103430907	103431079	COL11A1	NM_001854	2	67	38	-	103431043	103431096
267916479	chr1	103431030	103431204	103431054	103431174	COL11A1	NM_001854	2	67	38	-	103431043	103431096
269193904	chr1	103428056	103428258	103428084	103428237	COL11A1	NM_001854	2	67	39	-	103428209	103428316
269196827	chr1	103428204	103428388	103428228	103428360	COL11A1	NM_001854	2	67	39	-	103428209	103428316
268158870	chr1	103427768	103427957	103427789	103427929	COL11A1	NM_001854	2	67	40	-	103427732	103427821
285945377	chr1	103427677	103427812	103427707	103427788	COL11A1	NM_001854	2	67	40	-	103427732	103427821

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257321149	chr1	103427344	103427545	103427372	103427513	COL11A1	NM_001854	2	67	41	-	103427422	103427475
264439090	chr1	103412300	103412517	103412323	103412496	COL11A1	NM_001854	2	67	42	-	103412405	103412512
264452778	chr1	103412464	103412672	103412484	103412647	COL11A1	NM_001854	2	67	42	-	103412405	103412512
266869427	chr1	103405841	103406045	103405869	103406017	COL11A1	NM_001854	2	67	43	-	103405883	103405990
269340143	chr1	103404589	103404793	103404613	103404770	COL11A1	NM_001854	2	67	44	-	103404591	103404644
287501982	chr1	103404456	103404639	103404481	103404620	COL11A1	NM_001854	2	67	44	-	103404591	103404644
267638150	chr1	103400517	103400718	103400544	103400691	COL11A1	NM_001854	2	67	45	-	103400616	103400669
264502914	chr1	103399944	103400122	103399968	103400099	COL11A1	NM_001854	2	67	46	-	103400005	103400112
264521869	chr1	103400079	103400249	103400100	103400221	COL11A1	NM_001854	2	67	46	-	103400005	103400112
258812152	chr1	103388905	103389129	103388929	103389101	COL11A1	NM_001854	2	67	47	-	103388892	103388945
284987101	chr1	103388837	103388966	103388863	103388934	COL11A1	NM_001854	2	67	47	-	103388892	103388945
257911326	chr1	103386930	103387106	103386954	103387087	COL11A1	NM_001854	2	67	48	-	103387074	103387127
257915763	chr1	103387060	103387275	103387087	103387247	COL11A1	NM_001854	2	67	48	-	103387074	103387127
265677225	chr1	103385722	103385931	103385751	103385911	COL11A1	NM_001854	2	67	49	-	103385867	103385920
265677618	chr1	103385871	103386093	103385893	103386066	COL11A1	NM_001854	2	67	49	-	103385867	103385920
266371875	chr1	103381060	103381256	103381085	103381228	COL11A1	NM_001854	2	67	50	-	103381187	103381240
266382837	chr1	103381211	103381413	103381229	103381385	COL11A1	NM_001854	2	67	50	-	103381187	103381240
263154089	chr1	103380159	103380339	103380185	103380322	COL11A1	NM_001854	2	67	51	-	103380260	103380367
261551842	chr1	103379751	103379971	103379779	103379949	COL11A1	NM_001854	2	67	52	-	103379908	103379961
261556488	chr1	103379929	103380056	103379950	103380029	COL11A1	NM_001854	2	67	52	-	103379908	103379961
260147361	chr1	103379098	103379227	103379127	103379204	COL11A1	NM_001854	2	67	53	-	103379193	103379246
260151355	chr1	103379195	103379419	103379218	103379391	COL11A1	NM_001854	2	67	53	-	103379193	103379246
267830700	chr1	103377631	103377855	103377653	103377828	COL11A1	NM_001854	2	67	54	-	103377715	103377768
268784639	chr1	103364349	103364552	103364377	103364534	COL11A1	NM_001854	2	67	55	-	103364497	103364550
268786914	chr1	103364233	103364375	103364251	103364347	COL11A1	NM_001854	2	67	56	-	103364222	103364329
260581473	chr1	103363515	103363713	103363547	103363695	COL11A1	NM_001854	2	67	57	-	103363681	103363734
260581810	chr1	103363664	103363872	103363692	103363847	COL11A1	NM_001854	2	67	57	-	103363681	103363734
266630393	chr1	103355848	103356072	103355875	103356044	COL11A1	NM_001854	2	67	58	-	103356007	103356060
266634864	chr1	103356022	103356163	103356041	103356133	COL11A1	NM_001854	2	67	58	-	103356007	103356060
268213011	chr1	103354900	103355039	103354932	103355017	COL11A1	NM_001854	2	67	59	-	103355011	103355118
268216218	chr1	103355008	103355134	103355027	103355111	COL11A1	NM_001854	2	67	59	-	103355011	103355118
268216720	chr1	103355088	103355302	103355112	103355276	COL11A1	NM_001854	2	67	59	-	103355011	103355118
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_001854	2	67	60	-	103354422	103354475
263436532	chr1	103354432	103354626	103354453	103354598	COL11A1	NM_001854	2	67	60	-	103354422	103354475
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_001854	2	67	61	-	103354279	103354314
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_001854	2	67	61	-	103354279	103354314
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_001854	2	67	62	-	103354133	103354186
268814516	chr1	103354069	103354287	103354092	103354260	COL11A1	NM_001854	2	67	62	-	103354133	103354186
260880134	chr1	103352299	103352504	103352320	103352477	COL11A1	NM_001854	2	67	63	-	103352363	103352612
260938554	chr1	103352454	103352654	103352478	103352626	COL11A1	NM_001854	2	67	63	-	103352363	103352612
260975454	chr1	103348693	103348841	103348719	103348818	COL11A1	NM_001854	2	67	64	-	103348755	103348867

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
285945847	chr1	103348791	103348932	103348819	103348901	COL11A1	NM_001854	2	67	64	-	103348755	103348867
268004777	chr1	103347133	103347357	103347156	103347329	COL11A1	NM_001854	2	67	65	-	103347253	103347321
264528733	chr1	103345172	103345392	103345192	103345366	COL11A1	NM_001854	2	67	66	-	103345239	103345472
264566488	chr1	103345346	103345549	103345367	103345521	COL11A1	NM_001854	2	67	66	-	103345239	103345472
267664076	chr1	103343423	103343640	103343445	103343612	COL11A1	NM_001854	2	67	67	-	103342023	103343721
267668071	chr1	103343590	103343807	103343613	103343784	COL11A1	NM_001854	2	67	67	-	103342023	103343721
267640154	chr1	103573579	103573770	103573599	103573747	COL11A1	NM_080629	3	67	1	-	103573629	103574052
268808660	chr1	103548177	103548395	103548201	103548376	COL11A1	NM_080629	3	67	2	-	103548361	103548528
268813538	chr1	103548477	103548655	103548505	103548629	COL11A1	NM_080629	3	67	2	-	103548361	103548528
288659903	chr1	103548347	103548530	103548380	103548504	COL11A1	NM_080629	3	67	2	-	103548361	103548528
268922081	chr1	103544205	103544338	103544227	103544311	COL11A1	NM_080629	3	67	3	-	103544214	103544427
268926269	chr1	103544287	103544456	103544312	103544428	COL11A1	NM_080629	3	67	3	-	103544214	103544427
268929249	chr1	103544401	103544592	103544427	103544567	COL11A1	NM_080629	3	67	3	-	103544214	103544427
266350613	chr1	103540019	103540233	103540046	103540207	COL11A1	NM_080629	3	67	4	-	103540174	103540336
266372753	chr1	103540181	103540383	103540208	103540355	COL11A1	NM_080629	3	67	4	-	103540174	103540336
264825721	chr1	103496625	103496848	103496653	103496821	COL11A1	NM_080629	3	67	5	-	103496672	103496800
266476488	chr1	103491201	103491384	103491228	103491361	COL11A1	NM_080629	3	67	6	-	103491356	103491508
266484953	chr1	103491334	103491541	103491362	103491513	COL11A1	NM_080629	3	67	6	-	103491356	103491508
285261469	chr1	103491034	103491183	103491066	103491155	COL11A1	NM_080629	3	67	7	-	103491077	103491169
285264859	chr1	103491110	103491286	103491136	103491256	COL11A1	NM_080629	3	67	7	-	103491077	103491169
267355855	chr1	103488153	103488354	103488178	103488328	COL11A1	NM_080629	3	67	8	-	103488298	103488552
267357916	chr1	103488301	103488447	103488329	103488426	COL11A1	NM_080629	3	67	8	-	103488298	103488552
267358940	chr1	103488399	103488590	103488427	103488562	COL11A1	NM_080629	3	67	8	-	103488298	103488552
263920654	chr1	103487207	103487370	103487232	103487343	COL11A1	NM_080629	3	67	9	-	103487263	103487325
266363885	chr1	103484235	103484459	103484257	103484432	COL11A1	NM_080629	3	67	10	-	103484374	103484415
262530519	chr1	103483225	103483430	103483252	103483409	COL11A1	NM_080629	3	67	11	-	103483376	103483438
286215364	chr1	103483351	103483568	103483379	103483544	COL11A1	NM_080629	3	67	11	-	103483376	103483438
261443928	chr1	103481074	103481267	103481097	103481246	COL11A1	NM_080629	3	67	12	-	103481224	103481298
261449980	chr1	103481219	103481413	103481246	103481393	COL11A1	NM_080629	3	67	12	-	103481224	103481298
266666016	chr1	103480016	103480213	103480043	103480186	COL11A1	NM_080629	3	67	13	-	103480067	103480150
259414300	chr1	103477850	103478074	103477878	103478046	COL11A1	NM_080629	3	67	14	-	103477969	103478025
268594158	chr1	103473833	103474053	103473861	103474034	COL11A1	NM_080629	3	67	15	-	103474019	103474072
268595288	chr1	103474017	103474142	103474037	103474114	COL11A1	NM_080629	3	67	15	-	103474019	103474072
258136770	chr1	103471764	103471956	103471789	103471928	COL11A1	NM_080629	3	67	16	-	103471818	103471871
267389279	chr1	103471570	103471705	103471593	103471682	COL11A1	NM_080629	3	67	17	-	103471624	103471677
263904662	chr1	103471210	103471421	103471238	103471403	COL11A1	NM_080629	3	67	18	-	103471394	103471447
263904850	chr1	103471376	103471597	103471404	103471574	COL11A1	NM_080629	3	67	18	-	103471394	103471447
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_080629	3	67	19	-	103470164	103470217
269277244	chr1	103470166	103470322	103470189	103470301	COL11A1	NM_080629	3	67	19	-	103470164	103470217
264578556	chr1	103469863	103470033	103469889	103470009	COL11A1	NM_080629	3	67	20	-	103470000	103470044
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_080629	3	67	20	-	103470000	103470044

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269266422	chr1	103469984	103470181	103470010	103470153	COL11A1	NM_080629	3	67	20	-	103470000	103470044
267677208	chr1	103468684	103468903	103468705	103468876	COL11A1	NM_080629	3	67	21	-	103468771	103468824
268583156	chr1	103468126	103468350	103468151	103468328	COL11A1	NM_080629	3	67	22	-	103468303	103468347
268583898	chr1	103468298	103468502	103468322	103468474	COL11A1	NM_080629	3	67	22	-	103468303	103468347
263208014	chr1	103467947	103468123	103467971	103468095	COL11A1	NM_080629	3	67	23	-	103467984	103468037
266940616	chr1	103467310	103467524	103467334	103467503	COL11A1	NM_080629	3	67	24	-	103467481	103467525
266956643	chr1	103467477	103467696	103467503	103467672	COL11A1	NM_080629	3	67	24	-	103467481	103467525
285850381	chr1	103463828	103464019	103463859	103463992	COL11A1	NM_080629	3	67	25	-	103463866	103463919
287545341	chr1	103462567	103462692	103462595	103462666	COL11A1	NM_080629	3	67	26	-	103462636	103462680
287545346	chr1	103462645	103462816	103462667	103462788	COL11A1	NM_080629	3	67	26	-	103462636	103462680
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_080629	3	67	27	-	103461545	103461598
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_080629	3	67	27	-	103461545	103461598
267993173	chr1	103461303	103461463	103461331	103461442	COL11A1	NM_080629	3	67	28	-	103461420	103461464
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_080629	3	67	28	-	103461420	103461464
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_080629	3	67	28	-	103461420	103461464
268611523	chr1	103454944	103455105	103454976	103455080	COL11A1	NM_080629	3	67	29	-	103455074	103455127
268611531	chr1	103455047	103455257	103455079	103455230	COL11A1	NM_080629	3	67	29	-	103455074	103455127
267832844	chr1	103453142	103453316	103453165	103453293	COL11A1	NM_080629	3	67	30	-	103453189	103453296
267436171	chr1	103449546	103449729	103449568	103449703	COL11A1	NM_080629	3	67	31	-	103449694	103449747
267438589	chr1	103449679	103449869	103449704	103449841	COL11A1	NM_080629	3	67	31	-	103449694	103449747
263550626	chr1	103444931	103445087	103444953	103445062	COL11A1	NM_080629	3	67	32	-	103444938	103444991
266868808	chr1	103444496	103444720	103444523	103444691	COL11A1	NM_080629	3	67	33	-	103444616	103444660
267061252	chr1	103444340	103444506	103444367	103444478	COL11A1	NM_080629	3	67	34	-	103444416	103444469
268666431	chr1	103444158	103444364	103444186	103444336	COL11A1	NM_080629	3	67	35	-	103444264	103444308
267475919	chr1	103440357	103440561	103440383	103440534	COL11A1	NM_080629	3	67	36	-	103440386	103440439
265725259	chr1	103435768	103435957	103435789	103435926	COL11A1	NM_080629	3	67	37	-	103435775	103435828
267916351	chr1	103430880	103431103	103430907	103431079	COL11A1	NM_080629	3	67	38	-	103431043	103431096
267916479	chr1	103431030	103431204	103431054	103431174	COL11A1	NM_080629	3	67	38	-	103431043	103431096
269193904	chr1	103428056	103428258	103428084	103428237	COL11A1	NM_080629	3	67	39	-	103428209	103428316
269196827	chr1	103428204	103428388	103428228	103428360	COL11A1	NM_080629	3	67	39	-	103428209	103428316
268158870	chr1	103427768	103427957	103427789	103427929	COL11A1	NM_080629	3	67	40	-	103427732	103427821
285945377	chr1	103427677	103427812	103427707	103427788	COL11A1	NM_080629	3	67	40	-	103427732	103427821
257321149	chr1	103427344	103427545	103427372	103427513	COL11A1	NM_080629	3	67	41	-	103427422	103427475
264439090	chr1	103412300	103412517	103412323	103412496	COL11A1	NM_080629	3	67	42	-	103412405	103412512
264452778	chr1	103412464	103412672	103412484	103412647	COL11A1	NM_080629	3	67	42	-	103412405	103412512
266869427	chr1	103405841	103406045	103405869	103406017	COL11A1	NM_080629	3	67	43	-	103405883	103405990
269340143	chr1	103404589	103404793	103404613	103404770	COL11A1	NM_080629	3	67	44	-	103404591	103404644
287501982	chr1	103404456	103404639	103404481	103404620	COL11A1	NM_080629	3	67	44	-	103404591	103404644
267638150	chr1	103400517	103400718	103400544	103400691	COL11A1	NM_080629	3	67	45	-	103400616	103400669
264502914	chr1	103399944	103400122	103399968	103400099	COL11A1	NM_080629	3	67	46	-	103400005	103400112
264521869	chr1	103400079	103400249	103400100	103400221	COL11A1	NM_080629	3	67	46	-	103400005	103400112

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258812152	chr1	103388905	103389129	103388929	103389101	COL11A1	NM_080629	3	67	47	-	103388892	103388945
284987101	chr1	103388837	103388966	103388863	103388934	COL11A1	NM_080629	3	67	47	-	103388892	103388945
257911326	chr1	103386930	103387106	103386954	103387087	COL11A1	NM_080629	3	67	48	-	103387074	103387127
257915763	chr1	103387060	103387275	103387087	103387247	COL11A1	NM_080629	3	67	48	-	103387074	103387127
265677225	chr1	103385722	103385931	103385751	103385911	COL11A1	NM_080629	3	67	49	-	103385867	103385920
265677618	chr1	103385871	103386093	103385893	103386066	COL11A1	NM_080629	3	67	49	-	103385867	103385920
266371875	chr1	103381060	103381256	103381085	103381228	COL11A1	NM_080629	3	67	50	-	103381187	103381240
266382837	chr1	103381211	103381413	103381229	103381385	COL11A1	NM_080629	3	67	50	-	103381187	103381240
263154089	chr1	103380159	103380339	103380185	103380322	COL11A1	NM_080629	3	67	51	-	103380260	103380367
261551842	chr1	103379751	103379971	103379779	103379949	COL11A1	NM_080629	3	67	52	-	103379908	103379961
261556488	chr1	103379929	103380056	103379950	103380029	COL11A1	NM_080629	3	67	52	-	103379908	103379961
260147361	chr1	103379098	103379227	103379127	103379204	COL11A1	NM_080629	3	67	53	-	103379193	103379246
260151355	chr1	103379195	103379419	103379218	103379391	COL11A1	NM_080629	3	67	53	-	103379193	103379246
267830700	chr1	103377631	103377855	103377653	103377828	COL11A1	NM_080629	3	67	54	-	103377715	103377768
268784639	chr1	103364349	103364552	103364377	103364534	COL11A1	NM_080629	3	67	55	-	103364497	103364550
268786914	chr1	103364233	103364375	103364251	103364347	COL11A1	NM_080629	3	67	56	-	103364222	103364329
260581473	chr1	103363515	103363713	103363547	103363695	COL11A1	NM_080629	3	67	57	-	103363681	103363734
260581810	chr1	103363664	103363872	103363692	103363847	COL11A1	NM_080629	3	67	57	-	103363681	103363734
266630393	chr1	103355848	103356072	103355875	103356044	COL11A1	NM_080629	3	67	58	-	103356007	103356060
266634864	chr1	103356022	103356163	103356041	103356133	COL11A1	NM_080629	3	67	58	-	103356007	103356060
268213011	chr1	103354900	103355039	103354932	103355017	COL11A1	NM_080629	3	67	59	-	103355011	103355118
268216218	chr1	103355008	103355134	103355027	103355111	COL11A1	NM_080629	3	67	59	-	103355011	103355118
268216720	chr1	103355088	103355302	103355112	103355276	COL11A1	NM_080629	3	67	59	-	103355011	103355118
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_080629	3	67	60	-	103354422	103354475
263436532	chr1	103354432	103354626	103354453	103354598	COL11A1	NM_080629	3	67	60	-	103354422	103354475
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_080629	3	67	61	-	103354279	103354314
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_080629	3	67	61	-	103354279	103354314
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_080629	3	67	62	-	103354133	103354186
268814516	chr1	103354069	103354287	103354092	103354260	COL11A1	NM_080629	3	67	62	-	103354133	103354186
260880134	chr1	103352299	103352504	103352320	103352477	COL11A1	NM_080629	3	67	63	-	103352363	103352612
260938554	chr1	103352454	103352654	103352478	103352626	COL11A1	NM_080629	3	67	63	-	103352363	103352612
260975454	chr1	103348693	103348841	103348719	103348818	COL11A1	NM_080629	3	67	64	-	103348755	103348867
285945847	chr1	103348791	103348932	103348819	103348901	COL11A1	NM_080629	3	67	64	-	103348755	103348867
268004777	chr1	103347133	103347357	103347156	103347329	COL11A1	NM_080629	3	67	65	-	103347253	103347321
264528733	chr1	103345172	103345392	103345192	103345366	COL11A1	NM_080629	3	67	66	-	103345239	103345472
264566488	chr1	103345346	103345549	103345367	103345521	COL11A1	NM_080629	3	67	66	-	103345239	103345472
267664076	chr1	103343423	103343640	103343445	103343612	COL11A1	NM_080629	3	67	67	-	103342023	103343721
267668071	chr1	103343590	103343807	103343613	103343784	COL11A1	NM_080629	3	67	67	-	103342023	103343721
267640154	chr1	103573579	103573770	103573599	103573747	COL11A1	NM_080630	4	65	1	-	103573629	103574052
268808660	chr1	103548177	103548395	103548201	103548376	COL11A1	NM_080630	4	65	2	-	103548361	103548528
268813538	chr1	103548477	103548655	103548505	103548629	COL11A1	NM_080630	4	65	2	-	103548361	103548528

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288659903	chr1	103548347	103548530	103548380	103548504	COL11A1	NM_080630	4	65	2	-	103548361	103548528
268922081	chr1	103544205	103544338	103544227	103544311	COL11A1	NM_080630	4	65	3	-	103544214	103544427
268926269	chr1	103544287	103544456	103544312	103544428	COL11A1	NM_080630	4	65	3	-	103544214	103544427
268929249	chr1	103544401	103544592	103544427	103544567	COL11A1	NM_080630	4	65	3	-	103544214	103544427
266350613	chr1	103540019	103540233	103540046	103540207	COL11A1	NM_080630	4	65	4	-	103540174	103540336
266372753	chr1	103540181	103540383	103540208	103540355	COL11A1	NM_080630	4	65	4	-	103540174	103540336
264825721	chr1	103496625	103496848	103496653	103496821	COL11A1	NM_080630	4	65	5	-	103496672	103496800
268283839	chr1	103491708	103491931	103491731	103491903	COL11A1	NM_080630	4	65	6	-	103491772	103491888
263920654	chr1	103487207	103487370	103487232	103487343	COL11A1	NM_080630	4	65	7	-	103487263	103487325
266363885	chr1	103484235	103484459	103484257	103484432	COL11A1	NM_080630	4	65	8	-	103484374	103484415
262530519	chr1	103483225	103483430	103483252	103483409	COL11A1	NM_080630	4	65	9	-	103483376	103483438
286215364	chr1	103483351	103483568	103483379	103483544	COL11A1	NM_080630	4	65	9	-	103483376	103483438
261443928	chr1	103481074	103481267	103481097	103481246	COL11A1	NM_080630	4	65	10	-	103481224	103481298
261449980	chr1	103481219	103481413	103481246	103481393	COL11A1	NM_080630	4	65	10	-	103481224	103481298
266666016	chr1	103480016	103480213	103480043	103480186	COL11A1	NM_080630	4	65	11	-	103480067	103480150
259414300	chr1	103477850	103478074	103477878	103478046	COL11A1	NM_080630	4	65	12	-	103477969	103478025
268594158	chr1	103473833	103474053	103473861	103474034	COL11A1	NM_080630	4	65	13	-	103474019	103474072
268595288	chr1	103474017	103474142	103474037	103474114	COL11A1	NM_080630	4	65	13	-	103474019	103474072
258136770	chr1	103471764	103471956	103471789	103471928	COL11A1	NM_080630	4	65	14	-	103471818	103471871
267389279	chr1	103471570	103471705	103471593	103471682	COL11A1	NM_080630	4	65	15	-	103471624	103471677
263904662	chr1	103471210	103471421	103471238	103471403	COL11A1	NM_080630	4	65	16	-	103471394	103471447
263904850	chr1	103471376	103471597	103471404	103471574	COL11A1	NM_080630	4	65	16	-	103471394	103471447
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_080630	4	65	17	-	103470164	103470217
269277244	chr1	103470166	103470322	103470189	103470301	COL11A1	NM_080630	4	65	17	-	103470164	103470217
264578556	chr1	103469863	103470033	103469889	103470009	COL11A1	NM_080630	4	65	18	-	103470000	103470044
264591745	chr1	103470016	103470228	103470040	103470204	COL11A1	NM_080630	4	65	18	-	103470000	103470044
269266422	chr1	103469984	103470181	103470010	103470153	COL11A1	NM_080630	4	65	18	-	103470000	103470044
267677208	chr1	103468684	103468903	103468705	103468876	COL11A1	NM_080630	4	65	19	-	103468771	103468824
268583156	chr1	103468126	103468350	103468151	103468328	COL11A1	NM_080630	4	65	20	-	103468303	103468347
268583898	chr1	103468298	103468502	103468322	103468474	COL11A1	NM_080630	4	65	20	-	103468303	103468347
263208014	chr1	103467947	103468123	103467971	103468095	COL11A1	NM_080630	4	65	21	-	103467984	103468037
266940616	chr1	103467310	103467524	103467334	103467503	COL11A1	NM_080630	4	65	22	-	103467481	103467525
266956643	chr1	103467477	103467696	103467503	103467672	COL11A1	NM_080630	4	65	22	-	103467481	103467525
285850381	chr1	103463828	103464019	103463859	103463992	COL11A1	NM_080630	4	65	23	-	103463866	103463919
287545341	chr1	103462567	103462692	103462595	103462666	COL11A1	NM_080630	4	65	24	-	103462636	103462680
287545346	chr1	103462645	103462816	103462667	103462788	COL11A1	NM_080630	4	65	24	-	103462636	103462680
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_080630	4	65	25	-	103461545	103461598
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_080630	4	65	25	-	103461545	103461598
267993173	chr1	103461303	103461463	103461331	103461442	COL11A1	NM_080630	4	65	26	-	103461420	103461464
267994606	chr1	103461437	103461627	103461460	103461596	COL11A1	NM_080630	4	65	26	-	103461420	103461464
286190411	chr1	103461416	103461588	103461443	103461564	COL11A1	NM_080630	4	65	26	-	103461420	103461464

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268611523	chr1	103454944	103455105	103454976	103455080	COL11A1	NM_080630	4	65	27	-	103455074	103455127
268611531	chr1	103455047	103455257	103455079	103455230	COL11A1	NM_080630	4	65	27	-	103455074	103455127
267832844	chr1	103453142	103453316	103453165	103453293	COL11A1	NM_080630	4	65	28	-	103453189	103453296
267436171	chr1	103449546	103449729	103449568	103449703	COL11A1	NM_080630	4	65	29	-	103449694	103449747
267438589	chr1	103449679	103449869	103449704	103449841	COL11A1	NM_080630	4	65	29	-	103449694	103449747
263550626	chr1	103444931	103445087	103444953	103445062	COL11A1	NM_080630	4	65	30	-	103444938	103444991
266868808	chr1	103444496	103444720	103444523	103444691	COL11A1	NM_080630	4	65	31	-	103444616	103444660
267061252	chr1	103444340	103444506	103444367	103444478	COL11A1	NM_080630	4	65	32	-	103444416	103444469
268666431	chr1	103444158	103444364	103444186	103444336	COL11A1	NM_080630	4	65	33	-	103444264	103444308
267475919	chr1	103440357	103440561	103440383	103440534	COL11A1	NM_080630	4	65	34	-	103440386	103440439
265725259	chr1	103435768	103435957	103435789	103435926	COL11A1	NM_080630	4	65	35	-	103435775	103435828
267916351	chr1	103430880	103431103	103430907	103431079	COL11A1	NM_080630	4	65	36	-	103431043	103431096
267916479	chr1	103431030	103431204	103431054	103431174	COL11A1	NM_080630	4	65	36	-	103431043	103431096
269193904	chr1	103428056	103428258	103428084	103428237	COL11A1	NM_080630	4	65	37	-	103428209	103428316
269196827	chr1	103428204	103428388	103428228	103428360	COL11A1	NM_080630	4	65	37	-	103428209	103428316
268158870	chr1	103427768	103427957	103427789	103427929	COL11A1	NM_080630	4	65	38	-	103427732	103427821
285945377	chr1	103427677	103427812	103427707	103427788	COL11A1	NM_080630	4	65	38	-	103427732	103427821
257321149	chr1	103427344	103427545	103427372	103427513	COL11A1	NM_080630	4	65	39	-	103427422	103427475
264439090	chr1	103412300	103412517	103412323	103412496	COL11A1	NM_080630	4	65	40	-	103412405	103412512
264452778	chr1	103412464	103412672	103412484	103412647	COL11A1	NM_080630	4	65	40	-	103412405	103412512
266869427	chr1	103405841	103406045	103405869	103406017	COL11A1	NM_080630	4	65	41	-	103405883	103405990
269340143	chr1	103404589	103404793	103404613	103404770	COL11A1	NM_080630	4	65	42	-	103404591	103404644
287501982	chr1	103404456	103404639	103404481	103404620	COL11A1	NM_080630	4	65	42	-	103404591	103404644
267638150	chr1	103400517	103400718	103400544	103400691	COL11A1	NM_080630	4	65	43	-	103400616	103400669
264502914	chr1	103399944	103400122	103399968	103400099	COL11A1	NM_080630	4	65	44	-	103400005	103400112
264521869	chr1	103400079	103400249	103400100	103400221	COL11A1	NM_080630	4	65	44	-	103400005	103400112
258812152	chr1	103388905	103389129	103388929	103389101	COL11A1	NM_080630	4	65	45	-	103388892	103388945
284987101	chr1	103388837	103388966	103388863	103388934	COL11A1	NM_080630	4	65	45	-	103388892	103388945
257911326	chr1	103386930	103387106	103386954	103387087	COL11A1	NM_080630	4	65	46	-	103387074	103387127
257915763	chr1	103387060	103387275	103387087	103387247	COL11A1	NM_080630	4	65	46	-	103387074	103387127
265677225	chr1	103385722	103385931	103385751	103385911	COL11A1	NM_080630	4	65	47	-	103385867	103385920
265677618	chr1	103385871	103386093	103385893	103386066	COL11A1	NM_080630	4	65	47	-	103385867	103385920
266371875	chr1	103381060	103381256	103381085	103381228	COL11A1	NM_080630	4	65	48	-	103381187	103381240
266382837	chr1	103381211	103381413	103381229	103381385	COL11A1	NM_080630	4	65	48	-	103381187	103381240
263154089	chr1	103380159	103380339	103380185	103380322	COL11A1	NM_080630	4	65	49	-	103380260	103380367
261551842	chr1	103379751	103379971	103379779	103379949	COL11A1	NM_080630	4	65	50	-	103379908	103379961
261556488	chr1	103379929	103380056	103379950	103380029	COL11A1	NM_080630	4	65	50	-	103379908	103379961
260147361	chr1	103379098	103379227	103379127	103379204	COL11A1	NM_080630	4	65	51	-	103379193	103379246
260151355	chr1	103379195	103379419	103379218	103379391	COL11A1	NM_080630	4	65	51	-	103379193	103379246
267830700	chr1	103377631	103377855	103377653	103377828	COL11A1	NM_080630	4	65	52	-	103377715	103377768
268784639	chr1	103364349	103364552	103364377	103364534	COL11A1	NM_080630	4	65	53	-	103364497	103364550

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268786914	chr1	103364233	103364375	103364251	103364347	COL11A1	NM_080630	4	65	54	-	103364222	103364329
260581473	chr1	103363515	103363713	103363547	103363695	COL11A1	NM_080630	4	65	55	-	103363681	103363734
260581810	chr1	103363664	103363872	103363692	103363847	COL11A1	NM_080630	4	65	55	-	103363681	103363734
266630393	chr1	103355848	103356072	103355875	103356044	COL11A1	NM_080630	4	65	56	-	103356007	103356060
266634864	chr1	103356022	103356163	103356041	103356133	COL11A1	NM_080630	4	65	56	-	103356007	103356060
268213011	chr1	103354900	103355039	103354932	103355017	COL11A1	NM_080630	4	65	57	-	103355011	103355118
268216218	chr1	103355008	103355134	103355027	103355111	COL11A1	NM_080630	4	65	57	-	103355011	103355118
268216720	chr1	103355088	103355302	103355112	103355276	COL11A1	NM_080630	4	65	57	-	103355011	103355118
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_080630	4	65	58	-	103354422	103354475
263436532	chr1	103354432	103354626	103354453	103354598	COL11A1	NM_080630	4	65	58	-	103354422	103354475
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_080630	4	65	59	-	103354279	103354314
257302244	chr1	103354274	103354482	103354301	103354459	COL11A1	NM_080630	4	65	59	-	103354279	103354314
257283083	chr1	103354150	103354370	103354172	103354342	COL11A1	NM_080630	4	65	60	-	103354133	103354186
268814516	chr1	103354069	103354287	103354092	103354260	COL11A1	NM_080630	4	65	60	-	103354133	103354186
260880134	chr1	103352299	103352504	103352320	103352477	COL11A1	NM_080630	4	65	61	-	103352363	103352612
260938554	chr1	103352454	103352654	103352478	103352626	COL11A1	NM_080630	4	65	61	-	103352363	103352612
260975454	chr1	103348693	103348841	103348719	103348818	COL11A1	NM_080630	4	65	62	-	103348755	103348867
285945847	chr1	103348791	103348932	103348819	103348901	COL11A1	NM_080630	4	65	62	-	103348755	103348867
268004777	chr1	103347133	103347357	103347156	103347329	COL11A1	NM_080630	4	65	63	-	103347253	103347321
264528733	chr1	103345172	103345392	103345192	103345366	COL11A1	NM_080630	4	65	64	-	103345239	103345472
264566488	chr1	103345346	103345549	103345367	103345521	COL11A1	NM_080630	4	65	64	-	103345239	103345472
267664076	chr1	103343423	103343640	103343445	103343612	COL11A1	NM_080630	4	65	65	-	103342023	103343721
267668071	chr1	103343590	103343807	103343613	103343784	COL11A1	NM_080630	4	65	65	-	103342023	103343721
268544860	chr6	33159815	33160039	33159839	33160022	COL11A2	NM_001163771	1	5	1	-	33159936	33160245
261807702	chr6	33157072	33157283	33157091	33157258	COL11A2	NM_001163771	1	5	2	-	33157097	33157246
265825975	chr6	33156659	33156836	33156681	33156813	COL11A2	NM_001163771	1	5	3	-	33156755	33156965
265837609	chr6	33156785	33157004	33156804	33156980	COL11A2	NM_001163771	1	5	3	-	33156755	33156965
263478813	chr6	33156109	33156330	33156131	33156306	COL11A2	NM_001163771	1	5	4	-	33156139	33156301
267374697	chr6	33154295	33154457	33154318	33154435	COL11A2	NM_001163771	1	5	5	-	33154222	33154595
267379955	chr6	33154414	33154622	33154436	33154600	COL11A2	NM_001163771	1	5	5	-	33154222	33154595
268544860	chr6	33159815	33160039	33159839	33160022	COL11A2	NM_080679	2	63	1	-	33159936	33160245
261807702	chr6	33157072	33157283	33157091	33157258	COL11A2	NM_080679	2	63	2	-	33157097	33157246
265825975	chr6	33156659	33156836	33156681	33156813	COL11A2	NM_080679	2	63	3	-	33156755	33156965
265837609	chr6	33156785	33157004	33156804	33156980	COL11A2	NM_080679	2	63	3	-	33156755	33156965
263478813	chr6	33156109	33156330	33156131	33156306	COL11A2	NM_080679	2	63	4	-	33156139	33156301
267374697	chr6	33154295	33154457	33154318	33154435	COL11A2	NM_080679	2	63	5	-	33154404	33154595
267379955	chr6	33154414	33154622	33154436	33154600	COL11A2	NM_080679	2	63	5	-	33154404	33154595
268572053	chr6	33148796	33149019	33148820	33148996	COL11A2	NM_080679	2	63	6	-	33148888	33148947
267792033	chr6	33148602	33148813	33148623	33148787	COL11A2	NM_080679	2	63	7	-	33148741	33148782
257683131	chr6	33148320	33148536	33148341	33148512	COL11A2	NM_080679	2	63	8	-	33148445	33148507
268579270	chr6	33147939	33148143	33147962	33148119	COL11A2	NM_080679	2	63	9	-	33148035	33148109

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267473214	chr6	33147385	33147609	33147407	33147587	COL11A2	NM_080679	2	63	10	-	33147496	33147582
262650771	chr6	33147128	33147344	33147153	33147321	COL11A2	NM_080679	2	63	11	-	33147208	33147264
268657633	chr6	33146957	33147091	33146979	33147069	COL11A2	NM_080679	2	63	12	-	33147008	33147061
257438107	chr6	33146761	33146981	33146783	33146957	COL11A2	NM_080679	2	63	13	-	33146850	33146903
265267240	chr6	33146604	33146781	33146626	33146758	COL11A2	NM_080679	2	63	14	-	33146697	33146750
259630541	chr6	33146318	33146539	33146339	33146516	COL11A2	NM_080679	2	63	15	-	33146456	33146509
260241824	chr6	33146140	33146293	33146160	33146270	COL11A2	NM_080679	2	63	16	-	33146212	33146265
260206591	chr6	33145981	33146159	33146002	33146139	COL11A2	NM_080679	2	63	17	-	33146085	33146129
267576981	chr6	33145834	33146026	33145855	33145999	COL11A2	NM_080679	2	63	18	-	33145909	33145962
267731627	chr6	33145290	33145509	33145314	33145488	COL11A2	NM_080679	2	63	19	-	33145439	33145483
268689841	chr6	33145079	33145294	33145101	33145267	COL11A2	NM_080679	2	63	20	-	33145189	33145242
267952032	chr6	33144835	33145031	33144857	33145007	COL11A2	NM_080679	2	63	21	-	33144958	33145002
262131111	chr6	33144627	33144851	33144649	33144830	COL11A2	NM_080679	2	63	22	-	33144769	33144822
266569983	chr6	33144350	33144574	33144371	33144547	COL11A2	NM_080679	2	63	23	-	33144498	33144542
263035537	chr6	33144132	33144307	33144154	33144282	COL11A2	NM_080679	2	63	24	-	33144210	33144263
266127553	chr6	33143902	33144123	33143927	33144097	COL11A2	NM_080679	2	63	25	-	33144036	33144080
257282256	chr6	33143673	33143874	33143694	33143851	COL11A2	NM_080679	2	63	26	-	33143793	33143846
269236806	chr6	33143325	33143540	33143345	33143519	COL11A2	NM_080679	2	63	27	-	33143351	33143458
259432061	chr6	33142224	33142389	33142247	33142366	COL11A2	NM_080679	2	63	28	-	33142304	33142357
269205823	chr6	33141835	33142051	33141858	33142024	COL11A2	NM_080679	2	63	29	-	33141942	33141995
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080679	2	63	30	-	33141788	33141832
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080679	2	63	31	-	33141650	33141703
265658785	chr6	33141532	33141742	33141555	33141718	COL11A2	NM_080679	2	63	31	-	33141650	33141703
267485463	chr6	33141384	33141555	33141405	33141532	COL11A2	NM_080679	2	63	32	-	33141478	33141522
261045154	chr6	33141243	33141465	33141262	33141445	COL11A2	NM_080679	2	63	33	-	33141279	33141332
257303733	chr6	33141093	33141222	33141114	33141200	COL11A2	NM_080679	2	63	34	-	33141125	33141178
268753555	chr6	33140782	33140920	33140804	33140897	COL11A2	NM_080679	2	63	35	-	33140837	33140890
268889714	chr6	33140224	33140448	33140248	33140426	COL11A2	NM_080679	2	63	36	-	33140307	33140414
257466277	chr6	33140016	33140208	33140036	33140184	COL11A2	NM_080679	2	63	37	-	33140066	33140155
267991895	chr6	33139736	33139909	33139757	33139885	COL11A2	NM_080679	2	63	38	-	33139827	33139880
264363791	chr6	33139445	33139668	33139464	33139645	COL11A2	NM_080679	2	63	39	-	33139490	33139597
264857634	chr6	33139190	33139379	33139213	33139358	COL11A2	NM_080679	2	63	40	-	33139244	33139351
267078121	chr6	33138942	33139134	33138964	33139106	COL11A2	NM_080679	2	63	41	-	33139048	33139101
261604288	chr6	33138751	33138975	33138778	33138950	COL11A2	NM_080679	2	63	42	-	33138891	33138944
267432272	chr6	33138527	33138731	33138548	33138708	COL11A2	NM_080679	2	63	43	-	33138587	33138694
267342915	chr6	33138192	33138416	33138214	33138392	COL11A2	NM_080679	2	63	44	-	33138334	33138387
257869172	chr6	33137988	33138188	33138009	33138162	COL11A2	NM_080679	2	63	45	-	33138103	33138156
263943182	chr6	33137713	33137908	33137740	33137882	COL11A2	NM_080679	2	63	46	-	33137824	33137877
267971362	chr6	33137499	33137698	33137520	33137670	COL11A2	NM_080679	2	63	47	-	33137608	33137661
258830596	chr6	33137091	33137309	33137113	33137289	COL11A2	NM_080679	2	63	48	-	33137160	33137267
268268277	chr6	33136596	33136817	33136618	33136791	COL11A2	NM_080679	2	63	49	-	33136732	33136785

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266407806	chr6	33136348	33136564	33136369	33136542	COL11A2	NM_080679	2	63	50	-	33136483	33136536
263893543	chr6	33136213	33136374	33136231	33136354	COL11A2	NM_080679	2	63	51	-	33136296	33136349
268322332	chr6	33135449	33135662	33135469	33135641	COL11A2	NM_080679	2	63	52	-	33135576	33135629
267461591	chr6	33135125	33135349	33135144	33135327	COL11A2	NM_080679	2	63	53	-	33135203	33135310
267656646	chr6	33134895	33135118	33134915	33135100	COL11A2	NM_080679	2	63	54	-	33135041	33135094
264567485	chr6	33134773	33134933	33134793	33134907	COL11A2	NM_080679	2	63	55	-	33134847	33134900
268581784	chr6	33134455	33134647	33134476	33134622	COL11A2	NM_080679	2	63	56	-	33134497	33134604
259710812	chr6	33134149	33134373	33134170	33134353	COL11A2	NM_080679	2	63	57	-	33134290	33134343
268624743	chr6	33133791	33134013	33133813	33133988	COL11A2	NM_080679	2	63	58	-	33133948	33133983
267483453	chr6	33133618	33133791	33133639	33133766	COL11A2	NM_080679	2	63	59	-	33133708	33133761
265297255	chr6	33133292	33133512	33133313	33133490	COL11A2	NM_080679	2	63	60	-	33133326	33133593
265313759	chr6	33133437	33133642	33133459	33133620	COL11A2	NM_080679	2	63	60	-	33133326	33133593
257852819	chr6	33132478	33132696	33132506	33132673	COL11A2	NM_080679	2	63	61	-	33132629	33132741
257858861	chr6	33132638	33132861	33132658	33132837	COL11A2	NM_080679	2	63	61	-	33132629	33132741
261105121	chr6	33131870	33132087	33131892	33132066	COL11A2	NM_080679	2	63	62	-	33132044	33132250
261136625	chr6	33132045	33132268	33132067	33132245	COL11A2	NM_080679	2	63	62	-	33132044	33132250
261160974	chr6	33132226	33132350	33132246	33132330	COL11A2	NM_080679	2	63	62	-	33132044	33132250
264964366	chr6	33131418	33131636	33131438	33131613	COL11A2	NM_080679	2	63	63	-	33130469	33131595
268544860	chr6	33159815	33160039	33159839	33160022	COL11A2	NM_080680	3	66	1	-	33159936	33160245
261807702	chr6	33157072	33157283	33157091	33157258	COL11A2	NM_080680	3	66	2	-	33157097	33157246
265825975	chr6	33156659	33156836	33156681	33156813	COL11A2	NM_080680	3	66	3	-	33156755	33156965
265837609	chr6	33156785	33157004	33156804	33156980	COL11A2	NM_080680	3	66	3	-	33156755	33156965
263478813	chr6	33156109	33156330	33156131	33156306	COL11A2	NM_080680	3	66	4	-	33156139	33156301
267374697	chr6	33154295	33154457	33154318	33154435	COL11A2	NM_080680	3	66	5	-	33154404	33154595
267379955	chr6	33154414	33154622	33154436	33154600	COL11A2	NM_080680	3	66	5	-	33154404	33154595
267367169	chr6	33153355	33153565	33153380	33153547	COL11A2	NM_080680	3	66	6	-	33153478	33153555
264154798	chr6	33152639	33152863	33152663	33152839	COL11A2	NM_080680	3	66	7	-	33152769	33152831
269317089	chr6	33151793	33152014	33151820	33151989	COL11A2	NM_080680	3	66	8	-	33151922	33152101
269327248	chr6	33151966	33152160	33151990	33152140	COL11A2	NM_080680	3	66	8	-	33151922	33152101
268572053	chr6	33148796	33149019	33148820	33148996	COL11A2	NM_080680	3	66	9	-	33148888	33148947
267792033	chr6	33148602	33148813	33148623	33148787	COL11A2	NM_080680	3	66	10	-	33148741	33148782
257683131	chr6	33148320	33148536	33148341	33148512	COL11A2	NM_080680	3	66	11	-	33148445	33148507
268579270	chr6	33147939	33148143	33147962	33148119	COL11A2	NM_080680	3	66	12	-	33148035	33148109
267473214	chr6	33147385	33147609	33147407	33147587	COL11A2	NM_080680	3	66	13	-	33147496	33147582
262650771	chr6	33147128	33147344	33147153	33147321	COL11A2	NM_080680	3	66	14	-	33147208	33147264
268657633	chr6	33146957	33147091	33146979	33147069	COL11A2	NM_080680	3	66	15	-	33147008	33147061
257438107	chr6	33146761	33146981	33146783	33146957	COL11A2	NM_080680	3	66	16	-	33146850	33146903
265267240	chr6	33146604	33146781	33146626	33146758	COL11A2	NM_080680	3	66	17	-	33146697	33146750
259630541	chr6	33146318	33146539	33146339	33146516	COL11A2	NM_080680	3	66	18	-	33146456	33146509
260241824	chr6	33146140	33146293	33146160	33146270	COL11A2	NM_080680	3	66	19	-	33146212	33146265
260206591	chr6	33145981	33146159	33146002	33146139	COL11A2	NM_080680	3	66	20	-	33146085	33146129

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267576981	chr6	33145834	33146026	33145855	33145999	COL11A2	NM_080680	3	66	21	-	33145909	33145962
267731627	chr6	33145290	33145509	33145314	33145488	COL11A2	NM_080680	3	66	22	-	33145439	33145483
268689841	chr6	33145079	33145294	33145101	33145267	COL11A2	NM_080680	3	66	23	-	33145189	33145242
267952032	chr6	33144835	33145031	33144857	33145007	COL11A2	NM_080680	3	66	24	-	33144958	33145002
262131111	chr6	33144627	33144851	33144649	33144830	COL11A2	NM_080680	3	66	25	-	33144769	33144822
266569983	chr6	33144350	33144574	33144371	33144547	COL11A2	NM_080680	3	66	26	-	33144498	33144542
263035537	chr6	33144132	33144307	33144154	33144282	COL11A2	NM_080680	3	66	27	-	33144210	33144263
266127553	chr6	33143902	33144123	33143927	33144097	COL11A2	NM_080680	3	66	28	-	33144036	33144080
257282256	chr6	33143673	33143874	33143694	33143851	COL11A2	NM_080680	3	66	29	-	33143793	33143846
269236806	chr6	33143325	33143540	33143345	33143519	COL11A2	NM_080680	3	66	30	-	33143351	33143458
259432061	chr6	33142224	33142389	33142247	33142366	COL11A2	NM_080680	3	66	31	-	33142304	33142357
269205823	chr6	33141835	33142051	33141858	33142024	COL11A2	NM_080680	3	66	32	-	33141942	33141995
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080680	3	66	33	-	33141788	33141832
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080680	3	66	34	-	33141650	33141703
265658785	chr6	33141532	33141742	33141555	33141718	COL11A2	NM_080680	3	66	34	-	33141650	33141703
267485463	chr6	33141384	33141555	33141405	33141532	COL11A2	NM_080680	3	66	35	-	33141478	33141522
261045154	chr6	33141243	33141465	33141262	33141445	COL11A2	NM_080680	3	66	36	-	33141279	33141332
257303733	chr6	33141093	33141222	33141114	33141200	COL11A2	NM_080680	3	66	37	-	33141125	33141178
268753555	chr6	33140782	33140920	33140804	33140897	COL11A2	NM_080680	3	66	38	-	33140837	33140890
268889714	chr6	33140224	33140448	33140248	33140426	COL11A2	NM_080680	3	66	39	-	33140307	33140414
257466277	chr6	33140016	33140208	33140036	33140184	COL11A2	NM_080680	3	66	40	-	33140066	33140155
267991895	chr6	33139736	33139909	33139757	33139885	COL11A2	NM_080680	3	66	41	-	33139827	33139880
264363791	chr6	33139445	33139668	33139464	33139645	COL11A2	NM_080680	3	66	42	-	33139490	33139597
264857634	chr6	33139190	33139379	33139213	33139358	COL11A2	NM_080680	3	66	43	-	33139244	33139351
267078121	chr6	33138942	33139134	33138964	33139106	COL11A2	NM_080680	3	66	44	-	33139048	33139101
261604288	chr6	33138751	33138975	33138778	33138950	COL11A2	NM_080680	3	66	45	-	33138891	33138944
267432272	chr6	33138527	33138731	33138548	33138708	COL11A2	NM_080680	3	66	46	-	33138587	33138694
267342915	chr6	33138192	33138416	33138214	33138392	COL11A2	NM_080680	3	66	47	-	33138334	33138387
257869172	chr6	33137988	33138188	33138009	33138162	COL11A2	NM_080680	3	66	48	-	33138103	33138156
263943182	chr6	33137713	33137908	33137740	33137882	COL11A2	NM_080680	3	66	49	-	33137824	33137877
267971362	chr6	33137499	33137698	33137520	33137670	COL11A2	NM_080680	3	66	50	-	33137608	33137661
258830596	chr6	33137091	33137309	33137113	33137289	COL11A2	NM_080680	3	66	51	-	33137160	33137267
268268277	chr6	33136596	33136817	33136618	33136791	COL11A2	NM_080680	3	66	52	-	33136732	33136785
266407806	chr6	33136348	33136564	33136369	33136542	COL11A2	NM_080680	3	66	53	-	33136483	33136536
263893543	chr6	33136213	33136374	33136231	33136354	COL11A2	NM_080680	3	66	54	-	33136296	33136349
268322332	chr6	33135449	33135662	33135469	33135641	COL11A2	NM_080680	3	66	55	-	33135576	33135629
267461591	chr6	33135125	33135349	33135144	33135327	COL11A2	NM_080680	3	66	56	-	33135203	33135310
267656646	chr6	33134895	33135118	33134915	33135100	COL11A2	NM_080680	3	66	57	-	33135041	33135094
264567485	chr6	33134773	33134933	33134793	33134907	COL11A2	NM_080680	3	66	58	-	33134847	33134900
268581784	chr6	33134455	33134647	33134476	33134622	COL11A2	NM_080680	3	66	59	-	33134497	33134604
259710812	chr6	33134149	33134373	33134170	33134353	COL11A2	NM_080680	3	66	60	-	33134290	33134343

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268624743	chr6	33133791	33134013	33133813	33133988	COL11A2	NM_080680	3	66	61	-	33133948	33133983
267483453	chr6	33133618	33133791	33133639	33133766	COL11A2	NM_080680	3	66	62	-	33133708	33133761
265297255	chr6	33133292	33133512	33133313	33133490	COL11A2	NM_080680	3	66	63	-	33133326	33133593
265313759	chr6	33133437	33133642	33133459	33133620	COL11A2	NM_080680	3	66	63	-	33133326	33133593
257852819	chr6	33132478	33132696	33132506	33132673	COL11A2	NM_080680	3	66	64	-	33132629	33132741
257858861	chr6	33132638	33132861	33132658	33132837	COL11A2	NM_080680	3	66	64	-	33132629	33132741
261105121	chr6	33131870	33132087	33131892	33132066	COL11A2	NM_080680	3	66	65	-	33132044	33132250
261136625	chr6	33132045	33132268	33132067	33132245	COL11A2	NM_080680	3	66	65	-	33132044	33132250
261160974	chr6	33132226	33132350	33132246	33132330	COL11A2	NM_080680	3	66	65	-	33132044	33132250
264964366	chr6	33131418	33131636	33131438	33131613	COL11A2	NM_080680	3	66	66	-	33130469	33131595
268544860	chr6	33159815	33160039	33159839	33160022	COL11A2	NM_080681	4	64	1	-	33159936	33160245
261807702	chr6	33157072	33157283	33157091	33157258	COL11A2	NM_080681	4	64	2	-	33157097	33157246
265825975	chr6	33156659	33156836	33156681	33156813	COL11A2	NM_080681	4	64	3	-	33156755	33156965
265837609	chr6	33156785	33157004	33156804	33156980	COL11A2	NM_080681	4	64	3	-	33156755	33156965
263478813	chr6	33156109	33156330	33156131	33156306	COL11A2	NM_080681	4	64	4	-	33156139	33156301
267374697	chr6	33154295	33154457	33154318	33154435	COL11A2	NM_080681	4	64	5	-	33154404	33154595
267379955	chr6	33154414	33154622	33154436	33154600	COL11A2	NM_080681	4	64	5	-	33154404	33154595
264154798	chr6	33152639	33152863	33152663	33152839	COL11A2	NM_080681	4	64	6	-	33152769	33152831
268572053	chr6	33148796	33149019	33148820	33148996	COL11A2	NM_080681	4	64	7	-	33148888	33148947
267792033	chr6	33148602	33148813	33148623	33148787	COL11A2	NM_080681	4	64	8	-	33148741	33148782
257683131	chr6	33148320	33148536	33148341	33148512	COL11A2	NM_080681	4	64	9	-	33148445	33148507
268579270	chr6	33147939	33148143	33147962	33148119	COL11A2	NM_080681	4	64	10	-	33148035	33148109
267473214	chr6	33147385	33147609	33147407	33147587	COL11A2	NM_080681	4	64	11	-	33147496	33147582
262650771	chr6	33147128	33147344	33147153	33147321	COL11A2	NM_080681	4	64	12	-	33147208	33147264
268657633	chr6	33146957	33147091	33146979	33147069	COL11A2	NM_080681	4	64	13	-	33147008	33147061
257438107	chr6	33146761	33146981	33146783	33146957	COL11A2	NM_080681	4	64	14	-	33146850	33146903
265267240	chr6	33146604	33146781	33146626	33146758	COL11A2	NM_080681	4	64	15	-	33146697	33146750
259630541	chr6	33146318	33146539	33146339	33146516	COL11A2	NM_080681	4	64	16	-	33146456	33146509
260241824	chr6	33146140	33146293	33146160	33146270	COL11A2	NM_080681	4	64	17	-	33146212	33146265
260206591	chr6	33145981	33146159	33146002	33146139	COL11A2	NM_080681	4	64	18	-	33146085	33146129
267576981	chr6	33145834	33146026	33145855	33145999	COL11A2	NM_080681	4	64	19	-	33145909	33145962
267731627	chr6	33145290	33145509	33145314	33145488	COL11A2	NM_080681	4	64	20	-	33145439	33145483
268689841	chr6	33145079	33145294	33145101	33145267	COL11A2	NM_080681	4	64	21	-	33145189	33145242
267952032	chr6	33144835	33145031	33144857	33145007	COL11A2	NM_080681	4	64	22	-	33144958	33145002
262131111	chr6	33144627	33144851	33144649	33144830	COL11A2	NM_080681	4	64	23	-	33144769	33144822
266569983	chr6	33144350	33144574	33144371	33144547	COL11A2	NM_080681	4	64	24	-	33144498	33144542
263035537	chr6	33144132	33144307	33144154	33144282	COL11A2	NM_080681	4	64	25	-	33144210	33144263
266127553	chr6	33143902	33144123	33143927	33144097	COL11A2	NM_080681	4	64	26	-	33144036	33144080
257282256	chr6	33143673	33143874	33143694	33143851	COL11A2	NM_080681	4	64	27	-	33143793	33143846
269236806	chr6	33143325	33143540	33143345	33143519	COL11A2	NM_080681	4	64	28	-	33143351	33143458
259432061	chr6	33142224	33142389	33142247	33142366	COL11A2	NM_080681	4	64	29	-	33142304	33142357

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269205823	chr6	33141835	33142051	33141858	33142024	COL11A2	NM_080681	4	64	30	-	33141942	33141995
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080681	4	64	31	-	33141788	33141832
259425792	chr6	33141640	33141864	33141663	33141838	COL11A2	NM_080681	4	64	32	-	33141650	33141703
265658785	chr6	33141532	33141742	33141555	33141718	COL11A2	NM_080681	4	64	32	-	33141650	33141703
267485463	chr6	33141384	33141555	33141405	33141532	COL11A2	NM_080681	4	64	33	-	33141478	33141522
261045154	chr6	33141243	33141465	33141262	33141445	COL11A2	NM_080681	4	64	34	-	33141279	33141332
257303733	chr6	33141093	33141222	33141114	33141200	COL11A2	NM_080681	4	64	35	-	33141125	33141178
268753555	chr6	33140782	33140920	33140804	33140897	COL11A2	NM_080681	4	64	36	-	33140837	33140890
268889714	chr6	33140224	33140448	33140248	33140426	COL11A2	NM_080681	4	64	37	-	33140307	33140414
257466277	chr6	33140016	33140208	33140036	33140184	COL11A2	NM_080681	4	64	38	-	33140066	33140155
267991895	chr6	33139736	33139909	33139757	33139885	COL11A2	NM_080681	4	64	39	-	33139827	33139880
264363791	chr6	33139445	33139668	33139464	33139645	COL11A2	NM_080681	4	64	40	-	33139490	33139597
264857634	chr6	33139190	33139379	33139213	33139358	COL11A2	NM_080681	4	64	41	-	33139244	33139351
267078121	chr6	33138942	33139134	33138964	33139106	COL11A2	NM_080681	4	64	42	-	33139048	33139101
261604288	chr6	33138751	33138975	33138778	33138950	COL11A2	NM_080681	4	64	43	-	33138891	33138944
267432272	chr6	33138527	33138731	33138548	33138708	COL11A2	NM_080681	4	64	44	-	33138587	33138694
267342915	chr6	33138192	33138416	33138214	33138392	COL11A2	NM_080681	4	64	45	-	33138334	33138387
257869172	chr6	33137988	33138188	33138009	33138162	COL11A2	NM_080681	4	64	46	-	33138103	33138156
263943182	chr6	33137713	33137908	33137740	33137882	COL11A2	NM_080681	4	64	47	-	33137824	33137877
267971362	chr6	33137499	33137698	33137520	33137670	COL11A2	NM_080681	4	64	48	-	33137608	33137661
258830596	chr6	33137091	33137309	33137113	33137289	COL11A2	NM_080681	4	64	49	-	33137160	33137267
268268277	chr6	33136596	33136817	33136618	33136791	COL11A2	NM_080681	4	64	50	-	33136732	33136785
266407806	chr6	33136348	33136564	33136369	33136542	COL11A2	NM_080681	4	64	51	-	33136483	33136536
263893543	chr6	33136213	33136374	33136231	33136354	COL11A2	NM_080681	4	64	52	-	33136296	33136349
268322332	chr6	33135449	33135662	33135469	33135641	COL11A2	NM_080681	4	64	53	-	33135576	33135629
267461591	chr6	33135125	33135349	33135144	33135327	COL11A2	NM_080681	4	64	54	-	33135203	33135310
267656646	chr6	33134895	33135118	33134915	33135100	COL11A2	NM_080681	4	64	55	-	33135041	33135094
264567485	chr6	33134773	33134933	33134793	33134907	COL11A2	NM_080681	4	64	56	-	33134847	33134900
268581784	chr6	33134455	33134647	33134476	33134622	COL11A2	NM_080681	4	64	57	-	33134497	33134604
259710812	chr6	33134149	33134373	33134170	33134353	COL11A2	NM_080681	4	64	58	-	33134290	33134343
268624743	chr6	33133791	33134013	33133813	33133988	COL11A2	NM_080681	4	64	59	-	33133948	33133983
267483453	chr6	33133618	33133791	33133639	33133766	COL11A2	NM_080681	4	64	60	-	33133708	33133761
265297255	chr6	33133292	33133512	33133313	33133490	COL11A2	NM_080681	4	64	61	-	33133326	33133593
265313759	chr6	33133437	33133642	33133459	33133620	COL11A2	NM_080681	4	64	61	-	33133326	33133593
257852819	chr6	33132478	33132696	33132506	33132673	COL11A2	NM_080681	4	64	62	-	33132629	33132741
257858861	chr6	33132638	33132861	33132658	33132837	COL11A2	NM_080681	4	64	62	-	33132629	33132741
261105121	chr6	33131870	33132087	33131892	33132066	COL11A2	NM_080681	4	64	63	-	33132044	33132250
261136625	chr6	33132045	33132268	33132067	33132245	COL11A2	NM_080681	4	64	63	-	33132044	33132250
261160974	chr6	33132226	33132350	33132246	33132330	COL11A2	NM_080681	4	64	63	-	33132044	33132250
264964366	chr6	33131418	33131636	33131438	33131613	COL11A2	NM_080681	4	64	64	-	33130469	33131595
226082590	chr17	48278719	48278906	48278737	48278880	COL1A1	NM_000088	1	51	1	-	48278772	48279000

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253669462	chr17	48276976	48277200	48276998	48277178	COL1A1	NM_000088	1	51	2	-	48277114	48277308
253669697	chr17	48277167	48277341	48277186	48277320	COL1A1	NM_000088	1	51	2	-	48277114	48277308
329246933	chr17	48276763	48276980	48276783	48276960	COL1A1	NM_000088	1	51	3	-	48276917	48276951
225643961	chr17	48276641	48276850	48276659	48276828	COL1A1	NM_000088	1	51	4	-	48276779	48276814
329246933	chr17	48276763	48276980	48276783	48276960	COL1A1	NM_000088	1	51	4	-	48276779	48276814
225643961	chr17	48276641	48276850	48276659	48276828	COL1A1	NM_000088	1	51	5	-	48276587	48276688
227017398	chr17	48276561	48276782	48276580	48276762	COL1A1	NM_000088	1	51	5	-	48276587	48276688
226129532	chr17	48275671	48275895	48275692	48275870	COL1A1	NM_000088	1	51	6	-	48275794	48275865
328596651	chr17	48275386	48275610	48275409	48275588	COL1A1	NM_000088	1	51	7	-	48275522	48275566
225676299	chr17	48275202	48275400	48275225	48275372	COL1A1	NM_000088	1	51	8	-	48275310	48275363
253715048	chr17	48275008	48275232	48275029	48275207	COL1A1	NM_000088	1	51	9	-	48275093	48275146
328623261	chr17	48274421	48274629	48274444	48274608	COL1A1	NM_000088	1	51	10	-	48274541	48274594
329006000	chr17	48274238	48274455	48274260	48274431	COL1A1	NM_000088	1	51	11	-	48274371	48274424
253773466	chr17	48273845	48274064	48273866	48274038	COL1A1	NM_000088	1	51	12	-	48273978	48274031
226201195	chr17	48273735	48273940	48273760	48273915	COL1A1	NM_000088	1	51	13	-	48273845	48273889
253773466	chr17	48273845	48274064	48273866	48274038	COL1A1	NM_000088	1	51	13	-	48273845	48273889
226504563	chr17	48273575	48273759	48273594	48273733	COL1A1	NM_000088	1	51	14	-	48273675	48273728
226187372	chr17	48273423	48273605	48273446	48273583	COL1A1	NM_000088	1	51	15	-	48273516	48273560
328626251	chr17	48273154	48273367	48273177	48273342	COL1A1	NM_000088	1	51	16	-	48273284	48273337
226018350	chr17	48272846	48273064	48272868	48273042	COL1A1	NM_000088	1	51	17	-	48272928	48273026
225861671	chr17	48272762	48272905	48272781	48272883	COL1A1	NM_000088	1	51	18	-	48272795	48272839
225631151	chr17	48272517	48272738	48272537	48272718	COL1A1	NM_000088	1	51	19	-	48272593	48272691
225766511	chr17	48272301	48272494	48272321	48272471	COL1A1	NM_000088	1	51	20	-	48272408	48272461
226440627	chr17	48272036	48272250	48272054	48272232	COL1A1	NM_000088	1	51	21	-	48272082	48272189
329557948	chr17	48271817	48272026	48271840	48272007	COL1A1	NM_000088	1	51	22	-	48271934	48271987
225659492	chr17	48271628	48271839	48271648	48271816	COL1A1	NM_000088	1	51	23	-	48271710	48271808
225839989	chr17	48271402	48271577	48271422	48271554	COL1A1	NM_000088	1	51	24	-	48271491	48271544
225495550	chr17	48271271	48271492	48271292	48271468	COL1A1	NM_000088	1	51	25	-	48271304	48271402
226281609	chr17	48270313	48270503	48270334	48270476	COL1A1	NM_000088	1	51	26	-	48270355	48270408
226496635	chr17	48270052	48270247	48270074	48270225	COL1A1	NM_000088	1	51	27	-	48270158	48270211
225946458	chr17	48269911	48270082	48269936	48270059	COL1A1	NM_000088	1	51	28	-	48270001	48270054
227086360	chr17	48269746	48269935	48269771	48269909	COL1A1	NM_000088	1	51	29	-	48269836	48269889
225654024	chr17	48269231	48269425	48269251	48269402	COL1A1	NM_000088	1	51	30	-	48269341	48269385
226591875	chr17	48269117	48269306	48269135	48269286	COL1A1	NM_000088	1	51	31	-	48269149	48269247
225532498	chr17	48268659	48268879	48268684	48268856	COL1A1	NM_000088	1	51	32	-	48268744	48268851
225775851	chr17	48268126	48268317	48268148	48268290	COL1A1	NM_000088	1	51	33	-	48268178	48268285
328935844	chr17	48267759	48267981	48267780	48267962	COL1A1	NM_000088	1	51	34	-	48267904	48267957
329550528	chr17	48267552	48267772	48267573	48267746	COL1A1	NM_000088	1	51	35	-	48267688	48267741
226608355	chr17	48267287	48267497	48267306	48267479	COL1A1	NM_000088	1	51	36	-	48267362	48267469
328650207	chr17	48267079	48267300	48267100	48267279	COL1A1	NM_000088	1	51	37	-	48267220	48267273
253712235	chr17	48266937	48267126	48266957	48267101	COL1A1	NM_000088	1	51	38	-	48267040	48267093

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253968640	chr17	48266707	48266927	48266726	48266907	COL1A1	NM_000088	1	51	39	-	48266738	48266899
226042985	chr17	48266422	48266616	48266444	48266595	COL1A1	NM_000088	1	51	40	-	48266529	48266636
226050915	chr17	48266550	48266755	48266572	48266734	COL1A1	NM_000088	1	51	40	-	48266529	48266636
253781331	chr17	48266202	48266405	48266222	48266380	COL1A1	NM_000088	1	51	41	-	48266264	48266371
226530247	chr17	48266065	48266190	48266085	48266165	COL1A1	NM_000088	1	51	42	-	48266103	48266156
226255020	chr17	48265815	48266028	48265835	48266007	COL1A1	NM_000088	1	51	43	-	48265891	48265998
226423407	chr17	48265368	48265543	48265389	48265521	COL1A1	NM_000088	1	51	44	-	48265457	48265510
253629491	chr17	48265183	48265373	48265203	48265349	COL1A1	NM_000088	1	51	45	-	48265237	48265344
225558369	chr17	48264743	48264955	48264764	48264933	COL1A1	NM_000088	1	51	46	-	48264845	48264898
226986629	chr17	48264307	48264518	48264326	48264496	COL1A1	NM_000088	1	51	47	-	48264376	48264483
226580065	chr17	48263995	48264199	48264017	48264178	COL1A1	NM_000088	1	51	48	-	48264001	48264283
226587306	chr17	48264153	48264331	48264174	48264311	COL1A1	NM_000088	1	51	48	-	48264001	48264283
329536618	chr17	48263854	48264041	48263878	48264021	COL1A1	NM_000088	1	51	48	-	48264001	48264283
225525720	chr17	48263632	48263837	48263654	48263815	COL1A1	NM_000088	1	51	49	-	48263678	48263868
225531417	chr17	48263794	48263942	48263816	48263920	COL1A1	NM_000088	1	51	49	-	48263678	48263868
226700560	chr17	48263053	48263268	48263075	48263249	COL1A1	NM_000088	1	51	50	-	48263139	48263381
226706669	chr17	48263227	48263437	48263248	48263416	COL1A1	NM_000088	1	51	50	-	48263139	48263381
253693046	chr17	48262928	48263062	48262947	48263042	COL1A1	NM_000088	1	51	51	-	48261457	48263009
253699979	chr17	48262783	48262984	48262805	48262956	COL1A1	NM_000088	1	51	51	-	48261457	48263009
263407974	chr7	94024219	94024442	94024239	94024421	COL1A2	NM_000089	1	52	1	+	94023873	94024413
267253099	chr7	94026991	94027126	94027023	94027098	COL1A2	NM_000089	1	52	2	+	94027060	94027070
259316950	chr7	94028300	94028430	94028328	94028402	COL1A2	NM_000089	1	52	4	+	94028361	94028396
266332278	chr7	94029403	94029627	94029428	94029599	COL1A2	NM_000089	1	52	5	+	94029508	94029600
266335107	chr7	94029560	94029766	94029578	94029739	COL1A2	NM_000089	1	52	5	+	94029508	94029600
262071929	chr7	94030864	94031007	94030893	94030979	COL1A2	NM_000089	1	52	6	+	94030879	94030932
267316875	chr7	94033754	94033945	94033782	94033918	COL1A2	NM_000089	1	52	7	+	94033868	94033912
265227354	chr7	94033915	94034139	94033942	94034112	COL1A2	NM_000089	1	52	8	+	94034005	94034058
267866747	chr7	94034118	94034315	94034144	94034291	COL1A2	NM_000089	1	52	9	+	94034151	94034204
266940559	chr7	94034425	94034606	94034452	94034578	COL1A2	NM_000089	1	52	10	+	94034511	94034564
261646526	chr7	94034845	94035037	94034873	94035014	COL1A2	NM_000089	1	52	11	+	94034985	94035038
261653252	chr7	94034978	94035158	94035000	94035136	COL1A2	NM_000089	1	52	11	+	94034985	94035038
267250083	chr7	94035436	94035658	94035460	94035630	COL1A2	NM_000089	1	52	12	+	94035562	94035615
261072967	chr7	94037004	94037205	94037032	94037180	COL1A2	NM_000089	1	52	13	+	94037159	94037203
261074171	chr7	94037151	94037301	94037172	94037274	COL1A2	NM_000089	1	52	13	+	94037159	94037203
260507999	chr7	94037407	94037580	94037430	94037553	COL1A2	NM_000089	1	52	14	+	94037495	94037548
260522635	chr7	94037511	94037726	94037532	94037703	COL1A2	NM_000089	1	52	14	+	94037495	94037548
260522635	chr7	94037511	94037726	94037532	94037703	COL1A2	NM_000089	1	52	15	+	94037648	94037692
257857006	chr7	94037982	94038205	94038003	94038177	COL1A2	NM_000089	1	52	16	+	94038082	94038135
267290512	chr7	94038577	94038793	94038605	94038769	COL1A2	NM_000089	1	52	17	+	94038634	94038732
263632698	chr7	94038726	94038950	94038748	94038926	COL1A2	NM_000089	1	52	18	+	94038876	94038920
264894192	chr7	94038966	94039173	94038988	94039146	COL1A2	NM_000089	1	52	19	+	94039035	94039133

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261477450	chr7	94039447	94039671	94039472	94039645	COL1A2	NM_000089	1	52	20	+	94039554	94039607
265427958	chr7	94039599	94039811	94039622	94039790	COL1A2	NM_000089	1	52	21	+	94039732	94039839
265450408	chr7	94039763	94039979	94039787	94039951	COL1A2	NM_000089	1	52	21	+	94039732	94039839
268318980	chr7	94040065	94040288	94040086	94040260	COL1A2	NM_000089	1	52	22	+	94040201	94040254
269101048	chr7	94040299	94040499	94040320	94040471	COL1A2	NM_000089	1	52	23	+	94040368	94040466
258133019	chr7	94041287	94041484	94041310	94041456	COL1A2	NM_000089	1	52	24	+	94041380	94041433
264476951	chr7	94041805	94042025	94041829	94041999	COL1A2	NM_000089	1	52	25	+	94041896	94041994
269351526	chr7	94042301	94042503	94042326	94042475	COL1A2	NM_000089	1	52	26	+	94042395	94042448
268606928	chr7	94042862	94043085	94042883	94043060	COL1A2	NM_000089	1	52	27	+	94043002	94043055
267193567	chr7	94043093	94043301	94043121	94043279	COL1A2	NM_000089	1	52	28	+	94043206	94043259
263048367	chr7	94043425	94043602	94043451	94043576	COL1A2	NM_000089	1	52	29	+	94043534	94043587
263054196	chr7	94043557	94043758	94043576	94043731	COL1A2	NM_000089	1	52	29	+	94043534	94043587
265391241	chr7	94044434	94044658	94044459	94044632	COL1A2	NM_000089	1	52	30	+	94044538	94044582
261939298	chr7	94045668	94045855	94045692	94045834	COL1A2	NM_000089	1	52	31	+	94045717	94045815
268412690	chr7	94046869	94047090	94046895	94047069	COL1A2	NM_000089	1	52	32	+	94047036	94047143
268418940	chr7	94047028	94047240	94047049	94047219	COL1A2	NM_000089	1	52	32	+	94047036	94047143
267616770	chr7	94047663	94047883	94047690	94047857	COL1A2	NM_000089	1	52	33	+	94047811	94047864
261779464	chr7	94048689	94048913	94048711	94048886	COL1A2	NM_000089	1	52	34	+	94048810	94048863
258586616	chr7	94049408	94049632	94049429	94049604	COL1A2	NM_000089	1	52	35	+	94049545	94049598
267713759	chr7	94049589	94049810	94049612	94049783	COL1A2	NM_000089	1	52	36	+	94049703	94049756
268919490	chr7	94049802	94050007	94049822	94049984	COL1A2	NM_000089	1	52	37	+	94049853	94049960
263630779	chr7	94050228	94050402	94050252	94050379	COL1A2	NM_000089	1	52	38	+	94050321	94050374
269226333	chr7	94051088	94051307	94051112	94051280	COL1A2	NM_000089	1	52	39	+	94051211	94051264
266787551	chr7	94052213	94052378	94052235	94052356	COL1A2	NM_000089	1	52	40	+	94052269	94052430
266806714	chr7	94052338	94052526	94052357	94052498	COL1A2	NM_000089	1	52	40	+	94052269	94052430
268307652	chr7	94053566	94053788	94053594	94053760	COL1A2	NM_000089	1	52	41	+	94053648	94053755
267418452	chr7	94054369	94054589	94054392	94054561	COL1A2	NM_000089	1	52	42	+	94054429	94054536
268583761	chr7	94054812	94055036	94054833	94055008	COL1A2	NM_000089	1	52	43	+	94054922	94054975
264575487	chr7	94055006	94055198	94055035	94055174	COL1A2	NM_000089	1	52	44	+	94055062	94055169
258719747	chr7	94055201	94055395	94055222	94055368	COL1A2	NM_000089	1	52	45	+	94055310	94055363
268876211	chr7	94055653	94055873	94055681	94055847	COL1A2	NM_000089	1	52	46	+	94055735	94055842
268130882	chr7	94056199	94056416	94056224	94056388	COL1A2	NM_000089	1	52	47	+	94056320	94056373
268154225	chr7	94056455	94056657	94056476	94056630	COL1A2	NM_000089	1	52	48	+	94056500	94056607
265931310	chr7	94056875	94057091	94056898	94057063	COL1A2	NM_000089	1	52	49	+	94056939	94057197
265946596	chr7	94057043	94057228	94057064	94057207	COL1A2	NM_000089	1	52	49	+	94056939	94057197
263722914	chr7	94057434	94057655	94057455	94057629	COL1A2	NM_000089	1	52	50	+	94057605	94057789
263738274	chr7	94057604	94057818	94057630	94057795	COL1A2	NM_000089	1	52	50	+	94057605	94057789
267975036	chr7	94058444	94058610	94058472	94058587	COL1A2	NM_000089	1	52	51	+	94058500	94058742
267980415	chr7	94058567	94058782	94058588	94058756	COL1A2	NM_000089	1	52	51	+	94058500	94058742
265488160	chr7	94059438	94059660	94059462	94059640	COL1A2	NM_000089	1	52	52	+	94059559	94060544
265510395	chr7	94059619	94059810	94059641	94059783	COL1A2	NM_000089	1	52	52	+	94059559	94060544

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266936698	chr12	48397956	48398168	48397976	48398151	COL2A1	NM_001844	1	54	1	-	48398020	48398285
265191821	chr12	48393592	48393808	48393615	48393785	COL2A1	NM_001844	1	54	2	-	48393702	48393908
265209356	chr12	48393764	48393888	48393786	48393865	COL2A1	NM_001844	1	54	2	-	48393702	48393908
265230440	chr12	48393846	48394005	48393866	48393982	COL2A1	NM_001844	1	54	2	-	48393702	48393908
267736345	chr12	48392111	48392307	48392138	48392278	COL2A1	NM_001844	1	54	3	-	48392198	48392214
260783455	chr12	48391825	48392017	48391846	48391991	COL2A1	NM_001844	1	54	4	-	48391952	48391984
260783455	chr12	48391825	48392017	48391846	48391991	COL2A1	NM_001844	1	54	5	-	48391815	48391847
265604382	chr12	48391701	48391888	48391722	48391863	COL2A1	NM_001844	1	54	5	-	48391815	48391847
268371291	chr12	48391524	48391739	48391546	48391713	COL2A1	NM_001844	1	54	6	-	48391654	48391707
266605460	chr12	48391311	48391524	48391331	48391496	COL2A1	NM_001844	1	54	7	-	48391389	48391490
268544586	chr12	48390218	48390438	48390239	48390415	COL2A1	NM_001844	1	54	8	-	48390331	48390408
267336843	chr12	48389528	48389738	48389550	48389710	COL2A1	NM_001844	1	54	9	-	48389658	48389702
259085428	chr12	48389425	48389579	48389446	48389551	COL2A1	NM_001844	1	54	10	-	48389493	48389546
268572156	chr12	48388917	48389141	48388940	48389116	COL2A1	NM_001844	1	54	11	-	48389038	48389091
258258179	chr12	48388091	48388294	48388110	48388270	COL2A1	NM_001844	1	54	12	-	48388207	48388260
265097069	chr12	48387634	48387858	48387657	48387835	COL2A1	NM_001844	1	54	13	-	48387777	48387830
267435826	chr12	48387477	48387683	48387498	48387655	COL2A1	NM_001844	1	54	14	-	48387592	48387645
268486366	chr12	48387106	48387314	48387134	48387290	COL2A1	NM_001844	1	54	15	-	48387241	48387285
266129781	chr12	48386627	48386758	48386649	48386735	COL2A1	NM_001844	1	54	16	-	48386661	48386714
268219849	chr12	48383409	48383619	48383431	48383595	COL2A1	NM_001844	1	54	17	-	48383544	48383588
264524305	chr12	48382894	48383093	48382916	48383070	COL2A1	NM_001844	1	54	18	-	48383011	48383064
267728140	chr12	48381305	48381523	48381326	48381498	COL2A1	NM_001844	1	54	19	-	48381394	48381492
267033295	chr12	48380958	48381139	48380979	48381111	COL2A1	NM_001844	1	54	20	-	48381052	48381096
267018825	chr12	48380813	48381035	48380836	48381014	COL2A1	NM_001844	1	54	21	-	48380861	48380959
262987658	chr12	48380477	48380697	48380500	48380676	COL2A1	NM_001844	1	54	22	-	48380618	48380671
257319218	chr12	48380048	48380265	48380069	48380239	COL2A1	NM_001844	1	54	23	-	48380119	48380226
268642882	chr12	48379618	48379837	48379641	48379816	COL2A1	NM_001844	1	54	24	-	48379695	48379748
267845368	chr12	48379467	48379659	48379487	48379637	COL2A1	NM_001844	1	54	25	-	48379511	48379609
268889880	chr12	48379179	48379397	48379201	48379375	COL2A1	NM_001844	1	54	26	-	48379317	48379370
268099147	chr12	48378724	48378913	48378744	48378886	COL2A1	NM_001844	1	54	27	-	48378778	48378876
262245630	chr12	48378201	48378425	48378223	48378406	COL2A1	NM_001844	1	54	28	-	48378329	48378382
267513684	chr12	48377751	48377959	48377772	48377931	COL2A1	NM_001844	1	54	29	-	48377870	48377923
267663074	chr12	48377422	48377549	48377443	48377525	COL2A1	NM_001844	1	54	30	-	48377466	48377519
268631126	chr12	48377097	48377256	48377118	48377234	COL2A1	NM_001844	1	54	31	-	48377168	48377221
268785526	chr12	48376737	48376955	48376761	48376929	COL2A1	NM_001844	1	54	32	-	48376876	48376920
259667412	chr12	48376591	48376760	48376611	48376736	COL2A1	NM_001844	1	54	33	-	48376631	48376729
269062967	chr12	48376250	48376468	48376271	48376447	COL2A1	NM_001844	1	54	34	-	48376285	48376392
262348842	chr12	48375848	48376071	48375868	48376047	COL2A1	NM_001844	1	54	35	-	48375890	48375943
269346910	chr12	48375486	48375640	48375508	48375619	COL2A1	NM_001844	1	54	36	-	48375559	48375612
264560651	chr12	48375044	48375220	48375062	48375199	COL2A1	NM_001844	1	54	37	-	48375126	48375179
265555507	chr12	48374544	48374765	48374566	48374744	COL2A1	NM_001844	1	54	38	-	48374698	48374751

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265558472	chr12	48374678	48374897	48374702	48374877	COL2A1	NM_001844	1	54	38	-	48374698	48374751
267865639	chr12	48374293	48374502	48374314	48374481	COL2A1	NM_001844	1	54	39	-	48374337	48374444
267209816	chr12	48373749	48373957	48373769	48373933	COL2A1	NM_001844	1	54	40	-	48373792	48373845
268129907	chr12	48373182	48373398	48373202	48373377	COL2A1	NM_001844	1	54	41	-	48373294	48373347
267376888	chr12	48372313	48372516	48372333	48372493	COL2A1	NM_001844	1	54	42	-	48372380	48372541
267386604	chr12	48372471	48372595	48372491	48372573	COL2A1	NM_001844	1	54	42	-	48372380	48372541
268242894	chr12	48372005	48372221	48372026	48372199	COL2A1	NM_001844	1	54	43	-	48372074	48372181
267884790	chr12	48371708	48371931	48371728	48371908	COL2A1	NM_001844	1	54	44	-	48371793	48371900
268872447	chr12	48371256	48371471	48371280	48371445	COL2A1	NM_001844	1	54	45	-	48371383	48371436
269334895	chr12	48371068	48371245	48371090	48371222	COL2A1	NM_001844	1	54	46	-	48371103	48371210
268598628	chr12	48370855	48371034	48370876	48371013	COL2A1	NM_001844	1	54	47	-	48370885	48370938
257428720	chr12	48370533	48370733	48370553	48370710	COL2A1	NM_001844	1	54	48	-	48370595	48370702
268672488	chr12	48370167	48370377	48370188	48370355	COL2A1	NM_001844	1	54	49	-	48370297	48370350
261795216	chr12	48369659	48369883	48369680	48369860	COL2A1	NM_001844	1	54	50	-	48369746	48369853
269274009	chr12	48369023	48369237	48369043	48369220	COL2A1	NM_001844	1	54	51	-	48369100	48369388
269288466	chr12	48369201	48369423	48369221	48369400	COL2A1	NM_001844	1	54	51	-	48369100	48369388
266106271	chr12	48368341	48368540	48368367	48368518	COL2A1	NM_001844	1	54	52	-	48368458	48368645
266121996	chr12	48368496	48368715	48368519	48368693	COL2A1	NM_001844	1	54	52	-	48368458	48368645
261269959	chr12	48367837	48368037	48367858	48368016	COL2A1	NM_001844	1	54	53	-	48367872	48368114
261376128	chr12	48367996	48368211	48368017	48368187	COL2A1	NM_001844	1	54	53	-	48367872	48368114
258227924	chr12	48367148	48367369	48367169	48367346	COL2A1	NM_001844	1	54	54	-	48366748	48367336
266936698	chr12	48397956	48398168	48397976	48398151	COL2A1	NM_033150	2	53	1	-	48398020	48398285
267736345	chr12	48392111	48392307	48392138	48392278	COL2A1	NM_033150	2	53	2	-	48392198	48392214
260783455	chr12	48391825	48392017	48391846	48391991	COL2A1	NM_033150	2	53	3	-	48391952	48391984
260783455	chr12	48391825	48392017	48391846	48391991	COL2A1	NM_033150	2	53	4	-	48391815	48391847
265604382	chr12	48391701	48391888	48391722	48391863	COL2A1	NM_033150	2	53	4	-	48391815	48391847
268371291	chr12	48391524	48391739	48391546	48391713	COL2A1	NM_033150	2	53	5	-	48391654	48391707
266605460	chr12	48391311	48391524	48391331	48391496	COL2A1	NM_033150	2	53	6	-	48391389	48391490
268544586	chr12	48390218	48390438	48390239	48390415	COL2A1	NM_033150	2	53	7	-	48390331	48390408
267336843	chr12	48389528	48389738	48389550	48389710	COL2A1	NM_033150	2	53	8	-	48389658	48389702
259085428	chr12	48389425	48389579	48389446	48389551	COL2A1	NM_033150	2	53	9	-	48389493	48389546
268572156	chr12	48388917	48389141	48388940	48389116	COL2A1	NM_033150	2	53	10	-	48389038	48389091
258258179	chr12	48388091	48388294	48388110	48388270	COL2A1	NM_033150	2	53	11	-	48388207	48388260
265097069	chr12	48387634	48387858	48387657	48387835	COL2A1	NM_033150	2	53	12	-	48387777	48387830
267435826	chr12	48387477	48387683	48387498	48387655	COL2A1	NM_033150	2	53	13	-	48387592	48387645
268486366	chr12	48387106	48387314	48387134	48387290	COL2A1	NM_033150	2	53	14	-	48387241	48387285
266129781	chr12	48386627	48386758	48386649	48386735	COL2A1	NM_033150	2	53	15	-	48386661	48386714
268219849	chr12	48383409	48383619	48383431	48383595	COL2A1	NM_033150	2	53	16	-	48383544	48383588
264524305	chr12	48382894	48383093	48382916	48383070	COL2A1	NM_033150	2	53	17	-	48383011	48383064
267728140	chr12	48381305	48381523	48381326	48381498	COL2A1	NM_033150	2	53	18	-	48381394	48381492
267033295	chr12	48380958	48381139	48380979	48381111	COL2A1	NM_033150	2	53	19	-	48381052	48381096

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267018825	chr12	48380813	48381035	48380836	48381014	COL2A1	NM_033150	2	53	20	-	48380861	48380959
262987658	chr12	48380477	48380697	48380500	48380676	COL2A1	NM_033150	2	53	21	-	48380618	48380671
257319218	chr12	48380048	48380265	48380069	48380239	COL2A1	NM_033150	2	53	22	-	48380119	48380226
268642882	chr12	48379618	48379837	48379641	48379816	COL2A1	NM_033150	2	53	23	-	48379695	48379748
267845368	chr12	48379467	48379659	48379487	48379637	COL2A1	NM_033150	2	53	24	-	48379511	48379609
268889880	chr12	48379179	48379397	48379201	48379375	COL2A1	NM_033150	2	53	25	-	48379317	48379370
268099147	chr12	48378724	48378913	48378744	48378886	COL2A1	NM_033150	2	53	26	-	48378778	48378876
262245630	chr12	48378201	48378425	48378223	48378406	COL2A1	NM_033150	2	53	27	-	48378329	48378382
267513684	chr12	48377751	48377959	48377772	48377931	COL2A1	NM_033150	2	53	28	-	48377870	48377923
267663074	chr12	48377422	48377549	48377443	48377525	COL2A1	NM_033150	2	53	29	-	48377466	48377519
268631126	chr12	48377097	48377256	48377118	48377234	COL2A1	NM_033150	2	53	30	-	48377168	48377221
268785526	chr12	48376737	48376955	48376761	48376929	COL2A1	NM_033150	2	53	31	-	48376876	48376920
259667412	chr12	48376591	48376760	48376611	48376736	COL2A1	NM_033150	2	53	32	-	48376631	48376729
269062967	chr12	48376250	48376468	48376271	48376447	COL2A1	NM_033150	2	53	33	-	48376285	48376392
262348842	chr12	48375848	48376071	48375868	48376047	COL2A1	NM_033150	2	53	34	-	48375890	48375943
269346910	chr12	48375486	48375640	48375508	48375619	COL2A1	NM_033150	2	53	35	-	48375559	48375612
264560651	chr12	48375044	48375220	48375062	48375199	COL2A1	NM_033150	2	53	36	-	48375126	48375179
265555507	chr12	48374544	48374765	48374566	48374744	COL2A1	NM_033150	2	53	37	-	48374698	48374751
265558472	chr12	48374678	48374897	48374702	48374877	COL2A1	NM_033150	2	53	37	-	48374698	48374751
267865639	chr12	48374293	48374502	48374314	48374481	COL2A1	NM_033150	2	53	38	-	48374337	48374444
267209816	chr12	48373749	48373957	48373769	48373933	COL2A1	NM_033150	2	53	39	-	48373792	48373845
268129907	chr12	48373182	48373398	48373202	48373377	COL2A1	NM_033150	2	53	40	-	48373294	48373347
267376888	chr12	48372313	48372516	48372333	48372493	COL2A1	NM_033150	2	53	41	-	48372380	48372541
267386604	chr12	48372471	48372595	48372491	48372573	COL2A1	NM_033150	2	53	41	-	48372380	48372541
268242894	chr12	48372005	48372221	48372026	48372199	COL2A1	NM_033150	2	53	42	-	48372074	48372181
267884790	chr12	48371708	48371931	48371728	48371908	COL2A1	NM_033150	2	53	43	-	48371793	48371900
268872447	chr12	48371256	48371471	48371280	48371445	COL2A1	NM_033150	2	53	44	-	48371383	48371436
269334895	chr12	48371068	48371245	48371090	48371222	COL2A1	NM_033150	2	53	45	-	48371103	48371210
268598628	chr12	48370855	48371034	48370876	48371013	COL2A1	NM_033150	2	53	46	-	48370885	48370938
257428720	chr12	48370533	48370733	48370553	48370710	COL2A1	NM_033150	2	53	47	-	48370595	48370702
268672488	chr12	48370167	48370377	48370188	48370355	COL2A1	NM_033150	2	53	48	-	48370297	48370350
261795216	chr12	48369659	48369883	48369680	48369860	COL2A1	NM_033150	2	53	49	-	48369746	48369853
269274009	chr12	48369023	48369237	48369043	48369220	COL2A1	NM_033150	2	53	50	-	48369100	48369388
269288466	chr12	48369201	48369423	48369221	48369400	COL2A1	NM_033150	2	53	50	-	48369100	48369388
266106271	chr12	48368341	48368540	48368367	48368518	COL2A1	NM_033150	2	53	51	-	48368458	48368645
266121996	chr12	48368496	48368715	48368519	48368693	COL2A1	NM_033150	2	53	51	-	48368458	48368645
261269959	chr12	48367837	48368037	48367858	48368016	COL2A1	NM_033150	2	53	52	-	48367872	48368114
261376128	chr12	48367996	48368211	48368017	48368187	COL2A1	NM_033150	2	53	52	-	48367872	48368114
258227924	chr12	48367148	48367369	48367169	48367346	COL2A1	NM_033150	2	53	53	-	48366748	48367336
264015527	chr2	189839136	189839360	189839161	189839336	COL3A1	NM_000090	1	51	1	+	189839099	189839294
261112025	chr2	189849419	189849606	189849447	189849580	COL3A1	NM_000090	1	51	2	+	189849486	189849688

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261175165	chr2	189849556	189849779	189849581	189849751	COL3A1	NM_000090	1	51	2	+	189849486	189849688
269112202	chr2	189849754	189849958	189849781	189849937	COL3A1	NM_000090	1	51	3	+	189849923	189849973
269113526	chr2	189849915	189850110	189849938	189850082	COL3A1	NM_000090	1	51	3	+	189849923	189849973
267849444	chr2	189850325	189850503	189850354	189850482	COL3A1	NM_000090	1	51	4	+	189850391	189850504
267849948	chr2	189850394	189850520	189850418	189850494	COL3A1	NM_000090	1	51	4	+	189850391	189850504
267577652	chr2	189851654	189851830	189851678	189851801	COL3A1	NM_000090	1	51	5	+	189851785	189851865
267583171	chr2	189851778	189851937	189851802	189851909	COL3A1	NM_000090	1	51	5	+	189851785	189851865
265413432	chr2	189852727	189852947	189852750	189852919	COL3A1	NM_000090	1	51	6	+	189852807	189852860
267980719	chr2	189853215	189853364	189853244	189853346	COL3A1	NM_000090	1	51	7	+	189853316	189853369
268610822	chr2	189854035	189854163	189854063	189854140	COL3A1	NM_000090	1	51	8	+	189854122	189854175
268610928	chr2	189854110	189854267	189854132	189854239	COL3A1	NM_000090	1	51	8	+	189854122	189854175
267828505	chr2	189854668	189854889	189854693	189854868	COL3A1	NM_000090	1	51	9	+	189854822	189854875
267829269	chr2	189854844	189855059	189854864	189855038	COL3A1	NM_000090	1	51	9	+	189854822	189854875
263702910	chr2	189854864	189855079	189854885	189855054	COL3A1	NM_000090	1	51	10	+	189855033	189855086
263707543	chr2	189855034	189855162	189855055	189855134	COL3A1	NM_000090	1	51	10	+	189855033	189855086
267829269	chr2	189854844	189855059	189854864	189855038	COL3A1	NM_000090	1	51	10	+	189855033	189855086
269262344	chr2	189855711	189855878	189855739	189855848	COL3A1	NM_000090	1	51	11	+	189855730	189855783
262027668	chr2	189856115	189856254	189856148	189856233	COL3A1	NM_000090	1	51	12	+	189856213	189856257
262028298	chr2	189856205	189856406	189856232	189856385	COL3A1	NM_000090	1	51	12	+	189856213	189856257
269066917	chr2	189856299	189856482	189856325	189856454	COL3A1	NM_000090	1	51	13	+	189856395	189856448
261773039	chr2	189856817	189857011	189856844	189856984	COL3A1	NM_000090	1	51	14	+	189856910	189856954
266931078	chr2	189857614	189857831	189857632	189857803	COL3A1	NM_000090	1	51	15	+	189857613	189857666
264098045	chr2	189858006	189858220	189858030	189858191	COL3A1	NM_000090	1	51	16	+	189858087	189858185
257817812	chr2	189858637	189858842	189858665	189858819	COL3A1	NM_000090	1	51	17	+	189858764	189858808
257663835	chr2	189858851	189859071	189858875	189859050	COL3A1	NM_000090	1	51	18	+	189858960	189859058
257666052	chr2	189859014	189859238	189859033	189859215	COL3A1	NM_000090	1	51	18	+	189858960	189859058
265784438	chr2	189859200	189859356	189859228	189859329	COL3A1	NM_000090	1	51	19	+	189859267	189859320
261686276	chr2	189859309	189859519	189859329	189859496	COL3A1	NM_000090	1	51	20	+	189859450	189859557
261698498	chr2	189859476	189859603	189859497	189859575	COL3A1	NM_000090	1	51	20	+	189859450	189859557
269175633	chr2	189859729	189859872	189859758	189859847	COL3A1	NM_000090	1	51	21	+	189859772	189859825
269043701	chr2	189860357	189860579	189860383	189860551	COL3A1	NM_000090	1	51	22	+	189860418	189860516
263087242	chr2	189860681	189860894	189860709	189860872	COL3A1	NM_000090	1	51	23	+	189860851	189860904
263092761	chr2	189860831	189860980	189860856	189860958	COL3A1	NM_000090	1	51	23	+	189860851	189860904
265928841	chr2	189860949	189861149	189860976	189861129	COL3A1	NM_000090	1	51	24	+	189861124	189861222
265931329	chr2	189861116	189861326	189861144	189861301	COL3A1	NM_000090	1	51	24	+	189861124	189861222
260297021	chr2	189861850	189862015	189861876	189861989	COL3A1	NM_000090	1	51	25	+	189861891	189861944
269076963	chr2	189861937	189862159	189861957	189862130	COL3A1	NM_000090	1	51	26	+	189862062	189862115
268302928	chr2	189862304	189862521	189862326	189862495	COL3A1	NM_000090	1	51	27	+	189862426	189862479
267384422	chr2	189862874	189863054	189862899	189863031	COL3A1	NM_000090	1	51	28	+	189862992	189863045
263600503	chr2	189863273	189863488	189863298	189863462	COL3A1	NM_000090	1	51	29	+	189863400	189863444
257948705	chr2	189863917	189864137	189863943	189864114	COL3A1	NM_000090	1	51	30	+	189864011	189864109

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257973195	chr2	189864065	189864272	189864086	189864250	COL3A1	NM_000090	1	51	30	+	189864011	189864109
257973195	chr2	189864065	189864272	189864086	189864250	COL3A1	NM_000090	1	51	31	+	189864196	189864303
268878120	chr2	189864230	189864385	189864251	189864359	COL3A1	NM_000090	1	51	31	+	189864196	189864303
266114059	chr2	189864479	189864681	189864505	189864653	COL3A1	NM_000090	1	51	32	+	189864568	189864621
268096471	chr2	189865973	189866185	189866000	189866162	COL3A1	NM_000090	1	51	33	+	189866123	189866176
268099986	chr2	189866129	189866273	189866151	189866251	COL3A1	NM_000090	1	51	33	+	189866123	189866176
268784425	chr2	189866206	189866410	189866234	189866389	COL3A1	NM_000090	1	51	34	+	189866262	189866315
266990061	chr2	189866893	189867117	189866918	189867089	COL3A1	NM_000090	1	51	35	+	189867024	189867077
268588979	chr2	189867631	189867797	189867659	189867774	COL3A1	NM_000090	1	51	36	+	189867681	189867788
268590104	chr2	189867741	189867922	189867759	189867895	COL3A1	NM_000090	1	51	36	+	189867681	189867788
258732323	chr2	189868041	189868264	189868069	189868236	COL3A1	NM_000090	1	51	37	+	189868137	189868190
265145556	chr2	189868353	189868572	189868380	189868544	COL3A1	NM_000090	1	51	38	+	189868460	189868513
267646992	chr2	189868571	189868755	189868602	189868735	COL3A1	NM_000090	1	51	39	+	189868708	189868869
267647068	chr2	189868694	189868849	189868721	189868828	COL3A1	NM_000090	1	51	39	+	189868708	189868869
267648809	chr2	189868804	189868993	189868826	189868967	COL3A1	NM_000090	1	51	39	+	189868708	189868869
269444877	chr2	189868936	189869126	189868965	189869100	COL3A1	NM_000090	1	51	40	+	189868983	189869090
268456856	chr2	189869904	189870108	189869925	189870087	COL3A1	NM_000090	1	51	41	+	189870076	189870183
268457866	chr2	189870058	189870219	189870086	189870192	COL3A1	NM_000090	1	51	41	+	189870076	189870183
260993887	chr2	189870866	189871079	189870889	189871052	COL3A1	NM_000090	1	51	42	+	189870932	189870985
264204951	chr2	189870968	189871189	189870991	189871166	COL3A1	NM_000090	1	51	43	+	189871071	189871178
264235794	chr2	189871146	189871274	189871167	189871248	COL3A1	NM_000090	1	51	43	+	189871071	189871178
265562971	chr2	189872081	189872299	189872109	189872278	COL3A1	NM_000090	1	51	45	+	189872226	189872333
265563779	chr2	189872245	189872455	189872269	189872427	COL3A1	NM_000090	1	51	45	+	189872226	189872333
268731378	chr2	189872473	189872696	189872501	189872669	COL3A1	NM_000090	1	51	46	+	189872611	189872664
267656908	chr2	189872719	189872934	189872747	189872906	COL3A1	NM_000090	1	51	47	+	189872761	189872868
268916899	chr2	189873599	189873817	189873619	189873789	COL3A1	NM_000090	1	51	48	+	189873650	189873947
268922780	chr2	189873767	189873979	189873790	189873953	COL3A1	NM_000090	1	51	48	+	189873650	189873947
259305365	chr2	189874807	189875026	189874834	189875005	COL3A1	NM_000090	1	51	49	+	189874904	189875091
259342413	chr2	189874982	189875181	189875006	189875152	COL3A1	NM_000090	1	51	49	+	189874904	189875091
268160090	chr2	189875313	189875506	189875332	189875480	COL3A1	NM_000090	1	51	50	+	189875374	189875616
268189387	chr2	189875456	189875658	189875481	189875629	COL3A1	NM_000090	1	51	50	+	189875374	189875616
269086903	chr2	189876195	189876409	189876221	189876387	COL3A1	NM_000090	1	51	51	+	189876354	189877472
269096681	chr2	189876364	189876577	189876388	189876549	COL3A1	NM_000090	1	51	51	+	189876354	189877472
333300987	chr13	110959274	110959470	110959291	110959452	COL4A1	NM_001845	1	52	1	-	110959291	110959496
332261985	chr13	110894909	110895133	110894937	110895106	COL4A1	NM_001845	1	52	2	-	110895022	110895081
332840430	chr13	110866171	110866392	110866195	110866368	COL4A1	NM_001845	1	52	3	-	110866273	110866362
332832483	chr13	110866086	110866210	110866108	110866182	COL4A1	NM_001845	1	52	4	-	110866129	110866173
332268348	chr13	110864816	110865002	110864840	110864978	COL4A1	NM_001845	1	52	5	-	110864921	110864965
332647021	chr13	110864640	110864860	110864665	110864834	COL4A1	NM_001845	1	52	6	-	110864764	110864826
333406469	chr13	110864144	110864307	110864173	110864284	COL4A1	NM_001845	1	52	7	-	110864216	110864269
333222687	chr13	110863821	110864016	110863845	110863996	COL4A1	NM_001845	1	52	8	-	110863994	110864020

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333054255	chr13	110862434	110862638	110862456	110862610	COL4A1	NM_001845	1	52	9	-	110862476	110862559
332746535	chr13	110862203	110862425	110862225	110862398	COL4A1	NM_001845	1	52	10	-	110862327	110862389
332423362	chr13	110861653	110861824	110861683	110861797	COL4A1	NM_001845	1	52	11	-	110861739	110861774
333240641	chr13	110861101	110861305	110861127	110861277	COL4A1	NM_001845	1	52	12	-	110861196	110861237
333833401	chr13	110859593	110859803	110859618	110859779	COL4A1	NM_001845	1	52	13	-	110859750	110859836
333838283	chr13	110859759	110859907	110859780	110859879	COL4A1	NM_001845	1	52	13	-	110859750	110859836
333626195	chr13	110859052	110859267	110859074	110859243	COL4A1	NM_001845	1	52	14	-	110859212	110859238
332459977	chr13	110858857	110859050	110858878	110859029	COL4A1	NM_001845	1	52	15	-	110859012	110859062
332462631	chr13	110859007	110859211	110859030	110859182	COL4A1	NM_001845	1	52	15	-	110859012	110859062
333820349	chr13	110857762	110857939	110857785	110857913	COL4A1	NM_001845	1	52	16	-	110857841	110857885
333222164	chr13	110857599	110857780	110857627	110857758	COL4A1	NM_001845	1	52	17	-	110857700	110857753
332475552	chr13	110855878	110856025	110855897	110855997	COL4A1	NM_001845	1	52	18	-	110855913	110855954
332682083	chr13	110853771	110853895	110853793	110853869	COL4A1	NM_001845	1	52	19	-	110853785	110853869
332688764	chr13	110853846	110854054	110853869	110854031	COL4A1	NM_001845	1	52	19	-	110853785	110853869
332911079	chr13	110853045	110853269	110853073	110853241	COL4A1	NM_001845	1	52	20	-	110853201	110853236
333820725	chr13	110850700	110850918	110850723	110850897	COL4A1	NM_001845	1	52	21	-	110850814	110850978
333832580	chr13	110850877	110851005	110850898	110850983	COL4A1	NM_001845	1	52	21	-	110850814	110850978
332405368	chr13	110847295	110847516	110847318	110847488	COL4A1	NM_001845	1	52	22	-	110847370	110847465
333514452	chr13	110845073	110845291	110845095	110845265	COL4A1	NM_001845	1	52	23	-	110845177	110845260
332497916	chr13	110844464	110844674	110844485	110844649	COL4A1	NM_001845	1	52	24	-	110844561	110844631
332456602	chr13	110839420	110839617	110839445	110839594	COL4A1	NM_001845	1	52	25	-	110839485	110839676
332468608	chr13	110839574	110839704	110839595	110839681	COL4A1	NM_001845	1	52	25	-	110839485	110839676
333281335	chr13	110838697	110838916	110838719	110838892	COL4A1	NM_001845	1	52	26	-	110838732	110838900
333290729	chr13	110838872	110839014	110838893	110838985	COL4A1	NM_001845	1	52	26	-	110838732	110838900
332289863	chr13	110835437	110835660	110835458	110835636	COL4A1	NM_001845	1	52	27	-	110835531	110835623
333393109	chr13	110835249	110835473	110835273	110835451	COL4A1	NM_001845	1	52	28	-	110835340	110835444
333085048	chr13	110833605	110833794	110833627	110833768	COL4A1	NM_001845	1	52	29	-	110833639	110833736
333301886	chr13	110831482	110831662	110831504	110831642	COL4A1	NM_001845	1	52	30	-	110831618	110831768
333312224	chr13	110831610	110831812	110831634	110831785	COL4A1	NM_001845	1	52	30	-	110831618	110831768
333212579	chr13	110831204	110831420	110831227	110831396	COL4A1	NM_001845	1	52	31	-	110831270	110831383
332418925	chr13	110830352	110830571	110830375	110830545	COL4A1	NM_001845	1	52	32	-	110830411	110830578
332426106	chr13	110830522	110830743	110830543	110830722	COL4A1	NM_001845	1	52	32	-	110830411	110830578
333632510	chr13	110830124	110830326	110830146	110830300	COL4A1	NM_001845	1	52	33	-	110830189	110830278
333486015	chr13	110829202	110829414	110829221	110829392	COL4A1	NM_001845	1	52	34	-	110829232	110829384
333135140	chr13	110828880	110829104	110828905	110829078	COL4A1	NM_001845	1	52	35	-	110828973	110829071
332732494	chr13	110828670	110828890	110828692	110828865	COL4A1	NM_001845	1	52	36	-	110828771	110828860
332381982	chr13	110827452	110827659	110827475	110827638	COL4A1	NM_001845	1	52	37	-	110827565	110827704
332397305	chr13	110827615	110827743	110827639	110827715	COL4A1	NM_001845	1	52	37	-	110827565	110827704
333523759	chr13	110826922	110827145	110826950	110827117	COL4A1	NM_001845	1	52	38	-	110826970	110827096
332609892	chr13	110826705	110826914	110826727	110826887	COL4A1	NM_001845	1	52	39	-	110826793	110826873
332575061	chr13	110826150	110826374	110826173	110826350	COL4A1	NM_001845	1	52	40	-	110826247	110826345

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333276585	chr13	110824988	110825145	110825009	110825122	COL4A1	NM_001845	1	52	41	-	110825067	110825117
332430027	chr13	110822831	110823029	110822859	110823008	COL4A1	NM_001845	1	52	42	-	110822894	110823079
332431566	chr13	110822989	110823146	110823008	110823125	COL4A1	NM_001845	1	52	42	-	110822894	110823079
333155273	chr13	110821924	110822139	110821947	110822114	COL4A1	NM_001845	1	52	43	-	110821976	110822109
332396327	chr13	110819397	110819609	110819418	110819586	COL4A1	NM_001845	1	52	44	-	110819505	110819577
333397680	chr13	110818494	110818679	110818516	110818657	COL4A1	NM_001845	1	52	45	-	110818579	110818650
333744376	chr13	110817133	110817355	110817154	110817333	COL4A1	NM_001845	1	52	46	-	110817209	110817337
333756017	chr13	110817287	110817510	110817310	110817486	COL4A1	NM_001845	1	52	46	-	110817209	110817337
333453887	chr13	110815741	110815954	110815763	110815926	COL4A1	NM_001845	1	52	47	-	110815810	110815908
332357524	chr13	110814459	110814662	110814480	110814638	COL4A1	NM_001845	1	52	48	-	110814577	110814789
332369305	chr13	110814617	110814836	110814639	110814808	COL4A1	NM_001845	1	52	48	-	110814577	110814789
333261100	chr13	110813426	110813648	110813452	110813624	COL4A1	NM_001845	1	52	49	-	110813539	110813716
333279604	chr13	110813604	110813749	110813625	110813721	COL4A1	NM_001845	1	52	49	-	110813539	110813716
332518709	chr13	110807519	110807658	110807541	110807639	COL4A1	NM_001845	1	52	50	-	110807630	110807744
332523387	chr13	110807616	110807836	110807640	110807812	COL4A1	NM_001845	1	52	50	-	110807630	110807744
332574745	chr13	110804533	110804744	110804553	110804719	COL4A1	NM_001845	1	52	51	-	110804681	110804853
332590026	chr13	110804699	110804919	110804720	110804894	COL4A1	NM_001845	1	52	51	-	110804681	110804853
333027794	chr13	110802597	110802820	110802623	110802798	COL4A1	NM_001845	1	52	52	-	110801310	110802791
262474135	chrX	107683257	107683481	107683285	107683462	COL4A5	NM_000495	1	51	1	+	107683074	107683436
269297309	chrX	107782805	107782999	107782826	107782978	COL4A5	NM_000495	1	51	2	+	107782976	107783035
269305032	chrX	107782952	107783137	107782979	107783109	COL4A5	NM_000495	1	51	2	+	107782976	107783035
268256189	chrX	107802227	107802412	107802248	107802388	COL4A5	NM_000495	1	51	3	+	107802294	107802383
267525456	chrX	107806968	107807165	107806996	107807137	COL4A5	NM_000495	1	51	4	+	107807112	107807156
262494113	chrX	107811720	107811898	107811753	107811877	COL4A5	NM_000495	1	51	5	+	107811859	107811903
262495193	chrX	107811849	107812067	107811874	107812043	COL4A5	NM_000495	1	51	5	+	107811859	107811903
262495193	chrX	107811849	107812067	107811874	107812043	COL4A5	NM_000495	1	51	6	+	107811989	107812051
268737550	chrX	107812021	107812163	107812044	107812135	COL4A5	NM_000495	1	51	6	+	107811989	107812051
267731020	chrX	107814526	107814750	107814551	107814722	COL4A5	NM_000495	1	51	7	+	107814643	107814696
268867691	chrX	107814921	107815101	107814946	107815074	COL4A5	NM_000495	1	51	8	+	107815041	107815067
267634229	chrX	107816728	107816951	107816756	107816923	COL4A5	NM_000495	1	51	9	+	107816804	107816884
257472025	chrX	107821169	107821381	107821191	107821356	COL4A5	NM_000495	1	51	11	+	107821182	107821217
265980917	chrX	107821075	107821272	107821101	107821244	COL4A5	NM_000495	1	51	11	+	107821182	107821217
257472025	chrX	107821169	107821381	107821191	107821356	COL4A5	NM_000495	1	51	12	+	107821308	107821349
262648660	chrX	107821467	107821655	107821495	107821627	COL4A5	NM_000495	1	51	13	+	107821521	107821613
267630140	chrX	107823681	107823880	107823704	107823852	COL4A5	NM_000495	1	51	14	+	107823763	107823816
267756432	chrX	107823868	107824043	107823893	107824014	COL4A5	NM_000495	1	51	15	+	107823912	107823968
268755697	chrX	107824117	107824333	107824140	107824306	COL4A5	NM_000495	1	51	16	+	107824213	107824257
259736232	chrX	107826113	107826249	107826132	107826221	COL4A5	NM_000495	1	51	17	+	107826114	107826167
265798660	chrX	107827698	107827832	107827720	107827808	COL4A5	NM_000495	1	51	18	+	107827714	107827755
265226415	chrX	107829783	107830007	107829809	107829982	COL4A5	NM_000495	1	51	19	+	107829845	107829977
263037080	chrX	107834337	107834546	107834358	107834521	COL4A5	NM_000495	1	51	20	+	107834288	107834461

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265265860	chrX	107834706	107834888	107834730	107834862	COL4A5	NM_000495	1	51	21	+	107834791	107834874
259449291	chrX	107838640	107838847	107838663	107838822	COL4A5	NM_000495	1	51	22	+	107838739	107838831
259463743	chrX	107838794	107839015	107838813	107838987	COL4A5	NM_000495	1	51	22	+	107838739	107838831
268453469	chrX	107840142	107840267	107840169	107840244	COL4A5	NM_000495	1	51	23	+	107840228	107840298
268454099	chrX	107840220	107840442	107840245	107840415	COL4A5	NM_000495	1	51	23	+	107840228	107840298
267401146	chrX	107840504	107840714	107840530	107840691	COL4A5	NM_000495	1	51	24	+	107840607	107840798
267405985	chrX	107840664	107840887	107840692	107840861	COL4A5	NM_000495	1	51	24	+	107840607	107840798
268092023	chrX	107841856	107842080	107841881	107842059	COL4A5	NM_000495	1	51	25	+	107841932	107842100
268102116	chrX	107842038	107842177	107842060	107842149	COL4A5	NM_000495	1	51	25	+	107841932	107842100
266888261	chrX	107844598	107844757	107844625	107844729	COL4A5	NM_000495	1	51	26	+	107844623	107844715
262453311	chrX	107845057	107845258	107845079	107845234	COL4A5	NM_000495	1	51	27	+	107845115	107845219
266267812	chrX	107846149	107846341	107846170	107846313	COL4A5	NM_000495	1	51	28	+	107846194	107846291
263434055	chrX	107849930	107850149	107849957	107850128	COL4A5	NM_000495	1	51	29	+	107849972	107850122
269245809	chrX	107858072	107858290	107858097	107858262	COL4A5	NM_000495	1	51	30	+	107858141	107858254
268707335	chrX	107863376	107863580	107863403	107863559	COL4A5	NM_000495	1	51	31	+	107863489	107863656
268709093	chrX	107863525	107863733	107863547	107863706	COL4A5	NM_000495	1	51	31	+	107863489	107863656
267718007	chrX	107864926	107865148	107864948	107865127	COL4A5	NM_000495	1	51	32	+	107865033	107865122
267676814	chrX	107865803	107866012	107865823	107865989	COL4A5	NM_000495	1	51	33	+	107865906	107866055
267685891	chrX	107865951	107866173	107865977	107866148	COL4A5	NM_000495	1	51	33	+	107865906	107866055
266628086	chrX	107867383	107867595	107867405	107867570	COL4A5	NM_000495	1	51	34	+	107867466	107867564
263868675	chrX	107868861	107869079	107868886	107869052	COL4A5	NM_000495	1	51	35	+	107868935	107869024
258410085	chrX	107869327	107869522	107869352	107869500	COL4A5	NM_000495	1	51	36	+	107869440	107869579
258413741	chrX	107869468	107869616	107869490	107869588	COL4A5	NM_000495	1	51	36	+	107869440	107869579
261808994	chrX	107898553	107898739	107898573	107898711	COL4A5	NM_000495	1	51	37	+	107898561	107898687
268924779	chrX	107908678	107908900	107908706	107908875	COL4A5	NM_000495	1	51	38	+	107908737	107908817
257506456	chrX	107909681	107909904	107909707	107909878	COL4A5	NM_000495	1	51	39	+	107909726	107909824
262026705	chrX	107910199	107910420	107910225	107910395	COL4A5	NM_000495	1	51	40	+	107910363	107910413
262037268	chrX	107910362	107910553	107910383	107910525	COL4A5	NM_000495	1	51	40	+	107910363	107910413
260584038	chrX	107911488	107911703	107911516	107911680	COL4A5	NM_000495	1	51	41	+	107911549	107911734
260594845	chrX	107911622	107911843	107911642	107911820	COL4A5	NM_000495	1	51	41	+	107911549	107911734
267547327	chrX	107920689	107920908	107920717	107920880	COL4A5	NM_000495	1	51	42	+	107920730	107920863
262170131	chrX	107923836	107924040	107923861	107924012	COL4A5	NM_000495	1	51	43	+	107923909	107923981
267147755	chrX	107924058	107924271	107924080	107924244	COL4A5	NM_000495	1	51	44	+	107924115	107924186
263504421	chrX	107924912	107925136	107924935	107925111	COL4A5	NM_000495	1	51	45	+	107924990	107925118
269200362	chrX	107929166	107929388	107929190	107929364	COL4A5	NM_000495	1	51	46	+	107929261	107929359
265647213	chrX	107930653	107930818	107930680	107930794	COL4A5	NM_000495	1	51	47	+	107930712	107930924
265657475	chrX	107930774	107930992	107930795	107930966	COL4A5	NM_000495	1	51	47	+	107930712	107930924
267612587	chrX	107935861	107936031	107935888	107936009	COL4A5	NM_000495	1	51	48	+	107935978	107936155
267618007	chrX	107935990	107936192	107936010	107936164	COL4A5	NM_000495	1	51	48	+	107935978	107936155
262792323	chrX	107937962	107938183	107937983	107938156	COL4A5	NM_000495	1	51	49	+	107938037	107938151
257329044	chrX	107938383	107938584	107938407	107938562	COL4A5	NM_000495	1	51	50	+	107938497	107938669

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257393811	chrX	107938542	107938712	107938563	107938685	COL4A5	NM_000495	1	51	50	+	107938497	107938669
269450567	chrX	107939484	107939685	107939511	107939658	COL4A5	NM_000495	1	51	51	+	107939527	107940775
262474135	chrX	107683257	107683481	107683285	107683462	COL4A5	NM_033380	2	51	1	+	107683074	107683436
269297309	chrX	107782805	107782999	107782826	107782978	COL4A5	NM_033380	2	51	2	+	107782976	107783035
269305032	chrX	107782952	107783137	107782979	107783109	COL4A5	NM_033380	2	51	2	+	107782976	107783035
268256189	chrX	107802227	107802412	107802248	107802388	COL4A5	NM_033380	2	51	3	+	107802294	107802383
267525456	chrX	107806968	107807165	107806996	107807137	COL4A5	NM_033380	2	51	4	+	107807112	107807156
262494113	chrX	107811720	107811898	107811753	107811877	COL4A5	NM_033380	2	51	5	+	107811859	107811903
262495193	chrX	107811849	107812067	107811874	107812043	COL4A5	NM_033380	2	51	5	+	107811859	107811903
262495193	chrX	107811849	107812067	107811874	107812043	COL4A5	NM_033380	2	51	6	+	107811989	107812051
268737550	chrX	107812021	107812163	107812044	107812135	COL4A5	NM_033380	2	51	6	+	107811989	107812051
267731020	chrX	107814526	107814750	107814551	107814722	COL4A5	NM_033380	2	51	7	+	107814643	107814696
268867691	chrX	107814921	107815101	107814946	107815074	COL4A5	NM_033380	2	51	8	+	107815041	107815067
267634229	chrX	107816728	107816951	107816756	107816923	COL4A5	NM_033380	2	51	9	+	107816804	107816884
257472025	chrX	107821169	107821381	107821191	107821356	COL4A5	NM_033380	2	51	11	+	107821182	107821217
265980917	chrX	107821075	107821272	107821101	107821244	COL4A5	NM_033380	2	51	11	+	107821182	107821217
257472025	chrX	107821169	107821381	107821191	107821356	COL4A5	NM_033380	2	51	12	+	107821308	107821349
262648660	chrX	107821467	107821655	107821495	107821627	COL4A5	NM_033380	2	51	13	+	107821521	107821613
267630140	chrX	107823681	107823880	107823704	107823852	COL4A5	NM_033380	2	51	14	+	107823763	107823816
267756432	chrX	107823868	107824043	107823893	107824014	COL4A5	NM_033380	2	51	15	+	107823912	107823968
268755697	chrX	107824117	107824333	107824140	107824306	COL4A5	NM_033380	2	51	16	+	107824213	107824257
259736232	chrX	107826113	107826249	107826132	107826221	COL4A5	NM_033380	2	51	17	+	107826114	107826167
265798660	chrX	107827698	107827832	107827720	107827808	COL4A5	NM_033380	2	51	18	+	107827714	107827755
265226415	chrX	107829783	107830007	107829809	107829982	COL4A5	NM_033380	2	51	19	+	107829845	107829977
263037080	chrX	107834337	107834546	107834358	107834521	COL4A5	NM_033380	2	51	20	+	107834288	107834461
265265860	chrX	107834706	107834888	107834730	107834862	COL4A5	NM_033380	2	51	21	+	107834791	107834874
259449291	chrX	107838640	107838847	107838663	107838822	COL4A5	NM_033380	2	51	22	+	107838739	107838831
259463743	chrX	107838794	107839015	107838813	107838987	COL4A5	NM_033380	2	51	22	+	107838739	107838831
268453469	chrX	107840142	107840267	107840169	107840244	COL4A5	NM_033380	2	51	23	+	107840228	107840298
268454099	chrX	107840220	107840442	107840245	107840415	COL4A5	NM_033380	2	51	23	+	107840228	107840298
267401146	chrX	107840504	107840714	107840530	107840691	COL4A5	NM_033380	2	51	24	+	107840607	107840798
267405985	chrX	107840664	107840887	107840692	107840861	COL4A5	NM_033380	2	51	24	+	107840607	107840798
268092023	chrX	107841856	107842080	107841881	107842059	COL4A5	NM_033380	2	51	25	+	107841932	107842100
268102116	chrX	107842038	107842177	107842060	107842149	COL4A5	NM_033380	2	51	25	+	107841932	107842100
266888261	chrX	107844598	107844757	107844625	107844729	COL4A5	NM_033380	2	51	26	+	107844623	107844715
262453311	chrX	107845057	107845258	107845079	107845234	COL4A5	NM_033380	2	51	27	+	107845115	107845219
266267812	chrX	107846149	107846341	107846170	107846313	COL4A5	NM_033380	2	51	28	+	107846194	107846291
263434055	chrX	107849930	107850149	107849957	107850128	COL4A5	NM_033380	2	51	29	+	107849972	107850122
269245809	chrX	107858072	107858290	107858097	107858262	COL4A5	NM_033380	2	51	30	+	107858141	107858254
268707335	chrX	107863376	107863580	107863403	107863559	COL4A5	NM_033380	2	51	31	+	107863489	107863656
268709093	chrX	107863525	107863733	107863547	107863706	COL4A5	NM_033380	2	51	31	+	107863489	107863656

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267718007	chrX	107864926	107865148	107864948	107865127	COL4A5	NM_033380	2	51	32	+	107865033	107865122
267676814	chrX	107865803	107866012	107865823	107865989	COL4A5	NM_033380	2	51	33	+	107865906	107866055
267685891	chrX	107865951	107866173	107865977	107866148	COL4A5	NM_033380	2	51	33	+	107865906	107866055
266628086	chrX	107867383	107867595	107867405	107867570	COL4A5	NM_033380	2	51	34	+	107867466	107867564
263868675	chrX	107868861	107869079	107868886	107869052	COL4A5	NM_033380	2	51	35	+	107868935	107869024
258410085	chrX	107869327	107869522	107869352	107869500	COL4A5	NM_033380	2	51	36	+	107869440	107869579
258413741	chrX	107869468	107869616	107869490	107869588	COL4A5	NM_033380	2	51	36	+	107869440	107869579
261808994	chrX	107898553	107898739	107898573	107898711	COL4A5	NM_033380	2	51	37	+	107898561	107898687
268924779	chrX	107908678	107908900	107908706	107908875	COL4A5	NM_033380	2	51	38	+	107908737	107908817
257506456	chrX	107909681	107909904	107909707	107909878	COL4A5	NM_033380	2	51	39	+	107909726	107909824
262026705	chrX	107910199	107910420	107910225	107910395	COL4A5	NM_033380	2	51	40	+	107910363	107910413
262037268	chrX	107910362	107910553	107910383	107910525	COL4A5	NM_033380	2	51	40	+	107910363	107910413
260584038	chrX	107911488	107911703	107911516	107911680	COL4A5	NM_033380	2	51	41	+	107911549	107911736
260594845	chrX	107911622	107911843	107911642	107911820	COL4A5	NM_033380	2	51	41	+	107911549	107911736
267547327	chrX	107920689	107920908	107920717	107920880	COL4A5	NM_033380	2	51	42	+	107920727	107920863
262170131	chrX	107923836	107924040	107923861	107924012	COL4A5	NM_033380	2	51	43	+	107923909	107923981
267147755	chrX	107924058	107924271	107924080	107924244	COL4A5	NM_033380	2	51	44	+	107924115	107924186
263504421	chrX	107924912	107925136	107924935	107925111	COL4A5	NM_033380	2	51	45	+	107924990	107925118
269200362	chrX	107929166	107929388	107929190	107929364	COL4A5	NM_033380	2	51	46	+	107929261	107929359
265647213	chrX	107930653	107930818	107930680	107930794	COL4A5	NM_033380	2	51	47	+	107930712	107930924
265657475	chrX	107930774	107930992	107930795	107930966	COL4A5	NM_033380	2	51	47	+	107930712	107930924
267612587	chrX	107935861	107936031	107935888	107936009	COL4A5	NM_033380	2	51	48	+	107935978	107936155
267618007	chrX	107935990	107936192	107936010	107936164	COL4A5	NM_033380	2	51	48	+	107935978	107936155
262792323	chrX	107937962	107938183	107937983	107938156	COL4A5	NM_033380	2	51	49	+	107938037	107938151
257329044	chrX	107938383	107938584	107938407	107938562	COL4A5	NM_033380	2	51	50	+	107938497	107938669
257393811	chrX	107938542	107938712	107938563	107938685	COL4A5	NM_033380	2	51	50	+	107938497	107938669
269450567	chrX	107939484	107939685	107939511	107939658	COL4A5	NM_033380	2	51	51	+	107939527	107940775
266962582	chr9	137533902	137534061	137533919	137534044	COL5A1	NM_000093	1	66	1	+	137533652	137534142
266962722	chr9	137534039	137534258	137534058	137534239	COL5A1	NM_000093	1	66	1	+	137533652	137534142
263695232	chr9	137582721	137582944	137582741	137582925	COL5A1	NM_000093	1	66	2	+	137582758	137582925
263719001	chr9	137582904	137583095	137582923	137583073	COL5A1	NM_000093	1	66	2	+	137582758	137582925
264233117	chr9	137591676	137591866	137591696	137591846	COL5A1	NM_000093	1	66	3	+	137591755	137591968
264271893	chr9	137591825	137592045	137591846	137592023	COL5A1	NM_000093	1	66	3	+	137591755	137591968
257744133	chr9	137592925	137593149	137592947	137593127	COL5A1	NM_000093	1	66	4	+	137593017	137593179
257791753	chr9	137593108	137593315	137593128	137593294	COL5A1	NM_000093	1	66	4	+	137593017	137593179
267821332	chr9	137619071	137619270	137619095	137619248	COL5A1	NM_000093	1	66	5	+	137619112	137619243
265185616	chr9	137620428	137620649	137620448	137620627	COL5A1	NM_000093	1	66	6	+	137620516	137620653
265193388	chr9	137620561	137620751	137620582	137620729	COL5A1	NM_000093	1	66	6	+	137620516	137620653
267983153	chr9	137622048	137622234	137622069	137622213	COL5A1	NM_000093	1	66	7	+	137622082	137622321
267986417	chr9	137622194	137622404	137622214	137622383	COL5A1	NM_000093	1	66	7	+	137622082	137622321
268066147	chr9	137623217	137623406	137623238	137623383	COL5A1	NM_000093	1	66	8	+	137623342	137623509

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268069946	chr9	137623358	137623521	137623378	137623500	COL5A1	NM_000093	1	66	8	+	137623342	137623509
268074815	chr9	137623481	137623668	137623501	137623642	COL5A1	NM_000093	1	66	8	+	137623342	137623509
268008819	chr9	137623794	137624002	137623815	137623978	COL5A1	NM_000093	1	66	9	+	137623917	137623973
268914216	chr9	137630169	137630390	137630189	137630366	COL5A1	NM_000093	1	66	10	+	137630320	137630361
258384504	chr9	137630520	137630683	137630540	137630659	COL5A1	NM_000093	1	66	11	+	137630592	137630654
267449326	chr9	137642344	137642489	137642364	137642467	COL5A1	NM_000093	1	66	12	+	137642388	137642462
268337503	chr9	137642605	137642813	137642627	137642792	COL5A1	NM_000093	1	66	13	+	137642636	137642728
269173977	chr9	137644296	137644519	137644318	137644496	COL5A1	NM_000093	1	66	14	+	137644435	137644491
262135869	chr9	137645634	137645856	137645655	137645830	COL5A1	NM_000093	1	66	15	+	137645696	137645749
267875911	chr9	137645997	137646207	137646018	137646184	COL5A1	NM_000093	1	66	16	+	137646119	137646172
264744948	chr9	137648509	137648724	137648528	137648703	COL5A1	NM_000093	1	66	17	+	137648611	137648664
267671441	chr9	137649960	137650179	137649981	137650158	COL5A1	NM_000093	1	66	18	+	137650089	137650142
263963101	chr9	137653663	137653884	137653688	137653862	COL5A1	NM_000093	1	66	19	+	137653771	137653824
269254892	chr9	137655414	137655638	137655435	137655616	COL5A1	NM_000093	1	66	20	+	137655539	137655583
267314616	chr9	137657478	137657632	137657498	137657612	COL5A1	NM_000093	1	66	21	+	137657527	137657580
262099822	chr9	137658211	137658429	137658235	137658410	COL5A1	NM_000093	1	66	22	+	137658300	137658344
269074699	chr9	137658818	137659042	137658840	137659018	COL5A1	NM_000093	1	66	23	+	137658846	137658899
268927981	chr9	137659126	137659317	137659149	137659291	COL5A1	NM_000093	1	66	24	+	137659156	137659200
268788877	chr9	137660130	137660347	137660152	137660325	COL5A1	NM_000093	1	66	25	+	137660256	137660309
268016593	chr9	137664497	137664719	137664518	137664698	COL5A1	NM_000093	1	66	26	+	137664636	137664680
263815748	chr9	137666624	137666847	137666646	137666823	COL5A1	NM_000093	1	66	27	+	137666705	137666758
262601645	chr9	137671836	137672046	137671857	137672025	COL5A1	NM_000093	1	66	28	+	137671948	137671992
262056806	chr9	137674467	137674681	137674488	137674655	COL5A1	NM_000093	1	66	29	+	137674513	137674566
262261485	chr9	137676762	137676976	137676784	137676955	COL5A1	NM_000093	1	66	30	+	137676835	137676942
267835332	chr9	137677798	137678021	137677819	137677996	COL5A1	NM_000093	1	66	31	+	137677841	137677894
267319199	chr9	137680939	137681127	137680960	137681106	COL5A1	NM_000093	1	66	32	+	137681001	137681054
260444534	chr9	137686811	137687004	137686833	137686982	COL5A1	NM_000093	1	66	33	+	137686928	137686972
264121528	chr9	137687005	137687217	137687026	137687196	COL5A1	NM_000093	1	66	34	+	137687108	137687161
266458891	chr9	137688108	137688270	137688130	137688250	COL5A1	NM_000093	1	66	35	+	137688220	137688264
266483732	chr9	137688207	137688415	137688228	137688394	COL5A1	NM_000093	1	66	35	+	137688220	137688264
268290866	chr9	137688589	137688768	137688611	137688744	COL5A1	NM_000093	1	66	36	+	137688694	137688747
268293245	chr9	137688718	137688910	137688740	137688889	COL5A1	NM_000093	1	66	36	+	137688694	137688747
267449544	chr9	137690215	137690437	137690238	137690416	COL5A1	NM_000093	1	66	37	+	137690254	137690307
261248341	chr9	137693664	137693887	137693687	137693866	COL5A1	NM_000093	1	66	38	+	137693800	137693853
268646493	chr9	137694644	137694868	137694668	137694846	COL5A1	NM_000093	1	66	39	+	137694734	137694841
260922213	chr9	137696863	137697087	137696884	137697065	COL5A1	NM_000093	1	66	40	+	137696821	137696910
262372483	chr9	137696786	137697003	137696807	137696980	COL5A1	NM_000093	1	66	40	+	137696821	137696910
260922213	chr9	137696863	137697087	137696884	137697065	COL5A1	NM_000093	1	66	41	+	137697007	137697060
265340635	chr9	137697987	137698167	137698008	137698147	COL5A1	NM_000093	1	66	42	+	137698035	137698142
269257630	chr9	137700994	137701218	137701016	137701194	COL5A1	NM_000093	1	66	43	+	137701029	137701136
264266665	chr9	137702041	137702250	137702064	137702229	COL5A1	NM_000093	1	66	44	+	137702101	137702154

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263851749	chr9	137703044	137703268	137703065	137703244	COL5A1	NM_000093	1	66	45	+	137703185	137703238
269334746	chr9	137703246	137703464	137703270	137703443	COL5A1	NM_000093	1	66	46	+	137703338	137703445
269338298	chr9	137703388	137703601	137703411	137703578	COL5A1	NM_000093	1	66	46	+	137703338	137703445
267901937	chr9	137704216	137704402	137704236	137704380	COL5A1	NM_000093	1	66	47	+	137704295	137704348
267111778	chr9	137704378	137704601	137704398	137704580	COL5A1	NM_000093	1	66	48	+	137704451	137704558
258484795	chr9	137705739	137705930	137705760	137705913	COL5A1	NM_000093	1	66	49	+	137705829	137705882
267329272	chr9	137706603	137706777	137706624	137706755	COL5A1	NM_000093	1	66	50	+	137706643	137706750
257536378	chr9	137707368	137707579	137707389	137707556	COL5A1	NM_000093	1	66	51	+	137707422	137707475
265170570	chr9	137707669	137707883	137707691	137707860	COL5A1	NM_000093	1	66	52	+	137707781	137707834
258029260	chr9	137708770	137708970	137708790	137708948	COL5A1	NM_000093	1	66	53	+	137708872	137708925
265682779	chr9	137709592	137709781	137709613	137709760	COL5A1	NM_000093	1	66	54	+	137709624	137709677
260663775	chr9	137710460	137710684	137710481	137710663	COL5A1	NM_000093	1	66	55	+	137710502	137710609
260671943	chr9	137710662	137710792	137710681	137710771	COL5A1	NM_000093	1	66	56	+	137710694	137710747
268773411	chr9	137710772	137710987	137710792	137710961	COL5A1	NM_000093	1	66	57	+	137710846	137710899
267736792	chr9	137711927	137712123	137711948	137712100	COL5A1	NM_000093	1	66	58	+	137711962	137712069
267503168	chr9	137713894	137714087	137713914	137714063	COL5A1	NM_000093	1	66	59	+	137713943	137713996
268605716	chr9	137714701	137714924	137714725	137714904	COL5A1	NM_000093	1	66	60	+	137714844	137714879
269320925	chr9	137715167	137715341	137715188	137715320	COL5A1	NM_000093	1	66	61	+	137715262	137715315
268459408	chr9	137716395	137716608	137716415	137716585	COL5A1	NM_000093	1	66	62	+	137716446	137716701
268461921	chr9	137716565	137716784	137716586	137716763	COL5A1	NM_000093	1	66	62	+	137716446	137716701
267190063	chr9	137717450	137717665	137717472	137717642	COL5A1	NM_000093	1	66	63	+	137717638	137717750
267210388	chr9	137717621	137717840	137717643	137717813	COL5A1	NM_000093	1	66	63	+	137717638	137717750
268269270	chr9	137721758	137721932	137721778	137721907	COL5A1	NM_000093	1	66	64	+	137721822	137721890
267543452	chr9	137726758	137726974	137726777	137726956	COL5A1	NM_000093	1	66	65	+	137726817	137727050
267548200	chr9	137726908	137727130	137726930	137727110	COL5A1	NM_000093	1	66	65	+	137726817	137727050
263145809	chr9	137733968	137734191	137733988	137734172	COL5A1	NM_000093	1	66	66	+	137734003	137736688
258061602	chr2	190044151	190044371	190044172	190044348	COL5A2	NM_000393	1	54	1	-	190044234	190044605
266985518	chr2	189974857	189975074	189974881	189975050	COL5A2	NM_000393	1	54	2	-	189974951	189975175
267022975	chr2	189975031	189975251	189975051	189975223	COL5A2	NM_000393	1	54	2	-	189974951	189975175
268026085	chr2	189964677	189964883	189964703	189964855	COL5A2	NM_000393	1	54	4	-	189964833	189964865
268026633	chr2	189964833	189964957	189964856	189964929	COL5A2	NM_000393	1	54	4	-	189964833	189964865
258621639	chr2	189963270	189963482	189963296	189963463	COL5A2	NM_000393	1	54	5	-	189963453	189963485
258625200	chr2	189963441	189963620	189963464	189963592	COL5A2	NM_000393	1	54	5	-	189963453	189963485
259245594	chr2	189961963	189962181	189961983	189962153	COL5A2	NM_000393	1	54	6	-	189962003	189962056
268855615	chr2	189956992	189957180	189957017	189957152	COL5A2	NM_000393	1	54	7	-	189957036	189957146
269054852	chr2	189953246	189953470	189953272	189953444	COL5A2	NM_000393	1	54	8	-	189953421	189953498
269056619	chr2	189953423	189953643	189953445	189953619	COL5A2	NM_000393	1	54	8	-	189953421	189953498
268417448	chr2	189951356	189951527	189951377	189951502	COL5A2	NM_000393	1	54	9	-	189951452	189951496
268803709	chr2	189950391	189950597	189950419	189950569	COL5A2	NM_000393	1	54	10	-	189950445	189950498
260215631	chr2	189949733	189949933	189949758	189949912	COL5A2	NM_000393	1	54	11	-	189949886	189949939
260231802	chr2	189949877	189950011	189949902	189949979	COL5A2	NM_000393	1	54	11	-	189949886	189949939

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267578188	chr2	189948599	189948799	189948626	189948774	COL5A2	NM_000393	1	54	12	-	189948710	189948763
262896490	chr2	189945656	189945876	189945676	189945848	COL5A2	NM_000393	1	54	13	-	189945716	189945769
267861113	chr2	189944599	189944823	189944621	189944795	COL5A2	NM_000393	1	54	14	-	189944704	189944757
268630007	chr2	189943620	189943832	189943640	189943815	COL5A2	NM_000393	1	54	15	-	189943789	189943833
263076240	chr2	189943228	189943401	189943253	189943373	COL5A2	NM_000393	1	54	16	-	189943242	189943295
269256968	chr2	189940112	189940301	189940135	189940273	COL5A2	NM_000393	1	54	17	-	189940119	189940163
268716349	chr2	189936693	189936913	189936719	189936884	COL5A2	NM_000393	1	54	18	-	189936766	189936819
267728844	chr2	189933451	189933672	189933478	189933644	COL5A2	NM_000393	1	54	19	-	189933512	189933610
257451366	chr2	189932851	189933075	189932877	189933048	COL5A2	NM_000393	1	54	20	-	189932952	189932996
265737498	chr2	189932672	189932869	189932696	189932844	COL5A2	NM_000393	1	54	21	-	189932741	189932839
264300555	chr2	189931380	189931557	189931402	189931529	COL5A2	NM_000393	1	54	22	-	189931455	189931508
260469542	chr2	189931033	189931256	189931062	189931229	COL5A2	NM_000393	1	54	23	-	189931116	189931223
267425098	chr2	189929692	189929895	189929717	189929867	COL5A2	NM_000393	1	54	24	-	189929730	189929783
268304180	chr2	189929234	189929411	189929255	189929389	COL5A2	NM_000393	1	54	25	-	189929283	189929381
264621653	chr2	189928584	189928808	189928612	189928782	COL5A2	NM_000393	1	54	26	-	189928706	189928759
267284415	chr2	189927823	189928029	189927851	189928004	COL5A2	NM_000393	1	54	27	-	189927898	189927996
268931684	chr2	189927627	189927850	189927650	189927822	COL5A2	NM_000393	1	54	28	-	189927736	189927789
267760053	chr2	189927471	189927682	189927499	189927654	COL5A2	NM_000393	1	54	29	-	189927591	189927644
261365124	chr2	189926253	189926411	189926282	189926389	COL5A2	NM_000393	1	54	30	-	189926288	189926341
265774180	chr2	189925412	189925569	189925435	189925543	COL5A2	NM_000393	1	54	31	-	189925456	189925509
266096782	chr2	189923512	189923668	189923538	189923640	COL5A2	NM_000393	1	54	32	-	189923575	189923619
259718021	chr2	189923067	189923267	189923092	189923243	COL5A2	NM_000393	1	54	33	-	189923155	189923253
259750862	chr2	189923220	189923346	189923244	189923320	COL5A2	NM_000393	1	54	33	-	189923155	189923253
267409789	chr2	189921962	189922186	189921990	189922158	COL5A2	NM_000393	1	54	34	-	189922046	189922153
262495796	chr2	189921626	189921764	189921654	189921743	COL5A2	NM_000393	1	54	35	-	189921699	189921752
267661332	chr2	189918826	189919001	189918848	189918973	COL5A2	NM_000393	1	54	36	-	189918885	189918938
263360063	chr2	189918578	189918707	189918604	189918679	COL5A2	NM_000393	1	54	37	-	189918621	189918674
268011178	chr2	189917967	189918186	189917990	189918169	COL5A2	NM_000393	1	54	38	-	189918150	189918203
268011585	chr2	189918171	189918387	189918189	189918358	COL5A2	NM_000393	1	54	38	-	189918150	189918203
268804354	chr2	189917516	189917739	189917542	189917719	COL5A2	NM_000393	1	54	39	-	189917637	189917744
268809625	chr2	189917701	189917917	189917720	189917889	COL5A2	NM_000393	1	54	39	-	189917637	189917744
268081497	chr2	189917402	189917581	189917427	189917555	COL5A2	NM_000393	1	54	40	-	189917475	189917528
265627457	chr2	189916746	189916949	189916774	189916926	COL5A2	NM_000393	1	54	41	-	189916898	189916951
265628329	chr2	189916876	189917050	189916903	189917026	COL5A2	NM_000393	1	54	41	-	189916898	189916951
264844134	chr2	189915937	189916121	189915964	189916101	COL5A2	NM_000393	1	54	42	-	189916046	189916207
264855385	chr2	189916042	189916242	189916064	189916220	COL5A2	NM_000393	1	54	42	-	189916046	189916207
267880802	chr2	189915263	189915453	189915292	189915425	COL5A2	NM_000393	1	54	43	-	189915295	189915402
268867307	chr2	189914019	189914229	189914046	189914201	COL5A2	NM_000393	1	54	44	-	189914073	189914180
261828979	chr2	189912795	189912958	189912824	189912940	COL5A2	NM_000393	1	54	45	-	189912935	189912988
261828988	chr2	189912917	189913084	189912942	189913057	COL5A2	NM_000393	1	54	45	-	189912935	189912988
267896791	chr2	189910418	189910641	189910443	189910618	COL5A2	NM_000393	1	54	46	-	189910526	189910633

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267900913	chr2	189910528	189910661	189910551	189910628	COL5A2	NM_000393	1	54	46	-	189910526	189910633
268408474	chr2	189909795	189909935	189909824	189909917	COL5A2	NM_000393	1	54	47	-	189909905	189909958
268408644	chr2	189909915	189910139	189909933	189910113	COL5A2	NM_000393	1	54	47	-	189909905	189909958
267539236	chr2	189907811	189908002	189907836	189907974	COL5A2	NM_000393	1	54	48	-	189907877	189907984
260175546	chr2	189907333	189907554	189907355	189907528	COL5A2	NM_000393	1	54	49	-	189907446	189907499
265211627	chr2	189906232	189906439	189906254	189906416	COL5A2	NM_000393	1	54	50	-	189906312	189906419
269235345	chr2	189903967	189904190	189903988	189904166	COL5A2	NM_000393	1	54	51	-	189903998	189904289
269250723	chr2	189904148	189904369	189904167	189904344	COL5A2	NM_000393	1	54	51	-	189903998	189904289
258982148	chr2	189901337	189901474	189901364	189901450	COL5A2	NM_000393	1	54	52	-	189901342	189901529
258991442	chr2	189901426	189901612	189901451	189901584	COL5A2	NM_000393	1	54	52	-	189901342	189901529
268083085	chr2	189899543	189899759	189899566	189899733	COL5A2	NM_000393	1	54	53	-	189899642	189899881
268094681	chr2	189899713	189899923	189899734	189899897	COL5A2	NM_000393	1	54	53	-	189899642	189899881
266373975	chr2	189898647	189898835	189898668	189898813	COL5A2	NM_000393	1	54	54	-	189896641	189898942
266476175	chr2	189898787	189899010	189898814	189898983	COL5A2	NM_000393	1	54	54	-	189896641	189898942
265641210	chr3	48632400	48632620	48632419	48632598	COL7A1	NM_000094	1	118	1	-	48632508	48632593
258287370	chr3	48631631	48631833	48631655	48631812	COL7A1	NM_000094	1	118	2	-	48631801	48631981
258307700	chr3	48631792	48632013	48631812	48631992	COL7A1	NM_000094	1	118	2	-	48631801	48631981
268640171	chr3	48630855	48631075	48630877	48631054	COL7A1	NM_000094	1	118	3	-	48630970	48631129
268645214	chr3	48631010	48631234	48631032	48631212	COL7A1	NM_000094	1	118	3	-	48630970	48631129
257296336	chr3	48630706	48630909	48630727	48630889	COL7A1	NM_000094	1	118	4	-	48630789	48630882
268640171	chr3	48630855	48631075	48630877	48631054	COL7A1	NM_000094	1	118	4	-	48630789	48630882
266571112	chr3	48630443	48630641	48630464	48630614	COL7A1	NM_000094	1	118	5	-	48630535	48630696
266596575	chr3	48630592	48630805	48630615	48630781	COL7A1	NM_000094	1	118	5	-	48630535	48630696
261895822	chr3	48630180	48630403	48630202	48630384	COL7A1	NM_000094	1	118	6	-	48630208	48630371
267901627	chr3	48629977	48630167	48629997	48630143	COL7A1	NM_000094	1	118	7	-	48630003	48630132
268257037	chr3	48629711	48629929	48629733	48629909	COL7A1	NM_000094	1	118	8	-	48629784	48629900
267692223	chr3	48629424	48629614	48629445	48629594	COL7A1	NM_000094	1	118	9	-	48629535	48629681
267698470	chr3	48629567	48629791	48629586	48629768	COL7A1	NM_000094	1	118	9	-	48629535	48629681
267692223	chr3	48629424	48629614	48629445	48629594	COL7A1	NM_000094	1	118	10	-	48629331	48629447
268001523	chr3	48629255	48629477	48629277	48629457	COL7A1	NM_000094	1	118	10	-	48629331	48629447
267995835	chr3	48629160	48629284	48629180	48629263	COL7A1	NM_000094	1	118	11	-	48629106	48629255
268305518	chr3	48628991	48629215	48629012	48629196	COL7A1	NM_000094	1	118	11	-	48629106	48629255
257311772	chr3	48628845	48629052	48628866	48629031	COL7A1	NM_000094	1	118	12	-	48628897	48629025
268305518	chr3	48628991	48629215	48629012	48629196	COL7A1	NM_000094	1	118	12	-	48628897	48629025
268548206	chr3	48628068	48628277	48628086	48628258	COL7A1	NM_000094	1	118	13	-	48628106	48628249
269273651	chr3	48627835	48628049	48627855	48628022	COL7A1	NM_000094	1	118	14	-	48627892	48628017
268354367	chr3	48627592	48627816	48627613	48627795	COL7A1	NM_000094	1	118	15	-	48627646	48627789
269077792	chr3	48626962	48627186	48626982	48627166	COL7A1	NM_000094	1	118	16	-	48627032	48627151
267827932	chr3	48626719	48626941	48626739	48626922	COL7A1	NM_000094	1	118	17	-	48626760	48626903
268377195	chr3	48626229	48626453	48626251	48626433	COL7A1	NM_000094	1	118	18	-	48626303	48626428
260114075	chr3	48626039	48626263	48626058	48626242	COL7A1	NM_000094	1	118	19	-	48626075	48626221

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267952000	chr3	48625676	48625865	48625697	48625843	COL7A1	NM_000094	1	118	20	-	48625715	48625837
262345535	chr3	48625136	48625341	48625158	48625321	COL7A1	NM_000094	1	118	21	-	48625226	48625372
262358715	chr3	48625284	48625507	48625303	48625483	COL7A1	NM_000094	1	118	21	-	48625226	48625372
267131714	chr3	48624767	48624983	48624790	48624962	COL7A1	NM_000094	1	118	22	-	48624853	48624987
267159537	chr3	48624944	48625092	48624963	48625066	COL7A1	NM_000094	1	118	22	-	48624853	48624987
267212391	chr3	48624590	48624806	48624611	48624778	COL7A1	NM_000094	1	118	23	-	48624623	48624769
268352951	chr3	48624363	48624571	48624384	48624548	COL7A1	NM_000094	1	118	24	-	48624405	48624541
269343243	chr3	48623943	48624152	48623963	48624130	COL7A1	NM_000094	1	118	25	-	48623996	48624122
257320805	chr3	48623725	48623938	48623745	48623916	COL7A1	NM_000094	1	118	26	-	48623765	48623911
268040976	chr3	48623340	48623533	48623361	48623512	COL7A1	NM_000094	1	118	27	-	48623507	48623679
268257315	chr3	48623493	48623717	48623513	48623695	COL7A1	NM_000094	1	118	27	-	48623507	48623679
265413055	chr3	48623215	48623439	48623239	48623413	COL7A1	NM_000094	1	118	28	-	48623373	48623408
268040976	chr3	48623340	48623533	48623361	48623512	COL7A1	NM_000094	1	118	28	-	48623373	48623408
265413055	chr3	48623215	48623439	48623239	48623413	COL7A1	NM_000094	1	118	29	-	48623263	48623289
265545425	chr3	48622949	48623169	48622970	48623149	COL7A1	NM_000094	1	118	30	-	48623123	48623167
265545987	chr3	48622975	48623198	48622995	48623175	COL7A1	NM_000094	1	118	30	-	48623123	48623167
265545425	chr3	48622949	48623169	48622970	48623149	COL7A1	NM_000094	1	118	31	-	48622990	48623052
265545987	chr3	48622975	48623198	48622995	48623175	COL7A1	NM_000094	1	118	31	-	48622990	48623052
260813984	chr3	48622371	48622581	48622391	48622560	COL7A1	NM_000094	1	118	32	-	48622469	48622549
260804796	chr3	48622293	48622474	48622315	48622452	COL7A1	NM_000094	1	118	33	-	48622343	48622378
267858398	chr3	48622040	48622257	48622061	48622237	COL7A1	NM_000094	1	118	34	-	48622167	48622202
264293767	chr3	48621878	48622079	48621899	48622053	COL7A1	NM_000094	1	118	35	-	48621918	48621989
267524184	chr3	48621639	48621840	48621660	48621815	COL7A1	NM_000094	1	118	36	-	48621731	48621808
258176422	chr3	48621394	48621553	48621415	48621530	COL7A1	NM_000094	1	118	37	-	48621468	48621494
264393013	chr3	48621205	48621417	48621227	48621395	COL7A1	NM_000094	1	118	38	-	48621333	48621386
267990368	chr3	48621036	48621257	48621057	48621229	COL7A1	NM_000094	1	118	39	-	48621151	48621213
268375453	chr3	48620909	48621076	48620931	48621056	COL7A1	NM_000094	1	118	40	-	48620989	48621048
260050011	chr3	48620708	48620925	48620729	48620904	COL7A1	NM_000094	1	118	41	-	48620826	48620861
268799431	chr3	48620476	48620697	48620498	48620677	COL7A1	NM_000094	1	118	42	-	48620560	48620604
266735225	chr3	48620297	48620510	48620318	48620486	COL7A1	NM_000094	1	118	43	-	48620446	48620481
265735642	chr3	48619939	48620154	48619960	48620131	COL7A1	NM_000094	1	118	44	-	48620042	48620086
258828136	chr3	48619790	48619975	48619812	48619953	COL7A1	NM_000094	1	118	45	-	48619911	48619946
265162915	chr3	48619666	48619865	48619687	48619843	COL7A1	NM_000094	1	118	46	-	48619756	48619791
267683160	chr3	48619185	48619407	48619207	48619386	COL7A1	NM_000094	1	118	47	-	48619344	48619376
263763404	chr3	48619063	48619219	48619086	48619197	COL7A1	NM_000094	1	118	48	-	48619139	48619192
264437076	chr3	48618938	48619098	48618959	48619071	COL7A1	NM_000094	1	118	49	-	48619006	48619065
268293174	chr3	48618797	48619008	48618816	48618986	COL7A1	NM_000094	1	118	50	-	48618881	48618916
268842715	chr3	48618606	48618823	48618626	48618805	COL7A1	NM_000094	1	118	51	-	48618693	48618773
264059625	chr3	48618392	48618616	48618416	48618595	COL7A1	NM_000094	1	118	52	-	48618555	48618590
257710004	chr3	48618168	48618392	48618195	48618365	COL7A1	NM_000094	1	118	53	-	48618315	48618359
262747581	chr3	48617905	48618129	48617931	48618104	COL7A1	NM_000094	1	118	54	-	48618014	48618085

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266879583	chr3	48617646	48617824	48617667	48617803	COL7A1	NM_000094	1	118	55	-	48617733	48617777
266385969	chr3	48617365	48617530	48617387	48617502	COL7A1	NM_000094	1	118	56	-	48617464	48617490
268226363	chr3	48617095	48617279	48617117	48617255	COL7A1	NM_000094	1	118	57	-	48617218	48617247
257565423	chr3	48616926	48617132	48616946	48617107	COL7A1	NM_000094	1	118	58	-	48617021	48617101
257547016	chr3	48616756	48616977	48616778	48616953	COL7A1	NM_000094	1	118	59	-	48616913	48616948
257565423	chr3	48616926	48617132	48616946	48617107	COL7A1	NM_000094	1	118	59	-	48616913	48616948
257547016	chr3	48616756	48616977	48616778	48616953	COL7A1	NM_000094	1	118	60	-	48616802	48616837
266679331	chr3	48616564	48616741	48616586	48616719	COL7A1	NM_000094	1	118	61	-	48616630	48616710
268613659	chr3	48616202	48616423	48616223	48616397	COL7A1	NM_000094	1	118	62	-	48616352	48616387
267980943	chr3	48615792	48616004	48615813	48615983	COL7A1	NM_000094	1	118	63	-	48615886	48615948
258815871	chr3	48615610	48615826	48615638	48615803	COL7A1	NM_000094	1	118	64	-	48615754	48615798
261661626	chr3	48614286	48614496	48614308	48614473	COL7A1	NM_000094	1	118	65	-	48614425	48614460
261647792	chr3	48614159	48614379	48614180	48614357	COL7A1	NM_000094	1	118	66	-	48614317	48614352
261661626	chr3	48614286	48614496	48614308	48614473	COL7A1	NM_000094	1	118	66	-	48614317	48614352
261647792	chr3	48614159	48614379	48614180	48614357	COL7A1	NM_000094	1	118	67	-	48614109	48614204
267040651	chr3	48614040	48614260	48614061	48614236	COL7A1	NM_000094	1	118	67	-	48614109	48614204
267564452	chr3	48613835	48614016	48613856	48613995	COL7A1	NM_000094	1	118	68	-	48613955	48613990
264252976	chr3	48613727	48613897	48613749	48613875	COL7A1	NM_000094	1	118	69	-	48613833	48613868
267564452	chr3	48613835	48614016	48613856	48613995	COL7A1	NM_000094	1	118	69	-	48613833	48613868
264235062	chr3	48613537	48613760	48613557	48613734	COL7A1	NM_000094	1	118	70	-	48613682	48613729
257722831	chr3	48613137	48613361	48613158	48613341	COL7A1	NM_000094	1	118	71	-	48613300	48613335
257722831	chr3	48613137	48613361	48613158	48613341	COL7A1	NM_000094	1	118	72	-	48613059	48613181
265267947	chr3	48612987	48613211	48613007	48613192	COL7A1	NM_000094	1	118	72	-	48613059	48613181
260921447	chr3	48612635	48612849	48612655	48612828	COL7A1	NM_000094	1	118	73	-	48612772	48612972
268023044	chr3	48612785	48613008	48612804	48612987	COL7A1	NM_000094	1	118	73	-	48612772	48612972
260919681	chr3	48612558	48612700	48612581	48612680	COL7A1	NM_000094	1	118	74	-	48612640	48612675
260921447	chr3	48612635	48612849	48612655	48612828	COL7A1	NM_000094	1	118	74	-	48612640	48612675
261781026	chr3	48612367	48612588	48612391	48612565	COL7A1	NM_000094	1	118	75	-	48612497	48612559
267436226	chr3	48612161	48612327	48612185	48612306	COL7A1	NM_000094	1	118	76	-	48612230	48612298
268268222	chr3	48612037	48612182	48612059	48612159	COL7A1	NM_000094	1	118	77	-	48612110	48612154
263824908	chr3	48611865	48612088	48611889	48612065	COL7A1	NM_000094	1	118	78	-	48611921	48611983
269262720	chr3	48611672	48611826	48611690	48611804	COL7A1	NM_000094	1	118	79	-	48611695	48611739
267937034	chr3	48611155	48611369	48611176	48611348	COL7A1	NM_000094	1	118	80	-	48611288	48611323
268930773	chr3	48611013	48611192	48611034	48611168	COL7A1	NM_000094	1	118	81	-	48611123	48611158
266024106	chr3	48610828	48611036	48610849	48611014	COL7A1	NM_000094	1	118	82	-	48610946	48610990
260899590	chr3	48610635	48610808	48610656	48610786	COL7A1	NM_000094	1	118	83	-	48610749	48610781
260899590	chr3	48610635	48610808	48610656	48610786	COL7A1	NM_000094	1	118	84	-	48610607	48610669
267388986	chr3	48610486	48610698	48610507	48610676	COL7A1	NM_000094	1	118	84	-	48610607	48610669
264807116	chr3	48610307	48610517	48610330	48610496	COL7A1	NM_000094	1	118	85	-	48610454	48610489
264795633	chr3	48610221	48610403	48610241	48610383	COL7A1	NM_000094	1	118	86	-	48610295	48610375
264807116	chr3	48610307	48610517	48610330	48610496	COL7A1	NM_000094	1	118	86	-	48610295	48610375

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262588983	chr3	48610031	48610255	48610053	48610233	COL7A1	NM_000094	1	118	87	-	48610104	48610172
265699574	chr3	48609779	48610001	48609802	48609977	COL7A1	NM_000094	1	118	88	-	48609936	48609971
265699574	chr3	48609779	48610001	48609802	48609977	COL7A1	NM_000094	1	118	89	-	48609813	48609854
265749682	chr3	48609512	48609647	48609534	48609625	COL7A1	NM_000094	1	118	90	-	48609560	48609604
265743726	chr3	48609305	48609522	48609325	48609501	COL7A1	NM_000094	1	118	91	-	48609434	48609478
264360000	chr3	48608523	48608745	48608547	48608723	COL7A1	NM_000094	1	118	92	-	48608676	48608711
264334519	chr3	48608416	48608621	48608438	48608598	COL7A1	NM_000094	1	118	93	-	48608534	48608593
264360000	chr3	48608523	48608745	48608547	48608723	COL7A1	NM_000094	1	118	93	-	48608534	48608593
262881416	chr3	48608254	48608439	48608274	48608417	COL7A1	NM_000094	1	118	94	-	48608294	48608401
267247971	chr3	48608006	48608191	48608027	48608170	COL7A1	NM_000094	1	118	95	-	48608072	48608143
265799248	chr3	48607866	48608029	48607888	48608007	COL7A1	NM_000094	1	118	96	-	48607898	48607933
258981365	chr3	48607605	48607812	48607627	48607791	COL7A1	NM_000094	1	118	97	-	48607708	48607767
264516832	chr3	48607477	48607642	48607498	48607616	COL7A1	NM_000094	1	118	98	-	48607567	48607611
257539733	chr3	48607153	48607377	48607176	48607356	COL7A1	NM_000094	1	118	99	-	48607313	48607348
257539733	chr3	48607153	48607377	48607176	48607356	COL7A1	NM_000094	1	118	100	-	48607158	48607193
257800538	chr3	48607059	48607222	48607080	48607202	COL7A1	NM_000094	1	118	100	-	48607158	48607193
257796827	chr3	48606933	48607115	48606956	48607094	COL7A1	NM_000094	1	118	101	-	48607025	48607081
257800538	chr3	48607059	48607222	48607080	48607202	COL7A1	NM_000094	1	118	101	-	48607025	48607081
262377862	chr3	48606691	48606907	48606711	48606884	COL7A1	NM_000094	1	118	102	-	48606808	48606879
266689076	chr3	48606142	48606320	48606163	48606299	COL7A1	NM_000094	1	118	103	-	48606217	48606288
268130540	chr3	48605829	48606052	48605856	48606032	COL7A1	NM_000094	1	118	104	-	48605932	48605967
268689578	chr3	48605426	48605639	48605448	48605618	COL7A1	NM_000094	1	118	105	-	48605523	48605603
262244074	chr3	48605135	48605359	48605158	48605333	COL7A1	NM_000094	1	118	106	-	48605271	48605324
262244074	chr3	48605135	48605359	48605158	48605333	COL7A1	NM_000094	1	118	107	-	48605143	48605196
267567763	chr3	48604999	48605222	48605018	48605203	COL7A1	NM_000094	1	118	107	-	48605143	48605196
267566178	chr3	48604962	48605159	48604983	48605136	COL7A1	NM_000094	1	118	108	-	48605007	48605069
267567763	chr3	48604999	48605222	48605018	48605203	COL7A1	NM_000094	1	118	108	-	48605007	48605069
261406601	chr3	48604460	48604653	48604487	48604628	COL7A1	NM_000094	1	118	109	-	48604561	48604623
267857483	chr3	48604268	48604492	48604292	48604464	COL7A1	NM_000094	1	118	110	-	48604340	48604456
264214798	chr3	48604063	48604287	48604084	48604264	COL7A1	NM_000094	1	118	111	-	48604093	48604170
262527652	chr3	48603819	48604042	48603841	48604022	COL7A1	NM_000094	1	118	112	-	48603943	48603996
265552015	chr3	48603564	48603779	48603587	48603755	COL7A1	NM_000094	1	118	113	-	48603700	48603748
266338123	chr3	48602965	48603099	48602983	48603081	COL7A1	NM_000094	1	118	114	-	48603069	48603101
266333449	chr3	48602772	48602978	48602793	48602958	COL7A1	NM_000094	1	118	115	-	48602843	48602929
264583071	chr3	48602426	48602580	48602447	48602559	COL7A1	NM_000094	1	118	116	-	48602542	48602634
264603924	chr3	48602536	48602718	48602560	48602696	COL7A1	NM_000094	1	118	116	-	48602542	48602634
267262803	chr3	48602142	48602317	48602161	48602294	COL7A1	NM_000094	1	118	117	-	48602216	48602413
267270069	chr3	48602275	48602471	48602295	48602447	COL7A1	NM_000094	1	118	117	-	48602216	48602413
267390340	chr3	48601693	48601886	48601714	48601867	COL7A1	NM_000094	1	118	118	-	48601506	48601855
268656936	chr6	71012498	71012660	71012519	71012633	COL9A1	NM_001851	1	38	1	-	71012614	71012786
258901983	chr6	71011590	71011814	71011613	71011786	COL9A1	NM_001851	1	38	2	-	71011704	71011777

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262020108	chr6	71009974	71010129	71010001	71010101	COL9A1	NM_001851	1	38	3	-	71010012	71010089
262014505	chr6	71009839	71010003	71009864	71009975	COL9A1	NM_001851	1	38	4	-	71009746	71009878
266065748	chr6	71009582	71009800	71009610	71009778	COL9A1	NM_001851	1	38	4	-	71009746	71009878
266065911	chr6	71009744	71009892	71009772	71009863	COL9A1	NM_001851	1	38	4	-	71009746	71009878
269050431	chr6	71003755	71003976	71003778	71003948	COL9A1	NM_001851	1	38	5	-	71003870	71004266
269059371	chr6	71003928	71004152	71003949	71004127	COL9A1	NM_001851	1	38	5	-	71003870	71004266
269086259	chr6	71004100	71004314	71004128	71004290	COL9A1	NM_001851	1	38	5	-	71003870	71004266
261580786	chr6	70993359	70993556	70993380	70993529	COL9A1	NM_001851	1	38	6	-	70993440	70993523
268573780	chr6	70992432	70992653	70992454	70992626	COL9A1	NM_001851	1	38	7	-	70992601	70992621
264611319	chr6	70990985	70991201	70991006	70991176	COL9A1	NM_001851	1	38	8	-	70991093	70991167
258797559	chr6	70990605	70990782	70990629	70990759	COL9A1	NM_001851	1	38	9	-	70990707	70990742
268906480	chr6	70990441	70990634	70990465	70990609	COL9A1	NM_001851	1	38	10	-	70990515	70990577
267835224	chr6	70984390	70984530	70984415	70984502	COL9A1	NM_001851	1	38	11	-	70984422	70984475
263146612	chr6	70983564	70983785	70983592	70983767	COL9A1	NM_001851	1	38	12	-	70983750	70983785
258838822	chr6	70981672	70981839	70981700	70981807	COL9A1	NM_001851	1	38	13	-	70981768	70981791
268866598	chr6	70981230	70981378	70981257	70981359	COL9A1	NM_001851	1	38	14	-	70981358	70981411
268872668	chr6	70981337	70981533	70981360	70981505	COL9A1	NM_001851	1	38	14	-	70981358	70981411
267241523	chr6	70979879	70980102	70979904	70980077	COL9A1	NM_001851	1	38	15	-	70980017	70980070
267915050	chr6	70979266	70979456	70979292	70979428	COL9A1	NM_001851	1	38	16	-	70979336	70979368
265618725	chr6	70978389	70978606	70978411	70978578	COL9A1	NM_001851	1	38	17	-	70978507	70978563
265045936	chr6	70976267	70976452	70976295	70976427	COL9A1	NM_001851	1	38	18	-	70976420	70976473
265046045	chr6	70976405	70976531	70976429	70976505	COL9A1	NM_001851	1	38	18	-	70976420	70976473
268149036	chr6	70972828	70973052	70972852	70973023	COL9A1	NM_001851	1	38	19	-	70972947	70973000
267241116	chr6	70970345	70970499	70970372	70970471	COL9A1	NM_001851	1	38	20	-	70970360	70970413
265224530	chr6	70966384	70966583	70966410	70966554	COL9A1	NM_001851	1	38	21	-	70966471	70966524
267101951	chr6	70964965	70965182	70964992	70965154	COL9A1	NM_001851	1	38	22	-	70965040	70965093
268595215	chr6	70964799	70964995	70964827	70964967	COL9A1	NM_001851	1	38	23	-	70964853	70964906
257511073	chr6	70964582	70964775	70964609	70964747	COL9A1	NM_001851	1	38	24	-	70964666	70964719
264627686	chr6	70964074	70964275	70964102	70964249	COL9A1	NM_001851	1	38	25	-	70964179	70964232
263235645	chr6	70962902	70963125	70962929	70963104	COL9A1	NM_001851	1	38	26	-	70963088	70963132
263237282	chr6	70963088	70963283	70963109	70963256	COL9A1	NM_001851	1	38	26	-	70963088	70963132
266708416	chr6	70961865	70962055	70961885	70962027	COL9A1	NM_001851	1	38	27	-	70961965	70962018
266679745	chr6	70961719	70961943	70961744	70961915	COL9A1	NM_001851	1	38	28	-	70961823	70961876
262285176	chr6	70952319	70952534	70952342	70952511	COL9A1	NM_001851	1	38	29	-	70952365	70952418
268812968	chr6	70951567	70951788	70951591	70951764	COL9A1	NM_001851	1	38	30	-	70951667	70951738
261207416	chr6	70951017	70951233	70951044	70951207	COL9A1	NM_001851	1	38	31	-	70951122	70951157
264393994	chr6	70950233	70950447	70950261	70950421	COL9A1	NM_001851	1	38	32	-	70950392	70950436
264403129	chr6	70950398	70950618	70950418	70950592	COL9A1	NM_001851	1	38	32	-	70950392	70950436
257740555	chr6	70948940	70949109	70948969	70949084	COL9A1	NM_001851	1	38	33	-	70948957	70948989
268336740	chr6	70944450	70944673	70944471	70944648	COL9A1	NM_001851	1	38	34	-	70944497	70944643
266362181	chr6	70944145	70944339	70944171	70944312	COL9A1	NM_001851	1	38	35	-	70944242	70944296

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263016530	chr6	70942258	70942481	70942279	70942454	COL9A1	NM_001851	1	38	36	-	70942286	70942474
263032419	chr6	70942429	70942636	70942451	70942610	COL9A1	NM_001851	1	38	36	-	70942286	70942474
257715638	chr6	70935568	70935786	70935591	70935760	COL9A1	NM_001851	1	38	37	-	70935635	70935712
267894651	chr6	70926413	70926634	70926440	70926611	COL9A1	NM_001851	1	38	38	-	70925743	70926784
267899241	chr6	70926590	70926813	70926612	70926789	COL9A1	NM_001851	1	38	38	-	70925743	70926784
268371968	chr6	70992644	70992847	70992666	70992826	COL9A1	NM_078485	2	32	1	-	70992684	70992911
264611319	chr6	70990985	70991201	70991006	70991176	COL9A1	NM_078485	2	32	2	-	70991093	70991167
258797559	chr6	70990605	70990782	70990629	70990759	COL9A1	NM_078485	2	32	3	-	70990707	70990742
268906480	chr6	70990441	70990634	70990465	70990609	COL9A1	NM_078485	2	32	4	-	70990515	70990577
267835224	chr6	70984390	70984530	70984415	70984502	COL9A1	NM_078485	2	32	5	-	70984422	70984475
263146612	chr6	70983564	70983785	70983592	70983767	COL9A1	NM_078485	2	32	6	-	70983750	70983785
258838822	chr6	70981672	70981839	70981700	70981807	COL9A1	NM_078485	2	32	7	-	70981768	70981791
268866598	chr6	70981230	70981378	70981257	70981359	COL9A1	NM_078485	2	32	8	-	70981358	70981411
268872668	chr6	70981337	70981533	70981360	70981505	COL9A1	NM_078485	2	32	8	-	70981358	70981411
267241523	chr6	70979879	70980102	70979904	70980077	COL9A1	NM_078485	2	32	9	-	70980017	70980070
267915050	chr6	70979266	70979456	70979292	70979428	COL9A1	NM_078485	2	32	10	-	70979336	70979368
265618725	chr6	70978389	70978606	70978411	70978578	COL9A1	NM_078485	2	32	11	-	70978507	70978563
265045936	chr6	70976267	70976452	70976295	70976427	COL9A1	NM_078485	2	32	12	-	70976420	70976473
265046045	chr6	70976405	70976531	70976429	70976505	COL9A1	NM_078485	2	32	12	-	70976420	70976473
268149036	chr6	70972828	70973052	70972852	70973023	COL9A1	NM_078485	2	32	13	-	70972947	70973000
267241116	chr6	70970345	70970499	70970372	70970471	COL9A1	NM_078485	2	32	14	-	70970360	70970413
265224530	chr6	70966384	70966583	70966410	70966554	COL9A1	NM_078485	2	32	15	-	70966471	70966524
267101951	chr6	70964965	70965182	70964992	70965154	COL9A1	NM_078485	2	32	16	-	70965040	70965093
268595215	chr6	70964799	70964995	70964827	70964967	COL9A1	NM_078485	2	32	17	-	70964853	70964906
257511073	chr6	70964582	70964775	70964609	70964747	COL9A1	NM_078485	2	32	18	-	70964666	70964719
264627686	chr6	70964074	70964275	70964102	70964249	COL9A1	NM_078485	2	32	19	-	70964179	70964232
263235645	chr6	70962902	70963125	70962929	70963104	COL9A1	NM_078485	2	32	20	-	70963088	70963132
263237282	chr6	70963088	70963283	70963109	70963256	COL9A1	NM_078485	2	32	20	-	70963088	70963132
266708416	chr6	70961865	70962055	70961885	70962027	COL9A1	NM_078485	2	32	21	-	70961965	70962018
266679745	chr6	70961719	70961943	70961744	70961915	COL9A1	NM_078485	2	32	22	-	70961823	70961876
262285176	chr6	70952319	70952534	70952342	70952511	COL9A1	NM_078485	2	32	23	-	70952365	70952418
268812968	chr6	70951567	70951788	70951591	70951764	COL9A1	NM_078485	2	32	24	-	70951667	70951738
261207416	chr6	70951017	70951233	70951044	70951207	COL9A1	NM_078485	2	32	25	-	70951122	70951157
264393994	chr6	70950233	70950447	70950261	70950421	COL9A1	NM_078485	2	32	26	-	70950392	70950436
264403129	chr6	70950398	70950618	70950418	70950592	COL9A1	NM_078485	2	32	26	-	70950392	70950436
257740555	chr6	70948940	70949109	70948969	70949084	COL9A1	NM_078485	2	32	27	-	70948957	70948989
268336740	chr6	70944450	70944673	70944471	70944648	COL9A1	NM_078485	2	32	28	-	70944497	70944643
266362181	chr6	70944145	70944339	70944171	70944312	COL9A1	NM_078485	2	32	29	-	70944242	70944296
263016530	chr6	70942258	70942481	70942279	70942454	COL9A1	NM_078485	2	32	30	-	70942286	70942474
263032419	chr6	70942429	70942636	70942451	70942610	COL9A1	NM_078485	2	32	30	-	70942286	70942474
257715638	chr6	70935568	70935786	70935591	70935760	COL9A1	NM_078485	2	32	31	-	70935635	70935712

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267894651	chr6	70926413	70926634	70926440	70926611	COL9A1	NM_078485	2	32	32	-	70925743	70926784
267899241	chr6	70926590	70926813	70926612	70926789	COL9A1	NM_078485	2	32	32	-	70925743	70926784
269293862	chr1	197237461	197237647	197237484	197237624	CRB1	NM_001193640	1	10	1	+	197237334	197237612
264072914	chr1	197297971	197298180	197297996	197298154	CRB1	NM_001193640	1	10	2	+	197297552	197298133
264183644	chr1	197297471	197297691	197297497	197297664	CRB1	NM_001193640	1	10	2	+	197297552	197298133
264217566	chr1	197297641	197297847	197297665	197297825	CRB1	NM_001193640	1	10	2	+	197297552	197298133
264310030	chr1	197297799	197298020	197297824	197297996	CRB1	NM_001193640	1	10	2	+	197297552	197298133
269227472	chr1	197325819	197326042	197325841	197326021	CRB1	NM_001193640	1	10	3	+	197325961	197326143
269258245	chr1	197326000	197326179	197326022	197326151	CRB1	NM_001193640	1	10	3	+	197325961	197326143
266703310	chr1	197390644	197390792	197390664	197390763	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266706093	chr1	197390007	197390177	197390033	197390153	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266727165	chr1	197390134	197390336	197390154	197390308	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266750871	chr1	197390740	197390955	197390764	197390928	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266814611	chr1	197390903	197391121	197390929	197391101	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266823542	chr1	197390288	197390508	197390309	197390486	CRB1	NM_001193640	1	10	4	+	197390130	197391086
266924221	chr1	197390464	197390687	197390487	197390663	CRB1	NM_001193640	1	10	4	+	197390130	197391086
262480637	chr1	197396496	197396663	197396525	197396639	CRB1	NM_001193640	1	10	5	+	197396584	197397131
262516404	chr1	197396612	197396795	197396640	197396772	CRB1	NM_001193640	1	10	5	+	197396584	197397131
262528523	chr1	197396754	197396964	197396772	197396941	CRB1	NM_001193640	1	10	5	+	197396584	197397131
262559338	chr1	197396917	197397137	197396942	197397114	CRB1	NM_001193640	1	10	5	+	197396584	197397131
268296011	chr1	197397093	197397305	197397114	197397278	CRB1	NM_001193640	1	10	5	+	197396584	197397131
268817200	chr1	197398399	197398607	197398423	197398585	CRB1	NM_001193640	1	10	6	+	197398579	197398744
268823468	chr1	197398561	197398775	197398586	197398749	CRB1	NM_001193640	1	10	6	+	197398579	197398744
260009669	chr1	197404236	197404457	197404260	197404434	CRB1	NM_001193640	1	10	7	+	197403836	197404742
260070381	chr1	197404410	197404629	197404434	197404605	CRB1	NM_001193640	1	10	7	+	197403836	197404742
260212607	chr1	197404582	197404803	197404603	197404776	CRB1	NM_001193640	1	10	7	+	197403836	197404742
267997200	chr1	197403822	197403982	197403850	197403954	CRB1	NM_001193640	1	10	7	+	197403836	197404742
268003725	chr1	197403929	197404118	197403955	197404096	CRB1	NM_001193640	1	10	7	+	197403836	197404742
268008206	chr1	197404074	197404280	197404096	197404259	CRB1	NM_001193640	1	10	7	+	197403836	197404742
267755274	chr1	197407630	197407835	197407655	197407810	CRB1	NM_001193640	1	10	8	+	197407677	197407805
264905293	chr1	197411250	197411463	197411273	197411434	CRB1	NM_001193640	1	10	9	+	197411296	197411422
269254690	chr1	197446662	197446865	197446690	197446843	CRB1	NM_001193640	1	10	10	+	197446794	197447585
269290940	chr1	197446821	197447044	197446844	197447023	CRB1	NM_001193640	1	10	10	+	197446794	197447585
269293862	chr1	197237461	197237647	197237484	197237624	CRB1	NM_201253	2	12	1	+	197237334	197237612
264072914	chr1	197297971	197298180	197297996	197298154	CRB1	NM_201253	2	12	2	+	197297552	197298133
264183644	chr1	197297471	197297691	197297497	197297664	CRB1	NM_201253	2	12	2	+	197297552	197298133
264217566	chr1	197297641	197297847	197297665	197297825	CRB1	NM_201253	2	12	2	+	197297552	197298133
264310030	chr1	197297799	197298020	197297824	197297996	CRB1	NM_201253	2	12	2	+	197297552	197298133
261030069	chr1	197313299	197313483	197313324	197313461	CRB1	NM_201253	2	12	3	+	197313411	197313606
261051676	chr1	197313440	197313646	197313462	197313623	CRB1	NM_201253	2	12	3	+	197313411	197313606
268143017	chr1	197316381	197316605	197316408	197316582	CRB1	NM_201253	2	12	4	+	197316470	197316609

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268144176	chr1	197316555	197316774	197316582	197316748	CRB1	NM_201253	2	12	4	+	197316470	197316609
269227472	chr1	197325819	197326042	197325841	197326021	CRB1	NM_201253	2	12	5	+	197325961	197326143
269258245	chr1	197326000	197326179	197326022	197326151	CRB1	NM_201253	2	12	5	+	197325961	197326143
266703310	chr1	197390644	197390792	197390664	197390763	CRB1	NM_201253	2	12	6	+	197390130	197391086
266706093	chr1	197390007	197390177	197390033	197390153	CRB1	NM_201253	2	12	6	+	197390130	197391086
266727165	chr1	197390134	197390336	197390154	197390308	CRB1	NM_201253	2	12	6	+	197390130	197391086
266750871	chr1	197390740	197390955	197390764	197390928	CRB1	NM_201253	2	12	6	+	197390130	197391086
266814611	chr1	197390903	197391121	197390929	197391101	CRB1	NM_201253	2	12	6	+	197390130	197391086
266823542	chr1	197390288	197390508	197390309	197390486	CRB1	NM_201253	2	12	6	+	197390130	197391086
266924221	chr1	197390464	197390687	197390487	197390663	CRB1	NM_201253	2	12	6	+	197390130	197391086
262480637	chr1	197396496	197396663	197396525	197396639	CRB1	NM_201253	2	12	7	+	197396584	197397131
262516404	chr1	197396612	197396795	197396640	197396772	CRB1	NM_201253	2	12	7	+	197396584	197397131
262528523	chr1	197396754	197396964	197396772	197396941	CRB1	NM_201253	2	12	7	+	197396584	197397131
262559338	chr1	197396917	197397137	197396942	197397114	CRB1	NM_201253	2	12	7	+	197396584	197397131
268296011	chr1	197397093	197397305	197397114	197397278	CRB1	NM_201253	2	12	7	+	197396584	197397131
268817200	chr1	197398399	197398607	197398423	197398585	CRB1	NM_201253	2	12	8	+	197398579	197398744
268823468	chr1	197398561	197398775	197398586	197398749	CRB1	NM_201253	2	12	8	+	197398579	197398744
260009669	chr1	197404236	197404457	197404260	197404434	CRB1	NM_201253	2	12	9	+	197403836	197404742
260070381	chr1	197404410	197404629	197404434	197404605	CRB1	NM_201253	2	12	9	+	197403836	197404742
260212607	chr1	197404582	197404803	197404603	197404776	CRB1	NM_201253	2	12	9	+	197403836	197404742
267997200	chr1	197403822	197403982	197403850	197403954	CRB1	NM_201253	2	12	9	+	197403836	197404742
268003725	chr1	197403929	197404118	197403955	197404096	CRB1	NM_201253	2	12	9	+	197403836	197404742
268008206	chr1	197404074	197404280	197404096	197404259	CRB1	NM_201253	2	12	9	+	197403836	197404742
267755274	chr1	197407630	197407835	197407655	197407810	CRB1	NM_201253	2	12	10	+	197407677	197407805
264905293	chr1	197411250	197411463	197411273	197411434	CRB1	NM_201253	2	12	11	+	197411296	197411422
269254690	chr1	197446662	197446865	197446690	197446843	CRB1	NM_201253	2	12	12	+	197446794	197447585
269290940	chr1	197446821	197447044	197446844	197447023	CRB1	NM_201253	2	12	12	+	197446794	197447585
264876196	chr19	48337607	48337827	48337627	48337806	CRX	NM_000554	1	4	2	+	48337666	48337800
267638555	chr19	48339464	48339635	48339485	48339613	CRX	NM_000554	1	4	3	+	48339500	48339651
267639453	chr19	48339579	48339706	48339601	48339685	CRX	NM_000554	1	4	3	+	48339500	48339651
269369922	chr19	48342550	48342731	48342570	48342710	CRX	NM_000554	1	4	4	+	48342577	48346586
269370787	chr19	48342693	48342913	48342711	48342894	CRX	NM_000554	1	4	4	+	48342577	48346586
269372021	chr19	48343090	48343304	48343110	48343282	CRX	NM_000554	1	4	4	+	48342577	48346586
269372351	chr19	48342818	48343004	48342838	48342984	CRX	NM_000554	1	4	4	+	48342577	48346586
269374260	chr19	48342960	48343138	48342982	48343113	CRX	NM_000554	1	4	4	+	48342577	48346586
263345379	chr18	77455185	77455335	77455213	77455313	CTDP1	NM_001202504	1	13	2	+	77455225	77455308
266011911	chr18	77455943	77456166	77455963	77456148	CTDP1	NM_001202504	1	13	3	+	77455977	77456070
268768834	chr18	77457797	77458019	77457822	77457996	CTDP1	NM_001202504	1	13	4	+	77457860	77457988
259745912	chr18	77464732	77464955	77464754	77464935	CTDP1	NM_001202504	1	13	5	+	77464767	77464917
266564837	chr18	77470290	77470482	77470310	77470458	CTDP1	NM_001202504	1	13	6	+	77470346	77470436
268239174	chr18	77472863	77473087	77472886	77473064	CTDP1	NM_001202504	1	13	7	+	77472972	77473138

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268246578	chr18	77473040	77473170	77473065	77473142	CTDP1	NM_001202504	1	13	7	+	77472972	77473138
266015289	chr18	77475394	77475598	77475415	77475576	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268950787	chr18	77474992	77475149	77475010	77475129	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268950790	chr18	77474377	77474557	77474399	77474537	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268951758	chr18	77475099	77475315	77475117	77475294	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268958422	chr18	77474508	77474716	77474529	77474698	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268958831	chr18	77474662	77474839	77474682	77474818	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268959677	chr18	77474799	77474930	77474819	77474913	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268961006	chr18	77474875	77475050	77474893	77475031	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
268964329	chr18	77475274	77475434	77475295	77475414	CTDP1	NM_001202504	1	13	8	+	77474491	77475528
269281421	chr18	77477375	77477586	77477393	77477568	CTDP1	NM_001202504	1	13	9	+	77477535	77477676
269283569	chr18	77477526	77477750	77477546	77477730	CTDP1	NM_001202504	1	13	9	+	77477535	77477676
268199234	chr18	77477722	77477940	77477743	77477921	CTDP1	NM_001202504	1	13	10	+	77477810	77478016
268201139	chr18	77477902	77478069	77477921	77478048	CTDP1	NM_001202504	1	13	10	+	77477810	77478016
267422348	chr18	77488824	77489036	77488845	77489015	CTDP1	NM_001202504	1	13	11	+	77488907	77489069
267435318	chr18	77488995	77489196	77489016	77489172	CTDP1	NM_001202504	1	13	11	+	77488907	77489069
257457271	chr18	77496322	77496539	77496342	77496521	CTDP1	NM_001202504	1	13	12	+	77496355	77496521
257459291	chr18	77496478	77496699	77496495	77496677	CTDP1	NM_001202504	1	13	12	+	77496355	77496521
268502517	chr18	77513611	77513827	77513632	77513808	CTDP1	NM_001202504	1	13	13	+	77513652	77514510
268408182	chr18	77439835	77440058	77439856	77440040	CTDP1	NM_004715	2	13	1	+	77439801	77440261
268408220	chr18	77439940	77440155	77439957	77440136	CTDP1	NM_004715	2	13	1	+	77439801	77440261
268408274	chr18	77440133	77440280	77440152	77440263	CTDP1	NM_004715	2	13	1	+	77439801	77440261
263345379	chr18	77455185	77455335	77455213	77455313	CTDP1	NM_004715	2	13	2	+	77455225	77455308
266011911	chr18	77455943	77456166	77455963	77456148	CTDP1	NM_004715	2	13	3	+	77455977	77456070
268768834	chr18	77457797	77458019	77457822	77457996	CTDP1	NM_004715	2	13	4	+	77457860	77457988
259745912	chr18	77464732	77464955	77464754	77464935	CTDP1	NM_004715	2	13	5	+	77464767	77464917
266564837	chr18	77470290	77470482	77470310	77470458	CTDP1	NM_004715	2	13	6	+	77470346	77470436
268239174	chr18	77472863	77473087	77472886	77473064	CTDP1	NM_004715	2	13	7	+	77472972	77473138
268246578	chr18	77473040	77473170	77473065	77473142	CTDP1	NM_004715	2	13	7	+	77472972	77473138
266015289	chr18	77475394	77475598	77475415	77475576	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268950787	chr18	77474992	77475149	77475010	77475129	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268950790	chr18	77474377	77474557	77474399	77474537	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268951758	chr18	77475099	77475315	77475117	77475294	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268958422	chr18	77474508	77474716	77474529	77474698	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268958831	chr18	77474662	77474839	77474682	77474818	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268959677	chr18	77474799	77474930	77474819	77474913	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268961006	chr18	77474875	77475050	77474893	77475031	CTDP1	NM_004715	2	13	8	+	77474491	77475528
268964329	chr18	77475274	77475434	77475295	77475414	CTDP1	NM_004715	2	13	8	+	77474491	77475528
269281421	chr18	77477375	77477586	77477393	77477568	CTDP1	NM_004715	2	13	9	+	77477535	77477676
269283569	chr18	77477526	77477750	77477546	77477730	CTDP1	NM_004715	2	13	9	+	77477535	77477676
268199234	chr18	77477722	77477940	77477743	77477921	CTDP1	NM_004715	2	13	10	+	77477810	77478016

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268201139	chr18	77477902	77478069	77477921	77478048	CTDP1	NM_004715	2	13	10	+	77477810	77478016
267422348	chr18	77488824	77489036	77488845	77489015	CTDP1	NM_004715	2	13	11	+	77488907	77489069
267435318	chr18	77488995	77489196	77489016	77489172	CTDP1	NM_004715	2	13	11	+	77488907	77489069
257457271	chr18	77496322	77496539	77496342	77496521	CTDP1	NM_004715	2	13	12	+	77496355	77496521
257459291	chr18	77496478	77496699	77496495	77496677	CTDP1	NM_004715	2	13	12	+	77496355	77496521
268502517	chr18	77513611	77513827	77513632	77513808	CTDP1	NM_004715	2	13	13	+	77513652	77514510
268408182	chr18	77439835	77440058	77439856	77440040	CTDP1	NM_048368	3	12	1	+	77439801	77440261
268408220	chr18	77439940	77440155	77439957	77440136	CTDP1	NM_048368	3	12	1	+	77439801	77440261
268408274	chr18	77440133	77440280	77440152	77440263	CTDP1	NM_048368	3	12	1	+	77439801	77440261
263345379	chr18	77455185	77455335	77455213	77455313	CTDP1	NM_048368	3	12	2	+	77455225	77455308
266011911	chr18	77455943	77456166	77455963	77456148	CTDP1	NM_048368	3	12	3	+	77455977	77456070
268768834	chr18	77457797	77458019	77457822	77457996	CTDP1	NM_048368	3	12	4	+	77457860	77457988
259745912	chr18	77464732	77464955	77464754	77464935	CTDP1	NM_048368	3	12	5	+	77464767	77464917
266564837	chr18	77470290	77470482	77470310	77470458	CTDP1	NM_048368	3	12	6	+	77470346	77470436
268239174	chr18	77472863	77473087	77472886	77473064	CTDP1	NM_048368	3	12	7	+	77472972	77473138
268246578	chr18	77473040	77473170	77473065	77473142	CTDP1	NM_048368	3	12	7	+	77472972	77473138
266015289	chr18	77475394	77475598	77475415	77475576	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268950787	chr18	77474992	77475149	77475010	77475129	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268950790	chr18	77474377	77474557	77474399	77474537	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268951758	chr18	77475099	77475315	77475117	77475294	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268958422	chr18	77474508	77474716	77474529	77474698	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268958831	chr18	77474662	77474839	77474682	77474818	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268959677	chr18	77474799	77474930	77474819	77474913	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268961006	chr18	77474875	77475050	77474893	77475031	CTDP1	NM_048368	3	12	8	+	77474491	77475528
268964329	chr18	77475274	77475434	77475295	77475414	CTDP1	NM_048368	3	12	8	+	77474491	77475528
269281421	chr18	77477375	77477586	77477393	77477568	CTDP1	NM_048368	3	12	9	+	77477535	77477676
269283569	chr18	77477526	77477750	77477546	77477730	CTDP1	NM_048368	3	12	9	+	77477535	77477676
268199234	chr18	77477722	77477940	77477743	77477921	CTDP1	NM_048368	3	12	10	+	77477810	77478016
268201139	chr18	77477902	77478069	77477921	77478048	CTDP1	NM_048368	3	12	10	+	77477810	77478016
257457271	chr18	77496322	77496539	77496342	77496521	CTDP1	NM_048368	3	12	11	+	77496355	77496521
257459291	chr18	77496478	77496699	77496495	77496677	CTDP1	NM_048368	3	12	11	+	77496355	77496521
268502517	chr18	77513611	77513827	77513632	77513808	CTDP1	NM_048368	3	12	12	+	77513652	77514510
267219509	chr17	3543374	3543597	3543395	3543569	CTNS	NM_001031681	1	13	3	+	3543482	3543561
268446679	chr17	3550700	3550908	3550721	3550884	CTNS	NM_001031681	1	13	4	+	3550738	3550816
259958080	chr17	3552032	3552255	3552056	3552230	CTNS	NM_001031681	1	13	5	+	3552141	3552225
259472003	chr17	3558253	3558476	3558274	3558455	CTNS	NM_001031681	1	13	6	+	3558292	3558395
263349177	chr17	3558378	3558584	3558399	3558563	CTNS	NM_001031681	1	13	7	+	3558515	3558646
263380739	chr17	3558543	3558679	3558564	3558659	CTNS	NM_001031681	1	13	7	+	3558515	3558646
261988694	chr17	3559825	3560035	3559846	3560014	CTNS	NM_001031681	1	13	8	+	3559781	3559880
264071642	chr17	3559748	3559918	3559766	3559898	CTNS	NM_001031681	1	13	8	+	3559781	3559880
261988694	chr17	3559825	3560035	3559846	3560014	CTNS	NM_001031681	1	13	9	+	3559970	3560089

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262007802	chr17	3559996	3560201	3560015	3560177	CTNS	NM_001031681	1	13	9	+	3559970	3560089
269235463	chr17	3561258	3561474	3561279	3561449	CTNS	NM_001031681	1	13	10	+	3561299	3561469
269246862	chr17	3561426	3561583	3561447	3561561	CTNS	NM_001031681	1	13	10	+	3561299	3561469
260633502	chr17	3563048	3563272	3563072	3563250	CTNS	NM_001031681	1	13	11	+	3563152	3563269
260655723	chr17	3563229	3563438	3563250	3563416	CTNS	NM_001031681	1	13	11	+	3563152	3563269
268203191	chr17	3563480	3563686	3563500	3563668	CTNS	NM_001031681	1	13	12	+	3563530	3563644
268209254	chr17	3563882	3564090	3563902	3564068	CTNS	NM_001031681	1	13	13	+	3563911	3566397
267219509	chr17	3543374	3543597	3543395	3543569	CTNS	NM_004937	2	12	3	+	3543482	3543561
268446679	chr17	3550700	3550908	3550721	3550884	CTNS	NM_004937	2	12	4	+	3550738	3550816
259958080	chr17	3552032	3552255	3552056	3552230	CTNS	NM_004937	2	12	5	+	3552141	3552225
259472003	chr17	3558253	3558476	3558274	3558455	CTNS	NM_004937	2	12	6	+	3558292	3558395
263349177	chr17	3558378	3558584	3558399	3558563	CTNS	NM_004937	2	12	7	+	3558515	3558646
263380739	chr17	3558543	3558679	3558564	3558659	CTNS	NM_004937	2	12	7	+	3558515	3558646
261988694	chr17	3559825	3560035	3559846	3560014	CTNS	NM_004937	2	12	8	+	3559781	3559880
264071642	chr17	3559748	3559918	3559766	3559898	CTNS	NM_004937	2	12	8	+	3559781	3559880
261988694	chr17	3559825	3560035	3559846	3560014	CTNS	NM_004937	2	12	9	+	3559970	3560089
262007802	chr17	3559996	3560201	3560015	3560177	CTNS	NM_004937	2	12	9	+	3559970	3560089
269235463	chr17	3561258	3561474	3561279	3561449	CTNS	NM_004937	2	12	10	+	3561299	3561469
269246862	chr17	3561426	3561583	3561447	3561561	CTNS	NM_004937	2	12	10	+	3561299	3561469
260633502	chr17	3563048	3563272	3563072	3563250	CTNS	NM_004937	2	12	11	+	3563152	3563269
260655723	chr17	3563229	3563438	3563250	3563416	CTNS	NM_004937	2	12	11	+	3563152	3563269
268203191	chr17	3563480	3563686	3563500	3563668	CTNS	NM_004937	2	12	12	+	3563530	3566397
268209254	chr17	3563882	3564090	3563902	3564068	CTNS	NM_004937	2	12	12	+	3563530	3566397
267046622	chr2	219647005	219647226	219647022	219647204	CYP27A1	NM_000784	1	9	1	+	219646472	219647160
269170997	chr2	219646862	219647033	219646880	219647016	CYP27A1	NM_000784	1	9	1	+	219646472	219647160
268084182	chr2	219674260	219674450	219674282	219674428	CYP27A1	NM_000784	1	9	2	+	219674300	219674490
268103489	chr2	219674408	219674590	219674429	219674567	CYP27A1	NM_000784	1	9	2	+	219674300	219674490
267122146	chr2	219676871	219677061	219676897	219677033	CYP27A1	NM_000784	1	9	3	+	219676945	219677144
267153725	chr2	219677012	219677233	219677034	219677210	CYP27A1	NM_000784	1	9	3	+	219676945	219677144
268549983	chr2	219677175	219677390	219677196	219677365	CYP27A1	NM_000784	1	9	4	+	219677275	219677472
268563243	chr2	219677345	219677519	219677366	219677498	CYP27A1	NM_000784	1	9	4	+	219677275	219677472
264908082	chr2	219677546	219677769	219677567	219677749	CYP27A1	NM_000784	1	9	5	+	219677647	219677819
264961977	chr2	219677727	219677912	219677749	219677892	CYP27A1	NM_000784	1	9	5	+	219677647	219677819
267689875	chr2	219678701	219678923	219678722	219678902	CYP27A1	NM_000784	1	9	6	+	219678744	219678910
267708096	chr2	219678881	219679028	219678903	219679003	CYP27A1	NM_000784	1	9	6	+	219678744	219678910
268903974	chr2	219679000	219679211	219679021	219679192	CYP27A1	NM_000784	1	9	7	+	219679103	219679181
265478255	chr2	219679240	219679464	219679262	219679443	CYP27A1	NM_000784	1	9	8	+	219679268	219679480
265502616	chr2	219679392	219679611	219679413	219679589	CYP27A1	NM_000784	1	9	8	+	219679268	219679480
268331213	chr2	219679580	219679797	219679601	219679777	CYP27A1	NM_000784	1	9	9	+	219679634	219680016
268891891	chr1	100715247	100715425	100715273	100715403	DBT	NM_001918	1	11	1	-	100715326	100715409
267169440	chr1	100706189	100706365	100706209	100706336	DBT	NM_001918	1	11	2	-	100706317	100706440

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267177370	chr1	100706312	100706502	100706337	100706474	DBT	NM_001918	1	11	2	-	100706317	100706440
263089376	chr1	100700806	100701030	100700833	100701001	DBT	NM_001918	1	11	3	-	100700992	100701067
263090543	chr1	100701000	100701163	100701028	100701135	DBT	NM_001918	1	11	3	-	100700992	100701067
267635768	chr1	100696287	100696448	100696315	100696422	DBT	NM_001918	1	11	4	-	100696289	100696470
267636607	chr1	100696384	100696511	100696411	100696481	DBT	NM_001918	1	11	4	-	100696289	100696470
261752611	chr1	100684090	100684290	100684118	100684267	DBT	NM_001918	1	11	5	-	100684182	100684303
261754833	chr1	100684243	100684387	100684268	100684360	DBT	NM_001918	1	11	5	-	100684182	100684303
269193733	chr1	100681410	100681618	100681433	100681590	DBT	NM_001918	1	11	6	-	100681539	100681755
269204060	chr1	100681565	100681733	100681591	100681705	DBT	NM_001918	1	11	6	-	100681539	100681755
269207200	chr1	100681667	100681840	100681693	100681809	DBT	NM_001918	1	11	6	-	100681539	100681755
267922098	chr1	100680331	100680503	100680357	100680475	DBT	NM_001918	1	11	7	-	100680373	100680539
267923852	chr1	100680450	100680668	100680476	100680640	DBT	NM_001918	1	11	7	-	100680373	100680539
268883613	chr1	100676189	100676320	100676210	100676292	DBT	NM_001918	1	11	8	-	100676250	100676327
268886885	chr1	100676269	100676424	100676293	100676397	DBT	NM_001918	1	11	8	-	100676250	100676327
257288140	chr1	100671905	100672115	100671927	100672089	DBT	NM_001918	1	11	9	-	100672001	100672192
257317529	chr1	100672069	100672256	100672090	100672227	DBT	NM_001918	1	11	9	-	100672001	100672192
264746971	chr1	100671716	100671925	100671743	100671901	DBT	NM_001918	1	11	10	-	100671786	100671857
267014510	chr1	100661746	100661905	100661768	100661877	DBT	NM_001918	1	11	11	-	100652478	100661978
267028222	chr1	100661854	100662051	100661878	100662025	DBT	NM_001918	1	11	11	-	100652478	100661978
265917826	chrX	110653884	110654070	110653908	110654047	DCX	NM_000555	1	7	1	-	110653982	110654374
265929310	chrX	110654021	110654232	110654048	110654207	DCX	NM_000555	1	7	1	-	110653982	110654374
267457684	chrX	110653187	110653373	110653212	110653353	DCX	NM_000555	1	7	2	-	110653263	110653648
267473235	chrX	110653332	110653526	110653354	110653503	DCX	NM_000555	1	7	2	-	110653263	110653648
267495439	chrX	110653482	110653699	110653504	110653674	DCX	NM_000555	1	7	2	-	110653263	110653648
268732936	chrX	110644102	110644315	110644127	110644294	DCX	NM_000555	1	7	3	-	110644218	110644558
268750104	chrX	110644271	110644493	110644295	110644469	DCX	NM_000555	1	7	3	-	110644218	110644558
268759094	chrX	110644448	110644644	110644470	110644615	DCX	NM_000555	1	7	3	-	110644218	110644558
263727466	chrX	110576210	110576425	110576237	110576397	DCX	NM_000555	1	7	4	-	110576279	110576381
267270676	chrX	110574083	110574301	110574107	110574275	DCX	NM_000555	1	7	5	-	110574147	110574269
259647316	chrX	110555769	110555993	110555796	110555969	DCX	NM_000555	1	7	6	-	110555870	110555964
266295062	chrX	110544815	110545028	110544837	110545000	DCX	NM_000555	1	7	7	-	110537007	110544971
267457684	chrX	110653187	110653373	110653212	110653353	DCX	NM_001195553	2	7	2	-	110653263	110653648
267473235	chrX	110653332	110653526	110653354	110653503	DCX	NM_001195553	2	7	2	-	110653263	110653648
267495439	chrX	110653482	110653699	110653504	110653674	DCX	NM_001195553	2	7	2	-	110653263	110653648
268732936	chrX	110644102	110644315	110644127	110644294	DCX	NM_001195553	2	7	3	-	110644218	110644558
268750104	chrX	110644271	110644493	110644295	110644469	DCX	NM_001195553	2	7	3	-	110644218	110644558
268759094	chrX	110644448	110644644	110644470	110644615	DCX	NM_001195553	2	7	3	-	110644218	110644558
263727466	chrX	110576210	110576425	110576237	110576397	DCX	NM_001195553	2	7	4	-	110576279	110576381
267270676	chrX	110574083	110574301	110574107	110574275	DCX	NM_001195553	2	7	5	-	110574132	110574269
259647316	chrX	110555769	110555993	110555796	110555969	DCX	NM_001195553	2	7	6	-	110555867	110555964
266295062	chrX	110544815	110545028	110544837	110545000	DCX	NM_001195553	2	7	7	-	110537007	110544971

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267457684	chrX	110653187	110653373	110653212	110653353	DCX	NM_178151	3	7	2	-	110653263	110653648
267473235	chrX	110653332	110653526	110653354	110653503	DCX	NM_178151	3	7	2	-	110653263	110653648
267495439	chrX	110653482	110653699	110653504	110653674	DCX	NM_178151	3	7	2	-	110653263	110653648
268732936	chrX	110644102	110644315	110644127	110644294	DCX	NM_178151	3	7	3	-	110644218	110644558
268750104	chrX	110644271	110644493	110644295	110644469	DCX	NM_178151	3	7	3	-	110644218	110644558
268759094	chrX	110644448	110644644	110644470	110644615	DCX	NM_178151	3	7	3	-	110644218	110644558
263727466	chrX	110576210	110576425	110576237	110576397	DCX	NM_178151	3	7	4	-	110576279	110576381
267270676	chrX	110574083	110574301	110574107	110574275	DCX	NM_178151	3	7	5	-	110574147	110574269
259647316	chrX	110555769	110555993	110555796	110555969	DCX	NM_178151	3	7	6	-	110555870	110555964
266295062	chrX	110544815	110545028	110544837	110545000	DCX	NM_178151	3	7	7	-	110537007	110544971
267457684	chrX	110653187	110653373	110653212	110653353	DCX	NM_178152	4	7	2	-	110653263	110653648
267473235	chrX	110653332	110653526	110653354	110653503	DCX	NM_178152	4	7	2	-	110653263	110653648
267495439	chrX	110653482	110653699	110653504	110653674	DCX	NM_178152	4	7	2	-	110653263	110653648
268732936	chrX	110644102	110644315	110644127	110644294	DCX	NM_178152	4	7	3	-	110644218	110644558
268750104	chrX	110644271	110644493	110644295	110644469	DCX	NM_178152	4	7	3	-	110644218	110644558
268759094	chrX	110644448	110644644	110644470	110644615	DCX	NM_178152	4	7	3	-	110644218	110644558
263727466	chrX	110576210	110576425	110576237	110576397	DCX	NM_178152	4	7	4	-	110576279	110576381
267270676	chrX	110574083	110574301	110574107	110574275	DCX	NM_178152	4	7	5	-	110574132	110574269
259647316	chrX	110555769	110555993	110555796	110555969	DCX	NM_178152	4	7	6	-	110555870	110555964
266295062	chrX	110544815	110545028	110544837	110545000	DCX	NM_178152	4	7	7	-	110537007	110544971
267457684	chrX	110653187	110653373	110653212	110653353	DCX	NM_178153	5	7	2	-	110653263	110653648
267473235	chrX	110653332	110653526	110653354	110653503	DCX	NM_178153	5	7	2	-	110653263	110653648
267495439	chrX	110653482	110653699	110653504	110653674	DCX	NM_178153	5	7	2	-	110653263	110653648
268732936	chrX	110644102	110644315	110644127	110644294	DCX	NM_178153	5	7	3	-	110644218	110644558
268750104	chrX	110644271	110644493	110644295	110644469	DCX	NM_178153	5	7	3	-	110644218	110644558
268759094	chrX	110644448	110644644	110644470	110644615	DCX	NM_178153	5	7	3	-	110644218	110644558
263727466	chrX	110576210	110576425	110576237	110576397	DCX	NM_178153	5	7	4	-	110576279	110576381
267270676	chrX	110574083	110574301	110574107	110574275	DCX	NM_178153	5	7	5	-	110574147	110574269
259647316	chrX	110555769	110555993	110555796	110555969	DCX	NM_178153	5	7	6	-	110555870	110555964
266295062	chrX	110544815	110545028	110544837	110545000	DCX	NM_178153	5	7	7	-	110537007	110544971
267658825	chr2	220283108	220283326	220283125	220283307	DES	NM_001927	1	9	1	+	220283099	220283762
267659394	chr2	220283272	220283495	220283290	220283473	DES	NM_001927	1	9	1	+	220283099	220283762
267659656	chr2	220283530	220283700	220283550	220283679	DES	NM_001927	1	9	1	+	220283099	220283762
267660954	chr2	220283634	220283858	220283652	220283839	DES	NM_001927	1	9	1	+	220283099	220283762
267661364	chr2	220283443	220283568	220283463	220283549	DES	NM_001927	1	9	1	+	220283099	220283762
267781313	chr2	220284757	220284961	220284778	220284940	DES	NM_001927	1	9	2	+	220284817	220284877
267785091	chr2	220284819	220285042	220284842	220285019	DES	NM_001927	1	9	2	+	220284817	220284877
267785091	chr2	220284819	220285042	220284842	220285019	DES	NM_001927	1	9	3	+	220284973	220285068
268772456	chr2	220285000	220285222	220285020	220285200	DES	NM_001927	1	9	3	+	220284973	220285068
267942384	chr2	220285138	220285352	220285158	220285329	DES	NM_001927	1	9	4	+	220285217	220285378
267956167	chr2	220285309	220285468	220285330	220285447	DES	NM_001927	1	9	4	+	220285217	220285378

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261433337	chr2	220285441	220285652	220285462	220285631	DES	NM_001927	1	9	5	+	220285550	220285675
261499125	chr2	220285609	220285832	220285632	220285809	DES	NM_001927	1	9	5	+	220285550	220285675
267841527	chr2	220285998	220286206	220286020	220286187	DES	NM_001927	1	9	6	+	220286062	220286282
267853430	chr2	220286155	220286374	220286176	220286349	DES	NM_001927	1	9	6	+	220286062	220286282
267771047	chr2	220288455	220288677	220288481	220288654	DES	NM_001927	1	9	7	+	220288499	220288542
267390626	chr2	220290346	220290568	220290366	220290548	DES	NM_001927	1	9	8	+	220290385	220290467
268560938	chr2	220290615	220290799	220290636	220290778	DES	NM_001927	1	9	9	+	220290671	220291461
261787430	chr11	71155813	71156037	71155838	71156009	DHCR7	NM_001163817	1	9	3	-	71155901	71156004
265276441	chr11	71154944	71155110	71154967	71155090	DHCR7	NM_001163817	1	9	4	-	71155039	71155261
265300179	chr11	71155070	71155210	71155091	71155185	DHCR7	NM_001163817	1	9	4	-	71155039	71155261
265317849	chr11	71155165	71155354	71155186	71155333	DHCR7	NM_001163817	1	9	4	-	71155039	71155261
267772497	chr11	71153200	71153424	71153227	71153404	DHCR7	NM_001163817	1	9	5	-	71153309	71153399
265567607	chr11	71152221	71152399	71152244	71152379	DHCR7	NM_001163817	1	9	6	-	71152273	71152486
265574317	chr11	71152359	71152516	71152380	71152492	DHCR7	NM_001163817	1	9	6	-	71152273	71152486
257860724	chr11	71149836	71150059	71149861	71150033	DHCR7	NM_001163817	1	9	7	-	71149925	71150129
257887021	chr11	71149995	71150203	71150016	71150181	DHCR7	NM_001163817	1	9	7	-	71149925	71150129
268089883	chr11	71148716	71148892	71148737	71148871	DHCR7	NM_001163817	1	9	8	-	71148858	71148989
268108133	chr11	71148852	71149059	71148872	71149039	DHCR7	NM_001163817	1	9	8	-	71148858	71148989
267999045	chr11	71146369	71146574	71146388	71146553	DHCR7	NM_001163817	1	9	9	-	71145457	71146885
268002988	chr11	71146531	71146729	71146554	71146709	DHCR7	NM_001163817	1	9	9	-	71145457	71146885
268004438	chr11	71146689	71146817	71146708	71146796	DHCR7	NM_001163817	1	9	9	-	71145457	71146885
268005886	chr11	71146766	71146918	71146787	71146901	DHCR7	NM_001163817	1	9	9	-	71145457	71146885
261787430	chr11	71155813	71156037	71155838	71156009	DHCR7	NM_001360	2	9	3	-	71155901	71156004
265276441	chr11	71154944	71155110	71154967	71155090	DHCR7	NM_001360	2	9	4	-	71155039	71155261
265300179	chr11	71155070	71155210	71155091	71155185	DHCR7	NM_001360	2	9	4	-	71155039	71155261
265317849	chr11	71155165	71155354	71155186	71155333	DHCR7	NM_001360	2	9	4	-	71155039	71155261
267772497	chr11	71153200	71153424	71153227	71153404	DHCR7	NM_001360	2	9	5	-	71153309	71153399
265567607	chr11	71152221	71152399	71152244	71152379	DHCR7	NM_001360	2	9	6	-	71152273	71152486
265574317	chr11	71152359	71152516	71152380	71152492	DHCR7	NM_001360	2	9	6	-	71152273	71152486
257860724	chr11	71149836	71150059	71149861	71150033	DHCR7	NM_001360	2	9	7	-	71149925	71150129
257887021	chr11	71149995	71150203	71150016	71150181	DHCR7	NM_001360	2	9	7	-	71149925	71150129
268089883	chr11	71148716	71148892	71148737	71148871	DHCR7	NM_001360	2	9	8	-	71148858	71148989
268108133	chr11	71148852	71149059	71148872	71149039	DHCR7	NM_001360	2	9	8	-	71148858	71148989
267999045	chr11	71146369	71146574	71146388	71146553	DHCR7	NM_001360	2	9	9	-	71145457	71146885
268002988	chr11	71146531	71146729	71146554	71146709	DHCR7	NM_001360	2	9	9	-	71145457	71146885
268004438	chr11	71146689	71146817	71146708	71146796	DHCR7	NM_001360	2	9	9	-	71145457	71146885
268005886	chr11	71146766	71146918	71146787	71146901	DHCR7	NM_001360	2	9	9	-	71145457	71146885
262237613	chrX	153991136	153991301	153991154	153991283	DKC1	NM_001142463	1	15	1	+	153991031	153991256
265757724	chrX	153993072	153993259	153993098	153993232	DKC1	NM_001142463	1	15	2	+	153993174	153993241
265765929	chrX	153993211	153993341	153993233	153993313	DKC1	NM_001142463	1	15	2	+	153993174	153993241
267491306	chrX	153993630	153993850	153993657	153993826	DKC1	NM_001142463	1	15	3	+	153993719	153993805

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268068255	chrX	153994099	153994312	153994120	153994288	DKC1	NM_001142463	1	15	4	+	153994182	153994273
267740199	chrX	153994352	153994547	153994373	153994526	DKC1	NM_001142463	1	15	5	+	153994491	153994675
267765766	chrX	153994501	153994717	153994527	153994694	DKC1	NM_001142463	1	15	5	+	153994491	153994675
268652620	chrX	153995155	153995369	153995175	153995346	DKC1	NM_001142463	1	15	6	+	153995272	153995336
265386341	chrX	153995470	153995683	153995493	153995662	DKC1	NM_001142463	1	15	7	+	153995531	153995657
260311421	chrX	153996517	153996737	153996546	153996712	DKC1	NM_001142463	1	15	8	+	153996577	153996707
268823981	chrX	153997311	153997471	153997335	153997449	DKC1	NM_001142463	1	15	9	+	153997442	153997585
268839688	chrX	153997429	153997638	153997450	153997612	DKC1	NM_001142463	1	15	9	+	153997442	153997585
267265372	chrX	153998946	153999167	153998967	153999146	DKC1	NM_001142463	1	15	10	+	153999034	153999154
261246496	chrX	154001250	154001470	154001273	154001443	DKC1	NM_001142463	1	15	11	+	154001406	154001524
261281270	chrX	154001422	154001546	154001443	154001525	DKC1	NM_001142463	1	15	11	+	154001406	154001524
264962479	chrX	154002827	154003031	154002849	154003011	DKC1	NM_001142463	1	15	12	+	154002877	154002965
268124711	chrX	154003356	154003580	154003379	154003558	DKC1	NM_001142463	1	15	13	+	154003470	154003548
267541424	chrX	154004404	154004626	154004429	154004604	DKC1	NM_001142463	1	15	14	+	154004462	154004599
268385894	chrX	154004957	154005174	154004981	154005149	DKC1	NM_001142463	1	15	15	+	154005074	154005964
262237613	chrX	153991136	153991301	153991154	153991283	DKC1	NM_001363	2	15	1	+	153991031	153991256
265757724	chrX	153993072	153993259	153993098	153993232	DKC1	NM_001363	2	15	2	+	153993174	153993241
265765929	chrX	153993211	153993341	153993233	153993313	DKC1	NM_001363	2	15	2	+	153993174	153993241
267491306	chrX	153993630	153993850	153993657	153993826	DKC1	NM_001363	2	15	3	+	153993719	153993805
268068255	chrX	153994099	153994312	153994120	153994288	DKC1	NM_001363	2	15	4	+	153994182	153994273
267740199	chrX	153994352	153994547	153994373	153994526	DKC1	NM_001363	2	15	5	+	153994491	153994675
267765766	chrX	153994501	153994717	153994527	153994694	DKC1	NM_001363	2	15	5	+	153994491	153994675
268652620	chrX	153995155	153995369	153995175	153995346	DKC1	NM_001363	2	15	6	+	153995272	153995336
265386341	chrX	153995470	153995683	153995493	153995662	DKC1	NM_001363	2	15	7	+	153995531	153995657
260311421	chrX	153996517	153996737	153996546	153996712	DKC1	NM_001363	2	15	8	+	153996577	153996707
268823981	chrX	153997311	153997471	153997335	153997449	DKC1	NM_001363	2	15	9	+	153997442	153997585
268839688	chrX	153997429	153997638	153997450	153997612	DKC1	NM_001363	2	15	9	+	153997442	153997585
267265372	chrX	153998946	153999167	153998967	153999146	DKC1	NM_001363	2	15	10	+	153999034	153999154
261246496	chrX	154001250	154001470	154001273	154001443	DKC1	NM_001363	2	15	11	+	154001406	154001524
261281270	chrX	154001422	154001546	154001443	154001525	DKC1	NM_001363	2	15	11	+	154001406	154001524
264962479	chrX	154002827	154003031	154002849	154003011	DKC1	NM_001363	2	15	12	+	154002877	154002980
268124711	chrX	154003356	154003580	154003379	154003558	DKC1	NM_001363	2	15	13	+	154003470	154003548
267541424	chrX	154004404	154004626	154004429	154004604	DKC1	NM_001363	2	15	14	+	154004462	154004599
268385894	chrX	154004957	154005174	154004981	154005149	DKC1	NM_001363	2	15	15	+	154005074	154005964
259658195	chr7	107531577	107531765	107531595	107531743	DLD	NM_000108	1	14	1	+	107531586	107531734
269044788	chr7	107533551	107533775	107533575	107533749	DLD	NM_000108	1	14	2	+	107533645	107533723
260451296	chr7	107542044	107542220	107542072	107542195	DLD	NM_000108	1	14	3	+	107542183	107542262
260458542	chr7	107542169	107542356	107542196	107542331	DLD	NM_000108	1	14	3	+	107542183	107542262
265425278	chr7	107542653	107542870	107542678	107542844	DLD	NM_000108	1	14	4	+	107542770	107542838
267825756	chr7	107543914	107544041	107543943	107544013	DLD	NM_000108	1	14	5	+	107543923	107543992
263738968	chr7	107545225	107545447	107545251	107545418	DLD	NM_000108	1	14	6	+	107545403	107545503

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263751057	chr7	107545396	107545594	107545419	107545566	DLD	NM_000108	1	14	6	+	107545403	107545503
269306990	chr7	107545672	107545857	107545699	107545829	DLD	NM_000108	1	14	7	+	107545806	107545949
269307859	chr7	107545803	107545949	107545830	107545924	DLD	NM_000108	1	14	7	+	107545806	107545949
269312050	chr7	107545901	107546084	107545925	107546055	DLD	NM_000108	1	14	7	+	107545806	107545949
263006528	chr7	107546721	107546847	107546749	107546821	DLD	NM_000108	1	14	8	+	107546712	107546813
267255957	chr7	107555809	107556020	107555835	107555992	DLD	NM_000108	1	14	9	+	107555951	107556141
267268882	chr7	107555972	107556194	107555993	107556165	DLD	NM_000108	1	14	9	+	107555951	107556141
261633344	chr7	107557152	107557345	107557174	107557318	DLD	NM_000108	1	14	10	+	107557239	107557409
261643831	chr7	107557299	107557513	107557319	107557485	DLD	NM_000108	1	14	10	+	107557239	107557409
268113363	chr7	107557618	107557767	107557646	107557746	DLD	NM_000108	1	14	11	+	107557718	107557907
268116567	chr7	107557725	107557940	107557747	107557916	DLD	NM_000108	1	14	11	+	107557718	107557907
267905250	chr7	107558220	107558443	107558244	107558421	DLD	NM_000108	1	14	12	+	107558369	107558506
267919096	chr7	107558400	107558595	107558422	107558567	DLD	NM_000108	1	14	12	+	107558369	107558506
261731291	chr7	107559373	107559595	107559397	107559567	DLD	NM_000108	1	14	13	+	107559455	107559544
267876752	chr7	107559570	107559781	107559597	107559753	DLD	NM_000108	1	14	14	+	107559639	107561643
267055355	chrX	33357192	33357414	33357213	33357390	DMD	NM_000109	1	79	1	-	33357376	33357726
259413898	chrX	33038075	33038292	33038103	33038265	DMD	NM_000109	1	79	2	-	33038256	33038317
259414039	chrX	33038251	33038472	33038282	33038444	DMD	NM_000109	1	79	2	-	33038256	33038317
264713780	chrX	32867771	32867981	32867799	32867953	DMD	NM_000109	1	79	3	-	32867845	32867937
260476433	chrX	32862829	32863013	32862849	32862990	DMD	NM_000109	1	79	4	-	32862900	32862977
264347373	chrX	32841330	32841554	32841353	32841527	DMD	NM_000109	1	79	5	-	32841412	32841504
262352123	chrX	32834482	32834680	32834509	32834652	DMD	NM_000109	1	79	6	-	32834585	32834757
262360855	chrX	32834628	32834805	32834653	32834777	DMD	NM_000109	1	79	6	-	32834585	32834757
268830022	chrX	32827529	32827653	32827559	32827625	DMD	NM_000109	1	79	7	-	32827610	32827728
268831040	chrX	32827598	32827810	32827626	32827783	DMD	NM_000109	1	79	7	-	32827610	32827728
268057653	chrX	32717197	32717360	32717225	32717336	DMD	NM_000109	1	79	8	-	32717229	32717410
268060893	chrX	32717315	32717538	32717337	32717512	DMD	NM_000109	1	79	8	-	32717229	32717410
265555386	chrX	32715941	32716159	32715966	32716137	DMD	NM_000109	1	79	9	-	32715987	32716115
268416366	chrX	32662944	32663168	32662966	32663147	DMD	NM_000109	1	79	10	-	32663081	32663269
268425214	chrX	32663123	32663314	32663148	32663286	DMD	NM_000109	1	79	10	-	32663081	32663269
266953752	chrX	32662104	32662325	32662129	32662296	DMD	NM_000109	1	79	11	-	32662249	32662430
266987101	chrX	32662275	32662486	32662297	32662458	DMD	NM_000109	1	79	11	-	32662249	32662430
263807902	chrX	32632395	32632611	32632420	32632583	DMD	NM_000109	1	79	12	-	32632420	32632570
267431315	chrX	32613721	32613941	32613745	32613916	DMD	NM_000109	1	79	13	-	32613874	32613993
267435079	chrX	32613896	32614061	32613917	32614032	DMD	NM_000109	1	79	13	-	32613874	32613993
267795753	chrX	32591822	32591992	32591844	32591968	DMD	NM_000109	1	79	14	-	32591862	32591963
265989904	chrX	32591605	32591774	32591635	32591746	DMD	NM_000109	1	79	15	-	32591647	32591754
265995913	chrX	32591720	32591854	32591747	32591826	DMD	NM_000109	1	79	15	-	32591647	32591754
268500478	chrX	32583644	32583867	32583666	32583840	DMD	NM_000109	1	79	16	-	32583819	32583998
268512062	chrX	32583814	32584032	32583841	32584003	DMD	NM_000109	1	79	16	-	32583819	32583998
267264180	chrX	32563156	32563318	32563178	32563291	DMD	NM_000109	1	79	17	-	32563276	32563451

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267285698	chrX	32563264	32563486	32563292	32563458	DMD	NM_000109	1	79	17	-	32563276	32563451
266358909	chrX	32536051	32536192	32536075	32536167	DMD	NM_000109	1	79	18	-	32536125	32536248
266379337	chrX	32536147	32536363	32536168	32536341	DMD	NM_000109	1	79	18	-	32536125	32536248
263893404	chrX	32519853	32520046	32519881	32520023	DMD	NM_000109	1	79	19	-	32519872	32519959
259825716	chrX	32509352	32509522	32509380	32509493	DMD	NM_000109	1	79	20	-	32509394	32509635
259867182	chrX	32509470	32509692	32509494	32509666	DMD	NM_000109	1	79	20	-	32509394	32509635
268787517	chrX	32502963	32503166	32502986	32503140	DMD	NM_000109	1	79	21	-	32503036	32503216
268793852	chrX	32503120	32503322	32503141	32503294	DMD	NM_000109	1	79	21	-	32503036	32503216
269218594	chrX	32490157	32490336	32490178	32490311	DMD	NM_000109	1	79	22	-	32490281	32490426
269228807	chrX	32490291	32490480	32490312	32490451	DMD	NM_000109	1	79	22	-	32490281	32490426
258561160	chrX	32486451	32486674	32486476	32486653	DMD	NM_000109	1	79	23	-	32486615	32486827
258576289	chrX	32486626	32486829	32486654	32486804	DMD	NM_000109	1	79	23	-	32486615	32486827
258594401	chrX	32486785	32486948	32486810	32486915	DMD	NM_000109	1	79	23	-	32486615	32486827
266579266	chrX	32482703	32482848	32482724	32482823	DMD	NM_000109	1	79	24	-	32482703	32482816
268310868	chrX	32481448	32481643	32481476	32481619	DMD	NM_000109	1	79	25	-	32481556	32481711
268324540	chrX	32481597	32481807	32481620	32481780	DMD	NM_000109	1	79	25	-	32481556	32481711
265836702	chrX	32472661	32472883	32472687	32472860	DMD	NM_000109	1	79	26	-	32472779	32472949
265847985	chrX	32472833	32472960	32472861	32472936	DMD	NM_000109	1	79	26	-	32472779	32472949
265851010	chrX	32472905	32473117	32472930	32473090	DMD	NM_000109	1	79	26	-	32472779	32472949
258866001	chrX	32466508	32466723	32466535	32466696	DMD	NM_000109	1	79	27	-	32466573	32466755
258878704	chrX	32466671	32466861	32466697	32466833	DMD	NM_000109	1	79	27	-	32466573	32466755
267914085	chrX	32459195	32459415	32459221	32459387	DMD	NM_000109	1	79	28	-	32459297	32459431
267919003	chrX	32459361	32459575	32459388	32459549	DMD	NM_000109	1	79	28	-	32459297	32459431
264668639	chrX	32456225	32456416	32456249	32456388	DMD	NM_000109	1	79	29	-	32456358	32456507
264697306	chrX	32456363	32456580	32456389	32456554	DMD	NM_000109	1	79	29	-	32456358	32456507
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_000109	1	79	30	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_000109	1	79	30	-	32429869	32430030
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_000109	1	79	31	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_000109	1	79	32	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_000109	1	79	32	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_000109	1	79	33	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_000109	1	79	33	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_000109	1	79	34	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_000109	1	79	34	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_000109	1	79	34	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_000109	1	79	35	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_000109	1	79	35	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_000109	1	79	36	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_000109	1	79	36	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_000109	1	79	37	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_000109	1	79	37	-	32380905	32381075

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_000109	1	79	38	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_000109	1	79	38	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_000109	1	79	39	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_000109	1	79	39	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_000109	1	79	39	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_000109	1	79	40	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_000109	1	79	40	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_000109	1	79	41	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_000109	1	79	41	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_000109	1	79	42	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_000109	1	79	42	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_000109	1	79	43	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_000109	1	79	43	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_000109	1	79	44	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_000109	1	79	44	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_000109	1	79	45	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_000109	1	79	45	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_000109	1	79	46	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_000109	1	79	46	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_000109	1	79	47	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_000109	1	79	48	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_000109	1	79	48	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_000109	1	79	49	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_000109	1	79	50	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_000109	1	79	51	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_000109	1	79	51	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_000109	1	79	52	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_000109	1	79	53	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_000109	1	79	53	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_000109	1	79	53	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_000109	1	79	54	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_000109	1	79	54	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_000109	1	79	55	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_000109	1	79	55	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_000109	1	79	56	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_000109	1	79	56	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_000109	1	79	57	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_000109	1	79	58	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_000109	1	79	59	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_000109	1	79	59	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_000109	1	79	60	-	31462598	31462744

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_000109	1	79	60	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_000109	1	79	61	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_000109	1	79	61	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_000109	1	79	62	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_000109	1	79	63	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_000109	1	79	64	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_000109	1	79	65	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_000109	1	79	65	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_000109	1	79	66	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_000109	1	79	67	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_000109	1	79	67	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_000109	1	79	68	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_000109	1	79	68	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_000109	1	79	69	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_000109	1	79	69	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_000109	1	79	70	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_000109	1	79	71	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_000109	1	79	72	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_000109	1	79	73	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_000109	1	79	74	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_000109	1	79	74	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_000109	1	79	75	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_000109	1	79	75	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_000109	1	79	75	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_000109	1	79	76	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_000109	1	79	76	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_000109	1	79	77	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_000109	1	79	78	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_000109	1	79	79	-	31137345	31140047
267300908	chrX	33229279	33229503	33229308	33229475	DMD	NM_004006	2	79	1	-	33229399	33229673
259413898	chrX	33038075	33038292	33038103	33038265	DMD	NM_004006	2	79	2	-	33038256	33038317
259414039	chrX	33038251	33038472	33038282	33038444	DMD	NM_004006	2	79	2	-	33038256	33038317
264713780	chrX	32867771	32867981	32867799	32867953	DMD	NM_004006	2	79	3	-	32867845	32867937
260476433	chrX	32862829	32863013	32862849	32862990	DMD	NM_004006	2	79	4	-	32862900	32862977
264347373	chrX	32841330	32841554	32841353	32841527	DMD	NM_004006	2	79	5	-	32841412	32841504
262352123	chrX	32834482	32834680	32834509	32834652	DMD	NM_004006	2	79	6	-	32834585	32834757
262360855	chrX	32834628	32834805	32834653	32834777	DMD	NM_004006	2	79	6	-	32834585	32834757
268830022	chrX	32827529	32827653	32827559	32827625	DMD	NM_004006	2	79	7	-	32827610	32827728
268831040	chrX	32827598	32827810	32827626	32827783	DMD	NM_004006	2	79	7	-	32827610	32827728
268057653	chrX	32717197	32717360	32717225	32717336	DMD	NM_004006	2	79	8	-	32717229	32717410
268060893	chrX	32717315	32717538	32717337	32717512	DMD	NM_004006	2	79	8	-	32717229	32717410

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265555386	chrX	32715941	32716159	32715966	32716137	DMD	NM_004006	2	79	9	-	32715987	32716115
268416366	chrX	32662944	32663168	32662966	32663147	DMD	NM_004006	2	79	10	-	32663081	32663269
268425214	chrX	32663123	32663314	32663148	32663286	DMD	NM_004006	2	79	10	-	32663081	32663269
266953752	chrX	32662104	32662325	32662129	32662296	DMD	NM_004006	2	79	11	-	32662249	32662430
266987101	chrX	32662275	32662486	32662297	32662458	DMD	NM_004006	2	79	11	-	32662249	32662430
263807902	chrX	32632395	32632611	32632420	32632583	DMD	NM_004006	2	79	12	-	32632420	32632570
267431315	chrX	32613721	32613941	32613745	32613916	DMD	NM_004006	2	79	13	-	32613874	32613993
267435079	chrX	32613896	32614061	32613917	32614032	DMD	NM_004006	2	79	13	-	32613874	32613993
267795753	chrX	32591822	32591992	32591844	32591968	DMD	NM_004006	2	79	14	-	32591862	32591963
265989904	chrX	32591605	32591774	32591635	32591746	DMD	NM_004006	2	79	15	-	32591647	32591754
265995913	chrX	32591720	32591854	32591747	32591826	DMD	NM_004006	2	79	15	-	32591647	32591754
268500478	chrX	32583644	32583867	32583666	32583840	DMD	NM_004006	2	79	16	-	32583819	32583998
268512062	chrX	32583814	32584032	32583841	32584003	DMD	NM_004006	2	79	16	-	32583819	32583998
267264180	chrX	32563156	32563318	32563178	32563291	DMD	NM_004006	2	79	17	-	32563276	32563451
267285698	chrX	32563264	32563486	32563292	32563458	DMD	NM_004006	2	79	17	-	32563276	32563451
266358909	chrX	32536051	32536192	32536075	32536167	DMD	NM_004006	2	79	18	-	32536125	32536248
266379337	chrX	32536147	32536363	32536168	32536341	DMD	NM_004006	2	79	18	-	32536125	32536248
263893404	chrX	32519853	32520046	32519881	32520023	DMD	NM_004006	2	79	19	-	32519872	32519959
259825716	chrX	32509352	32509522	32509380	32509493	DMD	NM_004006	2	79	20	-	32509394	32509635
259867182	chrX	32509470	32509692	32509494	32509666	DMD	NM_004006	2	79	20	-	32509394	32509635
268787517	chrX	32502963	32503166	32502986	32503140	DMD	NM_004006	2	79	21	-	32503036	32503216
268793852	chrX	32503120	32503322	32503141	32503294	DMD	NM_004006	2	79	21	-	32503036	32503216
269218594	chrX	32490157	32490336	32490178	32490311	DMD	NM_004006	2	79	22	-	32490281	32490426
269228807	chrX	32490291	32490480	32490312	32490451	DMD	NM_004006	2	79	22	-	32490281	32490426
258561160	chrX	32486451	32486674	32486476	32486653	DMD	NM_004006	2	79	23	-	32486615	32486827
258576289	chrX	32486626	32486829	32486654	32486804	DMD	NM_004006	2	79	23	-	32486615	32486827
258594401	chrX	32486785	32486948	32486810	32486915	DMD	NM_004006	2	79	23	-	32486615	32486827
266579266	chrX	32482703	32482848	32482724	32482823	DMD	NM_004006	2	79	24	-	32482703	32482816
268310868	chrX	32481448	32481643	32481476	32481619	DMD	NM_004006	2	79	25	-	32481556	32481711
268324540	chrX	32481597	32481807	32481620	32481780	DMD	NM_004006	2	79	25	-	32481556	32481711
265836702	chrX	32472661	32472883	32472687	32472860	DMD	NM_004006	2	79	26	-	32472779	32472949
265847985	chrX	32472833	32472960	32472861	32472936	DMD	NM_004006	2	79	26	-	32472779	32472949
265851010	chrX	32472905	32473117	32472930	32473090	DMD	NM_004006	2	79	26	-	32472779	32472949
258866001	chrX	32466508	32466723	32466535	32466696	DMD	NM_004006	2	79	27	-	32466573	32466755
258878704	chrX	32466671	32466861	32466697	32466833	DMD	NM_004006	2	79	27	-	32466573	32466755
267914085	chrX	32459195	32459415	32459221	32459387	DMD	NM_004006	2	79	28	-	32459297	32459431
267919003	chrX	32459361	32459575	32459388	32459549	DMD	NM_004006	2	79	28	-	32459297	32459431
264668639	chrX	32456225	32456416	32456249	32456388	DMD	NM_004006	2	79	29	-	32456358	32456507
264697306	chrX	32456363	32456580	32456389	32456554	DMD	NM_004006	2	79	29	-	32456358	32456507
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004006	2	79	30	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004006	2	79	30	-	32429869	32430030

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004006	2	79	31	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004006	2	79	32	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004006	2	79	32	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004006	2	79	33	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004006	2	79	33	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004006	2	79	34	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004006	2	79	34	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004006	2	79	34	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004006	2	79	35	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004006	2	79	35	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004006	2	79	36	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004006	2	79	36	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004006	2	79	37	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004006	2	79	37	-	32380905	32381075
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004006	2	79	38	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004006	2	79	38	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004006	2	79	39	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004006	2	79	39	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004006	2	79	39	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004006	2	79	40	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004006	2	79	40	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004006	2	79	41	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004006	2	79	41	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004006	2	79	42	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004006	2	79	42	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004006	2	79	43	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004006	2	79	43	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004006	2	79	44	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004006	2	79	44	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004006	2	79	45	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004006	2	79	45	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004006	2	79	46	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004006	2	79	46	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004006	2	79	47	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004006	2	79	48	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004006	2	79	48	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004006	2	79	49	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004006	2	79	50	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004006	2	79	51	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004006	2	79	51	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004006	2	79	52	-	31747748	31747865

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004006	2	79	53	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004006	2	79	53	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004006	2	79	53	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004006	2	79	54	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004006	2	79	54	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004006	2	79	55	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004006	2	79	55	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004006	2	79	56	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004006	2	79	56	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004006	2	79	57	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004006	2	79	58	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004006	2	79	59	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004006	2	79	59	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004006	2	79	60	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004006	2	79	60	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004006	2	79	61	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004006	2	79	61	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004006	2	79	62	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004006	2	79	63	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004006	2	79	64	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004006	2	79	65	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004006	2	79	65	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004006	2	79	66	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004006	2	79	67	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004006	2	79	67	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004006	2	79	68	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004006	2	79	68	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004006	2	79	69	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004006	2	79	69	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004006	2	79	70	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004006	2	79	71	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004006	2	79	72	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004006	2	79	73	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004006	2	79	74	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004006	2	79	74	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004006	2	79	75	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004006	2	79	75	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004006	2	79	75	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004006	2	79	76	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004006	2	79	76	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004006	2	79	77	-	31152219	31152311

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004006	2	79	78	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004006	2	79	79	-	31137345	31140047
259413898	chrX	33038075	33038292	33038103	33038265	DMD	NM_004007	3	78	1	-	33038256	33038317
259414039	chrX	33038251	33038472	33038282	33038444	DMD	NM_004007	3	78	1	-	33038256	33038317
264713780	chrX	32867771	32867981	32867799	32867953	DMD	NM_004007	3	78	2	-	32867845	32867937
260476433	chrX	32862829	32863013	32862849	32862990	DMD	NM_004007	3	78	3	-	32862900	32862977
264347373	chrX	32841330	32841554	32841353	32841527	DMD	NM_004007	3	78	4	-	32841412	32841504
262352123	chrX	32834482	32834680	32834509	32834652	DMD	NM_004007	3	78	5	-	32834585	32834757
262360855	chrX	32834628	32834805	32834653	32834777	DMD	NM_004007	3	78	5	-	32834585	32834757
268830022	chrX	32827529	32827653	32827559	32827625	DMD	NM_004007	3	78	6	-	32827610	32827728
268831040	chrX	32827598	32827810	32827626	32827783	DMD	NM_004007	3	78	6	-	32827610	32827728
268057653	chrX	32717197	32717360	32717225	32717336	DMD	NM_004007	3	78	7	-	32717229	32717410
268060893	chrX	32717315	32717538	32717337	32717512	DMD	NM_004007	3	78	7	-	32717229	32717410
265555386	chrX	32715941	32716159	32715966	32716137	DMD	NM_004007	3	78	8	-	32715987	32716115
268416366	chrX	32662944	32663168	32662966	32663147	DMD	NM_004007	3	78	9	-	32663081	32663269
268425214	chrX	32663123	32663314	32663148	32663286	DMD	NM_004007	3	78	9	-	32663081	32663269
266953752	chrX	32662104	32662325	32662129	32662296	DMD	NM_004007	3	78	10	-	32662249	32662430
266987101	chrX	32662275	32662486	32662297	32662458	DMD	NM_004007	3	78	10	-	32662249	32662430
263807902	chrX	32632395	32632611	32632420	32632583	DMD	NM_004007	3	78	11	-	32632420	32632570
267431315	chrX	32613721	32613941	32613745	32613916	DMD	NM_004007	3	78	12	-	32613874	32613993
267435079	chrX	32613896	32614061	32613917	32614032	DMD	NM_004007	3	78	12	-	32613874	32613993
267795753	chrX	32591822	32591992	32591844	32591968	DMD	NM_004007	3	78	13	-	32591862	32591963
265989904	chrX	32591605	32591774	32591635	32591746	DMD	NM_004007	3	78	14	-	32591647	32591754
265995913	chrX	32591720	32591854	32591747	32591826	DMD	NM_004007	3	78	14	-	32591647	32591754
268500478	chrX	32583644	32583867	32583666	32583840	DMD	NM_004007	3	78	15	-	32583819	32583998
268512062	chrX	32583814	32584032	32583841	32584003	DMD	NM_004007	3	78	15	-	32583819	32583998
267264180	chrX	32563156	32563318	32563178	32563291	DMD	NM_004007	3	78	16	-	32563276	32563451
267285698	chrX	32563264	32563486	32563292	32563458	DMD	NM_004007	3	78	16	-	32563276	32563451
266358909	chrX	32536051	32536192	32536075	32536167	DMD	NM_004007	3	78	17	-	32536125	32536248
266379337	chrX	32536147	32536363	32536168	32536341	DMD	NM_004007	3	78	17	-	32536125	32536248
263893404	chrX	32519853	32520046	32519881	32520023	DMD	NM_004007	3	78	18	-	32519872	32519959
259825716	chrX	32509352	32509522	32509380	32509493	DMD	NM_004007	3	78	19	-	32509394	32509635
259867182	chrX	32509470	32509692	32509494	32509666	DMD	NM_004007	3	78	19	-	32509394	32509635
268787517	chrX	32502963	32503166	32502986	32503140	DMD	NM_004007	3	78	20	-	32503036	32503216
268793852	chrX	32503120	32503322	32503141	32503294	DMD	NM_004007	3	78	20	-	32503036	32503216
269218594	chrX	32490157	32490336	32490178	32490311	DMD	NM_004007	3	78	21	-	32490281	32490426
269228807	chrX	32490291	32490480	32490312	32490451	DMD	NM_004007	3	78	21	-	32490281	32490426
258561160	chrX	32486451	32486674	32486476	32486653	DMD	NM_004007	3	78	22	-	32486615	32486827
258576289	chrX	32486626	32486829	32486654	32486804	DMD	NM_004007	3	78	22	-	32486615	32486827
258594401	chrX	32486785	32486948	32486810	32486915	DMD	NM_004007	3	78	22	-	32486615	32486827
266579266	chrX	32482703	32482848	32482724	32482823	DMD	NM_004007	3	78	23	-	32482703	32482816

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268310868	chrX	32481448	32481643	32481476	32481619	DMD	NM_004007	3	78	24	-	32481556	32481711
268324540	chrX	32481597	32481807	32481620	32481780	DMD	NM_004007	3	78	24	-	32481556	32481711
265836702	chrX	32472661	32472883	32472687	32472860	DMD	NM_004007	3	78	25	-	32472779	32472949
265847985	chrX	32472833	32472960	32472861	32472936	DMD	NM_004007	3	78	25	-	32472779	32472949
265851010	chrX	32472905	32473117	32472930	32473090	DMD	NM_004007	3	78	25	-	32472779	32472949
258866001	chrX	32466508	32466723	32466535	32466696	DMD	NM_004007	3	78	26	-	32466573	32466755
258878704	chrX	32466671	32466861	32466697	32466833	DMD	NM_004007	3	78	26	-	32466573	32466755
267914085	chrX	32459195	32459415	32459221	32459387	DMD	NM_004007	3	78	27	-	32459297	32459431
267919003	chrX	32459361	32459575	32459388	32459549	DMD	NM_004007	3	78	27	-	32459297	32459431
264668639	chrX	32456225	32456416	32456249	32456388	DMD	NM_004007	3	78	28	-	32456358	32456507
264697306	chrX	32456363	32456580	32456389	32456554	DMD	NM_004007	3	78	28	-	32456358	32456507
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004007	3	78	29	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004007	3	78	29	-	32429869	32430030
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004007	3	78	30	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004007	3	78	31	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004007	3	78	31	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004007	3	78	32	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004007	3	78	32	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004007	3	78	33	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004007	3	78	33	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004007	3	78	33	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004007	3	78	34	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004007	3	78	34	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004007	3	78	35	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004007	3	78	35	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004007	3	78	36	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004007	3	78	36	-	32380905	32381075
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004007	3	78	37	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004007	3	78	37	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004007	3	78	38	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004007	3	78	38	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004007	3	78	38	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004007	3	78	39	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004007	3	78	39	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004007	3	78	40	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004007	3	78	40	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004007	3	78	41	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004007	3	78	41	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004007	3	78	42	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004007	3	78	42	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004007	3	78	43	-	32235033	32235180

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004007	3	78	43	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004007	3	78	44	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004007	3	78	44	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004007	3	78	45	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004007	3	78	45	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004007	3	78	46	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004007	3	78	47	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004007	3	78	47	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004007	3	78	48	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004007	3	78	49	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004007	3	78	50	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004007	3	78	50	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004007	3	78	51	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004007	3	78	52	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004007	3	78	52	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004007	3	78	52	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004007	3	78	53	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004007	3	78	53	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004007	3	78	54	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004007	3	78	54	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004007	3	78	55	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004007	3	78	55	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004007	3	78	56	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004007	3	78	57	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004007	3	78	58	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004007	3	78	58	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004007	3	78	59	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004007	3	78	59	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004007	3	78	60	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004007	3	78	60	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004007	3	78	61	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004007	3	78	62	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004007	3	78	63	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004007	3	78	64	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004007	3	78	64	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004007	3	78	65	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004007	3	78	66	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004007	3	78	66	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004007	3	78	67	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004007	3	78	67	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004007	3	78	68	-	31198487	31198598

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004007	3	78	68	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004007	3	78	69	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004007	3	78	70	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004007	3	78	71	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004007	3	78	72	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004007	3	78	73	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004007	3	78	73	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004007	3	78	74	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004007	3	78	74	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004007	3	78	74	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004007	3	78	75	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004007	3	78	75	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004007	3	78	76	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004007	3	78	77	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004007	3	78	78	-	31137345	31140047
263259812	chrX	33146113	33146324	33146137	33146300	DMD	NM_004009	4	79	1	-	33146264	33146545
259413898	chrX	33038075	33038292	33038103	33038265	DMD	NM_004009	4	79	2	-	33038256	33038317
259414039	chrX	33038251	33038472	33038282	33038444	DMD	NM_004009	4	79	2	-	33038256	33038317
264713780	chrX	32867771	32867981	32867799	32867953	DMD	NM_004009	4	79	3	-	32867845	32867937
260476433	chrX	32862829	32863013	32862849	32862990	DMD	NM_004009	4	79	4	-	32862900	32862977
264347373	chrX	32841330	32841554	32841353	32841527	DMD	NM_004009	4	79	5	-	32841412	32841504
262352123	chrX	32834482	32834680	32834509	32834652	DMD	NM_004009	4	79	6	-	32834585	32834757
262360855	chrX	32834628	32834805	32834653	32834777	DMD	NM_004009	4	79	6	-	32834585	32834757
268830022	chrX	32827529	32827653	32827559	32827625	DMD	NM_004009	4	79	7	-	32827610	32827728
268831040	chrX	32827598	32827810	32827626	32827783	DMD	NM_004009	4	79	7	-	32827610	32827728
268057653	chrX	32717197	32717360	32717225	32717336	DMD	NM_004009	4	79	8	-	32717229	32717410
268060893	chrX	32717315	32717538	32717337	32717512	DMD	NM_004009	4	79	8	-	32717229	32717410
265555386	chrX	32715941	32716159	32715966	32716137	DMD	NM_004009	4	79	9	-	32715987	32716115
268416366	chrX	32662944	32663168	32662966	32663147	DMD	NM_004009	4	79	10	-	32663081	32663269
268425214	chrX	32663123	32663314	32663148	32663286	DMD	NM_004009	4	79	10	-	32663081	32663269
266953752	chrX	32662104	32662325	32662129	32662296	DMD	NM_004009	4	79	11	-	32662249	32662430
266987101	chrX	32662275	32662486	32662297	32662458	DMD	NM_004009	4	79	11	-	32662249	32662430
263807902	chrX	32632395	32632611	32632420	32632583	DMD	NM_004009	4	79	12	-	32632420	32632570
267431315	chrX	32613721	32613941	32613745	32613916	DMD	NM_004009	4	79	13	-	32613874	32613993
267435079	chrX	32613896	32614061	32613917	32614032	DMD	NM_004009	4	79	13	-	32613874	32613993
267795753	chrX	32591822	32591992	32591844	32591968	DMD	NM_004009	4	79	14	-	32591862	32591963
265989904	chrX	32591605	32591774	32591635	32591746	DMD	NM_004009	4	79	15	-	32591647	32591754
265995913	chrX	32591720	32591854	32591747	32591826	DMD	NM_004009	4	79	15	-	32591647	32591754
268500478	chrX	32583644	32583867	32583666	32583840	DMD	NM_004009	4	79	16	-	32583819	32583998
268512062	chrX	32583814	32584032	32583841	32584003	DMD	NM_004009	4	79	16	-	32583819	32583998
267264180	chrX	32563156	32563318	32563178	32563291	DMD	NM_004009	4	79	17	-	32563276	32563451

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267285698	chrX	32563264	32563486	32563292	32563458	DMD	NM_004009	4	79	17	-	32563276	32563451
266358909	chrX	32536051	32536192	32536075	32536167	DMD	NM_004009	4	79	18	-	32536125	32536248
266379337	chrX	32536147	32536363	32536168	32536341	DMD	NM_004009	4	79	18	-	32536125	32536248
263893404	chrX	32519853	32520046	32519881	32520023	DMD	NM_004009	4	79	19	-	32519872	32519959
259825716	chrX	32509352	32509522	32509380	32509493	DMD	NM_004009	4	79	20	-	32509394	32509635
259867182	chrX	32509470	32509692	32509494	32509666	DMD	NM_004009	4	79	20	-	32509394	32509635
268787517	chrX	32502963	32503166	32502986	32503140	DMD	NM_004009	4	79	21	-	32503036	32503216
268793852	chrX	32503120	32503322	32503141	32503294	DMD	NM_004009	4	79	21	-	32503036	32503216
269218594	chrX	32490157	32490336	32490178	32490311	DMD	NM_004009	4	79	22	-	32490281	32490426
269228807	chrX	32490291	32490480	32490312	32490451	DMD	NM_004009	4	79	22	-	32490281	32490426
258561160	chrX	32486451	32486674	32486476	32486653	DMD	NM_004009	4	79	23	-	32486615	32486827
258576289	chrX	32486626	32486829	32486654	32486804	DMD	NM_004009	4	79	23	-	32486615	32486827
258594401	chrX	32486785	32486948	32486810	32486915	DMD	NM_004009	4	79	23	-	32486615	32486827
266579266	chrX	32482703	32482848	32482724	32482823	DMD	NM_004009	4	79	24	-	32482703	32482816
268310868	chrX	32481448	32481643	32481476	32481619	DMD	NM_004009	4	79	25	-	32481556	32481711
268324540	chrX	32481597	32481807	32481620	32481780	DMD	NM_004009	4	79	25	-	32481556	32481711
265836702	chrX	32472661	32472883	32472687	32472860	DMD	NM_004009	4	79	26	-	32472779	32472949
265847985	chrX	32472833	32472960	32472861	32472936	DMD	NM_004009	4	79	26	-	32472779	32472949
265851010	chrX	32472905	32473117	32472930	32473090	DMD	NM_004009	4	79	26	-	32472779	32472949
258866001	chrX	32466508	32466723	32466535	32466696	DMD	NM_004009	4	79	27	-	32466573	32466755
258878704	chrX	32466671	32466861	32466697	32466833	DMD	NM_004009	4	79	27	-	32466573	32466755
267914085	chrX	32459195	32459415	32459221	32459387	DMD	NM_004009	4	79	28	-	32459297	32459431
267919003	chrX	32459361	32459575	32459388	32459549	DMD	NM_004009	4	79	28	-	32459297	32459431
264668639	chrX	32456225	32456416	32456249	32456388	DMD	NM_004009	4	79	29	-	32456358	32456507
264697306	chrX	32456363	32456580	32456389	32456554	DMD	NM_004009	4	79	29	-	32456358	32456507
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004009	4	79	30	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004009	4	79	30	-	32429869	32430030
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004009	4	79	31	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004009	4	79	32	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004009	4	79	32	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004009	4	79	33	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004009	4	79	33	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004009	4	79	34	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004009	4	79	34	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004009	4	79	34	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004009	4	79	35	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004009	4	79	35	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004009	4	79	36	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004009	4	79	36	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004009	4	79	37	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004009	4	79	37	-	32380905	32381075

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004009	4	79	38	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004009	4	79	38	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004009	4	79	39	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004009	4	79	39	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004009	4	79	39	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004009	4	79	40	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004009	4	79	40	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004009	4	79	41	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004009	4	79	41	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004009	4	79	42	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004009	4	79	42	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004009	4	79	43	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004009	4	79	43	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004009	4	79	44	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004009	4	79	44	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004009	4	79	45	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004009	4	79	45	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004009	4	79	46	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004009	4	79	46	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004009	4	79	47	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004009	4	79	48	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004009	4	79	48	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004009	4	79	49	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004009	4	79	50	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004009	4	79	51	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004009	4	79	51	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004009	4	79	52	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004009	4	79	53	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004009	4	79	53	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004009	4	79	53	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004009	4	79	54	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004009	4	79	54	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004009	4	79	55	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004009	4	79	55	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004009	4	79	56	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004009	4	79	56	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004009	4	79	57	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004009	4	79	58	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004009	4	79	59	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004009	4	79	59	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004009	4	79	60	-	31462598	31462744

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004009	4	79	60	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004009	4	79	61	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004009	4	79	61	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004009	4	79	62	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004009	4	79	63	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004009	4	79	64	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004009	4	79	65	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004009	4	79	65	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004009	4	79	66	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004009	4	79	67	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004009	4	79	67	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004009	4	79	68	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004009	4	79	68	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004009	4	79	69	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004009	4	79	69	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004009	4	79	70	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004009	4	79	71	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004009	4	79	72	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004009	4	79	73	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004009	4	79	74	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004009	4	79	74	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004009	4	79	75	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004009	4	79	75	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004009	4	79	75	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004009	4	79	76	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004009	4	79	76	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004009	4	79	77	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004009	4	79	78	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004009	4	79	79	-	31137345	31140047
263259812	chrX	33146113	33146324	33146137	33146300	DMD	NM_004010	5	79	1	-	33146180	33146544
259413898	chrX	33038075	33038292	33038103	33038265	DMD	NM_004010	5	79	2	-	33038256	33038317
259414039	chrX	33038251	33038472	33038282	33038444	DMD	NM_004010	5	79	2	-	33038256	33038317
264713780	chrX	32867771	32867981	32867799	32867953	DMD	NM_004010	5	79	3	-	32867845	32867937
260476433	chrX	32862829	32863013	32862849	32862990	DMD	NM_004010	5	79	4	-	32862900	32862977
264347373	chrX	32841330	32841554	32841353	32841527	DMD	NM_004010	5	79	5	-	32841412	32841504
262352123	chrX	32834482	32834680	32834509	32834652	DMD	NM_004010	5	79	6	-	32834585	32834757
262360855	chrX	32834628	32834805	32834653	32834777	DMD	NM_004010	5	79	6	-	32834585	32834757
268830022	chrX	32827529	32827653	32827559	32827625	DMD	NM_004010	5	79	7	-	32827610	32827728
268831040	chrX	32827598	32827810	32827626	32827783	DMD	NM_004010	5	79	7	-	32827610	32827728
268057653	chrX	32717197	32717360	32717225	32717336	DMD	NM_004010	5	79	8	-	32717229	32717410
268060893	chrX	32717315	32717538	32717337	32717512	DMD	NM_004010	5	79	8	-	32717229	32717410

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265555386	chrX	32715941	32716159	32715966	32716137	DMD	NM_004010	5	79	9	-	32715987	32716115
268416366	chrX	32662944	32663168	32662966	32663147	DMD	NM_004010	5	79	10	-	32663081	32663269
268425214	chrX	32663123	32663314	32663148	32663286	DMD	NM_004010	5	79	10	-	32663081	32663269
266953752	chrX	32662104	32662325	32662129	32662296	DMD	NM_004010	5	79	11	-	32662249	32662430
266987101	chrX	32662275	32662486	32662297	32662458	DMD	NM_004010	5	79	11	-	32662249	32662430
263807902	chrX	32632395	32632611	32632420	32632583	DMD	NM_004010	5	79	12	-	32632420	32632570
267431315	chrX	32613721	32613941	32613745	32613916	DMD	NM_004010	5	79	13	-	32613874	32613993
267435079	chrX	32613896	32614061	32613917	32614032	DMD	NM_004010	5	79	13	-	32613874	32613993
267795753	chrX	32591822	32591992	32591844	32591968	DMD	NM_004010	5	79	14	-	32591862	32591963
265989904	chrX	32591605	32591774	32591635	32591746	DMD	NM_004010	5	79	15	-	32591647	32591754
265995913	chrX	32591720	32591854	32591747	32591826	DMD	NM_004010	5	79	15	-	32591647	32591754
268500478	chrX	32583644	32583867	32583666	32583840	DMD	NM_004010	5	79	16	-	32583819	32583998
268512062	chrX	32583814	32584032	32583841	32584003	DMD	NM_004010	5	79	16	-	32583819	32583998
267264180	chrX	32563156	32563318	32563178	32563291	DMD	NM_004010	5	79	17	-	32563276	32563451
267285698	chrX	32563264	32563486	32563292	32563458	DMD	NM_004010	5	79	17	-	32563276	32563451
266358909	chrX	32536051	32536192	32536075	32536167	DMD	NM_004010	5	79	18	-	32536125	32536248
266379337	chrX	32536147	32536363	32536168	32536341	DMD	NM_004010	5	79	18	-	32536125	32536248
263893404	chrX	32519853	32520046	32519881	32520023	DMD	NM_004010	5	79	19	-	32519872	32519959
259825716	chrX	32509352	32509522	32509380	32509493	DMD	NM_004010	5	79	20	-	32509394	32509635
259867182	chrX	32509470	32509692	32509494	32509666	DMD	NM_004010	5	79	20	-	32509394	32509635
268787517	chrX	32502963	32503166	32502986	32503140	DMD	NM_004010	5	79	21	-	32503036	32503216
268793852	chrX	32503120	32503322	32503141	32503294	DMD	NM_004010	5	79	21	-	32503036	32503216
269218594	chrX	32490157	32490336	32490178	32490311	DMD	NM_004010	5	79	22	-	32490281	32490426
269228807	chrX	32490291	32490480	32490312	32490451	DMD	NM_004010	5	79	22	-	32490281	32490426
258561160	chrX	32486451	32486674	32486476	32486653	DMD	NM_004010	5	79	23	-	32486615	32486827
258576289	chrX	32486626	32486829	32486654	32486804	DMD	NM_004010	5	79	23	-	32486615	32486827
258594401	chrX	32486785	32486948	32486810	32486915	DMD	NM_004010	5	79	23	-	32486615	32486827
266579266	chrX	32482703	32482848	32482724	32482823	DMD	NM_004010	5	79	24	-	32482703	32482816
268310868	chrX	32481448	32481643	32481476	32481619	DMD	NM_004010	5	79	25	-	32481556	32481711
268324540	chrX	32481597	32481807	32481620	32481780	DMD	NM_004010	5	79	25	-	32481556	32481711
265836702	chrX	32472661	32472883	32472687	32472860	DMD	NM_004010	5	79	26	-	32472779	32472949
265847985	chrX	32472833	32472960	32472861	32472936	DMD	NM_004010	5	79	26	-	32472779	32472949
265851010	chrX	32472905	32473117	32472930	32473090	DMD	NM_004010	5	79	26	-	32472779	32472949
258866001	chrX	32466508	32466723	32466535	32466696	DMD	NM_004010	5	79	27	-	32466573	32466755
258878704	chrX	32466671	32466861	32466697	32466833	DMD	NM_004010	5	79	27	-	32466573	32466755
267914085	chrX	32459195	32459415	32459221	32459387	DMD	NM_004010	5	79	28	-	32459297	32459431
267919003	chrX	32459361	32459575	32459388	32459549	DMD	NM_004010	5	79	28	-	32459297	32459431
264668639	chrX	32456225	32456416	32456249	32456388	DMD	NM_004010	5	79	29	-	32456358	32456507
264697306	chrX	32456363	32456580	32456389	32456554	DMD	NM_004010	5	79	29	-	32456358	32456507
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004010	5	79	30	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004010	5	79	30	-	32429869	32430030

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004010	5	79	31	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004010	5	79	32	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004010	5	79	32	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004010	5	79	33	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004010	5	79	33	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004010	5	79	34	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004010	5	79	34	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004010	5	79	34	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004010	5	79	35	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004010	5	79	35	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004010	5	79	36	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004010	5	79	36	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004010	5	79	37	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004010	5	79	37	-	32380905	32381075
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004010	5	79	38	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004010	5	79	38	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004010	5	79	39	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004010	5	79	39	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004010	5	79	39	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004010	5	79	40	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004010	5	79	40	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004010	5	79	41	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004010	5	79	41	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004010	5	79	42	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004010	5	79	42	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004010	5	79	43	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004010	5	79	43	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004010	5	79	44	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004010	5	79	44	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004010	5	79	45	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004010	5	79	45	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004010	5	79	46	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004010	5	79	46	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004010	5	79	47	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004010	5	79	48	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004010	5	79	48	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004010	5	79	49	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004010	5	79	50	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004010	5	79	51	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004010	5	79	51	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004010	5	79	52	-	31747748	31747865

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004010	5	79	53	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004010	5	79	53	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004010	5	79	53	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004010	5	79	54	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004010	5	79	54	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004010	5	79	55	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004010	5	79	55	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004010	5	79	56	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004010	5	79	56	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004010	5	79	57	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004010	5	79	58	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004010	5	79	59	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004010	5	79	59	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004010	5	79	60	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004010	5	79	60	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004010	5	79	61	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004010	5	79	61	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004010	5	79	62	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004010	5	79	63	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004010	5	79	64	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004010	5	79	65	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004010	5	79	65	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004010	5	79	66	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004010	5	79	67	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004010	5	79	67	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004010	5	79	68	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004010	5	79	68	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004010	5	79	69	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004010	5	79	69	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004010	5	79	70	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004010	5	79	71	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004010	5	79	72	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004010	5	79	73	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004010	5	79	74	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004010	5	79	74	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004010	5	79	75	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004010	5	79	75	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004010	5	79	75	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004010	5	79	76	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004010	5	79	76	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004010	5	79	77	-	31152219	31152311

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004010	5	79	78	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004010	5	79	79	-	31137345	31140047
268660765	chrX	32430133	32430356	32430159	32430331	DMD	NM_004011	6	51	1	-	32430279	32430371
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004011	6	51	2	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004011	6	51	2	-	32429869	32430030
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004011	6	51	3	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004011	6	51	4	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004011	6	51	4	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004011	6	51	5	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004011	6	51	5	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004011	6	51	6	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004011	6	51	6	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004011	6	51	6	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004011	6	51	7	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004011	6	51	7	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004011	6	51	8	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004011	6	51	8	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004011	6	51	9	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004011	6	51	9	-	32380905	32381075
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004011	6	51	10	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004011	6	51	10	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004011	6	51	11	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004011	6	51	11	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004011	6	51	11	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004011	6	51	12	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004011	6	51	12	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004011	6	51	13	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004011	6	51	13	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004011	6	51	14	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004011	6	51	14	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004011	6	51	15	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004011	6	51	15	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004011	6	51	16	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004011	6	51	16	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004011	6	51	17	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004011	6	51	17	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004011	6	51	18	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004011	6	51	18	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004011	6	51	19	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004011	6	51	20	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004011	6	51	20	-	31893308	31893490

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004011	6	51	21	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004011	6	51	22	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004011	6	51	23	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004011	6	51	23	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004011	6	51	24	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004011	6	51	25	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004011	6	51	25	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004011	6	51	25	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004011	6	51	26	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004011	6	51	26	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004011	6	51	27	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004011	6	51	27	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004011	6	51	28	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004011	6	51	28	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004011	6	51	29	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004011	6	51	30	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004011	6	51	31	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004011	6	51	31	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004011	6	51	32	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004011	6	51	32	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004011	6	51	33	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004011	6	51	33	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004011	6	51	34	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004011	6	51	35	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004011	6	51	36	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004011	6	51	37	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004011	6	51	37	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004011	6	51	38	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004011	6	51	39	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004011	6	51	39	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004011	6	51	40	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004011	6	51	40	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004011	6	51	41	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004011	6	51	41	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004011	6	51	42	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004011	6	51	43	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004011	6	51	44	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004011	6	51	45	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004011	6	51	46	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004011	6	51	46	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004011	6	51	47	-	31165392	31165635

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004011	6	51	47	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004011	6	51	47	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004011	6	51	48	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004011	6	51	48	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004011	6	51	49	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004011	6	51	50	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004011	6	51	51	-	31137345	31140047
268660765	chrX	32430133	32430356	32430159	32430331	DMD	NM_004012	7	51	1	-	32430136	32430371
269442115	chrX	32430070	32430246	32430098	32430218	DMD	NM_004012	7	51	1	-	32430136	32430371
267482188	chrX	32429714	32429935	32429738	32429914	DMD	NM_004012	7	51	2	-	32429869	32430030
267502450	chrX	32429894	32430096	32429915	32430068	DMD	NM_004012	7	51	2	-	32429869	32430030
268451768	chrX	32408131	32408345	32408154	32408316	DMD	NM_004012	7	51	3	-	32408188	32408298
265608736	chrX	32407470	32407679	32407498	32407655	DMD	NM_004012	7	51	4	-	32407618	32407791
265612924	chrX	32407632	32407852	32407656	32407827	DMD	NM_004012	7	51	4	-	32407618	32407791
261116945	chrX	32404361	32404554	32404388	32404526	DMD	NM_004012	7	51	5	-	32404427	32404582
261147548	chrX	32404501	32404719	32404527	32404691	DMD	NM_004012	7	51	5	-	32404427	32404582
265922075	chrX	32398452	32398675	32398480	32398647	DMD	NM_004012	7	51	6	-	32398627	32398797
265924827	chrX	32398627	32398805	32398648	32398777	DMD	NM_004012	7	51	6	-	32398627	32398797
265929880	chrX	32398762	32398984	32398785	32398956	DMD	NM_004012	7	51	6	-	32398627	32398797
258489220	chrX	32383021	32383218	32383049	32383190	DMD	NM_004012	7	51	7	-	32383137	32383316
258509808	chrX	32383167	32383349	32383191	32383322	DMD	NM_004012	7	51	7	-	32383137	32383316
267657785	chrX	32382634	32382772	32382663	32382748	DMD	NM_004012	7	51	8	-	32382699	32382827
267658590	chrX	32382723	32382866	32382749	32382838	DMD	NM_004012	7	51	8	-	32382699	32382827
265163882	chrX	32380725	32380934	32380745	32380906	DMD	NM_004012	7	51	9	-	32380905	32381075
265207924	chrX	32380882	32381105	32380907	32381080	DMD	NM_004012	7	51	9	-	32380905	32381075
267988509	chrX	32366479	32366631	32366507	32366602	DMD	NM_004012	7	51	10	-	32366523	32366645
267989019	chrX	32366577	32366747	32366603	32366719	DMD	NM_004012	7	51	10	-	32366523	32366645
260763022	chrX	32363949	32364117	32363976	32364089	DMD	NM_004012	7	51	11	-	32364060	32364197
260763712	chrX	32364059	32364201	32364088	32364173	DMD	NM_004012	7	51	11	-	32364060	32364197
260764550	chrX	32364146	32364359	32364172	32364333	DMD	NM_004012	7	51	11	-	32364060	32364197
261098978	chrX	32361112	32361323	32361139	32361295	DMD	NM_004012	7	51	12	-	32361251	32361403
261110291	chrX	32361274	32361464	32361296	32361438	DMD	NM_004012	7	51	12	-	32361251	32361403
269171924	chrX	32360035	32360251	32360063	32360227	DMD	NM_004012	7	51	13	-	32360217	32360399
269180858	chrX	32360202	32360426	32360228	32360405	DMD	NM_004012	7	51	13	-	32360217	32360399
262675831	chrX	32328083	32328275	32328109	32328251	DMD	NM_004012	7	51	14	-	32328199	32328393
262706247	chrX	32328228	32328450	32328252	32328425	DMD	NM_004012	7	51	14	-	32328199	32328393
269336029	chrX	32305560	32305736	32305589	32305716	DMD	NM_004012	7	51	15	-	32305646	32305818
269340667	chrX	32305696	32305920	32305717	32305896	DMD	NM_004012	7	51	15	-	32305646	32305818
267754806	chrX	32234933	32235154	32234959	32235126	DMD	NM_004012	7	51	16	-	32235033	32235180
267760205	chrX	32235099	32235313	32235127	32235285	DMD	NM_004012	7	51	16	-	32235033	32235180
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004012	7	51	17	-	31986456	31986631

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004012	7	51	17	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004012	7	51	18	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004012	7	51	18	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004012	7	51	19	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004012	7	51	20	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004012	7	51	20	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004012	7	51	21	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004012	7	51	22	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004012	7	51	23	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004012	7	51	23	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004012	7	51	24	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004012	7	51	25	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004012	7	51	25	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004012	7	51	25	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004012	7	51	26	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004012	7	51	26	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004012	7	51	27	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004012	7	51	27	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004012	7	51	28	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004012	7	51	28	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004012	7	51	29	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004012	7	51	30	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004012	7	51	31	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004012	7	51	31	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004012	7	51	32	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004012	7	51	32	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004012	7	51	33	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004012	7	51	33	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004012	7	51	34	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004012	7	51	35	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004012	7	51	36	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004012	7	51	37	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004012	7	51	37	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004012	7	51	38	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004012	7	51	39	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004012	7	51	39	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004012	7	51	40	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004012	7	51	40	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004012	7	51	41	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004012	7	51	41	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004012	7	51	42	-	31196786	31196922

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004012	7	51	43	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004012	7	51	44	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004012	7	51	45	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004012	7	51	46	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004012	7	51	46	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004012	7	51	47	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004012	7	51	47	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004012	7	51	47	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004012	7	51	48	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004012	7	51	48	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004012	7	51	49	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004012	7	51	50	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004012	7	51	51	-	31137345	31140047
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004013	8	36	2	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004013	8	36	2	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004013	8	36	3	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004013	8	36	3	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004013	8	36	4	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004013	8	36	5	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004013	8	36	5	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004013	8	36	6	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004013	8	36	7	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004013	8	36	8	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004013	8	36	8	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004013	8	36	9	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004013	8	36	10	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004013	8	36	10	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004013	8	36	10	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004013	8	36	11	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004013	8	36	11	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004013	8	36	12	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004013	8	36	12	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004013	8	36	13	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004013	8	36	13	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004013	8	36	14	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004013	8	36	15	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004013	8	36	16	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004013	8	36	16	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004013	8	36	17	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004013	8	36	17	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004013	8	36	18	-	31366673	31366751

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004013	8	36	18	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004013	8	36	19	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004013	8	36	20	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004013	8	36	21	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004013	8	36	22	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004013	8	36	22	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004013	8	36	23	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004013	8	36	24	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004013	8	36	24	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004013	8	36	25	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004013	8	36	25	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004013	8	36	26	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004013	8	36	26	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004013	8	36	27	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004013	8	36	28	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004013	8	36	29	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004013	8	36	30	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004013	8	36	31	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004013	8	36	31	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004013	8	36	32	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004013	8	36	32	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004013	8	36	32	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004013	8	36	33	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004013	8	36	33	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004013	8	36	34	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004013	8	36	35	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004013	8	36	36	-	31137345	31140047
267566601	chrX	31526199	31526418	31526223	31526393	DMD	NM_004014	9	25	1	-	31526325	31526415
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004014	9	25	2	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004014	9	25	2	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004014	9	25	3	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004014	9	25	4	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004014	9	25	5	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004014	9	25	5	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004014	9	25	6	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004014	9	25	6	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004014	9	25	7	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004014	9	25	7	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004014	9	25	8	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004014	9	25	9	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004014	9	25	10	-	31241164	31241238

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004014	9	25	11	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004014	9	25	11	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004014	9	25	12	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004014	9	25	13	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004014	9	25	13	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004014	9	25	14	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004014	9	25	14	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004014	9	25	15	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004014	9	25	15	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004014	9	25	16	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004014	9	25	17	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004014	9	25	18	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004014	9	25	19	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004014	9	25	20	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004014	9	25	20	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004014	9	25	21	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004014	9	25	21	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004014	9	25	21	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004014	9	25	22	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004014	9	25	22	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004014	9	25	23	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004014	9	25	24	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004014	9	25	25	-	31137345	31140047
265601143	chrX	31284834	31284997	31284854	31284976	DMD	NM_004015	10	18	1	-	31284927	31285024
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004015	10	18	2	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004015	10	18	3	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004015	10	18	4	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004015	10	18	4	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004015	10	18	5	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004015	10	18	6	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004015	10	18	6	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004015	10	18	7	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004015	10	18	7	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004015	10	18	8	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004015	10	18	8	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004015	10	18	9	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004015	10	18	10	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004015	10	18	11	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004015	10	18	12	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004015	10	18	13	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004015	10	18	13	-	31187560	31187718

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004015	10	18	14	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004015	10	18	14	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004015	10	18	14	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004015	10	18	15	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004015	10	18	15	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004015	10	18	16	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004015	10	18	17	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004015	10	18	18	-	31137345	31140047
265601143	chrX	31284834	31284997	31284854	31284976	DMD	NM_004016	11	17	1	-	31284927	31285024
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004016	11	17	2	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004016	11	17	3	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004016	11	17	4	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004016	11	17	4	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004016	11	17	5	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004016	11	17	6	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004016	11	17	6	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004016	11	17	7	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004016	11	17	7	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004016	11	17	8	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004016	11	17	8	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004016	11	17	9	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004016	11	17	10	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004016	11	17	11	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004016	11	17	12	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004016	11	17	13	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004016	11	17	13	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004016	11	17	14	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004016	11	17	14	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004016	11	17	14	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004016	11	17	15	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004016	11	17	15	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004016	11	17	16	-	31152219	31152311
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004016	11	17	17	-	31137345	31140047
265601143	chrX	31284834	31284997	31284854	31284976	DMD	NM_004017	12	17	1	-	31284927	31285024
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004017	12	17	2	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004017	12	17	3	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004017	12	17	4	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004017	12	17	4	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004017	12	17	5	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004017	12	17	6	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004017	12	17	6	-	31222078	31222235

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004017	12	17	7	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004017	12	17	7	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004017	12	17	8	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004017	12	17	8	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004017	12	17	9	-	31196786	31196922
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004017	12	17	10	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004017	12	17	11	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004017	12	17	12	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004017	12	17	12	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004017	12	17	13	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004017	12	17	13	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004017	12	17	13	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004017	12	17	14	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004017	12	17	14	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004017	12	17	15	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004017	12	17	16	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004017	12	17	17	-	31137345	31140047
265601143	chrX	31284834	31284997	31284854	31284976	DMD	NM_004018	13	16	1	-	31284927	31285024
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004018	13	16	2	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004018	13	16	3	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004018	13	16	4	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004018	13	16	4	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004018	13	16	5	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004018	13	16	6	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004018	13	16	6	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004018	13	16	7	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004018	13	16	7	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004018	13	16	8	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004018	13	16	8	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004018	13	16	9	-	31196786	31196922
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004018	13	16	10	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004018	13	16	11	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004018	13	16	12	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004018	13	16	12	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004018	13	16	13	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004018	13	16	13	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004018	13	16	13	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004018	13	16	14	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004018	13	16	14	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004018	13	16	15	-	31152219	31152311
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004018	13	16	16	-	31137345	31140047

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265601143	chrX	31284834	31284997	31284854	31284976	DMD	NM_004019	14	9	1	-	31284927	31285024
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004019	14	9	2	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004019	14	9	3	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004019	14	9	4	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004019	14	9	4	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004019	14	9	5	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004019	14	9	6	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004019	14	9	6	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004019	14	9	7	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004019	14	9	7	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004019	14	9	8	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004019	14	9	8	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004019	14	9	9	-	31196312	31196922
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004020	15	32	2	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004020	15	32	2	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004020	15	32	3	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004020	15	32	3	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004020	15	32	4	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004020	15	32	5	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004020	15	32	5	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004020	15	32	6	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004020	15	32	7	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004020	15	32	8	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004020	15	32	8	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004020	15	32	9	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004020	15	32	10	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004020	15	32	10	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004020	15	32	10	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004020	15	32	11	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004020	15	32	11	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004020	15	32	12	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004020	15	32	12	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004020	15	32	13	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004020	15	32	13	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004020	15	32	14	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004020	15	32	15	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004020	15	32	16	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004020	15	32	16	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004020	15	32	17	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004020	15	32	17	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004020	15	32	18	-	31366673	31366751

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004020	15	32	18	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004020	15	32	19	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004020	15	32	20	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004020	15	32	21	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004020	15	32	22	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004020	15	32	22	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004020	15	32	23	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004020	15	32	24	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004020	15	32	24	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004020	15	32	25	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004020	15	32	25	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004020	15	32	26	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004020	15	32	26	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004020	15	32	27	-	31196786	31196922
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004020	15	32	28	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004020	15	32	28	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004020	15	32	28	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004020	15	32	29	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004020	15	32	29	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004020	15	32	30	-	31152219	31152311
267991507	chrX	31144605	31144825	31144626	31144797	DMD	NM_004020	15	32	31	-	31144759	31144790
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004020	15	32	32	-	31137345	31140047
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004021	16	35	2	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004021	16	35	2	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004021	16	35	3	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004021	16	35	3	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004021	16	35	4	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004021	16	35	5	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004021	16	35	5	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004021	16	35	6	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004021	16	35	7	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004021	16	35	8	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004021	16	35	8	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004021	16	35	9	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004021	16	35	10	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004021	16	35	10	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004021	16	35	10	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004021	16	35	11	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004021	16	35	11	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004021	16	35	12	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004021	16	35	12	-	31645790	31645979

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004021	16	35	13	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004021	16	35	13	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004021	16	35	14	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004021	16	35	15	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004021	16	35	16	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004021	16	35	16	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004021	16	35	17	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004021	16	35	17	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004021	16	35	18	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004021	16	35	18	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004021	16	35	19	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004021	16	35	20	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004021	16	35	21	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004021	16	35	22	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004021	16	35	22	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004021	16	35	23	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004021	16	35	24	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004021	16	35	24	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004021	16	35	25	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004021	16	35	25	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004021	16	35	26	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004021	16	35	26	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004021	16	35	27	-	31196786	31196922
268691834	chrX	31195993	31196122	31196013	31196098	DMD	NM_004021	16	35	28	-	31196049	31196087
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004021	16	35	29	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004021	16	35	30	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004021	16	35	31	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004021	16	35	31	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004021	16	35	32	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004021	16	35	32	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004021	16	35	32	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004021	16	35	33	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004021	16	35	33	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004021	16	35	34	-	31152219	31152311
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004021	16	35	35	-	31137345	31140047
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004022	17	34	2	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004022	17	34	2	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004022	17	34	3	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004022	17	34	3	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004022	17	34	4	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004022	17	34	5	-	31893308	31893490

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004022	17	34	5	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004022	17	34	6	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004022	17	34	7	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004022	17	34	8	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004022	17	34	8	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004022	17	34	9	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004022	17	34	10	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004022	17	34	10	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004022	17	34	10	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004022	17	34	11	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004022	17	34	11	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004022	17	34	12	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004022	17	34	12	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004022	17	34	13	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004022	17	34	13	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004022	17	34	14	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004022	17	34	15	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004022	17	34	16	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004022	17	34	16	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004022	17	34	17	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004022	17	34	17	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004022	17	34	18	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004022	17	34	18	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004022	17	34	19	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004022	17	34	20	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004022	17	34	21	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004022	17	34	22	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004022	17	34	22	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004022	17	34	23	-	31224699	31224784
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004022	17	34	24	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004022	17	34	24	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004022	17	34	25	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004022	17	34	25	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004022	17	34	26	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004022	17	34	26	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004022	17	34	27	-	31196786	31196922
267930726	chrX	31191617	31191800	31191645	31191772	DMD	NM_004022	17	34	28	-	31191656	31191721
265699328	chrX	31190387	31190611	31190412	31190583	DMD	NM_004022	17	34	29	-	31190465	31190530
266375956	chrX	31187412	31187636	31187437	31187608	DMD	NM_004022	17	34	30	-	31187560	31187718
266427338	chrX	31187585	31187792	31187609	31187771	DMD	NM_004022	17	34	30	-	31187560	31187718
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004022	17	34	31	-	31165392	31165635

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004022	17	34	31	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004022	17	34	31	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004022	17	34	32	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004022	17	34	32	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004022	17	34	33	-	31152219	31152311
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004022	17	34	34	-	31137345	31140047
257485980	chrX	31986350	31986546	31986371	31986518	DMD	NM_004023	18	31	2	-	31986456	31986631
257506837	chrX	31986498	31986667	31986519	31986639	DMD	NM_004023	18	31	2	-	31986456	31986631
267644080	chrX	31950064	31950258	31950091	31950231	DMD	NM_004023	18	31	3	-	31950197	31950344
267646565	chrX	31950206	31950422	31950232	31950394	DMD	NM_004023	18	31	3	-	31950197	31950344
263422452	chrX	31947672	31947895	31947699	31947867	DMD	NM_004023	18	31	4	-	31947713	31947862
269244915	chrX	31893289	31893416	31893314	31893391	DMD	NM_004023	18	31	5	-	31893308	31893490
269250065	chrX	31893367	31893543	31893391	31893514	DMD	NM_004023	18	31	5	-	31893308	31893490
263144004	chrX	31854753	31854976	31854774	31854948	DMD	NM_004023	18	31	6	-	31854835	31854939
268371214	chrX	31838000	31838199	31838027	31838172	DMD	NM_004023	18	31	7	-	31838092	31838200
269197121	chrX	31791987	31792210	31792013	31792189	DMD	NM_004023	18	31	8	-	31792077	31792309
269207404	chrX	31792168	31792389	31792189	31792362	DMD	NM_004023	18	31	8	-	31792077	31792309
265654405	chrX	31747688	31747909	31747717	31747884	DMD	NM_004023	18	31	9	-	31747748	31747865
258868199	chrX	31697356	31697541	31697384	31697516	DMD	NM_004023	18	31	10	-	31697492	31697703
258869294	chrX	31697490	31697615	31697517	31697592	DMD	NM_004023	18	31	10	-	31697492	31697703
258882969	chrX	31697571	31697757	31697593	31697729	DMD	NM_004023	18	31	10	-	31697492	31697703
267714300	chrX	31675977	31676193	31676002	31676167	DMD	NM_004023	18	31	11	-	31676107	31676261
267724882	chrX	31676140	31676362	31676168	31676337	DMD	NM_004023	18	31	11	-	31676107	31676261
269411430	chrX	31645650	31645862	31645677	31645841	DMD	NM_004023	18	31	12	-	31645790	31645979
269437132	chrX	31645819	31646039	31645842	31646012	DMD	NM_004023	18	31	12	-	31645790	31645979
263061549	chrX	31525298	31525471	31525325	31525444	DMD	NM_004023	18	31	13	-	31525398	31525570
263099334	chrX	31525419	31525627	31525445	31525599	DMD	NM_004023	18	31	13	-	31525398	31525570
269102999	chrX	31514866	31515088	31514888	31515066	DMD	NM_004023	18	31	14	-	31514905	31515061
263137299	chrX	31497044	31497255	31497064	31497226	DMD	NM_004023	18	31	15	-	31497100	31497220
263299065	chrX	31496194	31496386	31496215	31496359	DMD	NM_004023	18	31	16	-	31496223	31496491
263348146	chrX	31496337	31496521	31496360	31496497	DMD	NM_004023	18	31	16	-	31496223	31496491
268721203	chrX	31462568	31462735	31462595	31462712	DMD	NM_004023	18	31	17	-	31462598	31462744
268744200	chrX	31462692	31462837	31462712	31462815	DMD	NM_004023	18	31	17	-	31462598	31462744
267638171	chrX	31366537	31366747	31366565	31366729	DMD	NM_004023	18	31	18	-	31366673	31366751
267638594	chrX	31366700	31366876	31366721	31366848	DMD	NM_004023	18	31	18	-	31366673	31366751
265624843	chrX	31341605	31341821	31341628	31341797	DMD	NM_004023	18	31	19	-	31341715	31341775
258709215	chrX	31279022	31279245	31279050	31279217	DMD	NM_004023	18	31	20	-	31279072	31279133
267975754	chrX	31241072	31241296	31241100	31241269	DMD	NM_004023	18	31	21	-	31241164	31241238
268938746	chrX	31227495	31227711	31227517	31227688	DMD	NM_004023	18	31	22	-	31227615	31227816
268948234	chrX	31227666	31227876	31227689	31227850	DMD	NM_004023	18	31	22	-	31227615	31227816
267955973	chrX	31224601	31224823	31224628	31224795	DMD	NM_004023	18	31	23	-	31224699	31224784

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266085870	chrX	31221927	31222149	31221950	31222127	DMD	NM_004023	18	31	24	-	31222078	31222235
266100059	chrX	31222106	31222273	31222128	31222245	DMD	NM_004023	18	31	24	-	31222078	31222235
267540981	chrX	31200741	31200909	31200763	31200886	DMD	NM_004023	18	31	25	-	31200855	31201021
267554089	chrX	31200862	31201062	31200887	31201039	DMD	NM_004023	18	31	25	-	31200855	31201021
268174717	chrX	31198330	31198521	31198354	31198497	DMD	NM_004023	18	31	26	-	31198487	31198598
268182295	chrX	31198475	31198658	31198498	31198631	DMD	NM_004023	18	31	26	-	31198487	31198598
263743122	chrX	31196747	31196958	31196772	31196930	DMD	NM_004023	18	31	27	-	31196786	31196922
267010858	chrX	31165262	31165465	31165284	31165443	DMD	NM_004023	18	31	28	-	31165392	31165635
267047398	chrX	31165417	31165623	31165444	31165598	DMD	NM_004023	18	31	28	-	31165392	31165635
267062875	chrX	31165578	31165766	31165599	31165745	DMD	NM_004023	18	31	28	-	31165392	31165635
268434596	chrX	31164293	31164517	31164314	31164496	DMD	NM_004023	18	31	29	-	31164408	31164531
268451559	chrX	31164472	31164649	31164497	31164621	DMD	NM_004023	18	31	29	-	31164408	31164531
269448034	chrX	31152173	31152394	31152194	31152366	DMD	NM_004023	18	31	30	-	31152219	31152311
264260543	chrX	31139917	31140093	31139938	31140066	DMD	NM_004023	18	31	31	-	31137345	31140047
265359853	chr7	21582815	21583033	21582832	21583016	DNAH11	NM_003777	1	83	1	+	21582833	21583214
265362411	chr7	21582913	21583122	21582932	21583098	DNAH11	NM_003777	1	83	1	+	21582833	21583214
265363744	chr7	21583075	21583272	21583097	21583250	DNAH11	NM_003777	1	83	1	+	21582833	21583214
257531266	chr7	21584511	21584735	21584536	21584710	DNAH11	NM_003777	1	83	2	+	21584624	21584767
257540926	chr7	21584683	21584873	21584711	21584849	DNAH11	NM_003777	1	83	2	+	21584624	21584767
257281653	chr7	21598330	21598554	21598356	21598526	DNAH11	NM_003777	1	83	3	+	21598420	21598616
257302636	chr7	21598463	21598667	21598492	21598646	DNAH11	NM_003777	1	83	3	+	21598420	21598616
268463531	chr7	21599061	21599283	21599084	21599255	DNAH11	NM_003777	1	83	4	+	21599221	21599410
268465474	chr7	21599227	21599353	21599256	21599328	DNAH11	NM_003777	1	83	4	+	21599221	21599410
268466543	chr7	21599307	21599464	21599329	21599435	DNAH11	NM_003777	1	83	4	+	21599221	21599410
269310884	chr7	21600545	21600726	21600574	21600698	DNAH11	NM_003777	1	83	5	+	21600689	21600788
269310968	chr7	21600679	21600823	21600703	21600800	DNAH11	NM_003777	1	83	5	+	21600689	21600788
268269781	chr7	21603687	21603905	21603711	21603881	DNAH11	NM_003777	1	83	6	+	21603804	21604015
268284139	chr7	21603861	21604069	21603882	21604042	DNAH11	NM_003777	1	83	6	+	21603804	21604015
267632534	chr7	21609621	21609835	21609645	21609808	DNAH11	NM_003777	1	83	7	+	21609687	21609917
267640663	chr7	21609755	21609968	21609783	21609947	DNAH11	NM_003777	1	83	7	+	21609687	21609917
268423964	chr7	21611370	21611508	21611397	21611480	DNAH11	NM_003777	1	83	8	+	21611424	21611591
268429739	chr7	21611458	21611629	21611481	21611604	DNAH11	NM_003777	1	83	8	+	21611424	21611591
263166771	chr7	21621369	21621576	21621394	21621549	DNAH11	NM_003777	1	83	9	+	21621523	21621639
263205805	chr7	21621522	21621713	21621550	21621684	DNAH11	NM_003777	1	83	9	+	21621523	21621639
257714694	chr7	21627642	21627850	21627668	21627824	DNAH11	NM_003777	1	83	10	+	21627682	21627819
268612758	chr7	21628064	21628288	21628087	21628260	DNAH11	NM_003777	1	83	11	+	21628130	21628254
268011970	chr7	21628684	21628890	21628709	21628862	DNAH11	NM_003777	1	83	12	+	21628826	21629021
268015492	chr7	21628835	21629018	21628863	21628992	DNAH11	NM_003777	1	83	12	+	21628826	21629021
268016381	chr7	21628965	21629145	21628993	21629120	DNAH11	NM_003777	1	83	12	+	21628826	21629021
267270106	chr7	21630595	21630819	21630622	21630791	DNAH11	NM_003777	1	83	13	+	21630536	21630640
267271847	chr7	21630607	21630830	21630632	21630807	DNAH11	NM_003777	1	83	13	+	21630536	21630640

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257637861	chr7	21630786	21630921	21630810	21630899	DNAH11	NM_003777	1	83	14	+	21630803	21631195
257660413	chr7	21630873	21631093	21630897	21631073	DNAH11	NM_003777	1	83	14	+	21630803	21631195
257673332	chr7	21631033	21631255	21631054	21631227	DNAH11	NM_003777	1	83	14	+	21630803	21631195
267271847	chr7	21630607	21630830	21630632	21630807	DNAH11	NM_003777	1	83	14	+	21630803	21631195
268933581	chr7	21639263	21639485	21639292	21639458	DNAH11	NM_003777	1	83	15	+	21639405	21639737
268942908	chr7	21639431	21639631	21639459	21639606	DNAH11	NM_003777	1	83	15	+	21639405	21639737
268957327	chr7	21639585	21639803	21639607	21639775	DNAH11	NM_003777	1	83	15	+	21639405	21639737
257477637	chr7	21640461	21640685	21640483	21640657	DNAH11	NM_003777	1	83	16	+	21640294	21640548
257485279	chr7	21640495	21640719	21640521	21640697	DNAH11	NM_003777	1	83	16	+	21640294	21640548
267960533	chr7	21640194	21640373	21640222	21640347	DNAH11	NM_003777	1	83	16	+	21640294	21640548
267968740	chr7	21640326	21640510	21640348	21640482	DNAH11	NM_003777	1	83	16	+	21640294	21640548
257477637	chr7	21640461	21640685	21640483	21640657	DNAH11	NM_003777	1	83	17	+	21640628	21640797
257485279	chr7	21640495	21640719	21640521	21640697	DNAH11	NM_003777	1	83	17	+	21640628	21640797
257498314	chr7	21640670	21640894	21640698	21640866	DNAH11	NM_003777	1	83	17	+	21640628	21640797
264923175	chr7	21640870	21641067	21640897	21641044	DNAH11	NM_003777	1	83	18	+	21641014	21641236
264924999	chr7	21641041	21641185	21641063	21641159	DNAH11	NM_003777	1	83	18	+	21641014	21641236
264943400	chr7	21641131	21641259	21641155	21641232	DNAH11	NM_003777	1	83	18	+	21641014	21641236
265303956	chr7	21646092	21646276	21646116	21646255	DNAH11	NM_003777	1	83	19	+	21646044	21646160
268019140	chr7	21646005	21646143	21646032	21646115	DNAH11	NM_003777	1	83	19	+	21646044	21646160
265309361	chr7	21646152	21646342	21646179	21646316	DNAH11	NM_003777	1	83	20	+	21646265	21646351
265311408	chr7	21646295	21646448	21646317	21646420	DNAH11	NM_003777	1	83	20	+	21646265	21646351
266639514	chr7	21654558	21654782	21654583	21654755	DNAH11	NM_003777	1	83	21	+	21654732	21654890
266692895	chr7	21654732	21654956	21654756	21654928	DNAH11	NM_003777	1	83	21	+	21654732	21654890
268462568	chr7	21655768	21655959	21655790	21655932	DNAH11	NM_003777	1	83	22	+	21655827	21655925
267611600	chr7	21657189	21657411	21657215	21657387	DNAH11	NM_003777	1	83	23	+	21657237	21657395
267620063	chr7	21657366	21657528	21657388	21657503	DNAH11	NM_003777	1	83	23	+	21657237	21657395
267764718	chr7	21658660	21658884	21658687	21658856	DNAH11	NM_003777	1	83	24	+	21658718	21658840
268719726	chr7	21659407	21659631	21659435	21659603	DNAH11	NM_003777	1	83	25	+	21659574	21659696
258352153	chr7	21675473	21675617	21675501	21675596	DNAH11	NM_003777	1	83	26	+	21675489	21675713
258386463	chr7	21675573	21675745	21675597	21675718	DNAH11	NM_003777	1	83	26	+	21675489	21675713
267869595	chr7	21677201	21677420	21677222	21677391	DNAH11	NM_003777	1	83	27	+	21677229	21677320
269352958	chr7	21678424	21678594	21678452	21678571	DNAH11	NM_003777	1	83	28	+	21678557	21678683
269354577	chr7	21678544	21678729	21678572	21678701	DNAH11	NM_003777	1	83	28	+	21678557	21678683
268865493	chr7	21695272	21695492	21695295	21695468	DNAH11	NM_003777	1	83	29	+	21695450	21695599
268869295	chr7	21695444	21695634	21695469	21695606	DNAH11	NM_003777	1	83	29	+	21695450	21695599
258038234	chr7	21698338	21698530	21698359	21698503	DNAH11	NM_003777	1	83	30	+	21698416	21698649
258107535	chr7	21698483	21698706	21698504	21698678	DNAH11	NM_003777	1	83	30	+	21698416	21698649
268178111	chr7	21721155	21721356	21721184	21721328	DNAH11	NM_003777	1	83	31	+	21721164	21721295
268178111	chr7	21721155	21721356	21721184	21721328	DNAH11	NM_003777	1	83	32	+	21721297	21721302
268054776	chr7	21723267	21723444	21723293	21723421	DNAH11	NM_003777	1	83	33	+	21723402	21723562
268067125	chr7	21723401	21723602	21723422	21723578	DNAH11	NM_003777	1	83	33	+	21723402	21723562

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262282412	chr7	21726823	21726989	21726850	21726962	DNAH11	NM_003777	1	83	34	+	21726717	21726873
266524326	chr7	21726569	21726766	21726599	21726744	DNAH11	NM_003777	1	83	34	+	21726717	21726873
266525595	chr7	21726684	21726875	21726713	21726849	DNAH11	NM_003777	1	83	34	+	21726717	21726873
262298686	chr7	21726950	21727171	21726977	21727150	DNAH11	NM_003777	1	83	35	+	21727000	21727145
267880551	chr7	21730311	21730534	21730336	21730513	DNAH11	NM_003777	1	83	36	+	21730383	21730499
268172565	chr7	21737536	21737755	21737563	21737727	DNAH11	NM_003777	1	83	37	+	21737693	21737831
268178943	chr7	21737708	21737860	21737728	21737832	DNAH11	NM_003777	1	83	37	+	21737693	21737831
258663146	chr7	21742245	21742462	21742273	21742435	DNAH11	NM_003777	1	83	38	+	21742328	21742420
268040455	chr7	21743901	21744104	21743927	21744078	DNAH11	NM_003777	1	83	39	+	21744052	21744246
268046128	chr7	21744051	21744273	21744079	21744251	DNAH11	NM_003777	1	83	39	+	21744052	21744246
268831940	chr7	21744985	21745206	21745011	21745179	DNAH11	NM_003777	1	83	40	+	21745078	21745155
267822206	chr7	21747134	21747345	21747161	21747318	DNAH11	NM_003777	1	83	41	+	21747317	21747453
267827600	chr7	21747296	21747515	21747319	21747489	DNAH11	NM_003777	1	83	41	+	21747317	21747453
268594749	chr7	21750047	21750244	21750066	21750217	DNAH11	NM_003777	1	83	42	+	21750171	21750321
268594847	chr7	21750192	21750396	21750218	21750368	DNAH11	NM_003777	1	83	42	+	21750171	21750321
267377410	chr7	21751255	21751479	21751280	21751459	DNAH11	NM_003777	1	83	43	+	21751330	21751478
262180545	chr7	21757267	21757416	21757292	21757394	DNAH11	NM_003777	1	83	44	+	21757393	21757543
262222801	chr7	21757370	21757583	21757395	21757555	DNAH11	NM_003777	1	83	44	+	21757393	21757543
266466898	chr7	21760175	21760392	21760201	21760367	DNAH11	NM_003777	1	83	45	+	21760343	21760474
266494527	chr7	21760342	21760514	21760368	21760486	DNAH11	NM_003777	1	83	45	+	21760343	21760474
267985095	chr7	21765294	21765501	21765322	21765480	DNAH11	NM_003777	1	83	46	+	21765429	21765602
267990471	chr7	21765457	21765633	21765480	21765605	DNAH11	NM_003777	1	83	46	+	21765429	21765602
264985202	chr7	21775089	21775293	21775116	21775271	DNAH11	NM_003777	1	83	47	+	21775258	21775462
265045629	chr7	21775251	21775385	21775272	21775359	DNAH11	NM_003777	1	83	47	+	21775258	21775462
265096724	chr7	21775335	21775513	21775360	21775485	DNAH11	NM_003777	1	83	47	+	21775258	21775462
269301385	chr7	21778166	21778369	21778186	21778342	DNAH11	NM_003777	1	83	48	+	21778319	21778484
269308070	chr7	21778315	21778516	21778343	21778489	DNAH11	NM_003777	1	83	48	+	21778319	21778484
261921738	chr7	21779129	21779328	21779156	21779300	DNAH11	NM_003777	1	83	49	+	21779189	21779291
268012726	chr7	21781479	21781642	21781505	21781618	DNAH11	NM_003777	1	83	50	+	21781545	21781784
268017996	chr7	21781591	21781815	21781619	21781789	DNAH11	NM_003777	1	83	50	+	21781545	21781784
265195269	chr7	21784030	21784253	21784056	21784225	DNAH11	NM_003777	1	83	51	+	21784056	21784217
268316667	chr7	21784326	21784550	21784351	21784529	DNAH11	NM_003777	1	83	52	+	21784488	21784681
268345718	chr7	21784507	21784712	21784530	21784686	DNAH11	NM_003777	1	83	52	+	21784488	21784681
267596048	chr7	21788171	21788392	21788190	21788371	DNAH11	NM_003777	1	83	53	+	21788198	21788360
267760050	chr7	21789244	21789454	21789265	21789426	DNAH11	NM_003777	1	83	54	+	21789296	21789419
264973316	chr7	21789662	21789886	21789682	21789859	DNAH11	NM_003777	1	83	55	+	21789840	21789982
264980118	chr7	21789836	21790030	21789860	21790002	DNAH11	NM_003777	1	83	55	+	21789840	21789982
259737630	chr7	21804907	21805122	21804930	21805099	DNAH11	NM_003777	1	83	56	+	21805046	21805207
259847201	chr7	21805078	21805296	21805100	21805271	DNAH11	NM_003777	1	83	56	+	21805046	21805207
268109133	chr7	21813201	21813421	21813228	21813395	DNAH11	NM_003777	1	83	57	+	21813384	21813617
268112030	chr7	21813374	21813596	21813396	21813576	DNAH11	NM_003777	1	83	57	+	21813384	21813617

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268121718	chr7	21813541	21813765	21813569	21813740	DNAH11	NM_003777	1	83	57	+	21813384	21813617
262657984	chr7	21818533	21818754	21818554	21818728	DNAH11	NM_003777	1	83	58	+	21818576	21818722
266395956	chr7	21823902	21824076	21823930	21824051	DNAH11	NM_003777	1	83	59	+	21824045	21824158
266438432	chr7	21824024	21824195	21824052	21824169	DNAH11	NM_003777	1	83	59	+	21824045	21824158
267670116	chr7	21826194	21826417	21826216	21826395	DNAH11	NM_003777	1	83	60	+	21826242	21826385
268657103	chr7	21826881	21827100	21826908	21827072	DNAH11	NM_003777	1	83	61	+	21827019	21827201
268666206	chr7	21827047	21827246	21827073	21827220	DNAH11	NM_003777	1	83	61	+	21827019	21827201
267362901	chr7	21828784	21828997	21828810	21828969	DNAH11	NM_003777	1	83	62	+	21828859	21828960
268724389	chr7	21840648	21840817	21840671	21840791	DNAH11	NM_003777	1	83	63	+	21840755	21840893
268728596	chr7	21840772	21840947	21840792	21840918	DNAH11	NM_003777	1	83	63	+	21840755	21840893
267474380	chr7	21847355	21847567	21847375	21847542	DNAH11	NM_003777	1	83	64	+	21847501	21847667
267500618	chr7	21847516	21847712	21847543	21847686	DNAH11	NM_003777	1	83	64	+	21847501	21847667
268095691	chr7	21855976	21856178	21856004	21856158	DNAH11	NM_003777	1	83	65	+	21856085	21856320
268117071	chr7	21856139	21856350	21856159	21856325	DNAH11	NM_003777	1	83	65	+	21856085	21856320
264387160	chr7	21857672	21857881	21857698	21857859	DNAH11	NM_003777	1	83	66	+	21857835	21857957
264388087	chr7	21857835	21858019	21857861	21857995	DNAH11	NM_003777	1	83	66	+	21857835	21857957
267853976	chr7	21882057	21882250	21882077	21882221	DNAH11	NM_003777	1	83	67	+	21882162	21882366
267879903	chr7	21882197	21882394	21882222	21882367	DNAH11	NM_003777	1	83	67	+	21882162	21882366
267287321	chr7	21892042	21892215	21892068	21892191	DNAH11	NM_003777	1	83	68	+	21892085	21892249
267299162	chr7	21892170	21892304	21892192	21892277	DNAH11	NM_003777	1	83	68	+	21892085	21892249
268496741	chr7	21893775	21893975	21893803	21893950	DNAH11	NM_003777	1	83	69	+	21893933	21894073
268506484	chr7	21893926	21894137	21893951	21894109	DNAH11	NM_003777	1	83	69	+	21893933	21894073
257342352	chr7	21901426	21901637	21901448	21901616	DNAH11	NM_003777	1	83	70	+	21901471	21901641
257372861	chr7	21901594	21901783	21901617	21901762	DNAH11	NM_003777	1	83	70	+	21901471	21901641
268671327	chr7	21904013	21904232	21904039	21904207	DNAH11	NM_003777	1	83	71	+	21904153	21904275
268683717	chr7	21904182	21904351	21904208	21904323	DNAH11	NM_003777	1	83	71	+	21904153	21904275
265812066	chr7	21906044	21906196	21906071	21906168	DNAH11	NM_003777	1	83	72	+	21906088	21906281
265829274	chr7	21906147	21906358	21906169	21906330	DNAH11	NM_003777	1	83	72	+	21906088	21906281
267642839	chr7	21907375	21907555	21907399	21907527	DNAH11	NM_003777	1	83	73	+	21907477	21907625
267651746	chr7	21907503	21907715	21907528	21907689	DNAH11	NM_003777	1	83	73	+	21907477	21907625
267059287	chr7	21908427	21908640	21908450	21908614	DNAH11	NM_003777	1	83	74	+	21908482	21908609
259326687	chr7	21912787	21913000	21912811	21912978	DNAH11	NM_003777	1	83	75	+	21912892	21913119
259376917	chr7	21912956	21913169	21912979	21913143	DNAH11	NM_003777	1	83	75	+	21912892	21913119
261114578	chr7	21920259	21920470	21920280	21920443	DNAH11	NM_003777	1	83	76	+	21920320	21920511
261154713	chr7	21920425	21920557	21920444	21920532	DNAH11	NM_003777	1	83	76	+	21920320	21920511
266688009	chr7	21923776	21923994	21923804	21923974	DNAH11	NM_003777	1	83	77	+	21923909	21924028
266717197	chr7	21923954	21924147	21923975	21924121	DNAH11	NM_003777	1	83	77	+	21923909	21924028
262913128	chr7	21931952	21932135	21931975	21932110	DNAH11	NM_003777	1	83	78	+	21932043	21932285
262979102	chr7	21932086	21932306	21932111	21932282	DNAH11	NM_003777	1	83	78	+	21932043	21932285
267244955	chr7	21934341	21934559	21934366	21934534	DNAH11	NM_003777	1	83	79	+	21934241	21934423
269212961	chr7	21934097	21934298	21934120	21934275	DNAH11	NM_003777	1	83	79	+	21934241	21934423

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269217310	chr7	21934249	21934458	21934276	21934430	DNAH11	NM_003777	1	83	79	+	21934241	21934423
267244955	chr7	21934341	21934559	21934366	21934534	DNAH11	NM_003777	1	83	80	+	21934502	21934617
267257255	chr7	21934513	21934716	21934535	21934693	DNAH11	NM_003777	1	83	80	+	21934502	21934617
268158442	chr7	21938923	21939124	21938948	21939103	DNAH11	NM_003777	1	83	81	+	21938954	21939066
267927888	chr7	21939483	21939697	21939506	21939670	DNAH11	NM_003777	1	83	82	+	21939598	21939738
267949416	chr7	21939648	21939782	21939671	21939756	DNAH11	NM_003777	1	83	82	+	21939598	21939738
264376786	chr7	21940587	21940810	21940607	21940788	DNAH11	NM_003777	1	83	83	+	21940625	21941457
264425864	chr7	21940756	21940963	21940782	21940936	DNAH11	NM_003777	1	83	83	+	21940625	21941457
258924889	chr5	13944367	13944591	13944393	13944571	DNAH5	NM_001369	1	79	1	-	13944491	13944589
264614871	chr5	13931173	13931397	13931194	13931369	DNAH5	NM_001369	1	79	2	-	13931219	13931353
267241986	chr5	13928037	13928253	13928057	13928226	DNAH5	NM_001369	1	79	3	-	13928203	13928287
267245941	chr5	13928203	13928422	13928227	13928393	DNAH5	NM_001369	1	79	3	-	13928203	13928287
268889140	chr5	13923302	13923453	13923327	13923430	DNAH5	NM_001369	1	79	4	-	13923389	13923549
268895797	chr5	13923410	13923596	13923431	13923569	DNAH5	NM_001369	1	79	4	-	13923389	13923549
262953073	chr5	13922159	13922383	13922181	13922363	DNAH5	NM_001369	1	79	5	-	13922216	13922437
262992709	chr5	13922342	13922501	13922364	13922473	DNAH5	NM_001369	1	79	5	-	13922216	13922437
266725631	chr5	13920555	13920778	13920583	13920750	DNAH5	NM_001369	1	79	6	-	13920589	13920726
261860084	chr5	13919130	13919353	13919151	13919329	DNAH5	NM_001369	1	79	7	-	13919285	13919461
261869051	chr5	13919281	13919496	13919303	13919475	DNAH5	NM_001369	1	79	7	-	13919285	13919461
269251508	chr5	13917079	13917278	13917103	13917256	DNAH5	NM_001369	1	79	8	-	13917252	13917365
269253460	chr5	13917230	13917430	13917257	13917402	DNAH5	NM_001369	1	79	8	-	13917252	13917365
268482733	chr5	13916276	13916489	13916302	13916463	DNAH5	NM_001369	1	79	9	-	13916457	13916564
268484642	chr5	13916436	13916655	13916464	13916622	DNAH5	NM_001369	1	79	9	-	13916457	13916564
267856241	chr5	13914621	13914811	13914648	13914783	DNAH5	NM_001369	1	79	10	-	13914629	13914751
265960351	chr5	13913666	13913890	13913695	13913868	DNAH5	NM_001369	1	79	11	-	13913852	13914067
265960484	chr5	13913846	13914061	13913872	13914038	DNAH5	NM_001369	1	79	11	-	13913852	13914067
265969606	chr5	13913951	13914170	13913976	13914142	DNAH5	NM_001369	1	79	11	-	13913852	13914067
267966225	chr5	13911400	13911616	13911422	13911590	DNAH5	NM_001369	1	79	12	-	13911495	13911602
267926049	chr5	13902033	13902257	13902055	13902233	DNAH5	NM_001369	1	79	13	-	13902162	13902247
265962112	chr5	13901230	13901451	13901255	13901426	DNAH5	NM_001369	1	79	14	-	13901361	13901682
265978752	chr5	13901406	13901623	13901427	13901597	DNAH5	NM_001369	1	79	14	-	13901361	13901682
265983462	chr5	13901601	13901820	13901629	13901787	DNAH5	NM_001369	1	79	14	-	13901361	13901682
267506076	chr5	13900268	13900411	13900291	13900392	DNAH5	NM_001369	1	79	15	-	13900315	13900521
267509464	chr5	13900372	13900584	13900393	13900556	DNAH5	NM_001369	1	79	15	-	13900315	13900521
262103516	chr5	13894697	13894870	13894721	13894849	DNAH5	NM_001369	1	79	16	-	13894759	13894930
262129542	chr5	13894829	13895044	13894850	13895021	DNAH5	NM_001369	1	79	16	-	13894759	13894930
267824186	chr5	13890971	13891189	13890995	13891167	DNAH5	NM_001369	1	79	17	-	13891085	13891230
267825536	chr5	13891146	13891356	13891168	13891328	DNAH5	NM_001369	1	79	17	-	13891085	13891230
264023711	chr5	13886043	13886183	13886067	13886156	DNAH5	NM_001369	1	79	18	-	13886073	13886238
264034163	chr5	13886131	13886306	13886157	13886279	DNAH5	NM_001369	1	79	18	-	13886073	13886238
259110172	chr5	13885041	13885180	13885062	13885153	DNAH5	NM_001369	1	79	19	-	13885098	13885337

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259151275	chr5	13885131	13885332	13885154	13885304	DNAH5	NM_001369	1	79	19	-	13885098	13885337
259166035	chr5	13885298	13885515	13885326	13885487	DNAH5	NM_001369	1	79	19	-	13885098	13885337
259050464	chr5	13882842	13883035	13882871	13883013	DNAH5	NM_001369	1	79	20	-	13883013	13883203
259057501	chr5	13882868	13883087	13882896	13883067	DNAH5	NM_001369	1	79	20	-	13883013	13883203
259108236	chr5	13883046	13883234	13883068	13883206	DNAH5	NM_001369	1	79	20	-	13883013	13883203
259050464	chr5	13882842	13883035	13882871	13883013	DNAH5	NM_001369	1	79	21	-	13882837	13882924
259057501	chr5	13882868	13883087	13882896	13883067	DNAH5	NM_001369	1	79	21	-	13882837	13882924
263805334	chr5	13882681	13882897	13882707	13882870	DNAH5	NM_001369	1	79	21	-	13882837	13882924
267842440	chr5	13876643	13876822	13876669	13876794	DNAH5	NM_001369	1	79	22	-	13876793	13876926
267851182	chr5	13876773	13876985	13876795	13876957	DNAH5	NM_001369	1	79	22	-	13876793	13876926
262669332	chr5	13871543	13871762	13871568	13871733	DNAH5	NM_001369	1	79	23	-	13871673	13871874
262701022	chr5	13871711	13871923	13871734	13871895	DNAH5	NM_001369	1	79	23	-	13871673	13871874
269357938	chr5	13870708	13870926	13870730	13870901	DNAH5	NM_001369	1	79	24	-	13870876	13871111
269360142	chr5	13870874	13871062	13870902	13871038	DNAH5	NM_001369	1	79	24	-	13870876	13871111
269372669	chr5	13871012	13871174	13871039	13871145	DNAH5	NM_001369	1	79	24	-	13870876	13871111
263841286	chr5	13867759	13867965	13867781	13867942	DNAH5	NM_001369	1	79	25	-	13867883	13868101
263847738	chr5	13867919	13868143	13867943	13868115	DNAH5	NM_001369	1	79	25	-	13867883	13868101
269083997	chr5	13866222	13866400	13866248	13866375	DNAH5	NM_001369	1	79	26	-	13866329	13866391
269085640	chr5	13866328	13866546	13866353	13866523	DNAH5	NM_001369	1	79	26	-	13866329	13866391
261855192	chr5	13865739	13865945	13865761	13865916	DNAH5	NM_001369	1	79	27	-	13865777	13866015
261859514	chr5	13865856	13866050	13865884	13866023	DNAH5	NM_001369	1	79	27	-	13865777	13866015
259070511	chr5	13864459	13864682	13864486	13864660	DNAH5	NM_001369	1	79	28	-	13864506	13864746
259120059	chr5	13864638	13864811	13864659	13864789	DNAH5	NM_001369	1	79	28	-	13864506	13864746
264764251	chr5	13862607	13862810	13862635	13862782	DNAH5	NM_001369	1	79	29	-	13862657	13862856
264831451	chr5	13862760	13862887	13862783	13862861	DNAH5	NM_001369	1	79	29	-	13862657	13862856
267692304	chr5	13859499	13859683	13859522	13859660	DNAH5	NM_001369	1	79	30	-	13859561	13859714
267698851	chr5	13859638	13859852	13859661	13859824	DNAH5	NM_001369	1	79	30	-	13859561	13859714
264120982	chr5	13850575	13850788	13850600	13850761	DNAH5	NM_001369	1	79	31	-	13850761	13850924
264152214	chr5	13850737	13850957	13850762	13850929	DNAH5	NM_001369	1	79	31	-	13850761	13850924
260274989	chr5	13844789	13844997	13844810	13844970	DNAH5	NM_001369	1	79	32	-	13844946	13845102
260401779	chr5	13844944	13845149	13844971	13845123	DNAH5	NM_001369	1	79	32	-	13844946	13845102
264767138	chr5	13841781	13841980	13841808	13841957	DNAH5	NM_001369	1	79	33	-	13841801	13842013
264796315	chr5	13841937	13842103	13841958	13842077	DNAH5	NM_001369	1	79	33	-	13841801	13842013
257281420	chr5	13840940	13841159	13840967	13841133	DNAH5	NM_001369	1	79	34	-	13841015	13841239
257317130	chr5	13841106	13841323	13841134	13841295	DNAH5	NM_001369	1	79	34	-	13841015	13841239
269034844	chr5	13839282	13839504	13839304	13839481	DNAH5	NM_001369	1	79	35	-	13839465	13839637
269038798	chr5	13839459	13839683	13839482	13839655	DNAH5	NM_001369	1	79	35	-	13839465	13839637
269188117	chr5	13830538	13830744	13830563	13830722	DNAH5	NM_001369	1	79	36	-	13830706	13830884
269203607	chr5	13830699	13830917	13830723	13830892	DNAH5	NM_001369	1	79	36	-	13830706	13830884
267706719	chr5	13830029	13830251	13830056	13830226	DNAH5	NM_001369	1	79	37	-	13830135	13830322
267714549	chr5	13830199	13830415	13830227	13830387	DNAH5	NM_001369	1	79	37	-	13830135	13830322

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263431208	chr5	13829524	13829670	13829550	13829645	DNAH5	NM_001369	1	79	38	-	13829619	13829813
263461125	chr5	13829625	13829849	13829646	13829823	DNAH5	NM_001369	1	79	38	-	13829619	13829813
257279184	chr5	13824169	13824339	13824193	13824311	DNAH5	NM_001369	1	79	39	-	13824308	13824442
257313112	chr5	13824287	13824511	13824312	13824483	DNAH5	NM_001369	1	79	39	-	13824308	13824442
268716401	chr5	13823349	13823555	13823372	13823527	DNAH5	NM_001369	1	79	40	-	13823372	13823479
263570996	chr5	13820364	13820496	13820388	13820476	DNAH5	NM_001369	1	79	41	-	13820455	13820608
263619062	chr5	13820455	13820654	13820477	13820629	DNAH5	NM_001369	1	79	41	-	13820455	13820608
267598978	chr5	13817579	13817721	13817608	13817694	DNAH5	NM_001369	1	79	42	-	13817657	13817803
267600493	chr5	13817667	13817851	13817695	13817825	DNAH5	NM_001369	1	79	42	-	13817657	13817803
264357422	chr5	13814630	13814853	13814654	13814833	DNAH5	NM_001369	1	79	43	-	13814714	13814955
264403341	chr5	13814808	13815020	13814832	13814995	DNAH5	NM_001369	1	79	43	-	13814714	13814955
258018609	chr5	13811703	13811861	13811731	13811835	DNAH5	NM_001369	1	79	44	-	13811756	13811932
258049712	chr5	13811811	13811995	13811836	13811967	DNAH5	NM_001369	1	79	44	-	13811756	13811932
268052084	chr5	13810131	13810335	13810148	13810318	DNAH5	NM_001369	1	79	45	-	13810168	13810369
268052362	chr5	13810275	13810488	13810292	13810466	DNAH5	NM_001369	1	79	45	-	13810168	13810369
267902842	chr5	13809099	13809323	13809126	13809300	DNAH5	NM_001369	1	79	46	-	13809153	13809295
269321295	chr5	13807660	13807852	13807685	13807826	DNAH5	NM_001369	1	79	47	-	13807700	13807834
261078291	chr5	13793889	13794112	13793912	13794084	DNAH5	NM_001369	1	79	48	-	13794045	13794167
261093291	chr5	13794053	13794209	13794081	13794181	DNAH5	NM_001369	1	79	48	-	13794045	13794167
268686664	chr5	13793542	13793763	13793569	13793742	DNAH5	NM_001369	1	79	49	-	13793624	13793837
268698660	chr5	13793722	13793910	13793743	13793887	DNAH5	NM_001369	1	79	49	-	13793624	13793837
262342591	chr5	13791969	13792134	13791995	13792109	DNAH5	NM_001369	1	79	50	-	13792103	13792326
262354325	chr5	13792082	13792248	13792110	13792228	DNAH5	NM_001369	1	79	50	-	13792103	13792326
262375703	chr5	13792199	13792410	13792227	13792383	DNAH5	NM_001369	1	79	50	-	13792103	13792326
267921316	chr5	13788808	13788951	13788834	13788922	DNAH5	NM_001369	1	79	51	-	13788825	13789023
267929955	chr5	13788900	13789070	13788923	13789042	DNAH5	NM_001369	1	79	51	-	13788825	13789023
268224658	chr5	13786113	13786333	13786138	13786310	DNAH5	NM_001369	1	79	52	-	13786288	13786460
268240267	chr5	13786287	13786505	13786311	13786477	DNAH5	NM_001369	1	79	52	-	13786288	13786460
266315246	chr5	13780877	13781083	13780899	13781054	DNAH5	NM_001369	1	79	53	-	13780938	13781068
266317976	chr5	13781034	13781192	13781055	13781163	DNAH5	NM_001369	1	79	53	-	13780938	13781068
263598964	chr5	13777207	13777428	13777233	13777405	DNAH5	NM_001369	1	79	54	-	13777311	13777464
263621165	chr5	13777378	13777529	13777406	13777501	DNAH5	NM_001369	1	79	54	-	13777311	13777464
263528046	chr5	13776473	13776697	13776495	13776678	DNAH5	NM_001369	1	79	55	-	13776548	13776815
263617206	chr5	13776655	13776846	13776679	13776821	DNAH5	NM_001369	1	79	55	-	13776548	13776815
265748464	chr5	13770853	13771071	13770872	13771043	DNAH5	NM_001369	1	79	56	-	13770858	13771089
265760077	chr5	13771020	13771205	13771044	13771177	DNAH5	NM_001369	1	79	56	-	13770858	13771089
265310518	chr5	13769559	13769763	13769587	13769735	DNAH5	NM_001369	1	79	57	-	13769610	13769724
261999071	chr5	13768942	13769127	13768970	13769102	DNAH5	NM_001369	1	79	58	-	13769069	13769245
262051857	chr5	13769080	13769283	13769103	13769258	DNAH5	NM_001369	1	79	58	-	13769069	13769245
269051842	chr5	13766015	13766143	13766041	13766118	DNAH5	NM_001369	1	79	59	-	13766085	13766288
269062833	chr5	13766093	13766317	13766119	13766294	DNAH5	NM_001369	1	79	59	-	13766085	13766288

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268508956	chr5	13762704	13762917	13762726	13762891	DNAH5	NM_001369	1	79	60	-	13762831	13763010
268520586	chr5	13762871	13763062	13762892	13763034	DNAH5	NM_001369	1	79	60	-	13762831	13763010
264079402	chr5	13758898	13759120	13758919	13759097	DNAH5	NM_001369	1	79	61	-	13758955	13759092
267459045	chr5	13754253	13754382	13754278	13754357	DNAH5	NM_001369	1	79	62	-	13754312	13754447
267463422	chr5	13754336	13754504	13754358	13754476	DNAH5	NM_001369	1	79	62	-	13754312	13754447
268416167	chr5	13753204	13753425	13753226	13753398	DNAH5	NM_001369	1	79	63	-	13753342	13753658
268425768	chr5	13753377	13753584	13753399	13753562	DNAH5	NM_001369	1	79	63	-	13753342	13753658
268438055	chr5	13753541	13753711	13753563	13753683	DNAH5	NM_001369	1	79	63	-	13753342	13753658
269221256	chr5	13752208	13752428	13752233	13752403	DNAH5	NM_001369	1	79	64	-	13752243	13752398
266897915	chr5	13751142	13751340	13751167	13751312	DNAH5	NM_001369	1	79	65	-	13751187	13751369
266929766	chr5	13751292	13751512	13751313	13751488	DNAH5	NM_001369	1	79	65	-	13751187	13751369
262355456	chr5	13737327	13737549	13737354	13737521	DNAH5	NM_001369	1	79	66	-	13737361	13737604
262386672	chr5	13737502	13737684	13737522	13737656	DNAH5	NM_001369	1	79	66	-	13737361	13737604
266573751	chr5	13735880	13736070	13735907	13736048	DNAH5	NM_001369	1	79	67	-	13735927	13736041
265700447	chr5	13735126	13735295	13735152	13735273	DNAH5	NM_001369	1	79	68	-	13735240	13735430
265721892	chr5	13735248	13735470	13735274	13735442	DNAH5	NM_001369	1	79	68	-	13735240	13735430
258783308	chr5	13729483	13729677	13729511	13729651	DNAH5	NM_001369	1	79	69	-	13729548	13729669
258803406	chr5	13729636	13729813	13729662	13729780	DNAH5	NM_001369	1	79	69	-	13729548	13729669
268762116	chr5	13727485	13727648	13727509	13727626	DNAH5	NM_001369	1	79	70	-	13727616	13727765
268765441	chr5	13727606	13727812	13727627	13727791	DNAH5	NM_001369	1	79	70	-	13727616	13727765
267795323	chr5	13721061	13721248	13721085	13721226	DNAH5	NM_001369	1	79	71	-	13721109	13721354
267806739	chr5	13721200	13721357	13721223	13721339	DNAH5	NM_001369	1	79	71	-	13721109	13721354
269299954	chr5	13718952	13719171	13718974	13719144	DNAH5	NM_001369	1	79	72	-	13718991	13719210
269318002	chr5	13719116	13719247	13719143	13719218	DNAH5	NM_001369	1	79	72	-	13718991	13719210
268101358	chr5	13717278	13717502	13717307	13717477	DNAH5	NM_001369	1	79	73	-	13717424	13717629
268110520	chr5	13717457	13717661	13717478	13717635	DNAH5	NM_001369	1	79	73	-	13717424	13717629
265756823	chr5	13716535	13716704	13716558	13716675	DNAH5	NM_001369	1	79	74	-	13716596	13716799
265769891	chr5	13716649	13716858	13716676	13716831	DNAH5	NM_001369	1	79	74	-	13716596	13716799
267906986	chr5	13714473	13714680	13714494	13714657	DNAH5	NM_001369	1	79	75	-	13714514	13714729
267914987	chr5	13714618	13714828	13714640	13714801	DNAH5	NM_001369	1	79	75	-	13714514	13714729
262980434	chr5	13708111	13708311	13708132	13708289	DNAH5	NM_001369	1	79	76	-	13708232	13708444
263033035	chr5	13708269	13708476	13708290	13708449	DNAH5	NM_001369	1	79	76	-	13708232	13708444
267617723	chr5	13701272	13701471	13701298	13701450	DNAH5	NM_001369	1	79	77	-	13701393	13701545
267625325	chr5	13701428	13701612	13701451	13701586	DNAH5	NM_001369	1	79	77	-	13701393	13701545
267686680	chr5	13700684	13700838	13700711	13700814	DNAH5	NM_001369	1	79	78	-	13700749	13700980
267708595	chr5	13700789	13701013	13700815	13700991	DNAH5	NM_001369	1	79	78	-	13700749	13700980
268704671	chr5	13691896	13692118	13691924	13692096	DNAH5	NM_001369	1	79	79	-	13690437	13692244
268714858	chr5	13692076	13692294	13692097	13692266	DNAH5	NM_001369	1	79	79	-	13690437	13692244
267654238	chr17	11501773	11501975	11501791	11501958	DNAH9	NM_001372	1	69	1	+	11501748	11502232
267654293	chr17	11501901	11502095	11501919	11502077	DNAH9	NM_001372	1	69	1	+	11501748	11502232
267654325	chr17	11502074	11502242	11502092	11502223	DNAH9	NM_001372	1	69	1	+	11501748	11502232

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267654719	chr17	11502200	11502366	11502218	11502346	DNAH9	NM_001372	1	69	1	+	11501748	11502232
264765877	chr17	11511331	11511520	11511353	11511500	DNAH9	NM_001372	1	69	2	+	11511446	11511642
264814045	chr17	11511481	11511687	11511501	11511663	DNAH9	NM_001372	1	69	2	+	11511446	11511642
262828421	chr17	11513643	11513785	11513665	11513761	DNAH9	NM_001372	1	69	3	+	11513713	11513871
262879486	chr17	11513739	11513937	11513762	11513909	DNAH9	NM_001372	1	69	3	+	11513713	11513871
264059829	chr17	11514903	11515127	11514927	11515102	DNAH9	NM_001372	1	69	4	+	11514967	11515097
269079316	chr17	11520697	11520883	11520719	11520863	DNAH9	NM_001372	1	69	5	+	11520728	11520939
269089200	chr17	11520842	11521018	11520863	11520994	DNAH9	NM_001372	1	69	5	+	11520728	11520939
268685036	chr17	11522780	11522983	11522804	11522958	DNAH9	NM_001372	1	69	6	+	11522865	11523098
268712801	chr17	11522936	11523155	11522959	11523133	DNAH9	NM_001372	1	69	6	+	11522865	11523098
257619571	chr17	11532712	11532869	11532737	11532845	DNAH9	NM_001372	1	69	7	+	11532734	11532901
257636957	chr17	11532819	11532984	11532846	11532956	DNAH9	NM_001372	1	69	7	+	11532734	11532901
268551549	chr17	11535850	11536063	11535875	11536043	DNAH9	NM_001372	1	69	8	+	11535904	11536020
263893649	chr17	11539921	11540144	11539945	11540117	DNAH9	NM_001372	1	69	9	+	11539951	11540101
267376054	chr17	11543532	11543730	11543553	11543707	DNAH9	NM_001372	1	69	10	+	11543587	11543701
268292919	chr17	11547873	11548092	11547894	11548070	DNAH9	NM_001372	1	69	11	+	11547948	11548016
266626127	chr17	11550355	11550567	11550378	11550541	DNAH9	NM_001372	1	69	12	+	11550389	11550515
267168002	chr17	11554308	11554514	11554331	11554487	DNAH9	NM_001372	1	69	13	+	11554386	11554641
267218024	chr17	11554465	11554677	11554488	11554651	DNAH9	NM_001372	1	69	13	+	11554386	11554641
268023150	chr17	11556000	11556210	11556027	11556181	DNAH9	NM_001372	1	69	14	+	11556078	11556319
268031531	chr17	11556154	11556353	11556182	11556332	DNAH9	NM_001372	1	69	14	+	11556078	11556319
269357488	chr17	11568096	11568319	11568124	11568291	DNAH9	NM_001372	1	69	15	+	11568150	11568285
261096879	chr17	11572258	11572467	11572281	11572442	DNAH9	NM_001372	1	69	16	+	11572381	11572577
261189785	chr17	11572421	11572644	11572443	11572623	DNAH9	NM_001372	1	69	16	+	11572381	11572577
268348058	chr17	11572621	11572821	11572642	11572801	DNAH9	NM_001372	1	69	17	+	11572687	11573111
268366243	chr17	11572781	11572976	11572802	11572950	DNAH9	NM_001372	1	69	17	+	11572687	11573111
268392165	chr17	11572925	11573141	11572951	11573116	DNAH9	NM_001372	1	69	17	+	11572687	11573111
266466791	chr17	11583003	11583193	11583031	11583168	DNAH9	NM_001372	1	69	18	+	11583074	11583296
266558051	chr17	11583147	11583369	11583169	11583342	DNAH9	NM_001372	1	69	18	+	11583074	11583296
268867629	chr17	11583885	11584090	11583907	11584066	DNAH9	NM_001372	1	69	19	+	11584040	11584206
268888446	chr17	11584042	11584251	11584067	11584227	DNAH9	NM_001372	1	69	19	+	11584040	11584206
258323046	chr17	11593409	11593624	11593433	11593601	DNAH9	NM_001372	1	69	20	+	11592883	11593753
258376698	chr17	11593578	11593799	11593602	11593771	DNAH9	NM_001372	1	69	20	+	11592883	11593753
258477665	chr17	11592790	11593014	11592819	11592990	DNAH9	NM_001372	1	69	20	+	11592883	11593753
258551994	chr17	11592967	11593191	11592991	11593169	DNAH9	NM_001372	1	69	20	+	11592883	11593753
258608470	chr17	11593150	11593340	11593170	11593318	DNAH9	NM_001372	1	69	20	+	11592883	11593753
258633276	chr17	11593253	11593458	11593275	11593432	DNAH9	NM_001372	1	69	20	+	11592883	11593753
267943376	chr17	11597147	11597370	11597170	11597342	DNAH9	NM_001372	1	69	21	+	11597185	11597315
264754404	chr17	11597575	11597798	11597602	11597775	DNAH9	NM_001372	1	69	22	+	11597638	11597764
267727189	chr17	11602881	11603093	11602904	11603072	DNAH9	NM_001372	1	69	23	+	11603048	11603200
267771204	chr17	11603049	11603272	11603073	11603244	DNAH9	NM_001372	1	69	23	+	11603048	11603200

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269378442	chr17	11604400	11604604	11604420	11604585	DNAH9	NM_001372	1	69	24	+	11604439	11604564
267354413	chr17	11607412	11607633	11607433	11607607	DNAH9	NM_001372	1	69	25	+	11607520	11607759
267369899	chr17	11607586	11607800	11607608	11607778	DNAH9	NM_001372	1	69	25	+	11607520	11607759
266502612	chr17	11608314	11608537	11608336	11608515	DNAH9	NM_001372	1	69	26	+	11608342	11608502
267960681	chr17	11622610	11622808	11622631	11622786	DNAH9	NM_001372	1	69	27	+	11622651	11622807
267969759	chr17	11622761	11622982	11622786	11622961	DNAH9	NM_001372	1	69	27	+	11622651	11622807
265108451	chr17	11631060	11631270	11631085	11631250	DNAH9	NM_001372	1	69	28	+	11631135	11631239
268585224	chr17	11642158	11642373	11642182	11642354	DNAH9	NM_001372	1	69	29	+	11642197	11642354
257720537	chr17	11645435	11645658	11645459	11645635	DNAH9	NM_001372	1	69	30	+	11645492	11645630
263886345	chr17	11648065	11648263	11648087	11648239	DNAH9	NM_001372	1	69	31	+	11648114	11648401
263911094	chr17	11648218	11648439	11648240	11648412	DNAH9	NM_001372	1	69	31	+	11648114	11648401
266641087	chr17	11650839	11651040	11650860	11651016	DNAH9	NM_001372	1	69	32	+	11650873	11651083
266665926	chr17	11650997	11651124	11651017	11651102	DNAH9	NM_001372	1	69	32	+	11650873	11651083
266793340	chr17	11656112	11656332	11656140	11656304	DNAH9	NM_001372	1	69	33	+	11656150	11656277
262405463	chr17	11659779	11659954	11659805	11659931	DNAH9	NM_001372	1	69	34	+	11659885	11659993
262443231	chr17	11659911	11660036	11659932	11660010	DNAH9	NM_001372	1	69	34	+	11659885	11659993
268908398	chr17	11660676	11660890	11660696	11660869	DNAH9	NM_001372	1	69	35	+	11660862	11661009
268923351	chr17	11660848	11661064	11660870	11661038	DNAH9	NM_001372	1	69	35	+	11660862	11661009
262550795	chr17	11666583	11666801	11666606	11666779	DNAH9	NM_001372	1	69	36	+	11666757	11666931
262627462	chr17	11666753	11666976	11666780	11666952	DNAH9	NM_001372	1	69	36	+	11666757	11666931
269279014	chr17	11671712	11671842	11671734	11671816	DNAH9	NM_001372	1	69	37	+	11671770	11671943
269289570	chr17	11671795	11671997	11671817	11671976	DNAH9	NM_001372	1	69	37	+	11671770	11671943
263763017	chr17	11672408	11672626	11672429	11672599	DNAH9	NM_001372	1	69	38	+	11672439	11672646
263775540	chr17	11672576	11672746	11672595	11672726	DNAH9	NM_001372	1	69	38	+	11672439	11672646
260055075	chr17	11684235	11684427	11684258	11684403	DNAH9	NM_001372	1	69	39	+	11684326	11684491
260129370	chr17	11684376	11684576	11684404	11684554	DNAH9	NM_001372	1	69	39	+	11684326	11684491
264767784	chr17	11686884	11687100	11686904	11687079	DNAH9	NM_001372	1	69	40	+	11686963	11687065
268144835	chr17	11687480	11687703	11687501	11687680	DNAH9	NM_001372	1	69	41	+	11687617	11687856
268161134	chr17	11687659	11687880	11687681	11687861	DNAH9	NM_001372	1	69	41	+	11687617	11687856
269264267	chr17	11696696	11696916	11696720	11696888	DNAH9	NM_001372	1	69	42	+	11696820	11696981
269283491	chr17	11696861	11697084	11696889	11697058	DNAH9	NM_001372	1	69	42	+	11696820	11696981
258760538	chr17	11700771	11700985	11700793	11700962	DNAH9	NM_001372	1	69	43	+	11700914	11701110
258830446	chr17	11700941	11701165	11700963	11701142	DNAH9	NM_001372	1	69	43	+	11700914	11701110
267114788	chr17	11710966	11711184	11710987	11711163	DNAH9	NM_001372	1	69	44	+	11711049	11711211
267167133	chr17	11711141	11711275	11711164	11711254	DNAH9	NM_001372	1	69	44	+	11711049	11711211
265335330	chr17	11713491	11713713	11713518	11713691	DNAH9	NM_001372	1	69	45	+	11713563	11713686
268036451	chr17	11725207	11725430	11725228	11725407	DNAH9	NM_001372	1	69	46	+	11725237	11725379
264997516	chr17	11725727	11725950	11725747	11725923	DNAH9	NM_001372	1	69	47	+	11725755	11725916
267789423	chr17	11726055	11726258	11726076	11726232	DNAH9	NM_001372	1	69	48	+	11726118	11726351
267817859	chr17	11726208	11726431	11726233	11726409	DNAH9	NM_001372	1	69	48	+	11726118	11726351
266789389	chr17	11737904	11738086	11737925	11738064	DNAH9	NM_001372	1	69	49	+	11737955	11738215

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266868044	chr17	11738042	11738253	11738065	11738232	DNAH9	NM_001372	1	69	49	+	11737955	11738215
268343847	chr17	11757281	11757480	11757304	11757459	DNAH9	NM_001372	1	69	50	+	11757320	11757745
268362473	chr17	11757436	11757658	11757457	11757630	DNAH9	NM_001372	1	69	50	+	11757320	11757745
268379754	chr17	11757607	11757791	11757631	11757771	DNAH9	NM_001372	1	69	50	+	11757320	11757745
260495790	chr17	11772396	11772611	11772418	11772585	DNAH9	NM_001372	1	69	51	+	11772451	11772570
268161794	chr17	11774808	11775031	11774828	11775003	DNAH9	NM_001372	1	69	52	+	11774915	11775103
268192262	chr17	11774977	11775193	11775004	11775171	DNAH9	NM_001372	1	69	52	+	11774915	11775103
258201049	chr17	11778181	11778405	11778207	11778383	DNAH9	NM_001372	1	69	53	+	11778266	11778501
258240571	chr17	11778364	11778530	11778384	11778508	DNAH9	NM_001372	1	69	53	+	11778266	11778501
265373990	chr17	11783358	11783580	11783381	11783557	DNAH9	NM_001372	1	69	54	+	11783395	11783517
268310788	chr17	11784405	11784604	11784431	11784583	DNAH9	NM_001372	1	69	55	+	11784526	11784730
268316261	chr17	11784559	11784782	11784580	11784760	DNAH9	NM_001372	1	69	55	+	11784526	11784730
267287487	chr17	11786872	11787096	11786894	11787076	DNAH9	NM_001372	1	69	56	+	11786903	11787067
261042748	chr17	11790097	11790310	11790117	11790287	DNAH9	NM_001372	1	69	57	+	11790142	11790282
267317736	chr17	11795005	11795199	11795033	11795175	DNAH9	NM_001372	1	69	58	+	11795094	11795264
267339142	chr17	11795156	11795319	11795176	11795292	DNAH9	NM_001372	1	69	58	+	11795094	11795264
264881581	chr17	11797634	11797856	11797659	11797832	DNAH9	NM_001372	1	69	59	+	11797691	11797813
267688227	chr17	11805972	11806117	11805996	11806093	DNAH9	NM_001372	1	69	60	+	11806036	11806229
267702329	chr17	11806072	11806291	11806094	11806271	DNAH9	NM_001372	1	69	60	+	11806036	11806229
265764716	chr17	11808798	11809018	11808819	11808994	DNAH9	NM_001372	1	69	61	+	11808978	11809126
265784843	chr17	11808969	11809188	11808995	11809166	DNAH9	NM_001372	1	69	61	+	11808978	11809126
260854576	chr17	11827092	11827308	11827119	11827282	DNAH9	NM_001372	1	69	62	+	11827131	11827258
265639084	chr17	11833127	11833349	11833150	11833323	DNAH9	NM_001372	1	69	63	+	11833183	11833410
265649310	chr17	11833263	11833470	11833284	11833448	DNAH9	NM_001372	1	69	63	+	11833183	11833410
261165271	chr17	11835272	11835476	11835293	11835453	DNAH9	NM_001372	1	69	64	+	11835331	11835522
261267734	chr17	11835432	11835602	11835454	11835576	DNAH9	NM_001372	1	69	64	+	11835331	11835522
267489746	chr17	11837145	11837274	11837166	11837250	DNAH9	NM_001372	1	69	65	+	11837197	11837388
267511526	chr17	11837227	11837422	11837251	11837400	DNAH9	NM_001372	1	69	65	+	11837197	11837388
263994616	chr17	11840557	11840768	11840578	11840745	DNAH9	NM_001372	1	69	66	+	11840669	11840839
264018136	chr17	11840725	11840908	11840746	11840883	DNAH9	NM_001372	1	69	66	+	11840669	11840839
259125465	chr17	11845458	11845661	11845479	11845640	DNAH9	NM_001372	1	69	67	+	11845620	11845802
259195417	chr17	11845619	11845831	11845641	11845810	DNAH9	NM_001372	1	69	67	+	11845620	11845802
264710446	chr17	11865121	11865341	11865142	11865317	DNAH9	NM_001372	1	69	68	+	11865184	11865573
264754214	chr17	11865297	11865512	11865318	11865484	DNAH9	NM_001372	1	69	68	+	11865184	11865573
264803239	chr17	11865464	11865607	11865485	11865585	DNAH9	NM_001372	1	69	68	+	11865184	11865573
264826262	chr17	11872567	11872754	11872588	11872734	DNAH9	NM_001372	1	69	69	+	11872617	11873065
264885042	chr17	11872712	11872930	11872735	11872910	DNAH9	NM_001372	1	69	69	+	11872617	11873065
267287487	chr17	11786872	11787096	11786894	11787076	DNAH9	NM_004662	2	15	2	+	11786903	11787067
261042748	chr17	11790097	11790310	11790117	11790287	DNAH9	NM_004662	2	15	3	+	11790142	11790282
267317736	chr17	11795005	11795199	11795033	11795175	DNAH9	NM_004662	2	15	4	+	11795094	11795264
267339142	chr17	11795156	11795319	11795176	11795292	DNAH9	NM_004662	2	15	4	+	11795094	11795264

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264881581	chr17	11797634	11797856	11797659	11797832	DNAH9	NM_004662	2	15	5	+	11797691	11797813
267688227	chr17	11805972	11806117	11805996	11806093	DNAH9	NM_004662	2	15	6	+	11806036	11806229
267702329	chr17	11806072	11806291	11806094	11806271	DNAH9	NM_004662	2	15	6	+	11806036	11806229
265764716	chr17	11808798	11809018	11808819	11808994	DNAH9	NM_004662	2	15	7	+	11808978	11809126
265784843	chr17	11808969	11809188	11808995	11809166	DNAH9	NM_004662	2	15	7	+	11808978	11809126
260854576	chr17	11827092	11827308	11827119	11827282	DNAH9	NM_004662	2	15	8	+	11827131	11827258
265639084	chr17	11833127	11833349	11833150	11833323	DNAH9	NM_004662	2	15	9	+	11833183	11833410
265649310	chr17	11833263	11833470	11833284	11833448	DNAH9	NM_004662	2	15	9	+	11833183	11833410
261165271	chr17	11835272	11835476	11835293	11835453	DNAH9	NM_004662	2	15	10	+	11835331	11835522
261267734	chr17	11835432	11835602	11835454	11835576	DNAH9	NM_004662	2	15	10	+	11835331	11835522
267489746	chr17	11837145	11837274	11837166	11837250	DNAH9	NM_004662	2	15	11	+	11837197	11837388
267511526	chr17	11837227	11837422	11837251	11837400	DNAH9	NM_004662	2	15	11	+	11837197	11837388
263994616	chr17	11840557	11840768	11840578	11840745	DNAH9	NM_004662	2	15	12	+	11840669	11840839
264018136	chr17	11840725	11840908	11840746	11840883	DNAH9	NM_004662	2	15	12	+	11840669	11840839
259125465	chr17	11845458	11845661	11845479	11845640	DNAH9	NM_004662	2	15	13	+	11845620	11845802
259195417	chr17	11845619	11845831	11845641	11845810	DNAH9	NM_004662	2	15	13	+	11845620	11845802
264710446	chr17	11865121	11865341	11865142	11865317	DNAH9	NM_004662	2	15	14	+	11865184	11865573
264754214	chr17	11865297	11865512	11865318	11865484	DNAH9	NM_004662	2	15	14	+	11865184	11865573
264803239	chr17	11865464	11865607	11865485	11865585	DNAH9	NM_004662	2	15	14	+	11865184	11865573
264826262	chr17	11872567	11872754	11872588	11872734	DNAH9	NM_004662	2	15	15	+	11872617	11873065
264885042	chr17	11872712	11872930	11872735	11872910	DNAH9	NM_004662	2	15	15	+	11872617	11873065
263347778	chr9	34458862	34459079	34458882	34459057	DNAI1	NM_012144	1	20	1	+	34458811	34459051
258292933	chr9	34483362	34483515	34483383	34483492	DNAI1	NM_012144	1	20	2	+	34483446	34483478
261533809	chr9	34485074	34485291	34485096	34485267	DNAI1	NM_012144	1	20	3	+	34485140	34485238
267633801	chr9	34485344	34485567	34485367	34485541	DNAI1	NM_012144	1	20	4	+	34485435	34485515
257942956	chr9	34489263	34489483	34489289	34489462	DNAI1	NM_012144	1	20	5	+	34489321	34489447
268714192	chr9	34489962	34490171	34489983	34490149	DNAI1	NM_012144	1	20	6	+	34490010	34490122
261262640	chr9	34490310	34490531	34490333	34490510	DNAI1	NM_012144	1	20	7	+	34490367	34490486
268827396	chr9	34491374	34491594	34491396	34491572	DNAI1	NM_012144	1	20	8	+	34491493	34491552
266833813	chr9	34493134	34493354	34493157	34493331	DNAI1	NM_012144	1	20	9	+	34493192	34493326
261482126	chr9	34497008	34497227	34497029	34497202	DNAI1	NM_012144	1	20	10	+	34497113	34497197
264563000	chr9	34500668	34500891	34500689	34500871	DNAI1	NM_012144	1	20	11	+	34500720	34500837
257292450	chr9	34501014	34501198	34501035	34501171	DNAI1	NM_012144	1	20	12	+	34501136	34501179
268724089	chr9	34506496	34506706	34506519	34506683	DNAI1	NM_012144	1	20	13	+	34506625	34506872
268727811	chr9	34506656	34506859	34506677	34506838	DNAI1	NM_012144	1	20	13	+	34506625	34506872
268741840	chr9	34506783	34507002	34506807	34506981	DNAI1	NM_012144	1	20	13	+	34506625	34506872
259115483	chr9	34512047	34512224	34512069	34512201	DNAI1	NM_012144	1	20	14	+	34512107	34512196
268808740	chr9	34512272	34512480	34512292	34512460	DNAI1	NM_012144	1	20	15	+	34512335	34512422
265809866	chr9	34513025	34513234	34513046	34513212	DNAI1	NM_012144	1	20	16	+	34513110	34513189
262449111	chr9	34514275	34514496	34514295	34514474	DNAI1	NM_012144	1	20	17	+	34514392	34514540
262515071	chr9	34514453	34514671	34514475	34514647	DNAI1	NM_012144	1	20	17	+	34514392	34514540

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262515071	chr9	34514453	34514671	34514475	34514647	DNAI1	NM_012144	1	20	18	+	34514638	34514737
264532244	chr9	34514579	34514773	34514598	34514750	DNAI1	NM_012144	1	20	18	+	34514638	34514737
267718983	chr9	34517161	34517329	34517182	34517307	DNAI1	NM_012144	1	20	19	+	34517283	34517465
267728148	chr9	34517283	34517505	34517308	34517484	DNAI1	NM_012144	1	20	19	+	34517283	34517465
268974256	chr9	34520616	34520789	34520638	34520767	DNAI1	NM_012144	1	20	20	+	34520656	34520982
267986228	chr17	72277841	72278063	72277862	72278043	DNAI2	NM_001172810	1	14	2	+	72277949	72278139
267991337	chr17	72278025	72278242	72278044	72278221	DNAI2	NM_001172810	1	14	2	+	72277949	72278139
265908185	chr17	72281122	72281319	72281143	72281291	DNAI2	NM_001172810	1	14	3	+	72281179	72281340
265910699	chr17	72281271	72281450	72281292	72281430	DNAI2	NM_001172810	1	14	3	+	72281179	72281340
258377128	chr17	72283060	72283264	72283083	72283244	DNAI2	NM_001172810	1	14	4	+	72283116	72283237
268751366	chr17	72285689	72285869	72285710	72285847	DNAI2	NM_001172810	1	14	5	+	72285733	72285875
268755742	chr17	72285805	72286027	72285829	72286005	DNAI2	NM_001172810	1	14	5	+	72285733	72285875
269436192	chr17	72287090	72287291	72287112	72287271	DNAI2	NM_001172810	1	14	6	+	72287159	72287272
264411200	chr17	72295821	72296032	72295844	72296011	DNAI2	NM_001172810	1	14	7	+	72295857	72295996
257906818	chr17	72297137	72297354	72297157	72297334	DNAI2	NM_001172810	1	14	8	+	72297185	72297307
268167968	chr17	72301292	72301511	72301313	72301489	DNAI2	NM_001172810	1	14	9	+	72301358	72301581
268185726	chr17	72301468	72301677	72301489	72301657	DNAI2	NM_001172810	1	14	9	+	72301358	72301581
261120133	chr17	72305352	72305565	72305373	72305545	DNAI2	NM_001172810	1	14	10	+	72305392	72305527
258611089	chr17	72306084	72306303	72306106	72306281	DNAI2	NM_001172810	1	14	11	+	72306192	72306302
258635441	chr17	72306260	72306385	72306282	72306360	DNAI2	NM_001172810	1	14	11	+	72306192	72306302
265909561	chr17	72308001	72308225	72308022	72308206	DNAI2	NM_001172810	1	14	12	+	72308142	72308369
265913086	chr17	72308190	72308378	72308207	72308361	DNAI2	NM_001172810	1	14	12	+	72308142	72308369
265916962	chr17	72308340	72308554	72308360	72308532	DNAI2	NM_001172810	1	14	12	+	72308142	72308369
262108782	chr17	72310214	72310418	72310235	72310396	DNAI2	NM_001172810	1	14	13	+	72310260	72310410
267986228	chr17	72277841	72278063	72277862	72278043	DNAI2	NM_023036	2	14	2	+	72277946	72278139
267991337	chr17	72278025	72278242	72278044	72278221	DNAI2	NM_023036	2	14	2	+	72277946	72278139
265908185	chr17	72281122	72281319	72281143	72281291	DNAI2	NM_023036	2	14	3	+	72281179	72281340
265910699	chr17	72281271	72281450	72281292	72281430	DNAI2	NM_023036	2	14	3	+	72281179	72281340
258377128	chr17	72283060	72283264	72283083	72283244	DNAI2	NM_023036	2	14	4	+	72283116	72283237
268751366	chr17	72285689	72285869	72285710	72285847	DNAI2	NM_023036	2	14	5	+	72285733	72285875
268755742	chr17	72285805	72286027	72285829	72286005	DNAI2	NM_023036	2	14	5	+	72285733	72285875
269436192	chr17	72287090	72287291	72287112	72287271	DNAI2	NM_023036	2	14	6	+	72287159	72287272
264411200	chr17	72295821	72296032	72295844	72296011	DNAI2	NM_023036	2	14	7	+	72295857	72295996
257906818	chr17	72297137	72297354	72297157	72297334	DNAI2	NM_023036	2	14	8	+	72297185	72297307
268167968	chr17	72301292	72301511	72301313	72301489	DNAI2	NM_023036	2	14	9	+	72301358	72301581
268185726	chr17	72301468	72301677	72301489	72301657	DNAI2	NM_023036	2	14	9	+	72301358	72301581
261120133	chr17	72305352	72305565	72305373	72305545	DNAI2	NM_023036	2	14	10	+	72305392	72305527
258611089	chr17	72306084	72306303	72306106	72306281	DNAI2	NM_023036	2	14	11	+	72306156	72306302
258635441	chr17	72306260	72306385	72306282	72306360	DNAI2	NM_023036	2	14	11	+	72306156	72306302
265909561	chr17	72308001	72308225	72308022	72308206	DNAI2	NM_023036	2	14	12	+	72308142	72308369
265913086	chr17	72308190	72308378	72308207	72308361	DNAI2	NM_023036	2	14	12	+	72308142	72308369

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265916962	chr17	72308340	72308554	72308360	72308532	DNAI2	NM_023036	2	14	12	+	72308142	72308369
262108782	chr17	72310214	72310418	72310235	72310396	DNAI2	NM_023036	2	14	13	+	72310260	72310410
262387186	chr19	10828850	10828992	10828867	10828974	DNM2	NM_001005360	1	21	1	+	10828729	10829079
262389686	chr19	10828945	10829080	10828965	10829062	DNM2	NM_001005360	1	21	1	+	10828729	10829079
262390017	chr19	10829050	10829255	10829068	10829238	DNM2	NM_001005360	1	21	1	+	10828729	10829079
269303842	chr19	10870308	10870528	10870328	10870507	DNM2	NM_001005360	1	21	2	+	10870414	10870487
269312004	chr19	10883124	10883348	10883149	10883327	DNM2	NM_001005360	1	21	3	+	10883155	10883304
268076884	chr19	10886282	10886483	10886302	10886460	DNM2	NM_001005360	1	21	4	+	10886379	10886582
268087477	chr19	10886438	10886662	10886461	10886640	DNM2	NM_001005360	1	21	4	+	10886379	10886582
266682354	chr19	10887759	10887949	10887777	10887925	DNM2	NM_001005360	1	21	5	+	10887794	10887892
266020640	chr19	10893483	10893679	10893507	10893658	DNM2	NM_001005360	1	21	6	+	10893636	10893796
266032291	chr19	10893636	10893824	10893656	10893804	DNM2	NM_001005360	1	21	6	+	10893636	10893796
265454894	chr19	10897176	10897342	10897196	10897317	DNM2	NM_001005360	1	21	7	+	10897240	10897382
265477332	chr19	10897273	10897479	10897295	10897459	DNM2	NM_001005360	1	21	7	+	10897240	10897382
267842940	chr19	10904311	10904533	10904333	10904512	DNM2	NM_001005360	1	21	8	+	10904396	10904531
267853769	chr19	10904494	10904635	10904513	10904610	DNM2	NM_001005360	1	21	8	+	10904396	10904531
264177937	chr19	10905965	10906143	10905986	10906123	DNM2	NM_001005360	1	21	9	+	10906048	10906115
263131618	chr19	10906616	10906802	10906637	10906782	DNM2	NM_001005360	1	21	10	+	10906737	10906875
263204557	chr19	10906762	10906917	10906783	10906895	DNM2	NM_001005360	1	21	10	+	10906737	10906875
257603185	chr19	10909046	10909258	10909067	10909239	DNM2	NM_001005360	1	21	11	+	10909162	10909248
265055473	chr19	10912882	10913062	10912903	10913039	DNM2	NM_001005360	1	21	12	+	10912964	10913034
259627294	chr19	10916549	10916709	10916569	10916686	DNM2	NM_001005360	1	21	13	+	10916592	10916643
266588928	chr19	10919207	10919392	10919231	10919366	DNM2	NM_001005360	1	21	14	+	10919245	10919256
267996543	chr19	10922902	10923049	10922922	10923026	DNM2	NM_001005360	1	21	15	+	10922940	10923053
268001170	chr19	10922999	10923189	10923021	10923169	DNM2	NM_001005360	1	21	15	+	10922940	10923053
269056446	chr19	10930601	10930823	10930622	10930801	DNM2	NM_001005360	1	21	16	+	10930656	10930765
262073382	chr19	10934419	10934643	10934438	10934625	DNM2	NM_001005360	1	21	17	+	10934464	10934575
267404692	chr19	10935632	10935836	10935655	10935816	DNM2	NM_001005360	1	21	18	+	10935733	10935897
267410308	chr19	10935796	10935935	10935816	10935910	DNM2	NM_001005360	1	21	18	+	10935733	10935897
267820329	chr19	10939670	10939876	10939691	10939855	DNM2	NM_001005360	1	21	19	+	10939712	10939944
267822532	chr19	10939837	10939983	10939856	10939964	DNM2	NM_001005360	1	21	19	+	10939712	10939944
263327687	chr19	10940774	10940991	10940795	10940970	DNM2	NM_001005360	1	21	20	+	10940803	10941054
263334051	chr19	10940952	10941157	10940970	10941140	DNM2	NM_001005360	1	21	20	+	10940803	10941054
268022486	chr19	10941622	10941790	10941643	10941770	DNM2	NM_001005360	1	21	21	+	10941654	10942586
262387186	chr19	10828850	10828992	10828867	10828974	DNM2	NM_001005361	2	21	1	+	10828729	10829079
262389686	chr19	10828945	10829080	10828965	10829062	DNM2	NM_001005361	2	21	1	+	10828729	10829079
262390017	chr19	10829050	10829255	10829068	10829238	DNM2	NM_001005361	2	21	1	+	10828729	10829079
269303842	chr19	10870308	10870528	10870328	10870507	DNM2	NM_001005361	2	21	2	+	10870414	10870487
269312004	chr19	10883124	10883348	10883149	10883327	DNM2	NM_001005361	2	21	3	+	10883155	10883304
268076884	chr19	10886282	10886483	10886302	10886460	DNM2	NM_001005361	2	21	4	+	10886379	10886582
268087477	chr19	10886438	10886662	10886461	10886640	DNM2	NM_001005361	2	21	4	+	10886379	10886582

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266682354	chr19	10887759	10887949	10887777	10887925	DNM2	NM_001005361	2	21	5	+	10887794	10887892
266020640	chr19	10893483	10893679	10893507	10893658	DNM2	NM_001005361	2	21	6	+	10893636	10893796
266032291	chr19	10893636	10893824	10893656	10893804	DNM2	NM_001005361	2	21	6	+	10893636	10893796
265454894	chr19	10897176	10897342	10897196	10897317	DNM2	NM_001005361	2	21	7	+	10897240	10897382
265477332	chr19	10897273	10897479	10897295	10897459	DNM2	NM_001005361	2	21	7	+	10897240	10897382
267842940	chr19	10904311	10904533	10904333	10904512	DNM2	NM_001005361	2	21	8	+	10904396	10904531
267853769	chr19	10904494	10904635	10904513	10904610	DNM2	NM_001005361	2	21	8	+	10904396	10904531
264177937	chr19	10905965	10906143	10905986	10906123	DNM2	NM_001005361	2	21	9	+	10906048	10906115
268042098	chr19	10908006	10908227	10908027	10908202	DNM2	NM_001005361	2	21	10	+	10908056	10908194
257603185	chr19	10909046	10909258	10909067	10909239	DNM2	NM_001005361	2	21	11	+	10909162	10909248
265055473	chr19	10912882	10913062	10912903	10913039	DNM2	NM_001005361	2	21	12	+	10912964	10913034
259627294	chr19	10916549	10916709	10916569	10916686	DNM2	NM_001005361	2	21	13	+	10916592	10916643
266588928	chr19	10919207	10919392	10919231	10919366	DNM2	NM_001005361	2	21	14	+	10919245	10919256
267996543	chr19	10922902	10923049	10922922	10923026	DNM2	NM_001005361	2	21	15	+	10922940	10923053
268001170	chr19	10922999	10923189	10923021	10923169	DNM2	NM_001005361	2	21	15	+	10922940	10923053
269056446	chr19	10930601	10930823	10930622	10930801	DNM2	NM_001005361	2	21	16	+	10930656	10930765
262073382	chr19	10934419	10934643	10934438	10934625	DNM2	NM_001005361	2	21	17	+	10934464	10934575
267404692	chr19	10935632	10935836	10935655	10935816	DNM2	NM_001005361	2	21	18	+	10935733	10935897
267410308	chr19	10935796	10935935	10935816	10935910	DNM2	NM_001005361	2	21	18	+	10935733	10935897
267820329	chr19	10939670	10939876	10939691	10939855	DNM2	NM_001005361	2	21	19	+	10939712	10939944
267822532	chr19	10939837	10939983	10939856	10939964	DNM2	NM_001005361	2	21	19	+	10939712	10939944
263327687	chr19	10940774	10940991	10940795	10940970	DNM2	NM_001005361	2	21	20	+	10940803	10941054
263334051	chr19	10940952	10941157	10940970	10941140	DNM2	NM_001005361	2	21	20	+	10940803	10941054
268022486	chr19	10941622	10941790	10941643	10941770	DNM2	NM_001005361	2	21	21	+	10941654	10942586
262387186	chr19	10828850	10828992	10828867	10828974	DNM2	NM_001005362	3	20	1	+	10828729	10829079
262389686	chr19	10828945	10829080	10828965	10829062	DNM2	NM_001005362	3	20	1	+	10828729	10829079
262390017	chr19	10829050	10829255	10829068	10829238	DNM2	NM_001005362	3	20	1	+	10828729	10829079
269303842	chr19	10870308	10870528	10870328	10870507	DNM2	NM_001005362	3	20	2	+	10870414	10870487
269312004	chr19	10883124	10883348	10883149	10883327	DNM2	NM_001005362	3	20	3	+	10883155	10883304
268076884	chr19	10886282	10886483	10886302	10886460	DNM2	NM_001005362	3	20	4	+	10886379	10886582
268087477	chr19	10886438	10886662	10886461	10886640	DNM2	NM_001005362	3	20	4	+	10886379	10886582
266682354	chr19	10887759	10887949	10887777	10887925	DNM2	NM_001005362	3	20	5	+	10887794	10887892
266020640	chr19	10893483	10893679	10893507	10893658	DNM2	NM_001005362	3	20	6	+	10893636	10893796
266032291	chr19	10893636	10893824	10893656	10893804	DNM2	NM_001005362	3	20	6	+	10893636	10893796
265454894	chr19	10897176	10897342	10897196	10897317	DNM2	NM_001005362	3	20	7	+	10897240	10897382
265477332	chr19	10897273	10897479	10897295	10897459	DNM2	NM_001005362	3	20	7	+	10897240	10897382
267842940	chr19	10904311	10904533	10904333	10904512	DNM2	NM_001005362	3	20	8	+	10904396	10904531
267853769	chr19	10904494	10904635	10904513	10904610	DNM2	NM_001005362	3	20	8	+	10904396	10904531
264177937	chr19	10905965	10906143	10905986	10906123	DNM2	NM_001005362	3	20	9	+	10906048	10906115
268042098	chr19	10908006	10908227	10908027	10908202	DNM2	NM_001005362	3	20	10	+	10908056	10908194
257603185	chr19	10909046	10909258	10909067	10909239	DNM2	NM_001005362	3	20	11	+	10909162	10909248

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265055473	chr19	10912882	10913062	10912903	10913039	DNM2	NM_001005362	3	20	12	+	10912964	10913034
259627294	chr19	10916549	10916709	10916569	10916686	DNM2	NM_001005362	3	20	13	+	10916592	10916643
267996543	chr19	10922902	10923049	10922922	10923026	DNM2	NM_001005362	3	20	14	+	10922940	10923053
268001170	chr19	10922999	10923189	10923021	10923169	DNM2	NM_001005362	3	20	14	+	10922940	10923053
269056446	chr19	10930601	10930823	10930622	10930801	DNM2	NM_001005362	3	20	15	+	10930656	10930765
262073382	chr19	10934419	10934643	10934438	10934625	DNM2	NM_001005362	3	20	16	+	10934464	10934575
267404692	chr19	10935632	10935836	10935655	10935816	DNM2	NM_001005362	3	20	17	+	10935733	10935897
267410308	chr19	10935796	10935935	10935816	10935910	DNM2	NM_001005362	3	20	17	+	10935733	10935897
267820329	chr19	10939670	10939876	10939691	10939855	DNM2	NM_001005362	3	20	18	+	10939712	10939944
267822532	chr19	10939837	10939983	10939856	10939964	DNM2	NM_001005362	3	20	18	+	10939712	10939944
263327687	chr19	10940774	10940991	10940795	10940970	DNM2	NM_001005362	3	20	19	+	10940803	10941054
263334051	chr19	10940952	10941157	10940970	10941140	DNM2	NM_001005362	3	20	19	+	10940803	10941054
268022486	chr19	10941622	10941790	10941643	10941770	DNM2	NM_001005362	3	20	20	+	10941654	10942586
262387186	chr19	10828850	10828992	10828867	10828974	DNM2	NM_001190716	4	21	1	+	10828729	10829079
262389686	chr19	10828945	10829080	10828965	10829062	DNM2	NM_001190716	4	21	1	+	10828729	10829079
262390017	chr19	10829050	10829255	10829068	10829238	DNM2	NM_001190716	4	21	1	+	10828729	10829079
269303842	chr19	10870308	10870528	10870328	10870507	DNM2	NM_001190716	4	21	2	+	10870414	10870487
269312004	chr19	10883124	10883348	10883149	10883327	DNM2	NM_001190716	4	21	3	+	10883155	10883304
268076884	chr19	10886282	10886483	10886302	10886460	DNM2	NM_001190716	4	21	4	+	10886379	10886582
268087477	chr19	10886438	10886662	10886461	10886640	DNM2	NM_001190716	4	21	4	+	10886379	10886582
266682354	chr19	10887759	10887949	10887777	10887925	DNM2	NM_001190716	4	21	5	+	10887794	10887892
266020640	chr19	10893483	10893679	10893507	10893658	DNM2	NM_001190716	4	21	6	+	10893636	10893796
266032291	chr19	10893636	10893824	10893656	10893804	DNM2	NM_001190716	4	21	6	+	10893636	10893796
265454894	chr19	10897176	10897342	10897196	10897317	DNM2	NM_001190716	4	21	7	+	10897240	10897382
265477332	chr19	10897273	10897479	10897295	10897459	DNM2	NM_001190716	4	21	7	+	10897240	10897382
267842940	chr19	10904311	10904533	10904333	10904512	DNM2	NM_001190716	4	21	8	+	10904396	10904531
267853769	chr19	10904494	10904635	10904513	10904610	DNM2	NM_001190716	4	21	8	+	10904396	10904531
264177937	chr19	10905965	10906143	10905986	10906123	DNM2	NM_001190716	4	21	9	+	10906048	10906115
263131618	chr19	10906616	10906802	10906637	10906782	DNM2	NM_001190716	4	21	10	+	10906737	10906875
263204557	chr19	10906762	10906917	10906783	10906895	DNM2	NM_001190716	4	21	10	+	10906737	10906875
257603185	chr19	10909046	10909258	10909067	10909239	DNM2	NM_001190716	4	21	11	+	10909162	10909248
265055473	chr19	10912882	10913062	10912903	10913039	DNM2	NM_001190716	4	21	12	+	10912964	10913034
259627294	chr19	10916549	10916709	10916569	10916686	DNM2	NM_001190716	4	21	13	+	10916592	10916643
266588928	chr19	10919207	10919392	10919231	10919366	DNM2	NM_001190716	4	21	14	+	10919245	10919256
267996543	chr19	10922902	10923049	10922922	10923026	DNM2	NM_001190716	4	21	15	+	10922940	10923053
268001170	chr19	10922999	10923189	10923021	10923169	DNM2	NM_001190716	4	21	15	+	10922940	10923053
269056446	chr19	10930601	10930823	10930622	10930801	DNM2	NM_001190716	4	21	16	+	10930656	10930765
262073382	chr19	10934419	10934643	10934438	10934625	DNM2	NM_001190716	4	21	17	+	10934464	10934575
267404692	chr19	10935632	10935836	10935655	10935816	DNM2	NM_001190716	4	21	18	+	10935733	10935897
267410308	chr19	10935796	10935935	10935816	10935910	DNM2	NM_001190716	4	21	18	+	10935733	10935897
267820329	chr19	10939670	10939876	10939691	10939855	DNM2	NM_001190716	4	21	19	+	10939712	10939944

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267822532	chr19	10939837	10939983	10939856	10939964	DNM2	NM_001190716	4	21	19	+	10939712	10939944
263327687	chr19	10940774	10940991	10940795	10940970	DNM2	NM_001190716	4	21	20	+	10940803	10941054
263334051	chr19	10940952	10941157	10940970	10941140	DNM2	NM_001190716	4	21	20	+	10940803	10941054
268022486	chr19	10941622	10941790	10941643	10941770	DNM2	NM_001190716	4	21	21	+	10941657	10942586
262387186	chr19	10828850	10828992	10828867	10828974	DNM2	NM_004945	5	20	1	+	10828729	10829079
262389686	chr19	10828945	10829080	10828965	10829062	DNM2	NM_004945	5	20	1	+	10828729	10829079
262390017	chr19	10829050	10829255	10829068	10829238	DNM2	NM_004945	5	20	1	+	10828729	10829079
269303842	chr19	10870308	10870528	10870328	10870507	DNM2	NM_004945	5	20	2	+	10870414	10870487
269312004	chr19	10883124	10883348	10883149	10883327	DNM2	NM_004945	5	20	3	+	10883155	10883304
268076884	chr19	10886282	10886483	10886302	10886460	DNM2	NM_004945	5	20	4	+	10886379	10886582
268087477	chr19	10886438	10886662	10886461	10886640	DNM2	NM_004945	5	20	4	+	10886379	10886582
266682354	chr19	10887759	10887949	10887777	10887925	DNM2	NM_004945	5	20	5	+	10887794	10887892
266020640	chr19	10893483	10893679	10893507	10893658	DNM2	NM_004945	5	20	6	+	10893636	10893796
266032291	chr19	10893636	10893824	10893656	10893804	DNM2	NM_004945	5	20	6	+	10893636	10893796
265454894	chr19	10897176	10897342	10897196	10897317	DNM2	NM_004945	5	20	7	+	10897240	10897382
265477332	chr19	10897273	10897479	10897295	10897459	DNM2	NM_004945	5	20	7	+	10897240	10897382
267842940	chr19	10904311	10904533	10904333	10904512	DNM2	NM_004945	5	20	8	+	10904396	10904531
267853769	chr19	10904494	10904635	10904513	10904610	DNM2	NM_004945	5	20	8	+	10904396	10904531
264177937	chr19	10905965	10906143	10905986	10906123	DNM2	NM_004945	5	20	9	+	10906048	10906115
263131618	chr19	10906616	10906802	10906637	10906782	DNM2	NM_004945	5	20	10	+	10906737	10906875
263204557	chr19	10906762	10906917	10906783	10906895	DNM2	NM_004945	5	20	10	+	10906737	10906875
257603185	chr19	10909046	10909258	10909067	10909239	DNM2	NM_004945	5	20	11	+	10909162	10909248
265055473	chr19	10912882	10913062	10912903	10913039	DNM2	NM_004945	5	20	12	+	10912964	10913034
259627294	chr19	10916549	10916709	10916569	10916686	DNM2	NM_004945	5	20	13	+	10916592	10916643
267996543	chr19	10922902	10923049	10922922	10923026	DNM2	NM_004945	5	20	14	+	10922940	10923053
268001170	chr19	10922999	10923189	10923021	10923169	DNM2	NM_004945	5	20	14	+	10922940	10923053
269056446	chr19	10930601	10930823	10930622	10930801	DNM2	NM_004945	5	20	15	+	10930656	10930765
262073382	chr19	10934419	10934643	10934438	10934625	DNM2	NM_004945	5	20	16	+	10934464	10934575
267404692	chr19	10935632	10935836	10935655	10935816	DNM2	NM_004945	5	20	17	+	10935733	10935897
267410308	chr19	10935796	10935935	10935816	10935910	DNM2	NM_004945	5	20	17	+	10935733	10935897
267820329	chr19	10939670	10939876	10939691	10939855	DNM2	NM_004945	5	20	18	+	10939712	10939944
267822532	chr19	10939837	10939983	10939856	10939964	DNM2	NM_004945	5	20	18	+	10939712	10939944
263327687	chr19	10940774	10940991	10940795	10940970	DNM2	NM_004945	5	20	19	+	10940803	10941054
263334051	chr19	10940952	10941157	10940970	10941140	DNM2	NM_004945	5	20	19	+	10940803	10941054
268022486	chr19	10941622	10941790	10941643	10941770	DNM2	NM_004945	5	20	20	+	10941654	10942586
263906362	chr4	3465121	3465332	3465139	3465314	DOK7	NM_001164673	1	7	1	+	3465033	3465156
264490187	chr4	3465027	3465251	3465051	3465230	DOK7	NM_001164673	1	7	1	+	3465033	3465156
263906362	chr4	3465121	3465332	3465139	3465314	DOK7	NM_001164673	1	7	2	+	3465233	3465278
264379159	chr4	3474963	3475181	3474983	3475160	DOK7	NM_001164673	1	7	3	+	3475133	3475363
264395624	chr4	3475140	3475311	3475161	3475290	DOK7	NM_001164673	1	7	3	+	3475133	3475363
264404761	chr4	3475259	3475479	3475277	3475460	DOK7	NM_001164673	1	7	3	+	3475133	3475363

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262494870	chr4	3478062	3478209	3478080	3478190	DOK7	NM_001164673	1	7	4	+	3478069	3478258
262509004	chr4	3478137	3478292	3478159	3478270	DOK7	NM_001164673	1	7	4	+	3478069	3478258
263994324	chr4	3487162	3487345	3487182	3487326	DOK7	NM_001164673	1	7	5	+	3487266	3487385
263999876	chr4	3487305	3487529	3487327	3487505	DOK7	NM_001164673	1	7	5	+	3487266	3487385
258312972	chr4	3491374	3491581	3491395	3491561	DOK7	NM_001164673	1	7	6	+	3491404	3491523
261684542	chr4	3494441	3494613	3494459	3494594	DOK7	NM_001164673	1	7	7	+	3494486	3496209
261688681	chr4	3494568	3494773	3494588	3494753	DOK7	NM_001164673	1	7	7	+	3494486	3496209
261691232	chr4	3494736	3494943	3494754	3494923	DOK7	NM_001164673	1	7	7	+	3494486	3496209
261790486	chr4	3494895	3495026	3494913	3495009	DOK7	NM_001164673	1	7	7	+	3494486	3496209
261790619	chr4	3495033	3495216	3495050	3495193	DOK7	NM_001164673	1	7	7	+	3494486	3496209
261792051	chr4	3495172	3495325	3495194	3495305	DOK7	NM_001164673	1	7	7	+	3494486	3496209
263906362	chr4	3465121	3465332	3465139	3465314	DOK7	NM_173660	2	7	1	+	3465033	3465156
264490187	chr4	3465027	3465251	3465051	3465230	DOK7	NM_173660	2	7	1	+	3465033	3465156
263906362	chr4	3465121	3465332	3465139	3465314	DOK7	NM_173660	2	7	2	+	3465233	3465278
264379159	chr4	3474963	3475181	3474983	3475160	DOK7	NM_173660	2	7	3	+	3475133	3475363
264395624	chr4	3475140	3475311	3475161	3475290	DOK7	NM_173660	2	7	3	+	3475133	3475363
264404761	chr4	3475259	3475479	3475277	3475460	DOK7	NM_173660	2	7	3	+	3475133	3475363
262494870	chr4	3478062	3478209	3478080	3478190	DOK7	NM_173660	2	7	4	+	3478069	3478269
262509004	chr4	3478137	3478292	3478159	3478270	DOK7	NM_173660	2	7	4	+	3478069	3478269
263994324	chr4	3487162	3487345	3487182	3487326	DOK7	NM_173660	2	7	5	+	3487266	3487385
263999876	chr4	3487305	3487529	3487327	3487505	DOK7	NM_173660	2	7	5	+	3487266	3487385
258312972	chr4	3491374	3491581	3491395	3491561	DOK7	NM_173660	2	7	6	+	3491404	3491523
261684542	chr4	3494441	3494613	3494459	3494594	DOK7	NM_173660	2	7	7	+	3494486	3496209
261688681	chr4	3494568	3494773	3494588	3494753	DOK7	NM_173660	2	7	7	+	3494486	3496209
261691232	chr4	3494736	3494943	3494754	3494923	DOK7	NM_173660	2	7	7	+	3494486	3496209
261790486	chr4	3494895	3495026	3494913	3495009	DOK7	NM_173660	2	7	7	+	3494486	3496209
261790619	chr4	3495033	3495216	3495050	3495193	DOK7	NM_173660	2	7	7	+	3494486	3496209
261792051	chr4	3495172	3495325	3495194	3495305	DOK7	NM_173660	2	7	7	+	3494486	3496209
268674498	chr18	28681726	28681949	28681749	28681932	DSC2	NM_004949	1	17	1	-	28681866	28682388
268674906	chr18	28681891	28682114	28681908	28682096	DSC2	NM_004949	1	17	1	-	28681866	28682388
261634037	chr18	28671979	28672196	28672006	28672168	DSC2	NM_004949	1	17	3	-	28672064	28672263
261641452	chr18	28672134	28672345	28672162	28672324	DSC2	NM_004949	1	17	3	-	28672064	28672263
268033741	chr18	28670939	28671065	28670967	28671042	DSC2	NM_004949	1	17	4	-	28670991	28671110
268036194	chr18	28671017	28671201	28671043	28671177	DSC2	NM_004949	1	17	4	-	28670991	28671110
262972438	chr18	28669343	28669556	28669366	28669536	DSC2	NM_004949	1	17	5	-	28669402	28669557
262993052	chr18	28669522	28669742	28669548	28669717	DSC2	NM_004949	1	17	5	-	28669402	28669557
267128373	chr18	28667550	28667766	28667575	28667745	DSC2	NM_004949	1	17	6	-	28667632	28667776
267139048	chr18	28667724	28667867	28667746	28667838	DSC2	NM_004949	1	17	6	-	28667632	28667776
257676222	chr18	28666356	28666576	28666384	28666554	DSC2	NM_004949	1	17	7	-	28666539	28666705
257681391	chr18	28666527	28666655	28666555	28666635	DSC2	NM_004949	1	17	7	-	28666539	28666705
257701867	chr18	28666616	28666788	28666636	28666761	DSC2	NM_004949	1	17	7	-	28666539	28666705

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267625298	chr18	28662818	28662969	28662843	28662941	DSC2	NM_004949	1	17	8	-	28662892	28663026
267626400	chr18	28662912	28663068	28662940	28663040	DSC2	NM_004949	1	17	8	-	28662892	28663026
264122906	chr18	28662059	28662258	28662089	28662229	DSC2	NM_004949	1	17	9	-	28662204	28662389
264122952	chr18	28662208	28662345	28662235	28662318	DSC2	NM_004949	1	17	9	-	28662204	28662389
264127330	chr18	28662294	28662468	28662319	28662440	DSC2	NM_004949	1	17	9	-	28662204	28662389
268829414	chr18	28659923	28660113	28659945	28660085	DSC2	NM_004949	1	17	10	-	28660062	28660318
269365337	chr18	28660061	28660258	28660086	28660235	DSC2	NM_004949	1	17	10	-	28660062	28660318
269378440	chr18	28660215	28660427	28660236	28660399	DSC2	NM_004949	1	17	10	-	28660062	28660318
268820610	chr18	28659742	28659900	28659768	28659873	DSC2	NM_004949	1	17	11	-	28659813	28659955
268825367	chr18	28659849	28660073	28659874	28660045	DSC2	NM_004949	1	17	11	-	28659813	28659955
268829414	chr18	28659923	28660113	28659945	28660085	DSC2	NM_004949	1	17	11	-	28659813	28659955
260012382	chr18	28654539	28654762	28654561	28654742	DSC2	NM_004949	1	17	12	-	28654649	28654873
260095660	chr18	28654722	28654938	28654743	28654912	DSC2	NM_004949	1	17	12	-	28654649	28654873
268659277	chr18	28651564	28651695	28651590	28651671	DSC2	NM_004949	1	17	13	-	28651571	28651807
268668519	chr18	28651649	28651775	28651672	28651747	DSC2	NM_004949	1	17	13	-	28651571	28651807
268673006	chr18	28651721	28651923	28651748	28651895	DSC2	NM_004949	1	17	13	-	28651571	28651807
257886170	chr18	28650638	28650786	28650665	28650762	DSC2	NM_004949	1	17	14	-	28650692	28650816
257903698	chr18	28650737	28650946	28650763	28650921	DSC2	NM_004949	1	17	14	-	28650692	28650816
269321884	chr18	28648826	28648971	28648857	28648954	DSC2	NM_004949	1	17	15	-	28648860	28649117
269328734	chr18	28648903	28649106	28648925	28649085	DSC2	NM_004949	1	17	15	-	28648860	28649117
269338995	chr18	28649059	28649205	28649080	28649180	DSC2	NM_004949	1	17	15	-	28648860	28649117
264230730	chr18	28648091	28648311	28648112	28648286	DSC2	NM_004949	1	17	16	-	28648265	28648310
264231315	chr18	28648124	28648346	28648145	28648319	DSC2	NM_004949	1	17	16	-	28648265	28648310
264230730	chr18	28648091	28648311	28648112	28648286	DSC2	NM_004949	1	17	17	-	28645942	28648178
264231315	chr18	28648124	28648346	28648145	28648319	DSC2	NM_004949	1	17	17	-	28645942	28648178
269127557	chr18	28647948	28648139	28647970	28648112	DSC2	NM_004949	1	17	17	-	28645942	28648178
268674498	chr18	28681726	28681949	28681749	28681932	DSC2	NM_024422	2	16	1	-	28681866	28682388
268674906	chr18	28681891	28682114	28681908	28682096	DSC2	NM_024422	2	16	1	-	28681866	28682388
261634037	chr18	28671979	28672196	28672006	28672168	DSC2	NM_024422	2	16	3	-	28672064	28672263
261641452	chr18	28672134	28672345	28672162	28672324	DSC2	NM_024422	2	16	3	-	28672064	28672263
268033741	chr18	28670939	28671065	28670967	28671042	DSC2	NM_024422	2	16	4	-	28670991	28671110
268036194	chr18	28671017	28671201	28671043	28671177	DSC2	NM_024422	2	16	4	-	28670991	28671110
262972438	chr18	28669343	28669556	28669366	28669536	DSC2	NM_024422	2	16	5	-	28669402	28669557
262993052	chr18	28669522	28669742	28669548	28669717	DSC2	NM_024422	2	16	5	-	28669402	28669557
267128373	chr18	28667550	28667766	28667575	28667745	DSC2	NM_024422	2	16	6	-	28667632	28667776
267139048	chr18	28667724	28667867	28667746	28667838	DSC2	NM_024422	2	16	6	-	28667632	28667776
257676222	chr18	28666356	28666576	28666384	28666554	DSC2	NM_024422	2	16	7	-	28666539	28666705
257681391	chr18	28666527	28666655	28666555	28666635	DSC2	NM_024422	2	16	7	-	28666539	28666705
257701867	chr18	28666616	28666788	28666636	28666761	DSC2	NM_024422	2	16	7	-	28666539	28666705
267625298	chr18	28662818	28662969	28662843	28662941	DSC2	NM_024422	2	16	8	-	28662892	28663026
267626400	chr18	28662912	28663068	28662940	28663040	DSC2	NM_024422	2	16	8	-	28662892	28663026

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264122906	chr18	28662059	28662258	28662089	28662229	DSC2	NM_024422	2	16	9	-	28662204	28662389
264122952	chr18	28662208	28662345	28662235	28662318	DSC2	NM_024422	2	16	9	-	28662204	28662389
264127330	chr18	28662294	28662468	28662319	28662440	DSC2	NM_024422	2	16	9	-	28662204	28662389
268829414	chr18	28659923	28660113	28659945	28660085	DSC2	NM_024422	2	16	10	-	28660062	28660318
269365337	chr18	28660061	28660258	28660086	28660235	DSC2	NM_024422	2	16	10	-	28660062	28660318
269378440	chr18	28660215	28660427	28660236	28660399	DSC2	NM_024422	2	16	10	-	28660062	28660318
268820610	chr18	28659742	28659900	28659768	28659873	DSC2	NM_024422	2	16	11	-	28659813	28659955
268825367	chr18	28659849	28660073	28659874	28660045	DSC2	NM_024422	2	16	11	-	28659813	28659955
268829414	chr18	28659923	28660113	28659945	28660085	DSC2	NM_024422	2	16	11	-	28659813	28659955
260012382	chr18	28654539	28654762	28654561	28654742	DSC2	NM_024422	2	16	12	-	28654649	28654873
260095660	chr18	28654722	28654938	28654743	28654912	DSC2	NM_024422	2	16	12	-	28654649	28654873
268659277	chr18	28651564	28651695	28651590	28651671	DSC2	NM_024422	2	16	13	-	28651571	28651807
268668519	chr18	28651649	28651775	28651672	28651747	DSC2	NM_024422	2	16	13	-	28651571	28651807
268673006	chr18	28651721	28651923	28651748	28651895	DSC2	NM_024422	2	16	13	-	28651571	28651807
257886170	chr18	28650638	28650786	28650665	28650762	DSC2	NM_024422	2	16	14	-	28650692	28650816
257903698	chr18	28650737	28650946	28650763	28650921	DSC2	NM_024422	2	16	14	-	28650692	28650816
269321884	chr18	28648826	28648971	28648857	28648954	DSC2	NM_024422	2	16	15	-	28648860	28649117
269328734	chr18	28648903	28649106	28648925	28649085	DSC2	NM_024422	2	16	15	-	28648860	28649117
269338995	chr18	28649059	28649205	28649080	28649180	DSC2	NM_024422	2	16	15	-	28648860	28649117
264230730	chr18	28648091	28648311	28648112	28648286	DSC2	NM_024422	2	16	16	-	28645942	28648178
264231315	chr18	28648124	28648346	28648145	28648319	DSC2	NM_024422	2	16	16	-	28645942	28648178
269127557	chr18	28647948	28648139	28647970	28648112	DSC2	NM_024422	2	16	16	-	28645942	28648178
268256788	chr18	29078237	29078437	29078254	29078420	DSG2	NM_001943	1	15	1	+	29078027	29078259
266538691	chr18	29098117	29098277	29098146	29098251	DSG2	NM_001943	1	15	2	+	29098202	29098237
267710554	chr18	29099618	29099824	29099646	29099800	DSG2	NM_001943	1	15	3	+	29099766	29099900
267712073	chr18	29099774	29099954	29099801	29099926	DSG2	NM_001943	1	15	3	+	29099766	29099900
267348791	chr18	29100723	29100911	29100749	29100885	DSG2	NM_001943	1	15	4	+	29100766	29100927
267349216	chr18	29100864	29101074	29100893	29101046	DSG2	NM_001943	1	15	4	+	29100766	29100927
267349865	chr18	29100893	29101102	29100920	29101076	DSG2	NM_001943	1	15	4	+	29100766	29100927
267349865	chr18	29100893	29101102	29100920	29101076	DSG2	NM_001943	1	15	5	+	29101062	29101206
267891462	chr18	29101052	29101181	29101077	29101158	DSG2	NM_001943	1	15	5	+	29101062	29101206
267895025	chr18	29101133	29101338	29101159	29101309	DSG2	NM_001943	1	15	5	+	29101062	29101206
262067788	chr18	29102039	29102255	29102067	29102227	DSG2	NM_001943	1	15	6	+	29102046	29102212
268477582	chr18	29104487	29104711	29104515	29104683	DSG2	NM_001943	1	15	7	+	29104411	29104548
268792327	chr18	29104319	29104496	29104345	29104469	DSG2	NM_001943	1	15	7	+	29104411	29104548
268798278	chr18	29104445	29104667	29104470	29104640	DSG2	NM_001943	1	15	7	+	29104411	29104548
268477582	chr18	29104487	29104711	29104515	29104683	DSG2	NM_001943	1	15	8	+	29104666	29104851
268480520	chr18	29104662	29104882	29104684	29104856	DSG2	NM_001943	1	15	8	+	29104666	29104851
266305307	chr18	29110810	29111029	29110835	29111002	DSG2	NM_001943	1	15	9	+	29110950	29111215
266308808	chr18	29110975	29111155	29111003	29111131	DSG2	NM_001943	1	15	9	+	29110950	29111215
266314847	chr18	29111106	29111316	29111132	29111289	DSG2	NM_001943	1	15	9	+	29110950	29111215

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268767340	chr18	29115156	29115356	29115184	29115328	DSG2	NM_001943	1	15	10	+	29115233	29115375
268769926	chr18	29115267	29115483	29115294	29115459	DSG2	NM_001943	1	15	10	+	29115233	29115375
269313953	chr18	29116063	29116228	29116089	29116202	DSG2	NM_001943	1	15	11	+	29116165	29116392
269326883	chr18	29116180	29116354	29116203	29116331	DSG2	NM_001943	1	15	11	+	29116165	29116392
269338777	chr18	29116311	29116528	29116332	29116500	DSG2	NM_001943	1	15	11	+	29116165	29116392
265250473	chr18	29118643	29118830	29118669	29118808	DSG2	NM_001943	1	15	12	+	29118714	29118941
265279817	chr18	29118783	29118971	29118809	29118946	DSG2	NM_001943	1	15	12	+	29118714	29118941
260009852	chr18	29120979	29121182	29121004	29121158	DSG2	NM_001943	1	15	13	+	29121156	29121277
260067958	chr18	29121132	29121343	29121159	29121321	DSG2	NM_001943	1	15	13	+	29121156	29121277
266663015	chr18	29122354	29122560	29122379	29122538	DSG2	NM_001943	1	15	14	+	29122483	29122815
266743397	chr18	29122515	29122666	29122539	29122644	DSG2	NM_001943	1	15	14	+	29122483	29122815
266774490	chr18	29122623	29122846	29122645	29122820	DSG2	NM_001943	1	15	14	+	29122483	29122815
262205322	chr18	29126119	29126293	29126140	29126266	DSG2	NM_001943	1	15	15	+	29125684	29128814
262287053	chr18	29126245	29126405	29126267	29126382	DSG2	NM_001943	1	15	15	+	29125684	29128814
262334130	chr18	29126359	29126573	29126383	29126553	DSG2	NM_001943	1	15	15	+	29125684	29128814
262394532	chr18	29126526	29126749	29126554	29126722	DSG2	NM_001943	1	15	15	+	29125684	29128814
268257852	chr18	29125671	29125861	29125698	29125834	DSG2	NM_001943	1	15	15	+	29125684	29128814
268285542	chr18	29125809	29126007	29125835	29125983	DSG2	NM_001943	1	15	15	+	29125684	29128814
268299492	chr18	29125956	29126167	29125984	29126139	DSG2	NM_001943	1	15	15	+	29125684	29128814
261828513	chr6	7542123	7542309	7542140	7542290	DSP	NM_001008844	1	24	1	+	7541870	7542318
261833181	chr6	7542255	7542452	7542279	7542432	DSP	NM_001008844	1	24	1	+	7541870	7542318
269233292	chr6	7555923	7556102	7555945	7556084	DSP	NM_001008844	1	24	2	+	7555951	7556053
267768395	chr6	7558303	7558522	7558330	7558502	DSP	NM_001008844	1	24	3	+	7558349	7558497
265135622	chr6	7559395	7559615	7559417	7559592	DSP	NM_001008844	1	24	4	+	7559459	7559633
265189179	chr6	7559572	7559731	7559593	7559705	DSP	NM_001008844	1	24	4	+	7559459	7559633
259065883	chr6	7562857	7563065	7562878	7563037	DSP	NM_001008844	1	24	5	+	7562885	7563013
268888935	chr6	7563848	7564056	7563875	7564028	DSP	NM_001008844	1	24	6	+	7563969	7564019
266278778	chr6	7565565	7565739	7565586	7565716	DSP	NM_001008844	1	24	7	+	7565592	7565753
266287457	chr6	7565697	7565834	7565717	7565813	DSP	NM_001008844	1	24	7	+	7565592	7565753
263433315	chr6	7566465	7566669	7566490	7566641	DSP	NM_001008844	1	24	8	+	7566610	7566714
263473862	chr6	7566614	7566815	7566642	7566788	DSP	NM_001008844	1	24	8	+	7566610	7566714
267670757	chr6	7567500	7567649	7567521	7567624	DSP	NM_001008844	1	24	9	+	7567587	7567682
267678893	chr6	7567605	7567813	7567625	7567785	DSP	NM_001008844	1	24	9	+	7567587	7567682
269285627	chr6	7567961	7568166	7567987	7568145	DSP	NM_001008844	1	24	10	+	7568014	7568139
262181786	chr6	7568553	7568775	7568577	7568752	DSP	NM_001008844	1	24	11	+	7568670	7568822
262208100	chr6	7568727	7568934	7568753	7568906	DSP	NM_001008844	1	24	11	+	7568670	7568822
269267507	chr6	7569255	7569442	7569277	7569421	DSP	NM_001008844	1	24	12	+	7569419	7569573
269283317	chr6	7569401	7569601	7569422	7569580	DSP	NM_001008844	1	24	12	+	7569419	7569573
259011022	chr6	7570569	7570742	7570592	7570721	DSP	NM_001008844	1	24	13	+	7570670	7570796
259075329	chr6	7570699	7570881	7570722	7570857	DSP	NM_001008844	1	24	13	+	7570670	7570796
266403520	chr6	7571496	7571676	7571518	7571650	DSP	NM_001008844	1	24	14	+	7571616	7571817

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266520495	chr6	7571628	7571851	7571651	7571823	DSP	NM_001008844	1	24	14	+	7571616	7571817
265294920	chr6	7572013	7572198	7572035	7572177	DSP	NM_001008844	1	24	15	+	7572075	7572301
265335562	chr6	7572155	7572333	7572178	7572306	DSP	NM_001008844	1	24	15	+	7572075	7572301
259196001	chr6	7574281	7574474	7574309	7574446	DSP	NM_001008844	1	24	16	+	7574319	7574485
259206149	chr6	7574375	7574581	7574397	7574555	DSP	NM_001008844	1	24	16	+	7574319	7574485
268594903	chr6	7574834	7575057	7574861	7575033	DSP	NM_001008844	1	24	17	+	7574890	7575028
267436583	chr6	7575448	7575619	7575468	7575596	DSP	NM_001008844	1	24	18	+	7575528	7575721
267454535	chr6	7575570	7575792	7575597	7575764	DSP	NM_001008844	1	24	18	+	7575528	7575721
267799145	chr6	7576524	7576736	7576546	7576708	DSP	NM_001008844	1	24	19	+	7576527	7576689
268767760	chr6	7577028	7577232	7577056	7577205	DSP	NM_001008844	1	24	20	+	7577192	7577275
268767880	chr6	7577178	7577348	7577206	7577320	DSP	NM_001008844	1	24	20	+	7577192	7577275
267606854	chr6	7577935	7578155	7577960	7578128	DSP	NM_001008844	1	24	21	+	7578012	7578119
267735550	chr6	7578527	7578734	7578549	7578706	DSP	NM_001008844	1	24	22	+	7578697	7578795
267738298	chr6	7578685	7578893	7578707	7578866	DSP	NM_001008844	1	24	22	+	7578697	7578795
258934940	chr6	7579440	7579653	7579467	7579632	DSP	NM_001008844	1	24	23	+	7579508	7580005
258976465	chr6	7579609	7579814	7579633	7579785	DSP	NM_001008844	1	24	23	+	7579508	7580005
259090081	chr6	7579759	7579960	7579786	7579937	DSP	NM_001008844	1	24	23	+	7579508	7580005
259143743	chr6	7579912	7580123	7579938	7580096	DSP	NM_001008844	1	24	23	+	7579508	7580005
263573626	chr6	7585817	7585961	7585840	7585939	DSP	NM_001008844	1	24	24	+	7582875	7586946
263586784	chr6	7585918	7586142	7585937	7586119	DSP	NM_001008844	1	24	24	+	7582875	7586946
268464265	chr6	7582724	7582944	7582747	7582922	DSP	NM_001008844	1	24	24	+	7582875	7586946
268467944	chr6	7582896	7583114	7582923	7583091	DSP	NM_001008844	1	24	24	+	7582875	7586946
268470117	chr6	7583894	7584116	7583918	7584093	DSP	NM_001008844	1	24	24	+	7582875	7586946
268475659	chr6	7583395	7583608	7583418	7583583	DSP	NM_001008844	1	24	24	+	7582875	7586946
268489637	chr6	7584893	7585089	7584918	7585061	DSP	NM_001008844	1	24	24	+	7582875	7586946
268492092	chr6	7584072	7584266	7584094	7584244	DSP	NM_001008844	1	24	24	+	7582875	7586946
268492677	chr6	7585363	7585586	7585390	7585564	DSP	NM_001008844	1	24	24	+	7582875	7586946
268495106	chr6	7584401	7584618	7584425	7584597	DSP	NM_001008844	1	24	24	+	7582875	7586946
268497138	chr6	7583060	7583275	7583087	7583254	DSP	NM_001008844	1	24	24	+	7582875	7586946
268499339	chr6	7583556	7583778	7583584	7583752	DSP	NM_001008844	1	24	24	+	7582875	7586946
268511771	chr6	7585524	7585740	7585546	7585719	DSP	NM_001008844	1	24	24	+	7582875	7586946
268512859	chr6	7585040	7585258	7585062	7585236	DSP	NM_001008844	1	24	24	+	7582875	7586946
268522908	chr6	7583732	7583941	7583753	7583918	DSP	NM_001008844	1	24	24	+	7582875	7586946
268525883	chr6	7585698	7585873	7585719	7585846	DSP	NM_001008844	1	24	24	+	7582875	7586946
268527094	chr6	7584578	7584795	7584598	7584767	DSP	NM_001008844	1	24	24	+	7582875	7586946
268529626	chr6	7583235	7583440	7583255	7583418	DSP	NM_001008844	1	24	24	+	7582875	7586946
268533959	chr6	7584220	7584444	7584245	7584424	DSP	NM_001008844	1	24	24	+	7582875	7586946
268534101	chr6	7585217	7585413	7585237	7585389	DSP	NM_001008844	1	24	24	+	7582875	7586946
268536789	chr6	7584743	7584941	7584768	7584917	DSP	NM_001008844	1	24	24	+	7582875	7586946
261828513	chr6	7542123	7542309	7542140	7542290	DSP	NM_004415	2	24	1	+	7541870	7542318
261833181	chr6	7542255	7542452	7542279	7542432	DSP	NM_004415	2	24	1	+	7541870	7542318

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269233292	chr6	7555923	7556102	7555945	7556084	DSP	NM_004415	2	24	2	+	7555951	7556053
267768395	chr6	7558303	7558522	7558330	7558502	DSP	NM_004415	2	24	3	+	7558349	7558497
265135622	chr6	7559395	7559615	7559417	7559592	DSP	NM_004415	2	24	4	+	7559459	7559633
265189179	chr6	7559572	7559731	7559593	7559705	DSP	NM_004415	2	24	4	+	7559459	7559633
259065883	chr6	7562857	7563065	7562878	7563037	DSP	NM_004415	2	24	5	+	7562885	7563013
268888935	chr6	7563848	7564056	7563875	7564028	DSP	NM_004415	2	24	6	+	7563969	7564019
266278778	chr6	7565565	7565739	7565586	7565716	DSP	NM_004415	2	24	7	+	7565592	7565753
266287457	chr6	7565697	7565834	7565717	7565813	DSP	NM_004415	2	24	7	+	7565592	7565753
263433315	chr6	7566465	7566669	7566490	7566641	DSP	NM_004415	2	24	8	+	7566610	7566714
263473862	chr6	7566614	7566815	7566642	7566788	DSP	NM_004415	2	24	8	+	7566610	7566714
267670757	chr6	7567500	7567649	7567521	7567624	DSP	NM_004415	2	24	9	+	7567587	7567682
267678893	chr6	7567605	7567813	7567625	7567785	DSP	NM_004415	2	24	9	+	7567587	7567682
269285627	chr6	7567961	7568166	7567987	7568145	DSP	NM_004415	2	24	10	+	7568014	7568139
262181786	chr6	7568553	7568775	7568577	7568752	DSP	NM_004415	2	24	11	+	7568670	7568822
262208100	chr6	7568727	7568934	7568753	7568906	DSP	NM_004415	2	24	11	+	7568670	7568822
269267507	chr6	7569255	7569442	7569277	7569421	DSP	NM_004415	2	24	12	+	7569419	7569573
269283317	chr6	7569401	7569601	7569422	7569580	DSP	NM_004415	2	24	12	+	7569419	7569573
259011022	chr6	7570569	7570742	7570592	7570721	DSP	NM_004415	2	24	13	+	7570670	7570796
259075329	chr6	7570699	7570881	7570722	7570857	DSP	NM_004415	2	24	13	+	7570670	7570796
266403520	chr6	7571496	7571676	7571518	7571650	DSP	NM_004415	2	24	14	+	7571616	7571817
266520495	chr6	7571628	7571851	7571651	7571823	DSP	NM_004415	2	24	14	+	7571616	7571817
265294920	chr6	7572013	7572198	7572035	7572177	DSP	NM_004415	2	24	15	+	7572075	7572301
265335562	chr6	7572155	7572333	7572178	7572306	DSP	NM_004415	2	24	15	+	7572075	7572301
259196001	chr6	7574281	7574474	7574309	7574446	DSP	NM_004415	2	24	16	+	7574319	7574485
259206149	chr6	7574375	7574581	7574397	7574555	DSP	NM_004415	2	24	16	+	7574319	7574485
268594903	chr6	7574834	7575057	7574861	7575033	DSP	NM_004415	2	24	17	+	7574890	7575028
267436583	chr6	7575448	7575619	7575468	7575596	DSP	NM_004415	2	24	18	+	7575528	7575721
267454535	chr6	7575570	7575792	7575597	7575764	DSP	NM_004415	2	24	18	+	7575528	7575721
267799145	chr6	7576524	7576736	7576546	7576708	DSP	NM_004415	2	24	19	+	7576527	7576689
268767760	chr6	7577028	7577232	7577056	7577205	DSP	NM_004415	2	24	20	+	7577192	7577275
268767880	chr6	7577178	7577348	7577206	7577320	DSP	NM_004415	2	24	20	+	7577192	7577275
267606854	chr6	7577935	7578155	7577960	7578128	DSP	NM_004415	2	24	21	+	7578012	7578119
267735550	chr6	7578527	7578734	7578549	7578706	DSP	NM_004415	2	24	22	+	7578697	7578795
267738298	chr6	7578685	7578893	7578707	7578866	DSP	NM_004415	2	24	22	+	7578697	7578795
258934940	chr6	7579440	7579653	7579467	7579632	DSP	NM_004415	2	24	23	+	7579508	7581802
258976465	chr6	7579609	7579814	7579633	7579785	DSP	NM_004415	2	24	23	+	7579508	7581802
259090081	chr6	7579759	7579960	7579786	7579937	DSP	NM_004415	2	24	23	+	7579508	7581802
259143743	chr6	7579912	7580123	7579938	7580096	DSP	NM_004415	2	24	23	+	7579508	7581802
265972026	chr6	7581445	7581657	7581470	7581636	DSP	NM_004415	2	24	23	+	7579508	7581802
265992653	chr6	7581612	7581835	7581634	7581808	DSP	NM_004415	2	24	23	+	7579508	7581802
266156664	chr6	7580973	7581197	7580994	7581175	DSP	NM_004415	2	24	23	+	7579508	7581802

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266167855	chr6	7581146	7581322	7581166	7581299	DSP	NM_004415	2	24	23	+	7579508	7581802
266178816	chr6	7581278	7581494	7581300	7581470	DSP	NM_004415	2	24	23	+	7579508	7581802
268961285	chr6	7580558	7580731	7580579	7580710	DSP	NM_004415	2	24	23	+	7579508	7581802
268972287	chr6	7580072	7580283	7580097	7580259	DSP	NM_004415	2	24	23	+	7579508	7581802
268978677	chr6	7580689	7580851	7580711	7580829	DSP	NM_004415	2	24	23	+	7579508	7581802
268985750	chr6	7580229	7580434	7580249	7580411	DSP	NM_004415	2	24	23	+	7579508	7581802
268993935	chr6	7580802	7581020	7580830	7580993	DSP	NM_004415	2	24	23	+	7579508	7581802
268996568	chr6	7580383	7580599	7580411	7580579	DSP	NM_004415	2	24	23	+	7579508	7581802
263573626	chr6	7585817	7585961	7585840	7585939	DSP	NM_004415	2	24	24	+	7582875	7586946
263586784	chr6	7585918	7586142	7585937	7586119	DSP	NM_004415	2	24	24	+	7582875	7586946
268464265	chr6	7582724	7582944	7582747	7582922	DSP	NM_004415	2	24	24	+	7582875	7586946
268467944	chr6	7582896	7583114	7582923	7583091	DSP	NM_004415	2	24	24	+	7582875	7586946
268470117	chr6	7583894	7584116	7583918	7584093	DSP	NM_004415	2	24	24	+	7582875	7586946
268475659	chr6	7583395	7583608	7583418	7583583	DSP	NM_004415	2	24	24	+	7582875	7586946
268489637	chr6	7584893	7585089	7584918	7585061	DSP	NM_004415	2	24	24	+	7582875	7586946
268492092	chr6	7584072	7584266	7584094	7584244	DSP	NM_004415	2	24	24	+	7582875	7586946
268492677	chr6	7585363	7585586	7585390	7585564	DSP	NM_004415	2	24	24	+	7582875	7586946
268495106	chr6	7584401	7584618	7584425	7584597	DSP	NM_004415	2	24	24	+	7582875	7586946
268497138	chr6	7583060	7583275	7583087	7583254	DSP	NM_004415	2	24	24	+	7582875	7586946
268499339	chr6	7583556	7583778	7583584	7583752	DSP	NM_004415	2	24	24	+	7582875	7586946
268511771	chr6	7585524	7585740	7585546	7585719	DSP	NM_004415	2	24	24	+	7582875	7586946
268512859	chr6	7585040	7585258	7585062	7585236	DSP	NM_004415	2	24	24	+	7582875	7586946
268522908	chr6	7583732	7583941	7583753	7583918	DSP	NM_004415	2	24	24	+	7582875	7586946
268525883	chr6	7585698	7585873	7585719	7585846	DSP	NM_004415	2	24	24	+	7582875	7586946
268527094	chr6	7584578	7584795	7584598	7584767	DSP	NM_004415	2	24	24	+	7582875	7586946
268529626	chr6	7583235	7583440	7583255	7583418	DSP	NM_004415	2	24	24	+	7582875	7586946
268533959	chr6	7584220	7584444	7584245	7584424	DSP	NM_004415	2	24	24	+	7582875	7586946
268534101	chr6	7585217	7585413	7585237	7585389	DSP	NM_004415	2	24	24	+	7582875	7586946
268536789	chr6	7584743	7584941	7584768	7584917	DSP	NM_004415	2	24	24	+	7582875	7586946
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130455	1	55	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130455	1	55	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130455	1	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130455	1	55	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130455	1	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130455	1	55	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130455	1	55	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130455	1	55	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130455	1	55	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130455	1	55	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130455	1	55	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130455	1	55	9	+	71744119	71744169

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130455	1	55	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130455	1	55	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130455	1	55	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130455	1	55	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130455	1	55	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130455	1	55	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130455	1	55	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130455	1	55	16	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_001130455	1	55	17	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130455	1	55	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130455	1	55	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130455	1	55	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130455	1	55	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130455	1	55	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130455	1	55	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130455	1	55	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130455	1	55	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130455	1	55	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130455	1	55	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130455	1	55	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130455	1	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130455	1	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130455	1	55	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130455	1	55	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130455	1	55	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130455	1	55	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130455	1	55	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130455	1	55	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130455	1	55	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130455	1	55	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130455	1	55	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130455	1	55	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130455	1	55	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130455	1	55	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130455	1	55	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130455	1	55	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130455	1	55	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130455	1	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130455	1	55	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130455	1	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130455	1	55	38	+	71838595	71838756

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130455	1	55	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130455	1	55	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130455	1	55	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130455	1	55	40	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130455	1	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130455	1	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130455	1	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130455	1	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130455	1	55	45	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130455	1	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130455	1	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130455	1	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130455	1	55	48	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130455	1	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130455	1	55	49	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130455	1	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130455	1	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130455	1	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130455	1	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130455	1	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130455	1	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130455	1	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130455	1	55	55	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130976	2	54	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130976	2	54	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130976	2	54	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130976	2	54	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130976	2	54	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130976	2	54	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130976	2	54	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130976	2	54	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130976	2	54	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130976	2	54	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130976	2	54	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130976	2	54	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130976	2	54	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130976	2	54	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130976	2	54	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130976	2	54	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130976	2	54	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130976	2	54	14	+	71762151	71762219

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130976	2	54	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130976	2	54	16	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130976	2	54	17	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130976	2	54	18	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130976	2	54	18	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130976	2	54	19	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130976	2	54	19	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130976	2	54	20	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130976	2	54	21	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130976	2	54	22	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130976	2	54	22	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130976	2	54	23	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130976	2	54	23	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130976	2	54	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130976	2	54	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130976	2	54	25	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130976	2	54	25	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130976	2	54	26	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130976	2	54	27	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130976	2	54	28	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130976	2	54	28	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130976	2	54	29	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130976	2	54	29	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130976	2	54	30	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130976	2	54	31	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130976	2	54	32	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130976	2	54	32	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130976	2	54	33	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130976	2	54	34	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130976	2	54	35	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130976	2	54	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130976	2	54	36	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130976	2	54	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130976	2	54	37	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130976	2	54	37	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130976	2	54	38	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130976	2	54	39	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130976	2	54	39	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130976	2	54	40	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130976	2	54	41	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130976	2	54	42	+	71886008	71886163

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130976	2	54	43	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130976	2	54	44	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130976	2	54	44	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130976	2	54	45	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130976	2	54	46	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130976	2	54	47	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130976	2	54	48	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130976	2	54	48	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130976	2	54	49	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130976	2	54	49	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130976	2	54	50	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130976	2	54	51	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130976	2	54	51	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130976	2	54	52	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130976	2	54	53	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130976	2	54	54	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130977	3	55	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130977	3	55	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130977	3	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130977	3	55	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130977	3	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130977	3	55	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130977	3	55	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130977	3	55	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130977	3	55	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130977	3	55	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130977	3	55	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130977	3	55	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130977	3	55	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130977	3	55	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130977	3	55	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130977	3	55	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130977	3	55	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130977	3	55	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130977	3	55	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130977	3	55	16	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130977	3	55	17	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130977	3	55	18	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130977	3	55	18	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130977	3	55	19	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130977	3	55	19	+	71780141	71780318

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130977	3	55	20	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130977	3	55	21	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130977	3	55	22	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130977	3	55	22	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130977	3	55	23	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130977	3	55	23	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130977	3	55	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130977	3	55	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130977	3	55	25	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130977	3	55	25	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130977	3	55	26	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130977	3	55	27	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130977	3	55	28	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130977	3	55	28	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130977	3	55	29	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130977	3	55	29	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130977	3	55	30	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130977	3	55	31	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130977	3	55	32	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130977	3	55	32	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130977	3	55	33	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130977	3	55	34	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130977	3	55	35	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130977	3	55	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130977	3	55	36	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130977	3	55	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130977	3	55	37	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130977	3	55	37	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130977	3	55	38	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130977	3	55	39	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130977	3	55	39	+	71840464	71840540
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130977	3	55	40	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130977	3	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130977	3	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130977	3	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130977	3	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130977	3	55	45	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130977	3	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130977	3	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130977	3	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130977	3	55	48	+	71895884	71895972

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130977	3	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130977	3	55	49	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130977	3	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130977	3	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130977	3	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130977	3	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130977	3	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130977	3	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130977	3	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130977	3	55	55	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130978	4	56	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130978	4	56	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130978	4	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130978	4	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130978	4	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130978	4	56	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130978	4	56	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130978	4	56	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130978	4	56	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130978	4	56	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130978	4	56	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130978	4	56	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130978	4	56	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130978	4	56	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130978	4	56	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130978	4	56	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130978	4	56	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130978	4	56	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130978	4	56	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130978	4	56	16	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_001130978	4	56	17	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130978	4	56	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130978	4	56	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130978	4	56	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130978	4	56	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130978	4	56	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130978	4	56	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130978	4	56	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130978	4	56	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130978	4	56	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130978	4	56	24	+	71791188	71791343

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130978	4	56	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130978	4	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130978	4	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130978	4	56	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130978	4	56	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130978	4	56	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130978	4	56	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130978	4	56	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130978	4	56	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130978	4	56	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130978	4	56	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130978	4	56	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130978	4	56	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130978	4	56	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130978	4	56	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130978	4	56	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130978	4	56	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130978	4	56	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130978	4	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130978	4	56	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130978	4	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130978	4	56	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130978	4	56	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130978	4	56	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130978	4	56	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130978	4	56	40	+	71840464	71840540
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130978	4	56	41	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130978	4	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130978	4	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130978	4	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130978	4	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130978	4	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130978	4	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130978	4	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130978	4	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130978	4	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130978	4	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130978	4	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130978	4	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130978	4	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130978	4	56	52	+	71901327	71901426

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130978	4	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130978	4	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130978	4	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130978	4	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130978	4	56	56	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130979	5	56	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130979	5	56	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130979	5	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130979	5	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130979	5	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130979	5	56	5	+	71738937	71739051
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130979	5	56	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130979	5	56	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130979	5	56	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130979	5	56	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130979	5	56	8	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130979	5	56	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130979	5	56	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130979	5	56	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130979	5	56	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130979	5	56	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130979	5	56	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130979	5	56	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130979	5	56	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130979	5	56	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130979	5	56	17	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_001130979	5	56	18	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130979	5	56	19	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130979	5	56	20	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130979	5	56	20	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130979	5	56	21	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130979	5	56	21	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130979	5	56	22	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130979	5	56	23	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130979	5	56	24	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130979	5	56	24	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130979	5	56	25	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130979	5	56	25	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130979	5	56	26	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130979	5	56	26	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130979	5	56	27	+	71795302	71795468

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130979	5	56	27	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130979	5	56	28	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130979	5	56	29	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130979	5	56	30	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130979	5	56	30	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130979	5	56	31	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130979	5	56	31	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130979	5	56	32	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130979	5	56	33	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130979	5	56	34	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130979	5	56	34	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130979	5	56	35	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130979	5	56	36	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130979	5	56	37	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130979	5	56	38	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130979	5	56	38	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130979	5	56	38	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130979	5	56	39	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130979	5	56	39	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130979	5	56	40	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130979	5	56	41	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130979	5	56	41	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130979	5	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130979	5	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130979	5	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130979	5	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130979	5	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130979	5	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130979	5	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130979	5	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130979	5	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130979	5	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130979	5	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130979	5	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130979	5	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130979	5	56	52	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130979	5	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130979	5	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130979	5	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130979	5	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130979	5	56	56	+	71913584	71913893

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130980	6	55	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130980	6	55	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130980	6	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130980	6	55	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130980	6	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130980	6	55	5	+	71738937	71739051
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130980	6	55	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130980	6	55	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130980	6	55	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130980	6	55	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130980	6	55	8	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130980	6	55	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130980	6	55	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130980	6	55	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130980	6	55	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130980	6	55	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130980	6	55	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130980	6	55	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130980	6	55	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130980	6	55	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130980	6	55	17	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130980	6	55	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130980	6	55	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130980	6	55	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130980	6	55	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130980	6	55	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130980	6	55	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130980	6	55	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130980	6	55	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130980	6	55	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130980	6	55	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130980	6	55	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130980	6	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130980	6	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130980	6	55	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130980	6	55	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130980	6	55	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130980	6	55	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130980	6	55	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130980	6	55	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130980	6	55	30	+	71801328	71801501

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130980	6	55	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130980	6	55	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130980	6	55	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130980	6	55	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130980	6	55	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130980	6	55	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130980	6	55	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130980	6	55	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130980	6	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130980	6	55	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130980	6	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130980	6	55	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130980	6	55	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130980	6	55	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130980	6	55	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130980	6	55	40	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130980	6	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130980	6	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130980	6	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130980	6	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130980	6	55	45	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130980	6	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130980	6	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130980	6	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130980	6	55	48	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130980	6	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130980	6	55	49	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130980	6	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130980	6	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130980	6	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130980	6	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130980	6	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130980	6	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130980	6	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130980	6	55	55	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_001130981	7	56	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_001130981	7	56	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130981	7	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130981	7	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130981	7	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130981	7	56	5	+	71738937	71739051

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130981	7	56	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130981	7	56	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130981	7	56	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130981	7	56	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130981	7	56	8	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130981	7	56	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130981	7	56	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130981	7	56	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130981	7	56	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130981	7	56	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130981	7	56	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130981	7	56	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130981	7	56	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130981	7	56	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130981	7	56	17	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130981	7	56	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130981	7	56	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130981	7	56	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130981	7	56	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130981	7	56	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130981	7	56	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130981	7	56	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130981	7	56	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130981	7	56	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130981	7	56	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130981	7	56	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130981	7	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130981	7	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130981	7	56	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130981	7	56	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130981	7	56	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130981	7	56	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130981	7	56	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130981	7	56	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130981	7	56	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130981	7	56	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130981	7	56	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130981	7	56	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130981	7	56	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130981	7	56	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130981	7	56	34	+	71827832	71827972

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130981	7	56	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130981	7	56	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130981	7	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130981	7	56	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130981	7	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130981	7	56	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130981	7	56	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130981	7	56	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130981	7	56	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130981	7	56	40	+	71840464	71840540
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130981	7	56	41	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130981	7	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130981	7	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130981	7	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130981	7	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130981	7	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130981	7	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130981	7	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130981	7	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130981	7	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130981	7	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130981	7	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130981	7	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130981	7	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130981	7	56	52	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130981	7	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130981	7	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130981	7	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130981	7	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130981	7	56	56	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130982	8	56	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130982	8	56	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130982	8	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130982	8	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130982	8	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130982	8	56	5	+	71738937	71739051
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130982	8	56	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130982	8	56	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130982	8	56	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130982	8	56	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130982	8	56	8	+	71742753	71742881

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130982	8	56	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130982	8	56	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130982	8	56	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130982	8	56	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130982	8	56	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130982	8	56	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130982	8	56	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130982	8	56	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130982	8	56	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130982	8	56	17	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_001130982	8	56	18	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130982	8	56	19	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130982	8	56	20	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130982	8	56	20	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130982	8	56	21	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130982	8	56	21	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130982	8	56	22	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130982	8	56	23	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130982	8	56	24	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130982	8	56	24	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130982	8	56	25	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130982	8	56	25	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130982	8	56	26	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130982	8	56	26	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130982	8	56	27	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130982	8	56	27	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130982	8	56	28	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130982	8	56	29	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130982	8	56	30	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130982	8	56	30	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130982	8	56	31	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130982	8	56	31	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130982	8	56	32	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130982	8	56	33	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130982	8	56	34	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130982	8	56	34	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130982	8	56	35	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130982	8	56	36	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130982	8	56	37	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130982	8	56	38	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130982	8	56	38	+	71838375	71838476

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130982	8	56	38	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130982	8	56	39	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130982	8	56	39	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130982	8	56	40	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130982	8	56	41	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130982	8	56	41	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130982	8	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130982	8	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130982	8	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130982	8	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130982	8	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130982	8	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130982	8	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130982	8	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130982	8	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130982	8	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130982	8	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130982	8	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130982	8	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130982	8	56	52	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130982	8	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130982	8	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130982	8	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130982	8	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130982	8	56	56	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130983	9	56	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130983	9	56	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130983	9	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130983	9	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130983	9	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130983	9	56	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130983	9	56	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130983	9	56	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130983	9	56	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130983	9	56	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130983	9	56	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130983	9	56	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130983	9	56	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130983	9	56	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130983	9	56	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130983	9	56	12	+	71753350	71753476

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130983	9	56	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130983	9	56	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130983	9	56	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130983	9	56	16	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_001130983	9	56	17	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130983	9	56	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130983	9	56	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130983	9	56	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130983	9	56	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130983	9	56	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130983	9	56	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130983	9	56	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130983	9	56	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130983	9	56	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130983	9	56	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130983	9	56	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130983	9	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130983	9	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130983	9	56	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130983	9	56	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130983	9	56	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130983	9	56	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130983	9	56	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130983	9	56	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130983	9	56	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130983	9	56	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130983	9	56	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130983	9	56	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130983	9	56	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130983	9	56	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130983	9	56	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130983	9	56	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130983	9	56	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130983	9	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130983	9	56	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130983	9	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130983	9	56	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130983	9	56	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130983	9	56	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130983	9	56	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130983	9	56	40	+	71840464	71840540

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130983	9	56	41	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130983	9	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130983	9	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130983	9	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130983	9	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130983	9	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130983	9	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130983	9	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130983	9	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130983	9	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130983	9	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130983	9	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130983	9	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130983	9	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130983	9	56	52	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130983	9	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130983	9	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130983	9	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130983	9	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130983	9	56	56	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130984	10	55	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130984	10	55	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130984	10	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130984	10	55	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130984	10	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130984	10	55	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130984	10	55	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130984	10	55	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130984	10	55	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130984	10	55	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130984	10	55	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130984	10	55	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130984	10	55	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130984	10	55	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130984	10	55	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130984	10	55	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130984	10	55	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130984	10	55	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130984	10	55	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130984	10	55	16	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130984	10	55	17	+	71778171	71778286

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130984	10	55	18	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130984	10	55	18	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130984	10	55	19	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130984	10	55	19	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130984	10	55	20	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130984	10	55	21	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130984	10	55	22	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130984	10	55	22	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130984	10	55	23	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130984	10	55	23	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130984	10	55	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130984	10	55	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130984	10	55	25	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130984	10	55	25	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130984	10	55	26	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130984	10	55	27	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130984	10	55	28	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130984	10	55	28	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130984	10	55	29	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130984	10	55	29	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130984	10	55	30	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130984	10	55	31	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130984	10	55	32	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130984	10	55	32	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130984	10	55	33	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130984	10	55	34	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130984	10	55	35	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130984	10	55	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130984	10	55	36	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130984	10	55	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130984	10	55	37	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130984	10	55	37	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130984	10	55	38	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130984	10	55	39	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130984	10	55	39	+	71840464	71840540
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130984	10	55	40	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130984	10	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130984	10	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130984	10	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130984	10	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130984	10	55	45	+	71891398	71891568

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130984	10	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130984	10	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130984	10	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130984	10	55	48	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130984	10	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130984	10	55	49	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130984	10	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130984	10	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130984	10	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130984	10	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130984	10	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130984	10	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130984	10	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130984	10	55	55	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130985	11	55	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130985	11	55	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130985	11	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130985	11	55	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130985	11	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130985	11	55	5	+	71738937	71739051
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130985	11	55	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130985	11	55	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130985	11	55	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130985	11	55	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130985	11	55	8	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130985	11	55	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130985	11	55	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130985	11	55	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130985	11	55	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130985	11	55	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130985	11	55	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130985	11	55	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130985	11	55	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130985	11	55	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130985	11	55	17	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130985	11	55	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130985	11	55	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130985	11	55	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130985	11	55	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130985	11	55	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130985	11	55	21	+	71780937	71781061

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130985	11	55	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130985	11	55	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130985	11	55	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130985	11	55	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130985	11	55	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130985	11	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130985	11	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130985	11	55	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130985	11	55	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130985	11	55	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130985	11	55	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130985	11	55	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130985	11	55	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130985	11	55	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130985	11	55	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130985	11	55	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130985	11	55	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130985	11	55	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130985	11	55	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130985	11	55	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130985	11	55	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130985	11	55	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130985	11	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130985	11	55	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130985	11	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130985	11	55	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130985	11	55	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130985	11	55	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130985	11	55	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130985	11	55	40	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130985	11	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130985	11	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130985	11	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130985	11	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130985	11	55	45	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130985	11	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130985	11	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130985	11	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130985	11	55	48	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130985	11	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130985	11	55	49	+	71896242	71896337

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130985	11	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130985	11	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130985	11	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130985	11	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130985	11	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130985	11	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130985	11	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130985	11	55	55	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130986	12	54	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130986	12	54	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130986	12	54	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130986	12	54	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130986	12	54	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130986	12	54	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130986	12	54	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130986	12	54	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130986	12	54	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130986	12	54	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130986	12	54	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130986	12	54	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130986	12	54	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130986	12	54	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130986	12	54	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130986	12	54	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130986	12	54	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130986	12	54	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130986	12	54	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130986	12	54	16	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130986	12	54	17	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130986	12	54	18	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130986	12	54	18	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130986	12	54	19	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130986	12	54	19	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130986	12	54	20	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130986	12	54	21	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130986	12	54	22	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130986	12	54	22	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130986	12	54	23	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130986	12	54	23	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130986	12	54	24	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130986	12	54	24	+	71795081	71795212

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130986	12	54	25	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130986	12	54	25	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130986	12	54	26	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130986	12	54	27	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130986	12	54	28	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130986	12	54	28	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130986	12	54	29	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130986	12	54	29	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130986	12	54	30	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130986	12	54	31	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130986	12	54	32	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130986	12	54	32	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130986	12	54	33	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130986	12	54	34	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130986	12	54	35	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130986	12	54	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130986	12	54	36	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130986	12	54	36	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130986	12	54	37	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130986	12	54	37	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130986	12	54	38	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130986	12	54	39	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130986	12	54	39	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130986	12	54	40	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130986	12	54	41	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130986	12	54	42	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130986	12	54	43	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130986	12	54	44	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130986	12	54	44	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130986	12	54	45	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130986	12	54	46	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130986	12	54	47	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130986	12	54	48	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130986	12	54	48	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130986	12	54	49	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130986	12	54	49	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130986	12	54	50	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130986	12	54	51	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130986	12	54	51	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130986	12	54	52	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130986	12	54	53	+	71909660	71909807

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130986	12	54	54	+	71913584	71913893
265605809	chr2	71693849	71694065	71693869	71694045	DYSF	NM_001130987	13	56	1	+	71693832	71694063
265606363	chr2	71694003	71694136	71694021	71694118	DYSF	NM_001130987	13	56	1	+	71693832	71694063
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_001130987	13	56	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_001130987	13	56	3	+	71709009	71709100
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_001130987	13	56	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_001130987	13	56	5	+	71738937	71739051
267410060	chr2	71740296	71740514	71740317	71740492	DYSF	NM_001130987	13	56	6	+	71740370	71740462
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_001130987	13	56	7	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_001130987	13	56	7	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_001130987	13	56	8	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_001130987	13	56	8	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_001130987	13	56	9	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_001130987	13	56	10	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_001130987	13	56	11	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_001130987	13	56	12	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_001130987	13	56	13	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_001130987	13	56	13	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_001130987	13	56	14	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_001130987	13	56	15	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_001130987	13	56	16	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_001130987	13	56	17	+	71766287	71766369
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_001130987	13	56	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_001130987	13	56	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_001130987	13	56	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_001130987	13	56	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_001130987	13	56	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_001130987	13	56	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_001130987	13	56	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_001130987	13	56	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_001130987	13	56	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_001130987	13	56	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_001130987	13	56	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_001130987	13	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130987	13	56	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_001130987	13	56	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_001130987	13	56	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_001130987	13	56	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_001130987	13	56	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_001130987	13	56	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_001130987	13	56	29	+	71797729	71797871

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_001130987	13	56	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_001130987	13	56	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_001130987	13	56	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_001130987	13	56	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_001130987	13	56	33	+	71825694	71825875
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_001130987	13	56	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_001130987	13	56	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_001130987	13	56	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_001130987	13	56	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_001130987	13	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130987	13	56	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_001130987	13	56	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_001130987	13	56	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_001130987	13	56	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_001130987	13	56	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_001130987	13	56	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_001130987	13	56	40	+	71840464	71840540
265697022	chr2	71847585	71847771	71847604	71847745	DYSF	NM_001130987	13	56	41	+	71847677	71847739
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_001130987	13	56	42	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_001130987	13	56	43	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_001130987	13	56	44	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_001130987	13	56	45	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_001130987	13	56	46	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_001130987	13	56	46	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_001130987	13	56	47	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_001130987	13	56	48	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_001130987	13	56	49	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_001130987	13	56	50	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_001130987	13	56	50	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_001130987	13	56	51	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_001130987	13	56	51	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_001130987	13	56	52	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_001130987	13	56	53	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_001130987	13	56	53	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_001130987	13	56	54	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_001130987	13	56	55	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_001130987	13	56	56	+	71913584	71913893
263469205	chr2	71680960	71681164	71680980	71681143	DYSF	NM_003494	14	55	1	+	71680753	71681216
263477422	chr2	71681123	71681313	71681144	71681291	DYSF	NM_003494	14	55	1	+	71680753	71681216
257540691	chr2	71707917	71708131	71707938	71708110	DYSF	NM_003494	14	55	2	+	71708013	71708068
267332243	chr2	71708987	71709154	71709013	71709131	DYSF	NM_003494	14	55	3	+	71709009	71709100

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
259921108	chr2	71730295	71730494	71730315	71730472	DYSF	NM_003494	14	55	4	+	71730344	71730449
263905997	chr2	71738911	71739073	71738930	71739056	DYSF	NM_003494	14	55	5	+	71738937	71739051
257301051	chr2	71740808	71741031	71740829	71741006	DYSF	NM_003494	14	55	6	+	71740846	71741051
257338612	chr2	71740982	71741190	71741005	71741168	DYSF	NM_003494	14	55	6	+	71740846	71741051
266633794	chr2	71742624	71742813	71742652	71742791	DYSF	NM_003494	14	55	7	+	71742753	71742881
266658808	chr2	71742749	71742972	71742770	71742948	DYSF	NM_003494	14	55	7	+	71742753	71742881
262753101	chr2	71743176	71743400	71743199	71743377	DYSF	NM_003494	14	55	8	+	71743310	71743372
269119277	chr2	71744030	71744209	71744055	71744181	DYSF	NM_003494	14	55	9	+	71744119	71744169
265457620	chr2	71747262	71747386	71747283	71747363	DYSF	NM_003494	14	55	10	+	71747308	71747338
266019492	chr2	71747889	71748113	71747911	71748090	DYSF	NM_003494	14	55	11	+	71747919	71748034
259442217	chr2	71753259	71753453	71753281	71753432	DYSF	NM_003494	14	55	12	+	71753350	71753476
259465360	chr2	71753382	71753596	71753404	71753574	DYSF	NM_003494	14	55	12	+	71753350	71753476
267322330	chr2	71755366	71755576	71755390	71755556	DYSF	NM_003494	14	55	13	+	71755428	71755531
257674686	chr2	71762107	71762331	71762128	71762310	DYSF	NM_003494	14	55	14	+	71762151	71762219
268186624	chr2	71762301	71762471	71762322	71762446	DYSF	NM_003494	14	55	15	+	71762398	71762441
264061688	chr2	71766238	71766455	71766260	71766427	DYSF	NM_003494	14	55	16	+	71766287	71766369
267488507	chr2	71776399	71776583	71776422	71776562	DYSF	NM_003494	14	55	17	+	71776480	71776521
262440751	chr2	71778105	71778326	71778123	71778307	DYSF	NM_003494	14	55	18	+	71778171	71778286
262275499	chr2	71778637	71778841	71778658	71778821	DYSF	NM_003494	14	55	19	+	71778737	71778850
262294780	chr2	71778798	71778939	71778820	71778920	DYSF	NM_003494	14	55	19	+	71778737	71778850
268938434	chr2	71780017	71780241	71780038	71780220	DYSF	NM_003494	14	55	20	+	71780141	71780318
268959684	chr2	71780200	71780370	71780221	71780348	DYSF	NM_003494	14	55	20	+	71780141	71780318
267943998	chr2	71780865	71781088	71780885	71781067	DYSF	NM_003494	14	55	21	+	71780937	71781061
264812016	chr2	71783071	71783291	71783088	71783273	DYSF	NM_003494	14	55	22	+	71783095	71783201
264652487	chr2	71788846	71788978	71788867	71788955	DYSF	NM_003494	14	55	23	+	71788882	71789074
264660095	chr2	71788924	71789147	71788945	71789126	DYSF	NM_003494	14	55	23	+	71788882	71789074
267654255	chr2	71791101	71791321	71791122	71791298	DYSF	NM_003494	14	55	24	+	71791188	71791343
267656162	chr2	71791231	71791412	71791251	71791388	DYSF	NM_003494	14	55	24	+	71791188	71791343
263315200	chr2	71795047	71795264	71795068	71795244	DYSF	NM_003494	14	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_003494	14	55	25	+	71795081	71795212
263343560	chr2	71795187	71795398	71795210	71795377	DYSF	NM_003494	14	55	26	+	71795302	71795468
266474737	chr2	71795353	71795539	71795376	71795518	DYSF	NM_003494	14	55	26	+	71795302	71795468
268901709	chr2	71796915	71797119	71796935	71797098	DYSF	NM_003494	14	55	27	+	71796950	71797064
267893206	chr2	71797329	71797539	71797351	71797519	DYSF	NM_003494	14	55	28	+	71797359	71797464
267313394	chr2	71797591	71797803	71797613	71797779	DYSF	NM_003494	14	55	29	+	71797729	71797871
267329214	chr2	71797729	71797942	71797751	71797922	DYSF	NM_003494	14	55	29	+	71797729	71797871
267813068	chr2	71801229	71801410	71801252	71801390	DYSF	NM_003494	14	55	30	+	71801328	71801501
267816153	chr2	71801367	71801560	71801390	71801538	DYSF	NM_003494	14	55	30	+	71801328	71801501
267758272	chr2	71816641	71816857	71816664	71816834	DYSF	NM_003494	14	55	31	+	71816723	71816816
267331231	chr2	71817247	71817465	71817269	71817444	DYSF	NM_003494	14	55	32	+	71817341	71817418
267932442	chr2	71825618	71825810	71825640	71825788	DYSF	NM_003494	14	55	33	+	71825694	71825875

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267940853	chr2	71825769	71825985	71825789	71825963	DYSF	NM_003494	14	55	33	+	71825694	71825875
265875985	chr2	71827787	71828003	71827808	71827979	DYSF	NM_003494	14	55	34	+	71827832	71827972
269076218	chr2	71828482	71828690	71828503	71828665	DYSF	NM_003494	14	55	35	+	71828629	71828658
265329296	chr2	71829769	71829993	71829789	71829972	DYSF	NM_003494	14	55	36	+	71829906	71829935
262053937	chr2	71838230	71838451	71838252	71838428	DYSF	NM_003494	14	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_003494	14	55	37	+	71838375	71838476
268870324	chr2	71838409	71838584	71838429	71838561	DYSF	NM_003494	14	55	37	+	71838375	71838476
262152075	chr2	71838430	71838647	71838452	71838627	DYSF	NM_003494	14	55	38	+	71838595	71838756
268881511	chr2	71838608	71838813	71838628	71838790	DYSF	NM_003494	14	55	38	+	71838595	71838756
267433052	chr2	71839738	71839962	71839757	71839942	DYSF	NM_003494	14	55	39	+	71839771	71839936
262817997	chr2	71840368	71840508	71840389	71840488	DYSF	NM_003494	14	55	40	+	71840464	71840540
262827425	chr2	71840465	71840651	71840487	71840624	DYSF	NM_003494	14	55	40	+	71840464	71840540
267932553	chr2	71871015	71871223	71871036	71871201	DYSF	NM_003494	14	55	41	+	71871095	71871193
264871928	chr2	71883270	71883476	71883291	71883454	DYSF	NM_003494	14	55	42	+	71883292	71883420
268853512	chr2	71885993	71886213	71886015	71886192	DYSF	NM_003494	14	55	43	+	71886008	71886163
258397144	chr2	71887612	71887833	71887633	71887812	DYSF	NM_003494	14	55	44	+	71887690	71887781
269185543	chr2	71891314	71891468	71891335	71891440	DYSF	NM_003494	14	55	45	+	71891398	71891568
269191432	chr2	71891420	71891641	71891441	71891618	DYSF	NM_003494	14	55	45	+	71891398	71891568
268185465	chr2	71892251	71892473	71892278	71892453	DYSF	NM_003494	14	55	46	+	71892292	71892434
267234648	chr2	71894466	71894671	71894486	71894652	DYSF	NM_003494	14	55	47	+	71894506	71894645
261889990	chr2	71895884	71896089	71895902	71896068	DYSF	NM_003494	14	55	48	+	71895884	71895972
268038610	chr2	71896072	71896272	71896092	71896244	DYSF	NM_003494	14	55	49	+	71896242	71896337
268053187	chr2	71896222	71896445	71896245	71896422	DYSF	NM_003494	14	55	49	+	71896242	71896337
268825151	chr2	71896551	71896774	71896576	71896748	DYSF	NM_003494	14	55	50	+	71896735	71896876
268843784	chr2	71896722	71896942	71896749	71896917	DYSF	NM_003494	14	55	50	+	71896735	71896876
267836253	chr2	71901263	71901463	71901285	71901440	DYSF	NM_003494	14	55	51	+	71901327	71901426
267557031	chr2	71906066	71906290	71906088	71906267	DYSF	NM_003494	14	55	52	+	71906187	71906365
267579922	chr2	71906247	71906469	71906268	71906441	DYSF	NM_003494	14	55	52	+	71906187	71906365
262934671	chr2	71908102	71908303	71908123	71908282	DYSF	NM_003494	14	55	53	+	71908131	71908240
267195366	chr2	71909615	71909835	71909637	71909816	DYSF	NM_003494	14	55	54	+	71909660	71909807
267637419	chr2	71913541	71913742	71913560	71913723	DYSF	NM_003494	14	55	55	+	71913584	71913893
227906350	chr7	73442472	73442668	73442493	73442647	ELN	NM_000501	1	33	1	+	73442427	73442599
332287035	chr7	73449560	73449774	73449586	73449750	ELN	NM_000501	1	33	2	+	73449694	73449744
230522602	chr7	73450835	73450992	73450854	73450970	ELN	NM_000501	1	33	3	+	73450885	73450914
230142763	chr7	73452000	73452165	73452020	73452140	ELN	NM_000501	1	33	4	+	73452037	73452069
333488196	chr7	73455403	73455610	73455423	73455586	ELN	NM_000501	1	33	5	+	73455546	73455581
230563775	chr7	73456880	73457067	73456901	73457046	ELN	NM_000501	1	33	6	+	73456944	73457036
232976845	chr7	73457265	73457403	73457285	73457382	ELN	NM_000501	1	33	7	+	73457314	73457364
230328840	chr7	73457357	73457578	73457377	73457558	ELN	NM_000501	1	33	8	+	73457448	73457498
227982516	chr7	73458167	73458291	73458188	73458264	ELN	NM_000501	1	33	9	+	73458209	73458250
229329616	chr7	73459519	73459706	73459543	73459685	ELN	NM_000501	1	33	10	+	73459552	73459623

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228373527	chr7	73460406	73460630	73460428	73460611	ELN	NM_000501	1	33	11	+	73460518	73460547
229946923	chr7	73460909	73461124	73460932	73461103	ELN	NM_000501	1	33	12	+	73461026	73461097
232082958	chr7	73461888	73462073	73461909	73462051	ELN	NM_000501	1	33	13	+	73462005	73462046
230677765	chr7	73462424	73462557	73462446	73462536	ELN	NM_000501	1	33	14	+	73462472	73462531
230412109	chr7	73462734	73462950	73462756	73462926	ELN	NM_000501	1	33	15	+	73462833	73462886
230770022	chr7	73466036	73466217	73466058	73466197	ELN	NM_000501	1	33	16	+	73466080	73466169
229294037	chr7	73466157	73466378	73466178	73466357	ELN	NM_000501	1	33	17	+	73466254	73466313
230003019	chr7	73467393	73467613	73467414	73467592	ELN	NM_000501	1	33	18	+	73467493	73467639
230013035	chr7	73467538	73467760	73467559	73467735	ELN	NM_000501	1	33	18	+	73467493	73467639
228163177	chr7	73468948	73469166	73468969	73469142	ELN	NM_000501	1	33	19	+	73469046	73469099
231730447	chr7	73470574	73470793	73470595	73470772	ELN	NM_000501	1	33	20	+	73470601	73470765
231478902	chr7	73470932	73471156	73470953	73471135	ELN	NM_000501	1	33	21	+	73471002	73471043
232300771	chr7	73471933	73472149	73471958	73472126	ELN	NM_000501	1	33	22	+	73471970	73472026
229106641	chr7	73474180	73474399	73474208	73474374	ELN	NM_000501	1	33	23	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_000501	1	33	23	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_000501	1	33	24	+	73474470	73474514
231235909	chr7	73474639	73474856	73474658	73474836	ELN	NM_000501	1	33	25	+	73474706	73474831
228166956	chr7	73475398	73475555	73475420	73475531	ELN	NM_000501	1	33	26	+	73475431	73475469
229086242	chr7	73477429	73477613	73477450	73477589	ELN	NM_000501	1	33	27	+	73477483	73477554
230091786	chr7	73477585	73477784	73477607	73477762	ELN	NM_000501	1	33	28	+	73477640	73477699
232262220	chr7	73477909	73478058	73477929	73478032	ELN	NM_000501	1	33	29	+	73477951	73478025
230661476	chr7	73479989	73480193	73480009	73480169	ELN	NM_000501	1	33	30	+	73480024	73480062
230460405	chr7	73480160	73480362	73480182	73480341	ELN	NM_000501	1	33	31	+	73480274	73480327
228482106	chr7	73481028	73481192	73481051	73481172	ELN	NM_000501	1	33	32	+	73481062	73481106
231534675	chr7	73482867	73483069	73482889	73483047	ELN	NM_000501	1	33	33	+	73482987	73484236
227906350	chr7	73442472	73442668	73442493	73442647	ELN	NM_001081752	2	30	1	+	73442427	73442599
332287035	chr7	73449560	73449774	73449586	73449750	ELN	NM_001081752	2	30	2	+	73449694	73449744
230142763	chr7	73452000	73452165	73452020	73452140	ELN	NM_001081752	2	30	3	+	73452037	73452069
333488196	chr7	73455403	73455610	73455423	73455586	ELN	NM_001081752	2	30	4	+	73455546	73455581
230563775	chr7	73456880	73457067	73456901	73457046	ELN	NM_001081752	2	30	5	+	73456944	73457036
232976845	chr7	73457265	73457403	73457285	73457382	ELN	NM_001081752	2	30	6	+	73457314	73457364
230328840	chr7	73457357	73457578	73457377	73457558	ELN	NM_001081752	2	30	7	+	73457448	73457498
227982516	chr7	73458167	73458291	73458188	73458264	ELN	NM_001081752	2	30	8	+	73458209	73458250
229329616	chr7	73459519	73459706	73459543	73459685	ELN	NM_001081752	2	30	9	+	73459552	73459623
228373527	chr7	73460406	73460630	73460428	73460611	ELN	NM_001081752	2	30	10	+	73460518	73460547
229946923	chr7	73460909	73461124	73460932	73461103	ELN	NM_001081752	2	30	11	+	73461026	73461097
232082958	chr7	73461888	73462073	73461909	73462051	ELN	NM_001081752	2	30	12	+	73462005	73462046
230677765	chr7	73462424	73462557	73462446	73462536	ELN	NM_001081752	2	30	13	+	73462472	73462531
230412109	chr7	73462734	73462950	73462756	73462926	ELN	NM_001081752	2	30	14	+	73462833	73462886
230770022	chr7	73466036	73466217	73466058	73466197	ELN	NM_001081752	2	30	15	+	73466080	73466169
229294037	chr7	73466157	73466378	73466178	73466357	ELN	NM_001081752	2	30	16	+	73466254	73466313

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230003019	chr7	73467393	73467613	73467414	73467592	ELN	NM_001081752	2	30	17	+	73467493	73467639
230013035	chr7	73467538	73467760	73467559	73467735	ELN	NM_001081752	2	30	17	+	73467493	73467639
228163177	chr7	73468948	73469166	73468969	73469142	ELN	NM_001081752	2	30	18	+	73469046	73469099
231730447	chr7	73470574	73470793	73470595	73470772	ELN	NM_001081752	2	30	19	+	73470601	73470765
231478902	chr7	73470932	73471156	73470953	73471135	ELN	NM_001081752	2	30	20	+	73471002	73471043
229106641	chr7	73474180	73474399	73474208	73474374	ELN	NM_001081752	2	30	21	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081752	2	30	21	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081752	2	30	22	+	73474470	73474514
231235909	chr7	73474639	73474856	73474658	73474836	ELN	NM_001081752	2	30	23	+	73474706	73474831
228166956	chr7	73475398	73475555	73475420	73475531	ELN	NM_001081752	2	30	24	+	73475431	73475469
229086242	chr7	73477429	73477613	73477450	73477589	ELN	NM_001081752	2	30	25	+	73477483	73477554
230091786	chr7	73477585	73477784	73477607	73477762	ELN	NM_001081752	2	30	26	+	73477640	73477699
232262220	chr7	73477909	73478058	73477929	73478032	ELN	NM_001081752	2	30	27	+	73477951	73478025
230661476	chr7	73479989	73480193	73480009	73480169	ELN	NM_001081752	2	30	28	+	73480024	73480062
228482106	chr7	73481028	73481192	73481051	73481172	ELN	NM_001081752	2	30	29	+	73481062	73481106
231534675	chr7	73482867	73483069	73482889	73483047	ELN	NM_001081752	2	30	30	+	73482987	73484236
227906350	chr7	73442472	73442668	73442493	73442647	ELN	NM_001081753	3	31	1	+	73442427	73442599
332287035	chr7	73449560	73449774	73449586	73449750	ELN	NM_001081753	3	31	2	+	73449694	73449744
230522602	chr7	73450835	73450992	73450854	73450970	ELN	NM_001081753	3	31	3	+	73450885	73450914
230142763	chr7	73452000	73452165	73452020	73452140	ELN	NM_001081753	3	31	4	+	73452037	73452069
333488196	chr7	73455403	73455610	73455423	73455586	ELN	NM_001081753	3	31	5	+	73455546	73455581
230563775	chr7	73456880	73457067	73456901	73457046	ELN	NM_001081753	3	31	6	+	73456944	73457036
232976845	chr7	73457265	73457403	73457285	73457382	ELN	NM_001081753	3	31	7	+	73457314	73457364
230328840	chr7	73457357	73457578	73457377	73457558	ELN	NM_001081753	3	31	8	+	73457433	73457498
227982516	chr7	73458167	73458291	73458188	73458264	ELN	NM_001081753	3	31	9	+	73458209	73458250
229329616	chr7	73459519	73459706	73459543	73459685	ELN	NM_001081753	3	31	10	+	73459552	73459623
228373527	chr7	73460406	73460630	73460428	73460611	ELN	NM_001081753	3	31	11	+	73460518	73460547
229946923	chr7	73460909	73461124	73460932	73461103	ELN	NM_001081753	3	31	12	+	73461026	73461097
232082958	chr7	73461888	73462073	73461909	73462051	ELN	NM_001081753	3	31	13	+	73462005	73462046
230677765	chr7	73462424	73462557	73462446	73462536	ELN	NM_001081753	3	31	14	+	73462472	73462531
230412109	chr7	73462734	73462950	73462756	73462926	ELN	NM_001081753	3	31	15	+	73462833	73462886
230770022	chr7	73466036	73466217	73466058	73466197	ELN	NM_001081753	3	31	16	+	73466080	73466169
229294037	chr7	73466157	73466378	73466178	73466357	ELN	NM_001081753	3	31	17	+	73466254	73466313
230003019	chr7	73467393	73467613	73467414	73467592	ELN	NM_001081753	3	31	18	+	73467493	73467639
230013035	chr7	73467538	73467760	73467559	73467735	ELN	NM_001081753	3	31	18	+	73467493	73467639
228163177	chr7	73468948	73469166	73468969	73469142	ELN	NM_001081753	3	31	19	+	73469046	73469099
231730447	chr7	73470574	73470793	73470595	73470772	ELN	NM_001081753	3	31	20	+	73470601	73470765
231478902	chr7	73470932	73471156	73470953	73471135	ELN	NM_001081753	3	31	21	+	73471002	73471043
229106641	chr7	73474180	73474399	73474208	73474374	ELN	NM_001081753	3	31	22	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081753	3	31	22	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081753	3	31	23	+	73474470	73474514

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231235909	chr7	73474639	73474856	73474658	73474836	ELN	NM_001081753	3	31	24	+	73474706	73474831
228166956	chr7	73475398	73475555	73475420	73475531	ELN	NM_001081753	3	31	25	+	73475431	73475469
229086242	chr7	73477429	73477613	73477450	73477589	ELN	NM_001081753	3	31	26	+	73477483	73477554
230091786	chr7	73477585	73477784	73477607	73477762	ELN	NM_001081753	3	31	27	+	73477640	73477699
232262220	chr7	73477909	73478058	73477929	73478032	ELN	NM_001081753	3	31	28	+	73477951	73478025
230661476	chr7	73479989	73480193	73480009	73480169	ELN	NM_001081753	3	31	29	+	73480024	73480062
228482106	chr7	73481028	73481192	73481051	73481172	ELN	NM_001081753	3	31	30	+	73481062	73481106
231534675	chr7	73482867	73483069	73482889	73483047	ELN	NM_001081753	3	31	31	+	73482987	73484236
227906350	chr7	73442472	73442668	73442493	73442647	ELN	NM_001081754	4	32	1	+	73442427	73442599
332287035	chr7	73449560	73449774	73449586	73449750	ELN	NM_001081754	4	32	2	+	73449694	73449744
230522602	chr7	73450835	73450992	73450854	73450970	ELN	NM_001081754	4	32	3	+	73450885	73450914
230142763	chr7	73452000	73452165	73452020	73452140	ELN	NM_001081754	4	32	4	+	73452037	73452069
333488196	chr7	73455403	73455610	73455423	73455586	ELN	NM_001081754	4	32	5	+	73455546	73455581
230563775	chr7	73456880	73457067	73456901	73457046	ELN	NM_001081754	4	32	6	+	73456944	73457036
232976845	chr7	73457265	73457403	73457285	73457382	ELN	NM_001081754	4	32	7	+	73457314	73457364
230328840	chr7	73457357	73457578	73457377	73457558	ELN	NM_001081754	4	32	8	+	73457433	73457498
227982516	chr7	73458167	73458291	73458188	73458264	ELN	NM_001081754	4	32	9	+	73458209	73458250
229329616	chr7	73459519	73459706	73459543	73459685	ELN	NM_001081754	4	32	10	+	73459552	73459623
228373527	chr7	73460406	73460630	73460428	73460611	ELN	NM_001081754	4	32	11	+	73460518	73460547
229946923	chr7	73460909	73461124	73460932	73461103	ELN	NM_001081754	4	32	12	+	73461026	73461097
232082958	chr7	73461888	73462073	73461909	73462051	ELN	NM_001081754	4	32	13	+	73462005	73462046
230677765	chr7	73462424	73462557	73462446	73462536	ELN	NM_001081754	4	32	14	+	73462472	73462531
230412109	chr7	73462734	73462950	73462756	73462926	ELN	NM_001081754	4	32	15	+	73462833	73462886
230770022	chr7	73466036	73466217	73466058	73466197	ELN	NM_001081754	4	32	16	+	73466080	73466169
229294037	chr7	73466157	73466378	73466178	73466357	ELN	NM_001081754	4	32	17	+	73466254	73466313
230003019	chr7	73467393	73467613	73467414	73467592	ELN	NM_001081754	4	32	18	+	73467493	73467639
230013035	chr7	73467538	73467760	73467559	73467735	ELN	NM_001081754	4	32	18	+	73467493	73467639
228163177	chr7	73468948	73469166	73468969	73469142	ELN	NM_001081754	4	32	19	+	73469046	73469099
231730447	chr7	73470574	73470793	73470595	73470772	ELN	NM_001081754	4	32	20	+	73470601	73470765
231478902	chr7	73470932	73471156	73470953	73471135	ELN	NM_001081754	4	32	21	+	73471002	73471043
232300771	chr7	73471933	73472149	73471958	73472126	ELN	NM_001081754	4	32	22	+	73471970	73472026
229106641	chr7	73474180	73474399	73474208	73474374	ELN	NM_001081754	4	32	23	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081754	4	32	23	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081754	4	32	24	+	73474470	73474514
231235909	chr7	73474639	73474856	73474658	73474836	ELN	NM_001081754	4	32	25	+	73474706	73474831
228166956	chr7	73475398	73475555	73475420	73475531	ELN	NM_001081754	4	32	26	+	73475431	73475469
229086242	chr7	73477429	73477613	73477450	73477589	ELN	NM_001081754	4	32	27	+	73477483	73477554
230091786	chr7	73477585	73477784	73477607	73477762	ELN	NM_001081754	4	32	28	+	73477640	73477699
232262220	chr7	73477909	73478058	73477929	73478032	ELN	NM_001081754	4	32	29	+	73477951	73478025
230661476	chr7	73479989	73480193	73480009	73480169	ELN	NM_001081754	4	32	30	+	73480024	73480062
228482106	chr7	73481028	73481192	73481051	73481172	ELN	NM_001081754	4	32	31	+	73481062	73481106

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231534675	chr7	73482867	73483069	73482889	73483047	ELN	NM_001081754	4	32	32	+	73482987	73484236
227906350	chr7	73442472	73442668	73442493	73442647	ELN	NM_001081755	5	32	1	+	73442427	73442599
332287035	chr7	73449560	73449774	73449586	73449750	ELN	NM_001081755	5	32	2	+	73449694	73449744
230522602	chr7	73450835	73450992	73450854	73450970	ELN	NM_001081755	5	32	3	+	73450885	73450914
230142763	chr7	73452000	73452165	73452020	73452140	ELN	NM_001081755	5	32	4	+	73452037	73452069
333488196	chr7	73455403	73455610	73455423	73455586	ELN	NM_001081755	5	32	5	+	73455546	73455581
230563775	chr7	73456880	73457067	73456901	73457046	ELN	NM_001081755	5	32	6	+	73456944	73457036
232976845	chr7	73457265	73457403	73457285	73457382	ELN	NM_001081755	5	32	7	+	73457314	73457364
230328840	chr7	73457357	73457578	73457377	73457558	ELN	NM_001081755	5	32	8	+	73457448	73457498
227982516	chr7	73458167	73458291	73458188	73458264	ELN	NM_001081755	5	32	9	+	73458209	73458250
229329616	chr7	73459519	73459706	73459543	73459685	ELN	NM_001081755	5	32	10	+	73459552	73459623
228373527	chr7	73460406	73460630	73460428	73460611	ELN	NM_001081755	5	32	11	+	73460518	73460547
229946923	chr7	73460909	73461124	73460932	73461103	ELN	NM_001081755	5	32	12	+	73461026	73461097
232082958	chr7	73461888	73462073	73461909	73462051	ELN	NM_001081755	5	32	13	+	73462005	73462046
230677765	chr7	73462424	73462557	73462446	73462536	ELN	NM_001081755	5	32	14	+	73462472	73462531
230412109	chr7	73462734	73462950	73462756	73462926	ELN	NM_001081755	5	32	15	+	73462833	73462886
230770022	chr7	73466036	73466217	73466058	73466197	ELN	NM_001081755	5	32	16	+	73466080	73466169
229294037	chr7	73466157	73466378	73466178	73466357	ELN	NM_001081755	5	32	17	+	73466254	73466313
230003019	chr7	73467393	73467613	73467414	73467592	ELN	NM_001081755	5	32	18	+	73467493	73467639
230013035	chr7	73467538	73467760	73467559	73467735	ELN	NM_001081755	5	32	18	+	73467493	73467639
228163177	chr7	73468948	73469166	73468969	73469142	ELN	NM_001081755	5	32	19	+	73469046	73469099
231730447	chr7	73470574	73470793	73470595	73470772	ELN	NM_001081755	5	32	20	+	73470601	73470765
231478902	chr7	73470932	73471156	73470953	73471135	ELN	NM_001081755	5	32	21	+	73471002	73471043
229106641	chr7	73474180	73474399	73474208	73474374	ELN	NM_001081755	5	32	22	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081755	5	32	22	+	73474216	73474377
332257145	chr7	73474355	73474571	73474374	73474549	ELN	NM_001081755	5	32	23	+	73474470	73474514
231235909	chr7	73474639	73474856	73474658	73474836	ELN	NM_001081755	5	32	24	+	73474706	73474831
228166956	chr7	73475398	73475555	73475420	73475531	ELN	NM_001081755	5	32	25	+	73475431	73475469
229086242	chr7	73477429	73477613	73477450	73477589	ELN	NM_001081755	5	32	26	+	73477483	73477554
230091786	chr7	73477585	73477784	73477607	73477762	ELN	NM_001081755	5	32	27	+	73477640	73477699
232262220	chr7	73477909	73478058	73477929	73478032	ELN	NM_001081755	5	32	28	+	73477951	73478025
230661476	chr7	73479989	73480193	73480009	73480169	ELN	NM_001081755	5	32	29	+	73480024	73480062
230460405	chr7	73480160	73480362	73480182	73480341	ELN	NM_001081755	5	32	30	+	73480274	73480327
228482106	chr7	73481028	73481192	73481051	73481172	ELN	NM_001081755	5	32	31	+	73481062	73481106
231534675	chr7	73482867	73483069	73482889	73483047	ELN	NM_001081755	5	32	32	+	73482987	73484236
267904497	chrX	153607674	153607889	153607692	153607871	EMD	NM_000117	1	6	1	+	153607597	153607926
267905502	chrX	153607848	153608070	153607872	153608047	EMD	NM_000117	1	6	1	+	153607597	153607926
266440885	chrX	153607910	153608100	153607930	153608078	EMD	NM_000117	1	6	2	+	153608050	153608154
266449415	chrX	153608046	153608265	153608070	153608244	EMD	NM_000117	1	6	2	+	153608050	153608154
261598032	chrX	153608268	153608428	153608289	153608409	EMD	NM_000117	1	6	3	+	153608302	153608379
263887764	chrX	153608408	153608632	153608428	153608604	EMD	NM_000117	1	6	4	+	153608594	153608727

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263914501	chrX	153608583	153608775	153608605	153608751	EMD	NM_000117	1	6	4	+	153608594	153608727
268737063	chrX	153609137	153609358	153609162	153609336	EMD	NM_000117	1	6	5	+	153609113	153609162
269176627	chrX	153609035	153609247	153609056	153609227	EMD	NM_000117	1	6	5	+	153609113	153609162
268737063	chrX	153609137	153609358	153609162	153609336	EMD	NM_000117	1	6	6	+	153609242	153609883
268748201	chrX	153609316	153609527	153609337	153609500	EMD	NM_000117	1	6	6	+	153609242	153609883
268755138	chrX	153609479	153609609	153609501	153609587	EMD	NM_000117	1	6	6	+	153609242	153609883
269206076	chr9	130616472	130616686	130616494	130616664	ENG	NM_000118	1	14	1	-	130616568	130617047
265627078	chr9	130605196	130605415	130605218	130605393	ENG	NM_000118	1	14	2	-	130605373	130605524
265637038	chr9	130605373	130605582	130605394	130605555	ENG	NM_000118	1	14	2	-	130605373	130605524
259251985	chr9	130591822	130592041	130591842	130592017	ENG	NM_000118	1	14	3	-	130591966	130592106
259313251	chr9	130591996	130592149	130592018	130592126	ENG	NM_000118	1	14	3	-	130591966	130592106
257557991	chr9	130588748	130588886	130588770	130588864	ENG	NM_000118	1	14	4	-	130588789	130588951
257563603	chr9	130588820	130589038	130588841	130589012	ENG	NM_000118	1	14	4	-	130588789	130588951
264184718	chr9	130587826	130588048	130587846	130588030	ENG	NM_000118	1	14	5	-	130587974	130588139
264186920	chr9	130588002	130588226	130588020	130588205	ENG	NM_000118	1	14	5	-	130587974	130588139
267260703	chr9	130587456	130587676	130587478	130587656	ENG	NM_000118	1	14	6	-	130587510	130587636
261863016	chr9	130587000	130587145	130587020	130587125	ENG	NM_000118	1	14	7	-	130587079	130587253
261869229	chr9	130587084	130587306	130587106	130587286	ENG	NM_000118	1	14	7	-	130587079	130587253
264173889	chr9	130586530	130586683	130586552	130586662	ENG	NM_000118	1	14	8	-	130586583	130586725
264195864	chr9	130586627	130586780	130586652	130586758	ENG	NM_000118	1	14	8	-	130586583	130586725
257761098	chr9	130582141	130582344	130582162	130582324	ENG	NM_000118	1	14	9	-	130582179	130582316
265489025	chr9	130581875	130582057	130581895	130582036	ENG	NM_000118	1	14	10	-	130581901	130581939
259788665	chr9	130580917	130581117	130580939	130581097	ENG	NM_000118	1	14	11	-	130580995	130581111
259801061	chr9	130581077	130581209	130581098	130581189	ENG	NM_000118	1	14	11	-	130580995	130581111
261890239	chr9	130580334	130580497	130580355	130580474	ENG	NM_000118	1	14	12	-	130580399	130580656
261900150	chr9	130580452	130580668	130580474	130580647	ENG	NM_000118	1	14	12	-	130580399	130580656
261911938	chr9	130580610	130580793	130580633	130580769	ENG	NM_000118	1	14	12	-	130580399	130580656
267271946	chr9	130579374	130579511	130579396	130579487	ENG	NM_000118	1	14	13	-	130579428	130579482
261868606	chr9	130577842	130578039	130577860	130578021	ENG	NM_000118	1	14	14	-	130577291	130578332
261870077	chr9	130578003	130578162	130578021	130578142	ENG	NM_000118	1	14	14	-	130577291	130578332
267334866	chr9	130578136	130578288	130578157	130578267	ENG	NM_000118	1	14	14	-	130577291	130578332
267338620	chr9	130578238	130578456	130578258	130578435	ENG	NM_000118	1	14	14	-	130577291	130578332
269206076	chr9	130616472	130616686	130616494	130616664	ENG	NM_001114753	2	15	1	-	130616568	130617047
265627078	chr9	130605196	130605415	130605218	130605393	ENG	NM_001114753	2	15	2	-	130605373	130605524
265637038	chr9	130605373	130605582	130605394	130605555	ENG	NM_001114753	2	15	2	-	130605373	130605524
259251985	chr9	130591822	130592041	130591842	130592017	ENG	NM_001114753	2	15	3	-	130591966	130592106
259313251	chr9	130591996	130592149	130592018	130592126	ENG	NM_001114753	2	15	3	-	130591966	130592106
257557991	chr9	130588748	130588886	130588770	130588864	ENG	NM_001114753	2	15	4	-	130588789	130588951
257563603	chr9	130588820	130589038	130588841	130589012	ENG	NM_001114753	2	15	4	-	130588789	130588951
264184718	chr9	130587826	130588048	130587846	130588030	ENG	NM_001114753	2	15	5	-	130587974	130588139
264186920	chr9	130588002	130588226	130588020	130588205	ENG	NM_001114753	2	15	5	-	130587974	130588139

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267260703	chr9	130587456	130587676	130587478	130587656	ENG	NM_001114753	2	15	6	-	130587510	130587636
261863016	chr9	130587000	130587145	130587020	130587125	ENG	NM_001114753	2	15	7	-	130587079	130587253
261869229	chr9	130587084	130587306	130587106	130587286	ENG	NM_001114753	2	15	7	-	130587079	130587253
264173889	chr9	130586530	130586683	130586552	130586662	ENG	NM_001114753	2	15	8	-	130586583	130586725
264195864	chr9	130586627	130586780	130586652	130586758	ENG	NM_001114753	2	15	8	-	130586583	130586725
257761098	chr9	130582141	130582344	130582162	130582324	ENG	NM_001114753	2	15	9	-	130582179	130582316
265489025	chr9	130581875	130582057	130581895	130582036	ENG	NM_001114753	2	15	10	-	130581901	130581939
259788665	chr9	130580917	130581117	130580939	130581097	ENG	NM_001114753	2	15	11	-	130580995	130581111
259801061	chr9	130581077	130581209	130581098	130581189	ENG	NM_001114753	2	15	11	-	130580995	130581111
261890239	chr9	130580334	130580497	130580355	130580474	ENG	NM_001114753	2	15	12	-	130580399	130580656
261900150	chr9	130580452	130580668	130580474	130580647	ENG	NM_001114753	2	15	12	-	130580399	130580656
261911938	chr9	130580610	130580793	130580633	130580769	ENG	NM_001114753	2	15	12	-	130580399	130580656
267271946	chr9	130579374	130579511	130579396	130579487	ENG	NM_001114753	2	15	13	-	130579428	130579482
267334866	chr9	130578136	130578288	130578157	130578267	ENG	NM_001114753	2	15	14	-	130578222	130578332
267338620	chr9	130578238	130578456	130578258	130578435	ENG	NM_001114753	2	15	14	-	130578222	130578332
261868606	chr9	130577842	130578039	130577860	130578021	ENG	NM_001114753	2	15	15	-	130577291	130578085
261870077	chr9	130578003	130578162	130578021	130578142	ENG	NM_001114753	2	15	15	-	130577291	130578085
231344745	chr8	119122250	119122451	119122271	119122427	EXT1	NM_000127	1	11	1	-	119122324	119124058
231368074	chr8	119122408	119122603	119122428	119122575	EXT1	NM_000127	1	11	1	-	119122324	119124058
231381890	chr8	119122868	119123087	119122888	119123063	EXT1	NM_000127	1	11	1	-	119122324	119124058
231393147	chr8	119122552	119122764	119122576	119122741	EXT1	NM_000127	1	11	1	-	119122324	119124058
231408410	chr8	119123043	119123226	119123064	119123203	EXT1	NM_000127	1	11	1	-	119122324	119124058
231410753	chr8	119122715	119122913	119122742	119122887	EXT1	NM_000127	1	11	1	-	119122324	119124058
231420020	chr8	119123185	119123341	119123204	119123314	EXT1	NM_000127	1	11	1	-	119122324	119124058
232756910	chr8	118849252	118849473	118849276	118849445	EXT1	NM_000127	1	11	2	-	118849347	118849440
228297369	chr8	118847634	118847821	118847656	118847798	EXT1	NM_000127	1	11	3	-	118847683	118847790
227906815	chr8	118842442	118842658	118842461	118842630	EXT1	NM_000127	1	11	4	-	118842469	118842588
228005291	chr8	118834650	118834870	118834677	118834842	EXT1	NM_000127	1	11	5	-	118834704	118834836
230794256	chr8	118831888	118832067	118831909	118832039	EXT1	NM_000127	1	11	6	-	118831915	118832033
232197308	chr8	118830586	118830808	118830609	118830785	EXT1	NM_000127	1	11	7	-	118830674	118830769
230104383	chr8	118825023	118825228	118825044	118825206	EXT1	NM_000127	1	11	8	-	118825111	118825200
229560074	chr8	118819430	118819648	118819456	118819624	EXT1	NM_000127	1	11	9	-	118819456	118819616
227708939	chr8	118816960	118817173	118816986	118817151	EXT1	NM_000127	1	11	10	-	118816961	118817132
333286106	chr8	118816788	118817009	118816814	118816985	EXT1	NM_000127	1	11	10	-	118816961	118817132
232636213	chr8	118812033	118812231	118812053	118812210	EXT1	NM_000127	1	11	11	-	118811602	118812136
232644468	chr8	118811852	118812076	118811874	118812054	EXT1	NM_000127	1	11	11	-	118811602	118812136
315904501	chr8	72268539	72268748	72268567	72268727	EYA1	NM_000503	1	18	2	-	72268697	72268746
317171079	chr8	72266961	72267172	72266989	72267145	EYA1	NM_000503	1	18	3	-	72267017	72267144
316644962	chr8	72246288	72246414	72246316	72246388	EYA1	NM_000503	1	18	4	-	72246332	72246409
315920684	chr8	72234354	72234556	72234375	72234527	EYA1	NM_000503	1	18	5	-	72234434	72234503
316575196	chr8	72233929	72234152	72233948	72234126	EYA1	NM_000503	1	18	6	-	72233969	72234114

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317230030	chr8	72229750	72229974	72229777	72229946	EYA1	NM_000503	1	18	7	-	72229787	72229924
320357420	chr8	72211760	72211956	72211788	72211928	EYA1	NM_000503	1	18	8	-	72211873	72211955
320358777	chr8	72211873	72212008	72211901	72211984	EYA1	NM_000503	1	18	8	-	72211873	72211955
317527466	chr8	72211167	72211368	72211189	72211347	EYA1	NM_000503	1	18	9	-	72211282	72211468
317549225	chr8	72211325	72211520	72211348	72211492	EYA1	NM_000503	1	18	9	-	72211282	72211468
316478561	chr8	72183960	72184181	72183984	72184153	EYA1	NM_000503	1	18	10	-	72183993	72184132
317483006	chr8	72181946	72182093	72181974	72182068	EYA1	NM_000503	1	18	11	-	72181975	72182058
315753077	chr8	72156784	72156989	72156811	72156962	EYA1	NM_000503	1	18	12	-	72156838	72156927
320430442	chr8	72129158	72129374	72129185	72129346	EYA1	NM_000503	1	18	13	-	72129200	72129258
319750534	chr8	72128896	72129119	72128918	72129093	EYA1	NM_000503	1	18	14	-	72128927	72129087
316632653	chr8	72127788	72128000	72127812	72127972	EYA1	NM_000503	1	18	15	-	72127849	72127963
316260122	chr8	72127466	72127680	72127493	72127652	EYA1	NM_000503	1	18	16	-	72127622	72127743
316260717	chr8	72127615	72127813	72127643	72127793	EYA1	NM_000503	1	18	16	-	72127622	72127743
316644218	chr8	72123351	72123558	72123378	72123531	EYA1	NM_000503	1	18	17	-	72123391	72123491
316330561	chr8	72111464	72111684	72111485	72111661	EYA1	NM_000503	1	18	18	-	72109668	72111655
315904501	chr8	72268539	72268748	72268567	72268727	EYA1	NM_172058	2	17	1	-	72268697	72268979
317171079	chr8	72266961	72267172	72266989	72267145	EYA1	NM_172058	2	17	2	-	72267017	72267144
316644962	chr8	72246288	72246414	72246316	72246388	EYA1	NM_172058	2	17	3	-	72246332	72246409
315920684	chr8	72234354	72234556	72234375	72234527	EYA1	NM_172058	2	17	4	-	72234434	72234503
316575196	chr8	72233929	72234152	72233948	72234126	EYA1	NM_172058	2	17	5	-	72233969	72234114
317230030	chr8	72229750	72229974	72229777	72229946	EYA1	NM_172058	2	17	6	-	72229787	72229924
320357420	chr8	72211760	72211956	72211788	72211928	EYA1	NM_172058	2	17	7	-	72211873	72211955
320358777	chr8	72211873	72212008	72211901	72211984	EYA1	NM_172058	2	17	7	-	72211873	72211955
317527466	chr8	72211167	72211368	72211189	72211347	EYA1	NM_172058	2	17	8	-	72211282	72211468
317549225	chr8	72211325	72211520	72211348	72211492	EYA1	NM_172058	2	17	8	-	72211282	72211468
316478561	chr8	72183960	72184181	72183984	72184153	EYA1	NM_172058	2	17	9	-	72183993	72184132
317483006	chr8	72181946	72182093	72181974	72182068	EYA1	NM_172058	2	17	10	-	72181975	72182058
315753077	chr8	72156784	72156989	72156811	72156962	EYA1	NM_172058	2	17	11	-	72156838	72156927
320430442	chr8	72129158	72129374	72129185	72129346	EYA1	NM_172058	2	17	12	-	72129200	72129258
319750534	chr8	72128896	72129119	72128918	72129093	EYA1	NM_172058	2	17	13	-	72128927	72129087
316632653	chr8	72127788	72128000	72127812	72127972	EYA1	NM_172058	2	17	14	-	72127849	72127963
316260122	chr8	72127466	72127680	72127493	72127652	EYA1	NM_172058	2	17	15	-	72127622	72127743
316260717	chr8	72127615	72127813	72127643	72127793	EYA1	NM_172058	2	17	15	-	72127622	72127743
316644218	chr8	72123351	72123558	72123378	72123531	EYA1	NM_172058	2	17	16	-	72123391	72123491
316330561	chr8	72111464	72111684	72111485	72111661	EYA1	NM_172058	2	17	17	-	72109668	72111655
315904501	chr8	72268539	72268748	72268567	72268727	EYA1	NM_172059	3	16	1	-	72268697	72268979
317171079	chr8	72266961	72267172	72266989	72267145	EYA1	NM_172059	3	16	2	-	72267017	72267144
316644962	chr8	72246288	72246414	72246316	72246388	EYA1	NM_172059	3	16	3	-	72246332	72246409
315920684	chr8	72234354	72234556	72234375	72234527	EYA1	NM_172059	3	16	4	-	72234434	72234503
316575196	chr8	72233929	72234152	72233948	72234126	EYA1	NM_172059	3	16	5	-	72233969	72234114
317230030	chr8	72229750	72229974	72229777	72229946	EYA1	NM_172059	3	16	6	-	72229787	72229909

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320357420	chr8	72211760	72211956	72211788	72211928	EYA1	NM_172059	3	16	7	-	72211873	72211955
320358777	chr8	72211873	72212008	72211901	72211984	EYA1	NM_172059	3	16	7	-	72211873	72211955
317527466	chr8	72211167	72211368	72211189	72211347	EYA1	NM_172059	3	16	8	-	72211282	72211468
317549225	chr8	72211325	72211520	72211348	72211492	EYA1	NM_172059	3	16	8	-	72211282	72211468
316478561	chr8	72183960	72184181	72183984	72184153	EYA1	NM_172059	3	16	9	-	72183993	72184132
317483006	chr8	72181946	72182093	72181974	72182068	EYA1	NM_172059	3	16	10	-	72181975	72182058
320430442	chr8	72129158	72129374	72129185	72129346	EYA1	NM_172059	3	16	11	-	72129200	72129258
319750534	chr8	72128896	72129119	72128918	72129093	EYA1	NM_172059	3	16	12	-	72128927	72129087
316632653	chr8	72127788	72128000	72127812	72127972	EYA1	NM_172059	3	16	13	-	72127849	72127963
316260122	chr8	72127466	72127680	72127493	72127652	EYA1	NM_172059	3	16	14	-	72127622	72127743
316260717	chr8	72127615	72127813	72127643	72127793	EYA1	NM_172059	3	16	14	-	72127622	72127743
316644218	chr8	72123351	72123558	72123378	72123531	EYA1	NM_172059	3	16	15	-	72123391	72123491
316330561	chr8	72111464	72111684	72111485	72111661	EYA1	NM_172059	3	16	16	-	72109668	72111655
315904501	chr8	72268539	72268748	72268567	72268727	EYA1	NM_172060	4	16	1	-	72268697	72268979
316644962	chr8	72246288	72246414	72246316	72246388	EYA1	NM_172060	4	16	2	-	72246332	72246409
315920684	chr8	72234354	72234556	72234375	72234527	EYA1	NM_172060	4	16	3	-	72234434	72234503
316575196	chr8	72233929	72234152	72233948	72234126	EYA1	NM_172060	4	16	4	-	72233969	72234114
317230030	chr8	72229750	72229974	72229777	72229946	EYA1	NM_172060	4	16	5	-	72229787	72229924
320357420	chr8	72211760	72211956	72211788	72211928	EYA1	NM_172060	4	16	6	-	72211873	72211955
320358777	chr8	72211873	72212008	72211901	72211984	EYA1	NM_172060	4	16	6	-	72211873	72211955
317527466	chr8	72211167	72211368	72211189	72211347	EYA1	NM_172060	4	16	7	-	72211282	72211468
317549225	chr8	72211325	72211520	72211348	72211492	EYA1	NM_172060	4	16	7	-	72211282	72211468
316478561	chr8	72183960	72184181	72183984	72184153	EYA1	NM_172060	4	16	8	-	72183993	72184132
317483006	chr8	72181946	72182093	72181974	72182068	EYA1	NM_172060	4	16	9	-	72181975	72182058
315753077	chr8	72156784	72156989	72156811	72156962	EYA1	NM_172060	4	16	10	-	72156838	72156927
320430442	chr8	72129158	72129374	72129185	72129346	EYA1	NM_172060	4	16	11	-	72129200	72129258
319750534	chr8	72128896	72129119	72128918	72129093	EYA1	NM_172060	4	16	12	-	72128927	72129087
316632653	chr8	72127788	72128000	72127812	72127972	EYA1	NM_172060	4	16	13	-	72127849	72127963
316260122	chr8	72127466	72127680	72127493	72127652	EYA1	NM_172060	4	16	14	-	72127622	72127743
316260717	chr8	72127615	72127813	72127643	72127793	EYA1	NM_172060	4	16	14	-	72127622	72127743
316644218	chr8	72123351	72123558	72123378	72123531	EYA1	NM_172060	4	16	15	-	72123391	72123491
316330561	chr8	72111464	72111684	72111485	72111661	EYA1	NM_172060	4	16	16	-	72109668	72111655
317608095	chr6	66204458	66204644	66204485	66204616	EYS	NM_001142800	1	43	4	-	66204556	66205500
317617557	chr6	66205083	66205243	66205111	66205218	EYS	NM_001142800	1	43	4	-	66204556	66205500
317623507	chr6	66204588	66204789	66204617	66204766	EYS	NM_001142800	1	43	4	-	66204556	66205500
317626313	chr6	66205197	66205325	66205219	66205297	EYS	NM_001142800	1	43	4	-	66204556	66205500
317638948	chr6	66204743	66204961	66204767	66204938	EYS	NM_001142800	1	43	4	-	66204556	66205500
317656341	chr6	66204915	66205134	66204939	66205111	EYS	NM_001142800	1	43	4	-	66204556	66205500
316471732	chr6	66200448	66200574	66200481	66200550	EYS	NM_001142800	1	43	5	-	66200487	66200600
316471883	chr6	66200549	66200740	66200572	66200710	EYS	NM_001142800	1	43	5	-	66200487	66200600
317862576	chr6	66114930	66115149	66114953	66115125	EYS	NM_001142800	1	43	6	-	66115067	66115260

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317864436	chr6	66115097	66115320	66115126	66115292	EYS	NM_001142800	1	43	6	-	66115067	66115260
316855570	chr6	66112369	66112577	66112397	66112549	EYS	NM_001142800	1	43	7	-	66112371	66112498
316819358	chr6	66094241	66094370	66094266	66094344	EYS	NM_001142800	1	43	8	-	66094279	66094393
316819834	chr6	66094323	66094546	66094347	66094518	EYS	NM_001142800	1	43	8	-	66094279	66094393
316999463	chr6	66063346	66063503	66063369	66063483	EYS	NM_001142800	1	43	9	-	66063351	66063510
317002662	chr6	66063387	66063524	66063414	66063496	EYS	NM_001142800	1	43	9	-	66063351	66063510
317368959	chr6	66053864	66053998	66053897	66053970	EYS	NM_001142800	1	43	10	-	66053931	66054070
317369263	chr6	66053940	66054067	66053962	66054046	EYS	NM_001142800	1	43	10	-	66053931	66054070
317370540	chr6	66054020	66054196	66054047	66054168	EYS	NM_001142800	1	43	10	-	66053931	66054070
315985942	chr6	66044783	66044964	66044811	66044938	EYS	NM_001142800	1	43	11	-	66044873	66045039
315988468	chr6	66044901	66045052	66044927	66045025	EYS	NM_001142800	1	43	11	-	66044873	66045039
317529702	chr6	66005626	66005839	66005655	66005818	EYS	NM_001142800	1	43	12	-	66005756	66006012
317541854	chr6	66005791	66005964	66005819	66005938	EYS	NM_001142800	1	43	12	-	66005756	66006012
317550652	chr6	66005919	66006139	66005939	66006112	EYS	NM_001142800	1	43	12	-	66005756	66006012
315945518	chr6	65767473	65767675	65767498	65767646	EYS	NM_001142800	1	43	13	-	65767507	65767620
316386692	chr6	65707382	65707571	65707406	65707546	EYS	NM_001142800	1	43	14	-	65707475	65707596
316393781	chr6	65707523	65707650	65707547	65707619	EYS	NM_001142800	1	43	14	-	65707475	65707596
316353242	chr6	65655524	65655728	65655548	65655703	EYS	NM_001142800	1	43	15	-	65655686	65655807
316363855	chr6	65655676	65655898	65655704	65655870	EYS	NM_001142800	1	43	15	-	65655686	65655807
317916934	chr6	65622238	65622438	65622264	65622412	EYS	NM_001142800	1	43	16	-	65622377	65622636
317932549	chr6	65622390	65622563	65622413	65622536	EYS	NM_001142800	1	43	16	-	65622377	65622636
317948492	chr6	65622512	65622732	65622537	65622705	EYS	NM_001142800	1	43	16	-	65622377	65622636
316112138	chr6	65612166	65612338	65612190	65612312	EYS	NM_001142800	1	43	17	-	65612297	65612393
316113333	chr6	65612285	65612429	65612313	65612401	EYS	NM_001142800	1	43	17	-	65612297	65612393
317099821	chr6	65611912	65612053	65611937	65612025	EYS	NM_001142800	1	43	18	-	65612006	65612113
317103933	chr6	65612003	65612194	65612026	65612166	EYS	NM_001142800	1	43	18	-	65612006	65612113
317494190	chr6	65596550	65596768	65596574	65596741	EYS	NM_001142800	1	43	19	-	65596590	65596735
317137569	chr6	65532404	65532595	65532437	65532571	EYS	NM_001142800	1	43	20	-	65532544	65532715
317138785	chr6	65532544	65532750	65532571	65532726	EYS	NM_001142800	1	43	20	-	65532544	65532715
316497916	chr6	65531390	65531598	65531418	65531571	EYS	NM_001142800	1	43	21	-	65531538	65531616
316502518	chr6	65531547	65531764	65531572	65531739	EYS	NM_001142800	1	43	21	-	65531538	65531616
316718171	chr6	65523187	65523325	65523212	65523299	EYS	NM_001142800	1	43	22	-	65523271	65523470
316725186	chr6	65523277	65523427	65523300	65523402	EYS	NM_001142800	1	43	22	-	65523271	65523470
316737786	chr6	65523383	65523600	65523403	65523574	EYS	NM_001142800	1	43	22	-	65523271	65523470
316850148	chr6	65335897	65336061	65335925	65336035	EYS	NM_001142800	1	43	23	-	65336014	65336138
316852244	chr6	65336013	65336207	65336036	65336179	EYS	NM_001142800	1	43	23	-	65336014	65336138
320546655	chr6	65327152	65327360	65327175	65327339	EYS	NM_001142800	1	43	24	-	65327311	65327426
320581301	chr6	65327311	65327448	65327339	65327420	EYS	NM_001142800	1	43	24	-	65327311	65327426
317509849	chr6	65302948	65303165	65302976	65303137	EYS	NM_001142800	1	43	25	-	65303010	65303202
317521238	chr6	65303111	65303303	65303136	65303275	EYS	NM_001142800	1	43	25	-	65303010	65303202
315527248	chr6	65300546	65300752	65300574	65300724	EYS	NM_001142800	1	43	26	-	65300116	65301882

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315534926	chr6	65300622	65300828	65300650	65300800	EYS	NM_001142800	1	43	26	-	65300116	65301882
315537396	chr6	65301087	65301306	65301115	65301287	EYS	NM_001142800	1	43	26	-	65300116	65301882
315544373	chr6	65300746	65300969	65300775	65300944	EYS	NM_001142800	1	43	26	-	65300116	65301882
315562772	chr6	65300920	65301140	65300945	65301116	EYS	NM_001142800	1	43	26	-	65300116	65301882
315568384	chr6	65301264	65301417	65301288	65301394	EYS	NM_001142800	1	43	26	-	65300116	65301882
315577902	chr6	65301372	65301499	65301395	65301476	EYS	NM_001142800	1	43	26	-	65300116	65301882
315584640	chr6	65301457	65301632	65301477	65301609	EYS	NM_001142800	1	43	26	-	65300116	65301882
317211807	chr6	65301587	65301764	65301610	65301740	EYS	NM_001142800	1	43	26	-	65300116	65301882
317237024	chr6	65300040	65300262	65300064	65300237	EYS	NM_001142800	1	43	26	-	65300116	65301882
317249941	chr6	65301718	65301942	65301741	65301917	EYS	NM_001142800	1	43	26	-	65300116	65301882
317261163	chr6	65300213	65300428	65300238	65300407	EYS	NM_001142800	1	43	26	-	65300116	65301882
317277161	chr6	65300385	65300606	65300408	65300578	EYS	NM_001142800	1	43	26	-	65300116	65301882
317919907	chr6	65148927	65149149	65148948	65149127	EYS	NM_001142800	1	43	27	-	65149055	65149245
317921097	chr6	65149111	65149252	65149135	65149225	EYS	NM_001142800	1	43	27	-	65149055	65149245
317924785	chr6	65149147	65149360	65149176	65149338	EYS	NM_001142800	1	43	27	-	65149055	65149245
316910496	chr6	65146002	65146201	65146028	65146173	EYS	NM_001142800	1	43	28	-	65146067	65146158
317532874	chr6	65098472	65098693	65098494	65098665	EYS	NM_001142800	1	43	29	-	65098583	65098733
317539099	chr6	65098643	65098865	65098666	65098837	EYS	NM_001142800	1	43	29	-	65098583	65098733
316472466	chr6	65016718	65016900	65016745	65016872	EYS	NM_001142800	1	43	30	-	65016863	65016975
316476109	chr6	65016845	65017059	65016873	65017031	EYS	NM_001142800	1	43	30	-	65016863	65016975
315723559	chr6	64940366	64940538	64940392	64940515	EYS	NM_001142800	1	43	31	-	64940485	64940717
315731400	chr6	64940494	64940684	64940516	64940659	EYS	NM_001142800	1	43	31	-	64940485	64940717
315739262	chr6	64940638	64940845	64940660	64940817	EYS	NM_001142800	1	43	31	-	64940485	64940717
315877280	chr6	64791693	64791884	64791721	64791856	EYS	NM_001142800	1	43	32	-	64791749	64791895
315877290	chr6	64791816	64792003	64791842	64791971	EYS	NM_001142800	1	43	32	-	64791749	64791895
317955022	chr6	64776200	64776378	64776223	64776350	EYS	NM_001142800	1	43	33	-	64776231	64776384
317956870	chr6	64776326	64776493	64776351	64776465	EYS	NM_001142800	1	43	33	-	64776231	64776384
316922208	chr6	64708916	64709119	64708942	64709091	EYS	NM_001142800	1	43	34	-	64708968	64709076
316419601	chr6	64694233	64694441	64694258	64694418	EYS	NM_001142800	1	43	35	-	64694276	64694496
316435204	chr6	64694398	64694555	64694419	64694527	EYS	NM_001142800	1	43	35	-	64694276	64694496
319858442	chr6	64574025	64574244	64574049	64574217	EYS	NM_001142800	1	43	36	-	64574079	64574251
316651555	chr6	64515964	64516186	64515985	64516159	EYS	NM_001142800	1	43	37	-	64516083	64516265
316674213	chr6	64516138	64516341	64516160	64516316	EYS	NM_001142800	1	43	37	-	64516083	64516265
317748331	chr6	64498922	64499145	64498945	64499122	EYS	NM_001142800	1	43	38	-	64498951	64499117
317376670	chr6	64497903	64498120	64497931	64498099	EYS	NM_001142800	1	43	39	-	64497998	64498142
317377491	chr6	64498076	64498298	64498100	64498269	EYS	NM_001142800	1	43	39	-	64497998	64498142
317084126	chr6	64487827	64487959	64487851	64487935	EYS	NM_001142800	1	43	40	-	64487899	64488073
317097805	chr6	64487913	64488101	64487936	64488075	EYS	NM_001142800	1	43	40	-	64487899	64488073
316190205	chr6	64472320	64472514	64472348	64472491	EYS	NM_001142800	1	43	41	-	64472354	64472526
316208599	chr6	64472456	64472580	64472482	64472551	EYS	NM_001142800	1	43	41	-	64472354	64472526
316096232	chr6	64436388	64436604	64436412	64436579	EYS	NM_001142800	1	43	42	-	64436412	64436573

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316063768	chr6	64430409	64430540	64430436	64430508	EYS	NM_001142800	1	43	43	-	64429876	64431693
316063791	chr6	64430489	64430697	64430520	64430670	EYS	NM_001142800	1	43	43	-	64429876	64431693
316064010	chr6	64430645	64430842	64430671	64430816	EYS	NM_001142800	1	43	43	-	64429876	64431693
316069507	chr6	64430789	64430975	64430817	64430947	EYS	NM_001142800	1	43	43	-	64429876	64431693
317458801	chr6	64430915	64431133	64430943	64431105	EYS	NM_001142800	1	43	43	-	64429876	64431693
317462071	chr6	64431083	64431292	64431104	64431270	EYS	NM_001142800	1	43	43	-	64429876	64431693
317462242	chr6	64431370	64431519	64431395	64431492	EYS	NM_001142800	1	43	43	-	64429876	64431693
317467204	chr6	64431467	64431664	64431493	64431641	EYS	NM_001142800	1	43	43	-	64429876	64431693
317475423	chr6	64431616	64431780	64431642	64431755	EYS	NM_001142800	1	43	43	-	64429876	64431693
317483957	chr6	64431245	64431422	64431271	64431394	EYS	NM_001142800	1	43	43	-	64429876	64431693
317608095	chr6	66204458	66204644	66204485	66204616	EYS	NM_001142801	2	12	4	-	66204556	66205500
317617557	chr6	66205083	66205243	66205111	66205218	EYS	NM_001142801	2	12	4	-	66204556	66205500
317623507	chr6	66204588	66204789	66204617	66204766	EYS	NM_001142801	2	12	4	-	66204556	66205500
317626313	chr6	66205197	66205325	66205219	66205297	EYS	NM_001142801	2	12	4	-	66204556	66205500
317638948	chr6	66204743	66204961	66204767	66204938	EYS	NM_001142801	2	12	4	-	66204556	66205500
317656341	chr6	66204915	66205134	66204939	66205111	EYS	NM_001142801	2	12	4	-	66204556	66205500
316471732	chr6	66200448	66200574	66200481	66200550	EYS	NM_001142801	2	12	5	-	66200487	66200600
316471883	chr6	66200549	66200740	66200572	66200710	EYS	NM_001142801	2	12	5	-	66200487	66200600
317862576	chr6	66114930	66115149	66114953	66115125	EYS	NM_001142801	2	12	6	-	66115067	66115260
317864436	chr6	66115097	66115320	66115126	66115292	EYS	NM_001142801	2	12	6	-	66115067	66115260
316855570	chr6	66112369	66112577	66112397	66112549	EYS	NM_001142801	2	12	7	-	66112371	66112498
316819358	chr6	66094241	66094370	66094266	66094344	EYS	NM_001142801	2	12	8	-	66094279	66094393
316819834	chr6	66094323	66094546	66094347	66094518	EYS	NM_001142801	2	12	8	-	66094279	66094393
316999463	chr6	66063346	66063503	66063369	66063483	EYS	NM_001142801	2	12	9	-	66063351	66063510
317002662	chr6	66063387	66063524	66063414	66063496	EYS	NM_001142801	2	12	9	-	66063351	66063510
317368959	chr6	66053864	66053998	66053897	66053970	EYS	NM_001142801	2	12	10	-	66053931	66054070
317369263	chr6	66053940	66054067	66053962	66054046	EYS	NM_001142801	2	12	10	-	66053931	66054070
317370540	chr6	66054020	66054196	66054047	66054168	EYS	NM_001142801	2	12	10	-	66053931	66054070
315985942	chr6	66044783	66044964	66044811	66044938	EYS	NM_001142801	2	12	11	-	66044873	66045039
315988468	chr6	66044901	66045052	66044927	66045025	EYS	NM_001142801	2	12	11	-	66044873	66045039
317608095	chr6	66204458	66204644	66204485	66204616	EYS	NM_198283	3	10	3	-	66204556	66205500
317617557	chr6	66205083	66205243	66205111	66205218	EYS	NM_198283	3	10	3	-	66204556	66205500
317623507	chr6	66204588	66204789	66204617	66204766	EYS	NM_198283	3	10	3	-	66204556	66205500
317626313	chr6	66205197	66205325	66205219	66205297	EYS	NM_198283	3	10	3	-	66204556	66205500
317638948	chr6	66204743	66204961	66204767	66204938	EYS	NM_198283	3	10	3	-	66204556	66205500
317656341	chr6	66204915	66205134	66204939	66205111	EYS	NM_198283	3	10	3	-	66204556	66205500
316471732	chr6	66200448	66200574	66200481	66200550	EYS	NM_198283	3	10	4	-	66200487	66200600
316471883	chr6	66200549	66200740	66200572	66200710	EYS	NM_198283	3	10	4	-	66200487	66200600
317862576	chr6	66114930	66115149	66114953	66115125	EYS	NM_198283	3	10	5	-	66115067	66115260
317864436	chr6	66115097	66115320	66115126	66115292	EYS	NM_198283	3	10	5	-	66115067	66115260
316855570	chr6	66112369	66112577	66112397	66112549	EYS	NM_198283	3	10	6	-	66112371	66112498

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316819358	chr6	66094241	66094370	66094266	66094344	EYS	NM_198283	3	10	7	-	66094279	66094393
316819834	chr6	66094323	66094546	66094347	66094518	EYS	NM_198283	3	10	7	-	66094279	66094393
316999463	chr6	66063346	66063503	66063369	66063483	EYS	NM_198283	3	10	8	-	66063351	66063510
317002662	chr6	66063387	66063524	66063414	66063496	EYS	NM_198283	3	10	8	-	66063351	66063510
317368959	chr6	66053864	66053998	66053897	66053970	EYS	NM_198283	3	10	9	-	66053931	66054070
317369263	chr6	66053940	66054067	66053962	66054046	EYS	NM_198283	3	10	9	-	66053931	66054070
317370540	chr6	66054020	66054196	66054047	66054168	EYS	NM_198283	3	10	9	-	66053931	66054070
315985942	chr6	66044783	66044964	66044811	66044938	EYS	NM_198283	3	10	10	-	66044806	66045039
315988468	chr6	66044901	66045052	66044927	66045025	EYS	NM_198283	3	10	10	-	66044806	66045039
317084416	chrX	154250655	154250860	154250675	154250834	F8	NM_000132	1	26	1	-	154250685	154250998
316354917	chrX	154227592	154227813	154227616	154227786	F8	NM_000132	1	26	2	-	154227754	154227875
316370047	chrX	154227766	154227910	154227787	154227882	F8	NM_000132	1	26	2	-	154227754	154227875
317107308	chrX	154225173	154225397	154225197	154225375	F8	NM_000132	1	26	3	-	154225248	154225370
315689861	chrX	154221107	154221303	154221130	154221277	F8	NM_000132	1	26	4	-	154221211	154221423
315707441	chrX	154221254	154221473	154221278	154221444	F8	NM_000132	1	26	4	-	154221211	154221423
315921138	chrX	154215357	154215581	154215386	154215560	F8	NM_000132	1	26	5	-	154215512	154215580
315923042	chrX	154215532	154215664	154215561	154215638	F8	NM_000132	1	26	5	-	154215512	154215580
316033628	chrX	154212888	154213111	154212914	154213086	F8	NM_000132	1	26	6	-	154212962	154213078
316083875	chrX	154197468	154197691	154197495	154197664	F8	NM_000132	1	26	7	-	154197606	154197827
316102166	chrX	154197643	154197864	154197665	154197836	F8	NM_000132	1	26	7	-	154197606	154197827
317567875	chrX	154194604	154194823	154194630	154194797	F8	NM_000132	1	26	8	-	154194701	154194962
317587909	chrX	154194773	154194994	154194798	154194968	F8	NM_000132	1	26	8	-	154194701	154194962
315525030	chrX	154194132	154194298	154194160	154194272	F8	NM_000132	1	26	9	-	154194245	154194416
315547610	chrX	154194250	154194467	154194273	154194440	F8	NM_000132	1	26	9	-	154194245	154194416
317341497	chrX	154189361	154189506	154189386	154189478	F8	NM_000132	1	26	10	-	154189350	154189443
316787247	chrX	154185182	154185340	154185206	154185312	F8	NM_000132	1	26	11	-	154185232	154185446
316800684	chrX	154185288	154185495	154185313	154185466	F8	NM_000132	1	26	11	-	154185232	154185446
320537155	chrX	154182003	154182196	154182031	154182175	F8	NM_000132	1	26	12	-	154182167	154182317
320548186	chrX	154182153	154182364	154182176	154182337	F8	NM_000132	1	26	12	-	154182167	154182317
316753628	chrX	154175843	154176043	154175869	154176019	F8	NM_000132	1	26	13	-	154175973	154176182
316783508	chrX	154175995	154176217	154176020	154176189	F8	NM_000132	1	26	13	-	154175973	154176182
317652120	chrX	154158308	154158530	154158332	154158506	F8	NM_000132	1	26	14	-	154156846	154159951
317653060	chrX	154158821	154158971	154158848	154158949	F8	NM_000132	1	26	14	-	154156846	154159951
317654653	chrX	154156781	154156918	154156809	154156892	F8	NM_000132	1	26	14	-	154156846	154159951
317656642	chrX	154156868	154157080	154156893	154157057	F8	NM_000132	1	26	14	-	154156846	154159951
317657241	chrX	154158920	154159115	154158948	154159090	F8	NM_000132	1	26	14	-	154156846	154159951
317660501	chrX	154157340	154157562	154157362	154157540	F8	NM_000132	1	26	14	-	154156846	154159951
317661638	chrX	154158481	154158702	154158507	154158681	F8	NM_000132	1	26	14	-	154156846	154159951
317664678	chrX	154159066	154159242	154159091	154159218	F8	NM_000132	1	26	14	-	154156846	154159951
317665047	chrX	154159324	154159541	154159352	154159515	F8	NM_000132	1	26	14	-	154156846	154159951
317666266	chrX	154157831	154158050	154157859	154158024	F8	NM_000132	1	26	14	-	154156846	154159951

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317672543	chrX	154157031	154157213	154157058	154157193	F8	NM_000132	1	26	14	-	154156846	154159951
317679718	chrX	154159198	154159406	154159219	154159378	F8	NM_000132	1	26	14	-	154156846	154159951
317680098	chrX	154159825	154160038	154159853	154160014	F8	NM_000132	1	26	14	-	154156846	154159951
317686621	chrX	154159489	154159713	154159511	154159687	F8	NM_000132	1	26	14	-	154156846	154159951
317692070	chrX	154158656	154158880	154158682	154158854	F8	NM_000132	1	26	14	-	154156846	154159951
317695301	chrX	154157510	154157728	154157538	154157705	F8	NM_000132	1	26	14	-	154156846	154159951
317700985	chrX	154157167	154157386	154157194	154157361	F8	NM_000132	1	26	14	-	154156846	154159951
317706783	chrX	154157997	154158191	154158025	154158167	F8	NM_000132	1	26	14	-	154156846	154159951
317709163	chrX	154159659	154159880	154159687	154159852	F8	NM_000132	1	26	14	-	154156846	154159951
317716731	chrX	154158139	154158358	154158168	154158331	F8	NM_000132	1	26	14	-	154156846	154159951
317717157	chrX	154157657	154157880	154157685	154157858	F8	NM_000132	1	26	14	-	154156846	154159951
317242614	chrX	154134669	154134833	154134696	154134809	F8	NM_000132	1	26	15	-	154134695	154134848
317258200	chrX	154134785	154134909	154134810	154134886	F8	NM_000132	1	26	15	-	154134695	154134848
316752929	chrX	154133052	154133274	154133077	154133246	F8	NM_000132	1	26	16	-	154133086	154133298
316765654	chrX	154133220	154133375	154133246	154133348	F8	NM_000132	1	26	16	-	154133086	154133298
315967956	chrX	154132449	154132673	154132475	154132647	F8	NM_000132	1	26	17	-	154132571	154132799
315992566	chrX	154132625	154132825	154132648	154132801	F8	NM_000132	1	26	17	-	154132571	154132799
316532899	chrX	154132159	154132285	154132183	154132263	F8	NM_000132	1	26	18	-	154132181	154132363
316543055	chrX	154132236	154132429	154132264	154132401	F8	NM_000132	1	26	18	-	154132181	154132363
317097921	chrX	154130232	154130358	154130256	154130335	F8	NM_000132	1	26	19	-	154130326	154130442
317103269	chrX	154130310	154130515	154130336	154130487	F8	NM_000132	1	26	19	-	154130326	154130442
316044342	chrX	154129560	154129745	154129588	154129722	F8	NM_000132	1	26	20	-	154129646	154129717
316070604	chrX	154128052	154128273	154128079	154128245	F8	NM_000132	1	26	21	-	154128141	154128226
316038176	chrX	154124248	154124443	154124277	154124416	F8	NM_000132	1	26	22	-	154124352	154124507
316048734	chrX	154124389	154124609	154124417	154124581	F8	NM_000132	1	26	22	-	154124352	154124507
315874264	chrX	154091311	154091535	154091333	154091507	F8	NM_000132	1	26	23	-	154091358	154091502
315525728	chrX	154089837	154090045	154089858	154090022	F8	NM_000132	1	26	24	-	154089993	154090141
315565956	chrX	154090002	154090182	154090023	154090155	F8	NM_000132	1	26	24	-	154089993	154090141
316103034	chrX	154088549	154088748	154088575	154088725	F8	NM_000132	1	26	25	-	154088707	154088883
316116860	chrX	154088700	154088912	154088726	154088888	F8	NM_000132	1	26	25	-	154088707	154088883
317577241	chrX	154065767	154065987	154065793	154065964	F8	NM_000132	1	26	26	-	154064064	154066027
317587194	chrX	154065943	154066067	154065965	154066039	F8	NM_000132	1	26	26	-	154064064	154066027
315874264	chrX	154091311	154091535	154091333	154091507	F8	NM_019863	2	5	2	-	154091358	154091502
315525728	chrX	154089837	154090045	154089858	154090022	F8	NM_019863	2	5	3	-	154089993	154090141
315565956	chrX	154090002	154090182	154090023	154090155	F8	NM_019863	2	5	3	-	154089993	154090141
316103034	chrX	154088549	154088748	154088575	154088725	F8	NM_019863	2	5	4	-	154088707	154088883
316116860	chrX	154088700	154088912	154088726	154088888	F8	NM_019863	2	5	4	-	154088707	154088883
317577241	chrX	154065767	154065987	154065793	154065964	F8	NM_019863	2	5	5	-	154064064	154066027
317587194	chrX	154065943	154066067	154065965	154066039	F8	NM_019863	2	5	5	-	154064064	154066027
316179608	chrX	138612781	138612996	138612802	138612968	F9	NM_000133	1	8	1	+	138612895	138613011
316197315	chrX	138612948	138613135	138612969	138613106	F9	NM_000133	1	8	1	+	138612895	138613011

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319785723	chrX	138619011	138619219	138619034	138619196	F9	NM_000133	1	8	2	+	138619169	138619332
319793495	chrX	138619171	138619365	138619197	138619338	F9	NM_000133	1	8	2	+	138619169	138619332
316508662	chrX	138619454	138619664	138619487	138619636	F9	NM_000133	1	8	3	+	138619521	138619545
317512183	chrX	138623175	138623394	138623195	138623366	F9	NM_000133	1	8	4	+	138623235	138623348
317900064	chrX	138630409	138630594	138630430	138630566	F9	NM_000133	1	8	5	+	138630522	138630650
317907209	chrX	138630546	138630755	138630567	138630727	F9	NM_000133	1	8	5	+	138630522	138630650
316918140	chrX	138633111	138633334	138633132	138633306	F9	NM_000133	1	8	6	+	138633221	138633423
316944969	chrX	138633279	138633456	138633307	138633428	F9	NM_000133	1	8	6	+	138633221	138633423
316963583	chrX	138642742	138642937	138642768	138642914	F9	NM_000133	1	8	7	+	138642900	138643014
316980980	chrX	138642888	138643055	138642915	138643027	F9	NM_000133	1	8	7	+	138642900	138643014
316590633	chrX	138643603	138643822	138643627	138643800	F9	NM_000133	1	8	8	+	138643683	138645617
316605530	chrX	138643779	138643980	138643801	138643956	F9	NM_000133	1	8	8	+	138643683	138645617
316636683	chrX	138643930	138644140	138643957	138644111	F9	NM_000133	1	8	8	+	138643683	138645617
316693546	chrX	138644089	138644284	138644112	138644257	F9	NM_000133	1	8	8	+	138643683	138645617
229299501	chr16	89882861	89883016	89882878	89882998	FANCA	NM_000135	1	43	1	-	89882945	89883065
228467884	chr16	89882225	89882440	89882246	89882417	FANCA	NM_000135	1	43	2	-	89882285	89882394
227685428	chr16	89880935	89881074	89880963	89881052	FANCA	NM_000135	1	43	3	-	89880928	89881021
328562978	chr16	89880779	89880987	89880806	89880962	FANCA	NM_000135	1	43	3	-	89880928	89881021
230673113	chr16	89877303	89877524	89877324	89877496	FANCA	NM_000135	1	43	4	-	89877337	89877479
230338959	chr16	89877063	89877286	89877085	89877257	FANCA	NM_000135	1	43	5	-	89877115	89877210
229932120	chr16	89874604	89874771	89874626	89874750	FANCA	NM_000135	1	43	6	-	89874702	89874775
329081687	chr16	89874730	89874924	89874751	89874896	FANCA	NM_000135	1	43	6	-	89874702	89874775
229172773	chr16	89871620	89871844	89871645	89871820	FANCA	NM_000135	1	43	7	-	89871688	89871800
229066910	chr16	89869589	89869803	89869618	89869781	FANCA	NM_000135	1	43	8	-	89869667	89869749
329574492	chr16	89865888	89866108	89865910	89866079	FANCA	NM_000135	1	43	9	-	89866013	89866046
230538666	chr16	89865476	89865678	89865497	89865654	FANCA	NM_000135	1	43	10	-	89865574	89865640
230804203	chr16	89862259	89862460	89862281	89862438	FANCA	NM_000135	1	43	11	-	89862314	89862426
230691580	chr16	89858798	89858997	89858821	89858969	FANCA	NM_000135	1	43	12	-	89858879	89858955
230585670	chr16	89858286	89858504	89858307	89858481	FANCA	NM_000135	1	43	13	-	89858335	89858476
230162479	chr16	89857761	89857975	89857783	89857950	FANCA	NM_000135	1	43	14	-	89857811	89857944
228553284	chr16	89851220	89851370	89851242	89851351	FANCA	NM_000135	1	43	15	-	89851262	89851372
328769875	chr16	89851329	89851539	89851349	89851520	FANCA	NM_000135	1	43	15	-	89851262	89851372
228334311	chr16	89849316	89849536	89849342	89849515	FANCA	NM_000135	1	43	16	-	89849415	89849510
231797331	chr16	89849157	89849368	89849178	89849340	FANCA	NM_000135	1	43	17	-	89849267	89849326
232788574	chr16	89846186	89846398	89846209	89846372	FANCA	NM_000135	1	43	18	-	89846277	89846365
230799413	chr16	89845281	89845440	89845305	89845418	FANCA	NM_000135	1	43	19	-	89845351	89845411
228350229	chr16	89845133	89845328	89845159	89845304	FANCA	NM_000135	1	43	20	-	89845209	89845258
228914735	chr16	89842068	89842243	89842090	89842219	FANCA	NM_000135	1	43	21	-	89842150	89842223
229671282	chr16	89839639	89839828	89839661	89839802	FANCA	NM_000135	1	43	22	-	89839679	89839792
230094656	chr16	89838048	89838259	89838069	89838231	FANCA	NM_000135	1	43	23	-	89838086	89838222
230398852	chr16	89836874	89837073	89836893	89837052	FANCA	NM_000135	1	43	24	-	89836972	89837042

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230710528	chr16	89836479	89836695	89836501	89836674	FANCA	NM_000135	1	43	25	-	89836574	89836667
227858245	chr16	89836214	89836345	89836234	89836326	FANCA	NM_000135	1	43	26	-	89836245	89836432
227864654	chr16	89836280	89836504	89836301	89836482	FANCA	NM_000135	1	43	26	-	89836245	89836432
228494722	chr16	89833482	89833609	89833500	89833582	FANCA	NM_000135	1	43	27	-	89833549	89833645
228498560	chr16	89833562	89833753	89833583	89833728	FANCA	NM_000135	1	43	27	-	89833549	89833645
228953917	chr16	89831195	89831351	89831215	89831329	FANCA	NM_000135	1	43	28	-	89831298	89831474
228971716	chr16	89831308	89831521	89831330	89831497	FANCA	NM_000135	1	43	28	-	89831298	89831474
229832790	chr16	89828329	89828481	89828350	89828454	FANCA	NM_000135	1	43	29	-	89828357	89828430
230482086	chr16	89824964	89825146	89824988	89825120	FANCA	NM_000135	1	43	30	-	89824985	89825113
230455340	chr16	89818469	89818669	89818496	89818641	FANCA	NM_000135	1	43	31	-	89818546	89818630
230129014	chr16	89816112	89816336	89816131	89816315	FANCA	NM_000135	1	43	32	-	89816138	89816310
232899129	chr16	89814977	89815201	89814996	89815180	FANCA	NM_000135	1	43	33	-	89815067	89815175
229359560	chr16	89813127	89813330	89813147	89813304	FANCA	NM_000135	1	43	34	-	89813239	89813298
231478428	chr16	89812934	89813156	89812955	89813132	FANCA	NM_000135	1	43	35	-	89812992	89813096
227694259	chr16	89811287	89811507	89811310	89811487	FANCA	NM_000135	1	43	36	-	89811367	89811479
228875513	chr16	89809154	89809374	89809181	89809354	FANCA	NM_000135	1	43	37	-	89809208	89809346
230679175	chr16	89807120	89807339	89807141	89807310	FANCA	NM_000135	1	43	38	-	89807212	89807274
227990399	chr16	89806319	89806541	89806340	89806520	FANCA	NM_000135	1	43	39	-	89806402	89806507
229505118	chr16	89805788	89805992	89805809	89805971	FANCA	NM_000135	1	43	40	-	89805886	89805961
230575658	chr16	89805438	89805635	89805459	89805612	FANCA	NM_000135	1	43	41	-	89805541	89805697
230585232	chr16	89805588	89805743	89805608	89805720	FANCA	NM_000135	1	43	41	-	89805541	89805697
329540886	chr16	89805186	89805410	89805212	89805387	FANCA	NM_000135	1	43	42	-	89805290	89805382
231337417	chr16	89804930	89805141	89804951	89805121	FANCA	NM_000135	1	43	43	-	89803959	89805116
229299501	chr16	89882861	89883016	89882878	89882998	FANCA	NM_001018112	2	11	1	-	89882945	89883065
228467884	chr16	89882225	89882440	89882246	89882417	FANCA	NM_001018112	2	11	2	-	89882285	89882394
227685428	chr16	89880935	89881074	89880963	89881052	FANCA	NM_001018112	2	11	3	-	89880928	89881021
328562978	chr16	89880779	89880987	89880806	89880962	FANCA	NM_001018112	2	11	3	-	89880928	89881021
230673113	chr16	89877303	89877524	89877324	89877496	FANCA	NM_001018112	2	11	4	-	89877337	89877479
230338959	chr16	89877063	89877286	89877085	89877257	FANCA	NM_001018112	2	11	5	-	89877115	89877210
229932120	chr16	89874604	89874771	89874626	89874750	FANCA	NM_001018112	2	11	6	-	89874702	89874775
329081687	chr16	89874730	89874924	89874751	89874896	FANCA	NM_001018112	2	11	6	-	89874702	89874775
229172773	chr16	89871620	89871844	89871645	89871820	FANCA	NM_001018112	2	11	7	-	89871688	89871800
229066910	chr16	89869589	89869803	89869618	89869781	FANCA	NM_001018112	2	11	8	-	89869667	89869749
329574492	chr16	89865888	89866108	89865910	89866079	FANCA	NM_001018112	2	11	9	-	89866013	89866046
230538666	chr16	89865476	89865678	89865497	89865654	FANCA	NM_001018112	2	11	10	-	89865574	89865640
232467100	chr16	89865331	89865537	89865352	89865513	FANCA	NM_001018112	2	11	11	-	89864767	89865487
232569651	chr9	98011391	98011601	98011417	98011578	FANCC	NM_000136	1	15	2	-	98011409	98011651
329211858	chr9	98011248	98011443	98011270	98011416	FANCC	NM_000136	1	15	2	-	98011409	98011651
230981295	chr9	98009629	98009842	98009656	98009814	FANCC	NM_000136	1	15	3	-	98009714	98009798
228877099	chr9	98002937	98003145	98002964	98003118	FANCC	NM_000136	1	15	4	-	98002931	98003025
328885928	chr9	98002776	98002961	98002804	98002934	FANCC	NM_000136	1	15	4	-	98002931	98003025

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229973491	chr9	97934181	97934405	97934203	97934377	FANCC	NM_000136	1	15	5	-	97934319	97934429
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_000136	1	15	5	-	97934319	97934429
232095859	chr9	97933253	97933458	97933280	97933430	FANCC	NM_000136	1	15	6	-	97933361	97933425
232122924	chr9	97912118	97912243	97912141	97912220	FANCC	NM_000136	1	15	7	-	97912205	97912369
232134571	chr9	97912199	97912415	97912221	97912389	FANCC	NM_000136	1	15	7	-	97912205	97912369
228759355	chr9	97897568	97897764	97897595	97897743	FANCC	NM_000136	1	15	8	-	97897628	97897784
228770475	chr9	97897714	97897918	97897736	97897893	FANCC	NM_000136	1	15	8	-	97897628	97897784
230062958	chr9	97888703	97888922	97888728	97888894	FANCC	NM_000136	1	15	9	-	97888811	97888863
227929253	chr9	97887291	97887498	97887318	97887474	FANCC	NM_000136	1	15	10	-	97887368	97887467
329438869	chr9	97879516	97879722	97879537	97879694	FANCC	NM_000136	1	15	11	-	97879597	97879672
230596386	chr9	97876804	97877024	97876825	97877002	FANCC	NM_000136	1	15	12	-	97876911	97876992
232655913	chr9	97873744	97873963	97873766	97873937	FANCC	NM_000136	1	15	13	-	97873745	97873919
329893949	chr9	97873601	97873802	97873623	97873781	FANCC	NM_000136	1	15	13	-	97873745	97873919
230193234	chr9	97869270	97869440	97869290	97869420	FANCC	NM_000136	1	15	14	-	97869348	97869551
230201006	chr9	97869395	97869587	97869417	97869565	FANCC	NM_000136	1	15	14	-	97869348	97869551
232187763	chr9	97863807	97864019	97863828	97863997	FANCC	NM_000136	1	15	15	-	97861336	97864132
232207121	chr9	97863977	97864165	97863998	97864137	FANCC	NM_000136	1	15	15	-	97861336	97864132
232569651	chr9	98011391	98011601	98011417	98011578	FANCC	NM_001243743	2	15	2	-	98011409	98011651
329211858	chr9	98011248	98011443	98011270	98011416	FANCC	NM_001243743	2	15	2	-	98011409	98011651
230981295	chr9	98009629	98009842	98009656	98009814	FANCC	NM_001243743	2	15	3	-	98009714	98009798
228877099	chr9	98002937	98003145	98002964	98003118	FANCC	NM_001243743	2	15	4	-	98002931	98003025
328885928	chr9	98002776	98002961	98002804	98002934	FANCC	NM_001243743	2	15	4	-	98002931	98003025
229973491	chr9	97934181	97934405	97934203	97934377	FANCC	NM_001243743	2	15	5	-	97934319	97934429
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_001243743	2	15	5	-	97934319	97934429
232095859	chr9	97933253	97933458	97933280	97933430	FANCC	NM_001243743	2	15	6	-	97933361	97933425
232122924	chr9	97912118	97912243	97912141	97912220	FANCC	NM_001243743	2	15	7	-	97912205	97912369
232134571	chr9	97912199	97912415	97912221	97912389	FANCC	NM_001243743	2	15	7	-	97912205	97912369
228759355	chr9	97897568	97897764	97897595	97897743	FANCC	NM_001243743	2	15	8	-	97897628	97897784
228770475	chr9	97897714	97897918	97897736	97897893	FANCC	NM_001243743	2	15	8	-	97897628	97897784
230062958	chr9	97888703	97888922	97888728	97888894	FANCC	NM_001243743	2	15	9	-	97888811	97888863
227929253	chr9	97887291	97887498	97887318	97887474	FANCC	NM_001243743	2	15	10	-	97887368	97887467
329438869	chr9	97879516	97879722	97879537	97879694	FANCC	NM_001243743	2	15	11	-	97879597	97879672
230596386	chr9	97876804	97877024	97876825	97877002	FANCC	NM_001243743	2	15	12	-	97876911	97876992
232655913	chr9	97873744	97873963	97873766	97873937	FANCC	NM_001243743	2	15	13	-	97873745	97873919
329893949	chr9	97873601	97873802	97873623	97873781	FANCC	NM_001243743	2	15	13	-	97873745	97873919
230193234	chr9	97869270	97869440	97869290	97869420	FANCC	NM_001243743	2	15	14	-	97869348	97869551
230201006	chr9	97869395	97869587	97869417	97869565	FANCC	NM_001243743	2	15	14	-	97869348	97869551
232187763	chr9	97863807	97864019	97863828	97863997	FANCC	NM_001243743	2	15	15	-	97861336	97864132
232207121	chr9	97863977	97864165	97863998	97864137	FANCC	NM_001243743	2	15	15	-	97861336	97864132
232569651	chr9	98011391	98011601	98011417	98011578	FANCC	NM_001243744	3	14	2	-	98011409	98011651
329211858	chr9	98011248	98011443	98011270	98011416	FANCC	NM_001243744	3	14	2	-	98011409	98011651

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230981295	chr9	98009629	98009842	98009656	98009814	FANCC	NM_001243744	3	14	3	-	98009714	98009798
228877099	chr9	98002937	98003145	98002964	98003118	FANCC	NM_001243744	3	14	4	-	98002931	98003025
328885928	chr9	98002776	98002961	98002804	98002934	FANCC	NM_001243744	3	14	4	-	98002931	98003025
229973491	chr9	97934181	97934405	97934203	97934377	FANCC	NM_001243744	3	14	5	-	97934319	97934429
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_001243744	3	14	5	-	97934319	97934429
232095859	chr9	97933253	97933458	97933280	97933430	FANCC	NM_001243744	3	14	6	-	97933361	97933425
232122924	chr9	97912118	97912243	97912141	97912220	FANCC	NM_001243744	3	14	7	-	97912205	97912369
232134571	chr9	97912199	97912415	97912221	97912389	FANCC	NM_001243744	3	14	7	-	97912205	97912369
228759355	chr9	97897568	97897764	97897595	97897743	FANCC	NM_001243744	3	14	8	-	97897628	97897784
228770475	chr9	97897714	97897918	97897736	97897893	FANCC	NM_001243744	3	14	8	-	97897628	97897784
230062958	chr9	97888703	97888922	97888728	97888894	FANCC	NM_001243744	3	14	9	-	97888811	97888863
227929253	chr9	97887291	97887498	97887318	97887474	FANCC	NM_001243744	3	14	10	-	97887368	97887467
329438869	chr9	97879516	97879722	97879537	97879694	FANCC	NM_001243744	3	14	11	-	97879597	97879672
230596386	chr9	97876804	97877024	97876825	97877002	FANCC	NM_001243744	3	14	12	-	97876911	97876992
232655913	chr9	97873744	97873963	97873766	97873937	FANCC	NM_001243744	3	14	13	-	97873745	97873919
329893949	chr9	97873601	97873802	97873623	97873781	FANCC	NM_001243744	3	14	13	-	97873745	97873919
232431157	chr9	97873450	97873661	97873471	97873640	FANCC	NM_001243744	3	14	14	-	97872508	97873627
329893949	chr9	97873601	97873802	97873623	97873781	FANCC	NM_001243744	3	14	14	-	97872508	97873627
230564557	chr11	22647007	22647230	22647027	22647211	FANCF	NM_022725	1	1	1	-	22644079	22647387
230567237	chr11	22647150	22647333	22647170	22647312	FANCF	NM_022725	1	1	1	-	22644079	22647387
230573648	chr11	22647288	22647511	22647310	22647486	FANCF	NM_022725	1	1	1	-	22644079	22647387
230646917	chr11	22646608	22646774	22646630	22646753	FANCF	NM_022725	1	1	1	-	22644079	22647387
230651561	chr11	22646734	22646916	22646754	22646891	FANCF	NM_022725	1	1	1	-	22644079	22647387
230654190	chr11	22646868	22647046	22646892	22647026	FANCF	NM_022725	1	1	1	-	22644079	22647387
232902356	chr11	22646142	22646339	22646167	22646315	FANCF	NM_022725	1	1	1	-	22644079	22647387
232936268	chr11	22646289	22646510	22646316	22646486	FANCF	NM_022725	1	1	1	-	22644079	22647387
232964567	chr11	22646465	22646651	22646487	22646630	FANCF	NM_022725	1	1	1	-	22644079	22647387
230445022	chr9	35079384	35079566	35079405	35079545	FANCG	NM_004629	1	14	1	-	35079438	35080013
230553247	chr9	35079045	35079263	35079067	35079243	FANCG	NM_004629	1	14	2	-	35079148	35079238
227746753	chr9	35078541	35078765	35078569	35078740	FANCG	NM_004629	1	14	3	-	35078602	35078733
230956472	chr9	35078154	35078372	35078177	35078345	FANCG	NM_004629	1	14	4	-	35078138	35078340
329534535	chr9	35078002	35078198	35078025	35078178	FANCG	NM_004629	1	14	4	-	35078138	35078340
228425956	chr9	35077204	35077425	35077227	35077401	FANCG	NM_004629	1	14	5	-	35077261	35077396
229651784	chr9	35076923	35077138	35076947	35077115	FANCG	NM_004629	1	14	6	-	35076968	35077098
231247220	chr9	35076649	35076873	35076672	35076849	FANCG	NM_004629	1	14	7	-	35076721	35076867
231279030	chr9	35076829	35076967	35076850	35076942	FANCG	NM_004629	1	14	7	-	35076721	35076867
228458041	chr9	35076331	35076497	35076355	35076477	FANCG	NM_004629	1	14	8	-	35076429	35076580
228472846	chr9	35076457	35076638	35076478	35076610	FANCG	NM_004629	1	14	8	-	35076429	35076580
231407847	chr9	35075844	35076054	35075867	35076031	FANCG	NM_004629	1	14	9	-	35075959	35076025
228762684	chr9	35075409	35075626	35075433	35075602	FANCG	NM_004629	1	14	10	-	35075462	35075751
228788812	chr9	35075574	35075790	35075596	35075767	FANCG	NM_004629	1	14	10	-	35075462	35075751

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329107672	chr9	35075129	35075348	35075152	35075327	FANCG	NM_004629	1	14	11	-	35075276	35075322
229521494	chr9	35074895	35075107	35074917	35075084	FANCG	NM_004629	1	14	12	-	35074924	35075079
230667946	chr9	35074309	35074532	35074332	35074504	FANCG	NM_004629	1	14	13	-	35074368	35074491
230744155	chr9	35074023	35074246	35074047	35074223	FANCG	NM_004629	1	14	14	-	35073835	35074213
317643286	chr15	48936712	48936923	48936733	48936901	FBN1	NM_000138	1	66	2	-	48936803	48937147
317650512	chr15	48936846	48936973	48936867	48936956	FBN1	NM_000138	1	66	2	-	48936803	48937147
317650743	chr15	48936925	48937136	48936945	48937119	FBN1	NM_000138	1	66	2	-	48936803	48937147
317155392	chr15	48905133	48905350	48905155	48905327	FBN1	NM_000138	1	66	3	-	48905207	48905289
316078907	chr15	48902778	48902957	48902803	48902935	FBN1	NM_000138	1	66	4	-	48902925	48903023
316081217	chr15	48902909	48903055	48902936	48903028	FBN1	NM_000138	1	66	4	-	48902925	48903023
317888564	chr15	48892197	48892370	48892221	48892345	FBN1	NM_000138	1	66	5	-	48892336	48892431
317903292	chr15	48892321	48892491	48892346	48892463	FBN1	NM_000138	1	66	5	-	48892336	48892431
316412699	chr15	48888382	48888603	48888405	48888580	FBN1	NM_000138	1	66	6	-	48888480	48888575
317020529	chr15	48829746	48829966	48829769	48829946	FBN1	NM_000138	1	66	7	-	48829808	48830005
317027027	chr15	48829921	48830144	48829943	48830122	FBN1	NM_000138	1	66	7	-	48829808	48830005
317082841	chr15	48826248	48826399	48826271	48826379	FBN1	NM_000138	1	66	8	-	48826277	48826402
317083967	chr15	48826345	48826472	48826373	48826439	FBN1	NM_000138	1	66	8	-	48826277	48826402
317338003	chr15	48818169	48818363	48818192	48818338	FBN1	NM_000138	1	66	9	-	48818327	48818452
317345093	chr15	48818311	48818524	48818339	48818499	FBN1	NM_000138	1	66	9	-	48818327	48818452
317421291	chr15	48812974	48813109	48812995	48813087	FBN1	NM_000138	1	66	10	-	48812856	48813014
319752627	chr15	48812812	48813015	48812833	48812994	FBN1	NM_000138	1	66	10	-	48812856	48813014
317518671	chr15	48808323	48808454	48808356	48808430	FBN1	NM_000138	1	66	11	-	48808380	48808559
317524582	chr15	48808402	48808599	48808425	48808575	FBN1	NM_000138	1	66	11	-	48808380	48808559
316574448	chr15	48807519	48807690	48807547	48807667	FBN1	NM_000138	1	66	12	-	48807584	48807724
316581197	chr15	48807648	48807849	48807668	48807826	FBN1	NM_000138	1	66	12	-	48807584	48807724
316344545	chr15	48805643	48805855	48805663	48805833	FBN1	NM_000138	1	66	13	-	48805746	48805865
316354258	chr15	48805808	48806028	48805833	48806000	FBN1	NM_000138	1	66	13	-	48805746	48805865
317039528	chr15	48802093	48802287	48802121	48802263	FBN1	NM_000138	1	66	14	-	48802241	48802366
317041984	chr15	48802241	48802462	48802264	48802437	FBN1	NM_000138	1	66	14	-	48802241	48802366
320391260	chr15	48800751	48800974	48800779	48800947	FBN1	NM_000138	1	66	15	-	48800779	48800901
315832481	chr15	48797074	48797295	48797098	48797272	FBN1	NM_000138	1	66	16	-	48797222	48797344
315857658	chr15	48797252	48797445	48797273	48797419	FBN1	NM_000138	1	66	16	-	48797222	48797344
316163626	chr15	48795952	48796169	48795972	48796144	FBN1	NM_000138	1	66	17	-	48795984	48796136
320525579	chr15	48791076	48791283	48791096	48791257	FBN1	NM_000138	1	66	18	-	48791182	48791235
317726396	chr15	48789344	48789564	48789370	48789538	FBN1	NM_000138	1	66	19	-	48789463	48789588
317737385	chr15	48789512	48789735	48789539	48789708	FBN1	NM_000138	1	66	19	-	48789463	48789588
316001418	chr15	48788190	48788395	48788218	48788367	FBN1	NM_000138	1	66	20	-	48788297	48788422
316003221	chr15	48788342	48788484	48788368	48788458	FBN1	NM_000138	1	66	20	-	48788297	48788422
316115445	chr15	48787586	48787772	48787613	48787747	FBN1	NM_000138	1	66	21	-	48787666	48787785
316117931	chr15	48787718	48787901	48787742	48787879	FBN1	NM_000138	1	66	21	-	48787666	48787785
315688875	chr15	48787248	48787431	48787275	48787410	FBN1	NM_000138	1	66	22	-	48787320	48787457

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315699054	chr15	48787388	48787611	48787411	48787584	FBN1	NM_000138	1	66	22	-	48787320	48787457
315729502	chr15	48786303	48786522	48786329	48786494	FBN1	NM_000138	1	66	23	-	48786401	48786451
315771257	chr15	48784549	48784773	48784572	48784751	FBN1	NM_000138	1	66	24	-	48784658	48784783
315777472	chr15	48784727	48784937	48784752	48784909	FBN1	NM_000138	1	66	24	-	48784658	48784783
316984142	chr15	48781942	48782165	48781965	48782144	FBN1	NM_000138	1	66	25	-	48782048	48782275
317001078	chr15	48782120	48782310	48782145	48782284	FBN1	NM_000138	1	66	25	-	48782048	48782275
315758743	chr15	48780514	48780732	48780538	48780705	FBN1	NM_000138	1	66	26	-	48780565	48780690
316742277	chr15	48780250	48780474	48780274	48780452	FBN1	NM_000138	1	66	27	-	48780310	48780438
316957965	chr15	48779442	48779666	48779469	48779639	FBN1	NM_000138	1	66	28	-	48779509	48779634
317164234	chr15	48779132	48779316	48779157	48779296	FBN1	NM_000138	1	66	29	-	48779272	48779397
317166006	chr15	48779272	48779437	48779297	48779409	FBN1	NM_000138	1	66	29	-	48779272	48779397
317768220	chr15	48777528	48777693	48777555	48777665	FBN1	NM_000138	1	66	30	-	48777571	48777693
316703497	chr15	48775844	48776046	48775867	48776021	FBN1	NM_000138	1	66	31	-	48776015	48776140
316710560	chr15	48775993	48776192	48776022	48776166	FBN1	NM_000138	1	66	31	-	48776015	48776140
316229767	chr15	48773842	48773974	48773863	48773948	FBN1	NM_000138	1	66	32	-	48773852	48773977
316232267	chr15	48773928	48774137	48773949	48774109	FBN1	NM_000138	1	66	32	-	48773852	48773977
317770215	chr15	48766674	48766887	48766702	48766861	FBN1	NM_000138	1	66	33	-	48766725	48766847
315530577	chr15	48766314	48766529	48766337	48766505	FBN1	NM_000138	1	66	34	-	48766452	48766574
315559121	chr15	48766486	48766704	48766506	48766677	FBN1	NM_000138	1	66	34	-	48766452	48766574
315984924	chr15	48764697	48764909	48764719	48764885	FBN1	NM_000138	1	66	35	-	48764748	48764873
317768826	chr15	48762718	48762940	48762741	48762919	FBN1	NM_000138	1	66	36	-	48762831	48762953
317784975	chr15	48762898	48763076	48762920	48763048	FBN1	NM_000138	1	66	36	-	48762831	48762953
316630172	chr15	48760535	48760758	48760560	48760736	FBN1	NM_000138	1	66	37	-	48760609	48760731
317039077	chr15	48759961	48760161	48759986	48760140	FBN1	NM_000138	1	66	38	-	48760135	48760299
317050628	chr15	48760118	48760332	48760141	48760304	FBN1	NM_000138	1	66	38	-	48760135	48760299
315597478	chr15	48757966	48758184	48757993	48758156	FBN1	NM_000138	1	66	39	-	48757987	48758055
316667432	chr15	48757815	48758018	48757837	48757992	FBN1	NM_000138	1	66	39	-	48757987	48758055
316644505	chr15	48757603	48757792	48757626	48757766	FBN1	NM_000138	1	66	40	-	48757765	48757890
316662549	chr15	48757743	48757967	48757767	48757939	FBN1	NM_000138	1	66	40	-	48757765	48757890
316667432	chr15	48757815	48758018	48757837	48757992	FBN1	NM_000138	1	66	40	-	48757765	48757890
316840291	chr15	48755952	48756169	48755978	48756148	FBN1	NM_000138	1	66	41	-	48756096	48756218
316859108	chr15	48756124	48756279	48756149	48756255	FBN1	NM_000138	1	66	41	-	48756096	48756218
317821743	chr15	48755121	48755308	48755142	48755287	FBN1	NM_000138	1	66	42	-	48755279	48755437
317842974	chr15	48755260	48755477	48755288	48755453	FBN1	NM_000138	1	66	42	-	48755279	48755437
317634013	chr15	48752412	48752551	48752435	48752529	FBN1	NM_000138	1	66	43	-	48752443	48752514
316220194	chr15	48748776	48748999	48748804	48748976	FBN1	NM_000138	1	66	44	-	48748834	48748959
316112930	chr15	48744705	48744926	48744730	48744899	FBN1	NM_000138	1	66	45	-	48744759	48744881
316937787	chr15	48740817	48741015	48740843	48740993	FBN1	NM_000138	1	66	46	-	48740965	48741090
316940677	chr15	48740955	48741089	48740978	48741062	FBN1	NM_000138	1	66	46	-	48740965	48741090
316941441	chr15	48741041	48741265	48741063	48741236	FBN1	NM_000138	1	66	46	-	48740965	48741090
317119725	chr15	48738866	48739087	48738888	48739062	FBN1	NM_000138	1	66	47	-	48738903	48739019

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315645433	chr15	48737536	48737760	48737563	48737733	FBN1	NM_000138	1	66	48	-	48737573	48737701
315901666	chr15	48736694	48736892	48736714	48736864	FBN1	NM_000138	1	66	49	-	48736738	48736857
317580376	chr15	48733864	48734079	48733889	48734050	FBN1	NM_000138	1	66	50	-	48733918	48734043
316489051	chr15	48729928	48730151	48729949	48730124	FBN1	NM_000138	1	66	51	-	48729965	48730114
316182255	chr15	48729460	48729645	48729489	48729617	FBN1	NM_000138	1	66	52	-	48729519	48729584
315910562	chr15	48729063	48729284	48729091	48729256	FBN1	NM_000138	1	66	53	-	48729158	48729274
317130385	chr15	48726720	48726940	48726747	48726915	FBN1	NM_000138	1	66	54	-	48726791	48726910
320429480	chr15	48725005	48725227	48725030	48725199	FBN1	NM_000138	1	66	55	-	48725063	48725185
320394718	chr15	48722758	48722980	48722779	48722952	FBN1	NM_000138	1	66	56	-	48722868	48722999
320453234	chr15	48722930	48723135	48722953	48723108	FBN1	NM_000138	1	66	56	-	48722868	48722999
317901665	chr15	48720501	48720708	48720523	48720680	FBN1	NM_000138	1	66	57	-	48720543	48720668
317379247	chr15	48719645	48719846	48719668	48719824	FBN1	NM_000138	1	66	58	-	48719764	48719970
317383437	chr15	48719798	48720019	48719822	48719992	FBN1	NM_000138	1	66	58	-	48719764	48719970
316557308	chr15	48717806	48717966	48717831	48717940	FBN1	NM_000138	1	66	59	-	48717936	48718061
316561950	chr15	48717913	48718130	48717941	48718103	FBN1	NM_000138	1	66	59	-	48717936	48718061
316710320	chr15	48717495	48717718	48717519	48717694	FBN1	NM_000138	1	66	60	-	48717566	48717688
319794966	chr15	48714094	48714301	48714123	48714278	FBN1	NM_000138	1	66	61	-	48714149	48714265
315886560	chr15	48713642	48713845	48713663	48713823	FBN1	NM_000138	1	66	62	-	48713755	48713883
315905983	chr15	48713803	48713982	48713824	48713958	FBN1	NM_000138	1	66	62	-	48713755	48713883
315609864	chr15	48712807	48713030	48712829	48713008	FBN1	NM_000138	1	66	63	-	48712884	48713003
317405737	chr15	48707641	48707865	48707667	48707844	FBN1	NM_000138	1	66	64	-	48707733	48707964
317412185	chr15	48707821	48707991	48707845	48707969	FBN1	NM_000138	1	66	64	-	48707733	48707964
316885563	chr15	48704603	48704794	48704624	48704771	FBN1	NM_000138	1	66	65	-	48704766	48704940
316902809	chr15	48704749	48704972	48704772	48704946	FBN1	NM_000138	1	66	65	-	48704766	48704940
317715191	chr15	48703414	48703632	48703442	48703604	FBN1	NM_000138	1	66	66	-	48700503	48703576
317720180	chr15	48703012	48703236	48703036	48703208	FBN1	NM_000138	1	66	66	-	48700503	48703576
317726796	chr15	48703181	48703374	48703209	48703353	FBN1	NM_000138	1	66	66	-	48700503	48703576
317737479	chr15	48703332	48703465	48703354	48703441	FBN1	NM_000138	1	66	66	-	48700503	48703576
316207845	chr22	32871330	32871488	32871347	32871462	FBXO7	NM_001033024	1	9	1	+	32871224	32871385
315662471	chr22	32874957	32875163	32874983	32875137	FBXO7	NM_001033024	1	9	2	+	32875120	32875262
315688282	chr22	32875113	32875337	32875138	32875310	FBXO7	NM_001033024	1	9	2	+	32875120	32875262
315790595	chr22	32879788	32879983	32879816	32879960	FBXO7	NM_001033024	1	9	3	+	32879884	32880111
315797314	chr22	32879939	32880140	32879961	32880116	FBXO7	NM_001033024	1	9	3	+	32879884	32880111
317048368	chr22	32880942	32881117	32880969	32881097	FBXO7	NM_001033024	1	9	4	+	32881055	32881196
317051202	chr22	32881078	32881227	32881098	32881203	FBXO7	NM_001033024	1	9	4	+	32881055	32881196
316898411	chr22	32883641	32883857	32883662	32883831	FBXO7	NM_001033024	1	9	5	+	32883732	32883815
315764002	chr22	32886935	32887123	32886963	32887100	FBXO7	NM_001033024	1	9	6	+	32887073	32887168
315766653	chr22	32887073	32887255	32887101	32887227	FBXO7	NM_001033024	1	9	6	+	32887073	32887168
315525228	chr22	32888994	32889141	32889021	32889120	FBXO7	NM_001033024	1	9	7	+	32889092	32889268
315545468	chr22	32889095	32889306	32889121	32889279	FBXO7	NM_001033024	1	9	7	+	32889092	32889268
316234235	chr22	32891417	32891568	32891442	32891537	FBXO7	NM_001033024	1	9	8	+	32891480	32891517

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317271043	chr22	32894066	32894231	32894094	32894207	FBXO7	NM_001033024	1	9	9	+	32894131	32894818
317284048	chr22	32894188	32894411	32894208	32894390	FBXO7	NM_001033024	1	9	9	+	32894131	32894818
317299413	chr22	32894368	32894591	32894390	32894570	FBXO7	NM_001033024	1	9	9	+	32894131	32894818
317917221	chr22	32870865	32871078	32870884	32871061	FBXO7	NM_012179	2	9	1	+	32870707	32871111
317917436	chr22	32870999	32871202	32871016	32871184	FBXO7	NM_012179	2	9	1	+	32870707	32871111
315662471	chr22	32874957	32875163	32874983	32875137	FBXO7	NM_012179	2	9	2	+	32874968	32875262
315688282	chr22	32875113	32875337	32875138	32875310	FBXO7	NM_012179	2	9	2	+	32874968	32875262
317157086	chr22	32874850	32875010	32874878	32874982	FBXO7	NM_012179	2	9	2	+	32874968	32875262
315790595	chr22	32879788	32879983	32879816	32879960	FBXO7	NM_012179	2	9	3	+	32879884	32880111
315797314	chr22	32879939	32880140	32879961	32880116	FBXO7	NM_012179	2	9	3	+	32879884	32880111
317048368	chr22	32880942	32881117	32880969	32881097	FBXO7	NM_012179	2	9	4	+	32881055	32881196
317051202	chr22	32881078	32881227	32881098	32881203	FBXO7	NM_012179	2	9	4	+	32881055	32881196
316898411	chr22	32883641	32883857	32883662	32883831	FBXO7	NM_012179	2	9	5	+	32883732	32883815
315764002	chr22	32886935	32887123	32886963	32887100	FBXO7	NM_012179	2	9	6	+	32887073	32887168
315766653	chr22	32887073	32887255	32887101	32887227	FBXO7	NM_012179	2	9	6	+	32887073	32887168
315525228	chr22	32888994	32889141	32889021	32889120	FBXO7	NM_012179	2	9	7	+	32889092	32889268
315545468	chr22	32889095	32889306	32889121	32889279	FBXO7	NM_012179	2	9	7	+	32889092	32889268
316234235	chr22	32891417	32891568	32891442	32891537	FBXO7	NM_012179	2	9	8	+	32891480	32891517
317271043	chr22	32894066	32894231	32894094	32894207	FBXO7	NM_012179	2	9	9	+	32894131	32894818
317284048	chr22	32894188	32894411	32894208	32894390	FBXO7	NM_012179	2	9	9	+	32894131	32894818
317299413	chr22	32894368	32894591	32894390	32894570	FBXO7	NM_012179	2	9	9	+	32894131	32894818
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_001174063	1	18	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_001174063	1	18	2	-	38314874	38315052
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_001174063	1	18	4	-	38285864	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_001174063	1	18	5	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_001174063	1	18	5	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_001174063	1	18	6	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_001174063	1	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174063	1	18	7	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_001174063	1	18	8	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_001174063	1	18	9	-	38277057	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_001174063	1	18	9	-	38277057	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_001174063	1	18	10	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_001174063	1	18	11	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_001174063	1	18	12	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_001174063	1	18	13	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_001174063	1	18	13	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_001174063	1	18	14	-	38272297	38272419

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_001174063	1	18	14	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_001174063	1	18	15	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_001174063	1	18	16	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_001174063	1	18	16	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_001174063	1	18	17	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_001174063	1	18	17	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_001174063	1	18	18	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_001174063	1	18	18	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_001174064	2	19	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_001174064	2	19	2	-	38314874	38315052
232244462	chr8	38297788	38297944	38297815	38297917	FGFR1	NM_001174064	2	19	3	-	38297824	38297891
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_001174064	2	19	5	-	38285864	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_001174064	2	19	6	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_001174064	2	19	6	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_001174064	2	19	7	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_001174064	2	19	8	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174064	2	19	8	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_001174064	2	19	9	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_001174064	2	19	10	-	38277057	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_001174064	2	19	10	-	38277057	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_001174064	2	19	11	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_001174064	2	19	12	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_001174064	2	19	13	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_001174064	2	19	14	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_001174064	2	19	14	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_001174064	2	19	15	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_001174064	2	19	15	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_001174064	2	19	16	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_001174064	2	19	17	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_001174064	2	19	17	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_001174064	2	19	18	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_001174064	2	19	18	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_001174064	2	19	19	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_001174064	2	19	19	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_001174065	3	18	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_001174065	3	18	2	-	38314874	38315052
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_001174065	3	18	3	-	38287200	38287466

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_001174065	3	18	4	-	38285870	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_001174065	3	18	5	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_001174065	3	18	5	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_001174065	3	18	6	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_001174065	3	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174065	3	18	7	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_001174065	3	18	8	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_001174065	3	18	9	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_001174065	3	18	9	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_001174065	3	18	10	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_001174065	3	18	11	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_001174065	3	18	12	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_001174065	3	18	13	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_001174065	3	18	13	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_001174065	3	18	14	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_001174065	3	18	14	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_001174065	3	18	15	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_001174065	3	18	16	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_001174065	3	18	16	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_001174065	3	18	17	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_001174065	3	18	17	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_001174065	3	18	18	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_001174065	3	18	18	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_001174066	4	17	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_001174066	4	17	2	-	38314874	38315052
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_001174066	4	17	3	-	38285864	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_001174066	4	17	4	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_001174066	4	17	4	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_001174066	4	17	5	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_001174066	4	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174066	4	17	6	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_001174066	4	17	7	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_001174066	4	17	8	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_001174066	4	17	8	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_001174066	4	17	9	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_001174066	4	17	10	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_001174066	4	17	11	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_001174066	4	17	12	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_001174066	4	17	12	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_001174066	4	17	13	-	38272297	38272419

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_001174066	4	17	13	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_001174066	4	17	14	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_001174066	4	17	15	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_001174066	4	17	15	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_001174066	4	17	16	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_001174066	4	17	16	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_001174066	4	17	17	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_001174066	4	17	17	-	38268656	38271322
232833813	chr8	38318490	38318698	38318511	38318673	FGFR1	NM_001174067	5	19	2	-	38318614	38318773
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_001174067	5	19	3	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_001174067	5	19	3	-	38314874	38315052
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_001174067	5	19	5	-	38285870	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_001174067	5	19	6	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_001174067	5	19	6	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_001174067	5	19	7	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_001174067	5	19	8	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174067	5	19	8	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_001174067	5	19	9	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_001174067	5	19	10	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_001174067	5	19	10	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_001174067	5	19	11	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_001174067	5	19	12	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_001174067	5	19	13	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_001174067	5	19	14	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_001174067	5	19	14	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_001174067	5	19	15	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_001174067	5	19	15	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_001174067	5	19	16	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_001174067	5	19	17	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_001174067	5	19	17	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_001174067	5	19	18	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_001174067	5	19	18	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_001174067	5	19	19	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_001174067	5	19	19	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_015850	6	18	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_015850	6	18	2	-	38314874	38315052
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_015850	6	18	3	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_015850	6	18	3	-	38287200	38287466

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_015850	6	18	3	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_015850	6	18	4	-	38285870	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_015850	6	18	5	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_015850	6	18	5	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_015850	6	18	6	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_015850	6	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_015850	6	18	7	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_015850	6	18	8	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_015850	6	18	9	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_015850	6	18	9	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_015850	6	18	10	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_015850	6	18	11	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_015850	6	18	12	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_015850	6	18	13	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_015850	6	18	13	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_015850	6	18	14	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_015850	6	18	14	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_015850	6	18	15	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_015850	6	18	16	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_015850	6	18	16	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_015850	6	18	17	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_015850	6	18	17	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_015850	6	18	18	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_015850	6	18	18	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_023105	7	17	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_023105	7	17	2	-	38314874	38315052
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_023105	7	17	3	-	38285864	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_023105	7	17	4	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_023105	7	17	4	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_023105	7	17	5	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_023105	7	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023105	7	17	6	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_023105	7	17	7	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_023105	7	17	8	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_023105	7	17	8	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_023105	7	17	9	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_023105	7	17	10	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_023105	7	17	11	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_023105	7	17	12	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_023105	7	17	12	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_023105	7	17	13	-	38272297	38272419

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_023105	7	17	13	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_023105	7	17	14	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_023105	7	17	15	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_023105	7	17	15	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_023105	7	17	16	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_023105	7	17	16	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_023105	7	17	17	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_023105	7	17	17	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_023106	8	17	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_023106	8	17	2	-	38314874	38315052
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_023106	8	17	3	-	38285870	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_023106	8	17	4	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_023106	8	17	4	-	38285439	38285611
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_023106	8	17	5	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_023106	8	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023106	8	17	6	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_023106	8	17	7	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_023106	8	17	8	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_023106	8	17	8	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_023106	8	17	9	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_023106	8	17	10	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_023106	8	17	11	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_023106	8	17	12	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_023106	8	17	12	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_023106	8	17	13	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_023106	8	17	13	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_023106	8	17	14	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_023106	8	17	15	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_023106	8	17	15	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_023106	8	17	16	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_023106	8	17	16	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_023106	8	17	17	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_023106	8	17	17	-	38268656	38271322
230738248	chr8	38314960	38315099	38314984	38315074	FGFR1	NM_023110	9	18	2	-	38314874	38315052
329436125	chr8	38314783	38315003	38314805	38314983	FGFR1	NM_023110	9	18	2	-	38314874	38315052
227977219	chr8	38287212	38287415	38287234	38287397	FGFR1	NM_023110	9	18	3	-	38287200	38287466
227982567	chr8	38287363	38287566	38287384	38287547	FGFR1	NM_023110	9	18	3	-	38287200	38287466
328650290	chr8	38287048	38287264	38287069	38287243	FGFR1	NM_023110	9	18	3	-	38287200	38287466
228001477	chr8	38285807	38285994	38285829	38285973	FGFR1	NM_023110	9	18	4	-	38285864	38285953
228278945	chr8	38285392	38285596	38285416	38285574	FGFR1	NM_023110	9	18	5	-	38285439	38285611
329648032	chr8	38285553	38285761	38285575	38285741	FGFR1	NM_023110	9	18	5	-	38285439	38285611

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229762274	chr8	38283590	38283795	38283611	38283770	FGFR1	NM_023110	9	18	6	-	38283640	38283763
229180966	chr8	38281974	38282154	38281995	38282132	FGFR1	NM_023110	9	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023110	9	18	7	-	38282027	38282217
232410604	chr8	38279282	38279487	38279304	38279464	FGFR1	NM_023110	9	18	8	-	38279315	38279459
229692679	chr8	38276942	38277149	38276966	38277122	FGFR1	NM_023110	9	18	9	-	38277051	38277253
229713390	chr8	38277102	38277279	38277123	38277258	FGFR1	NM_023110	9	18	9	-	38277051	38277253
228876952	chr8	38275699	38275921	38275722	38275901	FGFR1	NM_023110	9	18	10	-	38275746	38275891
231772097	chr8	38275328	38275543	38275349	38275519	FGFR1	NM_023110	9	18	11	-	38275388	38275509
228565350	chr8	38274747	38274967	38274768	38274941	FGFR1	NM_023110	9	18	12	-	38274824	38274934
228261140	chr8	38273342	38273565	38273362	38273544	FGFR1	NM_023110	9	18	13	-	38273388	38273578
329648453	chr8	38273523	38273729	38273541	38273704	FGFR1	NM_023110	9	18	13	-	38273388	38273578
227948825	chr8	38272240	38272384	38272262	38272359	FGFR1	NM_023110	9	18	14	-	38272297	38272419
227958207	chr8	38272340	38272521	38272360	38272495	FGFR1	NM_023110	9	18	14	-	38272297	38272419
230104831	chr8	38272045	38272263	38272066	38272239	FGFR1	NM_023110	9	18	15	-	38272077	38272147
229652415	chr8	38271562	38271692	38271582	38271672	FGFR1	NM_023110	9	18	16	-	38271670	38271807
229657918	chr8	38271651	38271853	38271672	38271833	FGFR1	NM_023110	9	18	16	-	38271670	38271807
229660052	chr8	38271309	38271490	38271331	38271469	FGFR1	NM_023110	9	18	17	-	38271436	38271541
229662222	chr8	38271430	38271602	38271451	38271578	FGFR1	NM_023110	9	18	17	-	38271436	38271541
230392874	chr8	38271102	38271294	38271123	38271274	FGFR1	NM_023110	9	18	18	-	38268656	38271322
230397695	chr8	38271241	38271451	38271260	38271429	FGFR1	NM_023110	9	18	18	-	38268656	38271322
229282611	chr4	1795518	1795742	1795536	1795724	FGFR3	NM_000142	1	18	2	+	1795560	1795770
328760002	chr4	1795718	1795901	1795735	1795882	FGFR3	NM_000142	1	18	2	+	1795560	1795770
227845110	chr4	1800953	1801172	1800972	1801153	FGFR3	NM_000142	1	18	3	+	1800981	1801250
227846601	chr4	1801083	1801293	1801103	1801272	FGFR3	NM_000142	1	18	3	+	1800981	1801250
227587450	chr4	1801444	1801654	1801462	1801635	FGFR3	NM_000142	1	18	4	+	1801474	1801539
229021837	chr4	1803049	1803256	1803067	1803239	FGFR3	NM_000142	1	18	5	+	1803094	1803263
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_000142	1	18	5	+	1803094	1803263
227974265	chr4	1803361	1803555	1803381	1803537	FGFR3	NM_000142	1	18	6	+	1803347	1803470
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_000142	1	18	6	+	1803347	1803470
227442268	chr4	1803535	1803691	1803552	1803671	FGFR3	NM_000142	1	18	7	+	1803562	1803752
227442769	chr4	1803638	1803858	1803660	1803837	FGFR3	NM_000142	1	18	7	+	1803562	1803752
227391156	chr4	1805392	1805545	1805413	1805523	FGFR3	NM_000142	1	18	8	+	1805419	1805563
227392369	chr4	1805504	1805667	1805524	1805646	FGFR3	NM_000142	1	18	8	+	1805419	1805563
227640662	chr4	1806037	1806259	1806057	1806235	FGFR3	NM_000142	1	18	9	+	1806057	1806247
328929345	chr4	1805891	1806111	1805911	1806090	FGFR3	NM_000142	1	18	9	+	1806057	1806247
328931069	chr4	1806214	1806407	1806234	1806383	FGFR3	NM_000142	1	18	9	+	1806057	1806247
227913054	chr4	1806435	1806619	1806458	1806600	FGFR3	NM_000142	1	18	10	+	1806551	1806696
227917304	chr4	1806574	1806769	1806595	1806749	FGFR3	NM_000142	1	18	10	+	1806551	1806696
227874749	chr4	1807042	1807211	1807062	1807188	FGFR3	NM_000142	1	18	11	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_000142	1	18	11	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_000142	1	18	12	+	1807286	1807396

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_000142	1	18	12	+	1807286	1807396
228569220	chr4	1807482	1807622	1807502	1807602	FGFR3	NM_000142	1	18	13	+	1807477	1807667
228572656	chr4	1807559	1807754	1807580	1807734	FGFR3	NM_000142	1	18	13	+	1807477	1807667
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_000142	1	18	13	+	1807477	1807667
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_000142	1	18	14	+	1807778	1807900
227995002	chr4	1807733	1807949	1807753	1807930	FGFR3	NM_000142	1	18	14	+	1807778	1807900
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_000142	1	18	15	+	1807984	1808054
227608653	chr4	1808245	1808447	1808264	1808429	FGFR3	NM_000142	1	18	16	+	1808273	1808410
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_000142	1	18	17	+	1808556	1808661
329689148	chr4	1808622	1808812	1808640	1808795	FGFR3	NM_000142	1	18	17	+	1808556	1808661
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_000142	1	18	18	+	1808843	1810599
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_000142	1	18	18	+	1808843	1810599
229282611	chr4	1795518	1795742	1795536	1795724	FGFR3	NM_001163213	2	18	2	+	1795560	1795770
328760002	chr4	1795718	1795901	1795735	1795882	FGFR3	NM_001163213	2	18	2	+	1795560	1795770
227845110	chr4	1800953	1801172	1800972	1801153	FGFR3	NM_001163213	2	18	3	+	1800981	1801250
227846601	chr4	1801083	1801293	1801103	1801272	FGFR3	NM_001163213	2	18	3	+	1800981	1801250
227587450	chr4	1801444	1801654	1801462	1801635	FGFR3	NM_001163213	2	18	4	+	1801474	1801539
229021837	chr4	1803049	1803256	1803067	1803239	FGFR3	NM_001163213	2	18	5	+	1803094	1803263
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_001163213	2	18	5	+	1803094	1803263
227974265	chr4	1803361	1803555	1803381	1803537	FGFR3	NM_001163213	2	18	6	+	1803347	1803470
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_001163213	2	18	6	+	1803347	1803470
227442268	chr4	1803535	1803691	1803552	1803671	FGFR3	NM_001163213	2	18	7	+	1803562	1803752
227442769	chr4	1803638	1803858	1803660	1803837	FGFR3	NM_001163213	2	18	7	+	1803562	1803752
227469618	chr4	1804614	1804838	1804631	1804818	FGFR3	NM_001163213	2	18	8	+	1804641	1804791
227640662	chr4	1806037	1806259	1806057	1806235	FGFR3	NM_001163213	2	18	9	+	1806057	1806247
328929345	chr4	1805891	1806111	1805911	1806090	FGFR3	NM_001163213	2	18	9	+	1806057	1806247
328931069	chr4	1806214	1806407	1806234	1806383	FGFR3	NM_001163213	2	18	9	+	1806057	1806247
227913054	chr4	1806435	1806619	1806458	1806600	FGFR3	NM_001163213	2	18	10	+	1806551	1806696
227917304	chr4	1806574	1806769	1806595	1806749	FGFR3	NM_001163213	2	18	10	+	1806551	1806696
227874749	chr4	1807042	1807211	1807062	1807188	FGFR3	NM_001163213	2	18	11	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_001163213	2	18	11	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_001163213	2	18	12	+	1807286	1807396
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_001163213	2	18	12	+	1807286	1807396
228569220	chr4	1807482	1807622	1807502	1807602	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
228572656	chr4	1807559	1807754	1807580	1807734	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_001163213	2	18	14	+	1807778	1807900
227995002	chr4	1807733	1807949	1807753	1807930	FGFR3	NM_001163213	2	18	14	+	1807778	1807900
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_001163213	2	18	15	+	1807984	1808054
227608653	chr4	1808245	1808447	1808264	1808429	FGFR3	NM_001163213	2	18	16	+	1808273	1808410
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_001163213	2	18	17	+	1808556	1808661

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329689148	chr4	1808622	1808812	1808640	1808795	FGFR3	NM_001163213	2	18	17	+	1808556	1808661
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_001163213	2	18	18	+	1808843	1810599
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_001163213	2	18	18	+	1808843	1810599
229282611	chr4	1795518	1795742	1795536	1795724	FGFR3	NM_022965	3	16	2	+	1795560	1795770
328760002	chr4	1795718	1795901	1795735	1795882	FGFR3	NM_022965	3	16	2	+	1795560	1795770
227845110	chr4	1800953	1801172	1800972	1801153	FGFR3	NM_022965	3	16	3	+	1800981	1801250
227846601	chr4	1801083	1801293	1801103	1801272	FGFR3	NM_022965	3	16	3	+	1800981	1801250
227587450	chr4	1801444	1801654	1801462	1801635	FGFR3	NM_022965	3	16	4	+	1801474	1801539
229021837	chr4	1803049	1803256	1803067	1803239	FGFR3	NM_022965	3	16	5	+	1803094	1803263
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_022965	3	16	5	+	1803094	1803263
227974265	chr4	1803361	1803555	1803381	1803537	FGFR3	NM_022965	3	16	6	+	1803347	1803470
328619261	chr4	1803204	1803421	1803224	1803402	FGFR3	NM_022965	3	16	6	+	1803347	1803470
227442268	chr4	1803535	1803691	1803552	1803671	FGFR3	NM_022965	3	16	7	+	1803562	1803752
227442769	chr4	1803638	1803858	1803660	1803837	FGFR3	NM_022965	3	16	7	+	1803562	1803752
227913054	chr4	1806435	1806619	1806458	1806600	FGFR3	NM_022965	3	16	8	+	1806551	1806696
227917304	chr4	1806574	1806769	1806595	1806749	FGFR3	NM_022965	3	16	8	+	1806551	1806696
227874749	chr4	1807042	1807211	1807062	1807188	FGFR3	NM_022965	3	16	9	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_022965	3	16	9	+	1807082	1807203
228335196	chr4	1807167	1807379	1807186	1807357	FGFR3	NM_022965	3	16	10	+	1807286	1807396
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_022965	3	16	10	+	1807286	1807396
228569220	chr4	1807482	1807622	1807502	1807602	FGFR3	NM_022965	3	16	11	+	1807477	1807667
228572656	chr4	1807559	1807754	1807580	1807734	FGFR3	NM_022965	3	16	11	+	1807477	1807667
329306679	chr4	1807317	1807533	1807343	1807512	FGFR3	NM_022965	3	16	11	+	1807477	1807667
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_022965	3	16	12	+	1807778	1807900
227995002	chr4	1807733	1807949	1807753	1807930	FGFR3	NM_022965	3	16	12	+	1807778	1807900
227627917	chr4	1807862	1808078	1807882	1808060	FGFR3	NM_022965	3	16	13	+	1807984	1808054
227608653	chr4	1808245	1808447	1808264	1808429	FGFR3	NM_022965	3	16	14	+	1808273	1808410
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_022965	3	16	15	+	1808556	1808661
329689148	chr4	1808622	1808812	1808640	1808795	FGFR3	NM_022965	3	16	15	+	1808556	1808661
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_022965	3	16	16	+	1808843	1810599
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_022965	3	16	16	+	1808843	1810599
320488133	chr1	171061754	171061978	171061782	171061950	FMO3	NM_001002294	1	9	2	+	171061794	171061931
319860590	chr1	171072848	171073009	171072870	171072984	FMO3	NM_001002294	1	9	3	+	171072926	171073114
319882132	chr1	171072957	171073162	171072985	171073134	FMO3	NM_001002294	1	9	3	+	171072926	171073114
316790144	chr1	171076752	171076968	171076778	171076942	FMO3	NM_001002294	1	9	4	+	171076816	171076978
316795325	chr1	171076919	171077142	171076943	171077114	FMO3	NM_001002294	1	9	4	+	171076816	171076978
317663748	chr1	171077182	171077395	171077208	171077375	FMO3	NM_001002294	1	9	5	+	171077220	171077362
315780084	chr1	171079901	171080060	171079929	171080034	FMO3	NM_001002294	1	9	6	+	171079939	171080138
315793012	chr1	171080014	171080182	171080035	171080158	FMO3	NM_001002294	1	9	6	+	171079939	171080138
315814376	chr1	171082989	171083183	171083016	171083158	FMO3	NM_001002294	1	9	7	+	171083147	171083502
315816594	chr1	171083134	171083282	171083159	171083260	FMO3	NM_001002294	1	9	7	+	171083147	171083502

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315827422	chr1	171083239	171083437	171083261	171083414	FMO3	NM_001002294	1	9	7	+	171083147	171083502
315838839	chr1	171083390	171083533	171083415	171083509	FMO3	NM_001002294	1	9	7	+	171083147	171083502
317578753	chr1	171085281	171085492	171085304	171085463	FMO3	NM_001002294	1	9	8	+	171085348	171085420
315604631	chr1	171086151	171086375	171086179	171086351	FMO3	NM_001002294	1	9	9	+	171086240	171086959
315625587	chr1	171086329	171086501	171086352	171086481	FMO3	NM_001002294	1	9	9	+	171086240	171086959
315639601	chr1	171086461	171086682	171086482	171086654	FMO3	NM_001002294	1	9	9	+	171086240	171086959
320488133	chr1	171061754	171061978	171061782	171061950	FMO3	NM_006894	2	9	2	+	171061794	171061931
319860590	chr1	171072848	171073009	171072870	171072984	FMO3	NM_006894	2	9	3	+	171072926	171073114
319882132	chr1	171072957	171073162	171072985	171073134	FMO3	NM_006894	2	9	3	+	171072926	171073114
316790144	chr1	171076752	171076968	171076778	171076942	FMO3	NM_006894	2	9	4	+	171076816	171076978
316795325	chr1	171076919	171077142	171076943	171077114	FMO3	NM_006894	2	9	4	+	171076816	171076978
317663748	chr1	171077182	171077395	171077208	171077375	FMO3	NM_006894	2	9	5	+	171077220	171077362
315780084	chr1	171079901	171080060	171079929	171080034	FMO3	NM_006894	2	9	6	+	171079939	171080138
315793012	chr1	171080014	171080182	171080035	171080158	FMO3	NM_006894	2	9	6	+	171079939	171080138
315814376	chr1	171082989	171083183	171083016	171083158	FMO3	NM_006894	2	9	7	+	171083147	171083502
315816594	chr1	171083134	171083282	171083159	171083260	FMO3	NM_006894	2	9	7	+	171083147	171083502
315827422	chr1	171083239	171083437	171083261	171083414	FMO3	NM_006894	2	9	7	+	171083147	171083502
315838839	chr1	171083390	171083533	171083415	171083509	FMO3	NM_006894	2	9	7	+	171083147	171083502
317578753	chr1	171085281	171085492	171085304	171085463	FMO3	NM_006894	2	9	8	+	171085348	171085420
315604631	chr1	171086151	171086375	171086179	171086351	FMO3	NM_006894	2	9	9	+	171086240	171086959
315625587	chr1	171086329	171086501	171086352	171086481	FMO3	NM_006894	2	9	9	+	171086240	171086959
315639601	chr1	171086461	171086682	171086482	171086654	FMO3	NM_006894	2	9	9	+	171086240	171086959
227673791	chr3	138665479	138665687	138665500	138665666	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229731695	chr3	138664324	138664540	138664342	138664523	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229745253	chr3	138664728	138664924	138664745	138664904	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229746185	chr3	138664776	138664992	138664794	138664973	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229746604	chr3	138664954	138665158	138664974	138665135	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229747046	chr3	138665103	138665268	138665121	138665247	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229752887	chr3	138665227	138665393	138665247	138665375	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229755698	chr3	138665331	138665522	138665349	138665505	FOXL2	NM_023067	1	1	1	-	138663066	138665982
317009085	chr4	190862103	190862279	190862124	190862259	FRG1	NM_004477	1	9	1	+	190861974	190862226
317802266	chr4	190864217	190864437	190864244	190864411	FRG1	NM_004477	1	9	2	+	190864357	190864427
316084246	chr4	190873315	190873478	190873340	190873458	FRG1	NM_004477	1	9	3	+	190873317	190873442
315727047	chr4	190874215	190874383	190874238	190874357	FRG1	NM_004477	1	9	4	+	190874223	190874280
316022702	chr4	190876108	190876266	190876131	190876246	FRG1	NM_004477	1	9	5	+	190876192	190876306
316026710	chr4	190876241	190876465	190876261	190876437	FRG1	NM_004477	1	9	5	+	190876192	190876306
317521388	chr4	190881741	190881965	190881769	190881938	FRG1	NM_004477	1	9	7	+	190881903	190881994
319752995	chr4	190884131	190884305	190884159	190884281	FRG1	NM_004477	1	9	9	+	190884248	190884359
316816541	chrX	131261732	131261941	131261756	131261917	FRMD7	NM_194277	1	12	1	-	131261816	131262050
317276043	chrX	131234563	131234787	131234587	131234759	FRMD7	NM_194277	1	12	2	-	131234640	131234744
316684228	chrX	131233414	131233582	131233442	131233557	FRMD7	NM_194277	1	12	3	-	131233496	131233538

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316776520	chrX	131231214	131231434	131231235	131231406	FRMD7	NM_194277	1	12	4	-	131231294	131231372
317470168	chrX	131228006	131228202	131228028	131228174	FRMD7	NM_194277	1	12	5	-	131228070	131228167
316517249	chrX	131219889	131220113	131219916	131220085	FRMD7	NM_194277	1	12	6	-	131219948	131220062
317239450	chrX	131219579	131219803	131219602	131219775	FRMD7	NM_194277	1	12	7	-	131219609	131219756
317514044	chrX	131218471	131218675	131218497	131218651	FRMD7	NM_194277	1	12	8	-	131218518	131218613
315645718	chrX	131216277	131216489	131216306	131216464	FRMD7	NM_194277	1	12	9	-	131216391	131216554
315663811	chrX	131216445	131216622	131216465	131216595	FRMD7	NM_194277	1	12	9	-	131216391	131216554
316810501	chrX	131214137	131214344	131214165	131214316	FRMD7	NM_194277	1	12	10	-	131214226	131214294
317792115	chrX	131213952	131214162	131213976	131214134	FRMD7	NM_194277	1	12	11	-	131214034	131214109
316292245	chrX	131212018	131212200	131212039	131212173	FRMD7	NM_194277	1	12	12	-	131211021	131212994
316321114	chrX	131212151	131212375	131212174	131212353	FRMD7	NM_194277	1	12	12	-	131211021	131212994
316330669	chrX	131212330	131212529	131212354	131212507	FRMD7	NM_194277	1	12	12	-	131211021	131212994
317639416	chrX	131212483	131212703	131212507	131212675	FRMD7	NM_194277	1	12	12	-	131211021	131212994
317666114	chrX	131212651	131212847	131212676	131212826	FRMD7	NM_194277	1	12	12	-	131211021	131212994
317673231	chrX	131211846	131212066	131211869	131212038	FRMD7	NM_194277	1	12	12	-	131211021	131212994
317695928	chrX	131212805	131213027	131212827	131213002	FRMD7	NM_194277	1	12	12	-	131211021	131212994
317466513	chr17	79495507	79495670	79495525	79495653	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317467327	chr17	79495917	79496137	79495934	79496119	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317469570	chr17	79495633	79495807	79495653	79495789	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317469829	chr17	79496101	79496228	79496120	79496208	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317470262	chr17	79495757	79495962	79495777	79495945	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317473152	chr17	79496183	79496374	79496204	79496355	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
317476059	chr17	79496310	79496507	79496333	79496485	FSCN2	NM_001077182	1	5	1	+	79495417	79496383
315741623	chr17	79501928	79502122	79501949	79502098	FSCN2	NM_001077182	1	5	2	+	79502078	79502234
315747868	chr17	79502078	79502266	79502099	79502244	FSCN2	NM_001077182	1	5	2	+	79502078	79502234
316593560	chr17	79503073	79503265	79503094	79503241	FSCN2	NM_001077182	1	5	3	+	79503172	79503293
316609309	chr17	79503215	79503437	79503236	79503411	FSCN2	NM_001077182	1	5	3	+	79503172	79503293
316094017	chr17	79503550	79503769	79503570	79503751	FSCN2	NM_001077182	1	5	4	+	79503576	79503815
316096256	chr17	79503734	79503932	79503752	79503913	FSCN2	NM_001077182	1	5	4	+	79503576	79503815
316893857	chr17	79503772	79503987	79503792	79503965	FSCN2	NM_001077182	1	5	4	+	79503576	79503815
316096256	chr17	79503734	79503932	79503752	79503913	FSCN2	NM_001077182	1	5	5	+	79503901	79504156
316893857	chr17	79503772	79503987	79503792	79503965	FSCN2	NM_001077182	1	5	5	+	79503901	79504156
316894209	chr17	79503905	79504111	79503925	79504091	FSCN2	NM_001077182	1	5	5	+	79503901	79504156
317466513	chr17	79495507	79495670	79495525	79495653	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317467327	chr17	79495917	79496137	79495934	79496119	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317469570	chr17	79495633	79495807	79495653	79495789	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317469829	chr17	79496101	79496228	79496120	79496208	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317470262	chr17	79495757	79495962	79495777	79495945	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317473152	chr17	79496183	79496374	79496204	79496355	FSCN2	NM_012418	2	5	1	+	79495417	79496383
317476059	chr17	79496310	79496507	79496333	79496485	FSCN2	NM_012418	2	5	1	+	79495417	79496383
315741623	chr17	79501928	79502122	79501949	79502098	FSCN2	NM_012418	2	5	2	+	79502078	79502234

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315747868	chr17	79502078	79502266	79502099	79502244	FSCN2	NM_012418	2	5	2	+	79502078	79502234
316593560	chr17	79503073	79503265	79503094	79503241	FSCN2	NM_012418	2	5	3	+	79503172	79503293
316609309	chr17	79503215	79503437	79503236	79503411	FSCN2	NM_012418	2	5	3	+	79503172	79503293
316094017	chr17	79503550	79503769	79503570	79503751	FSCN2	NM_012418	2	5	4	+	79503648	79503815
316096256	chr17	79503734	79503932	79503752	79503913	FSCN2	NM_012418	2	5	4	+	79503648	79503815
316893857	chr17	79503772	79503987	79503792	79503965	FSCN2	NM_012418	2	5	4	+	79503648	79503815
316096256	chr17	79503734	79503932	79503752	79503913	FSCN2	NM_012418	2	5	5	+	79503901	79504156
316893857	chr17	79503772	79503987	79503792	79503965	FSCN2	NM_012418	2	5	5	+	79503901	79504156
316894209	chr17	79503905	79504111	79503925	79504091	FSCN2	NM_012418	2	5	5	+	79503901	79504156
317501740	chr9	71650555	71650748	71650578	71650731	FXN	NM_000144	1	5	1	+	71650479	71650863
317502144	chr9	71650691	71650881	71650710	71650864	FXN	NM_000144	1	5	1	+	71650479	71650863
317870760	chr9	71661198	71661330	71661223	71661310	FXN	NM_000144	1	5	2	+	71661301	71661398
317875869	chr9	71661288	71661431	71661311	71661403	FXN	NM_000144	1	5	2	+	71661301	71661398
316142075	chr9	71668011	71668141	71668038	71668119	FXN	NM_000144	1	5	3	+	71668056	71668176
316153752	chr9	71668097	71668259	71668120	71668234	FXN	NM_000144	1	5	3	+	71668056	71668176
317212467	chr9	71679758	71679887	71679786	71679863	FXN	NM_000144	1	5	4	+	71679854	71679951
317215892	chr9	71679841	71680016	71679864	71679988	FXN	NM_000144	1	5	4	+	71679854	71679951
315649746	chr9	71687387	71687555	71687415	71687534	FXN	NM_000144	1	5	5	+	71687528	71693993
315658510	chr9	71687511	71687720	71687535	71687692	FXN	NM_000144	1	5	5	+	71687528	71693993
317501740	chr9	71650555	71650748	71650578	71650731	FXN	NM_001161706	2	5	1	+	71650479	71650863
317502144	chr9	71650691	71650881	71650710	71650864	FXN	NM_001161706	2	5	1	+	71650479	71650863
317870760	chr9	71661198	71661330	71661223	71661310	FXN	NM_001161706	2	5	2	+	71661301	71661398
317875869	chr9	71661288	71661431	71661311	71661403	FXN	NM_001161706	2	5	2	+	71661301	71661398
316142075	chr9	71668011	71668141	71668038	71668119	FXN	NM_001161706	2	5	3	+	71668056	71668176
316153752	chr9	71668097	71668259	71668120	71668234	FXN	NM_001161706	2	5	3	+	71668056	71668176
317212467	chr9	71679758	71679887	71679786	71679863	FXN	NM_001161706	2	5	4	+	71679854	71679951
317215892	chr9	71679841	71680016	71679864	71679988	FXN	NM_001161706	2	5	4	+	71679854	71679951
319835505	chr9	71714691	71714906	71714718	71714883	FXN	NM_001161706	2	5	5	+	71714817	71715094
317501740	chr9	71650555	71650748	71650578	71650731	FXN	NM_181425	3	5	1	+	71650479	71650863
317502144	chr9	71650691	71650881	71650710	71650864	FXN	NM_181425	3	5	1	+	71650479	71650863
317870760	chr9	71661198	71661330	71661223	71661310	FXN	NM_181425	3	5	2	+	71661301	71661398
317875869	chr9	71661288	71661431	71661311	71661403	FXN	NM_181425	3	5	2	+	71661301	71661398
316142075	chr9	71668011	71668141	71668038	71668119	FXN	NM_181425	3	5	3	+	71668056	71668176
316153752	chr9	71668097	71668259	71668120	71668234	FXN	NM_181425	3	5	3	+	71668056	71668176
317212467	chr9	71679758	71679887	71679786	71679863	FXN	NM_181425	3	5	4	+	71679854	71679959
317215892	chr9	71679841	71680016	71679864	71679988	FXN	NM_181425	3	5	4	+	71679854	71679959
315649746	chr9	71687387	71687555	71687415	71687534	FXN	NM_181425	3	5	5	+	71687528	71693993
315658510	chr9	71687511	71687720	71687535	71687692	FXN	NM_181425	3	5	5	+	71687528	71693993
316862580	chr17	78078326	78078522	78078343	78078503	GAA	NM_000152	1	20	2	+	78078354	78078931
316866446	chr17	78078476	78078686	78078500	78078667	GAA	NM_000152	1	20	2	+	78078354	78078931
316869479	chr17	78078642	78078832	78078661	78078810	GAA	NM_000152	1	20	2	+	78078354	78078931

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316874237	chr17	78078789	78079000	78078810	78078983	GAA	NM_000152	1	20	2	+	78078354	78078931
316342933	chr17	78079517	78079731	78079540	78079714	GAA	NM_000152	1	20	3	+	78079548	78079693
315991710	chr17	78081284	78081492	78081303	78081473	GAA	NM_000152	1	20	4	+	78081356	78081521
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_000152	1	20	4	+	78081356	78081521
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_000152	1	20	4	+	78081356	78081521
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_000152	1	20	5	+	78081599	78081695
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_000152	1	20	5	+	78081599	78081695
316254778	chr17	78081616	78081834	78081637	78081812	GAA	NM_000152	1	20	5	+	78081599	78081695
316739227	chr17	78082135	78082304	78082159	78082284	GAA	NM_000152	1	20	6	+	78082089	78082208
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_000152	1	20	6	+	78082089	78082208
320393998	chr17	78081995	78082207	78082016	78082187	GAA	NM_000152	1	20	6	+	78082089	78082208
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_000152	1	20	7	+	78082288	78082406
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_000152	1	20	7	+	78082288	78082406
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_000152	1	20	8	+	78082496	78082627
315783984	chr17	78082469	78082660	78082487	78082639	GAA	NM_000152	1	20	8	+	78082496	78082627
317490574	chr17	78083711	78083902	78083732	78083880	GAA	NM_000152	1	20	9	+	78083744	78083854
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_000152	1	20	10	+	78084526	78084639
319897411	chr17	78084417	78084641	78084437	78084621	GAA	NM_000152	1	20	10	+	78084526	78084639
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_000152	1	20	11	+	78084740	78084824
315987330	chr17	78084699	78084912	78084719	78084889	GAA	NM_000152	1	20	11	+	78084740	78084824
317964108	chr17	78085743	78085961	78085763	78085942	GAA	NM_000152	1	20	12	+	78085782	78085899
317029078	chr17	78086316	78086535	78086335	78086518	GAA	NM_000152	1	20	13	+	78086377	78086510
316425916	chr17	78086646	78086835	78086665	78086815	GAA	NM_000152	1	20	14	+	78086675	78086826
316429920	chr17	78086791	78086947	78086811	78086927	GAA	NM_000152	1	20	14	+	78086675	78086826
316681542	chr17	78086978	78087178	78086998	78087155	GAA	NM_000152	1	20	15	+	78087017	78087165
316684242	chr17	78087097	78087304	78087119	78087283	GAA	NM_000152	1	20	15	+	78087017	78087165
316798518	chr17	78090720	78090906	78090742	78090886	GAA	NM_000152	1	20	16	+	78090767	78090908
316803881	chr17	78090864	78091029	78090885	78091008	GAA	NM_000152	1	20	16	+	78090767	78090908
320447532	chr17	78091366	78091585	78091388	78091566	GAA	NM_000152	1	20	17	+	78091399	78091548
316325585	chr17	78091959	78092148	78091982	78092125	GAA	NM_000152	1	20	18	+	78091992	78092156
316328166	chr17	78092081	78092271	78092102	78092248	GAA	NM_000152	1	20	18	+	78091992	78092156
316596478	chr17	78092410	78092634	78092434	78092616	GAA	NM_000152	1	20	19	+	78092452	78092604
315882837	chr17	78093042	78093242	78093065	78093222	GAA	NM_000152	1	20	20	+	78093071	78093679
316862580	chr17	78078326	78078522	78078343	78078503	GAA	NM_001079803	2	21	3	+	78078354	78078931
316866446	chr17	78078476	78078686	78078500	78078667	GAA	NM_001079803	2	21	3	+	78078354	78078931
316869479	chr17	78078642	78078832	78078661	78078810	GAA	NM_001079803	2	21	3	+	78078354	78078931
316874237	chr17	78078789	78079000	78078810	78078983	GAA	NM_001079803	2	21	3	+	78078354	78078931
316342933	chr17	78079517	78079731	78079540	78079714	GAA	NM_001079803	2	21	4	+	78079548	78079693
315991710	chr17	78081284	78081492	78081303	78081473	GAA	NM_001079803	2	21	5	+	78081356	78081521
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_001079803	2	21	5	+	78081356	78081521
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_001079803	2	21	5	+	78081356	78081521

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_001079803	2	21	6	+	78081599	78081695
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_001079803	2	21	6	+	78081599	78081695
316254778	chr17	78081616	78081834	78081637	78081812	GAA	NM_001079803	2	21	6	+	78081599	78081695
316739227	chr17	78082135	78082304	78082159	78082284	GAA	NM_001079803	2	21	7	+	78082089	78082208
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_001079803	2	21	7	+	78082089	78082208
320393998	chr17	78081995	78082207	78082016	78082187	GAA	NM_001079803	2	21	7	+	78082089	78082208
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_001079803	2	21	8	+	78082288	78082406
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_001079803	2	21	8	+	78082288	78082406
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_001079803	2	21	9	+	78082496	78082627
315783984	chr17	78082469	78082660	78082487	78082639	GAA	NM_001079803	2	21	9	+	78082496	78082627
317490574	chr17	78083711	78083902	78083732	78083880	GAA	NM_001079803	2	21	10	+	78083744	78083854
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_001079803	2	21	11	+	78084526	78084639
319897411	chr17	78084417	78084641	78084437	78084621	GAA	NM_001079803	2	21	11	+	78084526	78084639
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_001079803	2	21	12	+	78084740	78084824
315987330	chr17	78084699	78084912	78084719	78084889	GAA	NM_001079803	2	21	12	+	78084740	78084824
317964108	chr17	78085743	78085961	78085763	78085942	GAA	NM_001079803	2	21	13	+	78085782	78085899
317029078	chr17	78086316	78086535	78086335	78086518	GAA	NM_001079803	2	21	14	+	78086377	78086510
316425916	chr17	78086646	78086835	78086665	78086815	GAA	NM_001079803	2	21	15	+	78086675	78086826
316429920	chr17	78086791	78086947	78086811	78086927	GAA	NM_001079803	2	21	15	+	78086675	78086826
316681542	chr17	78086978	78087178	78086998	78087155	GAA	NM_001079803	2	21	16	+	78087017	78087165
316684242	chr17	78087097	78087304	78087119	78087283	GAA	NM_001079803	2	21	16	+	78087017	78087165
316798518	chr17	78090720	78090906	78090742	78090886	GAA	NM_001079803	2	21	17	+	78090767	78090908
316803881	chr17	78090864	78091029	78090885	78091008	GAA	NM_001079803	2	21	17	+	78090767	78090908
320447532	chr17	78091366	78091585	78091388	78091566	GAA	NM_001079803	2	21	18	+	78091399	78091548
316325585	chr17	78091959	78092148	78091982	78092125	GAA	NM_001079803	2	21	19	+	78091992	78092156
316328166	chr17	78092081	78092271	78092102	78092248	GAA	NM_001079803	2	21	19	+	78091992	78092156
316596478	chr17	78092410	78092634	78092434	78092616	GAA	NM_001079803	2	21	20	+	78092452	78092604
315882837	chr17	78093042	78093242	78093065	78093222	GAA	NM_001079803	2	21	21	+	78093071	78093679
316862580	chr17	78078326	78078522	78078343	78078503	GAA	NM_001079804	3	20	2	+	78078354	78078931
316866446	chr17	78078476	78078686	78078500	78078667	GAA	NM_001079804	3	20	2	+	78078354	78078931
316869479	chr17	78078642	78078832	78078661	78078810	GAA	NM_001079804	3	20	2	+	78078354	78078931
316874237	chr17	78078789	78079000	78078810	78078983	GAA	NM_001079804	3	20	2	+	78078354	78078931
316342933	chr17	78079517	78079731	78079540	78079714	GAA	NM_001079804	3	20	3	+	78079548	78079693
315991710	chr17	78081284	78081492	78081303	78081473	GAA	NM_001079804	3	20	4	+	78081356	78081521
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_001079804	3	20	4	+	78081356	78081521
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_001079804	3	20	4	+	78081356	78081521
315995957	chr17	78081419	78081632	78081440	78081610	GAA	NM_001079804	3	20	5	+	78081599	78081695
316252452	chr17	78081483	78081690	78081503	78081667	GAA	NM_001079804	3	20	5	+	78081599	78081695
316254778	chr17	78081616	78081834	78081637	78081812	GAA	NM_001079804	3	20	5	+	78081599	78081695
316739227	chr17	78082135	78082304	78082159	78082284	GAA	NM_001079804	3	20	6	+	78082089	78082208
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_001079804	3	20	6	+	78082089	78082208

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320393998	chr17	78081995	78082207	78082016	78082187	GAA	NM_001079804	3	20	6	+	78082089	78082208
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_001079804	3	20	7	+	78082288	78082406
316741168	chr17	78082187	78082388	78082207	78082367	GAA	NM_001079804	3	20	7	+	78082288	78082406
315780568	chr17	78082343	78082562	78082364	78082540	GAA	NM_001079804	3	20	8	+	78082496	78082627
315783984	chr17	78082469	78082660	78082487	78082639	GAA	NM_001079804	3	20	8	+	78082496	78082627
317490574	chr17	78083711	78083902	78083732	78083880	GAA	NM_001079804	3	20	9	+	78083744	78083854
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_001079804	3	20	10	+	78084526	78084639
319897411	chr17	78084417	78084641	78084437	78084621	GAA	NM_001079804	3	20	10	+	78084526	78084639
315977058	chr17	78084591	78084812	78084612	78084790	GAA	NM_001079804	3	20	11	+	78084740	78084824
315987330	chr17	78084699	78084912	78084719	78084889	GAA	NM_001079804	3	20	11	+	78084740	78084824
317964108	chr17	78085743	78085961	78085763	78085942	GAA	NM_001079804	3	20	12	+	78085782	78085899
317029078	chr17	78086316	78086535	78086335	78086518	GAA	NM_001079804	3	20	13	+	78086377	78086510
316425916	chr17	78086646	78086835	78086665	78086815	GAA	NM_001079804	3	20	14	+	78086675	78086826
316429920	chr17	78086791	78086947	78086811	78086927	GAA	NM_001079804	3	20	14	+	78086675	78086826
316681542	chr17	78086978	78087178	78086998	78087155	GAA	NM_001079804	3	20	15	+	78087017	78087165
316684242	chr17	78087097	78087304	78087119	78087283	GAA	NM_001079804	3	20	15	+	78087017	78087165
316798518	chr17	78090720	78090906	78090742	78090886	GAA	NM_001079804	3	20	16	+	78090767	78090908
316803881	chr17	78090864	78091029	78090885	78091008	GAA	NM_001079804	3	20	16	+	78090767	78090908
320447532	chr17	78091366	78091585	78091388	78091566	GAA	NM_001079804	3	20	17	+	78091399	78091548
316325585	chr17	78091959	78092148	78091982	78092125	GAA	NM_001079804	3	20	18	+	78091992	78092156
316328166	chr17	78092081	78092271	78092102	78092248	GAA	NM_001079804	3	20	18	+	78091992	78092156
316596478	chr17	78092410	78092634	78092434	78092616	GAA	NM_001079804	3	20	19	+	78092452	78092604
315882837	chr17	78093042	78093242	78093065	78093222	GAA	NM_001079804	3	20	20	+	78093071	78093679
315638346	chr9	34646667	34646881	34646688	34646861	GALT	NM_000155	1	11	1	+	34646635	34646783
315841114	chr9	34647044	34647267	34647066	34647245	GALT	NM_000155	1	11	2	+	34647086	34647255
315854058	chr9	34647206	34647363	34647227	34647341	GALT	NM_000155	1	11	2	+	34647086	34647255
317441061	chr9	34647402	34647625	34647422	34647602	GALT	NM_000155	1	11	3	+	34647489	34647564
316273491	chr9	34647594	34647754	34647614	34647729	GALT	NM_000155	1	11	4	+	34647654	34647702
316486844	chr9	34647798	34648021	34647821	34647999	GALT	NM_000155	1	11	5	+	34647829	34647958
316565936	chr9	34648027	34648214	34648050	34648192	GALT	NM_000155	1	11	6	+	34648112	34648168
316269506	chr9	34648288	34648504	34648311	34648478	GALT	NM_000155	1	11	7	+	34648331	34648453
316036961	chr9	34648702	34648923	34648721	34648901	GALT	NM_000155	1	11	8	+	34648759	34648891
316544688	chr9	34648928	34649130	34648949	34649109	GALT	NM_000155	1	11	9	+	34648995	34649078
315956211	chr9	34649376	34649587	34649399	34649567	GALT	NM_000155	1	11	10	+	34649407	34649561
316841361	chr9	34650295	34650506	34650318	34650478	GALT	NM_000155	1	11	11	+	34650366	34650573
332319486	chr8	11565770	11565991	11565788	11565974	GATA4	NM_002052	1	7	2	+	11565365	11566437
332320426	chr8	11565918	11566121	11565935	11566104	GATA4	NM_002052	1	7	2	+	11565365	11566437
332320456	chr8	11566202	11566330	11566219	11566312	GATA4	NM_002052	1	7	2	+	11565365	11566437
333301485	chr8	11566288	11566506	11566307	11566488	GATA4	NM_002052	1	7	2	+	11565365	11566437
333567413	chr8	11606356	11606559	11606379	11606537	GATA4	NM_002052	1	7	3	+	11606428	11606594
333578789	chr8	11606507	11606720	11606528	11606700	GATA4	NM_002052	1	7	3	+	11606428	11606594

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332421760	chr8	11607577	11607800	11607603	11607778	GATA4	NM_002052	1	7	4	+	11607620	11607745
332389425	chr8	11612476	11612692	11612499	11612666	GATA4	NM_002052	1	7	5	+	11612555	11612642
332808886	chr8	11614410	11614576	11614432	11614556	GATA4	NM_002052	1	7	6	+	11614444	11614592
332814716	chr8	11614521	11614731	11614542	11614711	GATA4	NM_002052	1	7	6	+	11614444	11614592
333716193	chr8	11615753	11615977	11615772	11615955	GATA4	NM_002052	1	7	7	+	11615802	11617509
333741746	chr8	11615930	11616147	11615951	11616126	GATA4	NM_002052	1	7	7	+	11615802	11617509
316167692	chr1	155210805	155211027	155210831	155211002	GBA	NM_000157	1	11	1	-	155210877	155211069
317100535	chr1	155210320	155210511	155210347	155210489	GBA	NM_000157	1	11	2	-	155210421	155210508
317105229	chr1	155210400	155210545	155210421	155210523	GBA	NM_000157	1	11	2	-	155210421	155210508
315807488	chr1	155209554	155209751	155209575	155209729	GBA	NM_000157	1	11	3	-	155209677	155209868
315825533	chr1	155209707	155209930	155209727	155209905	GBA	NM_000157	1	11	3	-	155209677	155209868
317987313	chr1	155209360	155209584	155209387	155209559	GBA	NM_000157	1	11	4	-	155209407	155209553
316601934	chr1	155207860	155208022	155207884	155208000	GBA	NM_000157	1	11	6	-	155207925	155208097
316613638	chr1	155207977	155208188	155207998	155208167	GBA	NM_000157	1	11	6	-	155207925	155208097
317113500	chr1	155207016	155207222	155207038	155207204	GBA	NM_000157	1	11	7	-	155207132	155207369
317123673	chr1	155207183	155207401	155207205	155207379	GBA	NM_000157	1	11	7	-	155207132	155207369
317378287	chr1	155205962	155206144	155205991	155206123	GBA	NM_000157	1	11	8	-	155206036	155206260
317382145	chr1	155206088	155206293	155206109	155206272	GBA	NM_000157	1	11	8	-	155206036	155206260
318010922	chr1	155205386	155205571	155205407	155205548	GBA	NM_000157	1	11	9	-	155205472	155205635
320353838	chr1	155205523	155205720	155205548	155205698	GBA	NM_000157	1	11	9	-	155205472	155205635
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_000157	1	11	10	-	155204986	155205102
316968986	chr1	155204978	155205173	155204996	155205148	GBA	NM_000157	1	11	10	-	155204986	155205102
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_000157	1	11	11	-	155204239	155204891
316167692	chr1	155210805	155211027	155210831	155211002	GBA	NM_001005741	2	12	2	-	155210877	155210971
317100535	chr1	155210320	155210511	155210347	155210489	GBA	NM_001005741	2	12	3	-	155210421	155210508
317105229	chr1	155210400	155210545	155210421	155210523	GBA	NM_001005741	2	12	3	-	155210421	155210508
315807488	chr1	155209554	155209751	155209575	155209729	GBA	NM_001005741	2	12	4	-	155209677	155209868
315825533	chr1	155209707	155209930	155209727	155209905	GBA	NM_001005741	2	12	4	-	155209677	155209868
317987313	chr1	155209360	155209584	155209387	155209559	GBA	NM_001005741	2	12	5	-	155209407	155209553
316601934	chr1	155207860	155208022	155207884	155208000	GBA	NM_001005741	2	12	7	-	155207925	155208097
316613638	chr1	155207977	155208188	155207998	155208167	GBA	NM_001005741	2	12	7	-	155207925	155208097
317113500	chr1	155207016	155207222	155207038	155207204	GBA	NM_001005741	2	12	8	-	155207132	155207369
317123673	chr1	155207183	155207401	155207205	155207379	GBA	NM_001005741	2	12	8	-	155207132	155207369
317378287	chr1	155205962	155206144	155205991	155206123	GBA	NM_001005741	2	12	9	-	155206036	155206260
317382145	chr1	155206088	155206293	155206109	155206272	GBA	NM_001005741	2	12	9	-	155206036	155206260
318010922	chr1	155205386	155205571	155205407	155205548	GBA	NM_001005741	2	12	10	-	155205472	155205635
320353838	chr1	155205523	155205720	155205548	155205698	GBA	NM_001005741	2	12	10	-	155205472	155205635
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001005741	2	12	11	-	155204986	155205102
316968986	chr1	155204978	155205173	155204996	155205148	GBA	NM_001005741	2	12	11	-	155204986	155205102
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001005741	2	12	12	-	155204239	155204891
316167692	chr1	155210805	155211027	155210831	155211002	GBA	NM_001005742	3	12	2	-	155210877	155210952

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317100535	chr1	155210320	155210511	155210347	155210489	GBA	NM_001005742	3	12	3	-	155210421	155210508
317105229	chr1	155210400	155210545	155210421	155210523	GBA	NM_001005742	3	12	3	-	155210421	155210508
315807488	chr1	155209554	155209751	155209575	155209729	GBA	NM_001005742	3	12	4	-	155209677	155209868
315825533	chr1	155209707	155209930	155209727	155209905	GBA	NM_001005742	3	12	4	-	155209677	155209868
317987313	chr1	155209360	155209584	155209387	155209559	GBA	NM_001005742	3	12	5	-	155209407	155209553
316601934	chr1	155207860	155208022	155207884	155208000	GBA	NM_001005742	3	12	7	-	155207925	155208097
316613638	chr1	155207977	155208188	155207998	155208167	GBA	NM_001005742	3	12	7	-	155207925	155208097
317113500	chr1	155207016	155207222	155207038	155207204	GBA	NM_001005742	3	12	8	-	155207132	155207369
317123673	chr1	155207183	155207401	155207205	155207379	GBA	NM_001005742	3	12	8	-	155207132	155207369
317378287	chr1	155205962	155206144	155205991	155206123	GBA	NM_001005742	3	12	9	-	155206036	155206260
317382145	chr1	155206088	155206293	155206109	155206272	GBA	NM_001005742	3	12	9	-	155206036	155206260
318010922	chr1	155205386	155205571	155205407	155205548	GBA	NM_001005742	3	12	10	-	155205472	155205635
320353838	chr1	155205523	155205720	155205548	155205698	GBA	NM_001005742	3	12	10	-	155205472	155205635
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001005742	3	12	11	-	155204986	155205102
316968986	chr1	155204978	155205173	155204996	155205148	GBA	NM_001005742	3	12	11	-	155204986	155205102
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001005742	3	12	12	-	155204239	155204891
315807488	chr1	155209554	155209751	155209575	155209729	GBA	NM_001171811	4	10	2	-	155209677	155209868
315825533	chr1	155209707	155209930	155209727	155209905	GBA	NM_001171811	4	10	2	-	155209677	155209868
317987313	chr1	155209360	155209584	155209387	155209559	GBA	NM_001171811	4	10	3	-	155209407	155209553
316601934	chr1	155207860	155208022	155207884	155208000	GBA	NM_001171811	4	10	5	-	155207925	155208097
316613638	chr1	155207977	155208188	155207998	155208167	GBA	NM_001171811	4	10	5	-	155207925	155208097
317113500	chr1	155207016	155207222	155207038	155207204	GBA	NM_001171811	4	10	6	-	155207132	155207369
317123673	chr1	155207183	155207401	155207205	155207379	GBA	NM_001171811	4	10	6	-	155207132	155207369
317378287	chr1	155205962	155206144	155205991	155206123	GBA	NM_001171811	4	10	7	-	155206036	155206260
317382145	chr1	155206088	155206293	155206109	155206272	GBA	NM_001171811	4	10	7	-	155206036	155206260
318010922	chr1	155205386	155205571	155205407	155205548	GBA	NM_001171811	4	10	8	-	155205472	155205635
320353838	chr1	155205523	155205720	155205548	155205698	GBA	NM_001171811	4	10	8	-	155205472	155205635
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001171811	4	10	9	-	155204986	155205102
316968986	chr1	155204978	155205173	155204996	155205148	GBA	NM_001171811	4	10	9	-	155204986	155205102
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001171811	4	10	10	-	155204239	155204891
316167692	chr1	155210805	155211027	155210831	155211002	GBA	NM_001171812	5	10	1	-	155210877	155211066
317100535	chr1	155210320	155210511	155210347	155210489	GBA	NM_001171812	5	10	2	-	155210421	155210508
317105229	chr1	155210400	155210545	155210421	155210523	GBA	NM_001171812	5	10	2	-	155210421	155210508
315807488	chr1	155209554	155209751	155209575	155209729	GBA	NM_001171812	5	10	3	-	155209677	155209868
315825533	chr1	155209707	155209930	155209727	155209905	GBA	NM_001171812	5	10	3	-	155209677	155209868
316601934	chr1	155207860	155208022	155207884	155208000	GBA	NM_001171812	5	10	5	-	155207925	155208097
316613638	chr1	155207977	155208188	155207998	155208167	GBA	NM_001171812	5	10	5	-	155207925	155208097
317113500	chr1	155207016	155207222	155207038	155207204	GBA	NM_001171812	5	10	6	-	155207132	155207369
317123673	chr1	155207183	155207401	155207205	155207379	GBA	NM_001171812	5	10	6	-	155207132	155207369
317378287	chr1	155205962	155206144	155205991	155206123	GBA	NM_001171812	5	10	7	-	155206036	155206260
317382145	chr1	155206088	155206293	155206109	155206272	GBA	NM_001171812	5	10	7	-	155206036	155206260

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318010922	chr1	155205386	155205571	155205407	155205548	GBA	NM_001171812	5	10	8	-	155205472	155205635
320353838	chr1	155205523	155205720	155205548	155205698	GBA	NM_001171812	5	10	8	-	155205472	155205635
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001171812	5	10	9	-	155204986	155205102
316968986	chr1	155204978	155205173	155204996	155205148	GBA	NM_001171812	5	10	9	-	155204986	155205102
316557611	chr1	155204796	155205012	155204814	155204993	GBA	NM_001171812	5	10	10	-	155204239	155204891
317745918	chr3	81810482	81810699	81810500	81810682	GBE1	NM_000158	1	16	1	-	81810526	81810950
316258502	chr3	81754601	81754735	81754627	81754707	GBE1	NM_000158	1	16	2	-	81754595	81754764
316258703	chr3	81754646	81754773	81754672	81754744	GBE1	NM_000158	1	16	2	-	81754595	81754764
316259063	chr3	81754715	81754927	81754743	81754906	GBE1	NM_000158	1	16	2	-	81754595	81754764
316918325	chr3	81719827	81720049	81719854	81720021	GBE1	NM_000158	1	16	3	-	81719989	81720104
316923343	chr3	81720001	81720141	81720022	81720113	GBE1	NM_000158	1	16	3	-	81719989	81720104
316719050	chr3	81698821	81699017	81698848	81698990	GBE1	NM_000158	1	16	4	-	81698947	81699072
316726124	chr3	81698963	81699152	81698991	81699126	GBE1	NM_000158	1	16	4	-	81698947	81699072
316667771	chr3	81697841	81698039	81697869	81698011	GBE1	NM_000158	1	16	5	-	81698007	81698142
316668223	chr3	81697988	81698125	81698017	81698099	GBE1	NM_000158	1	16	5	-	81698007	81698142
316669803	chr3	81698073	81698283	81698099	81698262	GBE1	NM_000158	1	16	5	-	81698007	81698142
316569015	chr3	81695434	81695595	81695462	81695571	GBE1	NM_000158	1	16	6	-	81695543	81695633
316569304	chr3	81695548	81695755	81695572	81695727	GBE1	NM_000158	1	16	6	-	81695543	81695633
319818652	chr3	81691824	81692031	81691852	81692003	GBE1	NM_000158	1	16	7	-	81691932	81692141
319872818	chr3	81691975	81692199	81692003	81692174	GBE1	NM_000158	1	16	7	-	81691932	81692141
317530279	chr3	81642986	81643176	81643012	81643148	GBE1	NM_000158	1	16	8	-	81643059	81643174
317534939	chr3	81643123	81643296	81643150	81643264	GBE1	NM_000158	1	16	8	-	81643059	81643174
316313016	chr3	81640155	81640376	81640178	81640350	GBE1	NM_000158	1	16	9	-	81640188	81640315
316726062	chr3	81635192	81635376	81635219	81635348	GBE1	NM_000158	1	16	10	-	81635243	81635341
316827780	chr3	81630345	81630556	81630366	81630529	GBE1	NM_000158	1	16	11	-	81630316	81630426
315641122	chr3	81626918	81627107	81626947	81627086	GBE1	NM_000158	1	16	12	-	81627076	81627247
315641475	chr3	81627056	81627237	81627084	81627215	GBE1	NM_000158	1	16	12	-	81627076	81627247
315646672	chr3	81627188	81627361	81627216	81627334	GBE1	NM_000158	1	16	12	-	81627076	81627247
317428410	chr3	81586198	81586376	81586226	81586348	GBE1	NM_000158	1	16	13	-	81586062	81586246
319788579	chr3	81586028	81586249	81586053	81586225	GBE1	NM_000158	1	16	13	-	81586062	81586246
316026891	chr3	81584236	81584400	81584264	81584378	GBE1	NM_000158	1	16	14	-	81584344	81584476
316029511	chr3	81584358	81584504	81584379	81584476	GBE1	NM_000158	1	16	14	-	81584344	81584476
316030884	chr3	81584449	81584635	81584474	81584606	GBE1	NM_000158	1	16	14	-	81584344	81584476
316518675	chr3	81548102	81548326	81548125	81548305	GBE1	NM_000158	1	16	15	-	81548261	81548376
316530223	chr3	81548279	81548412	81548306	81548384	GBE1	NM_000158	1	16	15	-	81548261	81548376
317835595	chr3	81539433	81539657	81539455	81539630	GBE1	NM_000158	1	16	16	-	81538850	81539614
316040325	chr16	81129578	81129759	81129602	81129742	GCSH	NM_004483	1	5	1	-	81129736	81129980
315722238	chr16	81124120	81124316	81124146	81124290	GCSH	NM_004483	1	5	2	-	81124206	81124285
317034022	chr16	81121153	81121340	81121182	81121312	GCSH	NM_004483	1	5	3	-	81121206	81121269
316170471	chr16	81117977	81118196	81118003	81118173	GCSH	NM_004483	1	5	4	-	81118068	81118199
316172588	chr16	81118148	81118292	81118174	81118264	GCSH	NM_004483	1	5	4	-	81118068	81118199

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317422236	chr16	81116421	81116585	81116441	81116563	GCSH	NM_004483	1	5	5	-	81115552	81116568
317425940	chr16	81116538	81116663	81116564	81116635	GCSH	NM_004483	1	5	5	-	81115552	81116568
316040325	chr16	81129578	81129759	81129602	81129742	GCSH	NR_033249	2	4	1	-	81129736	81129980
315722238	chr16	81124120	81124316	81124146	81124290	GCSH	NR_033249	2	4	2	-	81124206	81124285
316170471	chr16	81117977	81118196	81118003	81118173	GCSH	NR_033249	2	4	3	-	81118068	81118199
316172588	chr16	81118148	81118292	81118174	81118264	GCSH	NR_033249	2	4	3	-	81118068	81118199
317422236	chr16	81116421	81116585	81116441	81116563	GCSH	NR_033249	2	4	4	-	81115552	81116568
317425940	chr16	81116538	81116663	81116564	81116635	GCSH	NR_033249	2	4	4	-	81115552	81116568
316972465	chr20	34025605	34025813	34025623	34025791	GDF5	NM_000557	1	2	1	-	34025078	34026027
320478284	chr20	34025006	34025212	34025029	34025193	GDF5	NM_000557	1	2	1	-	34025078	34026027
320493853	chr20	34025173	34025359	34025193	34025340	GDF5	NM_000557	1	2	1	-	34025078	34026027
320495756	chr20	34025319	34025506	34025339	34025488	GDF5	NM_000557	1	2	1	-	34025078	34026027
320502171	chr20	34025432	34025651	34025453	34025628	GDF5	NM_000557	1	2	1	-	34025078	34026027
316047572	chr20	34021562	34021768	34021584	34021745	GDF5	NM_000557	1	2	2	-	34021149	34022581
316066435	chr20	34021724	34021887	34021746	34021866	GDF5	NM_000557	1	2	2	-	34021149	34022581
316079072	chr20	34021845	34022005	34021867	34021984	GDF5	NM_000557	1	2	2	-	34021149	34022581
316083070	chr20	34021951	34022170	34021970	34022149	GDF5	NM_000557	1	2	2	-	34021149	34022581
316122240	chr20	34022126	34022350	34022149	34022330	GDF5	NM_000557	1	2	2	-	34021149	34022581
316126334	chr20	34022302	34022526	34022328	34022507	GDF5	NM_000557	1	2	2	-	34021149	34022581
316130918	chr20	34022473	34022695	34022493	34022672	GDF5	NM_000557	1	2	2	-	34021149	34022581
316720103	chr13	20762927	20763144	20762952	20763121	GJB2	NM_004004	1	2	2	-	20761604	20763742
317861409	chr13	20763098	20763322	20763122	20763301	GJB2	NM_004004	1	2	2	-	20761604	20763742
317871682	chr13	20763582	20763804	20763603	20763782	GJB2	NM_004004	1	2	2	-	20761604	20763742
317883990	chr13	20763280	20763487	20763302	20763467	GJB2	NM_004004	1	2	2	-	20761604	20763742
317908458	chr13	20763411	20763634	20763435	20763607	GJB2	NM_004004	1	2	2	-	20761604	20763742
316017202	chr1	35250313	35250529	35250341	35250507	GJB3	NM_001005752	1	2	2	+	35250339	35251967
316025167	chr1	35250466	35250650	35250486	35250633	GJB3	NM_001005752	1	2	2	+	35250339	35251967
316032937	chr1	35250602	35250809	35250623	35250786	GJB3	NM_001005752	1	2	2	+	35250339	35251967
317478871	chr1	35250763	35250987	35250787	35250966	GJB3	NM_001005752	1	2	2	+	35250339	35251967
317489585	chr1	35250948	35251163	35250967	35251145	GJB3	NM_001005752	1	2	2	+	35250339	35251967
317493206	chr1	35251116	35251336	35251138	35251315	GJB3	NM_001005752	1	2	2	+	35250339	35251967
316017202	chr1	35250313	35250529	35250341	35250507	GJB3	NM_024009	2	2	2	+	35250339	35251965
316025167	chr1	35250466	35250650	35250486	35250633	GJB3	NM_024009	2	2	2	+	35250339	35251965
316032937	chr1	35250602	35250809	35250623	35250786	GJB3	NM_024009	2	2	2	+	35250339	35251965
317478871	chr1	35250763	35250987	35250787	35250966	GJB3	NM_024009	2	2	2	+	35250339	35251965
317489585	chr1	35250948	35251163	35250967	35251145	GJB3	NM_024009	2	2	2	+	35250339	35251965
317493206	chr1	35251116	35251336	35251138	35251315	GJB3	NM_024009	2	2	2	+	35250339	35251965
316439953	chr13	20797132	20797295	20797158	20797267	GJB6	NM_001110219	1	5	5	-	20796101	20797634
316454240	chr13	20797240	20797452	20797268	20797431	GJB6	NM_001110219	1	5	5	-	20796101	20797634
316462638	chr13	20797409	20797557	20797431	20797534	GJB6	NM_001110219	1	5	5	-	20796101	20797634
316464145	chr13	20796792	20797008	20796816	20796987	GJB6	NM_001110219	1	5	5	-	20796101	20797634

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316473897	chr13	20797509	20797672	20797535	20797647	GJB6	NM_001110219	1	5	5	-	20796101	20797634
316488015	chr13	20796966	20797185	20796988	20797157	GJB6	NM_001110219	1	5	5	-	20796101	20797634
316439953	chr13	20797132	20797295	20797158	20797267	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316454240	chr13	20797240	20797452	20797268	20797431	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316462638	chr13	20797409	20797557	20797431	20797534	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316464145	chr13	20796792	20797008	20796816	20796987	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316473897	chr13	20797509	20797672	20797535	20797647	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316488015	chr13	20796966	20797185	20796988	20797157	GJB6	NM_001110220	2	4	4	-	20796101	20797634
316439953	chr13	20797132	20797295	20797158	20797267	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316454240	chr13	20797240	20797452	20797268	20797431	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316462638	chr13	20797409	20797557	20797431	20797534	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316464145	chr13	20796792	20797008	20796816	20796987	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316473897	chr13	20797509	20797672	20797535	20797647	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316488015	chr13	20796966	20797185	20796988	20797157	GJB6	NM_001110221	3	3	3	-	20796101	20797634
316439953	chr13	20797132	20797295	20797158	20797267	GJB6	NM_006783	4	3	3	-	20796101	20797634
316454240	chr13	20797240	20797452	20797268	20797431	GJB6	NM_006783	4	3	3	-	20796101	20797634
316462638	chr13	20797409	20797557	20797431	20797534	GJB6	NM_006783	4	3	3	-	20796101	20797634
316464145	chr13	20796792	20797008	20796816	20796987	GJB6	NM_006783	4	3	3	-	20796101	20797634
316473897	chr13	20797509	20797672	20797535	20797647	GJB6	NM_006783	4	3	3	-	20796101	20797634
316488015	chr13	20796966	20797185	20796988	20797157	GJB6	NM_006783	4	3	3	-	20796101	20797634
317553417	chrX	100662610	100662809	100662632	100662788	GLA	NM_000169	1	7	1	-	100662698	100663001
317566616	chrX	100662769	100662921	100662789	100662898	GLA	NM_000169	1	7	1	-	100662698	100663001
315539833	chrX	100658720	100658918	100658744	100658894	GLA	NM_000169	1	7	2	-	100658799	100658973
315568657	chrX	100658874	100659035	100658895	100659009	GLA	NM_000169	1	7	2	-	100658799	100658973
315749178	chrX	100656482	100656656	100656505	100656629	GLA	NM_000169	1	7	3	-	100656620	100656797
315757969	chrX	100656604	100656826	100656630	100656802	GLA	NM_000169	1	7	3	-	100656620	100656797
317155746	chrX	100655578	100655800	100655602	100655777	GLA	NM_000169	1	7	4	-	100655654	100655745
315763166	chrX	100653621	100653842	100653645	100653814	GLA	NM_000169	1	7	5	-	100653773	100653934
315779335	chrX	100653795	100654008	100653815	100653980	GLA	NM_000169	1	7	5	-	100653773	100653934
316754734	chrX	100653255	100653457	100653282	100653437	GLA	NM_000169	1	7	6	-	100653358	100653555
316759553	chrX	100653414	100653634	100653438	100653606	GLA	NM_000169	1	7	6	-	100653358	100653555
316967283	chrX	100652749	100652972	100652774	100652951	GLA	NM_000169	1	7	7	-	100652779	100653087
316997749	chrX	100652931	100653117	100652952	100653094	GLA	NM_000169	1	7	7	-	100652779	100653087
317184575	chr9	6645151	6645346	6645169	6645329	GLDC	NM_000170	1	25	1	-	6645245	6645692
320560561	chr9	6644500	6644721	6644521	6644697	GLDC	NM_000170	1	25	2	-	6644614	6644692
320406287	chr9	6620147	6620370	6620170	6620342	GLDC	NM_000170	1	25	3	-	6620184	6620319
316686056	chr9	6610040	6610252	6610068	6610232	GLDC	NM_000170	1	25	4	-	6610192	6610356
316687977	chr9	6610182	6610394	6610201	6610370	GLDC	NM_000170	1	25	4	-	6610192	6610356
316411497	chr9	6606484	6606701	6606506	6606675	GLDC	NM_000170	1	25	5	-	6606592	6606669
316287720	chr9	6604986	6605167	6605010	6605144	GLDC	NM_000170	1	25	6	-	6605131	6605278
316298791	chr9	6605120	6605309	6605145	6605283	GLDC	NM_000170	1	25	6	-	6605131	6605278

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316167074	chr9	6604462	6604640	6604490	6604618	GLDC	NM_000170	1	25	7	-	6604588	6604784
316175289	chr9	6604598	6604818	6604619	6604792	GLDC	NM_000170	1	25	7	-	6604588	6604784
316988683	chr9	6602049	6602249	6602077	6602223	GLDC	NM_000170	1	25	8	-	6602109	6602205
317086904	chr9	6594981	6595172	6595008	6595148	GLDC	NM_000170	1	25	9	-	6595014	6595119
316445667	chr9	6592689	6592885	6592712	6592860	GLDC	NM_000170	1	25	10	-	6592851	6592990
316449600	chr9	6592834	6593041	6592861	6593013	GLDC	NM_000170	1	25	10	-	6592851	6592990
317910752	chr9	6592075	6592270	6592099	6592242	GLDC	NM_000170	1	25	11	-	6592143	6592223
315859435	chr9	6589113	6589322	6589133	6589298	GLDC	NM_000170	1	25	12	-	6589195	6589292
316076997	chr9	6588527	6588731	6588549	6588708	GLDC	NM_000170	1	25	13	-	6588618	6588702
317186803	chr9	6588292	6588507	6588317	6588479	GLDC	NM_000170	1	25	14	-	6588401	6588442
317402445	chr9	6587130	6587298	6587151	6587270	GLDC	NM_000170	1	25	15	-	6587141	6587283
315758027	chr9	6565239	6565463	6565262	6565438	GLDC	NM_000170	1	25	16	-	6565354	6565429
317097085	chr9	6558526	6558729	6558547	6558701	GLDC	NM_000170	1	25	17	-	6558559	6558684
317843534	chr9	6556034	6556203	6556054	6556181	GLDC	NM_000170	1	25	18	-	6556153	6556302
317864123	chr9	6556158	6556333	6556182	6556307	GLDC	NM_000170	1	25	18	-	6556153	6556302
320399816	chr9	6554598	6554815	6554623	6554793	GLDC	NM_000170	1	25	19	-	6554669	6554781
317083878	chr9	6553336	6553484	6553356	6553460	GLDC	NM_000170	1	25	20	-	6553368	6553509
317091103	chr9	6553441	6553579	6553461	6553551	GLDC	NM_000170	1	25	20	-	6553368	6553509
315738668	chr9	6550719	6550943	6550740	6550919	GLDC	NM_000170	1	25	21	-	6550803	6550914
319793277	chr9	6539959	6540174	6539980	6540151	GLDC	NM_000170	1	25	22	-	6540051	6540146
317518704	chr9	6535970	6536154	6535992	6536130	GLDC	NM_000170	1	25	23	-	6536064	6536236
317536230	chr9	6536110	6536314	6536131	6536287	GLDC	NM_000170	1	25	23	-	6536064	6536236
316433244	chr9	6534621	6534829	6534646	6534808	GLDC	NM_000170	1	25	24	-	6534708	6534788
316619172	chr9	6532974	6533198	6532995	6533171	GLDC	NM_000170	1	25	25	-	6532464	6533160
317413768	chr9	36276787	36276950	36276812	36276928	GNE	NM_001128227	1	12	1	-	36276891	36277053
319753231	chr9	36276906	36277120	36276929	36277092	GNE	NM_001128227	1	12	1	-	36276891	36277053
320452334	chr9	36249150	36249277	36249179	36249255	GNE	NM_001128227	1	12	2	-	36249189	36249394
320468199	chr9	36249231	36249380	36249256	36249356	GNE	NM_001128227	1	12	2	-	36249189	36249394
320472369	chr9	36249332	36249556	36249361	36249532	GNE	NM_001128227	1	12	2	-	36249189	36249394
316360799	chr9	36245982	36246202	36246008	36246178	GNE	NM_001128227	1	12	3	-	36246028	36246479
316388606	chr9	36246159	36246367	36246179	36246346	GNE	NM_001128227	1	12	3	-	36246028	36246479
316406409	chr9	36246323	36246537	36246347	36246511	GNE	NM_001128227	1	12	3	-	36246028	36246479
316631876	chr9	36236737	36236955	36236762	36236934	GNE	NM_001128227	1	12	4	-	36236829	36236981
316637800	chr9	36236907	36237125	36236934	36237101	GNE	NM_001128227	1	12	4	-	36236829	36236981
315796280	chr9	36233865	36234059	36233893	36234036	GNE	NM_001128227	1	12	5	-	36233917	36234129
315816607	chr9	36234017	36234202	36234037	36234174	GNE	NM_001128227	1	12	5	-	36233917	36234129
315988841	chr9	36228962	36229139	36228984	36229113	GNE	NM_001128227	1	12	6	-	36229018	36229105
316823660	chr9	36227086	36227292	36227114	36227273	GNE	NM_001128227	1	12	7	-	36227245	36227455
316827223	chr9	36227252	36227429	36227274	36227401	GNE	NM_001128227	1	12	7	-	36227245	36227455
316833407	chr9	36227377	36227511	36227402	36227484	GNE	NM_001128227	1	12	7	-	36227245	36227455
316641578	chr9	36223204	36223413	36223226	36223390	GNE	NM_001128227	1	12	8	-	36223370	36223499

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316649921	chr9	36223365	36223533	36223391	36223506	GNE	NM_001128227	1	12	8	-	36223370	36223499
317944763	chr9	36222734	36222883	36222757	36222862	GNE	NM_001128227	1	12	9	-	36222774	36222995
317960508	chr9	36222842	36223027	36222863	36223001	GNE	NM_001128227	1	12	9	-	36222774	36222995
316189197	chr9	36219749	36219921	36219773	36219900	GNE	NM_001128227	1	12	10	-	36219835	36220017
316203546	chr9	36219880	36220053	36219901	36220027	GNE	NM_001128227	1	12	10	-	36219835	36220017
315840825	chr9	36218116	36218326	36218138	36218302	GNE	NM_001128227	1	12	11	-	36218180	36218296
315553045	chr9	36217474	36217646	36217494	36217619	GNE	NM_001128227	1	12	12	-	36214439	36217597
315590055	chr9	36217308	36217518	36217331	36217493	GNE	NM_001128227	1	12	12	-	36214439	36217597
320452334	chr9	36249150	36249277	36249179	36249255	GNE	NM_001190383	2	11	2	-	36249189	36249394
320468199	chr9	36249231	36249380	36249256	36249356	GNE	NM_001190383	2	11	2	-	36249189	36249394
320472369	chr9	36249332	36249556	36249361	36249532	GNE	NM_001190383	2	11	2	-	36249189	36249394
316360799	chr9	36245982	36246202	36246008	36246178	GNE	NM_001190383	2	11	3	-	36246028	36246479
316388606	chr9	36246159	36246367	36246179	36246346	GNE	NM_001190383	2	11	3	-	36246028	36246479
316406409	chr9	36246323	36246537	36246347	36246511	GNE	NM_001190383	2	11	3	-	36246028	36246479
316631876	chr9	36236737	36236955	36236762	36236934	GNE	NM_001190383	2	11	4	-	36236829	36236981
316637800	chr9	36236907	36237125	36236934	36237101	GNE	NM_001190383	2	11	4	-	36236829	36236981
315796280	chr9	36233865	36234059	36233893	36234036	GNE	NM_001190383	2	11	5	-	36233917	36234129
315816607	chr9	36234017	36234202	36234037	36234174	GNE	NM_001190383	2	11	5	-	36233917	36234129
315988841	chr9	36228962	36229139	36228984	36229113	GNE	NM_001190383	2	11	6	-	36229018	36229105
316823660	chr9	36227086	36227292	36227114	36227273	GNE	NM_001190383	2	11	7	-	36227245	36227455
316827223	chr9	36227252	36227429	36227274	36227401	GNE	NM_001190383	2	11	7	-	36227245	36227455
316833407	chr9	36227377	36227511	36227402	36227484	GNE	NM_001190383	2	11	7	-	36227245	36227455
316641578	chr9	36223204	36223413	36223226	36223390	GNE	NM_001190383	2	11	8	-	36223370	36223499
316649921	chr9	36223365	36223533	36223391	36223506	GNE	NM_001190383	2	11	8	-	36223370	36223499
316189197	chr9	36219749	36219921	36219773	36219900	GNE	NM_001190383	2	11	9	-	36219835	36220017
316203546	chr9	36219880	36220053	36219901	36220027	GNE	NM_001190383	2	11	9	-	36219835	36220017
315840825	chr9	36218116	36218326	36218138	36218302	GNE	NM_001190383	2	11	10	-	36218180	36218296
315553045	chr9	36217474	36217646	36217494	36217619	GNE	NM_001190383	2	11	11	-	36214439	36217597
315590055	chr9	36217308	36217518	36217331	36217493	GNE	NM_001190383	2	11	11	-	36214439	36217597
316360799	chr9	36245982	36246202	36246008	36246178	GNE	NM_001190384	3	10	2	-	36246028	36246479
316388606	chr9	36246159	36246367	36246179	36246346	GNE	NM_001190384	3	10	2	-	36246028	36246479
316406409	chr9	36246323	36246537	36246347	36246511	GNE	NM_001190384	3	10	2	-	36246028	36246479
315796280	chr9	36233865	36234059	36233893	36234036	GNE	NM_001190384	3	10	3	-	36233917	36234129
315816607	chr9	36234017	36234202	36234037	36234174	GNE	NM_001190384	3	10	3	-	36233917	36234129
315988841	chr9	36228962	36229139	36228984	36229113	GNE	NM_001190384	3	10	4	-	36229018	36229105
316823660	chr9	36227086	36227292	36227114	36227273	GNE	NM_001190384	3	10	5	-	36227245	36227455
316827223	chr9	36227252	36227429	36227274	36227401	GNE	NM_001190384	3	10	5	-	36227245	36227455
316833407	chr9	36227377	36227511	36227402	36227484	GNE	NM_001190384	3	10	5	-	36227245	36227455
316641578	chr9	36223204	36223413	36223226	36223390	GNE	NM_001190384	3	10	6	-	36223370	36223499
316649921	chr9	36223365	36223533	36223391	36223506	GNE	NM_001190384	3	10	6	-	36223370	36223499
317944763	chr9	36222734	36222883	36222757	36222862	GNE	NM_001190384	3	10	7	-	36222774	36222995

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317960508	chr9	36222842	36223027	36222863	36223001	GNE	NM_001190384	3	10	7	-	36222774	36222995
316189197	chr9	36219749	36219921	36219773	36219900	GNE	NM_001190384	3	10	8	-	36219835	36220017
316203546	chr9	36219880	36220053	36219901	36220027	GNE	NM_001190384	3	10	8	-	36219835	36220017
315840825	chr9	36218116	36218326	36218138	36218302	GNE	NM_001190384	3	10	9	-	36218180	36218296
315553045	chr9	36217474	36217646	36217494	36217619	GNE	NM_001190384	3	10	10	-	36214439	36217597
315590055	chr9	36217308	36217518	36217331	36217493	GNE	NM_001190384	3	10	10	-	36214439	36217597
317413768	chr9	36276787	36276950	36276812	36276928	GNE	NM_001190388	4	11	1	-	36276891	36277053
319753231	chr9	36276906	36277120	36276929	36277092	GNE	NM_001190388	4	11	1	-	36276891	36277053
316360799	chr9	36245982	36246202	36246008	36246178	GNE	NM_001190388	4	11	2	-	36246028	36246479
316388606	chr9	36246159	36246367	36246179	36246346	GNE	NM_001190388	4	11	2	-	36246028	36246479
316406409	chr9	36246323	36246537	36246347	36246511	GNE	NM_001190388	4	11	2	-	36246028	36246479
316631876	chr9	36236737	36236955	36236762	36236934	GNE	NM_001190388	4	11	3	-	36236829	36236981
316637800	chr9	36236907	36237125	36236934	36237101	GNE	NM_001190388	4	11	3	-	36236829	36236981
315796280	chr9	36233865	36234059	36233893	36234036	GNE	NM_001190388	4	11	4	-	36233917	36234129
315816607	chr9	36234017	36234202	36234037	36234174	GNE	NM_001190388	4	11	4	-	36233917	36234129
315988841	chr9	36228962	36229139	36228984	36229113	GNE	NM_001190388	4	11	5	-	36229018	36229105
316823660	chr9	36227086	36227292	36227114	36227273	GNE	NM_001190388	4	11	6	-	36227245	36227455
316827223	chr9	36227252	36227429	36227274	36227401	GNE	NM_001190388	4	11	6	-	36227245	36227455
316833407	chr9	36227377	36227511	36227402	36227484	GNE	NM_001190388	4	11	6	-	36227245	36227455
316641578	chr9	36223204	36223413	36223226	36223390	GNE	NM_001190388	4	11	7	-	36223370	36223499
316649921	chr9	36223365	36223533	36223391	36223506	GNE	NM_001190388	4	11	7	-	36223370	36223499
317944763	chr9	36222734	36222883	36222757	36222862	GNE	NM_001190388	4	11	8	-	36222774	36222995
317960508	chr9	36222842	36223027	36222863	36223001	GNE	NM_001190388	4	11	8	-	36222774	36222995
316189197	chr9	36219749	36219921	36219773	36219900	GNE	NM_001190388	4	11	9	-	36219835	36220017
316203546	chr9	36219880	36220053	36219901	36220027	GNE	NM_001190388	4	11	9	-	36219835	36220017
315840825	chr9	36218116	36218326	36218138	36218302	GNE	NM_001190388	4	11	10	-	36218180	36218296
315553045	chr9	36217474	36217646	36217494	36217619	GNE	NM_001190388	4	11	11	-	36214439	36217597
315590055	chr9	36217308	36217518	36217331	36217493	GNE	NM_001190388	4	11	11	-	36214439	36217597
320452334	chr9	36249150	36249277	36249179	36249255	GNE	NM_005476	5	12	2	-	36249189	36249394
320468199	chr9	36249231	36249380	36249256	36249356	GNE	NM_005476	5	12	2	-	36249189	36249394
320472369	chr9	36249332	36249556	36249361	36249532	GNE	NM_005476	5	12	2	-	36249189	36249394
316360799	chr9	36245982	36246202	36246008	36246178	GNE	NM_005476	5	12	3	-	36246028	36246479
316388606	chr9	36246159	36246367	36246179	36246346	GNE	NM_005476	5	12	3	-	36246028	36246479
316406409	chr9	36246323	36246537	36246347	36246511	GNE	NM_005476	5	12	3	-	36246028	36246479
316631876	chr9	36236737	36236955	36236762	36236934	GNE	NM_005476	5	12	4	-	36236829	36236981
316637800	chr9	36236907	36237125	36236934	36237101	GNE	NM_005476	5	12	4	-	36236829	36236981
315796280	chr9	36233865	36234059	36233893	36234036	GNE	NM_005476	5	12	5	-	36233917	36234129
315816607	chr9	36234017	36234202	36234037	36234174	GNE	NM_005476	5	12	5	-	36233917	36234129
315988841	chr9	36228962	36229139	36228984	36229113	GNE	NM_005476	5	12	6	-	36229018	36229105
316823660	chr9	36227086	36227292	36227114	36227273	GNE	NM_005476	5	12	7	-	36227245	36227455
316827223	chr9	36227252	36227429	36227274	36227401	GNE	NM_005476	5	12	7	-	36227245	36227455

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316833407	chr9	36227377	36227511	36227402	36227484	GNE	NM_005476	5	12	7	-	36227245	36227455
316641578	chr9	36223204	36223413	36223226	36223390	GNE	NM_005476	5	12	8	-	36223370	36223499
316649921	chr9	36223365	36223533	36223391	36223506	GNE	NM_005476	5	12	8	-	36223370	36223499
317944763	chr9	36222734	36222883	36222757	36222862	GNE	NM_005476	5	12	9	-	36222774	36222995
317960508	chr9	36222842	36223027	36222863	36223001	GNE	NM_005476	5	12	9	-	36222774	36222995
316189197	chr9	36219749	36219921	36219773	36219900	GNE	NM_005476	5	12	10	-	36219835	36220017
316203546	chr9	36219880	36220053	36219901	36220027	GNE	NM_005476	5	12	10	-	36219835	36220017
315840825	chr9	36218116	36218326	36218138	36218302	GNE	NM_005476	5	12	11	-	36218180	36218296
315553045	chr9	36217474	36217646	36217494	36217619	GNE	NM_005476	5	12	12	-	36214439	36217597
315590055	chr9	36217308	36217518	36217331	36217493	GNE	NM_005476	5	12	12	-	36214439	36217597
316853563	chr12	102224287	102224450	102224304	102224429	GNPTAB	NM_024312	1	21	1	-	102224337	102224645
316854566	chr12	102224407	102224599	102224427	102224582	GNPTAB	NM_024312	1	21	1	-	102224337	102224645
317168731	chr12	102190358	102190582	102190383	102190556	GNPTAB	NM_024312	1	21	2	-	102190455	102190540
315675427	chr12	102183706	102183868	102183732	102183841	GNPTAB	NM_024312	1	21	3	-	102183716	102183835
315895795	chr12	102182168	102182354	102182198	102182326	GNPTAB	NM_024312	1	21	4	-	102182326	102182367
315895895	chr12	102182299	102182442	102182327	102182420	GNPTAB	NM_024312	1	21	4	-	102182326	102182367
316207432	chr12	102179632	102179841	102179656	102179814	GNPTAB	NM_024312	1	21	5	-	102179790	102179995
316209083	chr12	102179797	102179925	102179825	102179904	GNPTAB	NM_024312	1	21	5	-	102179790	102179995
316215542	chr12	102179878	102180067	102179905	102180040	GNPTAB	NM_024312	1	21	5	-	102179790	102179995
316372292	chr12	102174174	102174371	102174207	102174345	GNPTAB	NM_024312	1	21	6	-	102174335	102174399
316372502	chr12	102174329	102174462	102174350	102174437	GNPTAB	NM_024312	1	21	6	-	102174335	102174399
317808007	chr12	102173889	102174112	102173911	102174089	GNPTAB	NM_024312	1	21	7	-	102173930	102174064
317937320	chr12	102164607	102164831	102164635	102164803	GNPTAB	NM_024312	1	21	8	-	102164774	102164935
317952047	chr12	102164780	102164984	102164804	102164956	GNPTAB	NM_024312	1	21	8	-	102164774	102164935
317070428	chr12	102164103	102164238	102164131	102164216	GNPTAB	NM_024312	1	21	9	-	102164184	102164363
317078898	chr12	102164190	102164402	102164217	102164374	GNPTAB	NM_024312	1	21	9	-	102164184	102164363
320572388	chr12	102163702	102163857	102163730	102163834	GNPTAB	NM_024312	1	21	10	-	102163799	102163969
320612528	chr12	102163807	102164017	102163835	102163990	GNPTAB	NM_024312	1	21	10	-	102163799	102163969
317837506	chr12	102161796	102161930	102161822	102161911	GNPTAB	NM_024312	1	21	11	-	102161815	102161938
317843436	chr12	102161873	102162095	102161895	102162071	GNPTAB	NM_024312	1	21	11	-	102161815	102161938
316561074	chr12	102159733	102159941	102159758	102159918	GNPTAB	NM_024312	1	21	12	-	102159869	102160072
316577762	chr12	102159897	102160101	102159919	102160078	GNPTAB	NM_024312	1	21	12	-	102159869	102160072
317018316	chr12	102157937	102158063	102157963	102158040	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
317019785	chr12	102158928	102159141	102158955	102159114	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
317024156	chr12	102158016	102158202	102158041	102158178	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
317038561	chr12	102158157	102158377	102158179	102158355	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
317053628	chr12	102158332	102158537	102158356	102158509	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
320502015	chr12	102158488	102158672	102158510	102158645	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
320542156	chr12	102158625	102158836	102158646	102158808	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
320600558	chr12	102158788	102158979	102158809	102158954	GNPTAB	NM_024312	1	21	13	-	102157980	102159082
316788299	chr12	102155279	102155497	102155306	102155470	GNPTAB	NM_024312	1	21	14	-	102155342	102155541

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316799452	chr12	102155444	102155590	102155471	102155563	GNPTAB	NM_024312	1	21	14	-	102155342	102155541
317112366	chr12	102154885	102155096	102154914	102155074	GNPTAB	NM_024312	1	21	15	-	102154905	102155124
317120200	chr12	102155047	102155195	102155075	102155167	GNPTAB	NM_024312	1	21	15	-	102154905	102155124
320379011	chr12	102153632	102153843	102153658	102153816	GNPTAB	NM_024312	1	21	16	-	102153808	102153921
320423263	chr12	102153795	102153972	102153817	102153944	GNPTAB	NM_024312	1	21	16	-	102153808	102153921
319864631	chr12	102151288	102151487	102151314	102151464	GNPTAB	NM_024312	1	21	17	-	102151350	102151435
317190716	chr12	102150832	102151046	102150856	102151023	GNPTAB	NM_024312	1	21	18	-	102150990	102151088
317197320	chr12	102150999	102151193	102151024	102151167	GNPTAB	NM_024312	1	21	18	-	102150990	102151088
317462027	chr12	102147094	102147225	102147120	102147201	GNPTAB	NM_024312	1	21	19	-	102147150	102147317
317471584	chr12	102147180	102147351	102147202	102147324	GNPTAB	NM_024312	1	21	19	-	102147150	102147317
316338908	chr12	102142798	102142968	102142831	102142941	GNPTAB	NM_024312	1	21	20	-	102142879	102142969
316339016	chr12	102142913	102143132	102142939	102143104	GNPTAB	NM_024312	1	21	20	-	102142879	102142969
315577990	chr12	102140901	102141100	102140929	102141072	GNPTAB	NM_024312	1	21	21	-	102139275	102141019
227394130	chrX	133119222	133119363	133119239	133119342	GPC3	NM_001164617	1	9	1	-	133119302	133119673
227395314	chrX	133119311	133119500	133119332	133119481	GPC3	NM_001164617	1	9	1	-	133119302	133119673
229286319	chrX	133087051	133087274	133087080	133087247	GPC3	NM_001164617	1	9	2	-	133087077	133087238
329656896	chrX	133086934	133087105	133086956	133087079	GPC3	NM_001164617	1	9	2	-	133087077	133087238
229055814	chrX	132887940	132888158	132887960	132888133	GPC3	NM_001164617	1	9	3	-	132887509	132888203
229057169	chrX	132887401	132887623	132887424	132887595	GPC3	NM_001164617	1	9	3	-	132887509	132888203
229076944	chrX	132888108	132888313	132888132	132888291	GPC3	NM_001164617	1	9	3	-	132887509	132888203
229096102	chrX	132887574	132887797	132887596	132887777	GPC3	NM_001164617	1	9	3	-	132887509	132888203
229148238	chrX	132887756	132887980	132887778	132887959	GPC3	NM_001164617	1	9	3	-	132887509	132888203
228432856	chrX	132838146	132838359	132838167	132838331	GPC3	NM_001164617	1	9	4	-	132838233	132838301
227472558	chrX	132833844	132834057	132833871	132834033	GPC3	NM_001164617	1	9	5	-	132833923	132834056
227474416	chrX	132834008	132834143	132834034	132834115	GPC3	NM_001164617	1	9	5	-	132833923	132834056
228922143	chrX	132826296	132826431	132826324	132826410	GPC3	NM_001164617	1	9	6	-	132826397	132826522
228922945	chrX	132826386	132826557	132826411	132826530	GPC3	NM_001164617	1	9	6	-	132826397	132826522
227194202	chrX	132795747	132795911	132795773	132795883	GPC3	NM_001164617	1	9	7	-	132795758	132795878
228149002	chrX	132730336	132730494	132730364	132730473	GPC3	NM_001164617	1	9	8	-	132730468	132730627
228185131	chrX	132730449	132730656	132730474	132730632	GPC3	NM_001164617	1	9	8	-	132730468	132730627
228105755	chrX	132670030	132670189	132670052	132670169	GPC3	NM_001164617	1	9	9	-	132669776	132670321
228118044	chrX	132670149	132670361	132670170	132670333	GPC3	NM_001164617	1	9	9	-	132669776	132670321
227394130	chrX	133119222	133119363	133119239	133119342	GPC3	NM_001164618	2	8	1	-	133119302	133119673
227395314	chrX	133119311	133119500	133119332	133119481	GPC3	NM_001164618	2	8	1	-	133119302	133119673
229286319	chrX	133087051	133087274	133087080	133087247	GPC3	NM_001164618	2	8	2	-	133087125	133087238
229055814	chrX	132887940	132888158	132887960	132888133	GPC3	NM_001164618	2	8	3	-	132887509	132888203
229057169	chrX	132887401	132887623	132887424	132887595	GPC3	NM_001164618	2	8	3	-	132887509	132888203
229076944	chrX	132888108	132888313	132888132	132888291	GPC3	NM_001164618	2	8	3	-	132887509	132888203
229096102	chrX	132887574	132887797	132887596	132887777	GPC3	NM_001164618	2	8	3	-	132887509	132888203
229148238	chrX	132887756	132887980	132887778	132887959	GPC3	NM_001164618	2	8	3	-	132887509	132888203
227472558	chrX	132833844	132834057	132833871	132834033	GPC3	NM_001164618	2	8	4	-	132833923	132834056

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227474416	chrX	132834008	132834143	132834034	132834115	GPC3	NM_001164618	2	8	4	-	132833923	132834056
228922143	chrX	132826296	132826431	132826324	132826410	GPC3	NM_001164618	2	8	5	-	132826397	132826522
228922945	chrX	132826386	132826557	132826411	132826530	GPC3	NM_001164618	2	8	5	-	132826397	132826522
227194202	chrX	132795747	132795911	132795773	132795883	GPC3	NM_001164618	2	8	6	-	132795758	132795878
228149002	chrX	132730336	132730494	132730364	132730473	GPC3	NM_001164618	2	8	7	-	132730468	132730627
228185131	chrX	132730449	132730656	132730474	132730632	GPC3	NM_001164618	2	8	7	-	132730468	132730627
228105755	chrX	132670030	132670189	132670052	132670169	GPC3	NM_001164618	2	8	8	-	132669776	132670321
228118044	chrX	132670149	132670361	132670170	132670333	GPC3	NM_001164618	2	8	8	-	132669776	132670321
227394130	chrX	133119222	133119363	133119239	133119342	GPC3	NM_001164619	3	7	1	-	133119302	133119673
227395314	chrX	133119311	133119500	133119332	133119481	GPC3	NM_001164619	3	7	1	-	133119302	133119673
229055814	chrX	132887940	132888158	132887960	132888133	GPC3	NM_001164619	3	7	2	-	132887509	132888203
229057169	chrX	132887401	132887623	132887424	132887595	GPC3	NM_001164619	3	7	2	-	132887509	132888203
229076944	chrX	132888108	132888313	132888132	132888291	GPC3	NM_001164619	3	7	2	-	132887509	132888203
229096102	chrX	132887574	132887797	132887596	132887777	GPC3	NM_001164619	3	7	2	-	132887509	132888203
229148238	chrX	132887756	132887980	132887778	132887959	GPC3	NM_001164619	3	7	2	-	132887509	132888203
227472558	chrX	132833844	132834057	132833871	132834033	GPC3	NM_001164619	3	7	3	-	132833923	132834056
227474416	chrX	132834008	132834143	132834034	132834115	GPC3	NM_001164619	3	7	3	-	132833923	132834056
228922143	chrX	132826296	132826431	132826324	132826410	GPC3	NM_001164619	3	7	4	-	132826397	132826522
228922945	chrX	132826386	132826557	132826411	132826530	GPC3	NM_001164619	3	7	4	-	132826397	132826522
227194202	chrX	132795747	132795911	132795773	132795883	GPC3	NM_001164619	3	7	5	-	132795758	132795878
228149002	chrX	132730336	132730494	132730364	132730473	GPC3	NM_001164619	3	7	6	-	132730468	132730627
228185131	chrX	132730449	132730656	132730474	132730632	GPC3	NM_001164619	3	7	6	-	132730468	132730627
228105755	chrX	132670030	132670189	132670052	132670169	GPC3	NM_001164619	3	7	7	-	132669776	132670321
228118044	chrX	132670149	132670361	132670170	132670333	GPC3	NM_001164619	3	7	7	-	132669776	132670321
227394130	chrX	133119222	133119363	133119239	133119342	GPC3	NM_004484	4	8	1	-	133119302	133119673
227395314	chrX	133119311	133119500	133119332	133119481	GPC3	NM_004484	4	8	1	-	133119302	133119673
229286319	chrX	133087051	133087274	133087080	133087247	GPC3	NM_004484	4	8	2	-	133087077	133087238
329656896	chrX	133086934	133087105	133086956	133087079	GPC3	NM_004484	4	8	2	-	133087077	133087238
229055814	chrX	132887940	132888158	132887960	132888133	GPC3	NM_004484	4	8	3	-	132887509	132888203
229057169	chrX	132887401	132887623	132887424	132887595	GPC3	NM_004484	4	8	3	-	132887509	132888203
229076944	chrX	132888108	132888313	132888132	132888291	GPC3	NM_004484	4	8	3	-	132887509	132888203
229096102	chrX	132887574	132887797	132887596	132887777	GPC3	NM_004484	4	8	3	-	132887509	132888203
229148238	chrX	132887756	132887980	132887778	132887959	GPC3	NM_004484	4	8	3	-	132887509	132888203
227472558	chrX	132833844	132834057	132833871	132834033	GPC3	NM_004484	4	8	4	-	132833923	132834056
227474416	chrX	132834008	132834143	132834034	132834115	GPC3	NM_004484	4	8	4	-	132833923	132834056
228922143	chrX	132826296	132826431	132826324	132826410	GPC3	NM_004484	4	8	5	-	132826397	132826522
228922945	chrX	132826386	132826557	132826411	132826530	GPC3	NM_004484	4	8	5	-	132826397	132826522
227194202	chrX	132795747	132795911	132795773	132795883	GPC3	NM_004484	4	8	6	-	132795758	132795878
228149002	chrX	132730336	132730494	132730364	132730473	GPC3	NM_004484	4	8	7	-	132730468	132730627
228185131	chrX	132730449	132730656	132730474	132730632	GPC3	NM_004484	4	8	7	-	132730468	132730627
228105755	chrX	132670030	132670189	132670052	132670169	GPC3	NM_004484	4	8	8	-	132669776	132670321

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228118044	chrX	132670149	132670361	132670170	132670333	GPC3	NM_004484	4	8	8	-	132669776	132670321
333181143	chr3	32148176	32148304	32148193	32148287	GPD1L	NM_015141	1	8	1	+	32148003	32148250
333179443	chr3	32169518	32169654	32169538	32169629	GPD1L	NM_015141	1	8	2	+	32169568	32169745
333183691	chr3	32169604	32169793	32169630	32169769	GPD1L	NM_015141	1	8	2	+	32169568	32169745
333666070	chr3	32179972	32180185	32179994	32180162	GPD1L	NM_015141	1	8	3	+	32180079	32180219
333688929	chr3	32180139	32180293	32180163	32180265	GPD1L	NM_015141	1	8	3	+	32180079	32180219
332450939	chr3	32181634	32181789	32181656	32181765	GPD1L	NM_015141	1	8	4	+	32181720	32181858
332469047	chr3	32181742	32181960	32181766	32181932	GPD1L	NM_015141	1	8	4	+	32181720	32181858
333640576	chr3	32187937	32188142	32187959	32188119	GPD1L	NM_015141	1	8	5	+	32188114	32188226
333642304	chr3	32188098	32188275	32188120	32188249	GPD1L	NM_015141	1	8	5	+	32188114	32188226
332795995	chr3	32200298	32200484	32200319	32200462	GPD1L	NM_015141	1	8	6	+	32200368	32200601
332816475	chr3	32200441	32200654	32200463	32200632	GPD1L	NM_015141	1	8	6	+	32200368	32200601
332990382	chr3	32201054	32201226	32201082	32201199	GPD1L	NM_015141	1	8	7	+	32201060	32201166
333782305	chr3	32207252	32207427	32207275	32207408	GPD1L	NM_015141	1	8	8	+	32207306	32210207
315832179	chrX	9733457	9733661	9733475	9733644	GPR143	NM_000273	1	9	1	-	9733608	9734005
315833403	chrX	9733824	9734003	9733842	9733985	GPR143	NM_000273	1	9	1	-	9733608	9734005
316217286	chrX	9727270	9727490	9727293	9727471	GPR143	NM_000273	1	9	3	-	9727372	9727466
316418701	chrX	9716537	9716724	9716559	9716704	GPR143	NM_000273	1	9	4	-	9716614	9716706
316428478	chrX	9716680	9716816	9716704	9716791	GPR143	NM_000273	1	9	4	-	9716614	9716706
316779403	chrX	9714056	9714230	9714078	9714201	GPR143	NM_000273	1	9	5	-	9714084	9714193
316901117	chrX	9711529	9711746	9711550	9711720	GPR143	NM_000273	1	9	6	-	9711605	9711713
317162186	chrX	9709369	9709529	9709397	9709504	GPR143	NM_000273	1	9	7	-	9709378	9709495
315946288	chrX	9707481	9707679	9707500	9707658	GPR143	NM_000273	1	9	8	-	9707525	9707759
315964458	chrX	9707639	9707787	9707659	9707764	GPR143	NM_000273	1	9	8	-	9707525	9707759
317021360	chrX	9693697	9693920	9693719	9693896	GPR143	NM_000273	1	9	9	-	9693453	9693880
315913987	chr17	7906888	7907034	7906905	7907016	GUCY2D	NM_000180	1	20	2	+	7906357	7907086
315914675	chr17	7906999	7907177	7907017	7907158	GUCY2D	NM_000180	1	20	2	+	7906357	7907086
319885604	chr17	7906643	7906793	7906660	7906776	GUCY2D	NM_000180	1	20	2	+	7906357	7907086
319885916	chr17	7906736	7906955	7906753	7906938	GUCY2D	NM_000180	1	20	2	+	7906357	7907086
317943657	chr17	7907108	7907307	7907125	7907288	GUCY2D	NM_000180	1	20	3	+	7907170	7907474
317946387	chr17	7907268	7907491	7907287	7907474	GUCY2D	NM_000180	1	20	3	+	7907170	7907474
317953823	chr17	7907448	7907646	7907469	7907623	GUCY2D	NM_000180	1	20	3	+	7907170	7907474
316010765	chr17	7909551	7909724	7909574	7909703	GUCY2D	NM_000180	1	20	4	+	7909681	7910032
316016993	chr17	7909685	7909902	7909704	7909884	GUCY2D	NM_000180	1	20	4	+	7909681	7910032
316021947	chr17	7909855	7910078	7909875	7910058	GUCY2D	NM_000180	1	20	4	+	7909681	7910032
316281608	chr17	7910305	7910496	7910325	7910470	GUCY2D	NM_000180	1	20	5	+	7910378	7910462
315691991	chr17	7910686	7910887	7910707	7910864	GUCY2D	NM_000180	1	20	6	+	7910744	7910846
316334303	chr17	7911169	7911392	7911191	7911371	GUCY2D	NM_000180	1	20	7	+	7911249	7911350
317366529	chr17	7912726	7912950	7912749	7912930	GUCY2D	NM_000180	1	20	8	+	7912824	7912904
316508178	chr17	7915606	7915770	7915630	7915748	GUCY2D	NM_000180	1	20	9	+	7915462	7915668
316514454	chr17	7915645	7915853	7915665	7915830	GUCY2D	NM_000180	1	20	9	+	7915462	7915668

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317089627	chr17	7915426	7915650	7915448	7915629	GUCY2D	NM_000180	1	20	9	+	7915462	7915668
316514454	chr17	7915645	7915853	7915665	7915830	GUCY2D	NM_000180	1	20	10	+	7915768	7915924
316523530	chr17	7915809	7915986	7915831	7915963	GUCY2D	NM_000180	1	20	10	+	7915768	7915924
316733287	chr17	7916367	7916532	7916387	7916509	GUCY2D	NM_000180	1	20	11	+	7916421	7916570
316739954	chr17	7916489	7916642	7916510	7916619	GUCY2D	NM_000180	1	20	11	+	7916421	7916570
317105408	chr17	7917103	7917299	7917125	7917279	GUCY2D	NM_000180	1	20	12	+	7917198	7917346
317109421	chr17	7917257	7917420	7917278	7917399	GUCY2D	NM_000180	1	20	12	+	7917198	7917346
317795818	chr17	7918047	7918255	7918067	7918229	GUCY2D	NM_000180	1	20	13	+	7917919	7918082
317921586	chr17	7917883	7918013	7917905	7917991	GUCY2D	NM_000180	1	20	13	+	7917919	7918082
317929019	chr17	7917970	7918189	7917992	7918169	GUCY2D	NM_000180	1	20	13	+	7917919	7918082
317795818	chr17	7918047	7918255	7918067	7918229	GUCY2D	NM_000180	1	20	14	+	7918177	7918369
317811584	chr17	7918209	7918421	7918230	7918398	GUCY2D	NM_000180	1	20	14	+	7918177	7918369
316191373	chr17	7918535	7918757	7918556	7918738	GUCY2D	NM_000180	1	20	15	+	7918646	7918820
316195671	chr17	7918717	7918900	7918739	7918876	GUCY2D	NM_000180	1	20	15	+	7918646	7918820
315685701	chr17	7918961	7919182	7918981	7919164	GUCY2D	NM_000180	1	20	16	+	7919061	7919159
315689630	chr17	7919090	7919284	7919107	7919263	GUCY2D	NM_000180	1	20	16	+	7919061	7919159
315689630	chr17	7919090	7919284	7919107	7919263	GUCY2D	NM_000180	1	20	17	+	7919245	7919339
315880890	chr17	7919244	7919467	7919264	7919447	GUCY2D	NM_000180	1	20	17	+	7919245	7919339
317354860	chr17	7919480	7919703	7919498	7919686	GUCY2D	NM_000180	1	20	18	+	7919523	7919608
320597683	chr17	7919720	7919943	7919739	7919926	GUCY2D	NM_000180	1	20	19	+	7919761	7919872
315961512	chr16	223181	223400	223198	223382	HBA2	NM_000517	1	3	2	+	223124	223328
316599924	chr16	223366	223582	223384	223565	HBA2	NM_000517	1	3	3	+	223471	223709
316606181	chr16	223545	223763	223566	223741	HBA2	NM_000517	1	3	3	+	223471	223709
316942689	chr11	5248082	5248305	5248105	5248280	HBB	NM_000518	1	3	1	-	5248160	5248301
316480986	chr11	5247775	5247980	5247800	5247958	HBB	NM_000518	1	3	2	-	5247807	5248029
316500873	chr11	5247936	5248061	5247959	5248036	HBB	NM_000518	1	3	2	-	5247807	5248029
316531462	chr11	5246789	5247001	5246817	5246974	HBB	NM_000518	1	3	3	-	5246696	5246956
332962615	chr15	73660339	73660552	73660356	73660535	HCN4	NM_005477	1	8	1	-	73659827	73661605
333719943	chr15	73659726	73659936	73659748	73659909	HCN4	NM_005477	1	8	1	-	73659827	73661605
333722763	chr15	73659887	73660066	73659904	73660049	HCN4	NM_005477	1	8	1	-	73659827	73661605
333725421	chr15	73660032	73660256	73660051	73660237	HCN4	NM_005477	1	8	1	-	73659827	73661605
333725575	chr15	73660041	73660259	73660062	73660240	HCN4	NM_005477	1	8	1	-	73659827	73661605
332609114	chr15	73635691	73635890	73635712	73635870	HCN4	NM_005477	1	8	2	-	73635726	73636149
332625723	chr15	73635849	73636045	73635871	73636022	HCN4	NM_005477	1	8	2	-	73635726	73636149
332644259	chr15	73636000	73636202	73636023	73636176	HCN4	NM_005477	1	8	2	-	73635726	73636149
333601338	chr15	73624367	73624535	73624388	73624513	HCN4	NM_005477	1	8	3	-	73624472	73624633
333609805	chr15	73624494	73624673	73624514	73624650	HCN4	NM_005477	1	8	3	-	73624472	73624633
332647807	chr15	73621869	73622040	73621890	73622022	HCN4	NM_005477	1	8	4	-	73621914	73622132
332654515	chr15	73621996	73622204	73622016	73622182	HCN4	NM_005477	1	8	4	-	73621914	73622132
333430109	chr15	73617549	73617773	73617568	73617749	HCN4	NM_005477	1	8	5	-	73617639	73617785
333434485	chr15	73617704	73617928	73617725	73617904	HCN4	NM_005477	1	8	5	-	73617639	73617785

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333611626	chr15	73617227	73617417	73617248	73617396	HCN4	NM_005477	1	8	6	-	73617296	73617536
333623221	chr15	73617370	73617571	73617396	73617551	HCN4	NM_005477	1	8	6	-	73617296	73617536
332489562	chr15	73616331	73616524	73616352	73616503	HCN4	NM_005477	1	8	7	-	73616430	73616594
332493138	chr15	73616484	73616625	73616504	73616604	HCN4	NM_005477	1	8	7	-	73616430	73616594
333254796	chr15	73615311	73615495	73615329	73615474	HCN4	NM_005477	1	8	8	-	73612200	73616290
333255187	chr15	73615456	73615623	73615473	73615606	HCN4	NM_005477	1	8	8	-	73612200	73616290
333255483	chr15	73615558	73615762	73615576	73615744	HCN4	NM_005477	1	8	8	-	73612200	73616290
333257842	chr15	73615721	73615897	73615739	73615880	HCN4	NM_005477	1	8	8	-	73612200	73616290
333258054	chr15	73614746	73614969	73614774	73614947	HCN4	NM_005477	1	8	8	-	73612200	73616290
333259202	chr15	73615855	73616079	73615878	73616061	HCN4	NM_005477	1	8	8	-	73612200	73616290
333260574	chr15	73616040	73616250	73616059	73616233	HCN4	NM_005477	1	8	8	-	73612200	73616290
333261943	chr15	73614920	73615141	73614941	73615124	HCN4	NM_005477	1	8	8	-	73612200	73616290
333262742	chr15	73615093	73615275	73615111	73615258	HCN4	NM_005477	1	8	8	-	73612200	73616290
333263738	chr15	73615171	73615395	73615191	73615374	HCN4	NM_005477	1	8	8	-	73612200	73616290
333270471	chr15	73616207	73616353	73616234	73616332	HCN4	NM_005477	1	8	8	-	73612200	73616290
316880198	chr15	72667917	72668100	72667939	72668080	HEXA	NM_000520	1	14	1	-	72668061	72668520
316887927	chr15	72668051	72668229	72668072	72668208	HEXA	NM_000520	1	14	1	-	72668061	72668520
316893163	chr15	72668183	72668405	72668207	72668384	HEXA	NM_000520	1	14	1	-	72668061	72668520
316640613	chr15	72648774	72648984	72648794	72648963	HEXA	NM_000520	1	14	2	-	72648866	72648958
315814968	chr15	72647844	72647968	72647866	72647941	HEXA	NM_000520	1	14	3	-	72647900	72647965
315817744	chr15	72647917	72648112	72647942	72648085	HEXA	NM_000520	1	14	3	-	72647900	72647965
320422474	chr15	72645888	72646112	72645913	72646085	HEXA	NM_000520	1	14	4	-	72646032	72646078
316533678	chr15	72645345	72645561	72645365	72645536	HEXA	NM_000520	1	14	5	-	72645409	72645519
317907040	chr15	72643380	72643604	72643404	72643581	HEXA	NM_000520	1	14	6	-	72643474	72643575
316679210	chr15	72642804	72643026	72642828	72643004	HEXA	NM_000520	1	14	7	-	72642859	72642991
316083160	chr15	72641293	72641516	72641314	72641488	HEXA	NM_000520	1	14	8	-	72641420	72641600
316103584	chr15	72641467	72641682	72641489	72641660	HEXA	NM_000520	1	14	8	-	72641420	72641600
317181755	chr15	72640311	72640530	72640331	72640506	HEXA	NM_000520	1	14	9	-	72640389	72640475
315672576	chr15	72639906	72640129	72639928	72640104	HEXA	NM_000520	1	14	10	-	72640027	72640099
315721574	chr15	72638720	72638928	72638741	72638905	HEXA	NM_000520	1	14	11	-	72638868	72639051
315739828	chr15	72638881	72639083	72638906	72639056	HEXA	NM_000520	1	14	11	-	72638868	72639051
316650631	chr15	72638472	72638696	72638497	72638672	HEXA	NM_000520	1	14	12	-	72638576	72638666
315798786	chr15	72637663	72637831	72637687	72637806	HEXA	NM_000520	1	14	13	-	72637787	72637891
315805537	chr15	72637786	72637934	72637807	72637913	HEXA	NM_000520	1	14	13	-	72637787	72637891
317966156	chr15	72636366	72636516	72636387	72636490	HEXA	NM_000520	1	14	14	-	72635778	72636481
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_000410	1	6	1	+	26087509	26087744
316048125	chr6	26091023	26091245	26091045	26091220	HFE	NM_000410	1	6	2	+	26091069	26091332
316083975	chr6	26091201	26091385	26091221	26091359	HFE	NM_000410	1	6	2	+	26091069	26091332
316573377	chr6	26091495	26091670	26091519	26091648	HFE	NM_000410	1	6	3	+	26091542	26091817
316592926	chr6	26091626	26091839	26091647	26091814	HFE	NM_000410	1	6	3	+	26091542	26091817
316602850	chr6	26091793	26091957	26091815	26091931	HFE	NM_000410	1	6	3	+	26091542	26091817

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_000410	1	6	4	+	26092913	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_000410	1	6	4	+	26092913	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_000410	1	6	5	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_000410	1	6	6	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139003	2	5	1	+	26087509	26087744
316048125	chr6	26091023	26091245	26091045	26091220	HFE	NM_139003	2	5	2	+	26091069	26091332
316083975	chr6	26091201	26091385	26091221	26091359	HFE	NM_139003	2	5	2	+	26091069	26091332
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139003	2	5	3	+	26092955	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139003	2	5	3	+	26092955	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139003	2	5	4	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139003	2	5	5	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139004	3	5	1	+	26087509	26087744
316048125	chr6	26091023	26091245	26091045	26091220	HFE	NM_139004	3	5	2	+	26091069	26091332
316083975	chr6	26091201	26091385	26091221	26091359	HFE	NM_139004	3	5	2	+	26091069	26091332
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139004	3	5	3	+	26092913	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139004	3	5	3	+	26092913	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139004	3	5	4	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139004	3	5	5	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139006	4	6	1	+	26087509	26087744
316048125	chr6	26091023	26091245	26091045	26091220	HFE	NM_139006	4	6	2	+	26091069	26091332
316083975	chr6	26091201	26091385	26091221	26091359	HFE	NM_139006	4	6	2	+	26091069	26091332
316573377	chr6	26091495	26091670	26091519	26091648	HFE	NM_139006	4	6	3	+	26091542	26091817
316592926	chr6	26091626	26091839	26091647	26091814	HFE	NM_139006	4	6	3	+	26091542	26091817
316602850	chr6	26091793	26091957	26091815	26091931	HFE	NM_139006	4	6	3	+	26091542	26091817
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139006	4	6	4	+	26092955	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139006	4	6	4	+	26092955	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139006	4	6	5	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139006	4	6	6	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139007	5	5	1	+	26087509	26087744
316573377	chr6	26091495	26091670	26091519	26091648	HFE	NM_139007	5	5	2	+	26091542	26091817
316592926	chr6	26091626	26091839	26091647	26091814	HFE	NM_139007	5	5	2	+	26091542	26091817
316602850	chr6	26091793	26091957	26091815	26091931	HFE	NM_139007	5	5	2	+	26091542	26091817
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139007	5	5	3	+	26092913	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139007	5	5	3	+	26092913	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139007	5	5	4	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139007	5	5	5	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139008	6	5	1	+	26087509	26087744
316573377	chr6	26091495	26091670	26091519	26091648	HFE	NM_139008	6	5	2	+	26091542	26091817
316592926	chr6	26091626	26091839	26091647	26091814	HFE	NM_139008	6	5	2	+	26091542	26091817
316602850	chr6	26091793	26091957	26091815	26091931	HFE	NM_139008	6	5	2	+	26091542	26091817
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139008	6	5	3	+	26092955	26093188

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139008	6	5	3	+	26092955	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139008	6	5	4	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139008	6	5	5	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139009	7	6	1	+	26087509	26087744
316048125	chr6	26091023	26091245	26091045	26091220	HFE	NM_139009	7	6	2	+	26091138	26091332
316083975	chr6	26091201	26091385	26091221	26091359	HFE	NM_139009	7	6	2	+	26091138	26091332
316573377	chr6	26091495	26091670	26091519	26091648	HFE	NM_139009	7	6	3	+	26091542	26091817
316592926	chr6	26091626	26091839	26091647	26091814	HFE	NM_139009	7	6	3	+	26091542	26091817
316602850	chr6	26091793	26091957	26091815	26091931	HFE	NM_139009	7	6	3	+	26091542	26091817
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139009	7	6	4	+	26092913	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139009	7	6	4	+	26092913	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139009	7	6	5	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139009	7	6	6	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139010	8	4	1	+	26087509	26087744
316134797	chr6	26092822	26093039	26092849	26093018	HFE	NM_139010	8	4	2	+	26092913	26093188
316169219	chr6	26092997	26093214	26093019	26093193	HFE	NM_139010	8	4	2	+	26092913	26093188
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139010	8	4	3	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139010	8	4	4	+	26094414	26095469
316593973	chr6	26087595	26087818	26087613	26087792	HFE	NM_139011	9	3	1	+	26087509	26087744
317950271	chr6	26093265	26093487	26093288	26093466	HFE	NM_139011	9	3	2	+	26093347	26093460
317169623	chr6	26094291	26094496	26094314	26094472	HFE	NM_139011	9	3	3	+	26094414	26095469
315904214	chr2	191184330	191184503	191184348	191184482	HIBCH	NM_014362	1	14	1	-	191184442	191184771
316443059	chr2	191175336	191175560	191175358	191175531	HIBCH	NM_014362	1	14	2	-	191175480	191175522
316715899	chr2	191161389	191161596	191161413	191161571	HIBCH	NM_014362	1	14	3	-	191161539	191161679
316720962	chr2	191161544	191161755	191161572	191161726	HIBCH	NM_014362	1	14	3	-	191161539	191161679
317832478	chr2	191159235	191159362	191159256	191159334	HIBCH	NM_014362	1	14	4	-	191159272	191159356
317835663	chr2	191159307	191159514	191159335	191159486	HIBCH	NM_014362	1	14	4	-	191159272	191159356
316196989	chr2	191155098	191155315	191155122	191155289	HIBCH	NM_014362	1	14	5	-	191155131	191155211
315715085	chr2	191152156	191152357	191152187	191152330	HIBCH	NM_014362	1	14	6	-	191152312	191152364
315715925	chr2	191152307	191152494	191152331	191152466	HIBCH	NM_014362	1	14	6	-	191152312	191152364
317435035	chr2	191125763	191125930	191125787	191125905	HIBCH	NM_014362	1	14	7	-	191125882	191125960
317446882	chr2	191125882	191126087	191125906	191126059	HIBCH	NM_014362	1	14	7	-	191125882	191125960
317405134	chr2	191116819	191116956	191116844	191116928	HIBCH	NM_014362	1	14	8	-	191116888	191117033
317407157	chr2	191116907	191117115	191116929	191117087	HIBCH	NM_014362	1	14	8	-	191116888	191117033
317122186	chr2	191114279	191114458	191114307	191114430	HIBCH	NM_014362	1	14	9	-	191114366	191114452
317124616	chr2	191114403	191114582	191114431	191114558	HIBCH	NM_014362	1	14	9	-	191114366	191114452
320366170	chr2	191110763	191110941	191110791	191110913	HIBCH	NM_014362	1	14	10	-	191110880	191110938
320367850	chr2	191110882	191111104	191110910	191111077	HIBCH	NM_014362	1	14	10	-	191110880	191110938
316827018	chr2	191109511	191109732	191109532	191109704	HIBCH	NM_014362	1	14	11	-	191109613	191109694
316107130	chr2	191077531	191077742	191077557	191077714	HIBCH	NM_014362	1	14	12	-	191077682	191077801
316109965	chr2	191077729	191077942	191077751	191077915	HIBCH	NM_014362	1	14	12	-	191077682	191077801

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316692928	chr2	191073550	191073701	191073574	191073674	HIBCH	NM_014362	1	14	13	-	191073606	191073639
315904214	chr2	191184330	191184503	191184348	191184482	HIBCH	NM_198047	2	13	1	-	191184442	191184771
316443059	chr2	191175336	191175560	191175358	191175531	HIBCH	NM_198047	2	13	2	-	191175480	191175522
316715899	chr2	191161389	191161596	191161413	191161571	HIBCH	NM_198047	2	13	3	-	191161539	191161679
316720962	chr2	191161544	191161755	191161572	191161726	HIBCH	NM_198047	2	13	3	-	191161539	191161679
317832478	chr2	191159235	191159362	191159256	191159334	HIBCH	NM_198047	2	13	4	-	191159272	191159356
317835663	chr2	191159307	191159514	191159335	191159486	HIBCH	NM_198047	2	13	4	-	191159272	191159356
316196989	chr2	191155098	191155315	191155122	191155289	HIBCH	NM_198047	2	13	5	-	191155131	191155211
315715085	chr2	191152156	191152357	191152187	191152330	HIBCH	NM_198047	2	13	6	-	191152312	191152364
315715925	chr2	191152307	191152494	191152331	191152466	HIBCH	NM_198047	2	13	6	-	191152312	191152364
317435035	chr2	191125763	191125930	191125787	191125905	HIBCH	NM_198047	2	13	7	-	191125882	191125960
317446882	chr2	191125882	191126087	191125906	191126059	HIBCH	NM_198047	2	13	7	-	191125882	191125960
317405134	chr2	191116819	191116956	191116844	191116928	HIBCH	NM_198047	2	13	8	-	191116888	191117033
317407157	chr2	191116907	191117115	191116929	191117087	HIBCH	NM_198047	2	13	8	-	191116888	191117033
317122186	chr2	191114279	191114458	191114307	191114430	HIBCH	NM_198047	2	13	9	-	191114366	191114452
317124616	chr2	191114403	191114582	191114431	191114558	HIBCH	NM_198047	2	13	9	-	191114366	191114452
320366170	chr2	191110763	191110941	191110791	191110913	HIBCH	NM_198047	2	13	10	-	191110880	191110938
320367850	chr2	191110882	191111104	191110910	191111077	HIBCH	NM_198047	2	13	10	-	191110880	191110938
316827018	chr2	191109511	191109732	191109532	191109704	HIBCH	NM_198047	2	13	11	-	191109613	191109694
316107130	chr2	191077531	191077742	191077557	191077714	HIBCH	NM_198047	2	13	12	-	191077682	191077801
316109965	chr2	191077729	191077942	191077751	191077915	HIBCH	NM_198047	2	13	12	-	191077682	191077801
317191864	chr11	118955714	118955866	118955736	118955843	HMBS	NM_000190	1	14	1	+	118955587	118955776
316133056	chr11	118958855	118959058	118958877	118959036	HMBS	NM_000190	1	14	2	+	118958965	118959018
319769338	chr11	118959228	118959448	118959251	118959422	HMBS	NM_000190	1	14	3	+	118959345	118959417
316362771	chr11	118959810	118960011	118959834	118959987	HMBS	NM_000190	1	14	4	+	118959792	118959841
317224974	chr11	118959756	118959915	118959784	118959892	HMBS	NM_000190	1	14	4	+	118959792	118959841
316362771	chr11	118959810	118960011	118959834	118959987	HMBS	NM_000190	1	14	5	+	118959927	118959982
316820848	chr11	118960291	118960497	118960311	118960475	HMBS	NM_000190	1	14	6	+	118960393	118960470
317805992	chr11	118960589	118960811	118960612	118960791	HMBS	NM_000190	1	14	7	+	118960700	118960777
316753118	chr11	118960843	118961009	118960864	118960984	HMBS	NM_000190	1	14	8	+	118960900	118960975
316738148	chr11	118962092	118962287	118962113	118962264	HMBS	NM_000190	1	14	9	+	118962123	118962236
320576791	chr11	118962707	118962920	118962732	118962896	HMBS	NM_000190	1	14	10	+	118962835	118962873
317261642	chr11	118963082	118963304	118963103	118963281	HMBS	NM_000190	1	14	11	+	118963114	118963233
315821349	chr11	118963377	118963576	118963399	118963553	HMBS	NM_000190	1	14	12	+	118963468	118963521
316552694	chr11	118963580	118963802	118963601	118963774	HMBS	NM_000190	1	14	13	+	118963645	118963731
315948027	chr11	118963782	118964002	118963805	118963979	HMBS	NM_000190	1	14	14	+	118963820	118964259
315970732	chr11	118963961	118964090	118963980	118964066	HMBS	NM_000190	1	14	14	+	118963820	118964259
316133056	chr11	118958855	118959058	118958877	118959036	HMBS	NM_001024382	2	14	2	+	118958965	118959018
319769338	chr11	118959228	118959448	118959251	118959422	HMBS	NM_001024382	2	14	3	+	118959345	118959417
316362771	chr11	118959810	118960011	118959834	118959987	HMBS	NM_001024382	2	14	4	+	118959792	118959841
317224974	chr11	118959756	118959915	118959784	118959892	HMBS	NM_001024382	2	14	4	+	118959792	118959841

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316362771	chr11	118959810	118960011	118959834	118959987	HMBS	NM_001024382	2	14	5	+	118959927	118959982
316820848	chr11	118960291	118960497	118960311	118960475	HMBS	NM_001024382	2	14	6	+	118960393	118960470
317805992	chr11	118960589	118960811	118960612	118960791	HMBS	NM_001024382	2	14	7	+	118960700	118960777
316753118	chr11	118960843	118961009	118960864	118960984	HMBS	NM_001024382	2	14	8	+	118960900	118960975
316738148	chr11	118962092	118962287	118962113	118962264	HMBS	NM_001024382	2	14	9	+	118962123	118962236
320576791	chr11	118962707	118962920	118962732	118962896	HMBS	NM_001024382	2	14	10	+	118962835	118962873
317261642	chr11	118963082	118963304	118963103	118963281	HMBS	NM_001024382	2	14	11	+	118963114	118963233
315821349	chr11	118963377	118963576	118963399	118963553	HMBS	NM_001024382	2	14	12	+	118963468	118963521
316552694	chr11	118963580	118963802	118963601	118963774	HMBS	NM_001024382	2	14	13	+	118963645	118963731
315948027	chr11	118963782	118964002	118963805	118963979	HMBS	NM_001024382	2	14	14	+	118963820	118964259
315970732	chr11	118963961	118964090	118963980	118964066	HMBS	NM_001024382	2	14	14	+	118963820	118964259
317145414	chr8	21985972	21986196	21985996	21986175	HR	NM_005144	1	19	2	-	21986072	21986723
317146791	chr8	21986567	21986782	21986587	21986761	HR	NM_005144	1	19	2	-	21986072	21986723
317150451	chr8	21986146	21986323	21986167	21986304	HR	NM_005144	1	19	2	-	21986072	21986723
317153615	chr8	21986276	21986478	21986298	21986457	HR	NM_005144	1	19	2	-	21986072	21986723
317156409	chr8	21986417	21986626	21986439	21986606	HR	NM_005144	1	19	2	-	21986072	21986723
317384500	chr8	21984442	21984654	21984462	21984633	HR	NM_005144	1	19	3	-	21984550	21985342
317386662	chr8	21985036	21985225	21985055	21985207	HR	NM_005144	1	19	3	-	21984550	21985342
317388673	chr8	21984580	21984799	21984604	21984782	HR	NM_005144	1	19	3	-	21984550	21985342
317391455	chr8	21984766	21984981	21984783	21984961	HR	NM_005144	1	19	3	-	21984550	21985342
317393466	chr8	21985187	21985378	21985208	21985355	HR	NM_005144	1	19	3	-	21984550	21985342
317397301	chr8	21984939	21985094	21984960	21985072	HR	NM_005144	1	19	3	-	21984550	21985342
316810940	chr8	21983008	21983212	21983028	21983191	HR	NM_005144	1	19	4	-	21983095	21983245
316815343	chr8	21983153	21983320	21983176	21983300	HR	NM_005144	1	19	4	-	21983095	21983245
316428020	chr8	21982709	21982909	21982730	21982891	HR	NM_005144	1	19	5	-	21982824	21983017
316429830	chr8	21982874	21983089	21982892	21983071	HR	NM_005144	1	19	5	-	21982824	21983017
317831668	chr8	21981085	21981272	21981106	21981251	HR	NM_005144	1	19	6	-	21981162	21981326
317836959	chr8	21981234	21981359	21981252	21981339	HR	NM_005144	1	19	6	-	21981162	21981326
315875615	chr8	21980234	21980432	21980254	21980409	HR	NM_005144	1	19	7	-	21980303	21980392
317158439	chr8	21979972	21980169	21979991	21980147	HR	NM_005144	1	19	8	-	21980006	21980121
317389730	chr8	21979027	21979217	21979048	21979189	HR	NM_005144	1	19	9	-	21979126	21979207
317401565	chr8	21979162	21979341	21979183	21979315	HR	NM_005144	1	19	9	-	21979126	21979207
316947802	chr8	21978410	21978632	21978430	21978611	HR	NM_005144	1	19	10	-	21978578	21978741
318002930	chr8	21978436	21978659	21978460	21978641	HR	NM_005144	1	19	10	-	21978578	21978741
318008997	chr8	21978623	21978765	21978642	21978746	HR	NM_005144	1	19	10	-	21978578	21978741
316944416	chr8	21978078	21978271	21978095	21978252	HR	NM_005144	1	19	11	-	21978229	21978471
316945753	chr8	21978235	21978459	21978253	21978438	HR	NM_005144	1	19	11	-	21978229	21978471
316947802	chr8	21978410	21978632	21978430	21978611	HR	NM_005144	1	19	11	-	21978229	21978471
318002930	chr8	21978436	21978659	21978460	21978641	HR	NM_005144	1	19	11	-	21978229	21978471
316429463	chr8	21977824	21978045	21977842	21978026	HR	NM_005144	1	19	12	-	21977855	21978020
316671913	chr8	21977491	21977715	21977513	21977696	HR	NM_005144	1	19	13	-	21977617	21977686

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
317532158	chr8	21977226	21977384	21977248	21977364	HR	NM_005144	1	19	14	-	21977273	21977403
317538128	chr8	21977336	21977519	21977358	21977497	HR	NM_005144	1	19	14	-	21977273	21977403
315710696	chr8	21976619	21976843	21976640	21976815	HR	NM_005144	1	19	15	-	21976677	21976796
315602156	chr8	21976398	21976603	21976416	21976585	HR	NM_005144	1	19	16	-	21976463	21976578
316012798	chr8	21974316	21974510	21974333	21974492	HR	NM_005144	1	19	17	-	21974388	21974552
316013587	chr8	21974439	21974628	21974457	21974608	HR	NM_005144	1	19	17	-	21974388	21974552
315535014	chr8	21973766	21973974	21973785	21973953	HR	NM_005144	1	19	18	-	21973813	21973941
317777450	chr8	21973102	21973313	21973124	21973285	HR	NM_005144	1	19	19	-	21971932	21973275
317145414	chr8	21985972	21986196	21985996	21986175	HR	NM_018411	2	18	2	-	21986072	21986723
317146791	chr8	21986567	21986782	21986587	21986761	HR	NM_018411	2	18	2	-	21986072	21986723
317150451	chr8	21986146	21986323	21986167	21986304	HR	NM_018411	2	18	2	-	21986072	21986723
317153615	chr8	21986276	21986478	21986298	21986457	HR	NM_018411	2	18	2	-	21986072	21986723
317156409	chr8	21986417	21986626	21986439	21986606	HR	NM_018411	2	18	2	-	21986072	21986723
317384500	chr8	21984442	21984654	21984462	21984633	HR	NM_018411	2	18	3	-	21984550	21985342
317386662	chr8	21985036	21985225	21985055	21985207	HR	NM_018411	2	18	3	-	21984550	21985342
317388673	chr8	21984580	21984799	21984604	21984782	HR	NM_018411	2	18	3	-	21984550	21985342
317391455	chr8	21984766	21984981	21984783	21984961	HR	NM_018411	2	18	3	-	21984550	21985342
317393466	chr8	21985187	21985378	21985208	21985355	HR	NM_018411	2	18	3	-	21984550	21985342
317397301	chr8	21984939	21985094	21984960	21985072	HR	NM_018411	2	18	3	-	21984550	21985342
316810940	chr8	21983008	21983212	21983028	21983191	HR	NM_018411	2	18	4	-	21983095	21983245
316815343	chr8	21983153	21983320	21983176	21983300	HR	NM_018411	2	18	4	-	21983095	21983245
316428020	chr8	21982709	21982909	21982730	21982891	HR	NM_018411	2	18	5	-	21982824	21983017
316429830	chr8	21982874	21983089	21982892	21983071	HR	NM_018411	2	18	5	-	21982824	21983017
317831668	chr8	21981085	21981272	21981106	21981251	HR	NM_018411	2	18	6	-	21981162	21981326
317836959	chr8	21981234	21981359	21981252	21981339	HR	NM_018411	2	18	6	-	21981162	21981326
315875615	chr8	21980234	21980432	21980254	21980409	HR	NM_018411	2	18	7	-	21980303	21980392
317158439	chr8	21979972	21980169	21979991	21980147	HR	NM_018411	2	18	8	-	21980006	21980121
317389730	chr8	21979027	21979217	21979048	21979189	HR	NM_018411	2	18	9	-	21979126	21979207
317401565	chr8	21979162	21979341	21979183	21979315	HR	NM_018411	2	18	9	-	21979126	21979207
316947802	chr8	21978410	21978632	21978430	21978611	HR	NM_018411	2	18	10	-	21978578	21978741
318002930	chr8	21978436	21978659	21978460	21978641	HR	NM_018411	2	18	10	-	21978578	21978741
318008997	chr8	21978623	21978765	21978642	21978746	HR	NM_018411	2	18	10	-	21978578	21978741
316944416	chr8	21978078	21978271	21978095	21978252	HR	NM_018411	2	18	11	-	21978229	21978471
316945753	chr8	21978235	21978459	21978253	21978438	HR	NM_018411	2	18	11	-	21978229	21978471
316947802	chr8	21978410	21978632	21978430	21978611	HR	NM_018411	2	18	11	-	21978229	21978471
318002930	chr8	21978436	21978659	21978460	21978641	HR	NM_018411	2	18	11	-	21978229	21978471
316429463	chr8	21977824	21978045	21977842	21978026	HR	NM_018411	2	18	12	-	21977855	21978020
316671913	chr8	21977491	21977715	21977513	21977696	HR	NM_018411	2	18	13	-	21977617	21977686
317532158	chr8	21977226	21977384	21977248	21977364	HR	NM_018411	2	18	14	-	21977273	21977403
317538128	chr8	21977336	21977519	21977358	21977497	HR	NM_018411	2	18	14	-	21977273	21977403
315710696	chr8	21976619	21976843	21976640	21976815	HR	NM_018411	2	18	15	-	21976677	21976796

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315602156	chr8	21976398	21976603	21976416	21976585	HR	NM_018411	2	18	16	-	21976463	21976578
315535014	chr8	21973766	21973974	21973785	21973953	HR	NM_018411	2	18	17	-	21973813	21973941
317777450	chr8	21973102	21973313	21973124	21973285	HR	NM_018411	2	18	18	-	21971932	21973275
333305161	chrX	148586415	148586625	148586440	148586605	IDS	NM_000202	1	9	1	-	148586565	148586884
333309169	chrX	148586560	148586777	148586579	148586758	IDS	NM_000202	1	9	1	-	148586565	148586884
332459508	chrX	148585656	148585880	148585677	148585860	IDS	NM_000202	1	9	2	-	148585687	148585823
332688340	chrX	148584809	148584961	148584831	148584941	IDS	NM_000202	1	9	3	-	148584842	148585019
332690211	chrX	148584923	148585130	148584942	148585108	IDS	NM_000202	1	9	3	-	148584842	148585019
332773688	chrX	148582393	148582617	148582418	148582589	IDS	NM_000202	1	9	4	-	148582480	148582568
333091863	chrX	148579563	148579736	148579584	148579709	IDS	NM_000202	1	9	5	-	148579638	148579838
333103236	chrX	148579688	148579897	148579710	148579871	IDS	NM_000202	1	9	5	-	148579638	148579838
333391365	chrX	148577734	148577901	148577755	148577878	IDS	NM_000202	1	9	6	-	148577877	148578047
333406372	chrX	148577854	148578077	148577879	148578052	IDS	NM_000202	1	9	6	-	148577877	148578047
333585219	chrX	148571657	148571871	148571684	148571845	IDS	NM_000202	1	9	7	-	148571845	148571971
333612120	chrX	148571820	148572040	148571846	148572012	IDS	NM_000202	1	9	7	-	148571845	148571971
332741648	chrX	148568358	148568576	148568379	148568553	IDS	NM_000202	1	9	8	-	148568456	148568629
332756489	chrX	148568533	148568730	148568554	148568702	IDS	NM_000202	1	9	8	-	148568456	148568629
333024166	chrX	148564246	148564464	148564269	148564439	IDS	NM_000202	1	9	9	-	148560295	148564749
333044804	chrX	148564417	148564615	148564440	148564591	IDS	NM_000202	1	9	9	-	148560295	148564749
333060052	chrX	148564570	148564777	148564592	148564756	IDS	NM_000202	1	9	9	-	148560295	148564749
333305161	chrX	148586415	148586625	148586440	148586605	IDS	NM_001166550	2	9	1	-	148586565	148586884
333309169	chrX	148586560	148586777	148586579	148586758	IDS	NM_001166550	2	9	1	-	148586565	148586884
332459508	chrX	148585656	148585880	148585677	148585860	IDS	NM_001166550	2	9	2	-	148585687	148585823
332688340	chrX	148584809	148584961	148584831	148584941	IDS	NM_001166550	2	9	3	-	148584842	148584975
332690211	chrX	148584923	148585130	148584942	148585108	IDS	NM_001166550	2	9	3	-	148584842	148584975
332773688	chrX	148582393	148582617	148582418	148582589	IDS	NM_001166550	2	9	4	-	148582480	148582568
333091863	chrX	148579563	148579736	148579584	148579709	IDS	NM_001166550	2	9	5	-	148579638	148579838
333103236	chrX	148579688	148579897	148579710	148579871	IDS	NM_001166550	2	9	5	-	148579638	148579838
333391365	chrX	148577734	148577901	148577755	148577878	IDS	NM_001166550	2	9	6	-	148577877	148578047
333406372	chrX	148577854	148578077	148577879	148578052	IDS	NM_001166550	2	9	6	-	148577877	148578047
333585219	chrX	148571657	148571871	148571684	148571845	IDS	NM_001166550	2	9	7	-	148571845	148571971
333612120	chrX	148571820	148572040	148571846	148572012	IDS	NM_001166550	2	9	7	-	148571845	148571971
332741648	chrX	148568358	148568576	148568379	148568553	IDS	NM_001166550	2	9	8	-	148568456	148568629
332756489	chrX	148568533	148568730	148568554	148568702	IDS	NM_001166550	2	9	8	-	148568456	148568629
333024166	chrX	148564246	148564464	148564269	148564439	IDS	NM_001166550	2	9	9	-	148560295	148564749
333044804	chrX	148564417	148564615	148564440	148564591	IDS	NM_001166550	2	9	9	-	148560295	148564749
333060052	chrX	148564570	148564777	148564592	148564756	IDS	NM_001166550	2	9	9	-	148560295	148564749
333305161	chrX	148586415	148586625	148586440	148586605	IDS	NM_006123	3	8	1	-	148586565	148586884
333309169	chrX	148586560	148586777	148586579	148586758	IDS	NM_006123	3	8	1	-	148586565	148586884
332459508	chrX	148585656	148585880	148585677	148585860	IDS	NM_006123	3	8	2	-	148585687	148585823
332688340	chrX	148584809	148584961	148584831	148584941	IDS	NM_006123	3	8	3	-	148584842	148585019

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332690211	chrX	148584923	148585130	148584942	148585108	IDS	NM_006123	3	8	3	-	148584842	148585019
332773688	chrX	148582393	148582617	148582418	148582589	IDS	NM_006123	3	8	4	-	148582480	148582568
333091863	chrX	148579563	148579736	148579584	148579709	IDS	NM_006123	3	8	5	-	148579638	148579838
333103236	chrX	148579688	148579897	148579710	148579871	IDS	NM_006123	3	8	5	-	148579638	148579838
333391365	chrX	148577734	148577901	148577755	148577878	IDS	NM_006123	3	8	6	-	148577877	148578047
333406372	chrX	148577854	148578077	148577879	148578052	IDS	NM_006123	3	8	6	-	148577877	148578047
333585219	chrX	148571657	148571871	148571684	148571845	IDS	NM_006123	3	8	7	-	148571845	148571971
333612120	chrX	148571820	148572040	148571846	148572012	IDS	NM_006123	3	8	7	-	148571845	148571971
332672775	chrX	148568711	148568925	148568738	148568897	IDS	NM_006123	3	8	8	-	148568662	148568844
332756489	chrX	148568533	148568730	148568554	148568702	IDS	NM_006123	3	8	8	-	148568662	148568844
328551274	chr4	980959	981119	980977	981098	IDUA	NM_000203	1	14	1	+	980785	981030
329258406	chr4	981573	981795	981590	981773	IDUA	NM_000203	1	14	2	+	981597	981737
329363604	chr4	994368	994591	994387	994571	IDUA	NM_000203	1	14	3	+	994400	994485
329263011	chr4	994558	994748	994581	994725	IDUA	NM_000203	1	14	4	+	994670	994777
329269423	chr4	994702	994926	994725	994905	IDUA	NM_000203	1	14	4	+	994670	994777
329107786	chr4	995157	995314	995178	995293	IDUA	NM_000203	1	14	5	+	995256	995351
329114344	chr4	995271	995457	995294	995438	IDUA	NM_000203	1	14	5	+	995256	995351
328674656	chr4	995646	995857	995668	995840	IDUA	NM_000203	1	14	6	+	995467	995669
328832557	chr4	995410	995632	995429	995613	IDUA	NM_000203	1	14	6	+	995467	995669
328834405	chr4	995597	995804	995614	995784	IDUA	NM_000203	1	14	6	+	995467	995669
328674656	chr4	995646	995857	995668	995840	IDUA	NM_000203	1	14	7	+	995770	995949
328675494	chr4	995820	996002	995839	995984	IDUA	NM_000203	1	14	7	+	995770	995949
328675749	chr4	995914	996092	995931	996072	IDUA	NM_000203	1	14	7	+	995770	995949
328834405	chr4	995597	995804	995614	995784	IDUA	NM_000203	1	14	7	+	995770	995949
328675749	chr4	995914	996092	995931	996072	IDUA	NM_000203	1	14	8	+	996057	996273
328759634	chr4	996055	996212	996072	996195	IDUA	NM_000203	1	14	8	+	996057	996273
328760104	chr4	996183	996373	996200	996356	IDUA	NM_000203	1	14	8	+	996057	996273
328779126	chr4	996410	996586	996429	996569	IDUA	NM_000203	1	14	9	+	996520	996732
328779354	chr4	996530	996749	996547	996731	IDUA	NM_000203	1	14	9	+	996520	996732
328779965	chr4	996644	996867	996662	996850	IDUA	NM_000203	1	14	9	+	996520	996732
328779965	chr4	996644	996867	996662	996850	IDUA	NM_000203	1	14	10	+	996824	996945
328886463	chr4	997089	997273	997107	997256	IDUA	NM_000203	1	14	11	+	997133	997258
328887349	chr4	997211	997415	997230	997397	IDUA	NM_000203	1	14	11	+	997133	997258
328887349	chr4	997211	997415	997230	997397	IDUA	NM_000203	1	14	12	+	997337	997413
329282720	chr4	997259	997464	997278	997446	IDUA	NM_000203	1	14	12	+	997337	997413
328630790	chr4	997743	997956	997763	997937	IDUA	NM_000203	1	14	13	+	997800	997900
329017035	chr4	998013	998226	998031	998209	IDUA	NM_000203	1	14	14	+	998048	998317
279023073	chr9	111693233	111693454	111693254	111693431	IKBKAP	NM_003640	1	37	2	-	111693277	111693481
279308123	chr9	111691962	111692143	111691988	111692122	IKBKAP	NM_003640	1	37	3	-	111692049	111692201
279316717	chr9	111692102	111692238	111692123	111692210	IKBKAP	NM_003640	1	37	3	-	111692049	111692201
278209117	chr9	111689588	111689812	111689616	111689784	IKBKAP	NM_003640	1	37	4	-	111689652	111689733

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279781491	chr9	111688726	111688948	111688750	111688919	IKBKAP	NM_003640	1	37	5	-	111688803	111688883
278339098	chr9	111685016	111685240	111685044	111685213	IKBKAP	NM_003640	1	37	6	-	111685122	111685207
317188474	chr9	111681391	111681608	111681418	111681582	IKBKAP	NM_003640	1	37	7	-	111681533	111681629
317196780	chr9	111681539	111681761	111681560	111681738	IKBKAP	NM_003640	1	37	7	-	111681533	111681629
279789336	chr9	111681011	111681212	111681039	111681188	IKBKAP	NM_003640	1	37	8	-	111681091	111681181
279036664	chr9	111679766	111679983	111679793	111679955	IKBKAP	NM_003640	1	37	9	-	111679827	111679950
279976003	chr9	111678406	111678620	111678433	111678593	IKBKAP	NM_003640	1	37	10	-	111678484	111678577
278208296	chr9	111674452	111674639	111674474	111674618	IKBKAP	NM_003640	1	37	11	-	111674544	111674774
278236801	chr9	111674599	111674807	111674619	111674781	IKBKAP	NM_003640	1	37	11	-	111674544	111674774
281269601	chr9	111673188	111673354	111673213	111673329	IKBKAP	NM_003640	1	37	12	-	111673290	111673460
281283711	chr9	111673303	111673498	111673330	111673469	IKBKAP	NM_003640	1	37	12	-	111673290	111673460
280099502	chr9	111670535	111670752	111670556	111670724	IKBKAP	NM_003640	1	37	13	-	111670585	111670684
280822163	chr9	111668611	111668828	111668634	111668801	IKBKAP	NM_003640	1	37	14	-	111668583	111668765
315926031	chr9	111668455	111668655	111668481	111668633	IKBKAP	NM_003640	1	37	14	-	111668583	111668765
279460240	chr9	111665806	111665984	111665834	111665957	IKBKAP	NM_003640	1	37	15	-	111665843	111665949
278171601	chr9	111665063	111665261	111665085	111665233	IKBKAP	NM_003640	1	37	16	-	111665119	111665222
279707578	chr9	111663832	111664045	111663854	111664017	IKBKAP	NM_003640	1	37	17	-	111663908	111663961
278612512	chr9	111663641	111663865	111663667	111663840	IKBKAP	NM_003640	1	37	18	-	111663705	111663810
279446848	chr9	111662479	111662703	111662502	111662675	IKBKAP	NM_003640	1	37	19	-	111662540	111662655
278350091	chr9	111662046	111662253	111662075	111662225	IKBKAP	NM_003640	1	37	20	-	111662102	111662175
280564998	chr9	111660873	111661085	111660899	111661057	IKBKAP	NM_003640	1	37	21	-	111660951	111661029
317152186	chr9	111660811	111661007	111660841	111660980	IKBKAP	NM_003640	1	37	21	-	111660951	111661029
277938824	chr9	111660708	111660866	111660740	111660840	IKBKAP	NM_003640	1	37	22	-	111660782	111660861
317152186	chr9	111660811	111661007	111660841	111660980	IKBKAP	NM_003640	1	37	22	-	111660782	111660861
278835241	chr9	111659371	111659595	111659395	111659570	IKBKAP	NM_003640	1	37	23	-	111659428	111659565
278228582	chr9	111659132	111659355	111659157	111659327	IKBKAP	NM_003640	1	37	24	-	111659233	111659318
279552721	chr9	111658750	111658967	111658778	111658940	IKBKAP	NM_003640	1	37	25	-	111658776	111658924
316735071	chr9	111658620	111658801	111658642	111658777	IKBKAP	NM_003640	1	37	25	-	111658776	111658924
316417175	chr9	111656067	111656253	111656092	111656232	IKBKAP	NM_003640	1	37	26	-	111656223	111656346
281238800	chr9	111655170	111655394	111655194	111655368	IKBKAP	NM_003640	1	37	27	-	111655266	111655363
278439149	chr9	111653376	111653577	111653401	111653555	IKBKAP	NM_003640	1	37	28	-	111653483	111653684
278441734	chr9	111653507	111653730	111653532	111653702	IKBKAP	NM_003640	1	37	28	-	111653483	111653684
315857673	chr9	111651487	111651705	111651509	111651679	IKBKAP	NM_003640	1	37	29	-	111651612	111651673
317112891	chr9	111644275	111644497	111644299	111644472	IKBKAP	NM_003640	1	37	30	-	111644405	111644467
280404001	chr9	111643898	111644095	111643926	111644067	IKBKAP	NM_003640	1	37	31	-	111643985	111644045
280204795	chr9	111642259	111642482	111642282	111642454	IKBKAP	NM_003640	1	37	32	-	111642332	111642445
279098870	chr9	111641650	111641866	111641678	111641842	IKBKAP	NM_003640	1	37	33	-	111641726	111641837
277892366	chr9	111640821	111641028	111640843	111641004	IKBKAP	NM_003640	1	37	34	-	111640903	111641030
315782298	chr9	111640974	111641152	111640997	111641129	IKBKAP	NM_003640	1	37	34	-	111640903	111641030
278859813	chr9	111640277	111640484	111640299	111640457	IKBKAP	NM_003640	1	37	35	-	111640275	111640429
317316210	chr9	111640117	111640326	111640144	111640298	IKBKAP	NM_003640	1	37	35	-	111640275	111640429

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278633307	chr9	111637195	111637319	111637221	111637297	IKBKAP	NM_003640	1	37	36	-	111637175	111637250
316988673	chr9	111637025	111637248	111637052	111637220	IKBKAP	NM_003640	1	37	36	-	111637175	111637250
281194809	chr9	111631298	111631492	111631321	111631467	IKBKAP	NM_003640	1	37	37	-	111629800	111631462
317255790	chrX	70331201	70331421	70331221	70331398	IL2RG	NM_000206	1	8	1	-	70331275	70331481
317034341	chrX	70330612	70330835	70330634	70330810	IL2RG	NM_000206	1	8	2	-	70330747	70330900
317061632	chrX	70330788	70330954	70330811	70330928	IL2RG	NM_000206	1	8	2	-	70330747	70330900
315938364	chrX	70330225	70330449	70330246	70330425	IL2RG	NM_000206	1	8	3	-	70330354	70330538
315973059	chrX	70330405	70330569	70330426	70330545	IL2RG	NM_000206	1	8	3	-	70330354	70330538
315897533	chrX	70329961	70330177	70329984	70330152	IL2RG	NM_000206	1	8	4	-	70330006	70330145
316036682	chrX	70328984	70329123	70329005	70329102	IL2RG	NM_000206	1	8	5	-	70329078	70329240
316055833	chrX	70329081	70329280	70329103	70329256	IL2RG	NM_000206	1	8	5	-	70329078	70329240
316382437	chrX	70328322	70328546	70328346	70328521	IL2RG	NM_000206	1	8	6	-	70328449	70328545
316706637	chrX	70328076	70328239	70328098	70328216	IL2RG	NM_000206	1	8	7	-	70328127	70328196
316904791	chrX	70327507	70327731	70327528	70327710	IL2RG	NM_000206	1	8	8	-	70327254	70327771
316917782	chrX	70327690	70327824	70327711	70327798	IL2RG	NM_000206	1	8	8	-	70327254	70327771
316891038	chr7	128049806	128049948	128049824	128049930	IMPDH1	NM_000883	1	17	1	-	128049810	128050036
316891062	chr7	128049866	128050046	128049883	128050029	IMPDH1	NM_000883	1	17	1	-	128049810	128050036
315719151	chr7	128049357	128049579	128049378	128049555	IMPDH1	NM_000883	1	17	2	-	128049495	128049538
315719151	chr7	128049357	128049579	128049378	128049555	IMPDH1	NM_000883	1	17	3	-	128049343	128049406
316916378	chr7	128049263	128049452	128049284	128049431	IMPDH1	NM_000883	1	17	3	-	128049343	128049406
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_000883	1	17	4	-	128045821	128045919
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_000883	1	17	4	-	128045821	128045919
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_000883	1	17	5	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_000883	1	17	6	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_000883	1	17	7	-	128040871	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_000883	1	17	7	-	128040871	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_000883	1	17	8	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_000883	1	17	8	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_000883	1	17	9	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_000883	1	17	10	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_000883	1	17	10	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_000883	1	17	11	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_000883	1	17	12	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_000883	1	17	13	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_000883	1	17	14	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_000883	1	17	15	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_000883	1	17	15	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_000883	1	17	16	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_000883	1	17	17	-	128032331	128033082
316891038	chr7	128049806	128049948	128049824	128049930	IMPDH1	NM_001102605	2	16	1	-	128049810	128050036
316891062	chr7	128049866	128050046	128049883	128050029	IMPDH1	NM_001102605	2	16	1	-	128049810	128050036

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315719151	chr7	128049357	128049579	128049378	128049555	IMPDH1	NM_001102605	2	16	2	-	128049343	128049420
316916378	chr7	128049263	128049452	128049284	128049431	IMPDH1	NM_001102605	2	16	2	-	128049343	128049420
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_001102605	2	16	3	-	128045821	128045919
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_001102605	2	16	3	-	128045821	128045919
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_001102605	2	16	4	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_001102605	2	16	5	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_001102605	2	16	6	-	128040871	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_001102605	2	16	6	-	128040871	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_001102605	2	16	7	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_001102605	2	16	7	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_001102605	2	16	8	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_001102605	2	16	9	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_001102605	2	16	9	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_001102605	2	16	10	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_001102605	2	16	11	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_001102605	2	16	12	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_001102605	2	16	13	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_001102605	2	16	14	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_001102605	2	16	14	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_001102605	2	16	15	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_001102605	2	16	16	-	128032331	128033082
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_001142573	3	14	1	-	128045821	128046024
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_001142573	3	14	1	-	128045821	128046024
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_001142573	3	14	2	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_001142573	3	14	3	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_001142573	3	14	4	-	128040871	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_001142573	3	14	4	-	128040871	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_001142573	3	14	5	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_001142573	3	14	5	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_001142573	3	14	6	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_001142573	3	14	7	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_001142573	3	14	7	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_001142573	3	14	8	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_001142573	3	14	9	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_001142573	3	14	10	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_001142573	3	14	11	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_001142573	3	14	12	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_001142573	3	14	12	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_001142573	3	14	13	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_001142573	3	14	14	-	128032331	128033082
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_001142574	4	14	1	-	128045821	128046024

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_001142574	4	14	1	-	128045821	128046024
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_001142574	4	14	2	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_001142574	4	14	3	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_001142574	4	14	4	-	128040886	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_001142574	4	14	4	-	128040886	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_001142574	4	14	5	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_001142574	4	14	5	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_001142574	4	14	6	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_001142574	4	14	7	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_001142574	4	14	7	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_001142574	4	14	8	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_001142574	4	14	9	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_001142574	4	14	10	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_001142574	4	14	11	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_001142574	4	14	12	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_001142574	4	14	12	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_001142574	4	14	13	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_001142574	4	14	14	-	128032331	128033082
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_001142575	5	13	1	-	128045821	128046024
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_001142575	5	13	1	-	128045821	128046024
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_001142575	5	13	2	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_001142575	5	13	3	-	128041069	128041170
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_001142575	5	13	4	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_001142575	5	13	4	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_001142575	5	13	5	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_001142575	5	13	6	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_001142575	5	13	6	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_001142575	5	13	7	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_001142575	5	13	8	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_001142575	5	13	9	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_001142575	5	13	10	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_001142575	5	13	11	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_001142575	5	13	11	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_001142575	5	13	12	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_001142575	5	13	13	-	128032331	128033082
316891038	chr7	128049806	128049948	128049824	128049930	IMPDH1	NM_001142576	6	16	1	-	128049810	128050036
316891062	chr7	128049866	128050046	128049883	128050029	IMPDH1	NM_001142576	6	16	1	-	128049810	128050036
315719151	chr7	128049357	128049579	128049378	128049555	IMPDH1	NM_001142576	6	16	2	-	128049495	128049538
315719151	chr7	128049357	128049579	128049378	128049555	IMPDH1	NM_001142576	6	16	3	-	128049343	128049406
316916378	chr7	128049263	128049452	128049284	128049431	IMPDH1	NM_001142576	6	16	3	-	128049343	128049406
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_001142576	6	16	4	-	128043760	128043808

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_001142576	6	16	5	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_001142576	6	16	6	-	128040871	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_001142576	6	16	6	-	128040871	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_001142576	6	16	7	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_001142576	6	16	7	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_001142576	6	16	8	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_001142576	6	16	9	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_001142576	6	16	9	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_001142576	6	16	10	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_001142576	6	16	11	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_001142576	6	16	12	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_001142576	6	16	13	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_001142576	6	16	14	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_001142576	6	16	14	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_001142576	6	16	15	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_001142576	6	16	16	-	128032331	128033082
316891038	chr7	128049806	128049948	128049824	128049930	IMPDH1	NM_183243	7	15	1	-	128049810	128050036
316891062	chr7	128049866	128050046	128049883	128050029	IMPDH1	NM_183243	7	15	1	-	128049810	128050036
316597329	chr7	128045666	128045887	128045683	128045870	IMPDH1	NM_183243	7	15	2	-	128045821	128045919
316598233	chr7	128045812	128045960	128045833	128045943	IMPDH1	NM_183243	7	15	2	-	128045821	128045919
316385407	chr7	128043628	128043851	128043655	128043830	IMPDH1	NM_183243	7	15	3	-	128043760	128043808
316369862	chr7	128041011	128041209	128041030	128041184	IMPDH1	NM_183243	7	15	4	-	128041069	128041170
316365871	chr7	128040919	128041081	128040945	128041059	IMPDH1	NM_183243	7	15	5	-	128040871	128040945
316696142	chr7	128040749	128040970	128040770	128040946	IMPDH1	NM_183243	7	15	5	-	128040871	128040945
315845253	chr7	128040334	128040497	128040354	128040477	IMPDH1	NM_183243	7	15	6	-	128040387	128040593
315853071	chr7	128040413	128040634	128040437	128040612	IMPDH1	NM_183243	7	15	6	-	128040387	128040593
316024655	chr7	128040046	128040269	128040067	128040248	IMPDH1	NM_183243	7	15	7	-	128040149	128040236
316909762	chr7	128038388	128038604	128038409	128038581	IMPDH1	NM_183243	7	15	8	-	128038468	128038667
316927520	chr7	128038555	128038772	128038576	128038750	IMPDH1	NM_183243	7	15	8	-	128038468	128038667
317165765	chr7	128036888	128037102	128036910	128037081	IMPDH1	NM_183243	7	15	9	-	128036986	128037076
315848815	chr7	128036629	128036795	128036648	128036773	IMPDH1	NM_183243	7	15	10	-	128036654	128036749
316789740	chr7	128035157	128035369	128035177	128035346	IMPDH1	NM_183243	7	15	11	-	128035185	128035328
317503231	chr7	128034895	128035118	128034915	128035097	IMPDH1	NM_183243	7	15	12	-	128034943	128035087
315542977	chr7	128034401	128034607	128034426	128034582	IMPDH1	NM_183243	7	15	13	-	128034510	128034653
315560982	chr7	128034563	128034736	128034583	128034712	IMPDH1	NM_183243	7	15	13	-	128034510	128034653
316581658	chr7	128034249	128034445	128034271	128034423	IMPDH1	NM_183243	7	15	14	-	128034332	128034415
317581212	chr7	128032950	128033127	128032972	128033106	IMPDH1	NM_183243	7	15	15	-	128032331	128033082
279394023	chr17	73720737	73720958	73720758	73720935	ITGB4	NM_000213	1	40	2	+	73720774	73720862
278482519	chr17	73723212	73723428	73723233	73723402	ITGB4	NM_000213	1	40	3	+	73723275	73723357
281054791	chr17	73723458	73723645	73723477	73723623	ITGB4	NM_000213	1	40	4	+	73723485	73723586
281031221	chr17	73723685	73723897	73723704	73723876	ITGB4	NM_000213	1	40	5	+	73723732	73723936

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
281042172	chr17	73723855	73724054	73723877	73724029	ITGB4	NM_000213	1	40	5	+	73723732	73723936
280307613	chr17	73724422	73724631	73724443	73724608	ITGB4	NM_000213	1	40	6	+	73724458	73724554
279735502	chr17	73725259	73725435	73725282	73725409	ITGB4	NM_000213	1	40	7	+	73725346	73725517
279741631	chr17	73725388	73725572	73725410	73725554	ITGB4	NM_000213	1	40	7	+	73725346	73725517
278533815	chr17	73726356	73726575	73726375	73726549	ITGB4	NM_000213	1	40	8	+	73726322	73726585
278542110	chr17	73726528	73726656	73726550	73726634	ITGB4	NM_000213	1	40	8	+	73726322	73726585
316840287	chr17	73726175	73726395	73726197	73726374	ITGB4	NM_000213	1	40	8	+	73726322	73726585
277849702	chr17	73726913	73727136	73726936	73727116	ITGB4	NM_000213	1	40	9	+	73726956	73727045
281232165	chr17	73727290	73727494	73727310	73727477	ITGB4	NM_000213	1	40	10	+	73727327	73727449
278696811	chr17	73727786	73728005	73727810	73727984	ITGB4	NM_000213	1	40	11	+	73727893	73728054
278700239	chr17	73727964	73728133	73727985	73728111	ITGB4	NM_000213	1	40	11	+	73727893	73728054
316553874	chr17	73728115	73728293	73728136	73728272	ITGB4	NM_000213	1	40	12	+	73728244	73728320
316560903	chr17	73728243	73728461	73728263	73728439	ITGB4	NM_000213	1	40	12	+	73728244	73728320
279406389	chr17	73729525	73729748	73729546	73729724	ITGB4	NM_000213	1	40	13	+	73729571	73729773
279414016	chr17	73729704	73729849	73729723	73729829	ITGB4	NM_000213	1	40	13	+	73729571	73729773
279048269	chr17	73732085	73732303	73732107	73732280	ITGB4	NM_000213	1	40	14	+	73732132	73732235
278521940	chr17	73732280	73732494	73732302	73732473	ITGB4	NM_000213	1	40	15	+	73732369	73732467
281266945	chr17	73732606	73732812	73732625	73732793	ITGB4	NM_000213	1	40	16	+	73732646	73732775
279777522	chr17	73733303	73733467	73733323	73733446	ITGB4	NM_000213	1	40	17	+	73733403	73733525
279779170	chr17	73733427	73733583	73733446	73733566	ITGB4	NM_000213	1	40	17	+	73733403	73733525
280296074	chr17	73733515	73733739	73733536	73733722	ITGB4	NM_000213	1	40	18	+	73733619	73733725
281062873	chr17	73735648	73735843	73735669	73735821	ITGB4	NM_000213	1	40	19	+	73735753	73735786
280796666	chr17	73735912	73736129	73735930	73736111	ITGB4	NM_000213	1	40	20	+	73735961	73736152
317450681	chr17	73736078	73736301	73736099	73736279	ITGB4	NM_000213	1	40	20	+	73735961	73736152
280591251	chr17	73736337	73736549	73736358	73736527	ITGB4	NM_000213	1	40	21	+	73736439	73736542
317216289	chr17	73736482	73736660	73736502	73736638	ITGB4	NM_000213	1	40	21	+	73736439	73736542
280077460	chr17	73736765	73736939	73736786	73736919	ITGB4	NM_000213	1	40	22	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_000213	1	40	22	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_000213	1	40	23	+	73737063	73737086
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_000213	1	40	24	+	73738422	73738570
280065868	chr17	73738396	73738525	73738414	73738506	ITGB4	NM_000213	1	40	24	+	73738422	73738570
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_000213	1	40	24	+	73738422	73738570
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_000213	1	40	25	+	73738663	73738842
278953812	chr17	73738710	73738864	73738727	73738846	ITGB4	NM_000213	1	40	25	+	73738663	73738842
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_000213	1	40	25	+	73738663	73738842
278335516	chr17	73739756	73739971	73739775	73739954	ITGB4	NM_000213	1	40	26	+	73739794	73739942
278719167	chr17	73744970	73745172	73744991	73745150	ITGB4	NM_000213	1	40	27	+	73744922	73745126
317112833	chr17	73744793	73745015	73744815	73744993	ITGB4	NM_000213	1	40	27	+	73744922	73745126
278019155	chr17	73746111	73746319	73746132	73746295	ITGB4	NM_000213	1	40	28	+	73746192	73746349
315976071	chr17	73746265	73746485	73746285	73746465	ITGB4	NM_000213	1	40	28	+	73746192	73746349
278589431	chr17	73746657	73746875	73746682	73746849	ITGB4	NM_000213	1	40	29	+	73746761	73746941

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278595310	chr17	73746830	73747043	73746850	73747020	ITGB4	NM_000213	1	40	29	+	73746761	73746941
279808701	chr17	73747014	73747219	73747034	73747197	ITGB4	NM_000213	1	40	30	+	73747055	73747192
278318901	chr17	73748225	73748415	73748246	73748395	ITGB4	NM_000213	1	40	31	+	73748255	73748437
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_000213	1	40	31	+	73748255	73748437
279644234	chr17	73748523	73748719	73748543	73748697	ITGB4	NM_000213	1	40	32	+	73748527	73748658
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_000213	1	40	32	+	73748527	73748658
278181212	chr17	73750629	73750838	73750647	73750819	ITGB4	NM_000213	1	40	34	+	73750657	73750896
278192836	chr17	73750799	73750946	73750819	73750923	ITGB4	NM_000213	1	40	34	+	73750657	73750896
278430136	chr17	73751717	73751938	73751737	73751921	ITGB4	NM_000213	1	40	35	+	73751782	73751931
316669523	chr17	73751897	73752049	73751918	73752028	ITGB4	NM_000213	1	40	35	+	73751782	73751931
279690394	chr17	73752463	73752670	73752485	73752650	ITGB4	NM_000213	1	40	36	+	73752510	73752698
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_000213	1	40	36	+	73752510	73752698
278851751	chr17	73752753	73752937	73752775	73752917	ITGB4	NM_000213	1	40	37	+	73752785	73752940
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_000213	1	40	37	+	73752785	73752940
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_000213	1	40	37	+	73752785	73752940
279848819	chr17	73752994	73753214	73753014	73753193	ITGB4	NM_000213	1	40	38	+	73753024	73753188
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_000213	1	40	38	+	73753024	73753188
279281759	chr17	73753248	73753424	73753268	73753406	ITGB4	NM_000213	1	40	39	+	73753281	73753391
278080208	chr17	73753460	73753641	73753481	73753619	ITGB4	NM_000213	1	40	40	+	73753497	73753899
278083961	chr17	73753598	73753724	73753619	73753703	ITGB4	NM_000213	1	40	40	+	73753497	73753899
279394023	chr17	73720737	73720958	73720758	73720935	ITGB4	NM_001005619	2	39	1	+	73720776	73720862
278482519	chr17	73723212	73723428	73723233	73723402	ITGB4	NM_001005619	2	39	2	+	73723275	73723357
281054791	chr17	73723458	73723645	73723477	73723623	ITGB4	NM_001005619	2	39	3	+	73723485	73723586
281031221	chr17	73723685	73723897	73723704	73723876	ITGB4	NM_001005619	2	39	4	+	73723732	73723936
281042172	chr17	73723855	73724054	73723877	73724029	ITGB4	NM_001005619	2	39	4	+	73723732	73723936
280307613	chr17	73724422	73724631	73724443	73724608	ITGB4	NM_001005619	2	39	5	+	73724458	73724554
279735502	chr17	73725259	73725435	73725282	73725409	ITGB4	NM_001005619	2	39	6	+	73725346	73725517
279741631	chr17	73725388	73725572	73725410	73725554	ITGB4	NM_001005619	2	39	6	+	73725346	73725517
278533815	chr17	73726356	73726575	73726375	73726549	ITGB4	NM_001005619	2	39	7	+	73726322	73726585
278542110	chr17	73726528	73726656	73726550	73726634	ITGB4	NM_001005619	2	39	7	+	73726322	73726585
316840287	chr17	73726175	73726395	73726197	73726374	ITGB4	NM_001005619	2	39	7	+	73726322	73726585
277849702	chr17	73726913	73727136	73726936	73727116	ITGB4	NM_001005619	2	39	8	+	73726956	73727045
281232165	chr17	73727290	73727494	73727310	73727477	ITGB4	NM_001005619	2	39	9	+	73727327	73727449
278696811	chr17	73727786	73728005	73727810	73727984	ITGB4	NM_001005619	2	39	10	+	73727893	73728054
278700239	chr17	73727964	73728133	73727985	73728111	ITGB4	NM_001005619	2	39	10	+	73727893	73728054
316553874	chr17	73728115	73728293	73728136	73728272	ITGB4	NM_001005619	2	39	11	+	73728244	73728320
316560903	chr17	73728243	73728461	73728263	73728439	ITGB4	NM_001005619	2	39	11	+	73728244	73728320
279406389	chr17	73729525	73729748	73729546	73729724	ITGB4	NM_001005619	2	39	12	+	73729571	73729773
279414016	chr17	73729704	73729849	73729723	73729829	ITGB4	NM_001005619	2	39	12	+	73729571	73729773
279048269	chr17	73732085	73732303	73732107	73732280	ITGB4	NM_001005619	2	39	13	+	73732132	73732235
278521940	chr17	73732280	73732494	73732302	73732473	ITGB4	NM_001005619	2	39	14	+	73732369	73732467

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
281266945	chr17	73732606	73732812	73732625	73732793	ITGB4	NM_001005619	2	39	15	+	73732646	73732775
279777522	chr17	73733303	73733467	73733323	73733446	ITGB4	NM_001005619	2	39	16	+	73733403	73733525
279779170	chr17	73733427	73733583	73733446	73733566	ITGB4	NM_001005619	2	39	16	+	73733403	73733525
280296074	chr17	73733515	73733739	73733536	73733722	ITGB4	NM_001005619	2	39	17	+	73733619	73733725
281062873	chr17	73735648	73735843	73735669	73735821	ITGB4	NM_001005619	2	39	18	+	73735753	73735786
280796666	chr17	73735912	73736129	73735930	73736111	ITGB4	NM_001005619	2	39	19	+	73735961	73736152
317450681	chr17	73736078	73736301	73736099	73736279	ITGB4	NM_001005619	2	39	19	+	73735961	73736152
280591251	chr17	73736337	73736549	73736358	73736527	ITGB4	NM_001005619	2	39	20	+	73736439	73736542
317216289	chr17	73736482	73736660	73736502	73736638	ITGB4	NM_001005619	2	39	20	+	73736439	73736542
280077460	chr17	73736765	73736939	73736786	73736919	ITGB4	NM_001005619	2	39	21	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_001005619	2	39	21	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_001005619	2	39	22	+	73737063	73737086
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_001005619	2	39	23	+	73738422	73738570
280065868	chr17	73738396	73738525	73738414	73738506	ITGB4	NM_001005619	2	39	23	+	73738422	73738570
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_001005619	2	39	23	+	73738422	73738570
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_001005619	2	39	24	+	73738663	73738842
278953812	chr17	73738710	73738864	73738727	73738846	ITGB4	NM_001005619	2	39	24	+	73738663	73738842
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_001005619	2	39	24	+	73738663	73738842
278335516	chr17	73739756	73739971	73739775	73739954	ITGB4	NM_001005619	2	39	25	+	73739794	73739942
278719167	chr17	73744970	73745172	73744991	73745150	ITGB4	NM_001005619	2	39	26	+	73744922	73745126
317112833	chr17	73744793	73745015	73744815	73744993	ITGB4	NM_001005619	2	39	26	+	73744922	73745126
278019155	chr17	73746111	73746319	73746132	73746295	ITGB4	NM_001005619	2	39	27	+	73746192	73746349
315976071	chr17	73746265	73746485	73746285	73746465	ITGB4	NM_001005619	2	39	27	+	73746192	73746349
278589431	chr17	73746657	73746875	73746682	73746849	ITGB4	NM_001005619	2	39	28	+	73746761	73746941
278595310	chr17	73746830	73747043	73746850	73747020	ITGB4	NM_001005619	2	39	28	+	73746761	73746941
279808701	chr17	73747014	73747219	73747034	73747197	ITGB4	NM_001005619	2	39	29	+	73747055	73747192
278318901	chr17	73748225	73748415	73748246	73748395	ITGB4	NM_001005619	2	39	30	+	73748255	73748437
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_001005619	2	39	30	+	73748255	73748437
279644234	chr17	73748523	73748719	73748543	73748697	ITGB4	NM_001005619	2	39	31	+	73748527	73748658
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_001005619	2	39	31	+	73748527	73748658
278181212	chr17	73750629	73750838	73750647	73750819	ITGB4	NM_001005619	2	39	32	+	73750657	73750896
278192836	chr17	73750799	73750946	73750819	73750923	ITGB4	NM_001005619	2	39	32	+	73750657	73750896
280280368	chr17	73751100	73751264	73751121	73751240	ITGB4	NM_001005619	2	39	33	+	73751136	73751294
280286172	chr17	73751200	73751360	73751221	73751338	ITGB4	NM_001005619	2	39	33	+	73751136	73751294
278430136	chr17	73751717	73751938	73751737	73751921	ITGB4	NM_001005619	2	39	34	+	73751782	73751931
316669523	chr17	73751897	73752049	73751918	73752028	ITGB4	NM_001005619	2	39	34	+	73751782	73751931
279690394	chr17	73752463	73752670	73752485	73752650	ITGB4	NM_001005619	2	39	35	+	73752510	73752698
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_001005619	2	39	35	+	73752510	73752698
278851751	chr17	73752753	73752937	73752775	73752917	ITGB4	NM_001005619	2	39	36	+	73752785	73752940
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_001005619	2	39	36	+	73752785	73752940
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_001005619	2	39	36	+	73752785	73752940

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279848819	chr17	73752994	73753214	73753014	73753193	ITGB4	NM_001005619	2	39	37	+	73753024	73753188
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_001005619	2	39	37	+	73753024	73753188
279281759	chr17	73753248	73753424	73753268	73753406	ITGB4	NM_001005619	2	39	38	+	73753281	73753391
278080208	chr17	73753460	73753641	73753481	73753619	ITGB4	NM_001005619	2	39	39	+	73753497	73753899
278083961	chr17	73753598	73753724	73753619	73753703	ITGB4	NM_001005619	2	39	39	+	73753497	73753899
279394023	chr17	73720737	73720958	73720758	73720935	ITGB4	NM_001005731	3	39	2	+	73720774	73720862
278482519	chr17	73723212	73723428	73723233	73723402	ITGB4	NM_001005731	3	39	3	+	73723275	73723357
281054791	chr17	73723458	73723645	73723477	73723623	ITGB4	NM_001005731	3	39	4	+	73723485	73723586
281031221	chr17	73723685	73723897	73723704	73723876	ITGB4	NM_001005731	3	39	5	+	73723732	73723936
281042172	chr17	73723855	73724054	73723877	73724029	ITGB4	NM_001005731	3	39	5	+	73723732	73723936
280307613	chr17	73724422	73724631	73724443	73724608	ITGB4	NM_001005731	3	39	6	+	73724458	73724554
279735502	chr17	73725259	73725435	73725282	73725409	ITGB4	NM_001005731	3	39	7	+	73725346	73725517
279741631	chr17	73725388	73725572	73725410	73725554	ITGB4	NM_001005731	3	39	7	+	73725346	73725517
278533815	chr17	73726356	73726575	73726375	73726549	ITGB4	NM_001005731	3	39	8	+	73726322	73726585
278542110	chr17	73726528	73726656	73726550	73726634	ITGB4	NM_001005731	3	39	8	+	73726322	73726585
316840287	chr17	73726175	73726395	73726197	73726374	ITGB4	NM_001005731	3	39	8	+	73726322	73726585
277849702	chr17	73726913	73727136	73726936	73727116	ITGB4	NM_001005731	3	39	9	+	73726956	73727045
281232165	chr17	73727290	73727494	73727310	73727477	ITGB4	NM_001005731	3	39	10	+	73727327	73727449
278696811	chr17	73727786	73728005	73727810	73727984	ITGB4	NM_001005731	3	39	11	+	73727893	73728054
278700239	chr17	73727964	73728133	73727985	73728111	ITGB4	NM_001005731	3	39	11	+	73727893	73728054
316553874	chr17	73728115	73728293	73728136	73728272	ITGB4	NM_001005731	3	39	12	+	73728244	73728320
316560903	chr17	73728243	73728461	73728263	73728439	ITGB4	NM_001005731	3	39	12	+	73728244	73728320
279406389	chr17	73729525	73729748	73729546	73729724	ITGB4	NM_001005731	3	39	13	+	73729571	73729773
279414016	chr17	73729704	73729849	73729723	73729829	ITGB4	NM_001005731	3	39	13	+	73729571	73729773
279048269	chr17	73732085	73732303	73732107	73732280	ITGB4	NM_001005731	3	39	14	+	73732132	73732235
278521940	chr17	73732280	73732494	73732302	73732473	ITGB4	NM_001005731	3	39	15	+	73732369	73732467
281266945	chr17	73732606	73732812	73732625	73732793	ITGB4	NM_001005731	3	39	16	+	73732646	73732775
279777522	chr17	73733303	73733467	73733323	73733446	ITGB4	NM_001005731	3	39	17	+	73733403	73733525
279779170	chr17	73733427	73733583	73733446	73733566	ITGB4	NM_001005731	3	39	17	+	73733403	73733525
280296074	chr17	73733515	73733739	73733536	73733722	ITGB4	NM_001005731	3	39	18	+	73733619	73733725
281062873	chr17	73735648	73735843	73735669	73735821	ITGB4	NM_001005731	3	39	19	+	73735753	73735786
280796666	chr17	73735912	73736129	73735930	73736111	ITGB4	NM_001005731	3	39	20	+	73735961	73736152
317450681	chr17	73736078	73736301	73736099	73736279	ITGB4	NM_001005731	3	39	20	+	73735961	73736152
280591251	chr17	73736337	73736549	73736358	73736527	ITGB4	NM_001005731	3	39	21	+	73736439	73736542
317216289	chr17	73736482	73736660	73736502	73736638	ITGB4	NM_001005731	3	39	21	+	73736439	73736542
280077460	chr17	73736765	73736939	73736786	73736919	ITGB4	NM_001005731	3	39	22	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_001005731	3	39	22	+	73736874	73736932
316832733	chr17	73736894	73737107	73736916	73737084	ITGB4	NM_001005731	3	39	23	+	73737063	73737086
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_001005731	3	39	24	+	73738422	73738570
280065868	chr17	73738396	73738525	73738414	73738506	ITGB4	NM_001005731	3	39	24	+	73738422	73738570
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_001005731	3	39	24	+	73738422	73738570

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278949328	chr17	73738541	73738746	73738561	73738726	ITGB4	NM_001005731	3	39	25	+	73738663	73738842
278953812	chr17	73738710	73738864	73738727	73738846	ITGB4	NM_001005731	3	39	25	+	73738663	73738842
315899233	chr17	73738484	73738693	73738507	73738673	ITGB4	NM_001005731	3	39	25	+	73738663	73738842
278335516	chr17	73739756	73739971	73739775	73739954	ITGB4	NM_001005731	3	39	26	+	73739794	73739942
278719167	chr17	73744970	73745172	73744991	73745150	ITGB4	NM_001005731	3	39	27	+	73744922	73745126
317112833	chr17	73744793	73745015	73744815	73744993	ITGB4	NM_001005731	3	39	27	+	73744922	73745126
278019155	chr17	73746111	73746319	73746132	73746295	ITGB4	NM_001005731	3	39	28	+	73746192	73746349
315976071	chr17	73746265	73746485	73746285	73746465	ITGB4	NM_001005731	3	39	28	+	73746192	73746349
278589431	chr17	73746657	73746875	73746682	73746849	ITGB4	NM_001005731	3	39	29	+	73746761	73746941
278595310	chr17	73746830	73747043	73746850	73747020	ITGB4	NM_001005731	3	39	29	+	73746761	73746941
279808701	chr17	73747014	73747219	73747034	73747197	ITGB4	NM_001005731	3	39	30	+	73747055	73747192
278318901	chr17	73748225	73748415	73748246	73748395	ITGB4	NM_001005731	3	39	31	+	73748255	73748437
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_001005731	3	39	31	+	73748255	73748437
279644234	chr17	73748523	73748719	73748543	73748697	ITGB4	NM_001005731	3	39	32	+	73748527	73748658
316350568	chr17	73748339	73748561	73748358	73748542	ITGB4	NM_001005731	3	39	32	+	73748527	73748658
278181212	chr17	73750629	73750838	73750647	73750819	ITGB4	NM_001005731	3	39	33	+	73750657	73750896
278192836	chr17	73750799	73750946	73750819	73750923	ITGB4	NM_001005731	3	39	33	+	73750657	73750896
278430136	chr17	73751717	73751938	73751737	73751921	ITGB4	NM_001005731	3	39	34	+	73751782	73751931
316669523	chr17	73751897	73752049	73751918	73752028	ITGB4	NM_001005731	3	39	34	+	73751782	73751931
279690394	chr17	73752463	73752670	73752485	73752650	ITGB4	NM_001005731	3	39	35	+	73752510	73752698
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_001005731	3	39	35	+	73752510	73752698
278851751	chr17	73752753	73752937	73752775	73752917	ITGB4	NM_001005731	3	39	36	+	73752785	73752940
279696725	chr17	73752630	73752815	73752650	73752795	ITGB4	NM_001005731	3	39	36	+	73752785	73752940
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_001005731	3	39	36	+	73752785	73752940
279848819	chr17	73752994	73753214	73753014	73753193	ITGB4	NM_001005731	3	39	37	+	73753024	73753188
317134186	chr17	73752895	73753116	73752916	73753094	ITGB4	NM_001005731	3	39	37	+	73753024	73753188
279281759	chr17	73753248	73753424	73753268	73753406	ITGB4	NM_001005731	3	39	38	+	73753281	73753391
278080208	chr17	73753460	73753641	73753481	73753619	ITGB4	NM_001005731	3	39	39	+	73753497	73753899
278083961	chr17	73753598	73753724	73753619	73753703	ITGB4	NM_001005731	3	39	39	+	73753497	73753899
316217559	chr20	10653323	10653520	10653342	10653495	JAG1	NM_000214	1	26	2	-	10653349	10653654
316221108	chr20	10653476	10653640	10653496	10653619	JAG1	NM_000214	1	26	2	-	10653349	10653654
316229103	chr20	10653600	10653797	10653620	10653773	JAG1	NM_000214	1	26	2	-	10653349	10653654
315716933	chr20	10644497	10644704	10644519	10644676	JAG1	NM_000214	1	26	3	-	10644611	10644662
315859914	chr20	10639055	10639259	10639080	10639235	JAG1	NM_000214	1	26	4	-	10639116	10639370
315871593	chr20	10639213	10639436	10639236	10639413	JAG1	NM_000214	1	26	4	-	10639116	10639370
316402877	chr20	10636960	10637133	10636989	10637112	JAG1	NM_000214	1	26	5	-	10637046	10637106
316822810	chr20	10633086	10633282	10633107	10633260	JAG1	NM_000214	1	26	6	-	10633116	10633246
316256503	chr20	10632732	10632930	10632760	10632904	JAG1	NM_000214	1	26	7	-	10632779	10632898
316114527	chr20	10632163	10632376	10632183	10632355	JAG1	NM_000214	1	26	8	-	10632229	10632342
315784931	chr20	10630814	10631038	10630834	10631016	JAG1	NM_000214	1	26	9	-	10630895	10631008
317417682	chr20	10630110	10630314	10630129	10630290	JAG1	NM_000214	1	26	10	-	10630170	10630283

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
316810597	chr20	10629623	10629822	10629644	10629794	JAG1	NM_000214	1	26	11	-	10629709	10629755
316516869	chr20	10629163	10629383	10629185	10629355	JAG1	NM_000214	1	26	12	-	10629197	10629370
316543151	chr20	10629333	10629457	10629356	10629435	JAG1	NM_000214	1	26	12	-	10629197	10629370
316449074	chr20	10628556	10628770	10628578	10628744	JAG1	NM_000214	1	26	13	-	10628608	10628758
316469040	chr20	10628725	10628869	10628745	10628844	JAG1	NM_000214	1	26	13	-	10628608	10628758
316126438	chr20	10627556	10627780	10627576	10627756	JAG1	NM_000214	1	26	14	-	10627587	10627751
316027750	chr20	10626555	10626779	10626576	10626753	JAG1	NM_000214	1	26	15	-	10626619	10626732
315824363	chr20	10625961	10626143	10625982	10626122	JAG1	NM_000214	1	26	16	-	10626004	10626117
320474322	chr20	10625824	10626026	10625848	10626004	JAG1	NM_000214	1	26	16	-	10626004	10626117
320458773	chr20	10625653	10625869	10625675	10625848	JAG1	NM_000214	1	26	17	-	10625791	10625904
320474322	chr20	10625824	10626026	10625848	10626004	JAG1	NM_000214	1	26	17	-	10625791	10625904
317935422	chr20	10625433	10625655	10625454	10625635	JAG1	NM_000214	1	26	18	-	10625511	10625627
320420438	chr20	10624959	10625099	10624981	10625074	JAG1	NM_000214	1	26	19	-	10625005	10625032
316870189	chr20	10624318	10624539	10624343	10624516	JAG1	NM_000214	1	26	20	-	10624426	10624511
315605134	chr20	10623060	10623281	10623085	10623254	JAG1	NM_000214	1	26	21	-	10623136	10623249
315832851	chr20	10622371	10622589	10622391	10622562	JAG1	NM_000214	1	26	22	-	10622431	10622540
316818203	chr20	10622000	10622222	10622025	10622202	JAG1	NM_000214	1	26	23	-	10622108	10622341
316842534	chr20	10622183	10622402	10622203	10622378	JAG1	NM_000214	1	26	23	-	10622108	10622341
316360319	chr20	10621711	10621931	10621731	10621904	JAG1	NM_000214	1	26	24	-	10621761	10621892
316133650	chr20	10621395	10621614	10621422	10621586	JAG1	NM_000214	1	26	25	-	10621431	10621581
317417455	chr20	10620407	10620576	10620429	10620551	JAG1	NM_000214	1	26	26	-	10618332	10620603
317424093	chr20	10619958	10620178	10619977	10620153	JAG1	NM_000214	1	26	26	-	10618332	10620603
317436626	chr20	10620531	10620673	10620552	10620648	JAG1	NM_000214	1	26	26	-	10618332	10620603
317446257	chr20	10620136	10620349	10620154	10620322	JAG1	NM_000214	1	26	26	-	10618332	10620603
319892457	chr20	10620301	10620451	10620323	10620428	JAG1	NM_000214	1	26	26	-	10618332	10620603
332841014	chr17	39927861	39928065	39927884	39928044	JUP	NM_002230	1	14	2	-	39927899	39928114
332852086	chr17	39928024	39928218	39928045	39928195	JUP	NM_002230	1	14	2	-	39927899	39928114
333168608	chr17	39925598	39925782	39925616	39925763	JUP	NM_002230	1	14	3	-	39925670	39925929
333173260	chr17	39925735	39925957	39925759	39925938	JUP	NM_002230	1	14	3	-	39925670	39925929
332727422	chr17	39925195	39925367	39925214	39925349	JUP	NM_002230	1	14	4	-	39925221	39925459
332736635	chr17	39925328	39925531	39925349	39925510	JUP	NM_002230	1	14	4	-	39925221	39925459
332690380	chr17	39923493	39923717	39923520	39923696	JUP	NM_002230	1	14	5	-	39923631	39923832
332697158	chr17	39923678	39923872	39923697	39923851	JUP	NM_002230	1	14	5	-	39923631	39923832
332995471	chr17	39921150	39921366	39921167	39921343	JUP	NM_002230	1	14	6	-	39921175	39921319
332705854	chr17	39920875	39921096	39920896	39921077	JUP	NM_002230	1	14	7	-	39920965	39921068
333022304	chr17	39919207	39919417	39919226	39919399	JUP	NM_002230	1	14	8	-	39919235	39919573
333036024	chr17	39919375	39919568	39919395	39919545	JUP	NM_002230	1	14	8	-	39919235	39919573
333053153	chr17	39919525	39919650	39919546	39919626	JUP	NM_002230	1	14	8	-	39919235	39919573
332795208	chr17	39914930	39915150	39914949	39915129	JUP	NM_002230	1	14	9	-	39914967	39915122
333228405	chr17	39914575	39914784	39914598	39914763	JUP	NM_002230	1	14	10	-	39914651	39914770
333237853	chr17	39914742	39914871	39914764	39914847	JUP	NM_002230	1	14	10	-	39914651	39914770

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332879041	chr17	39913727	39913923	39913748	39913903	JUP	NM_002230	1	14	11	-	39913886	39914036
332965814	chr17	39913881	39914085	39913899	39914065	JUP	NM_002230	1	14	11	-	39913886	39914036
332875838	chr17	39913630	39913816	39913653	39913793	JUP	NM_002230	1	14	12	-	39913667	39913788
332879041	chr17	39913727	39913923	39913748	39913903	JUP	NM_002230	1	14	12	-	39913667	39913788
333693994	chr17	39912274	39912495	39912295	39912472	JUP	NM_002230	1	14	13	-	39912427	39912466
333179433	chr17	39911927	39912127	39911952	39912106	JUP	NM_002230	1	14	14	-	39910859	39912147
333181400	chr17	39912060	39912191	39912083	39912170	JUP	NM_002230	1	14	14	-	39910859	39912147
332841014	chr17	39927861	39928065	39927884	39928044	JUP	NM_021991	2	15	2	-	39927899	39928114
332852086	chr17	39928024	39928218	39928045	39928195	JUP	NM_021991	2	15	2	-	39927899	39928114
333168608	chr17	39925598	39925782	39925616	39925763	JUP	NM_021991	2	15	3	-	39925670	39925929
333173260	chr17	39925735	39925957	39925759	39925938	JUP	NM_021991	2	15	3	-	39925670	39925929
332727422	chr17	39925195	39925367	39925214	39925349	JUP	NM_021991	2	15	4	-	39925221	39925459
332736635	chr17	39925328	39925531	39925349	39925510	JUP	NM_021991	2	15	4	-	39925221	39925459
332690380	chr17	39923493	39923717	39923520	39923696	JUP	NM_021991	2	15	5	-	39923631	39923832
332697158	chr17	39923678	39923872	39923697	39923851	JUP	NM_021991	2	15	5	-	39923631	39923832
332995471	chr17	39921150	39921366	39921167	39921343	JUP	NM_021991	2	15	6	-	39921175	39921319
332705854	chr17	39920875	39921096	39920896	39921077	JUP	NM_021991	2	15	7	-	39920965	39921068
333022304	chr17	39919207	39919417	39919226	39919399	JUP	NM_021991	2	15	8	-	39919235	39919573
333036024	chr17	39919375	39919568	39919395	39919545	JUP	NM_021991	2	15	8	-	39919235	39919573
333053153	chr17	39919525	39919650	39919546	39919626	JUP	NM_021991	2	15	8	-	39919235	39919573
332795208	chr17	39914930	39915150	39914949	39915129	JUP	NM_021991	2	15	9	-	39914967	39915122
333228405	chr17	39914575	39914784	39914598	39914763	JUP	NM_021991	2	15	10	-	39914651	39914770
333237853	chr17	39914742	39914871	39914764	39914847	JUP	NM_021991	2	15	10	-	39914651	39914770
332879041	chr17	39913727	39913923	39913748	39913903	JUP	NM_021991	2	15	11	-	39913886	39914036
332965814	chr17	39913881	39914085	39913899	39914065	JUP	NM_021991	2	15	11	-	39913886	39914036
332875838	chr17	39913630	39913816	39913653	39913793	JUP	NM_021991	2	15	12	-	39913667	39913788
332879041	chr17	39913727	39913923	39913748	39913903	JUP	NM_021991	2	15	12	-	39913667	39913788
333693994	chr17	39912274	39912495	39912295	39912472	JUP	NM_021991	2	15	13	-	39912427	39912466
333179433	chr17	39911927	39912127	39911952	39912106	JUP	NM_021991	2	15	14	-	39911982	39912147
333181400	chr17	39912060	39912191	39912083	39912170	JUP	NM_021991	2	15	14	-	39911982	39912147
313839339	chr21	35821401	35821621	35821424	35821598	KCNE1	NM_000219	1	3	3	-	35818988	35821982
313861100	chr21	35821576	35821791	35821599	35821768	KCNE1	NM_000219	1	3	3	-	35818988	35821982
313879348	chr21	35821747	35821952	35821768	35821930	KCNE1	NM_000219	1	3	3	-	35818988	35821982
313895285	chr21	35821909	35822035	35821930	35822013	KCNE1	NM_000219	1	3	3	-	35818988	35821982
313839339	chr21	35821401	35821621	35821424	35821598	KCNE1	NM_001127668	2	3	3	-	35818988	35821982
313861100	chr21	35821576	35821791	35821599	35821768	KCNE1	NM_001127668	2	3	3	-	35818988	35821982
313879348	chr21	35821747	35821952	35821768	35821930	KCNE1	NM_001127668	2	3	3	-	35818988	35821982
313895285	chr21	35821909	35822035	35821930	35822013	KCNE1	NM_001127668	2	3	3	-	35818988	35821982
313839339	chr21	35821401	35821621	35821424	35821598	KCNE1	NM_001127669	3	3	3	-	35818988	35821982
313861100	chr21	35821576	35821791	35821599	35821768	KCNE1	NM_001127669	3	3	3	-	35818988	35821982
313879348	chr21	35821747	35821952	35821768	35821930	KCNE1	NM_001127669	3	3	3	-	35818988	35821982

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313895285	chr21	35821909	35822035	35821930	35822013	KCNE1	NM_001127669	3	3	3	-	35818988	35821982
313839339	chr21	35821401	35821621	35821424	35821598	KCNE1	NM_001127670	4	2	2	-	35818988	35821982
313861100	chr21	35821576	35821791	35821599	35821768	KCNE1	NM_001127670	4	2	2	-	35818988	35821982
313879348	chr21	35821747	35821952	35821768	35821930	KCNE1	NM_001127670	4	2	2	-	35818988	35821982
313895285	chr21	35821909	35822035	35821930	35822013	KCNE1	NM_001127670	4	2	2	-	35818988	35821982
314104909	chr21	35742722	35742940	35742748	35742913	KCNE2	NM_172201	1	2	2	+	35742766	35743440
314128308	chr21	35742891	35743103	35742914	35743077	KCNE2	NM_172201	1	2	2	+	35742766	35743440
314159925	chr21	35743053	35743257	35743078	35743230	KCNE2	NM_172201	1	2	2	+	35742766	35743440
332281258	chr11	74168252	74168451	74168273	74168423	KCNE3	NM_005472	1	3	3	-	74165886	74168648
332301214	chr11	74168393	74168617	74168422	74168594	KCNE3	NM_005472	1	3	3	-	74165886	74168648
332314809	chr11	74168574	74168705	74168595	74168684	KCNE3	NM_005472	1	3	3	-	74165886	74168648
312732660	chr7	150674811	150674969	150674830	150674948	KCNH2	NM_000238	1	15	1	-	150674926	150675402
313947041	chr7	150671786	150672009	150671803	150671991	KCNH2	NM_000238	1	15	2	-	150671799	150672029
313952758	chr7	150671965	150672117	150671985	150672095	KCNH2	NM_000238	1	15	2	-	150671799	150672029
313117317	chr7	150656630	150656848	150656650	150656829	KCNH2	NM_000238	1	15	3	-	150656660	150656824
314902096	chr7	150655039	150655252	150655058	150655235	KCNH2	NM_000238	1	15	4	-	150655147	150655590
314902141	chr7	150655187	150655411	150655204	150655393	KCNH2	NM_000238	1	15	4	-	150655147	150655590
314902223	chr7	150655229	150655433	150655246	150655415	KCNH2	NM_000238	1	15	4	-	150655147	150655590
314902365	chr7	150655394	150655618	150655412	150655601	KCNH2	NM_000238	1	15	4	-	150655147	150655590
313699188	chr7	150654331	150654530	150654351	150654507	KCNH2	NM_000238	1	15	5	-	150654379	150654590
313710589	chr7	150654483	150654675	150654506	150654652	KCNH2	NM_000238	1	15	5	-	150654379	150654590
314006299	chr7	150649447	150649664	150649468	150649644	KCNH2	NM_000238	1	15	6	-	150649513	150649941
314022452	chr7	150649625	150649846	150649645	150649827	KCNH2	NM_000238	1	15	6	-	150649513	150649941
314035627	chr7	150649794	150650016	150649816	150649996	KCNH2	NM_000238	1	15	6	-	150649513	150649941
313987312	chr7	150648463	150648669	150648484	150648646	KCNH2	NM_000238	1	15	7	-	150648536	150648923
313997688	chr7	150648628	150648831	150648647	150648809	KCNH2	NM_000238	1	15	7	-	150648536	150648923
314008798	chr7	150648767	150648965	150648787	150648945	KCNH2	NM_000238	1	15	7	-	150648536	150648923
313672201	chr7	150647921	150648140	150647942	150648120	KCNH2	NM_000238	1	15	8	-	150648009	150648208
313677277	chr7	150648091	150648310	150648111	150648289	KCNH2	NM_000238	1	15	8	-	150648009	150648208
314711874	chr7	150647167	150647386	150647186	150647363	KCNH2	NM_000238	1	15	9	-	150647256	150647508
314717636	chr7	150647336	150647553	150647355	150647535	KCNH2	NM_000238	1	15	9	-	150647256	150647508
315019241	chr7	150645798	150646015	150645820	150645994	KCNH2	NM_000238	1	15	10	-	150645944	150646137
315050033	chr7	150645975	150646165	150645995	150646146	KCNH2	NM_000238	1	15	10	-	150645944	150646137
312881912	chr7	150645437	150645658	150645456	150645636	KCNH2	NM_000238	1	15	11	-	150645532	150645631
314219745	chr7	150644563	150644743	150644586	150644725	KCNH2	NM_000238	1	15	12	-	150644694	150644966
314399198	chr7	150644706	150644875	150644725	150644858	KCNH2	NM_000238	1	15	12	-	150644694	150644966
314400794	chr7	150644825	150644996	150644846	150644974	KCNH2	NM_000238	1	15	12	-	150644694	150644966
314217515	chr7	150644333	150644544	150644354	150644524	KCNH2	NM_000238	1	15	13	-	150644416	150644602
314219003	chr7	150644442	150644651	150644460	150644634	KCNH2	NM_000238	1	15	13	-	150644416	150644602
314219745	chr7	150644563	150644743	150644586	150644725	KCNH2	NM_000238	1	15	13	-	150644416	150644602
313906010	chr7	150643919	150644100	150643938	150644079	KCNH2	NM_000238	1	15	14	-	150643965	150644142

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313911326	chr7	150644045	150644182	150644065	150644161	KCNH2	NM_000238	1	15	14	-	150643965	150644142
315264231	chr7	150642326	150642536	150642346	150642518	KCNH2	NM_000238	1	15	15	-	150642044	150642602
315266090	chr7	150642465	150642643	150642482	150642625	KCNH2	NM_000238	1	15	15	-	150642044	150642602
313406303	chr7	150652303	150652510	150652321	150652492	KCNH2	NM_001204798	2	5	1	-	150652484	150652917
313408456	chr7	150652464	150652660	150652483	150652643	KCNH2	NM_001204798	2	5	1	-	150652484	150652917
314006299	chr7	150649447	150649664	150649468	150649644	KCNH2	NM_001204798	2	5	2	-	150649513	150649941
314022452	chr7	150649625	150649846	150649645	150649827	KCNH2	NM_001204798	2	5	2	-	150649513	150649941
314035627	chr7	150649794	150650016	150649816	150649996	KCNH2	NM_001204798	2	5	2	-	150649513	150649941
313987312	chr7	150648463	150648669	150648484	150648646	KCNH2	NM_001204798	2	5	3	-	150648536	150648923
313997688	chr7	150648628	150648831	150648647	150648809	KCNH2	NM_001204798	2	5	3	-	150648536	150648923
314008798	chr7	150648767	150648965	150648787	150648945	KCNH2	NM_001204798	2	5	3	-	150648536	150648923
313672201	chr7	150647921	150648140	150647942	150648120	KCNH2	NM_001204798	2	5	4	-	150648009	150648208
313677277	chr7	150648091	150648310	150648111	150648289	KCNH2	NM_001204798	2	5	4	-	150648009	150648208
313018739	chr7	150646844	150647051	150646866	150647028	KCNH2	NM_001204798	2	5	5	-	150646516	150647508
314698994	chr7	150647009	150647204	150647029	150647185	KCNH2	NM_001204798	2	5	5	-	150646516	150647508
314711874	chr7	150647167	150647386	150647186	150647363	KCNH2	NM_001204798	2	5	5	-	150646516	150647508
314717636	chr7	150647336	150647553	150647355	150647535	KCNH2	NM_001204798	2	5	5	-	150646516	150647508
312732660	chr7	150674811	150674969	150674830	150674948	KCNH2	NM_172056	3	9	1	-	150674926	150675402
313947041	chr7	150671786	150672009	150671803	150671991	KCNH2	NM_172056	3	9	2	-	150671799	150672029
313952758	chr7	150671965	150672117	150671985	150672095	KCNH2	NM_172056	3	9	2	-	150671799	150672029
313117317	chr7	150656630	150656848	150656650	150656829	KCNH2	NM_172056	3	9	3	-	150656660	150656824
314902096	chr7	150655039	150655252	150655058	150655235	KCNH2	NM_172056	3	9	4	-	150655147	150655590
314902141	chr7	150655187	150655411	150655204	150655393	KCNH2	NM_172056	3	9	4	-	150655147	150655590
314902223	chr7	150655229	150655433	150655246	150655415	KCNH2	NM_172056	3	9	4	-	150655147	150655590
314902365	chr7	150655394	150655618	150655412	150655601	KCNH2	NM_172056	3	9	4	-	150655147	150655590
313699188	chr7	150654331	150654530	150654351	150654507	KCNH2	NM_172056	3	9	5	-	150654379	150654590
313710589	chr7	150654483	150654675	150654506	150654652	KCNH2	NM_172056	3	9	5	-	150654379	150654590
314006299	chr7	150649447	150649664	150649468	150649644	KCNH2	NM_172056	3	9	6	-	150649513	150649941
314022452	chr7	150649625	150649846	150649645	150649827	KCNH2	NM_172056	3	9	6	-	150649513	150649941
314035627	chr7	150649794	150650016	150649816	150649996	KCNH2	NM_172056	3	9	6	-	150649513	150649941
313987312	chr7	150648463	150648669	150648484	150648646	KCNH2	NM_172056	3	9	7	-	150648536	150648923
313997688	chr7	150648628	150648831	150648647	150648809	KCNH2	NM_172056	3	9	7	-	150648536	150648923
314008798	chr7	150648767	150648965	150648787	150648945	KCNH2	NM_172056	3	9	7	-	150648536	150648923
313672201	chr7	150647921	150648140	150647942	150648120	KCNH2	NM_172056	3	9	8	-	150648009	150648208
313677277	chr7	150648091	150648310	150648111	150648289	KCNH2	NM_172056	3	9	8	-	150648009	150648208
313018739	chr7	150646844	150647051	150646866	150647028	KCNH2	NM_172056	3	9	9	-	150646516	150647508
314698994	chr7	150647009	150647204	150647029	150647185	KCNH2	NM_172056	3	9	9	-	150646516	150647508
314711874	chr7	150647167	150647386	150647186	150647363	KCNH2	NM_172056	3	9	9	-	150646516	150647508
314717636	chr7	150647336	150647553	150647355	150647535	KCNH2	NM_172056	3	9	9	-	150646516	150647508
313406303	chr7	150652303	150652510	150652321	150652492	KCNH2	NM_172057	4	11	1	-	150652484	150652917
313408456	chr7	150652464	150652660	150652483	150652643	KCNH2	NM_172057	4	11	1	-	150652484	150652917

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314006299	chr7	150649447	150649664	150649468	150649644	KCNH2	NM_172057	4	11	2	-	150649513	150649941
314022452	chr7	150649625	150649846	150649645	150649827	KCNH2	NM_172057	4	11	2	-	150649513	150649941
314035627	chr7	150649794	150650016	150649816	150649996	KCNH2	NM_172057	4	11	2	-	150649513	150649941
313987312	chr7	150648463	150648669	150648484	150648646	KCNH2	NM_172057	4	11	3	-	150648536	150648923
313997688	chr7	150648628	150648831	150648647	150648809	KCNH2	NM_172057	4	11	3	-	150648536	150648923
314008798	chr7	150648767	150648965	150648787	150648945	KCNH2	NM_172057	4	11	3	-	150648536	150648923
313672201	chr7	150647921	150648140	150647942	150648120	KCNH2	NM_172057	4	11	4	-	150648009	150648208
313677277	chr7	150648091	150648310	150648111	150648289	KCNH2	NM_172057	4	11	4	-	150648009	150648208
314711874	chr7	150647167	150647386	150647186	150647363	KCNH2	NM_172057	4	11	5	-	150647256	150647508
314717636	chr7	150647336	150647553	150647355	150647535	KCNH2	NM_172057	4	11	5	-	150647256	150647508
315019241	chr7	150645798	150646015	150645820	150645994	KCNH2	NM_172057	4	11	6	-	150645944	150646137
315050033	chr7	150645975	150646165	150645995	150646146	KCNH2	NM_172057	4	11	6	-	150645944	150646137
312881912	chr7	150645437	150645658	150645456	150645636	KCNH2	NM_172057	4	11	7	-	150645532	150645631
314219745	chr7	150644563	150644743	150644586	150644725	KCNH2	NM_172057	4	11	8	-	150644694	150644966
314399198	chr7	150644706	150644875	150644725	150644858	KCNH2	NM_172057	4	11	8	-	150644694	150644966
314400794	chr7	150644825	150644996	150644846	150644974	KCNH2	NM_172057	4	11	8	-	150644694	150644966
314217515	chr7	150644333	150644544	150644354	150644524	KCNH2	NM_172057	4	11	9	-	150644416	150644602
314219003	chr7	150644442	150644651	150644460	150644634	KCNH2	NM_172057	4	11	9	-	150644416	150644602
314219745	chr7	150644563	150644743	150644586	150644725	KCNH2	NM_172057	4	11	9	-	150644416	150644602
313906010	chr7	150643919	150644100	150643938	150644079	KCNH2	NM_172057	4	11	10	-	150643965	150644142
313911326	chr7	150644045	150644182	150644065	150644161	KCNH2	NM_172057	4	11	10	-	150643965	150644142
315264231	chr7	150642326	150642536	150642346	150642518	KCNH2	NM_172057	4	11	11	-	150642044	150642602
315266090	chr7	150642465	150642643	150642482	150642625	KCNH2	NM_172057	4	11	11	-	150642044	150642602
333034994	chr17	68172159	68172383	68172182	68172360	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333038350	chr17	68171674	68171869	68171694	68171848	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333051402	chr17	68171828	68172047	68171849	68172019	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333058123	chr17	68172337	68172485	68172361	68172461	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333068269	chr17	68172443	68172656	68172462	68172631	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333069911	chr17	68171988	68172209	68172016	68172182	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333087187	chr17	68171147	68171371	68171168	68171346	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333108074	chr17	68171322	68171545	68171347	68171523	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
333126840	chr17	68171492	68171715	68171514	68171695	KCNJ2	NM_000891	1	2	2	+	68170965	68176183
314381911	chr11	2466412	2466618	2466430	2466599	KCNQ1	NM_000218	1	16	1	+	2466221	2466714
314383080	chr11	2466576	2466768	2466593	2466749	KCNQ1	NM_000218	1	16	1	+	2466221	2466714
315488736	chr11	2549034	2549216	2549057	2549195	KCNQ1	NM_000218	1	16	2	+	2549158	2549248
315496163	chr11	2549174	2549385	2549194	2549364	KCNQ1	NM_000218	1	16	2	+	2549158	2549248
314074787	chr11	2591738	2591895	2591760	2591875	KCNQ1	NM_000218	1	16	3	+	2591858	2591984
314079141	chr11	2591843	2592040	2591863	2592019	KCNQ1	NM_000218	1	16	3	+	2591858	2591984
313956327	chr11	2592511	2592735	2592531	2592714	KCNQ1	NM_000218	1	16	4	+	2592555	2592633
313624153	chr11	2593216	2593387	2593234	2593369	KCNQ1	NM_000218	1	16	5	+	2593243	2593339
313570127	chr11	2594047	2594241	2594067	2594221	KCNQ1	NM_000218	1	16	6	+	2594076	2594216

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314619154	chr11	2604621	2604824	2604638	2604806	KCNQ1	NM_000218	1	16	7	+	2604665	2604775
314784484	chr11	2606364	2606588	2606383	2606560	KCNQ1	NM_000218	1	16	8	+	2606442	2606537
314371647	chr11	2608725	2608920	2608747	2608898	KCNQ1	NM_000218	1	16	9	+	2608800	2608922
314374660	chr11	2608844	2609025	2608867	2609004	KCNQ1	NM_000218	1	16	9	+	2608800	2608922
314433179	chr11	2609901	2610031	2609922	2610012	KCNQ1	NM_000218	1	16	10	+	2609943	2610084
314438379	chr11	2609991	2610171	2610013	2610150	KCNQ1	NM_000218	1	16	10	+	2609943	2610084
315229185	chr11	2683154	2683339	2683173	2683320	KCNQ1	NM_000218	1	16	11	+	2683191	2683311
314127973	chr11	2790034	2790245	2790054	2790224	KCNQ1	NM_000218	1	16	12	+	2790074	2790149
312897655	chr11	2797154	2797364	2797173	2797347	KCNQ1	NM_000218	1	16	13	+	2797190	2797284
314753698	chr11	2798145	2798290	2798165	2798267	KCNQ1	NM_000218	1	16	14	+	2798216	2798262
314816548	chr11	2799166	2799354	2799186	2799334	KCNQ1	NM_000218	1	16	15	+	2799206	2799267
312972514	chr11	2868965	2869188	2868986	2869169	KCNQ1	NM_000218	1	16	16	+	2868997	2870340
312974728	chr11	2869143	2869342	2869162	2869320	KCNQ1	NM_000218	1	16	16	+	2868997	2870340
315488736	chr11	2549034	2549216	2549057	2549195	KCNQ1	NR_040711	2	16	2	+	2549158	2549248
315496163	chr11	2549174	2549385	2549194	2549364	KCNQ1	NR_040711	2	16	2	+	2549158	2549248
314074787	chr11	2591738	2591895	2591760	2591875	KCNQ1	NR_040711	2	16	3	+	2591858	2591984
314079141	chr11	2591843	2592040	2591863	2592019	KCNQ1	NR_040711	2	16	3	+	2591858	2591984
313956327	chr11	2592511	2592735	2592531	2592714	KCNQ1	NR_040711	2	16	4	+	2592555	2592633
313624153	chr11	2593216	2593387	2593234	2593369	KCNQ1	NR_040711	2	16	5	+	2593243	2593339
313570127	chr11	2594047	2594241	2594067	2594221	KCNQ1	NR_040711	2	16	6	+	2594076	2594216
314619154	chr11	2604621	2604824	2604638	2604806	KCNQ1	NR_040711	2	16	7	+	2604665	2604775
314784484	chr11	2606364	2606588	2606383	2606560	KCNQ1	NR_040711	2	16	8	+	2606442	2606537
314371647	chr11	2608725	2608920	2608747	2608898	KCNQ1	NR_040711	2	16	9	+	2608800	2608922
314374660	chr11	2608844	2609025	2608867	2609004	KCNQ1	NR_040711	2	16	9	+	2608800	2608922
314433179	chr11	2609901	2610031	2609922	2610012	KCNQ1	NR_040711	2	16	10	+	2609943	2610084
314438379	chr11	2609991	2610171	2610013	2610150	KCNQ1	NR_040711	2	16	10	+	2609943	2610084
315229185	chr11	2683154	2683339	2683173	2683320	KCNQ1	NR_040711	2	16	11	+	2683191	2683311
314127973	chr11	2790034	2790245	2790054	2790224	KCNQ1	NR_040711	2	16	12	+	2790074	2790149
312897655	chr11	2797154	2797364	2797173	2797347	KCNQ1	NR_040711	2	16	13	+	2797190	2797284
314753698	chr11	2798145	2798290	2798165	2798267	KCNQ1	NR_040711	2	16	14	+	2798216	2798262
314816548	chr11	2799166	2799354	2799186	2799334	KCNQ1	NR_040711	2	16	15	+	2799206	2799267
312972514	chr11	2868965	2869188	2868986	2869169	KCNQ1	NR_040711	2	16	16	+	2868997	2870340
312974728	chr11	2869143	2869342	2869162	2869320	KCNQ1	NR_040711	2	16	16	+	2868997	2870340
314511384	chr1	41249679	41249866	41249696	41249849	KCNQ4	NM_004700	1	14	1	+	41249684	41250079
314511449	chr1	41249828	41250044	41249845	41250027	KCNQ4	NM_004700	1	14	1	+	41249684	41250079
314511463	chr1	41250010	41250232	41250028	41250212	KCNQ4	NM_004700	1	14	1	+	41249684	41250079
314254953	chr1	41282830	41283046	41282858	41283028	KCNQ4	NM_004700	1	14	2	+	41282937	41283027
315283080	chr1	41283683	41283874	41283702	41283852	KCNQ4	NM_004700	1	14	3	+	41283836	41283962
315287383	chr1	41283830	41284039	41283853	41284017	KCNQ4	NM_004700	1	14	3	+	41283836	41283962
313692561	chr1	41284138	41284354	41284158	41284334	KCNQ4	NM_004700	1	14	4	+	41284177	41284352
313696070	chr1	41284316	41284516	41284334	41284498	KCNQ4	NM_004700	1	14	4	+	41284177	41284352

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314024587	chr1	41284880	41285093	41284904	41285072	KCNQ4	NM_004700	1	14	5	+	41285019	41285144
314027322	chr1	41285022	41285241	41285043	41285220	KCNQ4	NM_004700	1	14	5	+	41285019	41285144
313687146	chr1	41285510	41285733	41285530	41285713	KCNQ4	NM_004700	1	14	6	+	41285547	41285657
312670060	chr1	41285767	41285966	41285787	41285946	KCNQ4	NM_004700	1	14	7	+	41285837	41285932
314477155	chr1	41287934	41288137	41287954	41288115	KCNQ4	NM_004700	1	14	8	+	41287986	41288074
312863425	chr1	41289614	41289824	41289634	41289807	KCNQ4	NM_004700	1	14	9	+	41289769	41289930
312865780	chr1	41289780	41290004	41289801	41289979	KCNQ4	NM_004700	1	14	9	+	41289769	41289930
314893401	chr1	41296712	41296925	41296733	41296901	KCNQ4	NM_004700	1	14	10	+	41296756	41296976
314895765	chr1	41296825	41297010	41296846	41296992	KCNQ4	NM_004700	1	14	10	+	41296756	41296976
314940124	chr1	41298587	41298808	41298612	41298791	KCNQ4	NM_004700	1	14	11	+	41298686	41298785
313554698	chr1	41300573	41300722	41300595	41300699	KCNQ4	NM_004700	1	14	12	+	41300639	41300770
313560070	chr1	41300683	41300906	41300700	41300883	KCNQ4	NM_004700	1	14	12	+	41300639	41300770
315303966	chr1	41303309	41303509	41303330	41303488	KCNQ4	NM_004700	1	14	13	+	41303337	41303466
315494339	chr1	41303827	41304010	41303849	41303991	KCNQ4	NM_004700	1	14	14	+	41303983	41306124
315495662	chr1	41303975	41304168	41303992	41304149	KCNQ4	NM_004700	1	14	14	+	41303983	41306124
315503533	chr1	41304120	41304342	41304140	41304322	KCNQ4	NM_004700	1	14	14	+	41303983	41306124
314511384	chr1	41249679	41249866	41249696	41249849	KCNQ4	NM_172163	2	13	1	+	41249684	41250079
314511449	chr1	41249828	41250044	41249845	41250027	KCNQ4	NM_172163	2	13	1	+	41249684	41250079
314511463	chr1	41250010	41250232	41250028	41250212	KCNQ4	NM_172163	2	13	1	+	41249684	41250079
314254953	chr1	41282830	41283046	41282858	41283028	KCNQ4	NM_172163	2	13	2	+	41282937	41283027
315283080	chr1	41283683	41283874	41283702	41283852	KCNQ4	NM_172163	2	13	3	+	41283836	41283962
315287383	chr1	41283830	41284039	41283853	41284017	KCNQ4	NM_172163	2	13	3	+	41283836	41283962
313692561	chr1	41284138	41284354	41284158	41284334	KCNQ4	NM_172163	2	13	4	+	41284177	41284352
313696070	chr1	41284316	41284516	41284334	41284498	KCNQ4	NM_172163	2	13	4	+	41284177	41284352
314024587	chr1	41284880	41285093	41284904	41285072	KCNQ4	NM_172163	2	13	5	+	41285019	41285144
314027322	chr1	41285022	41285241	41285043	41285220	KCNQ4	NM_172163	2	13	5	+	41285019	41285144
313687146	chr1	41285510	41285733	41285530	41285713	KCNQ4	NM_172163	2	13	6	+	41285547	41285657
312670060	chr1	41285767	41285966	41285787	41285946	KCNQ4	NM_172163	2	13	7	+	41285837	41285932
314477155	chr1	41287934	41288137	41287954	41288115	KCNQ4	NM_172163	2	13	8	+	41287986	41288074
314893401	chr1	41296712	41296925	41296733	41296901	KCNQ4	NM_172163	2	13	9	+	41296756	41296976
314895765	chr1	41296825	41297010	41296846	41296992	KCNQ4	NM_172163	2	13	9	+	41296756	41296976
314940124	chr1	41298587	41298808	41298612	41298791	KCNQ4	NM_172163	2	13	10	+	41298686	41298785
313554698	chr1	41300573	41300722	41300595	41300699	KCNQ4	NM_172163	2	13	11	+	41300639	41300770
313560070	chr1	41300683	41300906	41300700	41300883	KCNQ4	NM_172163	2	13	11	+	41300639	41300770
315303966	chr1	41303309	41303509	41303330	41303488	KCNQ4	NM_172163	2	13	12	+	41303337	41303466
315494339	chr1	41303827	41304010	41303849	41303991	KCNQ4	NM_172163	2	13	13	+	41303983	41306124
315495662	chr1	41303975	41304168	41303992	41304149	KCNQ4	NM_172163	2	13	13	+	41303983	41306124
315503533	chr1	41304120	41304342	41304140	41304322	KCNQ4	NM_172163	2	13	13	+	41303983	41306124
315129537	chr8	126095879	126096039	126095902	126096011	KIAA0196	NM_014846	1	29	2	-	126095955	126096264
315134295	chr8	126095985	126096175	126096012	126096154	KIAA0196	NM_014846	1	29	2	-	126095955	126096264
313335752	chr8	126095293	126095496	126095316	126095469	KIAA0196	NM_014846	1	29	3	-	126095355	126095500

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313337527	chr8	126095443	126095620	126095470	126095596	KIAA0196	NM_014846	1	29	3	-	126095355	126095500
313464851	chr8	126094468	126094676	126094492	126094651	KIAA0196	NM_014846	1	29	4	-	126094625	126094709
313466372	chr8	126094636	126094806	126094661	126094778	KIAA0196	NM_014846	1	29	4	-	126094625	126094709
313026994	chr8	126093815	126094037	126093842	126094011	KIAA0196	NM_014846	1	29	5	-	126093903	126094003
312854046	chr8	126090919	126091131	126090947	126091108	KIAA0196	NM_014846	1	29	6	-	126090980	126091172
312869843	chr8	126091088	126091298	126091109	126091271	KIAA0196	NM_014846	1	29	6	-	126090980	126091172
312663961	chr8	126088508	126088663	126088529	126088641	KIAA0196	NM_014846	1	29	7	-	126088590	126088742
312680125	chr8	126088614	126088802	126088642	126088779	KIAA0196	NM_014846	1	29	7	-	126088590	126088742
313884449	chr8	126087184	126087404	126087209	126087376	KIAA0196	NM_014846	1	29	8	-	126087240	126087353
313607301	chr8	126085360	126085566	126085385	126085541	KIAA0196	NM_014846	1	29	9	-	126085395	126085566
313620616	chr8	126085521	126085708	126085542	126085679	KIAA0196	NM_014846	1	29	9	-	126085395	126085566
313253246	chr8	126079706	126079902	126079733	126079881	KIAA0196	NM_014846	1	29	10	-	126079834	126079961
313260309	chr8	126079859	126079984	126079882	126079958	KIAA0196	NM_014846	1	29	10	-	126079834	126079961
313920221	chr8	126075727	126075949	126075754	126075921	KIAA0196	NM_014846	1	29	11	-	126075764	126075893
312889381	chr8	126073261	126073485	126073281	126073460	KIAA0196	NM_014846	1	29	12	-	126073324	126073436
313200445	chr8	126071560	126071764	126071584	126071737	KIAA0196	NM_014846	1	29	13	-	126071618	126071784
313214911	chr8	126071713	126071837	126071738	126071809	KIAA0196	NM_014846	1	29	13	-	126071618	126071784
314081726	chr8	126071382	126071578	126071407	126071550	KIAA0196	NM_014846	1	29	14	-	126071464	126071539
312855912	chr8	126069625	126069849	126069651	126069825	KIAA0196	NM_014846	1	29	15	-	126069798	126069908
312859465	chr8	126069799	126070022	126069826	126070001	KIAA0196	NM_014846	1	29	15	-	126069798	126069908
314507664	chr8	126068776	126068965	126068798	126068941	KIAA0196	NM_014846	1	29	16	-	126068919	126069059
314517880	chr8	126068922	126069090	126068942	126069067	KIAA0196	NM_014846	1	29	16	-	126068919	126069059
312873674	chr8	126067746	126067970	126067773	126067941	KIAA0196	NM_014846	1	29	17	-	126067833	126067913
313998829	chr8	126062698	126062898	126062723	126062876	KIAA0196	NM_014846	1	29	18	-	126062806	126062907
314015921	chr8	126062854	126062981	126062877	126062957	KIAA0196	NM_014846	1	29	18	-	126062806	126062907
313753412	chr8	126061115	126061318	126061138	126061289	KIAA0196	NM_014846	1	29	19	-	126061248	126061427
313761707	chr8	126061263	126061466	126061290	126061439	KIAA0196	NM_014846	1	29	19	-	126061248	126061427
314387682	chr8	126059396	126059582	126059417	126059554	KIAA0196	NM_014846	1	29	20	-	126059449	126059573
314394886	chr8	126059539	126059690	126059562	126059658	KIAA0196	NM_014846	1	29	20	-	126059449	126059573
314035362	chr8	126056624	126056841	126056646	126056817	KIAA0196	NM_014846	1	29	21	-	126056778	126056940
314049893	chr8	126056793	126057014	126056818	126056986	KIAA0196	NM_014846	1	29	21	-	126056778	126056940
312896956	chr8	126056177	126056363	126056203	126056341	KIAA0196	NM_014846	1	29	22	-	126056234	126056336
313104849	chr8	126056027	126056201	126056055	126056173	KIAA0196	NM_014846	1	29	23	-	126056067	126056146
314439946	chr8	126051976	126052173	126052001	126052148	KIAA0196	NM_014846	1	29	24	-	126052037	126052140
312835344	chr8	126050971	126051194	126050992	126051170	KIAA0196	NM_014846	1	29	25	-	126051072	126051201
312846449	chr8	126051149	126051356	126051171	126051330	KIAA0196	NM_014846	1	29	25	-	126051072	126051201
313881258	chr8	126049373	126049559	126049400	126049532	KIAA0196	NM_014846	1	29	26	-	126049479	126049575
313884025	chr8	126049506	126049631	126049533	126049604	KIAA0196	NM_014846	1	29	26	-	126049479	126049575
313926761	chr8	126044442	126044662	126044464	126044641	KIAA0196	NM_014846	1	29	27	-	126044483	126044636
314205966	chr8	126040777	126041000	126040799	126040975	KIAA0196	NM_014846	1	29	28	-	126040862	126040949
313897591	chr8	126036798	126037009	126036825	126036982	KIAA0196	NM_014846	1	29	29	-	126036503	126036915

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313387801	chr7	23145551	23145757	23145571	23145735	KLHL7	NM_001031710	1	11	1	+	23145353	23145765
313392967	chr7	23145713	23145929	23145736	23145909	KLHL7	NM_001031710	1	11	1	+	23145353	23145765
312668319	chr7	23163253	23163441	23163278	23163415	KLHL7	NM_001031710	1	11	2	+	23163396	23163498
312684963	chr7	23163390	23163612	23163416	23163584	KLHL7	NM_001031710	1	11	2	+	23163396	23163498
314245585	chr7	23164237	23164454	23164257	23164426	KLHL7	NM_001031710	1	11	3	+	23164307	23164400
313040147	chr7	23164585	23164751	23164610	23164723	KLHL7	NM_001031710	1	11	4	+	23164667	23164791
313041454	chr7	23164701	23164905	23164724	23164877	KLHL7	NM_001031710	1	11	4	+	23164667	23164791
313043904	chr7	23180305	23180529	23180331	23180504	KLHL7	NM_001031710	1	11	5	+	23180388	23180563
313058432	chr7	23180431	23180654	23180458	23180630	KLHL7	NM_001031710	1	11	5	+	23180388	23180563
313422189	chr7	23183297	23183516	23183325	23183489	KLHL7	NM_001031710	1	11	6	+	23183470	23183644
313439476	chr7	23183464	23183688	23183490	23183660	KLHL7	NM_001031710	1	11	6	+	23183470	23183644
314859671	chr7	23191659	23191880	23191686	23191852	KLHL7	NM_001031710	1	11	7	+	23191686	23191828
314063781	chr7	23205241	23205415	23205269	23205388	KLHL7	NM_001031710	1	11	8	+	23205317	23205557
314070505	chr7	23205368	23205589	23205389	23205562	KLHL7	NM_001031710	1	11	8	+	23205317	23205557
313913509	chr7	23207406	23207600	23207427	23207572	KLHL7	NM_001031710	1	11	9	+	23207455	23207656
313921568	chr7	23207552	23207727	23207573	23207700	KLHL7	NM_001031710	1	11	9	+	23207455	23207656
314275595	chr7	23212526	23212697	23212554	23212669	KLHL7	NM_001031710	1	11	10	+	23212567	23212664
314451874	chr7	23213616	23213784	23213644	23213762	KLHL7	NM_001031710	1	11	11	+	23213634	23215038
314473435	chr7	23213736	23213947	23213763	23213922	KLHL7	NM_001031710	1	11	11	+	23213634	23215038
313387801	chr7	23145551	23145757	23145571	23145735	KLHL7	NM_001172428	2	5	1	+	23145353	23145765
313392967	chr7	23145713	23145929	23145736	23145909	KLHL7	NM_001172428	2	5	1	+	23145353	23145765
312668319	chr7	23163253	23163441	23163278	23163415	KLHL7	NM_001172428	2	5	2	+	23163396	23163498
312684963	chr7	23163390	23163612	23163416	23163584	KLHL7	NM_001172428	2	5	2	+	23163396	23163498
314245585	chr7	23164237	23164454	23164257	23164426	KLHL7	NM_001172428	2	5	3	+	23164307	23164400
313040147	chr7	23164585	23164751	23164610	23164723	KLHL7	NM_001172428	2	5	4	+	23164667	23164791
313041454	chr7	23164701	23164905	23164724	23164877	KLHL7	NM_001172428	2	5	4	+	23164667	23164791
313177797	chr7	23165251	23165468	23165273	23165444	KLHL7	NM_001172428	2	5	5	+	23165380	23165669
312668319	chr7	23163253	23163441	23163278	23163415	KLHL7	NM_018846	3	11	2	+	23163396	23163498
312684963	chr7	23163390	23163612	23163416	23163584	KLHL7	NM_018846	3	11	2	+	23163396	23163498
314245585	chr7	23164237	23164454	23164257	23164426	KLHL7	NM_018846	3	11	3	+	23164307	23164400
313040147	chr7	23164585	23164751	23164610	23164723	KLHL7	NM_018846	3	11	4	+	23164667	23164791
313041454	chr7	23164701	23164905	23164724	23164877	KLHL7	NM_018846	3	11	4	+	23164667	23164791
313043904	chr7	23180305	23180529	23180331	23180504	KLHL7	NM_018846	3	11	5	+	23180388	23180563
313058432	chr7	23180431	23180654	23180458	23180630	KLHL7	NM_018846	3	11	5	+	23180388	23180563
313422189	chr7	23183297	23183516	23183325	23183489	KLHL7	NM_018846	3	11	6	+	23183470	23183644
313439476	chr7	23183464	23183688	23183490	23183660	KLHL7	NM_018846	3	11	6	+	23183470	23183644
314859671	chr7	23191659	23191880	23191686	23191852	KLHL7	NM_018846	3	11	7	+	23191686	23191828
314063781	chr7	23205241	23205415	23205269	23205388	KLHL7	NM_018846	3	11	8	+	23205317	23205557
314070505	chr7	23205368	23205589	23205389	23205562	KLHL7	NM_018846	3	11	8	+	23205317	23205557
313913509	chr7	23207406	23207600	23207427	23207572	KLHL7	NM_018846	3	11	9	+	23207455	23207656
313921568	chr7	23207552	23207727	23207573	23207700	KLHL7	NM_018846	3	11	9	+	23207455	23207656

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314275595	chr7	23212526	23212697	23212554	23212669	KLHL7	NM_018846	3	11	10	+	23212567	23212664
314451874	chr7	23213616	23213784	23213644	23213762	KLHL7	NM_018846	3	11	11	+	23213634	23215038
314473435	chr7	23213736	23213947	23213763	23213922	KLHL7	NM_018846	3	11	11	+	23213634	23215038
313387801	chr7	23145551	23145757	23145571	23145735	KLHL7	NR_033328	4	12	1	+	23145353	23145765
313392967	chr7	23145713	23145929	23145736	23145909	KLHL7	NR_033328	4	12	1	+	23145353	23145765
312668319	chr7	23163253	23163441	23163278	23163415	KLHL7	NR_033328	4	12	3	+	23163396	23163498
312684963	chr7	23163390	23163612	23163416	23163584	KLHL7	NR_033328	4	12	3	+	23163396	23163498
314245585	chr7	23164237	23164454	23164257	23164426	KLHL7	NR_033328	4	12	4	+	23164307	23164400
313040147	chr7	23164585	23164751	23164610	23164723	KLHL7	NR_033328	4	12	5	+	23164667	23164791
313041454	chr7	23164701	23164905	23164724	23164877	KLHL7	NR_033328	4	12	5	+	23164667	23164791
313043904	chr7	23180305	23180529	23180331	23180504	KLHL7	NR_033328	4	12	6	+	23180388	23180563
313058432	chr7	23180431	23180654	23180458	23180630	KLHL7	NR_033328	4	12	6	+	23180388	23180563
313422189	chr7	23183297	23183516	23183325	23183489	KLHL7	NR_033328	4	12	7	+	23183470	23183644
313439476	chr7	23183464	23183688	23183490	23183660	KLHL7	NR_033328	4	12	7	+	23183470	23183644
314859671	chr7	23191659	23191880	23191686	23191852	KLHL7	NR_033328	4	12	8	+	23191686	23191828
314063781	chr7	23205241	23205415	23205269	23205388	KLHL7	NR_033328	4	12	9	+	23205317	23205557
314070505	chr7	23205368	23205589	23205389	23205562	KLHL7	NR_033328	4	12	9	+	23205317	23205557
313913509	chr7	23207406	23207600	23207427	23207572	KLHL7	NR_033328	4	12	10	+	23207455	23207656
313921568	chr7	23207552	23207727	23207573	23207700	KLHL7	NR_033328	4	12	10	+	23207455	23207656
314275595	chr7	23212526	23212697	23212554	23212669	KLHL7	NR_033328	4	12	11	+	23212567	23212664
314451874	chr7	23213616	23213784	23213644	23213762	KLHL7	NR_033328	4	12	12	+	23213634	23215038
314473435	chr7	23213736	23213947	23213763	23213922	KLHL7	NR_033328	4	12	12	+	23213634	23215038
313387801	chr7	23145551	23145757	23145571	23145735	KLHL7	NR_033329	5	6	1	+	23145353	23145765
313392967	chr7	23145713	23145929	23145736	23145909	KLHL7	NR_033329	5	6	1	+	23145353	23145765
312668319	chr7	23163253	23163441	23163278	23163415	KLHL7	NR_033329	5	6	3	+	23163396	23163498
312684963	chr7	23163390	23163612	23163416	23163584	KLHL7	NR_033329	5	6	3	+	23163396	23163498
314245585	chr7	23164237	23164454	23164257	23164426	KLHL7	NR_033329	5	6	4	+	23164307	23164400
313040147	chr7	23164585	23164751	23164610	23164723	KLHL7	NR_033329	5	6	5	+	23164667	23164791
313041454	chr7	23164701	23164905	23164724	23164877	KLHL7	NR_033329	5	6	5	+	23164667	23164791
313177797	chr7	23165251	23165468	23165273	23165444	KLHL7	NR_033329	5	6	6	+	23165380	23165669
231133876	chr12	25398214	25398415	25398242	25398388	KRAS	NM_004985	1	5	2	-	25398208	25398329
326888191	chr12	25398123	25398267	25398149	25398241	KRAS	NM_004985	1	5	2	-	25398208	25398329
234355242	chr12	25380223	25380385	25380241	25380358	KRAS	NM_004985	1	5	3	-	25380168	25380346
326772204	chr12	25380138	25380262	25380169	25380240	KRAS	NM_004985	1	5	3	-	25380168	25380346
233467333	chr12	25378548	25378679	25378576	25378651	KRAS	NM_004985	1	5	4	-	25378548	25378707
329963600	chr12	25378390	25378605	25378414	25378577	KRAS	NM_004985	1	5	4	-	25378548	25378707
329967168	chr12	25378620	25378842	25378648	25378814	KRAS	NM_004985	1	5	4	-	25378548	25378707
234764769	chr12	25362590	25362768	25362619	25362738	KRAS	NM_004985	1	5	5	-	25358180	25362845
234764991	chr12	25362740	25362903	25362770	25362877	KRAS	NM_004985	1	5	5	-	25358180	25362845
231133876	chr12	25398214	25398415	25398242	25398388	KRAS	NM_033360	2	6	2	-	25398208	25398329
326888191	chr12	25398123	25398267	25398149	25398241	KRAS	NM_033360	2	6	2	-	25398208	25398329

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234355242	chr12	25380223	25380385	25380241	25380358	KRAS	NM_033360	2	6	3	-	25380168	25380346
326772204	chr12	25380138	25380262	25380169	25380240	KRAS	NM_033360	2	6	3	-	25380168	25380346
233467333	chr12	25378548	25378679	25378576	25378651	KRAS	NM_033360	2	6	4	-	25378548	25378707
329963600	chr12	25378390	25378605	25378414	25378577	KRAS	NM_033360	2	6	4	-	25378548	25378707
329967168	chr12	25378620	25378842	25378648	25378814	KRAS	NM_033360	2	6	4	-	25378548	25378707
233359144	chr12	25368325	25368536	25368353	25368508	KRAS	NM_033360	2	6	5	-	25368371	25368494
234764769	chr12	25362590	25362768	25362619	25362738	KRAS	NM_033360	2	6	6	-	25358180	25362845
234764991	chr12	25362740	25362903	25362770	25362877	KRAS	NM_033360	2	6	6	-	25358180	25362845
313183271	chr17	39742409	39742605	39742431	39742580	KRT14	NM_000526	1	8	1	-	39742562	39743147
313201279	chr17	39742560	39742750	39742581	39742730	KRT14	NM_000526	1	8	1	-	39742562	39743147
313212016	chr17	39742709	39742933	39742729	39742913	KRT14	NM_000526	1	8	1	-	39742562	39743147
313213468	chr17	39742739	39742944	39742759	39742927	KRT14	NM_000526	1	8	1	-	39742562	39743147
315027573	chr17	39741197	39741348	39741218	39741323	KRT14	NM_000526	1	8	2	-	39741227	39741309
315334412	chr17	39740464	39740634	39740489	39740614	KRT14	NM_000526	1	8	3	-	39740509	39740665
315353271	chr17	39740561	39740712	39740581	39740688	KRT14	NM_000526	1	8	3	-	39740509	39740665
313916389	chr17	39739941	39740100	39739963	39740081	KRT14	NM_000526	1	8	4	-	39740012	39740173
313938660	chr17	39740058	39740250	39740082	39740226	KRT14	NM_000526	1	8	4	-	39740012	39740173
314485131	chr17	39739777	39739958	39739796	39739933	KRT14	NM_000526	1	8	5	-	39739803	39739928
313092870	chr17	39739327	39739534	39739349	39739515	KRT14	NM_000526	1	8	6	-	39739487	39739707
314246050	chr17	39739471	39739677	39739490	39739657	KRT14	NM_000526	1	8	6	-	39739487	39739707
314255787	chr17	39739625	39739806	39739648	39739783	KRT14	NM_000526	1	8	6	-	39739487	39739707
313089502	chr17	39739222	39739439	39739243	39739417	KRT14	NM_000526	1	8	7	-	39739346	39739392
313092870	chr17	39739327	39739534	39739349	39739515	KRT14	NM_000526	1	8	7	-	39739346	39739392
314714909	chr17	39738621	39738819	39738643	39738798	KRT14	NM_000526	1	8	8	-	39738531	39738784
314805685	chr12	52913455	52913676	52913482	52913655	KRT5	NM_000424	1	9	1	-	52913526	52914243
314822582	chr12	52913632	52913856	52913654	52913836	KRT5	NM_000424	1	9	1	-	52913526	52914243
314826900	chr12	52913815	52913992	52913835	52913973	KRT5	NM_000424	1	9	1	-	52913526	52914243
314830220	chr12	52913900	52914107	52913921	52914086	KRT5	NM_000424	1	9	1	-	52913526	52914243
314815588	chr12	52912635	52912854	52912658	52912834	KRT5	NM_000424	1	9	2	-	52912730	52912944
314830474	chr12	52912813	52913019	52912834	52912998	KRT5	NM_000424	1	9	2	-	52912730	52912944
313259503	chr12	52911780	52911990	52911801	52911966	KRT5	NM_000424	1	9	3	-	52911887	52911947
315080186	chr12	52911589	52911803	52911617	52911781	KRT5	NM_000424	1	9	4	-	52911681	52911776
313832034	chr12	52911244	52911461	52911269	52911439	KRT5	NM_000424	1	9	5	-	52911374	52911538
313847203	chr12	52911418	52911568	52911440	52911546	KRT5	NM_000424	1	9	5	-	52911374	52911538
314232256	chr12	52910859	52911047	52910881	52911023	KRT5	NM_000424	1	9	6	-	52910891	52911016
312901721	chr12	52910274	52910497	52910298	52910476	KRT5	NM_000424	1	9	7	-	52910421	52910641
312912605	chr12	52910452	52910670	52910471	52910648	KRT5	NM_000424	1	9	7	-	52910421	52910641
313130827	chr12	52909433	52909657	52909457	52909630	KRT5	NM_000424	1	9	8	-	52909582	52909616
313360462	chr12	52908658	52908876	52908681	52908857	KRT5	NM_000424	1	9	9	-	52908359	52909024
314905239	chr12	52908830	52909054	52908849	52909033	KRT5	NM_000424	1	9	9	-	52908359	52909024
314295419	chrX	153141131	153141303	153141152	153141285	L1CAM	NM_000425	1	28	1	-	153141216	153141399

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314118657	chrX	153138541	153138744	153138562	153138719	L1CAM	NM_000425	1	28	2	-	153138683	153138697
312915925	chrX	153137954	153138166	153137975	153138145	L1CAM	NM_000425	1	28	3	-	153138047	153138152
312927049	chrX	153138122	153138328	153138143	153138304	L1CAM	NM_000425	1	28	3	-	153138047	153138152
313182255	chrX	153137548	153137691	153137569	153137670	L1CAM	NM_000425	1	28	4	-	153137607	153137809
313186748	chrX	153137647	153137787	153137668	153137764	L1CAM	NM_000425	1	28	4	-	153137607	153137809
313197004	chrX	153137741	153137961	153137761	153137939	L1CAM	NM_000425	1	28	4	-	153137607	153137809
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_000425	1	28	5	-	153136512	153136634
314497788	chrX	153136440	153136659	153136459	153136641	L1CAM	NM_000425	1	28	5	-	153136512	153136634
313640662	chrX	153136142	153136364	153136164	153136341	L1CAM	NM_000425	1	28	6	-	153136245	153136415
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_000425	1	28	6	-	153136245	153136415
314944170	chrX	153135773	153135978	153135792	153135959	L1CAM	NM_000425	1	28	7	-	153135843	153135954
314513877	chrX	153135466	153135593	153135487	153135572	L1CAM	NM_000425	1	28	8	-	153135511	153135695
314517429	chrX	153135517	153135737	153135538	153135714	L1CAM	NM_000425	1	28	8	-	153135511	153135695
314511840	chrX	153135344	153135528	153135365	153135506	L1CAM	NM_000425	1	28	9	-	153135258	153135389
314921322	chrX	153135176	153135385	153135197	153135367	L1CAM	NM_000425	1	28	9	-	153135258	153135389
315343504	chrX	153134933	153135076	153134957	153135056	L1CAM	NM_000425	1	28	10	-	153134975	153135118
315349364	chrX	153135026	153135174	153135048	153135155	L1CAM	NM_000425	1	28	10	-	153134975	153135118
312722746	chrX	153134258	153134436	153134278	153134416	L1CAM	NM_000425	1	28	11	-	153134296	153134407
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_000425	1	28	12	-	153134016	153134182
313525557	chrX	153133936	153134145	153133958	153134124	L1CAM	NM_000425	1	28	12	-	153134016	153134182
313533937	chrX	153134074	153134294	153134095	153134273	L1CAM	NM_000425	1	28	12	-	153134016	153134182
312755216	chrX	153133699	153133915	153133720	153133892	L1CAM	NM_000425	1	28	13	-	153133757	153133913
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_000425	1	28	13	-	153133757	153133913
313245100	chrX	153133376	153133582	153133396	153133559	L1CAM	NM_000425	1	28	14	-	153133453	153133577
313251633	chrX	153133532	153133731	153133553	153133710	L1CAM	NM_000425	1	28	14	-	153133453	153133577
314387885	chrX	153133093	153133288	153133114	153133266	L1CAM	NM_000425	1	28	15	-	153133255	153133365
314394185	chrX	153133240	153133464	153133264	153133442	L1CAM	NM_000425	1	28	15	-	153133255	153133365
313745458	chrX	153132701	153132918	153132725	153132898	L1CAM	NM_000425	1	28	16	-	153132811	153133008
313760969	chrX	153132875	153133038	153132899	153133013	L1CAM	NM_000425	1	28	16	-	153132811	153133008
313958463	chrX	153132412	153132617	153132433	153132592	L1CAM	NM_000425	1	28	17	-	153132509	153132579
315094959	chrX	153132023	153132208	153132045	153132189	L1CAM	NM_000425	1	28	18	-	153132104	153132326
315101848	chrX	153132166	153132364	153132189	153132343	L1CAM	NM_000425	1	28	18	-	153132104	153132326
313622191	chrX	153131094	153131302	153131115	153131279	L1CAM	NM_000425	1	28	19	-	153131159	153131274
313122836	chrX	153130676	153130868	153130695	153130847	L1CAM	NM_000425	1	28	20	-	153130754	153130955
313126759	chrX	153130821	153130980	153130844	153130960	L1CAM	NM_000425	1	28	20	-	153130754	153130955
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_000425	1	28	21	-	153130543	153130665
312983916	chrX	153130504	153130709	153130522	153130692	L1CAM	NM_000425	1	28	21	-	153130543	153130665
312909638	chrX	153130247	153130429	153130267	153130408	L1CAM	NM_000425	1	28	22	-	153130276	153130449
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_000425	1	28	22	-	153130276	153130449
314333197	chrX	153130034	153130219	153130055	153130199	L1CAM	NM_000425	1	28	23	-	153130040	153130159
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_000425	1	28	23	-	153130040	153130159

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315351902	chrX	153129705	153129912	153129728	153129889	L1CAM	NM_000425	1	28	24	-	153129777	153129932
315367362	chrX	153129870	153130059	153129890	153130036	L1CAM	NM_000425	1	28	24	-	153129777	153129932
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_000425	1	28	24	-	153129777	153129932
313965371	chrX	153129215	153129385	153129235	153129362	L1CAM	NM_000425	1	28	25	-	153129338	153129472
313967663	chrX	153129337	153129559	153129357	153129537	L1CAM	NM_000425	1	28	25	-	153129338	153129472
315068283	chrX	153128818	153129034	153128840	153129012	L1CAM	NM_000425	1	28	26	-	153128932	153129004
313294264	chrX	153128759	153128951	153128779	153128931	L1CAM	NM_000425	1	28	27	-	153128823	153128834
312956891	chrX	153128002	153128226	153128022	153128206	L1CAM	NM_000425	1	28	28	-	153126971	153128349
312965181	chrX	153128186	153128383	153128207	153128365	L1CAM	NM_000425	1	28	28	-	153126971	153128349
314295419	chrX	153141131	153141303	153141152	153141285	L1CAM	NM_001143963	2	26	1	-	153141216	153141399
312915925	chrX	153137954	153138166	153137975	153138145	L1CAM	NM_001143963	2	26	2	-	153138047	153138152
312927049	chrX	153138122	153138328	153138143	153138304	L1CAM	NM_001143963	2	26	2	-	153138047	153138152
313182255	chrX	153137548	153137691	153137569	153137670	L1CAM	NM_001143963	2	26	3	-	153137607	153137809
313186748	chrX	153137647	153137787	153137668	153137764	L1CAM	NM_001143963	2	26	3	-	153137607	153137809
313197004	chrX	153137741	153137961	153137761	153137939	L1CAM	NM_001143963	2	26	3	-	153137607	153137809
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_001143963	2	26	4	-	153136512	153136634
314497788	chrX	153136440	153136659	153136459	153136641	L1CAM	NM_001143963	2	26	4	-	153136512	153136634
313640662	chrX	153136142	153136364	153136164	153136341	L1CAM	NM_001143963	2	26	5	-	153136245	153136415
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_001143963	2	26	5	-	153136245	153136415
314944170	chrX	153135773	153135978	153135792	153135959	L1CAM	NM_001143963	2	26	6	-	153135843	153135954
314513877	chrX	153135466	153135593	153135487	153135572	L1CAM	NM_001143963	2	26	7	-	153135511	153135695
314517429	chrX	153135517	153135737	153135538	153135714	L1CAM	NM_001143963	2	26	7	-	153135511	153135695
314511840	chrX	153135344	153135528	153135365	153135506	L1CAM	NM_001143963	2	26	8	-	153135258	153135389
314921322	chrX	153135176	153135385	153135197	153135367	L1CAM	NM_001143963	2	26	8	-	153135258	153135389
315343504	chrX	153134933	153135076	153134957	153135056	L1CAM	NM_001143963	2	26	9	-	153134975	153135118
315349364	chrX	153135026	153135174	153135048	153135155	L1CAM	NM_001143963	2	26	9	-	153134975	153135118
312722746	chrX	153134258	153134436	153134278	153134416	L1CAM	NM_001143963	2	26	10	-	153134296	153134407
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_001143963	2	26	11	-	153134016	153134182
313525557	chrX	153133936	153134145	153133958	153134124	L1CAM	NM_001143963	2	26	11	-	153134016	153134182
313533937	chrX	153134074	153134294	153134095	153134273	L1CAM	NM_001143963	2	26	11	-	153134016	153134182
312755216	chrX	153133699	153133915	153133720	153133892	L1CAM	NM_001143963	2	26	12	-	153133757	153133913
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_001143963	2	26	12	-	153133757	153133913
313245100	chrX	153133376	153133582	153133396	153133559	L1CAM	NM_001143963	2	26	13	-	153133453	153133577
313251633	chrX	153133532	153133731	153133553	153133710	L1CAM	NM_001143963	2	26	13	-	153133453	153133577
314387885	chrX	153133093	153133288	153133114	153133266	L1CAM	NM_001143963	2	26	14	-	153133255	153133365
314394185	chrX	153133240	153133464	153133264	153133442	L1CAM	NM_001143963	2	26	14	-	153133255	153133365
313745458	chrX	153132701	153132918	153132725	153132898	L1CAM	NM_001143963	2	26	15	-	153132811	153133008
313760969	chrX	153132875	153133038	153132899	153133013	L1CAM	NM_001143963	2	26	15	-	153132811	153133008
313958463	chrX	153132412	153132617	153132433	153132592	L1CAM	NM_001143963	2	26	16	-	153132509	153132579
315094959	chrX	153132023	153132208	153132045	153132189	L1CAM	NM_001143963	2	26	17	-	153132104	153132326
315101848	chrX	153132166	153132364	153132189	153132343	L1CAM	NM_001143963	2	26	17	-	153132104	153132326

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313622191	chrX	153131094	153131302	153131115	153131279	L1CAM	NM_001143963	2	26	18	-	153131159	153131274
313122836	chrX	153130676	153130868	153130695	153130847	L1CAM	NM_001143963	2	26	19	-	153130754	153130955
313126759	chrX	153130821	153130980	153130844	153130960	L1CAM	NM_001143963	2	26	19	-	153130754	153130955
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_001143963	2	26	20	-	153130543	153130665
312983916	chrX	153130504	153130709	153130522	153130692	L1CAM	NM_001143963	2	26	20	-	153130543	153130665
312909638	chrX	153130247	153130429	153130267	153130408	L1CAM	NM_001143963	2	26	21	-	153130276	153130449
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_001143963	2	26	21	-	153130276	153130449
314333197	chrX	153130034	153130219	153130055	153130199	L1CAM	NM_001143963	2	26	22	-	153130040	153130159
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_001143963	2	26	22	-	153130040	153130159
315351902	chrX	153129705	153129912	153129728	153129889	L1CAM	NM_001143963	2	26	23	-	153129777	153129932
315367362	chrX	153129870	153130059	153129890	153130036	L1CAM	NM_001143963	2	26	23	-	153129777	153129932
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_001143963	2	26	23	-	153129777	153129932
313965371	chrX	153129215	153129385	153129235	153129362	L1CAM	NM_001143963	2	26	24	-	153129338	153129472
313967663	chrX	153129337	153129559	153129357	153129537	L1CAM	NM_001143963	2	26	24	-	153129338	153129472
315068283	chrX	153128818	153129034	153128840	153129012	L1CAM	NM_001143963	2	26	25	-	153128932	153129004
312956891	chrX	153128002	153128226	153128022	153128206	L1CAM	NM_001143963	2	26	26	-	153126971	153128349
312965181	chrX	153128186	153128383	153128207	153128365	L1CAM	NM_001143963	2	26	26	-	153126971	153128349
314295419	chrX	153141131	153141303	153141152	153141285	L1CAM	NM_024003	3	27	1	-	153141216	153141399
314118657	chrX	153138541	153138744	153138562	153138719	L1CAM	NM_024003	3	27	2	-	153138683	153138697
312915925	chrX	153137954	153138166	153137975	153138145	L1CAM	NM_024003	3	27	3	-	153138047	153138152
312927049	chrX	153138122	153138328	153138143	153138304	L1CAM	NM_024003	3	27	3	-	153138047	153138152
313182255	chrX	153137548	153137691	153137569	153137670	L1CAM	NM_024003	3	27	4	-	153137607	153137809
313186748	chrX	153137647	153137787	153137668	153137764	L1CAM	NM_024003	3	27	4	-	153137607	153137809
313197004	chrX	153137741	153137961	153137761	153137939	L1CAM	NM_024003	3	27	4	-	153137607	153137809
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_024003	3	27	5	-	153136512	153136634
314497788	chrX	153136440	153136659	153136459	153136641	L1CAM	NM_024003	3	27	5	-	153136512	153136634
313640662	chrX	153136142	153136364	153136164	153136341	L1CAM	NM_024003	3	27	6	-	153136245	153136415
313658010	chrX	153136322	153136537	153136342	153136513	L1CAM	NM_024003	3	27	6	-	153136245	153136415
314944170	chrX	153135773	153135978	153135792	153135959	L1CAM	NM_024003	3	27	7	-	153135843	153135954
314513877	chrX	153135466	153135593	153135487	153135572	L1CAM	NM_024003	3	27	8	-	153135511	153135695
314517429	chrX	153135517	153135737	153135538	153135714	L1CAM	NM_024003	3	27	8	-	153135511	153135695
314511840	chrX	153135344	153135528	153135365	153135506	L1CAM	NM_024003	3	27	9	-	153135258	153135389
314921322	chrX	153135176	153135385	153135197	153135367	L1CAM	NM_024003	3	27	9	-	153135258	153135389
315343504	chrX	153134933	153135076	153134957	153135056	L1CAM	NM_024003	3	27	10	-	153134975	153135118
315349364	chrX	153135026	153135174	153135048	153135155	L1CAM	NM_024003	3	27	10	-	153134975	153135118
312722746	chrX	153134258	153134436	153134278	153134416	L1CAM	NM_024003	3	27	11	-	153134296	153134407
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_024003	3	27	12	-	153134016	153134182
313525557	chrX	153133936	153134145	153133958	153134124	L1CAM	NM_024003	3	27	12	-	153134016	153134182
313533937	chrX	153134074	153134294	153134095	153134273	L1CAM	NM_024003	3	27	12	-	153134016	153134182
312755216	chrX	153133699	153133915	153133720	153133892	L1CAM	NM_024003	3	27	13	-	153133757	153133913
312774806	chrX	153133862	153134056	153133886	153134029	L1CAM	NM_024003	3	27	13	-	153133757	153133913

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313245100	chrX	153133376	153133582	153133396	153133559	L1CAM	NM_024003	3	27	14	-	153133453	153133577
313251633	chrX	153133532	153133731	153133553	153133710	L1CAM	NM_024003	3	27	14	-	153133453	153133577
314387885	chrX	153133093	153133288	153133114	153133266	L1CAM	NM_024003	3	27	15	-	153133255	153133365
314394185	chrX	153133240	153133464	153133264	153133442	L1CAM	NM_024003	3	27	15	-	153133255	153133365
313745458	chrX	153132701	153132918	153132725	153132898	L1CAM	NM_024003	3	27	16	-	153132811	153133008
313760969	chrX	153132875	153133038	153132899	153133013	L1CAM	NM_024003	3	27	16	-	153132811	153133008
313958463	chrX	153132412	153132617	153132433	153132592	L1CAM	NM_024003	3	27	17	-	153132509	153132579
315094959	chrX	153132023	153132208	153132045	153132189	L1CAM	NM_024003	3	27	18	-	153132104	153132326
315101848	chrX	153132166	153132364	153132189	153132343	L1CAM	NM_024003	3	27	18	-	153132104	153132326
313622191	chrX	153131094	153131302	153131115	153131279	L1CAM	NM_024003	3	27	19	-	153131159	153131274
313122836	chrX	153130676	153130868	153130695	153130847	L1CAM	NM_024003	3	27	20	-	153130754	153130955
313126759	chrX	153130821	153130980	153130844	153130960	L1CAM	NM_024003	3	27	20	-	153130754	153130955
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_024003	3	27	21	-	153130543	153130665
312983916	chrX	153130504	153130709	153130522	153130692	L1CAM	NM_024003	3	27	21	-	153130543	153130665
312909638	chrX	153130247	153130429	153130267	153130408	L1CAM	NM_024003	3	27	22	-	153130276	153130449
312914119	chrX	153130381	153130567	153130402	153130547	L1CAM	NM_024003	3	27	22	-	153130276	153130449
314333197	chrX	153130034	153130219	153130055	153130199	L1CAM	NM_024003	3	27	23	-	153130040	153130159
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_024003	3	27	23	-	153130040	153130159
315351902	chrX	153129705	153129912	153129728	153129889	L1CAM	NM_024003	3	27	24	-	153129777	153129932
315367362	chrX	153129870	153130059	153129890	153130036	L1CAM	NM_024003	3	27	24	-	153129777	153129932
315367965	chrX	153129871	153130079	153129892	153130054	L1CAM	NM_024003	3	27	24	-	153129777	153129932
313965371	chrX	153129215	153129385	153129235	153129362	L1CAM	NM_024003	3	27	25	-	153129338	153129472
313967663	chrX	153129337	153129559	153129357	153129537	L1CAM	NM_024003	3	27	25	-	153129338	153129472
315068283	chrX	153128818	153129034	153128840	153129012	L1CAM	NM_024003	3	27	26	-	153128932	153129004
312956891	chrX	153128002	153128226	153128022	153128206	L1CAM	NM_024003	3	27	27	-	153126971	153128349
312965181	chrX	153128186	153128383	153128207	153128365	L1CAM	NM_024003	3	27	27	-	153126971	153128349
313256547	chr1	209824117	209824341	209824140	209824318	LAMB3	NM_000228	1	23	2	-	209824262	209824326
312994770	chr1	209823281	209823498	209823302	209823477	LAMB3	NM_000228	1	23	3	-	209823309	209823463
314683640	chr1	209811796	209812020	209811818	209811998	LAMB3	NM_000228	1	23	4	-	209811879	209811993
314057393	chr1	209811162	209811367	209811183	209811339	LAMB3	NM_000228	1	23	5	-	209811253	209811326
313318839	chr1	209807751	209807960	209807774	209807940	LAMB3	NM_000228	1	23	6	-	209807792	209807983
313326684	chr1	209807922	209808144	209807941	209808123	LAMB3	NM_000228	1	23	6	-	209807792	209807983
314596450	chr1	209806303	209806514	209806327	209806491	LAMB3	NM_000228	1	23	7	-	209806415	209806478
313092774	chr1	209805826	209806039	209805851	209806017	LAMB3	NM_000228	1	23	8	-	209805928	209806121
313098172	chr1	209805982	209806199	209806001	209806172	LAMB3	NM_000228	1	23	8	-	209805928	209806121
313414123	chr1	209803914	209804127	209803933	209804101	LAMB3	NM_000228	1	23	9	-	209803960	209804080
315298544	chr1	209802949	209803157	209802972	209803137	LAMB3	NM_000228	1	23	10	-	209803082	209803270
315315983	chr1	209803117	209803296	209803137	209803276	LAMB3	NM_000228	1	23	10	-	209803082	209803270
313315601	chr1	209801343	209801558	209801360	209801540	LAMB3	NM_000228	1	23	11	-	209801380	209801535
313427569	chr1	209800636	209800860	209800655	209800841	LAMB3	NM_000228	1	23	12	-	209800728	209800924
313436764	chr1	209800814	209800969	209800835	209800949	LAMB3	NM_000228	1	23	12	-	209800728	209800924

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313688429	chr1	209800187	209800403	209800205	209800380	LAMB3	NM_000228	1	23	13	-	209800212	209800323
313435719	chr1	209798938	209799103	209798958	209799078	LAMB3	NM_000228	1	23	14	-	209798993	209799371
313445591	chr1	209799057	209799263	209799079	209799241	LAMB3	NM_000228	1	23	14	-	209798993	209799371
313455109	chr1	209799203	209799407	209799225	209799386	LAMB3	NM_000228	1	23	14	-	209798993	209799371
314054805	chr1	209797077	209797259	209797100	209797230	LAMB3	NM_000228	1	23	15	-	209797185	209797345
314227812	chr1	209797207	209797393	209797231	209797365	LAMB3	NM_000228	1	23	15	-	209797185	209797345
314046978	chr1	209796818	209797018	209796838	209797000	LAMB3	NM_000228	1	23	16	-	209796850	209797070
314052871	chr1	209796978	209797198	209796998	209797177	LAMB3	NM_000228	1	23	16	-	209796850	209797070
314396542	chr1	209796270	209796483	209796292	209796463	LAMB3	NM_000228	1	23	17	-	209796327	209796524
314404310	chr1	209796442	209796651	209796462	209796629	LAMB3	NM_000228	1	23	17	-	209796327	209796524
314449350	chr1	209795740	209795950	209795761	209795929	LAMB3	NM_000228	1	23	18	-	209795881	209796025
314456893	chr1	209795906	209796130	209795925	209796106	LAMB3	NM_000228	1	23	18	-	209795881	209796025
312855913	chr1	209791754	209791941	209791776	209791918	LAMB3	NM_000228	1	23	19	-	209791797	209792004
312867261	chr1	209791895	209792033	209791919	209792009	LAMB3	NM_000228	1	23	19	-	209791797	209792004
313956077	chr1	209791091	209791282	209791114	209791261	LAMB3	NM_000228	1	23	20	-	209791252	209791393
313966381	chr1	209791239	209791459	209791261	209791434	LAMB3	NM_000228	1	23	20	-	209791252	209791393
312678683	chr1	209790710	209790901	209790731	209790880	LAMB3	NM_000228	1	23	21	-	209790755	209790931
312699224	chr1	209790854	209791064	209790875	209791042	LAMB3	NM_000228	1	23	21	-	209790755	209790931
313350389	chr1	209789782	209790004	209789802	209789976	LAMB3	NM_000228	1	23	22	-	209789816	209789969
313750751	chr1	209788489	209788699	209788511	209788678	LAMB3	NM_000228	1	23	23	-	209788218	209788752
315114129	chr1	209788652	209788858	209788672	209788834	LAMB3	NM_000228	1	23	23	-	209788218	209788752
313256547	chr1	209824117	209824341	209824140	209824318	LAMB3	NM_001017402	2	22	1	-	209824262	209824679
312994770	chr1	209823281	209823498	209823302	209823477	LAMB3	NM_001017402	2	22	2	-	209823309	209823463
314683640	chr1	209811796	209812020	209811818	209811998	LAMB3	NM_001017402	2	22	3	-	209811879	209811993
314057393	chr1	209811162	209811367	209811183	209811339	LAMB3	NM_001017402	2	22	4	-	209811253	209811326
313318839	chr1	209807751	209807960	209807774	209807940	LAMB3	NM_001017402	2	22	5	-	209807792	209807983
313326684	chr1	209807922	209808144	209807941	209808123	LAMB3	NM_001017402	2	22	5	-	209807792	209807983
314596450	chr1	209806303	209806514	209806327	209806491	LAMB3	NM_001017402	2	22	6	-	209806415	209806478
313092774	chr1	209805826	209806039	209805851	209806017	LAMB3	NM_001017402	2	22	7	-	209805928	209806121
313098172	chr1	209805982	209806199	209806001	209806172	LAMB3	NM_001017402	2	22	7	-	209805928	209806121
313414123	chr1	209803914	209804127	209803933	209804101	LAMB3	NM_001017402	2	22	8	-	209803960	209804080
315298544	chr1	209802949	209803157	209802972	209803137	LAMB3	NM_001017402	2	22	9	-	209803082	209803270
315315983	chr1	209803117	209803296	209803137	209803276	LAMB3	NM_001017402	2	22	9	-	209803082	209803270
313315601	chr1	209801343	209801558	209801360	209801540	LAMB3	NM_001017402	2	22	10	-	209801380	209801535
313427569	chr1	209800636	209800860	209800655	209800841	LAMB3	NM_001017402	2	22	11	-	209800728	209800924
313436764	chr1	209800814	209800969	209800835	209800949	LAMB3	NM_001017402	2	22	11	-	209800728	209800924
313688429	chr1	209800187	209800403	209800205	209800380	LAMB3	NM_001017402	2	22	12	-	209800212	209800323
313435719	chr1	209798938	209799103	209798958	209799078	LAMB3	NM_001017402	2	22	13	-	209798993	209799371
313445591	chr1	209799057	209799263	209799079	209799241	LAMB3	NM_001017402	2	22	13	-	209798993	209799371
313455109	chr1	209799203	209799407	209799225	209799386	LAMB3	NM_001017402	2	22	13	-	209798993	209799371
314054805	chr1	209797077	209797259	209797100	209797230	LAMB3	NM_001017402	2	22	14	-	209797185	209797345

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314227812	chr1	209797207	209797393	209797231	209797365	LAMB3	NM_001017402	2	22	14	-	209797185	209797345
314046978	chr1	209796818	209797018	209796838	209797000	LAMB3	NM_001017402	2	22	15	-	209796850	209797070
314052871	chr1	209796978	209797198	209796998	209797177	LAMB3	NM_001017402	2	22	15	-	209796850	209797070
314396542	chr1	209796270	209796483	209796292	209796463	LAMB3	NM_001017402	2	22	16	-	209796327	209796524
314404310	chr1	209796442	209796651	209796462	209796629	LAMB3	NM_001017402	2	22	16	-	209796327	209796524
314449350	chr1	209795740	209795950	209795761	209795929	LAMB3	NM_001017402	2	22	17	-	209795881	209796025
314456893	chr1	209795906	209796130	209795925	209796106	LAMB3	NM_001017402	2	22	17	-	209795881	209796025
312855913	chr1	209791754	209791941	209791776	209791918	LAMB3	NM_001017402	2	22	18	-	209791797	209792004
312867261	chr1	209791895	209792033	209791919	209792009	LAMB3	NM_001017402	2	22	18	-	209791797	209792004
313956077	chr1	209791091	209791282	209791114	209791261	LAMB3	NM_001017402	2	22	19	-	209791252	209791393
313966381	chr1	209791239	209791459	209791261	209791434	LAMB3	NM_001017402	2	22	19	-	209791252	209791393
312678683	chr1	209790710	209790901	209790731	209790880	LAMB3	NM_001017402	2	22	20	-	209790755	209790931
312699224	chr1	209790854	209791064	209790875	209791042	LAMB3	NM_001017402	2	22	20	-	209790755	209790931
313350389	chr1	209789782	209790004	209789802	209789976	LAMB3	NM_001017402	2	22	21	-	209789816	209789969
313750751	chr1	209788489	209788699	209788511	209788678	LAMB3	NM_001017402	2	22	22	-	209788218	209788752
315114129	chr1	209788652	209788858	209788672	209788834	LAMB3	NM_001017402	2	22	22	-	209788218	209788752
313256547	chr1	209824117	209824341	209824140	209824318	LAMB3	NM_001127641	3	23	2	-	209824262	209824326
312994770	chr1	209823281	209823498	209823302	209823477	LAMB3	NM_001127641	3	23	3	-	209823309	209823463
314683640	chr1	209811796	209812020	209811818	209811998	LAMB3	NM_001127641	3	23	4	-	209811879	209811993
314057393	chr1	209811162	209811367	209811183	209811339	LAMB3	NM_001127641	3	23	5	-	209811253	209811326
313318839	chr1	209807751	209807960	209807774	209807940	LAMB3	NM_001127641	3	23	6	-	209807792	209807983
313326684	chr1	209807922	209808144	209807941	209808123	LAMB3	NM_001127641	3	23	6	-	209807792	209807983
314596450	chr1	209806303	209806514	209806327	209806491	LAMB3	NM_001127641	3	23	7	-	209806415	209806478
313092774	chr1	209805826	209806039	209805851	209806017	LAMB3	NM_001127641	3	23	8	-	209805928	209806121
313098172	chr1	209805982	209806199	209806001	209806172	LAMB3	NM_001127641	3	23	8	-	209805928	209806121
313414123	chr1	209803914	209804127	209803933	209804101	LAMB3	NM_001127641	3	23	9	-	209803960	209804080
315298544	chr1	209802949	209803157	209802972	209803137	LAMB3	NM_001127641	3	23	10	-	209803082	209803270
315315983	chr1	209803117	209803296	209803137	209803276	LAMB3	NM_001127641	3	23	10	-	209803082	209803270
313315601	chr1	209801343	209801558	209801360	209801540	LAMB3	NM_001127641	3	23	11	-	209801380	209801535
313427569	chr1	209800636	209800860	209800655	209800841	LAMB3	NM_001127641	3	23	12	-	209800728	209800924
313436764	chr1	209800814	209800969	209800835	209800949	LAMB3	NM_001127641	3	23	12	-	209800728	209800924
313688429	chr1	209800187	209800403	209800205	209800380	LAMB3	NM_001127641	3	23	13	-	209800212	209800323
313435719	chr1	209798938	209799103	209798958	209799078	LAMB3	NM_001127641	3	23	14	-	209798993	209799371
313445591	chr1	209799057	209799263	209799079	209799241	LAMB3	NM_001127641	3	23	14	-	209798993	209799371
313455109	chr1	209799203	209799407	209799225	209799386	LAMB3	NM_001127641	3	23	14	-	209798993	209799371
314054805	chr1	209797077	209797259	209797100	209797230	LAMB3	NM_001127641	3	23	15	-	209797185	209797345
314227812	chr1	209797207	209797393	209797231	209797365	LAMB3	NM_001127641	3	23	15	-	209797185	209797345
314046978	chr1	209796818	209797018	209796838	209797000	LAMB3	NM_001127641	3	23	16	-	209796850	209797070
314052871	chr1	209796978	209797198	209796998	209797177	LAMB3	NM_001127641	3	23	16	-	209796850	209797070
314396542	chr1	209796270	209796483	209796292	209796463	LAMB3	NM_001127641	3	23	17	-	209796327	209796524
314404310	chr1	209796442	209796651	209796462	209796629	LAMB3	NM_001127641	3	23	17	-	209796327	209796524

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314449350	chr1	209795740	209795950	209795761	209795929	LAMB3	NM_001127641	3	23	18	-	209795881	209796025
314456893	chr1	209795906	209796130	209795925	209796106	LAMB3	NM_001127641	3	23	18	-	209795881	209796025
312855913	chr1	209791754	209791941	209791776	209791918	LAMB3	NM_001127641	3	23	19	-	209791797	209792004
312867261	chr1	209791895	209792033	209791919	209792009	LAMB3	NM_001127641	3	23	19	-	209791797	209792004
313956077	chr1	209791091	209791282	209791114	209791261	LAMB3	NM_001127641	3	23	20	-	209791252	209791393
313966381	chr1	209791239	209791459	209791261	209791434	LAMB3	NM_001127641	3	23	20	-	209791252	209791393
312678683	chr1	209790710	209790901	209790731	209790880	LAMB3	NM_001127641	3	23	21	-	209790755	209790931
312699224	chr1	209790854	209791064	209790875	209791042	LAMB3	NM_001127641	3	23	21	-	209790755	209790931
313350389	chr1	209789782	209790004	209789802	209789976	LAMB3	NM_001127641	3	23	22	-	209789816	209789969
313750751	chr1	209788489	209788699	209788511	209788678	LAMB3	NM_001127641	3	23	23	-	209788218	209788752
315114129	chr1	209788652	209788858	209788672	209788834	LAMB3	NM_001127641	3	23	23	-	209788218	209788752
313407811	chrX	119602878	119603084	119602900	119603062	LAMP2	NM_001122606	1	9	1	-	119602961	119603204
312677994	chrX	119590386	119590577	119590412	119590553	LAMP2	NM_001122606	1	9	2	-	119590506	119590624
312684956	chrX	119590530	119590704	119590554	119590679	LAMP2	NM_001122606	1	9	2	-	119590506	119590624
313984161	chrX	119589092	119589305	119589119	119589277	LAMP2	NM_001122606	1	9	3	-	119589212	119589425
313997788	chrX	119589253	119589464	119589278	119589442	LAMP2	NM_001122606	1	9	3	-	119589212	119589425
313077562	chrX	119582750	119582887	119582778	119582863	LAMP2	NM_001122606	1	9	4	-	119582825	119582983
313079850	chrX	119582839	119583025	119582864	119582998	LAMP2	NM_001122606	1	9	4	-	119582825	119582983
314353537	chrX	119581623	119581779	119581645	119581751	LAMP2	NM_001122606	1	9	5	-	119581696	119581880
314363586	chrX	119581729	119581920	119581752	119581897	LAMP2	NM_001122606	1	9	5	-	119581696	119581880
315040647	chrX	119579990	119580198	119580011	119580170	LAMP2	NM_001122606	1	9	6	-	119580160	119580282
315056519	chrX	119580145	119580314	119580171	119580287	LAMP2	NM_001122606	1	9	6	-	119580160	119580282
313738912	chrX	119576399	119576579	119576425	119576551	LAMP2	NM_001122606	1	9	7	-	119576454	119576517
315275113	chrX	119575455	119575668	119575479	119575640	LAMP2	NM_001122606	1	9	8	-	119575585	119575749
315279194	chrX	119575616	119575814	119575641	119575788	LAMP2	NM_001122606	1	9	8	-	119575585	119575749
314103744	chrX	119562196	119562420	119562220	119562392	LAMP2	NM_001122606	1	9	9	-	119560003	119562481
314129299	chrX	119562356	119562528	119562385	119562500	LAMP2	NM_001122606	1	9	9	-	119560003	119562481
313407811	chrX	119602878	119603084	119602900	119603062	LAMP2	NM_002294	2	9	1	-	119602961	119603204
312677994	chrX	119590386	119590577	119590412	119590553	LAMP2	NM_002294	2	9	2	-	119590506	119590624
312684956	chrX	119590530	119590704	119590554	119590679	LAMP2	NM_002294	2	9	2	-	119590506	119590624
313984161	chrX	119589092	119589305	119589119	119589277	LAMP2	NM_002294	2	9	3	-	119589212	119589425
313997788	chrX	119589253	119589464	119589278	119589442	LAMP2	NM_002294	2	9	3	-	119589212	119589425
313077562	chrX	119582750	119582887	119582778	119582863	LAMP2	NM_002294	2	9	4	-	119582825	119582983
313079850	chrX	119582839	119583025	119582864	119582998	LAMP2	NM_002294	2	9	4	-	119582825	119582983
314353537	chrX	119581623	119581779	119581645	119581751	LAMP2	NM_002294	2	9	5	-	119581696	119581880
314363586	chrX	119581729	119581920	119581752	119581897	LAMP2	NM_002294	2	9	5	-	119581696	119581880
315040647	chrX	119579990	119580198	119580011	119580170	LAMP2	NM_002294	2	9	6	-	119580160	119580282
315056519	chrX	119580145	119580314	119580171	119580287	LAMP2	NM_002294	2	9	6	-	119580160	119580282
313738912	chrX	119576399	119576579	119576425	119576551	LAMP2	NM_002294	2	9	7	-	119576454	119576517
315275113	chrX	119575455	119575668	119575479	119575640	LAMP2	NM_002294	2	9	8	-	119575585	119575749
315279194	chrX	119575616	119575814	119575641	119575788	LAMP2	NM_002294	2	9	8	-	119575585	119575749

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314103744	chrX	119562196	119562420	119562220	119562392	LAMP2	NM_002294	2	9	9	-	119560003	119565317
314129299	chrX	119562356	119562528	119562385	119562500	LAMP2	NM_002294	2	9	9	-	119560003	119565317
315376390	chrX	119565032	119565211	119565058	119565188	LAMP2	NM_002294	2	9	9	-	119560003	119565317
315381388	chrX	119565161	119565347	119565189	119565322	LAMP2	NM_002294	2	9	9	-	119560003	119565317
313407811	chrX	119602878	119603084	119602900	119603062	LAMP2	NM_013995	3	9	1	-	119602961	119603204
312677994	chrX	119590386	119590577	119590412	119590553	LAMP2	NM_013995	3	9	2	-	119590506	119590624
312684956	chrX	119590530	119590704	119590554	119590679	LAMP2	NM_013995	3	9	2	-	119590506	119590624
313984161	chrX	119589092	119589305	119589119	119589277	LAMP2	NM_013995	3	9	3	-	119589212	119589425
313997788	chrX	119589253	119589464	119589278	119589442	LAMP2	NM_013995	3	9	3	-	119589212	119589425
313077562	chrX	119582750	119582887	119582778	119582863	LAMP2	NM_013995	3	9	4	-	119582825	119582983
313079850	chrX	119582839	119583025	119582864	119582998	LAMP2	NM_013995	3	9	4	-	119582825	119582983
314353537	chrX	119581623	119581779	119581645	119581751	LAMP2	NM_013995	3	9	5	-	119581696	119581880
314363586	chrX	119581729	119581920	119581752	119581897	LAMP2	NM_013995	3	9	5	-	119581696	119581880
315040647	chrX	119579990	119580198	119580011	119580170	LAMP2	NM_013995	3	9	6	-	119580160	119580282
315056519	chrX	119580145	119580314	119580171	119580287	LAMP2	NM_013995	3	9	6	-	119580160	119580282
313738912	chrX	119576399	119576579	119576425	119576551	LAMP2	NM_013995	3	9	7	-	119576454	119576517
315275113	chrX	119575455	119575668	119575479	119575640	LAMP2	NM_013995	3	9	8	-	119575585	119575749
315279194	chrX	119575616	119575814	119575641	119575788	LAMP2	NM_013995	3	9	8	-	119575585	119575749
313634317	chrX	119572825	119573048	119572850	119573021	LAMP2	NM_013995	3	9	9	-	119570349	119573148
313647056	chrX	119572993	119573216	119573022	119573188	LAMP2	NM_013995	3	9	9	-	119570349	119573148
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_001080114	1	13	1	+	88428426	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_001080114	1	13	2	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_001080114	1	13	2	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_001080114	1	13	3	+	88439839	88439914
314808437	chr10	88445264	88445485	88445285	88445463	LDB3	NM_001080114	1	13	4	+	88445435	88445457
313892711	chr10	88446756	88446971	88446776	88446949	LDB3	NM_001080114	1	13	5	+	88446826	88447029
313901334	chr10	88446928	88447131	88446949	88447110	LDB3	NM_001080114	1	13	5	+	88446826	88447029
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_001080114	1	13	6	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_001080114	1	13	6	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_001080114	1	13	7	+	88452292	88452328
315089751	chr10	88469621	88469828	88469642	88469808	LDB3	NM_001080114	1	13	8	+	88469662	88469807
315094128	chr10	88469781	88469990	88469801	88469969	LDB3	NM_001080114	1	13	8	+	88469662	88469807
313338426	chr10	88475916	88476139	88475940	88476116	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313342676	chr10	88476081	88476271	88476102	88476250	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313342915	chr10	88476118	88476342	88476142	88476319	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313344591	chr10	88476252	88476380	88476273	88476360	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313347138	chr10	88476324	88476540	88476349	88476520	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313353008	chr10	88476501	88476660	88476521	88476640	LDB3	NM_001080114	1	13	9	+	88476084	88476528
313314880	chr10	88477674	88477839	88477695	88477814	LDB3	NM_001080114	1	13	10	+	88477721	88477901
313325445	chr10	88477794	88477939	88477815	88477916	LDB3	NM_001080114	1	13	10	+	88477721	88477901
312720394	chr10	88478442	88478630	88478465	88478609	LDB3	NM_001080114	1	13	11	+	88478484	88478604

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314530245	chr10	88485868	88486056	88485894	88486034	LDB3	NM_001080114	1	13	12	+	88485894	88486009
314163258	chr10	88492585	88492805	88492606	88492784	LDB3	NM_001080114	1	13	13	+	88492644	88495824
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_001080115	2	7	1	+	88428426	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_001080115	2	7	2	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_001080115	2	7	2	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_001080115	2	7	3	+	88439839	88439914
314870567	chr10	88441133	88441342	88441151	88441323	LDB3	NM_001080115	2	7	4	+	88441193	88441560
314872169	chr10	88441291	88441514	88441312	88441492	LDB3	NM_001080115	2	7	4	+	88441193	88441560
314876134	chr10	88441459	88441592	88441479	88441570	LDB3	NM_001080115	2	7	4	+	88441193	88441560
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_001080115	2	7	5	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_001080115	2	7	5	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_001080115	2	7	6	+	88452292	88452328
314935247	chr10	88458931	88459093	88458954	88459074	LDB3	NM_001080115	2	7	7	+	88459035	88459810
314961597	chr10	88459055	88459243	88459075	88459216	LDB3	NM_001080115	2	7	7	+	88459035	88459810
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_001080116	3	8	1	+	88428321	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_001080116	3	8	2	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_001080116	3	8	2	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_001080116	3	8	3	+	88439839	88439914
314808437	chr10	88445264	88445485	88445285	88445463	LDB3	NM_001080116	3	8	4	+	88445435	88445457
313892711	chr10	88446756	88446971	88446776	88446949	LDB3	NM_001080116	3	8	5	+	88446826	88447029
313901334	chr10	88446928	88447131	88446949	88447110	LDB3	NM_001080116	3	8	5	+	88446826	88447029
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_001080116	3	8	6	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_001080116	3	8	6	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_001080116	3	8	7	+	88452292	88452328
314935247	chr10	88458931	88459093	88458954	88459074	LDB3	NM_001080116	3	8	8	+	88459035	88459810
314961597	chr10	88459055	88459243	88459075	88459216	LDB3	NM_001080116	3	8	8	+	88459035	88459810
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_001171610	4	14	2	+	88428426	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_001171610	4	14	3	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_001171610	4	14	3	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_001171610	4	14	4	+	88439839	88439914
314870567	chr10	88441133	88441342	88441151	88441323	LDB3	NM_001171610	4	14	5	+	88441193	88441560
314872169	chr10	88441291	88441514	88441312	88441492	LDB3	NM_001171610	4	14	5	+	88441193	88441560
314876134	chr10	88441459	88441592	88441479	88441570	LDB3	NM_001171610	4	14	5	+	88441193	88441560
313892711	chr10	88446756	88446971	88446776	88446949	LDB3	NM_001171610	4	14	6	+	88446826	88447029
313901334	chr10	88446928	88447131	88446949	88447110	LDB3	NM_001171610	4	14	6	+	88446826	88447029
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_001171610	4	14	7	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_001171610	4	14	7	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_001171610	4	14	8	+	88452292	88452328
315089751	chr10	88469621	88469828	88469642	88469808	LDB3	NM_001171610	4	14	9	+	88469662	88469807
315094128	chr10	88469781	88469990	88469801	88469969	LDB3	NM_001171610	4	14	9	+	88469662	88469807
313338426	chr10	88475916	88476139	88475940	88476116	LDB3	NM_001171610	4	14	10	+	88476084	88476528

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313342676	chr10	88476081	88476271	88476102	88476250	LDB3	NM_001171610	4	14	10	+	88476084	88476528
313342915	chr10	88476118	88476342	88476142	88476319	LDB3	NM_001171610	4	14	10	+	88476084	88476528
313344591	chr10	88476252	88476380	88476273	88476360	LDB3	NM_001171610	4	14	10	+	88476084	88476528
313347138	chr10	88476324	88476540	88476349	88476520	LDB3	NM_001171610	4	14	10	+	88476084	88476528
313353008	chr10	88476501	88476660	88476521	88476640	LDB3	NM_001171610	4	14	10	+	88476084	88476528
313314880	chr10	88477674	88477839	88477695	88477814	LDB3	NM_001171610	4	14	11	+	88477721	88477901
313325445	chr10	88477794	88477939	88477815	88477916	LDB3	NM_001171610	4	14	11	+	88477721	88477901
312720394	chr10	88478442	88478630	88478465	88478609	LDB3	NM_001171610	4	14	12	+	88478484	88478604
314530245	chr10	88485868	88486056	88485894	88486034	LDB3	NM_001171610	4	14	13	+	88485894	88486009
314163258	chr10	88492585	88492805	88492606	88492784	LDB3	NM_001171610	4	14	14	+	88492644	88495824
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_001171611	5	8	1	+	88428426	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_001171611	5	8	2	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_001171611	5	8	2	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_001171611	5	8	3	+	88439839	88439914
314870567	chr10	88441133	88441342	88441151	88441323	LDB3	NM_001171611	5	8	4	+	88441193	88441560
314872169	chr10	88441291	88441514	88441312	88441492	LDB3	NM_001171611	5	8	4	+	88441193	88441560
314876134	chr10	88441459	88441592	88441479	88441570	LDB3	NM_001171611	5	8	4	+	88441193	88441560
313892711	chr10	88446756	88446971	88446776	88446949	LDB3	NM_001171611	5	8	5	+	88446826	88447029
313901334	chr10	88446928	88447131	88446949	88447110	LDB3	NM_001171611	5	8	5	+	88446826	88447029
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_001171611	5	8	6	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_001171611	5	8	6	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_001171611	5	8	7	+	88452292	88452328
314935247	chr10	88458931	88459093	88458954	88459074	LDB3	NM_001171611	5	8	8	+	88459035	88459810
314961597	chr10	88459055	88459243	88459075	88459216	LDB3	NM_001171611	5	8	8	+	88459035	88459810
313109786	chr10	88428382	88428606	88428400	88428587	LDB3	NM_007078	6	13	1	+	88428426	88428541
313126531	chr10	88439071	88439270	88439093	88439248	LDB3	NM_007078	6	13	2	+	88439124	88439275
313135100	chr10	88439225	88439410	88439248	88439385	LDB3	NM_007078	6	13	2	+	88439124	88439275
314382869	chr10	88439803	88440027	88439827	88440008	LDB3	NM_007078	6	13	3	+	88439839	88439914
314870567	chr10	88441133	88441342	88441151	88441323	LDB3	NM_007078	6	13	4	+	88441193	88441560
314872169	chr10	88441291	88441514	88441312	88441492	LDB3	NM_007078	6	13	4	+	88441193	88441560
314876134	chr10	88441459	88441592	88441479	88441570	LDB3	NM_007078	6	13	4	+	88441193	88441560
312797232	chr10	88451502	88451725	88451525	88451702	LDB3	NM_007078	6	13	5	+	88451653	88451822
312812365	chr10	88451684	88451869	88451701	88451849	LDB3	NM_007078	6	13	5	+	88451653	88451822
313936813	chr10	88452264	88452418	88452285	88452396	LDB3	NM_007078	6	13	6	+	88452292	88452328
312930443	chr10	88466248	88466468	88466271	88466449	LDB3	NM_007078	6	13	7	+	88466288	88466476
312934488	chr10	88466409	88466632	88466426	88466612	LDB3	NM_007078	6	13	7	+	88466288	88466476
315089751	chr10	88469621	88469828	88469642	88469808	LDB3	NM_007078	6	13	8	+	88469662	88469807
315094128	chr10	88469781	88469990	88469801	88469969	LDB3	NM_007078	6	13	8	+	88469662	88469807
313338426	chr10	88475916	88476139	88475940	88476116	LDB3	NM_007078	6	13	9	+	88476084	88476528
313342676	chr10	88476081	88476271	88476102	88476250	LDB3	NM_007078	6	13	9	+	88476084	88476528
313342915	chr10	88476118	88476342	88476142	88476319	LDB3	NM_007078	6	13	9	+	88476084	88476528

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313344591	chr10	88476252	88476380	88476273	88476360	LDB3	NM_007078	6	13	9	+	88476084	88476528
313347138	chr10	88476324	88476540	88476349	88476520	LDB3	NM_007078	6	13	9	+	88476084	88476528
313353008	chr10	88476501	88476660	88476521	88476640	LDB3	NM_007078	6	13	9	+	88476084	88476528
313314880	chr10	88477674	88477839	88477695	88477814	LDB3	NM_007078	6	13	10	+	88477721	88477901
313325445	chr10	88477794	88477939	88477815	88477916	LDB3	NM_007078	6	13	10	+	88477721	88477901
312720394	chr10	88478442	88478630	88478465	88478609	LDB3	NM_007078	6	13	11	+	88478484	88478604
314530245	chr10	88485868	88486056	88485894	88486034	LDB3	NM_007078	6	13	12	+	88485894	88486009
314163258	chr10	88492585	88492805	88492606	88492784	LDB3	NM_007078	6	13	13	+	88492644	88495824
313058164	chr1	156084972	156085192	156084991	156085167	LMNA	NM_005572	1	10	1	+	156084461	156085065
314804406	chr1	156084622	156084844	156084642	156084824	LMNA	NM_005572	1	10	1	+	156084461	156085065
314805437	chr1	156084807	156085007	156084825	156084990	LMNA	NM_005572	1	10	1	+	156084461	156085065
314606917	chr1	156100254	156100450	156100276	156100431	LMNA	NM_005572	1	10	2	+	156100408	156100564
314619747	chr1	156100407	156100629	156100430	156100602	LMNA	NM_005572	1	10	2	+	156100408	156100564
314281496	chr1	156104155	156104379	156104178	156104358	LMNA	NM_005572	1	10	3	+	156104194	156104319
315262670	chr1	156104538	156104760	156104560	156104734	LMNA	NM_005572	1	10	4	+	156104596	156104766
315274090	chr1	156104713	156104838	156104735	156104818	LMNA	NM_005572	1	10	4	+	156104596	156104766
313627461	chr1	156104937	156105156	156104958	156105137	LMNA	NM_005572	1	10	5	+	156104978	156105103
313433055	chr1	156105629	156105844	156105651	156105823	LMNA	NM_005572	1	10	6	+	156105692	156105912
313438206	chr1	156105763	156105981	156105781	156105962	LMNA	NM_005572	1	10	6	+	156105692	156105912
313277097	chr1	156105967	156106113	156105988	156106092	LMNA	NM_005572	1	10	7	+	156106005	156106227
313285533	chr1	156106058	156106276	156106079	156106255	LMNA	NM_005572	1	10	7	+	156106005	156106227
312784348	chr1	156106597	156106785	156106619	156106765	LMNA	NM_005572	1	10	8	+	156106712	156106819
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_005572	1	10	8	+	156106712	156106819
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_005572	1	10	9	+	156106904	156107023
314376618	chr1	156106882	156107086	156106906	156107066	LMNA	NM_005572	1	10	9	+	156106904	156107023
314910422	chr1	156107356	156107515	156107378	156107492	LMNA	NM_005572	1	10	10	+	156107445	156107657
314912383	chr1	156107471	156107666	156107493	156107644	LMNA	NM_005572	1	10	10	+	156107445	156107657
313058164	chr1	156084972	156085192	156084991	156085167	LMNA	NM_170707	2	12	1	+	156084461	156085065
314804406	chr1	156084622	156084844	156084642	156084824	LMNA	NM_170707	2	12	1	+	156084461	156085065
314805437	chr1	156084807	156085007	156084825	156084990	LMNA	NM_170707	2	12	1	+	156084461	156085065
314606917	chr1	156100254	156100450	156100276	156100431	LMNA	NM_170707	2	12	2	+	156100408	156100564
314619747	chr1	156100407	156100629	156100430	156100602	LMNA	NM_170707	2	12	2	+	156100408	156100564
314281496	chr1	156104155	156104379	156104178	156104358	LMNA	NM_170707	2	12	3	+	156104194	156104319
315262670	chr1	156104538	156104760	156104560	156104734	LMNA	NM_170707	2	12	4	+	156104596	156104766
315274090	chr1	156104713	156104838	156104735	156104818	LMNA	NM_170707	2	12	4	+	156104596	156104766
313627461	chr1	156104937	156105156	156104958	156105137	LMNA	NM_170707	2	12	5	+	156104978	156105103
313433055	chr1	156105629	156105844	156105651	156105823	LMNA	NM_170707	2	12	6	+	156105692	156105912
313438206	chr1	156105763	156105981	156105781	156105962	LMNA	NM_170707	2	12	6	+	156105692	156105912
313277097	chr1	156105967	156106113	156105988	156106092	LMNA	NM_170707	2	12	7	+	156106005	156106227
313285533	chr1	156106058	156106276	156106079	156106255	LMNA	NM_170707	2	12	7	+	156106005	156106227
312784348	chr1	156106597	156106785	156106619	156106765	LMNA	NM_170707	2	12	8	+	156106712	156106819

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_170707	2	12	8	+	156106712	156106819
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_170707	2	12	9	+	156106904	156107023
314376618	chr1	156106882	156107086	156106906	156107066	LMNA	NM_170707	2	12	9	+	156106904	156107023
314910422	chr1	156107356	156107515	156107378	156107492	LMNA	NM_170707	2	12	10	+	156107445	156107534
314912383	chr1	156107471	156107666	156107493	156107644	LMNA	NM_170707	2	12	10	+	156107445	156107534
312716650	chr1	156108222	156108442	156108241	156108421	LMNA	NM_170707	2	12	11	+	156108279	156108548
312718145	chr1	156108404	156108616	156108422	156108597	LMNA	NM_170707	2	12	11	+	156108279	156108548
314783850	chr1	156108838	156108994	156108859	156108976	LMNA	NM_170707	2	12	12	+	156108871	156109878
313058164	chr1	156084972	156085192	156084991	156085167	LMNA	NM_170708	3	11	1	+	156084461	156085065
314804406	chr1	156084622	156084844	156084642	156084824	LMNA	NM_170708	3	11	1	+	156084461	156085065
314805437	chr1	156084807	156085007	156084825	156084990	LMNA	NM_170708	3	11	1	+	156084461	156085065
314606917	chr1	156100254	156100450	156100276	156100431	LMNA	NM_170708	3	11	2	+	156100408	156100564
314619747	chr1	156100407	156100629	156100430	156100602	LMNA	NM_170708	3	11	2	+	156100408	156100564
314281496	chr1	156104155	156104379	156104178	156104358	LMNA	NM_170708	3	11	3	+	156104194	156104319
315262670	chr1	156104538	156104760	156104560	156104734	LMNA	NM_170708	3	11	4	+	156104596	156104766
315274090	chr1	156104713	156104838	156104735	156104818	LMNA	NM_170708	3	11	4	+	156104596	156104766
313627461	chr1	156104937	156105156	156104958	156105137	LMNA	NM_170708	3	11	5	+	156104978	156105103
313433055	chr1	156105629	156105844	156105651	156105823	LMNA	NM_170708	3	11	6	+	156105692	156105912
313438206	chr1	156105763	156105981	156105781	156105962	LMNA	NM_170708	3	11	6	+	156105692	156105912
313277097	chr1	156105967	156106113	156105988	156106092	LMNA	NM_170708	3	11	7	+	156106005	156106227
313285533	chr1	156106058	156106276	156106079	156106255	LMNA	NM_170708	3	11	7	+	156106005	156106227
312784348	chr1	156106597	156106785	156106619	156106765	LMNA	NM_170708	3	11	8	+	156106712	156106819
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_170708	3	11	8	+	156106712	156106819
312796180	chr1	156106736	156106960	156106757	156106940	LMNA	NM_170708	3	11	9	+	156106904	156107023
314376618	chr1	156106882	156107086	156106906	156107066	LMNA	NM_170708	3	11	9	+	156106904	156107023
312716650	chr1	156108222	156108442	156108241	156108421	LMNA	NM_170708	3	11	10	+	156108279	156108548
312718145	chr1	156108404	156108616	156108422	156108597	LMNA	NM_170708	3	11	10	+	156108279	156108548
314783850	chr1	156108838	156108994	156108859	156108976	LMNA	NM_170708	3	11	11	+	156108871	156109878
312830998	chr4	155665342	155665521	155665361	155665496	LRAT	NM_004744	1	3	1	+	155665163	155665374
312830998	chr4	155665342	155665521	155665361	155665496	LRAT	NM_004744	1	3	2	+	155665478	155666018
312835928	chr4	155665476	155665689	155665497	155665668	LRAT	NM_004744	1	3	2	+	155665478	155666018
312845641	chr4	155665648	155665868	155665669	155665847	LRAT	NM_004744	1	3	2	+	155665478	155666018
312861938	chr4	155665827	155665994	155665847	155665972	LRAT	NM_004744	1	3	2	+	155665478	155666018
314640186	chr4	155665954	155666088	155665973	155666066	LRAT	NM_004744	1	3	2	+	155665478	155666018
314406444	chr4	155670085	155670219	155670109	155670196	LRAT	NM_004744	1	3	3	+	155670136	155674270
314410583	chr4	155670174	155670321	155670197	155670297	LRAT	NM_004744	1	3	3	+	155670136	155674270
278509725	chr12	40618884	40619032	40618902	40619004	LRRK2	NM_198578	1	51	1	+	40618813	40619084
278512567	chr12	40618979	40619195	40619005	40619173	LRRK2	NM_198578	1	51	1	+	40618813	40619084
278043070	chr12	40619262	40619478	40619286	40619450	LRRK2	NM_198578	1	51	2	+	40619357	40619442
280333064	chr12	40626079	40626252	40626100	40626224	LRRK2	NM_198578	1	51	3	+	40626076	40626185
313568761	chr12	40625904	40626127	40625927	40626099	LRRK2	NM_198578	1	51	3	+	40626076	40626185

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279402333	chr12	40629447	40629638	40629475	40629610	LRRK2	NM_198578	1	51	4	+	40629428	40629516
313470288	chr12	40629297	40629501	40629323	40629474	LRRK2	NM_198578	1	51	4	+	40629428	40629516
278603846	chr12	40631660	40631871	40631684	40631846	LRRK2	NM_198578	1	51	5	+	40631771	40631905
314201151	chr12	40631823	40632042	40631847	40632014	LRRK2	NM_198578	1	51	5	+	40631771	40631905
279474455	chr12	40634165	40634389	40634198	40634365	LRRK2	NM_198578	1	51	6	+	40634285	40634419
279477864	chr12	40634295	40634436	40634321	40634408	LRRK2	NM_198578	1	51	6	+	40634285	40634419
279479927	chr12	40634386	40634533	40634409	40634505	LRRK2	NM_198578	1	51	6	+	40634285	40634419
278043356	chr12	40637241	40637422	40637267	40637398	LRRK2	NM_198578	1	51	7	+	40637352	40637483
278048187	chr12	40637372	40637496	40637399	40637466	LRRK2	NM_198578	1	51	7	+	40637352	40637483
280882765	chr12	40643583	40643789	40643611	40643761	LRRK2	NM_198578	1	51	8	+	40643628	40643747
277831338	chr12	40644959	40645163	40644987	40645136	LRRK2	NM_198578	1	51	9	+	40645034	40645176
312671677	chr12	40645115	40645302	40645137	40645274	LRRK2	NM_198578	1	51	9	+	40645034	40645176
312676967	chr12	40645137	40645343	40645163	40645314	LRRK2	NM_198578	1	51	9	+	40645034	40645176
312671677	chr12	40645115	40645302	40645137	40645274	LRRK2	NM_198578	1	51	10	+	40645267	40645346
312676967	chr12	40645137	40645343	40645163	40645314	LRRK2	NM_198578	1	51	10	+	40645267	40645346
314688430	chr12	40645277	40645478	40645305	40645450	LRRK2	NM_198578	1	51	10	+	40645267	40645346
279439020	chr12	40646717	40646841	40646740	40646819	LRRK2	NM_198578	1	51	11	+	40646712	40646818
313491413	chr12	40646577	40646779	40646600	40646751	LRRK2	NM_198578	1	51	11	+	40646712	40646818
279394327	chr12	40650929	40651137	40650958	40651111	LRRK2	NM_198578	1	51	12	+	40651050	40651179
279395161	chr12	40651085	40651307	40651112	40651279	LRRK2	NM_198578	1	51	12	+	40651050	40651179
280376905	chr12	40653190	40653360	40653211	40653333	LRRK2	NM_198578	1	51	13	+	40653282	40653406
280383037	chr12	40653308	40653522	40653334	40653494	LRRK2	NM_198578	1	51	13	+	40653282	40653406
278712027	chr12	40657514	40657693	40657542	40657667	LRRK2	NM_198578	1	51	14	+	40657591	40657703
312730668	chr12	40657605	40657828	40657633	40657803	LRRK2	NM_198578	1	51	14	+	40657591	40657703
278211317	chr12	40668293	40668472	40668326	40668444	LRRK2	NM_198578	1	51	15	+	40668385	40668529
278213286	chr12	40668397	40668590	40668425	40668569	LRRK2	NM_198578	1	51	15	+	40668385	40668529
279065058	chr12	40668569	40668750	40668590	40668726	LRRK2	NM_198578	1	51	16	+	40668656	40668795
279067787	chr12	40668699	40668850	40668727	40668825	LRRK2	NM_198578	1	51	16	+	40668656	40668795
279419619	chr12	40671630	40671756	40671660	40671734	LRRK2	NM_198578	1	51	17	+	40671690	40671818
279420063	chr12	40671708	40671916	40671735	40671889	LRRK2	NM_198578	1	51	17	+	40671690	40671818
278700684	chr12	40671892	40672094	40671919	40672068	LRRK2	NM_198578	1	51	18	+	40671893	40672063
279421461	chr12	40671800	40671945	40671826	40671918	LRRK2	NM_198578	1	51	18	+	40671893	40672063
279544386	chr12	40677561	40677730	40677591	40677703	LRRK2	NM_198578	1	51	19	+	40677677	40677935
279550605	chr12	40677681	40677868	40677704	40677840	LRRK2	NM_198578	1	51	19	+	40677677	40677935
279559748	chr12	40677819	40678028	40677841	40677999	LRRK2	NM_198578	1	51	19	+	40677677	40677935
277862074	chr12	40681056	40681277	40681083	40681248	LRRK2	NM_198578	1	51	20	+	40681153	40681341
277873146	chr12	40681226	40681410	40681249	40681384	LRRK2	NM_198578	1	51	20	+	40681153	40681341
278769489	chr12	40687350	40687574	40687377	40687549	LRRK2	NM_198578	1	51	21	+	40687347	40687465
314443268	chr12	40687203	40687416	40687231	40687388	LRRK2	NM_198578	1	51	21	+	40687347	40687465
279380191	chr12	40688549	40688771	40688581	40688743	LRRK2	NM_198578	1	51	22	+	40688647	40688716
278446570	chr12	40689222	40689384	40689249	40689357	LRRK2	NM_198578	1	51	23	+	40689229	40689446

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278457765	chr12	40689333	40689557	40689358	40689529	LRRK2	NM_198578	1	51	23	+	40689229	40689446
280769224	chr12	40691987	40692197	40692015	40692169	LRRK2	NM_198578	1	51	24	+	40692045	40692295
280776917	chr12	40692147	40692344	40692170	40692315	LRRK2	NM_198578	1	51	24	+	40692045	40692295
278200195	chr12	40692803	40692993	40692829	40692964	LRRK2	NM_198578	1	51	25	+	40692911	40693059
278203587	chr12	40692937	40693104	40692965	40693082	LRRK2	NM_198578	1	51	25	+	40692911	40693059
278706503	chr12	40696499	40696665	40696526	40696636	LRRK2	NM_198578	1	51	26	+	40696591	40696684
278709010	chr12	40696604	40696747	40696632	40696719	LRRK2	NM_198578	1	51	26	+	40696591	40696684
279631766	chr12	40697754	40697953	40697780	40697924	LRRK2	NM_198578	1	51	27	+	40697750	40697936
314021488	chr12	40697586	40697802	40697608	40697779	LRRK2	NM_198578	1	51	27	+	40697750	40697936
314030660	chr12	40697890	40698092	40697918	40698060	LRRK2	NM_198578	1	51	27	+	40697750	40697936
278494415	chr12	40699485	40699708	40699509	40699681	LRRK2	NM_198578	1	51	28	+	40699587	40699768
278503027	chr12	40699647	40699842	40699675	40699816	LRRK2	NM_198578	1	51	28	+	40699587	40699768
279758255	chr12	40702257	40702408	40702285	40702380	LRRK2	NM_198578	1	51	29	+	40702269	40702498
279765271	chr12	40702353	40702568	40702381	40702543	LRRK2	NM_198578	1	51	29	+	40702269	40702498
278213074	chr12	40702937	40703140	40702958	40703113	LRRK2	NM_198578	1	51	30	+	40702908	40703035
313265128	chr12	40702758	40702982	40702786	40702957	LRRK2	NM_198578	1	51	30	+	40702908	40703035
279399776	chr12	40704139	40704344	40704162	40704318	LRRK2	NM_198578	1	51	31	+	40704233	40704451
279428723	chr12	40704298	40704512	40704319	40704484	LRRK2	NM_198578	1	51	31	+	40704233	40704451
278128787	chr12	40707694	40707888	40707717	40707864	LRRK2	NM_198578	1	51	32	+	40707774	40707975
278139024	chr12	40707844	40708011	40707865	40707983	LRRK2	NM_198578	1	51	32	+	40707774	40707975
279093783	chr12	40709008	40709132	40709036	40709108	LRRK2	NM_198578	1	51	33	+	40709014	40709102
278122269	chr12	40713787	40713974	40713813	40713946	LRRK2	NM_198578	1	51	34	+	40713790	40713977
313225874	chr12	40713626	40713834	40713647	40713812	LRRK2	NM_198578	1	51	34	+	40713790	40713977
313243210	chr12	40713919	40714113	40713947	40714085	LRRK2	NM_198578	1	51	34	+	40713790	40713977
279368663	chr12	40714780	40715003	40714803	40714975	LRRK2	NM_198578	1	51	35	+	40714836	40714990
278630632	chr12	40715858	40716080	40715882	40716054	LRRK2	NM_198578	1	51	36	+	40715837	40715983
315413595	chr12	40715700	40715910	40715727	40715881	LRRK2	NM_198578	1	51	36	+	40715837	40715983
279614586	chr12	40716087	40716307	40716111	40716280	LRRK2	NM_198578	1	51	37	+	40716121	40716312
279623712	chr12	40716215	40716355	40716243	40716324	LRRK2	NM_198578	1	51	37	+	40716121	40716312
280680180	chr12	40716992	40717122	40717018	40717092	LRRK2	NM_198578	1	51	38	+	40716962	40717108
312663140	chr12	40716833	40717043	40716858	40717020	LRRK2	NM_198578	1	51	38	+	40716962	40717108
280421692	chr12	40722117	40722260	40722143	40722232	LRRK2	NM_198578	1	51	39	+	40722162	40722262
315285684	chr12	40722203	40722427	40722231	40722400	LRRK2	NM_198578	1	51	39	+	40722162	40722262
280782406	chr12	40728656	40728868	40728684	40728846	LRRK2	NM_198578	1	51	40	+	40728769	40728959
280809382	chr12	40728827	40729003	40728847	40728976	LRRK2	NM_198578	1	51	40	+	40728769	40728959
279935416	chr12	40734124	40734309	40734146	40734281	LRRK2	NM_198578	1	51	41	+	40734096	40734256
314482759	chr12	40733965	40734168	40733990	40734145	LRRK2	NM_198578	1	51	41	+	40734096	40734256
278295799	chr12	40740481	40740679	40740504	40740651	LRRK2	NM_198578	1	51	42	+	40740555	40740725
278300258	chr12	40740651	40740824	40740679	40740791	LRRK2	NM_198578	1	51	42	+	40740555	40740725
279692599	chr12	40742117	40742299	40742146	40742273	LRRK2	NM_198578	1	51	43	+	40742211	40742311
278502182	chr12	40745375	40745542	40745401	40745514	LRRK2	NM_198578	1	51	44	+	40745341	40745535

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313978413	chr12	40745204	40745428	40745227	40745400	LRRK2	NM_198578	1	51	44	+	40745341	40745535
313990072	chr12	40745486	40745701	40745514	40745673	LRRK2	NM_198578	1	51	44	+	40745341	40745535
278966678	chr12	40748106	40748230	40748134	40748202	LRRK2	NM_198578	1	51	45	+	40748101	40748294
278971585	chr12	40748181	40748365	40748203	40748337	LRRK2	NM_198578	1	51	45	+	40748101	40748294
312861313	chr12	40747926	40748149	40747953	40748127	LRRK2	NM_198578	1	51	45	+	40748101	40748294
279952653	chr12	40753005	40753192	40753033	40753167	LRRK2	NM_198578	1	51	47	+	40753062	40753246
279956162	chr12	40753132	40753258	40753160	40753228	LRRK2	NM_198578	1	51	47	+	40753062	40753246
279070544	chr12	40757199	40757417	40757226	40757389	LRRK2	NM_198578	1	51	48	+	40757204	40757356
313016979	chr12	40757035	40757251	40757065	40757225	LRRK2	NM_198578	1	51	48	+	40757204	40757356
279465625	chr12	40758523	40758728	40758545	40758706	LRRK2	NM_198578	1	51	49	+	40758644	40758852
279471719	chr12	40758679	40758807	40758707	40758778	LRRK2	NM_198578	1	51	49	+	40758644	40758852
279481389	chr12	40758754	40758949	40758779	40758922	LRRK2	NM_198578	1	51	49	+	40758644	40758852
279511781	chr12	40760693	40760857	40760721	40760831	LRRK2	NM_198578	1	51	50	+	40760808	40760879
279512880	chr12	40760802	40760931	40760830	40760907	LRRK2	NM_198578	1	51	50	+	40760808	40760879
280297283	chr12	40761353	40761570	40761383	40761542	LRRK2	NM_198578	1	51	51	+	40761446	40763086
280299321	chr12	40761474	40761694	40761502	40761666	LRRK2	NM_198578	1	51	51	+	40761446	40763086
314604190	chr18	32585357	32585555	32585377	32585526	MAPRE2	NM_001143826	1	8	2	+	32585456	32585517
313950598	chr18	32650036	32650209	32650057	32650181	MAPRE2	NM_001143826	1	8	3	+	32650159	32650286
313954493	chr18	32650162	32650347	32650182	32650319	MAPRE2	NM_001143826	1	8	3	+	32650159	32650286
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NM_001143826	1	8	4	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NM_001143826	1	8	5	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NM_001143826	1	8	5	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NM_001143826	1	8	6	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NM_001143826	1	8	6	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NM_001143826	1	8	7	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NM_001143826	1	8	7	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NM_001143826	1	8	8	+	32720259	32723432
315042838	chr18	32558393	32558557	32558412	32558532	MAPRE2	NM_001143827	2	8	1	+	32558208	32558505
314604190	chr18	32585357	32585555	32585377	32585526	MAPRE2	NM_001143827	2	8	2	+	32585456	32585517
313950598	chr18	32650036	32650209	32650057	32650181	MAPRE2	NM_001143827	2	8	3	+	32650159	32650286
313954493	chr18	32650162	32650347	32650182	32650319	MAPRE2	NM_001143827	2	8	3	+	32650159	32650286
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NM_001143827	2	8	4	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NM_001143827	2	8	5	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NM_001143827	2	8	5	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NM_001143827	2	8	6	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NM_001143827	2	8	6	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NM_001143827	2	8	7	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NM_001143827	2	8	7	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NM_001143827	2	8	8	+	32720259	32723432
315119712	chr18	32621472	32621597	32621492	32621574	MAPRE2	NM_001256420	3	6	1	+	32621324	32621625
315123420	chr18	32621543	32621765	32621572	32621741	MAPRE2	NM_001256420	3	6	1	+	32621324	32621625

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NM_001256420	3	6	2	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NM_001256420	3	6	3	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NM_001256420	3	6	3	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NM_001256420	3	6	4	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NM_001256420	3	6	4	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NM_001256420	3	6	5	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NM_001256420	3	6	5	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NM_001256420	3	6	6	+	32720259	32723432
315119712	chr18	32621472	32621597	32621492	32621574	MAPRE2	NM_014268	4	7	1	+	32621324	32621625
315123420	chr18	32621543	32621765	32621572	32621741	MAPRE2	NM_014268	4	7	1	+	32621324	32621625
313950598	chr18	32650036	32650209	32650057	32650181	MAPRE2	NM_014268	4	7	2	+	32650159	32650286
313954493	chr18	32650162	32650347	32650182	32650319	MAPRE2	NM_014268	4	7	2	+	32650159	32650286
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NM_014268	4	7	3	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NM_014268	4	7	4	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NM_014268	4	7	4	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NM_014268	4	7	5	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NM_014268	4	7	5	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NM_014268	4	7	6	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NM_014268	4	7	6	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NM_014268	4	7	7	+	32720259	32723432
315119712	chr18	32621472	32621597	32621492	32621574	MAPRE2	NR_026570	5	6	1	+	32621324	32621625
315123420	chr18	32621543	32621765	32621572	32621741	MAPRE2	NR_026570	5	6	1	+	32621324	32621625
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NR_026570	5	6	2	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NR_026570	5	6	3	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NR_026570	5	6	3	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NR_026570	5	6	4	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NR_026570	5	6	4	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NR_026570	5	6	5	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NR_026570	5	6	5	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NR_026570	5	6	6	+	32720259	32722378
315123420	chr18	32621543	32621765	32621572	32621741	MAPRE2	NR_046177	6	7	1	+	32621614	32621730
313950598	chr18	32650036	32650209	32650057	32650181	MAPRE2	NR_046177	6	7	2	+	32650159	32650286
313954493	chr18	32650162	32650347	32650182	32650319	MAPRE2	NR_046177	6	7	2	+	32650159	32650286
312699815	chr18	32677376	32677589	32677402	32677560	MAPRE2	NR_046177	6	7	3	+	32677410	32677555
314144083	chr18	32681899	32682032	32681927	32682009	MAPRE2	NR_046177	6	7	4	+	32681910	32682123
314152804	chr18	32681984	32682151	32682010	32682129	MAPRE2	NR_046177	6	7	4	+	32681910	32682123
313909453	chr18	32706724	32706943	32706750	32706920	MAPRE2	NR_046177	6	7	5	+	32706912	32707051
313918070	chr18	32706899	32707097	32706921	32707076	MAPRE2	NR_046177	6	7	5	+	32706912	32707051
315301196	chr18	32711850	32712025	32711871	32711998	MAPRE2	NR_046177	6	7	6	+	32711996	32712154
315330421	chr18	32711978	32712190	32711999	32712165	MAPRE2	NR_046177	6	7	6	+	32711996	32712154
315450023	chr18	32720208	32720366	32720229	32720343	MAPRE2	NR_046177	6	7	7	+	32720259	32723432

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_001123066	1	15	2	+	44039687	44039836
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_001123066	1	15	3	+	44049225	44049311
312964666	chr17	44051718	44051921	44051738	44051899	MAPT	NM_001123066	1	15	4	+	44051751	44051837
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_001123066	1	15	5	+	44055741	44055806
312924552	chr17	44060972	44061106	44060997	44061085	MAPT	NM_001123066	1	15	6	+	44060544	44061296
312929488	chr17	44061061	44061251	44061080	44061232	MAPT	NM_001123066	1	15	6	+	44060544	44061296
312934620	chr17	44061208	44061427	44061230	44061405	MAPT	NM_001123066	1	15	6	+	44060544	44061296
312937973	chr17	44060518	44060685	44060536	44060668	MAPT	NM_001123066	1	15	6	+	44060544	44061296
312942565	chr17	44060636	44060845	44060653	44060828	MAPT	NM_001123066	1	15	6	+	44060544	44061296
312943826	chr17	44060809	44061018	44060829	44060998	MAPT	NM_001123066	1	15	6	+	44060544	44061296
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_001123066	1	15	7	+	44064406	44064461
313354423	chr17	44067080	44067295	44067108	44067271	MAPT	NM_001123066	1	15	8	+	44067244	44067441
313372709	chr17	44067249	44067471	44067272	44067446	MAPT	NM_001123066	1	15	8	+	44067244	44067441
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_001123066	1	15	9	+	44068826	44068952
313422808	chr17	44071214	44071419	44071234	44071395	MAPT	NM_001123066	1	15	10	+	44071290	44071343
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_001123066	1	15	11	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_001123066	1	15	11	+	44073765	44074030
314160066	chr17	44087640	44087822	44087661	44087796	MAPT	NM_001123066	1	15	12	+	44087676	44087768
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_001123066	1	15	13	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_001123066	1	15	14	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_001123066	1	15	15	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_001123066	1	15	15	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_001123067	2	11	2	+	44039687	44039836
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_001123067	2	11	3	+	44049225	44049311
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_001123067	2	11	4	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_001123067	2	11	5	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_001123067	2	11	6	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_001123067	2	11	7	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_001123067	2	11	7	+	44073765	44074030
314160066	chr17	44087640	44087822	44087661	44087796	MAPT	NM_001123067	2	11	8	+	44087676	44087768
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_001123067	2	11	9	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_001123067	2	11	10	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_001123067	2	11	11	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_001123067	2	11	11	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_001203251	3	10	2	+	44039687	44039836
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_001203251	3	10	3	+	44049225	44049311
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_001203251	3	10	4	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_001203251	3	10	5	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_001203251	3	10	6	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_001203251	3	10	7	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_001203251	3	10	7	+	44073765	44074030

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_001203251	3	10	8	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_001203251	3	10	9	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_001203251	3	10	10	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_001203251	3	10	10	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_001203252	4	11	2	+	44039687	44039836
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_001203252	4	11	3	+	44049225	44049311
312964666	chr17	44051718	44051921	44051738	44051899	MAPT	NM_001203252	4	11	4	+	44051751	44051837
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_001203252	4	11	5	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_001203252	4	11	6	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_001203252	4	11	7	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_001203252	4	11	8	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_001203252	4	11	8	+	44073765	44074030
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_001203252	4	11	9	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_001203252	4	11	10	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_001203252	4	11	11	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_001203252	4	11	11	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_005910	5	12	2	+	44039687	44039836
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_005910	5	12	3	+	44049225	44049311
312964666	chr17	44051718	44051921	44051738	44051899	MAPT	NM_005910	5	12	4	+	44051751	44051837
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_005910	5	12	5	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_005910	5	12	6	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_005910	5	12	7	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_005910	5	12	8	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_005910	5	12	8	+	44073765	44074030
314160066	chr17	44087640	44087822	44087661	44087796	MAPT	NM_005910	5	12	9	+	44087676	44087768
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_005910	5	12	10	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_005910	5	12	11	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_005910	5	12	12	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_005910	5	12	12	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_016834	6	10	2	+	44039687	44039836
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_016834	6	10	3	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_016834	6	10	4	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_016834	6	10	5	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_016834	6	10	6	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_016834	6	10	6	+	44073765	44074030
314160066	chr17	44087640	44087822	44087661	44087796	MAPT	NM_016834	6	10	7	+	44087676	44087768
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_016834	6	10	8	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_016834	6	10	9	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_016834	6	10	10	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_016834	6	10	10	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_016835	7	14	2	+	44039687	44039836

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312731535	chr17	44049150	44049373	44049171	44049354	MAPT	NM_016835	7	14	3	+	44049225	44049311
312964666	chr17	44051718	44051921	44051738	44051899	MAPT	NM_016835	7	14	4	+	44051751	44051837
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_016835	7	14	5	+	44055741	44055806
312924552	chr17	44060972	44061106	44060997	44061085	MAPT	NM_016835	7	14	6	+	44060544	44061296
312929488	chr17	44061061	44061251	44061080	44061232	MAPT	NM_016835	7	14	6	+	44060544	44061296
312934620	chr17	44061208	44061427	44061230	44061405	MAPT	NM_016835	7	14	6	+	44060544	44061296
312937973	chr17	44060518	44060685	44060536	44060668	MAPT	NM_016835	7	14	6	+	44060544	44061296
312942565	chr17	44060636	44060845	44060653	44060828	MAPT	NM_016835	7	14	6	+	44060544	44061296
312943826	chr17	44060809	44061018	44060829	44060998	MAPT	NM_016835	7	14	6	+	44060544	44061296
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_016835	7	14	7	+	44064406	44064461
313354423	chr17	44067080	44067295	44067108	44067271	MAPT	NM_016835	7	14	8	+	44067244	44067441
313372709	chr17	44067249	44067471	44067272	44067446	MAPT	NM_016835	7	14	8	+	44067244	44067441
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_016835	7	14	9	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_016835	7	14	10	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_016835	7	14	10	+	44073765	44074030
314160066	chr17	44087640	44087822	44087661	44087796	MAPT	NM_016835	7	14	11	+	44087676	44087768
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_016835	7	14	12	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_016835	7	14	13	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_016835	7	14	14	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_016835	7	14	14	+	44101322	44105699
313402560	chr17	44039672	44039883	44039696	44039863	MAPT	NM_016841	8	9	2	+	44039687	44039836
314875183	chr17	44055610	44055833	44055637	44055812	MAPT	NM_016841	8	9	3	+	44055741	44055806
314004640	chr17	44064288	44064506	44064313	44064483	MAPT	NM_016841	8	9	4	+	44064406	44064461
314504319	chr17	44068769	44068992	44068791	44068965	MAPT	NM_016841	8	9	5	+	44068826	44068952
313518207	chr17	44073727	44073933	44073747	44073915	MAPT	NM_016841	8	9	6	+	44073765	44074030
313525070	chr17	44073893	44074107	44073913	44074089	MAPT	NM_016841	8	9	6	+	44073765	44074030
314010204	chr17	44091495	44091716	44091521	44091696	MAPT	NM_016841	8	9	7	+	44091609	44091690
313156360	chr17	44095919	44096125	44095945	44096105	MAPT	NM_016841	8	9	8	+	44095984	44096096
313190837	chr17	44101268	44101477	44101289	44101455	MAPT	NM_016841	8	9	9	+	44101322	44105699
313204485	chr17	44101430	44101617	44101453	44101596	MAPT	NM_016841	8	9	9	+	44101322	44105699
313034049	chr16	89985742	89985941	89985760	89985924	MC1R	NM_002386	1	1	1	+	89984287	89987385
313038759	chr16	89985907	89986119	89985924	89986100	MC1R	NM_002386	1	1	1	+	89984287	89987385
313047378	chr16	89986082	89986297	89986101	89986278	MC1R	NM_002386	1	1	1	+	89984287	89987385
314720259	chr16	89985570	89985793	89985590	89985772	MC1R	NM_002386	1	1	1	+	89984287	89987385
314723961	chr16	89986245	89986419	89986266	89986397	MC1R	NM_002386	1	1	1	+	89984287	89987385
314727212	chr16	89986375	89986547	89986395	89986524	MC1R	NM_002386	1	1	1	+	89984287	89987385
314733993	chr16	89986490	89986681	89986518	89986657	MC1R	NM_002386	1	1	1	+	89984287	89987385
312729176	chrX	153297626	153297850	153297649	153297828	MECP2	NM_001110792	1	3	2	-	153297658	153298008
312731126	chrX	153297760	153297964	153297778	153297937	MECP2	NM_001110792	1	3	2	-	153297658	153298008
312742730	chrX	153297909	153298053	153297938	153298027	MECP2	NM_001110792	1	3	2	-	153297658	153298008
313749001	chrX	153295717	153295896	153295742	153295874	MECP2	NM_001110792	1	3	3	-	153295686	153296901

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313756595	chrX	153295852	153296047	153295873	153296024	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313763388	chrX	153295968	153296174	153295989	153296153	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313765729	chrX	153296100	153296303	153296117	153296284	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313791416	chrX	153296790	153296932	153296811	153296907	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313801236	chrX	153296259	153296424	153296283	153296402	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313806252	chrX	153296383	153296552	153296403	153296530	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313814965	chrX	153296476	153296667	153296497	153296646	MECP2	NM_001110792	1	3	3	-	153295686	153296901
313824392	chrX	153296625	153296835	153296646	153296810	MECP2	NM_001110792	1	3	3	-	153295686	153296901
314887625	chrX	153357475	153357693	153357496	153357672	MECP2	NM_004992	2	4	2	-	153357642	153357765
312729176	chrX	153297626	153297850	153297649	153297828	MECP2	NM_004992	2	4	3	-	153297658	153298008
312731126	chrX	153297760	153297964	153297778	153297937	MECP2	NM_004992	2	4	3	-	153297658	153298008
312742730	chrX	153297909	153298053	153297938	153298027	MECP2	NM_004992	2	4	3	-	153297658	153298008
313749001	chrX	153295717	153295896	153295742	153295874	MECP2	NM_004992	2	4	4	-	153287264	153296901
313756595	chrX	153295852	153296047	153295873	153296024	MECP2	NM_004992	2	4	4	-	153287264	153296901
313763388	chrX	153295968	153296174	153295989	153296153	MECP2	NM_004992	2	4	4	-	153287264	153296901
313765729	chrX	153296100	153296303	153296117	153296284	MECP2	NM_004992	2	4	4	-	153287264	153296901
313791416	chrX	153296790	153296932	153296811	153296907	MECP2	NM_004992	2	4	4	-	153287264	153296901
313801236	chrX	153296259	153296424	153296283	153296402	MECP2	NM_004992	2	4	4	-	153287264	153296901
313806252	chrX	153296383	153296552	153296403	153296530	MECP2	NM_004992	2	4	4	-	153287264	153296901
313814965	chrX	153296476	153296667	153296497	153296646	MECP2	NM_004992	2	4	4	-	153287264	153296901
313824392	chrX	153296625	153296835	153296646	153296810	MECP2	NM_004992	2	4	4	-	153287264	153296901
292121619	chrX	70338535	70338731	70338553	70338711	MED12	NM_005120	1	45	1	+	70338406	70338703
291688986	chrX	70339193	70339374	70339215	70339347	MED12	NM_005120	1	45	2	+	70339223	70339327
292913808	chrX	70339546	70339755	70339570	70339733	MED12	NM_005120	1	45	3	+	70339536	70339727
313626710	chrX	70339704	70339892	70339725	70339866	MED12	NM_005120	1	45	3	+	70339536	70339727
315511019	chrX	70339387	70339597	70339408	70339569	MED12	NM_005120	1	45	3	+	70339536	70339727
293369865	chrX	70339842	70340050	70339867	70340025	MED12	NM_005120	1	45	4	+	70339864	70340020
313626710	chrX	70339704	70339892	70339725	70339866	MED12	NM_005120	1	45	4	+	70339864	70340020
290774660	chrX	70340753	70340884	70340779	70340857	MED12	NM_005120	1	45	5	+	70340821	70341002
290781760	chrX	70340834	70341055	70340858	70341030	MED12	NM_005120	1	45	5	+	70340821	70341002
289648372	chrX	70341093	70341317	70341119	70341294	MED12	NM_005120	1	45	6	+	70341177	70341287
290517850	chrX	70341322	70341544	70341348	70341518	MED12	NM_005120	1	45	7	+	70341412	70341666
290529982	chrX	70341497	70341714	70341519	70341689	MED12	NM_005120	1	45	7	+	70341412	70341666
291963135	chrX	70342003	70342227	70342026	70342205	MED12	NM_005120	1	45	8	+	70342050	70342196
291791288	chrX	70342299	70342513	70342321	70342486	MED12	NM_005120	1	45	9	+	70342358	70342457
314007323	chrX	70342405	70342620	70342425	70342594	MED12	NM_005120	1	45	9	+	70342358	70342457
292729123	chrX	70342571	70342793	70342595	70342765	MED12	NM_005120	1	45	10	+	70342588	70342724
314007323	chrX	70342405	70342620	70342425	70342594	MED12	NM_005120	1	45	10	+	70342588	70342724
291355444	chrX	70342896	70343112	70342917	70343085	MED12	NM_005120	1	45	11	+	70342945	70343076
289986298	chrX	70343384	70343603	70343408	70343578	MED12	NM_005120	1	45	12	+	70343444	70343570
291170022	chrX	70343874	70344098	70343896	70344074	MED12	NM_005120	1	45	13	+	70344009	70344238

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
291202266	chrX	70344049	70344268	70344075	70344245	MED12	NM_005120	1	45	13	+	70344009	70344238
289311762	chrX	70344505	70344723	70344527	70344703	MED12	NM_005120	1	45	14	+	70344614	70344694
313252895	chrX	70344638	70344858	70344662	70344838	MED12	NM_005120	1	45	14	+	70344614	70344694
289538718	chrX	70344814	70345037	70344839	70345011	MED12	NM_005120	1	45	15	+	70344826	70344996
313252895	chrX	70344638	70344858	70344662	70344838	MED12	NM_005120	1	45	15	+	70344826	70344996
290748951	chrX	70345162	70345375	70345183	70345350	MED12	NM_005120	1	45	16	+	70345201	70345345
290213833	chrX	70345420	70345641	70345441	70345617	MED12	NM_005120	1	45	17	+	70345513	70345563
289833770	chrX	70345822	70346044	70345845	70346024	MED12	NM_005120	1	45	18	+	70345886	70346004
290851747	chrX	70346147	70346360	70346170	70346339	MED12	NM_005120	1	45	19	+	70346191	70346334
289530665	chrX	70346803	70347022	70346825	70346998	MED12	NM_005120	1	45	20	+	70346819	70346982
314768712	chrX	70346648	70346849	70346675	70346824	MED12	NM_005120	1	45	20	+	70346819	70346982
292301886	chrX	70347140	70347347	70347160	70347327	MED12	NM_005120	1	45	21	+	70347186	70347317
289756287	chrX	70347634	70347858	70347658	70347837	MED12	NM_005120	1	45	22	+	70347743	70347970
289801314	chrX	70347814	70347998	70347838	70347977	MED12	NM_005120	1	45	22	+	70347743	70347970
291569419	chrX	70348111	70348329	70348135	70348309	MED12	NM_005120	1	45	23	+	70348146	70348290
290402164	chrX	70348406	70348628	70348426	70348601	MED12	NM_005120	1	45	24	+	70348448	70348568
290160439	chrX	70348898	70349103	70348922	70349078	MED12	NM_005120	1	45	25	+	70348964	70349065
290663714	chrX	70349114	70349321	70349134	70349298	MED12	NM_005120	1	45	26	+	70349166	70349279
289306128	chrX	70349417	70349587	70349439	70349563	MED12	NM_005120	1	45	27	+	70349530	70349705
289320371	chrX	70349542	70349739	70349564	70349716	MED12	NM_005120	1	45	27	+	70349530	70349705
290271180	chrX	70349818	70350013	70349840	70349991	MED12	NM_005120	1	45	28	+	70349885	70350064
290297715	chrX	70349972	70350131	70349992	70350105	MED12	NM_005120	1	45	28	+	70349885	70350064
290246616	chrX	70351303	70351524	70351328	70351503	MED12	NM_005120	1	45	29	+	70351400	70351471
291811929	chrX	70351864	70352086	70351887	70352061	MED12	NM_005120	1	45	30	+	70351923	70352056
290588157	chrX	70352200	70352415	70352221	70352395	MED12	NM_005120	1	45	31	+	70352227	70352388
289361657	chrX	70352715	70352870	70352735	70352847	MED12	NM_005120	1	45	32	+	70352695	70352806
314594164	chrX	70352538	70352758	70352566	70352734	MED12	NM_005120	1	45	32	+	70352695	70352806
291779886	chrX	70352891	70353103	70352919	70353080	MED12	NM_005120	1	45	33	+	70352973	70353062
289871915	chrX	70354144	70354365	70354166	70354341	MED12	NM_005120	1	45	34	+	70354207	70354316
289258300	chrX	70354518	70354741	70354546	70354718	MED12	NM_005120	1	45	35	+	70354563	70354698
290857425	chrX	70354877	70355091	70354898	70355069	MED12	NM_005120	1	45	36	+	70354942	70355103
290883853	chrX	70355046	70355174	70355070	70355153	MED12	NM_005120	1	45	36	+	70354942	70355103
292955758	chrX	70356066	70356289	70356093	70356269	MED12	NM_005120	1	45	37	+	70356131	70356505
292970486	chrX	70356213	70356426	70356233	70356406	MED12	NM_005120	1	45	37	+	70356131	70356505
292984093	chrX	70356370	70356564	70356393	70356544	MED12	NM_005120	1	45	37	+	70356131	70356505
291343086	chrX	70356689	70356913	70356710	70356892	MED12	NM_005120	1	45	38	+	70356729	70356879
292982255	chrX	70356960	70357184	70356983	70357162	MED12	NM_005120	1	45	39	+	70357037	70357233
293001527	chrX	70357139	70357337	70357163	70357315	MED12	NM_005120	1	45	39	+	70357037	70357233
291894593	chrX	70357299	70357519	70357321	70357496	MED12	NM_005120	1	45	40	+	70357408	70357485
290795186	chrX	70357492	70357715	70357513	70357688	MED12	NM_005120	1	45	41	+	70357576	70357793
290818304	chrX	70357669	70357825	70357689	70357799	MED12	NM_005120	1	45	41	+	70357576	70357793

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289543418	chrX	70360361	70360585	70360388	70360564	MED12	NM_005120	1	45	42	+	70360485	70360707
289558279	chrX	70360515	70360737	70360543	70360716	MED12	NM_005120	1	45	42	+	70360485	70360707
290674952	chrX	70361045	70361269	70361072	70361252	MED12	NM_005120	1	45	43	+	70361080	70361220
292010765	chrX	70361678	70361900	70361704	70361874	MED12	NM_005120	1	45	44	+	70361733	70361814
293381127	chrX	70361913	70362132	70361934	70362107	MED12	NM_005120	1	45	45	+	70362025	70362304
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_000244	1	10	2	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_000244	1	10	2	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_000244	1	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_000244	1	10	2	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_000244	1	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_000244	1	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_000244	1	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_000244	1	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_000244	1	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_000244	1	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_000244	1	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_000244	1	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_000244	1	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_000244	1	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_000244	1	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_000244	1	10	9	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_000244	1	10	10	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_000244	1	10	10	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_000244	1	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_000244	1	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130799	2	10	2	-	64577137	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130799	2	10	2	-	64577137	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130799	2	10	2	-	64577137	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130799	2	10	2	-	64577137	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130799	2	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130799	2	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130799	2	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130799	2	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130799	2	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130799	2	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130799	2	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130799	2	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130799	2	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130799	2	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130799	2	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130799	2	10	9	-	64572506	64572670

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130799	2	10	10	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130799	2	10	10	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130799	2	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130799	2	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130800	3	10	2	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130800	3	10	2	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130800	3	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130800	3	10	2	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130800	3	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130800	3	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130800	3	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130800	3	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130800	3	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130800	3	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130800	3	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130800	3	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130800	3	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130800	3	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130800	3	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130800	3	10	9	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130800	3	10	10	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130800	3	10	10	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130800	3	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130800	3	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130801	4	10	2	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130801	4	10	2	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130801	4	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130801	4	10	2	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130801	4	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130801	4	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130801	4	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130801	4	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130801	4	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130801	4	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130801	4	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130801	4	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130801	4	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130801	4	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130801	4	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130801	4	10	9	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130801	4	10	10	-	64570986	64572288

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130801	4	10	10	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130801	4	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130801	4	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130802	5	10	2	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130802	5	10	2	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130802	5	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130802	5	10	2	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130802	5	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130802	5	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130802	5	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130802	5	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130802	5	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130802	5	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130802	5	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130802	5	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130802	5	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130802	5	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130802	5	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130802	5	10	9	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130802	5	10	10	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130802	5	10	10	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130802	5	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130802	5	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130803	6	10	2	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130803	6	10	2	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130803	6	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130803	6	10	2	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130803	6	10	3	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130803	6	10	3	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130803	6	10	4	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130803	6	10	5	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130803	6	10	6	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130803	6	10	6	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130803	6	10	7	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130803	6	10	7	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130803	6	10	8	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130803	6	10	8	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130803	6	10	9	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130803	6	10	9	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130803	6	10	10	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130803	6	10	10	-	64570986	64572288

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130803	6	10	10	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130803	6	10	10	-	64570986	64572288
231175888	chr11	64577083	64577273	64577107	64577251	MEN1	NM_130804	7	11	3	-	64577122	64577604
231197582	chr11	64577217	64577438	64577239	64577420	MEN1	NM_130804	7	11	3	-	64577122	64577604
231207483	chr11	64577399	64577566	64577418	64577548	MEN1	NM_130804	7	11	3	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130804	7	11	3	-	64577122	64577604
233659805	chr11	64575278	64575477	64575299	64575456	MEN1	NM_130804	7	11	4	-	64575363	64575571
233661775	chr11	64575427	64575608	64575447	64575584	MEN1	NM_130804	7	11	4	-	64575363	64575571
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130804	7	11	5	-	64575024	64575152
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130804	7	11	6	-	64574651	64574691
231999899	chr11	64574530	64574723	64574552	64574700	MEN1	NM_130804	7	11	7	-	64574483	64574570
232652555	chr11	64574384	64574600	64574407	64574577	MEN1	NM_130804	7	11	7	-	64574483	64574570
233055134	chr11	64573635	64573817	64573656	64573793	MEN1	NM_130804	7	11	8	-	64573704	64573840
233058664	chr11	64573772	64573958	64573794	64573937	MEN1	NM_130804	7	11	8	-	64573704	64573840
231863204	chr11	64573000	64573222	64573022	64573196	MEN1	NM_130804	7	11	9	-	64573107	64573242
231871856	chr11	64573174	64573362	64573197	64573343	MEN1	NM_130804	7	11	9	-	64573107	64573242
233521715	chr11	64572427	64572624	64572449	64572604	MEN1	NM_130804	7	11	10	-	64572506	64572670
233524291	chr11	64572582	64572794	64572602	64572770	MEN1	NM_130804	7	11	10	-	64572506	64572670
233335526	chr11	64571779	64571933	64571797	64571913	MEN1	NM_130804	7	11	11	-	64570986	64572288
234682094	chr11	64571896	64572119	64571914	64572101	MEN1	NM_130804	7	11	11	-	64570986	64572288
234683263	chr11	64572062	64572273	64572079	64572254	MEN1	NM_130804	7	11	11	-	64570986	64572288
234684087	chr11	64572165	64572327	64572184	64572307	MEN1	NM_130804	7	11	11	-	64570986	64572288
314046002	chr2	112656272	112656487	112656291	112656468	MERTK	NM_006343	1	19	1	+	112656191	112656373
314264974	chr2	112686544	112686741	112686572	112686720	MERTK	NM_006343	1	19	2	+	112686697	112687117
314280444	chr2	112686697	112686903	112686720	112686881	MERTK	NM_006343	1	19	2	+	112686697	112687117
314291900	chr2	112686858	112687045	112686879	112687021	MERTK	NM_006343	1	19	2	+	112686697	112687117
314307122	chr2	112686989	112687127	112687018	112687101	MERTK	NM_006343	1	19	2	+	112686697	112687117
313055723	chr2	112702452	112702672	112702480	112702651	MERTK	NM_006343	1	19	3	+	112702537	112702637
314925760	chr2	112704871	112705007	112704899	112704985	MERTK	NM_006343	1	19	4	+	112704971	112705144
314938486	chr2	112704965	112705180	112704986	112705152	MERTK	NM_006343	1	19	4	+	112704971	112705144
314483962	chr2	112722727	112722896	112722749	112722876	MERTK	NM_006343	1	19	5	+	112722768	112722854
313287347	chr2	112725641	112725855	112725665	112725834	MERTK	NM_006343	1	19	6	+	112725714	112725829
313004422	chr2	112732702	112732917	112732724	112732891	MERTK	NM_006343	1	19	7	+	112732866	112733049
313034065	chr2	112732871	112733079	112732892	112733054	MERTK	NM_006343	1	19	7	+	112732866	112733049
313674351	chr2	112740378	112740602	112740406	112740575	MERTK	NM_006343	1	19	8	+	112740419	112740570
313674349	chr2	112751791	112752015	112751818	112751989	MERTK	NM_006343	1	19	9	+	112751828	112751981
313456269	chr2	112754866	112755087	112754891	112755063	MERTK	NM_006343	1	19	10	+	112754900	112755053
314313811	chr2	112758659	112758845	112758684	112758818	MERTK	NM_006343	1	19	11	+	112758778	112758863
314318895	chr2	112758791	112758960	112758819	112758932	MERTK	NM_006343	1	19	11	+	112758778	112758863
314089952	chr2	112760607	112760817	112760635	112760789	MERTK	NM_006343	1	19	12	+	112760669	112760764
312955485	chr2	112761373	112761597	112761397	112761571	MERTK	NM_006343	1	19	13	+	112761481	112761561

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313930534	chr2	112765861	112766077	112765885	112766057	MERTK	NM_006343	1	19	14	+	112765960	112766052
313874326	chr2	112767467	112767691	112767493	112767667	MERTK	NM_006343	1	19	15	+	112767525	112767643
315238274	chr2	112776922	112777132	112776943	112777111	MERTK	NM_006343	1	19	16	+	112776990	112777099
315407654	chr2	112778964	112779185	112778984	112779164	MERTK	NM_006343	1	19	17	+	112778999	112779158
314375962	chr2	112779787	112780006	112779808	112779983	MERTK	NM_006343	1	19	18	+	112779835	112779971
314341314	chr2	112785859	112786016	112785882	112785991	MERTK	NM_006343	1	19	19	+	112785928	112786945
314359016	chr2	112785971	112786164	112785992	112786140	MERTK	NM_006343	1	19	19	+	112785928	112786945
314370964	chr2	112786120	112786321	112786141	112786300	MERTK	NM_006343	1	19	19	+	112785928	112786945
314389211	chr2	112786280	112786486	112786301	112786458	MERTK	NM_006343	1	19	19	+	112785928	112786945
313027932	chr1	12049070	12049294	12049097	12049266	MFN2	NM_001127660	1	18	2	+	12049222	12049400
313065701	chr1	12049244	12049468	12049267	12049440	MFN2	NM_001127660	1	18	2	+	12049222	12049400
313272458	chr1	12052578	12052793	12052599	12052770	MFN2	NM_001127660	1	18	3	+	12052612	12052747
314318081	chr1	12056136	12056268	12056156	12056246	MFN2	NM_001127660	1	18	4	+	12056213	12056375
314327943	chr1	12056224	12056441	12056245	12056420	MFN2	NM_001127660	1	18	4	+	12056213	12056375
314990984	chr1	12057314	12057536	12057337	12057514	MFN2	NM_001127660	1	18	5	+	12057354	12057478
313266571	chr1	12058650	12058855	12058673	12058834	MFN2	NM_001127660	1	18	6	+	12058827	12058935
313293684	chr1	12058813	12059037	12058835	12059017	MFN2	NM_001127660	1	18	6	+	12058827	12058935
314485266	chr1	12059013	12059184	12059033	12059162	MFN2	NM_001127660	1	18	7	+	12059045	12059152
314683298	chr1	12061363	12061575	12061387	12061554	MFN2	NM_001127660	1	18	8	+	12061458	12061611
314696583	chr1	12061534	12061676	12061555	12061654	MFN2	NM_001127660	1	18	8	+	12061458	12061611
315316343	chr1	12061721	12061921	12061743	12061898	MFN2	NM_001127660	1	18	9	+	12061826	12061893
314262552	chr1	12061972	12062189	12061993	12062167	MFN2	NM_001127660	1	18	10	+	12062039	12062160
313552987	chr1	12063986	12064202	12064007	12064180	MFN2	NM_001127660	1	18	11	+	12064049	12064175
313733448	chr1	12064476	12064698	12064498	12064677	MFN2	NM_001127660	1	18	12	+	12064566	12064670
313080043	chr1	12064825	12065048	12064848	12065027	MFN2	NM_001127660	1	18	13	+	12064882	12064984
313443411	chr1	12065683	12065874	12065704	12065851	MFN2	NM_001127660	1	18	14	+	12065768	12065988
313471617	chr1	12065829	12066015	12065852	12065993	MFN2	NM_001127660	1	18	14	+	12065768	12065988
315469198	chr1	12066564	12066776	12066584	12066756	MFN2	NM_001127660	1	18	15	+	12066595	12066750
315038427	chr1	12066957	12067178	12066981	12067154	MFN2	NM_001127660	1	18	16	+	12067110	12067306
315056599	chr1	12067133	12067357	12067154	12067336	MFN2	NM_001127660	1	18	16	+	12067110	12067306
312932826	chr1	12069619	12069822	12069640	12069802	MFN2	NM_001127660	1	18	17	+	12069649	12069783
313658757	chr1	12071491	12071690	12071518	12071670	MFN2	NM_001127660	1	18	18	+	12071553	12073572
313027932	chr1	12049070	12049294	12049097	12049266	MFN2	NM_014874	2	19	3	+	12049222	12049400
313065701	chr1	12049244	12049468	12049267	12049440	MFN2	NM_014874	2	19	3	+	12049222	12049400
313272458	chr1	12052578	12052793	12052599	12052770	MFN2	NM_014874	2	19	4	+	12052612	12052747
314318081	chr1	12056136	12056268	12056156	12056246	MFN2	NM_014874	2	19	5	+	12056213	12056375
314327943	chr1	12056224	12056441	12056245	12056420	MFN2	NM_014874	2	19	5	+	12056213	12056375
314990984	chr1	12057314	12057536	12057337	12057514	MFN2	NM_014874	2	19	6	+	12057354	12057478
313266571	chr1	12058650	12058855	12058673	12058834	MFN2	NM_014874	2	19	7	+	12058827	12058935
313293684	chr1	12058813	12059037	12058835	12059017	MFN2	NM_014874	2	19	7	+	12058827	12058935
314485266	chr1	12059013	12059184	12059033	12059162	MFN2	NM_014874	2	19	8	+	12059045	12059152

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314683298	chr1	12061363	12061575	12061387	12061554	MFN2	NM_014874	2	19	9	+	12061458	12061611
314696583	chr1	12061534	12061676	12061555	12061654	MFN2	NM_014874	2	19	9	+	12061458	12061611
315316343	chr1	12061721	12061921	12061743	12061898	MFN2	NM_014874	2	19	10	+	12061826	12061893
314262552	chr1	12061972	12062189	12061993	12062167	MFN2	NM_014874	2	19	11	+	12062039	12062160
313552987	chr1	12063986	12064202	12064007	12064180	MFN2	NM_014874	2	19	12	+	12064049	12064175
313733448	chr1	12064476	12064698	12064498	12064677	MFN2	NM_014874	2	19	13	+	12064566	12064670
313080043	chr1	12064825	12065048	12064848	12065027	MFN2	NM_014874	2	19	14	+	12064882	12064984
313443411	chr1	12065683	12065874	12065704	12065851	MFN2	NM_014874	2	19	15	+	12065768	12065988
313471617	chr1	12065829	12066015	12065852	12065993	MFN2	NM_014874	2	19	15	+	12065768	12065988
315469198	chr1	12066564	12066776	12066584	12066756	MFN2	NM_014874	2	19	16	+	12066595	12066750
315038427	chr1	12066957	12067178	12066981	12067154	MFN2	NM_014874	2	19	17	+	12067110	12067306
315056599	chr1	12067133	12067357	12067154	12067336	MFN2	NM_014874	2	19	17	+	12067110	12067306
312932826	chr1	12069619	12069822	12069640	12069802	MFN2	NM_014874	2	19	18	+	12069649	12069783
313658757	chr1	12071491	12071690	12071518	12071670	MFN2	NM_014874	2	19	19	+	12071553	12073572
234691924	chr3	37034983	37035203	37035003	37035182	MLH1	NM_000249	1	19	1	+	37034841	37035154
233154267	chr3	37038020	37038233	37038045	37038208	MLH1	NM_000249	1	19	2	+	37038110	37038200
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_000249	1	19	3	+	37042446	37042544
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_000249	1	19	3	+	37042446	37042544
233506067	chr3	37045815	37046039	37045837	37046013	MLH1	NM_000249	1	19	4	+	37045892	37045965
233175804	chr3	37048414	37048592	37048441	37048564	MLH1	NM_000249	1	19	5	+	37048482	37048554
233350901	chr3	37050206	37050427	37050232	37050404	MLH1	NM_000249	1	19	6	+	37050305	37050396
231631673	chr3	37053247	37053383	37053269	37053358	MLH1	NM_000249	1	19	7	+	37053311	37053353
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_000249	1	19	8	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_000249	1	19	8	+	37053502	37053590
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_000249	1	19	9	+	37055923	37056035
232268195	chr3	37055922	37056067	37055950	37056040	MLH1	NM_000249	1	19	9	+	37055923	37056035
232109369	chr3	37058897	37059117	37058923	37059095	MLH1	NM_000249	1	19	10	+	37058997	37059090
233194742	chr3	37061696	37061872	37061720	37061850	MLH1	NM_000249	1	19	11	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_000249	1	19	11	+	37061801	37061954
233218426	chr3	37067005	37067206	37067032	37067181	MLH1	NM_000249	1	19	12	+	37067128	37067498
233218701	chr3	37067159	37067359	37067182	37067334	MLH1	NM_000249	1	19	12	+	37067128	37067498
233225397	chr3	37067314	37067529	37067335	37067504	MLH1	NM_000249	1	19	12	+	37067128	37067498
234245975	chr3	37070156	37070316	37070177	37070290	MLH1	NM_000249	1	19	13	+	37070275	37070423
234252676	chr3	37070268	37070474	37070291	37070454	MLH1	NM_000249	1	19	13	+	37070275	37070423
232047370	chr3	37081597	37081820	37081618	37081797	MLH1	NM_000249	1	19	14	+	37081677	37081785
234336842	chr3	37083662	37083886	37083689	37083858	MLH1	NM_000249	1	19	15	+	37083759	37083822
232901699	chr3	37088902	37089118	37088928	37089092	MLH1	NM_000249	1	19	16	+	37089010	37089174
232951907	chr3	37089070	37089204	37089093	37089176	MLH1	NM_000249	1	19	16	+	37089010	37089174
234600799	chr3	37089924	37090135	37089946	37090108	MLH1	NM_000249	1	19	17	+	37090008	37090100
234741715	chr3	37090272	37090425	37090300	37090397	MLH1	NM_000249	1	19	18	+	37090395	37090508
234742951	chr3	37090372	37090566	37090398	37090539	MLH1	NM_000249	1	19	18	+	37090395	37090508

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233386372	chr3	37091857	37092031	37091884	37092008	MLH1	NM_000249	1	19	19	+	37091977	37092337
233393018	chr3	37091988	37092177	37092009	37092150	MLH1	NM_000249	1	19	19	+	37091977	37092337
233154267	chr3	37038020	37038233	37038045	37038208	MLH1	NM_001167617	2	19	2	+	37038110	37038200
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167617	2	19	3	+	37042446	37042539
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167617	2	19	3	+	37042446	37042539
233506067	chr3	37045815	37046039	37045837	37046013	MLH1	NM_001167617	2	19	4	+	37045892	37045965
233175804	chr3	37048414	37048592	37048441	37048564	MLH1	NM_001167617	2	19	5	+	37048482	37048554
233350901	chr3	37050206	37050427	37050232	37050404	MLH1	NM_001167617	2	19	6	+	37050305	37050396
231631673	chr3	37053247	37053383	37053269	37053358	MLH1	NM_001167617	2	19	7	+	37053311	37053353
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167617	2	19	8	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167617	2	19	8	+	37053502	37053590
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167617	2	19	9	+	37055923	37056035
232268195	chr3	37055922	37056067	37055950	37056040	MLH1	NM_001167617	2	19	9	+	37055923	37056035
232109369	chr3	37058897	37059117	37058923	37059095	MLH1	NM_001167617	2	19	10	+	37058997	37059090
233194742	chr3	37061696	37061872	37061720	37061850	MLH1	NM_001167617	2	19	11	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167617	2	19	11	+	37061801	37061954
233218426	chr3	37067005	37067206	37067032	37067181	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233218701	chr3	37067159	37067359	37067182	37067334	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233225397	chr3	37067314	37067529	37067335	37067504	MLH1	NM_001167617	2	19	12	+	37067128	37067498
234245975	chr3	37070156	37070316	37070177	37070290	MLH1	NM_001167617	2	19	13	+	37070275	37070423
234252676	chr3	37070268	37070474	37070291	37070454	MLH1	NM_001167617	2	19	13	+	37070275	37070423
232047370	chr3	37081597	37081820	37081618	37081797	MLH1	NM_001167617	2	19	14	+	37081677	37081785
234336842	chr3	37083662	37083886	37083689	37083858	MLH1	NM_001167617	2	19	15	+	37083759	37083822
232901699	chr3	37088902	37089118	37088928	37089092	MLH1	NM_001167617	2	19	16	+	37089010	37089174
232951907	chr3	37089070	37089204	37089093	37089176	MLH1	NM_001167617	2	19	16	+	37089010	37089174
234600799	chr3	37089924	37090135	37089946	37090108	MLH1	NM_001167617	2	19	17	+	37090008	37090100
234741715	chr3	37090272	37090425	37090300	37090397	MLH1	NM_001167617	2	19	18	+	37090395	37090508
234742951	chr3	37090372	37090566	37090398	37090539	MLH1	NM_001167617	2	19	18	+	37090395	37090508
233386372	chr3	37091857	37092031	37091884	37092008	MLH1	NM_001167617	2	19	19	+	37091977	37092337
233393018	chr3	37091988	37092177	37092009	37092150	MLH1	NM_001167617	2	19	19	+	37091977	37092337
233154267	chr3	37038020	37038233	37038045	37038208	MLH1	NM_001167618	3	19	2	+	37038115	37038200
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167618	3	19	3	+	37042446	37042544
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167618	3	19	3	+	37042446	37042544
233506067	chr3	37045815	37046039	37045837	37046013	MLH1	NM_001167618	3	19	4	+	37045892	37045965
233175804	chr3	37048414	37048592	37048441	37048564	MLH1	NM_001167618	3	19	5	+	37048482	37048554
233350901	chr3	37050206	37050427	37050232	37050404	MLH1	NM_001167618	3	19	6	+	37050305	37050396
231631673	chr3	37053247	37053383	37053269	37053358	MLH1	NM_001167618	3	19	7	+	37053311	37053353
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167618	3	19	8	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167618	3	19	8	+	37053502	37053590
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167618	3	19	9	+	37055923	37056035
232268195	chr3	37055922	37056067	37055950	37056040	MLH1	NM_001167618	3	19	9	+	37055923	37056035

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232109369	chr3	37058897	37059117	37058923	37059095	MLH1	NM_001167618	3	19	10	+	37058997	37059090
233194742	chr3	37061696	37061872	37061720	37061850	MLH1	NM_001167618	3	19	11	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167618	3	19	11	+	37061801	37061954
233218426	chr3	37067005	37067206	37067032	37067181	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233218701	chr3	37067159	37067359	37067182	37067334	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233225397	chr3	37067314	37067529	37067335	37067504	MLH1	NM_001167618	3	19	12	+	37067128	37067498
234245975	chr3	37070156	37070316	37070177	37070290	MLH1	NM_001167618	3	19	13	+	37070275	37070423
234252676	chr3	37070268	37070474	37070291	37070454	MLH1	NM_001167618	3	19	13	+	37070275	37070423
232047370	chr3	37081597	37081820	37081618	37081797	MLH1	NM_001167618	3	19	14	+	37081677	37081785
234336842	chr3	37083662	37083886	37083689	37083858	MLH1	NM_001167618	3	19	15	+	37083759	37083822
232901699	chr3	37088902	37089118	37088928	37089092	MLH1	NM_001167618	3	19	16	+	37089010	37089174
232951907	chr3	37089070	37089204	37089093	37089176	MLH1	NM_001167618	3	19	16	+	37089010	37089174
234600799	chr3	37089924	37090135	37089946	37090108	MLH1	NM_001167618	3	19	17	+	37090008	37090100
234741715	chr3	37090272	37090425	37090300	37090397	MLH1	NM_001167618	3	19	18	+	37090395	37090508
234742951	chr3	37090372	37090566	37090398	37090539	MLH1	NM_001167618	3	19	18	+	37090395	37090508
233386372	chr3	37091857	37092031	37091884	37092008	MLH1	NM_001167618	3	19	19	+	37091977	37092337
233393018	chr3	37091988	37092177	37092009	37092150	MLH1	NM_001167618	3	19	19	+	37091977	37092337
233154267	chr3	37038020	37038233	37038045	37038208	MLH1	NM_001167619	4	18	2	+	37038110	37038200
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167619	4	18	3	+	37042446	37042544
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167619	4	18	3	+	37042446	37042544
233506067	chr3	37045815	37046039	37045837	37046013	MLH1	NM_001167619	4	18	4	+	37045892	37045965
233175804	chr3	37048414	37048592	37048441	37048564	MLH1	NM_001167619	4	18	5	+	37048482	37048554
231631673	chr3	37053247	37053383	37053269	37053358	MLH1	NM_001167619	4	18	6	+	37053311	37053353
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167619	4	18	7	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167619	4	18	7	+	37053502	37053590
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167619	4	18	8	+	37055923	37056035
232268195	chr3	37055922	37056067	37055950	37056040	MLH1	NM_001167619	4	18	8	+	37055923	37056035
232109369	chr3	37058897	37059117	37058923	37059095	MLH1	NM_001167619	4	18	9	+	37058997	37059090
233194742	chr3	37061696	37061872	37061720	37061850	MLH1	NM_001167619	4	18	10	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167619	4	18	10	+	37061801	37061954
233218426	chr3	37067005	37067206	37067032	37067181	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233218701	chr3	37067159	37067359	37067182	37067334	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233225397	chr3	37067314	37067529	37067335	37067504	MLH1	NM_001167619	4	18	11	+	37067128	37067498
234245975	chr3	37070156	37070316	37070177	37070290	MLH1	NM_001167619	4	18	12	+	37070275	37070423
234252676	chr3	37070268	37070474	37070291	37070454	MLH1	NM_001167619	4	18	12	+	37070275	37070423
232047370	chr3	37081597	37081820	37081618	37081797	MLH1	NM_001167619	4	18	13	+	37081677	37081785
234336842	chr3	37083662	37083886	37083689	37083858	MLH1	NM_001167619	4	18	14	+	37083759	37083822
232901699	chr3	37088902	37089118	37088928	37089092	MLH1	NM_001167619	4	18	15	+	37089010	37089174
232951907	chr3	37089070	37089204	37089093	37089176	MLH1	NM_001167619	4	18	15	+	37089010	37089174
234600799	chr3	37089924	37090135	37089946	37090108	MLH1	NM_001167619	4	18	16	+	37090008	37090100
234741715	chr3	37090272	37090425	37090300	37090397	MLH1	NM_001167619	4	18	17	+	37090395	37090508

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234742951	chr3	37090372	37090566	37090398	37090539	MLH1	NM_001167619	4	18	17	+	37090395	37090508
233386372	chr3	37091857	37092031	37091884	37092008	MLH1	NM_001167619	4	18	18	+	37091977	37092337
233393018	chr3	37091988	37092177	37092009	37092150	MLH1	NM_001167619	4	18	18	+	37091977	37092337
315296115	chr4	146560195	146560388	146560222	146560360	MMAA	NM_172250	1	7	2	+	146560227	146560730
315325121	chr4	146560336	146560541	146560361	146560513	MMAA	NM_172250	1	7	2	+	146560227	146560730
315363005	chr4	146560487	146560699	146560513	146560671	MMAA	NM_172250	1	7	2	+	146560227	146560730
315367999	chr4	146560647	146560826	146560672	146560797	MMAA	NM_172250	1	7	2	+	146560227	146560730
313652895	chr4	146563456	146563591	146563487	146563567	MMAA	NM_172250	1	7	3	+	146563515	146563637
313663237	chr4	146563529	146563749	146563557	146563725	MMAA	NM_172250	1	7	3	+	146563515	146563637
314517491	chr4	146567042	146567203	146567066	146567176	MMAA	NM_172250	1	7	4	+	146567138	146567308
314533131	chr4	146567149	146567318	146567177	146567296	MMAA	NM_172250	1	7	4	+	146567138	146567308
314535939	chr4	146567269	146567397	146567297	146567367	MMAA	NM_172250	1	7	4	+	146567138	146567308
314301158	chr4	146572223	146572446	146572243	146572418	MMAA	NM_172250	1	7	5	+	146572214	146572299
312977335	chr4	146575005	146575218	146575030	146575191	MMAA	NM_172250	1	7	6	+	146575146	146575295
312987640	chr4	146575168	146575327	146575192	146575300	MMAA	NM_172250	1	7	6	+	146575146	146575295
314531612	chr4	146576266	146576461	146576293	146576435	MMAA	NM_172250	1	7	7	+	146576299	146581187
314541490	chr4	146576412	146576559	146576436	146576536	MMAA	NM_172250	1	7	7	+	146576299	146581187
314543643	chr4	146576503	146576726	146576527	146576703	MMAA	NM_172250	1	7	7	+	146576299	146581187
314429145	chr12	110011105	110011314	110011123	110011296	MMAB	NM_052845	1	9	1	-	110011152	110011358
312946979	chr12	110009405	110009551	110009432	110009528	MMAB	NM_052845	1	9	2	-	110009454	110009515
312952543	chr12	110006496	110006709	110006517	110006681	MMAB	NM_052845	1	9	3	-	110006575	110006668
314879247	chr12	110002856	110003027	110002876	110002999	MMAB	NM_052845	1	9	4	-	110002924	110002981
315446662	chr12	109999509	109999700	109999530	109999673	MMAB	NM_052845	1	9	5	-	109999585	109999657
313605379	chr12	109999127	109999351	109999152	109999331	MMAB	NM_052845	1	9	6	-	109999225	109999322
313373451	chr12	109998693	109998916	109998713	109998895	MMAB	NM_052845	1	9	7	-	109998845	109998909
313383159	chr12	109998833	109999018	109998853	109998999	MMAB	NM_052845	1	9	7	-	109998845	109998909
314405406	chr12	109996837	109997049	109996858	109997023	MMAB	NM_052845	1	9	8	-	109996901	109996960
312768346	chr12	109994804	109994977	109994825	109994952	MMAB	NM_052845	1	9	9	-	109991521	109994941
314429145	chr12	110011105	110011314	110011123	110011296	MMAB	NR_038118	2	10	1	-	110011152	110011358
312946979	chr12	110009405	110009551	110009432	110009528	MMAB	NR_038118	2	10	2	-	110009454	110009515
312952543	chr12	110006496	110006709	110006517	110006681	MMAB	NR_038118	2	10	3	-	110006575	110006668
314879247	chr12	110002856	110003027	110002876	110002999	MMAB	NR_038118	2	10	4	-	110002924	110002981
315446662	chr12	109999509	109999700	109999530	109999673	MMAB	NR_038118	2	10	5	-	109999585	109999657
313605379	chr12	109999127	109999351	109999152	109999331	MMAB	NR_038118	2	10	6	-	109999225	109999322
313373451	chr12	109998693	109998916	109998713	109998895	MMAB	NR_038118	2	10	8	-	109998845	109998909
313383159	chr12	109998833	109999018	109998853	109998999	MMAB	NR_038118	2	10	8	-	109998845	109998909
314405406	chr12	109996837	109997049	109996858	109997023	MMAB	NR_038118	2	10	9	-	109996901	109996960
312768346	chr12	109994804	109994977	109994825	109994952	MMAB	NR_038118	2	10	10	-	109991521	109994941
314188172	chr1	45965915	45966131	45965937	45966104	MMACHC	NM_015506	1	4	1	+	45965856	45966085
315466772	chr1	45972941	45973153	45972964	45973132	MMACHC	NM_015506	1	4	2	+	45973028	45973222
315485872	chr1	45973091	45973309	45973111	45973287	MMACHC	NM_015506	1	4	2	+	45973028	45973222

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
315313733	chr1	45973729	45973929	45973750	45973907	MMACHC	NM_015506	1	4	3	+	45973884	45974036
315355835	chr1	45973886	45974081	45973908	45974055	MMACHC	NM_015506	1	4	3	+	45973884	45974036
314995455	chr1	45974378	45974602	45974399	45974578	MMACHC	NM_015506	1	4	4	+	45974468	45976739
315020152	chr1	45974558	45974778	45974579	45974755	MMACHC	NM_015506	1	4	4	+	45974468	45976739
315037401	chr1	45974727	45974946	45974747	45974919	MMACHC	NM_015506	1	4	4	+	45974468	45976739
315107214	chr1	161279520	161279741	161279543	161279719	MPZ	NM_000530	1	6	1	-	161279629	161279762
313132054	chr1	161276913	161277132	161276938	161277111	MPZ	NM_000530	1	6	2	-	161277048	161277214
313147120	chr1	161277088	161277244	161277112	161277222	MPZ	NM_000530	1	6	2	-	161277048	161277214
314749361	chr1	161276346	161276564	161276368	161276542	MPZ	NM_000530	1	6	3	-	161276498	161276711
314770829	chr1	161276522	161276740	161276543	161276718	MPZ	NM_000530	1	6	3	-	161276498	161276711
314038850	chr1	161276052	161276275	161276072	161276253	MPZ	NM_000530	1	6	4	-	161276119	161276254
314046814	chr1	161276231	161276410	161276252	161276390	MPZ	NM_000530	1	6	4	-	161276119	161276254
314633928	chr1	161275780	161275987	161275799	161275963	MPZ	NM_000530	1	6	5	-	161275898	161275958
314927061	chr1	161275581	161275803	161275602	161275784	MPZ	NM_000530	1	6	6	-	161274525	161275767
236941969	chr2	47630265	47630470	47630285	47630450	MSH2	NM_000251	1	16	1	+	47630263	47630541
236947701	chr2	47630426	47630614	47630445	47630595	MSH2	NM_000251	1	16	1	+	47630263	47630541
237654990	chr2	47635534	47635664	47635560	47635635	MSH2	NM_000251	1	16	2	+	47635540	47635694
237657546	chr2	47635608	47635824	47635636	47635796	MSH2	NM_000251	1	16	2	+	47635540	47635694
237721752	chr2	47637228	47637405	47637251	47637381	MSH2	NM_000251	1	16	3	+	47637233	47637511
237760205	chr2	47637356	47637551	47637382	47637527	MSH2	NM_000251	1	16	3	+	47637233	47637511
235692106	chr2	47639424	47639583	47639456	47639556	MSH2	NM_000251	1	16	4	+	47639553	47639699
235692136	chr2	47639556	47639692	47639584	47639667	MSH2	NM_000251	1	16	4	+	47639553	47639699
235692642	chr2	47639631	47639829	47639652	47639797	MSH2	NM_000251	1	16	4	+	47639553	47639699
239680547	chr2	47641290	47641481	47641314	47641454	MSH2	NM_000251	1	16	5	+	47641408	47641557
239694657	chr2	47641420	47641559	47641445	47641535	MSH2	NM_000251	1	16	5	+	47641408	47641557
239694744	chr2	47641514	47641654	47641540	47641623	MSH2	NM_000251	1	16	5	+	47641408	47641557
235555845	chr2	47643368	47643527	47643393	47643502	MSH2	NM_000251	1	16	6	+	47643435	47643568
235559334	chr2	47643477	47643631	47643503	47643603	MSH2	NM_000251	1	16	6	+	47643435	47643568
239502259	chr2	47656789	47656985	47656816	47656961	MSH2	NM_000251	1	16	7	+	47656881	47657080
239514182	chr2	47656936	47657148	47656962	47657121	MSH2	NM_000251	1	16	7	+	47656881	47657080
258191416	chr2	47672581	47672741	47672608	47672715	MSH2	NM_000251	1	16	8	+	47672687	47672796
258191801	chr2	47672688	47672911	47672716	47672883	MSH2	NM_000251	1	16	8	+	47672687	47672796
242651479	chr2	47690149	47690325	47690172	47690298	MSH2	NM_000251	1	16	9	+	47690170	47690293
242478548	chr2	47693735	47693959	47693768	47693936	MSH2	NM_000251	1	16	10	+	47693797	47693947
242484850	chr2	47693834	47693959	47693862	47693939	MSH2	NM_000251	1	16	10	+	47693797	47693947
238698772	chr2	47698026	47698243	47698054	47698215	MSH2	NM_000251	1	16	11	+	47698104	47698201
236815587	chr2	47702160	47702285	47702184	47702262	MSH2	NM_000251	1	16	12	+	47702164	47702409
236818060	chr2	47702221	47702351	47702242	47702323	MSH2	NM_000251	1	16	12	+	47702164	47702409
236818141	chr2	47702315	47702537	47702336	47702510	MSH2	NM_000251	1	16	12	+	47702164	47702409
241364791	chr2	47703377	47703596	47703405	47703574	MSH2	NM_000251	1	16	13	+	47703506	47703710
241383357	chr2	47703549	47703769	47703575	47703743	MSH2	NM_000251	1	16	13	+	47703506	47703710

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240387263	chr2	47705299	47705488	47705326	47705465	MSH2	NM_000251	1	16	14	+	47705411	47705658
240406328	chr2	47705438	47705583	47705466	47705559	MSH2	NM_000251	1	16	14	+	47705411	47705658
240418863	chr2	47705534	47705714	47705560	47705686	MSH2	NM_000251	1	16	14	+	47705411	47705658
235399185	chr2	47707706	47707862	47707733	47707835	MSH2	NM_000251	1	16	15	+	47707835	47708010
235410093	chr2	47707810	47708033	47707836	47708004	MSH2	NM_000251	1	16	15	+	47707835	47708010
237702371	chr2	47709831	47709961	47709860	47709938	MSH2	NM_000251	1	16	16	+	47709918	47710360
237702442	chr2	47709897	47710113	47709921	47710085	MSH2	NM_000251	1	16	16	+	47709918	47710360
314791122	chrX	149760935	149761129	149760963	149761101	MTM1	NM_000252	1	15	2	+	149761067	149761139
314796672	chrX	149761076	149761218	149761102	149761191	MTM1	NM_000252	1	15	2	+	149761067	149761139
313794353	chrX	149764880	149765066	149764905	149765039	MTM1	NM_000252	1	15	3	+	149764962	149765034
313879459	chrX	149766991	149767126	149767019	149767097	MTM1	NM_000252	1	15	4	+	149767056	149767150
313879543	chrX	149767072	149767237	149767098	149767209	MTM1	NM_000252	1	15	4	+	149767056	149767150
314763393	chrX	149782905	149783129	149782930	149783111	MTM1	NM_000252	1	15	5	+	149783062	149783172
314767331	chrX	149783089	149783215	149783112	149783191	MTM1	NM_000252	1	15	5	+	149783062	149783172
315468224	chrX	149787461	149787662	149787489	149787641	MTM1	NM_000252	1	15	6	+	149787511	149787612
313939431	chrX	149807367	149807537	149807389	149807509	MTM1	NM_000252	1	15	7	+	149807416	149807499
312871723	chrX	149809619	149809843	149809640	149809822	MTM1	NM_000252	1	15	8	+	149809742	149809891
312880030	chrX	149809800	149809947	149809823	149809919	MTM1	NM_000252	1	15	8	+	149809742	149809891
314332887	chrX	149814063	149814202	149814087	149814178	MTM1	NM_000252	1	15	9	+	149814156	149814344
314341782	chrX	149814156	149814378	149814179	149814352	MTM1	NM_000252	1	15	9	+	149814156	149814344
312982713	chrX	149818028	149818241	149818053	149818215	MTM1	NM_000252	1	15	10	+	149818189	149818374
312985846	chrX	149818190	149818377	149818216	149818348	MTM1	NM_000252	1	15	10	+	149818189	149818374
312989223	chrX	149818318	149818538	149818345	149818505	MTM1	NM_000252	1	15	10	+	149818189	149818374
313602384	chrX	149826142	149826350	149826165	149826323	MTM1	NM_000252	1	15	11	+	149826294	149826500
313613518	chrX	149826302	149826470	149826324	149826442	MTM1	NM_000252	1	15	11	+	149826294	149826500
313618960	chrX	149826415	149826638	149826443	149826612	MTM1	NM_000252	1	15	11	+	149826294	149826500
315221711	chrX	149828041	149828265	149828067	149828238	MTM1	NM_000252	1	15	12	+	149828137	149828229
313934701	chrX	149828797	149829013	149828822	149828985	MTM1	NM_000252	1	15	13	+	149828844	149828957
313198147	chrX	149831818	149832040	149831841	149832017	MTM1	NM_000252	1	15	14	+	149831906	149832082
313211366	chrX	149831990	149832124	149832018	149832096	MTM1	NM_000252	1	15	14	+	149831906	149832082
315007312	chrX	149839739	149839963	149839767	149839937	MTM1	NM_000252	1	15	15	+	149839901	149841616
315036406	chrX	149839918	149840128	149839938	149840101	MTM1	NM_000252	1	15	15	+	149839901	149841616
313101642	chr6	49426821	49427041	49426848	49427016	MUT	NM_000255	1	13	2	-	49426795	49427218
313119433	chr6	49426993	49427212	49427017	49427184	MUT	NM_000255	1	13	2	-	49426795	49427218
314377134	chr6	49425339	49425523	49425369	49425497	MUT	NM_000255	1	13	3	-	49425404	49425771
314378674	chr6	49425443	49425588	49425471	49425561	MUT	NM_000255	1	13	3	-	49425404	49425771
314390827	chr6	49425531	49425745	49425559	49425724	MUT	NM_000255	1	13	3	-	49425404	49425771
314396405	chr6	49425697	49425821	49425722	49425793	MUT	NM_000255	1	13	3	-	49425404	49425771
314750130	chr6	49423776	49423918	49423803	49423895	MUT	NM_000255	1	13	4	-	49423793	49423950
314750284	chr6	49423792	49423919	49423818	49423896	MUT	NM_000255	1	13	4	-	49423793	49423950
314884362	chr6	49421212	49421398	49421235	49421369	MUT	NM_000255	1	13	5	-	49421298	49421469

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314889577	chr6	49421318	49421484	49421343	49421453	MUT	NM_000255	1	13	5	-	49421298	49421469
314889746	chr6	49421407	49421626	49421435	49421597	MUT	NM_000255	1	13	5	-	49421298	49421469
312919126	chr6	49419144	49419336	49419171	49419315	MUT	NM_000255	1	13	6	-	49419179	49419427
312932682	chr6	49419294	49419513	49419316	49419484	MUT	NM_000255	1	13	6	-	49419179	49419427
313274742	chr6	49416349	49416569	49416373	49416549	MUT	NM_000255	1	13	7	-	49416529	49416640
313275399	chr6	49416594	49416817	49416614	49416784	MUT	NM_000255	1	13	7	-	49416529	49416640
315309951	chr6	49415382	49415515	49415410	49415487	MUT	NM_000255	1	13	8	-	49415383	49415498
315313770	chr6	49415447	49415666	49415475	49415644	MUT	NM_000255	1	13	8	-	49415383	49415498
312816834	chr6	49412288	49412504	49412315	49412476	MUT	NM_000255	1	13	9	-	49412352	49412467
315120604	chr6	49409498	49409628	49409523	49409606	MUT	NM_000255	1	13	10	-	49409553	49409684
315124806	chr6	49409585	49409713	49409607	49409685	MUT	NM_000255	1	13	10	-	49409553	49409684
314990847	chr6	49407900	49408032	49407925	49408007	MUT	NM_000255	1	13	11	-	49407919	49408066
314993581	chr6	49407944	49408068	49407971	49408041	MUT	NM_000255	1	13	11	-	49407919	49408066
314051780	chr6	49403113	49403254	49403141	49403228	MUT	NM_000255	1	13	12	-	49403169	49403336
314055821	chr6	49403209	49403353	49403229	49403327	MUT	NM_000255	1	13	12	-	49403169	49403336
314101438	chr6	49399277	49399496	49399301	49399469	MUT	NM_000255	1	13	13	-	49398073	49399569
314105161	chr6	49399445	49399621	49399470	49399593	MUT	NM_000255	1	13	13	-	49398073	49399569
313281001	chr11	47374076	47374290	47374096	47374266	MYBPC3	NM_000256	1	34	1	-	47374174	47374253
314061165	chr11	47372764	47372951	47372784	47372933	MYBPC3	NM_000256	1	34	2	-	47372790	47373056
314065294	chr11	47372910	47373105	47372929	47373088	MYBPC3	NM_000256	1	34	2	-	47372790	47373056
312902042	chr11	47371977	47372195	47371999	47372175	MYBPC3	NM_000256	1	34	3	-	47372053	47372166
313192410	chr11	47371525	47371680	47371543	47371660	MYBPC3	NM_000256	1	34	4	-	47371565	47371663
314478027	chr11	47371261	47371421	47371282	47371400	MYBPC3	NM_000256	1	34	5	-	47371325	47371473
314482635	chr11	47371378	47371574	47371398	47371556	MYBPC3	NM_000256	1	34	5	-	47371325	47371473
313889238	chr11	47369860	47370018	47369880	47369993	MYBPC3	NM_000256	1	34	6	-	47369975	47370092
313896596	chr11	47369972	47370156	47369994	47370139	MYBPC3	NM_000256	1	34	6	-	47369975	47370092
315379835	chr11	47369336	47369483	47369355	47369462	MYBPC3	NM_000256	1	34	7	-	47369408	47369456
314074949	chr11	47369060	47369263	47369082	47369239	MYBPC3	NM_000256	1	34	8	-	47369202	47369231
314327791	chr11	47368797	47369011	47368820	47368989	MYBPC3	NM_000256	1	34	9	-	47368976	47369030
314349282	chr11	47368967	47369091	47368990	47369069	MYBPC3	NM_000256	1	34	9	-	47368976	47369030
314327791	chr11	47368797	47369011	47368820	47368989	MYBPC3	NM_000256	1	34	10	-	47368973	47368974
314198545	chr11	47368144	47368309	47368165	47368284	MYBPC3	NM_000256	1	34	11	-	47368178	47368195
313422313	chr11	47367683	47367868	47367704	47367849	MYBPC3	NM_000256	1	34	12	-	47367758	47367921
313427245	chr11	47367818	47368012	47367837	47367992	MYBPC3	NM_000256	1	34	12	-	47367758	47367921
313854230	chr11	47364895	47365093	47364920	47365072	MYBPC3	NM_000256	1	34	13	-	47365043	47365175
313861285	chr11	47365051	47365252	47365073	47365233	MYBPC3	NM_000256	1	34	13	-	47365043	47365175
313345461	chr11	47364541	47364702	47364561	47364678	MYBPC3	NM_000256	1	34	14	-	47364572	47364699
313350498	chr11	47364652	47364815	47364672	47364792	MYBPC3	NM_000256	1	34	14	-	47364572	47364699
312688273	chr11	47364227	47364422	47364247	47364397	MYBPC3	NM_000256	1	34	15	-	47364381	47364486
313241268	chr11	47364367	47364591	47364392	47364570	MYBPC3	NM_000256	1	34	15	-	47364381	47364486
312675540	chr11	47364086	47364270	47364107	47364248	MYBPC3	NM_000256	1	34	16	-	47364129	47364295

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312688273	chr11	47364227	47364422	47364247	47364397	MYBPC3	NM_000256	1	34	16	-	47364129	47364295
312886343	chr11	47363506	47363655	47363525	47363635	MYBPC3	NM_000256	1	34	17	-	47363542	47363707
312890904	chr11	47363610	47363745	47363633	47363726	MYBPC3	NM_000256	1	34	17	-	47363542	47363707
313863444	chr11	47362512	47362711	47362536	47362690	MYBPC3	NM_000256	1	34	18	-	47362689	47362795
313866989	chr11	47362576	47362800	47362599	47362780	MYBPC3	NM_000256	1	34	18	-	47362689	47362795
313869257	chr11	47362760	47362983	47362780	47362959	MYBPC3	NM_000256	1	34	18	-	47362689	47362795
313863444	chr11	47362512	47362711	47362536	47362690	MYBPC3	NM_000256	1	34	19	-	47362554	47362583
312952546	chr11	47361065	47361267	47361084	47361246	MYBPC3	NM_000256	1	34	20	-	47361202	47361341
312964350	chr11	47361213	47361379	47361234	47361356	MYBPC3	NM_000256	1	34	20	-	47361202	47361341
312955911	chr11	47360808	47360998	47360828	47360978	MYBPC3	NM_000256	1	34	21	-	47360875	47360955
312695397	chr11	47359930	47360153	47359952	47360131	MYBPC3	NM_000256	1	34	22	-	47360071	47360230
312705071	chr11	47360112	47360264	47360132	47360242	MYBPC3	NM_000256	1	34	22	-	47360071	47360230
313850460	chr11	47359086	47359302	47359106	47359281	MYBPC3	NM_000256	1	34	23	-	47359241	47359345
314460224	chr11	47359182	47359376	47359202	47359357	MYBPC3	NM_000256	1	34	23	-	47359241	47359345
313845146	chr11	47358929	47359126	47358948	47359105	MYBPC3	NM_000256	1	34	24	-	47358942	47359130
313850460	chr11	47359086	47359302	47359106	47359281	MYBPC3	NM_000256	1	34	24	-	47358942	47359130
314224846	chr11	47357371	47357593	47357391	47357572	MYBPC3	NM_000256	1	34	25	-	47357428	47357562
313482333	chr11	47356553	47356718	47356572	47356695	MYBPC3	NM_000256	1	34	26	-	47356593	47356760
313484980	chr11	47356641	47356854	47356661	47356828	MYBPC3	NM_000256	1	34	26	-	47356593	47356760
313859597	chr11	47355392	47355592	47355415	47355566	MYBPC3	NM_000256	1	34	27	-	47355473	47355561
314582625	chr11	47354993	47355187	47355015	47355166	MYBPC3	NM_000256	1	34	28	-	47355108	47355303
314586850	chr11	47355131	47355348	47355155	47355326	MYBPC3	NM_000256	1	34	28	-	47355108	47355303
313408623	chr11	47354599	47354779	47354621	47354759	MYBPC3	NM_000256	1	34	29	-	47354745	47354884
313411071	chr11	47354738	47354911	47354759	47354891	MYBPC3	NM_000256	1	34	29	-	47354745	47354884
315401008	chr11	47354254	47354477	47354275	47354455	MYBPC3	NM_000256	1	34	30	-	47354365	47354524
315414333	chr11	47354435	47354639	47354456	47354614	MYBPC3	NM_000256	1	34	30	-	47354365	47354524
313968792	chr11	47354091	47354281	47354111	47354260	MYBPC3	NM_000256	1	34	31	-	47354117	47354253
313350658	chr11	47353531	47353745	47353548	47353725	MYBPC3	NM_000256	1	34	32	-	47353623	47353809
313358091	chr11	47353704	47353843	47353726	47353821	MYBPC3	NM_000256	1	34	32	-	47353623	47353809
315414608	chr11	47353267	47353491	47353291	47353469	MYBPC3	NM_000256	1	34	33	-	47353396	47353432
235094211	chr16	15931715	15931922	15931739	15931900	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235117895	chr16	15931877	15932080	15931901	15932054	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235132139	chr16	15932034	15932159	15932055	15932131	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235266587	chr16	15917023	15917223	15917045	15917202	MYH11	NM_001040113	1	43	3	-	15917112	15917268
235288000	chr16	15917182	15917306	15917203	15917284	MYH11	NM_001040113	1	43	3	-	15917112	15917268
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_001040113	1	43	4	-	15892517	15892544
236236349	chr16	15880398	15880617	15880425	15880594	MYH11	NM_001040113	1	43	5	-	15880487	15880589
239091356	chr16	15878432	15878613	15878453	15878584	MYH11	NM_001040113	1	43	6	-	15878555	15878575
239338678	chr16	15876159	15876374	15876179	15876346	MYH11	NM_001040113	1	43	7	-	15876242	15876334
241641206	chr16	15872508	15872732	15872535	15872709	MYH11	NM_001040113	1	43	8	-	15872637	15872700
239876856	chr16	15869863	15870061	15869884	15870038	MYH11	NM_001040113	1	43	9	-	15869935	15870033

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257621923	chr16	15865394	15865604	15865415	15865580	MYH11	NM_001040113	1	43	10	-	15865426	15865569
237455671	chr16	15857609	15857791	15857630	15857768	MYH11	NM_001040113	1	43	11	-	15857653	15857748
235190727	chr16	15854390	15854545	15854417	15854520	MYH11	NM_001040113	1	43	12	-	15854397	15854515
235862638	chr16	15853304	15853467	15853330	15853441	MYH11	NM_001040113	1	43	13	-	15853433	15853585
235871594	chr16	15853420	15853627	15853442	15853604	MYH11	NM_001040113	1	43	13	-	15853433	15853585
237032059	chr16	15851628	15851832	15851648	15851809	MYH11	NM_001040113	1	43	14	-	15851684	15851857
237044500	chr16	15851780	15851920	15851804	15851896	MYH11	NM_001040113	1	43	14	-	15851684	15851857
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_001040113	1	43	15	-	15850198	15850371
239188299	chr16	15850192	15850403	15850215	15850378	MYH11	NM_001040113	1	43	15	-	15850198	15850371
235085723	chr16	15847201	15847425	15847225	15847398	MYH11	NM_001040113	1	43	16	-	15847251	15847365
238054094	chr16	15843866	15844063	15843888	15844044	MYH11	NM_001040113	1	43	17	-	15843995	15844188
238061913	chr16	15844017	15844228	15844035	15844211	MYH11	NM_001040113	1	43	17	-	15843995	15844188
235850442	chr16	15841834	15842056	15841855	15842036	MYH11	NM_001040113	1	43	18	-	15841904	15842025
235912395	chr16	15841629	15841852	15841650	15841830	MYH11	NM_001040113	1	43	19	-	15841731	15841800
235677714	chr16	15841396	15841615	15841420	15841592	MYH11	NM_001040113	1	43	20	-	15841427	15841587
241165400	chr16	15838917	15839141	15838939	15839122	MYH11	NM_001040113	1	43	21	-	15838986	15839094
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_001040113	1	43	22	-	15835617	15835748
236982469	chr16	15835571	15835773	15835591	15835753	MYH11	NM_001040113	1	43	22	-	15835617	15835748
235593926	chr16	15835299	15835517	15835316	15835494	MYH11	NM_001040113	1	43	23	-	15835320	15835526
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_001040113	1	43	23	-	15835320	15835526
241726329	chr16	15833893	15834110	15833913	15834086	MYH11	NM_001040113	1	43	24	-	15833908	15834045
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_001040113	1	43	25	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_001040113	1	43	25	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_001040113	1	43	25	-	15832422	15832545
238394426	chr16	15831261	15831485	15831282	15831463	MYH11	NM_001040113	1	43	26	-	15831306	15831477
238435747	chr16	15831443	15831576	15831464	15831552	MYH11	NM_001040113	1	43	26	-	15831306	15831477
235993401	chr16	15829188	15829401	15829210	15829380	MYH11	NM_001040113	1	43	27	-	15829223	15829435
236012954	chr16	15829354	15829565	15829375	15829542	MYH11	NM_001040113	1	43	27	-	15829223	15829435
235964651	chr16	15826372	15826595	15826399	15826573	MYH11	NM_001040113	1	43	28	-	15826421	15826565
237072766	chr16	15820641	15820825	15820660	15820801	MYH11	NM_001040113	1	43	29	-	15820705	15820911
237077663	chr16	15820784	15820941	15820802	15820920	MYH11	NM_001040113	1	43	29	-	15820705	15820911
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_001040113	1	43	30	-	15818745	15818849
238723188	chr16	15818711	15818892	15818731	15818867	MYH11	NM_001040113	1	43	30	-	15818745	15818849
236860074	chr16	15818455	15818676	15818478	15818654	MYH11	NM_001040113	1	43	31	-	15818504	15818656
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_001040113	1	43	31	-	15818504	15818656
235076112	chr16	15817937	15818145	15817956	15818119	MYH11	NM_001040113	1	43	32	-	15818018	15818266
235102341	chr16	15818099	15818299	15818120	15818279	MYH11	NM_001040113	1	43	32	-	15818018	15818266
240392505	chr16	15815164	15815342	15815191	15815317	MYH11	NM_001040113	1	43	33	-	15815279	15815491
240404527	chr16	15815297	15815517	15815318	15815496	MYH11	NM_001040113	1	43	33	-	15815279	15815491
242141683	chr16	15814608	15814786	15814631	15814767	MYH11	NM_001040113	1	43	34	-	15814696	15814908
242158745	chr16	15814742	15814956	15814765	15814930	MYH11	NM_001040113	1	43	34	-	15814696	15814908

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236507399	chr16	15813980	15814198	15814000	15814176	MYH11	NM_001040113	1	43	35	-	15814008	15814169
258675034	chr16	15813408	15813614	15813429	15813590	MYH11	NM_001040113	1	43	36	-	15813442	15813570
238362046	chr16	15813044	15813255	15813065	15813233	MYH11	NM_001040113	1	43	37	-	15813077	15813165
235710460	chr16	15812048	15812218	15812069	15812199	MYH11	NM_001040113	1	43	38	-	15812172	15812295
235711009	chr16	15812169	15812384	15812188	15812364	MYH11	NM_001040113	1	43	38	-	15812172	15812295
240643159	chr16	15810927	15811108	15810951	15811088	MYH11	NM_001040113	1	43	39	-	15810997	15811205
240651582	chr16	15811056	15811268	15811079	15811248	MYH11	NM_001040113	1	43	39	-	15810997	15811205
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_001040113	1	43	40	-	15809021	15809129
236868309	chr16	15808937	15809156	15808955	15809134	MYH11	NM_001040113	1	43	40	-	15809021	15809129
236539858	chr16	15808714	15808921	15808735	15808901	MYH11	NM_001040113	1	43	41	-	15808766	15808938
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_001040113	1	43	41	-	15808766	15808938
241613566	chr16	15802535	15802750	15802562	15802725	MYH11	NM_001040113	1	43	42	-	15802660	15802698
237725648	chr16	15797813	15798033	15797834	15798006	MYH11	NM_001040113	1	43	43	-	15796992	15797980
235094211	chr16	15931715	15931922	15931739	15931900	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235117895	chr16	15931877	15932080	15931901	15932054	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235132139	chr16	15932034	15932159	15932055	15932131	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235266587	chr16	15917023	15917223	15917045	15917202	MYH11	NM_001040114	2	42	3	-	15917112	15917268
235288000	chr16	15917182	15917306	15917203	15917284	MYH11	NM_001040114	2	42	3	-	15917112	15917268
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_001040114	2	42	4	-	15892517	15892544
236236349	chr16	15880398	15880617	15880425	15880594	MYH11	NM_001040114	2	42	5	-	15880487	15880589
239091356	chr16	15878432	15878613	15878453	15878584	MYH11	NM_001040114	2	42	6	-	15878555	15878575
239338678	chr16	15876159	15876374	15876179	15876346	MYH11	NM_001040114	2	42	7	-	15876242	15876334
241641206	chr16	15872508	15872732	15872535	15872709	MYH11	NM_001040114	2	42	8	-	15872637	15872700
239876856	chr16	15869863	15870061	15869884	15870038	MYH11	NM_001040114	2	42	9	-	15869935	15870033
257621923	chr16	15865394	15865604	15865415	15865580	MYH11	NM_001040114	2	42	10	-	15865426	15865569
237455671	chr16	15857609	15857791	15857630	15857768	MYH11	NM_001040114	2	42	11	-	15857653	15857748
235190727	chr16	15854390	15854545	15854417	15854520	MYH11	NM_001040114	2	42	12	-	15854397	15854515
235862638	chr16	15853304	15853467	15853330	15853441	MYH11	NM_001040114	2	42	13	-	15853433	15853585
235871594	chr16	15853420	15853627	15853442	15853604	MYH11	NM_001040114	2	42	13	-	15853433	15853585
237032059	chr16	15851628	15851832	15851648	15851809	MYH11	NM_001040114	2	42	14	-	15851684	15851857
237044500	chr16	15851780	15851920	15851804	15851896	MYH11	NM_001040114	2	42	14	-	15851684	15851857
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_001040114	2	42	15	-	15850198	15850371
239188299	chr16	15850192	15850403	15850215	15850378	MYH11	NM_001040114	2	42	15	-	15850198	15850371
235085723	chr16	15847201	15847425	15847225	15847398	MYH11	NM_001040114	2	42	16	-	15847251	15847365
238054094	chr16	15843866	15844063	15843888	15844044	MYH11	NM_001040114	2	42	17	-	15843995	15844188
238061913	chr16	15844017	15844228	15844035	15844211	MYH11	NM_001040114	2	42	17	-	15843995	15844188
235850442	chr16	15841834	15842056	15841855	15842036	MYH11	NM_001040114	2	42	18	-	15841904	15842025
235912395	chr16	15841629	15841852	15841650	15841830	MYH11	NM_001040114	2	42	19	-	15841731	15841800
235677714	chr16	15841396	15841615	15841420	15841592	MYH11	NM_001040114	2	42	20	-	15841427	15841587
241165400	chr16	15838917	15839141	15838939	15839122	MYH11	NM_001040114	2	42	21	-	15838986	15839094
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_001040114	2	42	22	-	15835617	15835748

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236982469	chr16	15835571	15835773	15835591	15835753	MYH11	NM_001040114	2	42	22	-	15835617	15835748
235593926	chr16	15835299	15835517	15835316	15835494	MYH11	NM_001040114	2	42	23	-	15835320	15835526
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_001040114	2	42	23	-	15835320	15835526
241726329	chr16	15833893	15834110	15833913	15834086	MYH11	NM_001040114	2	42	24	-	15833908	15834045
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_001040114	2	42	25	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_001040114	2	42	25	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_001040114	2	42	25	-	15832422	15832545
238394426	chr16	15831261	15831485	15831282	15831463	MYH11	NM_001040114	2	42	26	-	15831306	15831477
238435747	chr16	15831443	15831576	15831464	15831552	MYH11	NM_001040114	2	42	26	-	15831306	15831477
235993401	chr16	15829188	15829401	15829210	15829380	MYH11	NM_001040114	2	42	27	-	15829223	15829435
236012954	chr16	15829354	15829565	15829375	15829542	MYH11	NM_001040114	2	42	27	-	15829223	15829435
235964651	chr16	15826372	15826595	15826399	15826573	MYH11	NM_001040114	2	42	28	-	15826421	15826565
237072766	chr16	15820641	15820825	15820660	15820801	MYH11	NM_001040114	2	42	29	-	15820705	15820911
237077663	chr16	15820784	15820941	15820802	15820920	MYH11	NM_001040114	2	42	29	-	15820705	15820911
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_001040114	2	42	30	-	15818745	15818849
238723188	chr16	15818711	15818892	15818731	15818867	MYH11	NM_001040114	2	42	30	-	15818745	15818849
236860074	chr16	15818455	15818676	15818478	15818654	MYH11	NM_001040114	2	42	31	-	15818504	15818656
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_001040114	2	42	31	-	15818504	15818656
235076112	chr16	15817937	15818145	15817956	15818119	MYH11	NM_001040114	2	42	32	-	15818018	15818266
235102341	chr16	15818099	15818299	15818120	15818279	MYH11	NM_001040114	2	42	32	-	15818018	15818266
240392505	chr16	15815164	15815342	15815191	15815317	MYH11	NM_001040114	2	42	33	-	15815279	15815491
240404527	chr16	15815297	15815517	15815318	15815496	MYH11	NM_001040114	2	42	33	-	15815279	15815491
242141683	chr16	15814608	15814786	15814631	15814767	MYH11	NM_001040114	2	42	34	-	15814696	15814908
242158745	chr16	15814742	15814956	15814765	15814930	MYH11	NM_001040114	2	42	34	-	15814696	15814908
236507399	chr16	15813980	15814198	15814000	15814176	MYH11	NM_001040114	2	42	35	-	15814008	15814169
258675034	chr16	15813408	15813614	15813429	15813590	MYH11	NM_001040114	2	42	36	-	15813442	15813570
238362046	chr16	15813044	15813255	15813065	15813233	MYH11	NM_001040114	2	42	37	-	15813077	15813165
235710460	chr16	15812048	15812218	15812069	15812199	MYH11	NM_001040114	2	42	38	-	15812172	15812295
235711009	chr16	15812169	15812384	15812188	15812364	MYH11	NM_001040114	2	42	38	-	15812172	15812295
240643159	chr16	15810927	15811108	15810951	15811088	MYH11	NM_001040114	2	42	39	-	15810997	15811205
240651582	chr16	15811056	15811268	15811079	15811248	MYH11	NM_001040114	2	42	39	-	15810997	15811205
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_001040114	2	42	40	-	15809021	15809129
236868309	chr16	15808937	15809156	15808955	15809134	MYH11	NM_001040114	2	42	40	-	15809021	15809129
236539858	chr16	15808714	15808921	15808735	15808901	MYH11	NM_001040114	2	42	41	-	15808766	15808938
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_001040114	2	42	41	-	15808766	15808938
237725648	chr16	15797813	15798033	15797834	15798006	MYH11	NM_001040114	2	42	42	-	15796992	15797980
235094211	chr16	15931715	15931922	15931739	15931900	MYH11	NM_002474	3	41	2	-	15931765	15932126
235117895	chr16	15931877	15932080	15931901	15932054	MYH11	NM_002474	3	41	2	-	15931765	15932126
235132139	chr16	15932034	15932159	15932055	15932131	MYH11	NM_002474	3	41	2	-	15931765	15932126
235266587	chr16	15917023	15917223	15917045	15917202	MYH11	NM_002474	3	41	3	-	15917112	15917268
235288000	chr16	15917182	15917306	15917203	15917284	MYH11	NM_002474	3	41	3	-	15917112	15917268

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_002474	3	41	4	-	15892517	15892544
236236349	chr16	15880398	15880617	15880425	15880594	MYH11	NM_002474	3	41	5	-	15880487	15880589
239338678	chr16	15876159	15876374	15876179	15876346	MYH11	NM_002474	3	41	6	-	15876242	15876334
241641206	chr16	15872508	15872732	15872535	15872709	MYH11	NM_002474	3	41	7	-	15872637	15872700
239876856	chr16	15869863	15870061	15869884	15870038	MYH11	NM_002474	3	41	8	-	15869935	15870033
257621923	chr16	15865394	15865604	15865415	15865580	MYH11	NM_002474	3	41	9	-	15865426	15865569
237455671	chr16	15857609	15857791	15857630	15857768	MYH11	NM_002474	3	41	10	-	15857653	15857748
235190727	chr16	15854390	15854545	15854417	15854520	MYH11	NM_002474	3	41	11	-	15854397	15854515
235862638	chr16	15853304	15853467	15853330	15853441	MYH11	NM_002474	3	41	12	-	15853433	15853585
235871594	chr16	15853420	15853627	15853442	15853604	MYH11	NM_002474	3	41	12	-	15853433	15853585
237032059	chr16	15851628	15851832	15851648	15851809	MYH11	NM_002474	3	41	13	-	15851684	15851857
237044500	chr16	15851780	15851920	15851804	15851896	MYH11	NM_002474	3	41	13	-	15851684	15851857
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_002474	3	41	14	-	15850198	15850371
239188299	chr16	15850192	15850403	15850215	15850378	MYH11	NM_002474	3	41	14	-	15850198	15850371
235085723	chr16	15847201	15847425	15847225	15847398	MYH11	NM_002474	3	41	15	-	15847251	15847365
238054094	chr16	15843866	15844063	15843888	15844044	MYH11	NM_002474	3	41	16	-	15843995	15844188
238061913	chr16	15844017	15844228	15844035	15844211	MYH11	NM_002474	3	41	16	-	15843995	15844188
235850442	chr16	15841834	15842056	15841855	15842036	MYH11	NM_002474	3	41	17	-	15841904	15842025
235912395	chr16	15841629	15841852	15841650	15841830	MYH11	NM_002474	3	41	18	-	15841731	15841800
235677714	chr16	15841396	15841615	15841420	15841592	MYH11	NM_002474	3	41	19	-	15841427	15841587
241165400	chr16	15838917	15839141	15838939	15839122	MYH11	NM_002474	3	41	20	-	15838986	15839094
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_002474	3	41	21	-	15835617	15835748
236982469	chr16	15835571	15835773	15835591	15835753	MYH11	NM_002474	3	41	21	-	15835617	15835748
235593926	chr16	15835299	15835517	15835316	15835494	MYH11	NM_002474	3	41	22	-	15835320	15835526
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_002474	3	41	22	-	15835320	15835526
241726329	chr16	15833893	15834110	15833913	15834086	MYH11	NM_002474	3	41	23	-	15833908	15834045
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_002474	3	41	24	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_002474	3	41	24	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_002474	3	41	24	-	15832422	15832545
238394426	chr16	15831261	15831485	15831282	15831463	MYH11	NM_002474	3	41	25	-	15831306	15831477
238435747	chr16	15831443	15831576	15831464	15831552	MYH11	NM_002474	3	41	25	-	15831306	15831477
235993401	chr16	15829188	15829401	15829210	15829380	MYH11	NM_002474	3	41	26	-	15829223	15829435
236012954	chr16	15829354	15829565	15829375	15829542	MYH11	NM_002474	3	41	26	-	15829223	15829435
235964651	chr16	15826372	15826595	15826399	15826573	MYH11	NM_002474	3	41	27	-	15826421	15826565
237072766	chr16	15820641	15820825	15820660	15820801	MYH11	NM_002474	3	41	28	-	15820705	15820911
237077663	chr16	15820784	15820941	15820802	15820920	MYH11	NM_002474	3	41	28	-	15820705	15820911
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_002474	3	41	29	-	15818745	15818849
238723188	chr16	15818711	15818892	15818731	15818867	MYH11	NM_002474	3	41	29	-	15818745	15818849
236860074	chr16	15818455	15818676	15818478	15818654	MYH11	NM_002474	3	41	30	-	15818504	15818656
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_002474	3	41	30	-	15818504	15818656
235076112	chr16	15817937	15818145	15817956	15818119	MYH11	NM_002474	3	41	31	-	15818018	15818266

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235102341	chr16	15818099	15818299	15818120	15818279	MYH11	NM_002474	3	41	31	-	15818018	15818266
240392505	chr16	15815164	15815342	15815191	15815317	MYH11	NM_002474	3	41	32	-	15815279	15815491
240404527	chr16	15815297	15815517	15815318	15815496	MYH11	NM_002474	3	41	32	-	15815279	15815491
242141683	chr16	15814608	15814786	15814631	15814767	MYH11	NM_002474	3	41	33	-	15814696	15814908
242158745	chr16	15814742	15814956	15814765	15814930	MYH11	NM_002474	3	41	33	-	15814696	15814908
236507399	chr16	15813980	15814198	15814000	15814176	MYH11	NM_002474	3	41	34	-	15814008	15814169
258675034	chr16	15813408	15813614	15813429	15813590	MYH11	NM_002474	3	41	35	-	15813442	15813570
238362046	chr16	15813044	15813255	15813065	15813233	MYH11	NM_002474	3	41	36	-	15813077	15813165
235710460	chr16	15812048	15812218	15812069	15812199	MYH11	NM_002474	3	41	37	-	15812172	15812295
235711009	chr16	15812169	15812384	15812188	15812364	MYH11	NM_002474	3	41	37	-	15812172	15812295
240643159	chr16	15810927	15811108	15810951	15811088	MYH11	NM_002474	3	41	38	-	15810997	15811205
240651582	chr16	15811056	15811268	15811079	15811248	MYH11	NM_002474	3	41	38	-	15810997	15811205
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_002474	3	41	39	-	15809021	15809129
236868309	chr16	15808937	15809156	15808955	15809134	MYH11	NM_002474	3	41	39	-	15809021	15809129
236539858	chr16	15808714	15808921	15808735	15808901	MYH11	NM_002474	3	41	40	-	15808766	15808938
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_002474	3	41	40	-	15808766	15808938
237725648	chr16	15797813	15798033	15797834	15798006	MYH11	NM_002474	3	41	41	-	15796992	15797980
235094211	chr16	15931715	15931922	15931739	15931900	MYH11	NM_022844	4	42	2	-	15931765	15932126
235117895	chr16	15931877	15932080	15931901	15932054	MYH11	NM_022844	4	42	2	-	15931765	15932126
235132139	chr16	15932034	15932159	15932055	15932131	MYH11	NM_022844	4	42	2	-	15931765	15932126
235266587	chr16	15917023	15917223	15917045	15917202	MYH11	NM_022844	4	42	3	-	15917112	15917268
235288000	chr16	15917182	15917306	15917203	15917284	MYH11	NM_022844	4	42	3	-	15917112	15917268
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_022844	4	42	4	-	15892517	15892544
236236349	chr16	15880398	15880617	15880425	15880594	MYH11	NM_022844	4	42	5	-	15880487	15880589
239338678	chr16	15876159	15876374	15876179	15876346	MYH11	NM_022844	4	42	6	-	15876242	15876334
241641206	chr16	15872508	15872732	15872535	15872709	MYH11	NM_022844	4	42	7	-	15872637	15872700
239876856	chr16	15869863	15870061	15869884	15870038	MYH11	NM_022844	4	42	8	-	15869935	15870033
257621923	chr16	15865394	15865604	15865415	15865580	MYH11	NM_022844	4	42	9	-	15865426	15865569
237455671	chr16	15857609	15857791	15857630	15857768	MYH11	NM_022844	4	42	10	-	15857653	15857748
235190727	chr16	15854390	15854545	15854417	15854520	MYH11	NM_022844	4	42	11	-	15854397	15854515
235862638	chr16	15853304	15853467	15853330	15853441	MYH11	NM_022844	4	42	12	-	15853433	15853585
235871594	chr16	15853420	15853627	15853442	15853604	MYH11	NM_022844	4	42	12	-	15853433	15853585
237032059	chr16	15851628	15851832	15851648	15851809	MYH11	NM_022844	4	42	13	-	15851684	15851857
237044500	chr16	15851780	15851920	15851804	15851896	MYH11	NM_022844	4	42	13	-	15851684	15851857
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_022844	4	42	14	-	15850198	15850371
239188299	chr16	15850192	15850403	15850215	15850378	MYH11	NM_022844	4	42	14	-	15850198	15850371
235085723	chr16	15847201	15847425	15847225	15847398	MYH11	NM_022844	4	42	15	-	15847251	15847365
238054094	chr16	15843866	15844063	15843888	15844044	MYH11	NM_022844	4	42	16	-	15843995	15844188
238061913	chr16	15844017	15844228	15844035	15844211	MYH11	NM_022844	4	42	16	-	15843995	15844188
235850442	chr16	15841834	15842056	15841855	15842036	MYH11	NM_022844	4	42	17	-	15841904	15842025
235912395	chr16	15841629	15841852	15841650	15841830	MYH11	NM_022844	4	42	18	-	15841731	15841800

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235677714	chr16	15841396	15841615	15841420	15841592	MYH11	NM_022844	4	42	19	-	15841427	15841587
241165400	chr16	15838917	15839141	15838939	15839122	MYH11	NM_022844	4	42	20	-	15838986	15839094
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_022844	4	42	21	-	15835617	15835748
236982469	chr16	15835571	15835773	15835591	15835753	MYH11	NM_022844	4	42	21	-	15835617	15835748
235593926	chr16	15835299	15835517	15835316	15835494	MYH11	NM_022844	4	42	22	-	15835320	15835526
235599692	chr16	15835463	15835654	15835486	15835630	MYH11	NM_022844	4	42	22	-	15835320	15835526
241726329	chr16	15833893	15834110	15833913	15834086	MYH11	NM_022844	4	42	23	-	15833908	15834045
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_022844	4	42	24	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_022844	4	42	24	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_022844	4	42	24	-	15832422	15832545
238394426	chr16	15831261	15831485	15831282	15831463	MYH11	NM_022844	4	42	25	-	15831306	15831477
238435747	chr16	15831443	15831576	15831464	15831552	MYH11	NM_022844	4	42	25	-	15831306	15831477
235993401	chr16	15829188	15829401	15829210	15829380	MYH11	NM_022844	4	42	26	-	15829223	15829435
236012954	chr16	15829354	15829565	15829375	15829542	MYH11	NM_022844	4	42	26	-	15829223	15829435
235964651	chr16	15826372	15826595	15826399	15826573	MYH11	NM_022844	4	42	27	-	15826421	15826565
237072766	chr16	15820641	15820825	15820660	15820801	MYH11	NM_022844	4	42	28	-	15820705	15820911
237077663	chr16	15820784	15820941	15820802	15820920	MYH11	NM_022844	4	42	28	-	15820705	15820911
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_022844	4	42	29	-	15818745	15818849
238723188	chr16	15818711	15818892	15818731	15818867	MYH11	NM_022844	4	42	29	-	15818745	15818849
236860074	chr16	15818455	15818676	15818478	15818654	MYH11	NM_022844	4	42	30	-	15818504	15818656
238712230	chr16	15818632	15818856	15818653	15818832	MYH11	NM_022844	4	42	30	-	15818504	15818656
235076112	chr16	15817937	15818145	15817956	15818119	MYH11	NM_022844	4	42	31	-	15818018	15818266
235102341	chr16	15818099	15818299	15818120	15818279	MYH11	NM_022844	4	42	31	-	15818018	15818266
240392505	chr16	15815164	15815342	15815191	15815317	MYH11	NM_022844	4	42	32	-	15815279	15815491
240404527	chr16	15815297	15815517	15815318	15815496	MYH11	NM_022844	4	42	32	-	15815279	15815491
242141683	chr16	15814608	15814786	15814631	15814767	MYH11	NM_022844	4	42	33	-	15814696	15814908
242158745	chr16	15814742	15814956	15814765	15814930	MYH11	NM_022844	4	42	33	-	15814696	15814908
236507399	chr16	15813980	15814198	15814000	15814176	MYH11	NM_022844	4	42	34	-	15814008	15814169
258675034	chr16	15813408	15813614	15813429	15813590	MYH11	NM_022844	4	42	35	-	15813442	15813570
238362046	chr16	15813044	15813255	15813065	15813233	MYH11	NM_022844	4	42	36	-	15813077	15813165
235710460	chr16	15812048	15812218	15812069	15812199	MYH11	NM_022844	4	42	37	-	15812172	15812295
235711009	chr16	15812169	15812384	15812188	15812364	MYH11	NM_022844	4	42	37	-	15812172	15812295
240643159	chr16	15810927	15811108	15810951	15811088	MYH11	NM_022844	4	42	38	-	15810997	15811205
240651582	chr16	15811056	15811268	15811079	15811248	MYH11	NM_022844	4	42	38	-	15810997	15811205
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_022844	4	42	39	-	15809021	15809129
236868309	chr16	15808937	15809156	15808955	15809134	MYH11	NM_022844	4	42	39	-	15809021	15809129
236539858	chr16	15808714	15808921	15808735	15808901	MYH11	NM_022844	4	42	40	-	15808766	15808938
236543421	chr16	15808860	15809049	15808878	15809030	MYH11	NM_022844	4	42	40	-	15808766	15808938
241613566	chr16	15802535	15802750	15802562	15802725	MYH11	NM_022844	4	42	41	-	15802660	15802698
237725648	chr16	15797813	15798033	15797834	15798006	MYH11	NM_022844	4	42	42	-	15796992	15797980
313858123	chr14	23876175	23876315	23876197	23876293	MYH6	NM_002471	1	39	3	-	23876232	23876445

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313869275	chr14	23876272	23876474	23876294	23876450	MYH6	NM_002471	1	39	3	-	23876232	23876445
315459531	chr14	23874668	23874881	23874689	23874859	MYH6	NM_002471	1	39	4	-	23874836	23874979
315471086	chr14	23874835	23875015	23874858	23874993	MYH6	NM_002471	1	39	4	-	23874836	23874979
312818027	chr14	23874423	23874618	23874442	23874599	MYH6	NM_002471	1	39	5	-	23874432	23874588
314401894	chr14	23874245	23874464	23874266	23874442	MYH6	NM_002471	1	39	5	-	23874432	23874588
314401894	chr14	23874245	23874464	23874266	23874442	MYH6	NM_002471	1	39	6	-	23874309	23874336
312820683	chr14	23873761	23873985	23873783	23873963	MYH6	NM_002471	1	39	7	-	23873920	23874031
312832603	chr14	23873942	23874164	23873963	23874141	MYH6	NM_002471	1	39	7	-	23873920	23874031
312920942	chr14	23873402	23873623	23873427	23873602	MYH6	NM_002471	1	39	8	-	23873505	23873597
313031432	chr14	23872827	23873018	23872850	23872996	MYH6	NM_002471	1	39	9	-	23872924	23872987
313256998	chr14	23872509	23872719	23872527	23872693	MYH6	NM_002471	1	39	10	-	23872557	23872655
313985222	chr14	23871747	23871944	23871767	23871924	MYH6	NM_002471	1	39	11	-	23871906	23872009
313988875	chr14	23871800	23872000	23871820	23871978	MYH6	NM_002471	1	39	11	-	23871906	23872009
315129032	chr14	23871959	23872179	23871979	23872158	MYH6	NM_002471	1	39	11	-	23871906	23872009
313977253	chr14	23871585	23871794	23871606	23871771	MYH6	NM_002471	1	39	12	-	23871673	23871811
313985222	chr14	23871747	23871944	23871767	23871924	MYH6	NM_002471	1	39	12	-	23871673	23871811
313620815	chr14	23869868	23870074	23869890	23870053	MYH6	NM_002471	1	39	13	-	23869918	23870186
313633111	chr14	23870015	23870215	23870041	23870191	MYH6	NM_002471	1	39	13	-	23869918	23870186
315265595	chr14	23869439	23869644	23869459	23869624	MYH6	NM_002471	1	39	14	-	23869465	23869635
314215343	chr14	23867840	23868027	23867860	23868005	MYH6	NM_002471	1	39	15	-	23867937	23868246
314225855	chr14	23867984	23868158	23868005	23868136	MYH6	NM_002471	1	39	15	-	23867937	23868246
314235992	chr14	23868115	23868335	23868136	23868312	MYH6	NM_002471	1	39	15	-	23867937	23868246
312847569	chr14	23866630	23866853	23866651	23866828	MYH6	NM_002471	1	39	16	-	23866752	23866822
313079635	chr14	23866315	23866495	23866339	23866473	MYH6	NM_002471	1	39	17	-	23866379	23866466
312751362	chr14	23866131	23866343	23866153	23866321	MYH6	NM_002471	1	39	18	-	23866172	23866289
314913992	chr14	23865837	23866053	23865858	23866032	MYH6	NM_002471	1	39	19	-	23865903	23866026
313478517	chr14	23865441	23865657	23865465	23865636	MYH6	NM_002471	1	39	20	-	23865493	23865629
312861903	chr14	23863200	23863407	23863220	23863385	MYH6	NM_002471	1	39	21	-	23863277	23863532
312869871	chr14	23863360	23863576	23863383	23863553	MYH6	NM_002471	1	39	21	-	23863277	23863532
313100695	chr14	23862811	23863034	23862835	23863011	MYH6	NM_002471	1	39	22	-	23862875	23863117
313127704	chr14	23862987	23863197	23863006	23863174	MYH6	NM_002471	1	39	22	-	23862875	23863117
315381253	chr14	23862393	23862606	23862419	23862586	MYH6	NM_002471	1	39	23	-	23862551	23862727
315397536	chr14	23862565	23862788	23862587	23862766	MYH6	NM_002471	1	39	23	-	23862551	23862727
314356280	chr14	23862017	23862147	23862037	23862123	MYH6	NM_002471	1	39	24	-	23862121	23862266
314362115	chr14	23862103	23862312	23862124	23862283	MYH6	NM_002471	1	39	24	-	23862121	23862266
313445436	chr14	23861712	23861908	23861734	23861886	MYH6	NM_002471	1	39	25	-	23861771	23861861
313462483	chr14	23859464	23859672	23859482	23859652	MYH6	NM_002471	1	39	26	-	23859266	23859655
313467800	chr14	23859586	23859745	23859606	23859719	MYH6	NM_002471	1	39	26	-	23859266	23859655
313288429	chr14	23858744	23858960	23858766	23858938	MYH6	NM_002471	1	39	27	-	23858802	23858928
313468593	chr14	23858527	23858745	23858549	23858725	MYH6	NM_002471	1	39	28	-	23858602	23858720
312775582	chr14	23858021	23858226	23858041	23858208	MYH6	NM_002471	1	39	29	-	23858068	23858264

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312781879	chr14	23858180	23858399	23858202	23858378	MYH6	NM_002471	1	39	29	-	23858068	23858264
315240928	chr14	23857290	23857463	23857310	23857441	MYH6	NM_002471	1	39	30	-	23857364	23857547
315251151	chr14	23857420	23857594	23857442	23857573	MYH6	NM_002471	1	39	30	-	23857364	23857547
313236335	chr14	23856931	23857110	23856953	23857088	MYH6	NM_002471	1	39	31	-	23856967	23857132
313244797	chr14	23857066	23857245	23857087	23857223	MYH6	NM_002471	1	39	31	-	23856967	23857132
314524914	chr14	23856669	23856890	23856688	23856870	MYH6	NM_002471	1	39	32	-	23856738	23856862
315095293	chr14	23855352	23855554	23855372	23855534	MYH6	NM_002471	1	39	33	-	23855524	23855832
315101312	chr14	23855513	23855706	23855533	23855689	MYH6	NM_002471	1	39	33	-	23855524	23855832
315107148	chr14	23855680	23855904	23855697	23855878	MYH6	NM_002471	1	39	33	-	23855524	23855832
313190045	chr14	23855089	23855309	23855110	23855291	MYH6	NM_002471	1	39	34	-	23855137	23855340
313198915	chr14	23855269	23855475	23855289	23855455	MYH6	NM_002471	1	39	34	-	23855137	23855340
314938521	chr14	23854023	23854246	23854044	23854224	MYH6	NM_002471	1	39	35	-	23854125	23854250
314951847	chr14	23854203	23854387	23854225	23854359	MYH6	NM_002471	1	39	35	-	23854125	23854250
313742065	chr14	23853600	23853810	23853624	23853792	MYH6	NM_002471	1	39	36	-	23853651	23853926
313744557	chr14	23853766	23853959	23853786	23853938	MYH6	NM_002471	1	39	36	-	23853651	23853926
314613482	chr14	23852374	23852590	23852402	23852567	MYH6	NM_002471	1	39	37	-	23852434	23852529
313593035	chr14	23851588	23851811	23851608	23851789	MYH6	NM_002471	1	39	38	-	23851637	23851771
315351995	chr14	23851087	23851301	23851108	23851277	MYH6	NM_002471	1	39	39	-	23851199	23851272
313499518	chr14	23902679	23902900	23902700	23902879	MYH7	NM_000257	1	40	3	-	23902741	23902949
313510273	chr14	23902840	23903064	23902861	23903042	MYH7	NM_000257	1	40	3	-	23902741	23902949
313316474	chr14	23902237	23902447	23902259	23902427	MYH7	NM_000257	1	40	4	-	23902293	23902436
313330338	chr14	23902407	23902532	23902428	23902511	MYH7	NM_000257	1	40	4	-	23902293	23902436
315394814	chr14	23901809	23902033	23901830	23902009	MYH7	NM_000257	1	40	5	-	23901848	23902004
313881820	chr14	23901637	23901825	23901658	23901803	MYH7	NM_000257	1	40	6	-	23901688	23901715
313925255	chr14	23900929	23901129	23900949	23901104	MYH7	NM_000257	1	40	7	-	23900970	23901078
313073814	chr14	23900724	23900948	23900748	23900928	MYH7	NM_000257	1	40	8	-	23900794	23900886
312804562	chr14	23900556	23900719	23900580	23900695	MYH7	NM_000257	1	40	9	-	23900627	23900690
312758691	chr14	23900062	23900252	23900083	23900223	MYH7	NM_000257	1	40	10	-	23900110	23900208
314256238	chr14	23899684	23899904	23899705	23899882	MYH7	NM_000257	1	40	11	-	23899769	23899872
314031052	chr14	23898915	23899059	23898936	23899036	MYH7	NM_000257	1	40	12	-	23898984	23899122
314038761	chr14	23899016	23899184	23899037	23899156	MYH7	NM_000257	1	40	12	-	23898984	23899122
315155833	chr14	23898399	23898585	23898419	23898561	MYH7	NM_000257	1	40	13	-	23898438	23898556
313541814	chr14	23898117	23898341	23898139	23898318	MYH7	NM_000257	1	40	14	-	23898164	23898313
313051581	chr14	23897636	23897857	23897658	23897834	MYH7	NM_000257	1	40	15	-	23897709	23897879
313070606	chr14	23897802	23897963	23897826	23897945	MYH7	NM_000257	1	40	15	-	23897709	23897879
314854602	chr14	23896748	23896954	23896770	23896932	MYH7	NM_000257	1	40	16	-	23896794	23897103
314878018	chr14	23896906	23897130	23896930	23897108	MYH7	NM_000257	1	40	16	-	23896794	23897103
313323038	chr14	23896322	23896546	23896341	23896521	MYH7	NM_000257	1	40	17	-	23896449	23896516
313963632	chr14	23895911	23896131	23895933	23896108	MYH7	NM_000257	1	40	18	-	23895986	23896073
314236080	chr14	23895132	23895321	23895154	23895296	MYH7	NM_000257	1	40	19	-	23895173	23895290
315328300	chr14	23894834	23895054	23894858	23895033	MYH7	NM_000257	1	40	20	-	23894904	23895027

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314408000	chr14	23894463	23894663	23894483	23894642	MYH7	NM_000257	1	40	21	-	23894491	23894627
313172110	chr14	23893942	23894097	23893963	23894077	MYH7	NM_000257	1	40	22	-	23893978	23894233
313175550	chr14	23894058	23894266	23894078	23894244	MYH7	NM_000257	1	40	22	-	23893978	23894233
314711984	chr14	23893043	23893261	23893064	23893237	MYH7	NM_000257	1	40	23	-	23893116	23893358
314730711	chr14	23893217	23893420	23893238	23893395	MYH7	NM_000257	1	40	23	-	23893116	23893358
313583384	chr14	23892699	23892894	23892720	23892872	MYH7	NM_000257	1	40	24	-	23892756	23892932
313604780	chr14	23892850	23893060	23892873	23893040	MYH7	NM_000257	1	40	24	-	23892756	23892932
312839867	chr14	23891327	23891551	23891350	23891528	MYH7	NM_000257	1	40	25	-	23891389	23891534
312852465	chr14	23891505	23891703	23891527	23891677	MYH7	NM_000257	1	40	25	-	23891389	23891534
315275331	chr14	23890064	23890286	23890089	23890264	MYH7	NM_000257	1	40	26	-	23890167	23890257
315433331	chr14	23888947	23889155	23888970	23889138	MYH7	NM_000257	1	40	27	-	23889054	23889443
315438581	chr14	23889252	23889453	23889270	23889435	MYH7	NM_000257	1	40	27	-	23889054	23889443
315440326	chr14	23889353	23889565	23889372	23889544	MYH7	NM_000257	1	40	27	-	23889054	23889443
314327004	chr14	23888650	23888851	23888670	23888823	MYH7	NM_000257	1	40	28	-	23888692	23888818
313551804	chr14	23888309	23888533	23888333	23888509	MYH7	NM_000257	1	40	29	-	23888386	23888504
313377752	chr14	23887293	23887510	23887316	23887490	MYH7	NM_000257	1	40	30	-	23887419	23887615
313381853	chr14	23887452	23887657	23887472	23887636	MYH7	NM_000257	1	40	30	-	23887419	23887615
313723167	chr14	23886624	23886831	23886644	23886811	MYH7	NM_000257	1	40	31	-	23886712	23886895
313737662	chr14	23886784	23887006	23886807	23886980	MYH7	NM_000257	1	40	31	-	23886712	23886895
313168062	chr14	23886210	23886420	23886231	23886396	MYH7	NM_000257	1	40	32	-	23886362	23886527
313177517	chr14	23886372	23886594	23886393	23886574	MYH7	NM_000257	1	40	32	-	23886362	23886527
314922110	chr14	23886022	23886232	23886042	23886210	MYH7	NM_000257	1	40	33	-	23886077	23886201
312667567	chr14	23885078	23885237	23885099	23885217	MYH7	NM_000257	1	40	34	-	23885213	23885521
312682364	chr14	23885196	23885384	23885216	23885366	MYH7	NM_000257	1	40	34	-	23885213	23885521
312692196	chr14	23885348	23885563	23885366	23885544	MYH7	NM_000257	1	40	34	-	23885213	23885521
314614812	chr14	23884740	23884889	23884764	23884868	MYH7	NM_000257	1	40	35	-	23884838	23885041
314618550	chr14	23884852	23885067	23884869	23885047	MYH7	NM_000257	1	40	35	-	23884838	23885041
314775459	chr14	23884544	23884758	23884565	23884736	MYH7	NM_000257	1	40	36	-	23884590	23884715
314324104	chr14	23884145	23884363	23884166	23884344	MYH7	NM_000257	1	40	37	-	23884204	23884479
314326639	chr14	23884320	23884525	23884340	23884503	MYH7	NM_000257	1	40	37	-	23884204	23884479
315081800	chr14	23883139	23883361	23883159	23883336	MYH7	NM_000257	1	40	38	-	23883216	23883311
314053643	chr14	23882936	23883160	23882959	23883139	MYH7	NM_000257	1	40	39	-	23882968	23883102
314675540	chr14	23881912	23882112	23881933	23882086	MYH7	NM_000257	1	40	40	-	23881947	23882080
313608585	chr12	111358268	111358470	111358290	111358448	MYL2	NM_000432	1	7	1	-	111358331	111358404
315430808	chr12	111356815	111357033	111356837	111357005	MYL2	NM_000432	1	7	2	-	111356908	111356997
312950643	chr12	111353457	111353669	111353478	111353648	MYL2	NM_000432	1	7	3	-	111353519	111353594
314000329	chr12	111351933	111352122	111351957	111352099	MYL2	NM_000432	1	7	4	-	111351990	111352094
313803347	chr12	111350955	111351154	111350977	111351133	MYL2	NM_000432	1	7	5	-	111351050	111351128
312668647	chr12	111350765	111350986	111350786	111350965	MYL2	NM_000432	1	7	6	-	111350900	111350948
315509544	chr12	111348792	111349011	111348812	111348991	MYL2	NM_000432	1	7	7	-	111348624	111348979
314382701	chr3	46904691	46904912	46904713	46904887	MYL3	NM_000258	1	7	1	-	46904752	46904973

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314658782	chr3	46902286	46902491	46902307	46902466	MYL3	NM_000258	1	7	2	-	46902450	46902477
315332933	chr3	46902295	46902517	46902318	46902496	MYL3	NM_000258	1	7	2	-	46902450	46902477
314650481	chr3	46902116	46902328	46902137	46902307	MYL3	NM_000258	1	7	3	-	46902166	46902315
314658782	chr3	46902286	46902491	46902307	46902466	MYL3	NM_000258	1	7	3	-	46902166	46902315
312975923	chr3	46900901	46901094	46900923	46901070	MYL3	NM_000258	1	7	4	-	46900965	46901138
312983533	chr3	46901050	46901256	46901071	46901231	MYL3	NM_000258	1	7	4	-	46900965	46901138
313153338	chr3	46899717	46899901	46899737	46899880	MYL3	NM_000258	1	7	5	-	46899874	46899951
314956995	chr3	46899861	46900034	46899881	46900011	MYL3	NM_000258	1	7	5	-	46899874	46899951
313144289	chr3	46899588	46899789	46899609	46899767	MYL3	NM_000258	1	7	6	-	46899721	46899762
313153338	chr3	46899717	46899901	46899737	46899880	MYL3	NM_000258	1	7	6	-	46899721	46899762
332121800	chr3	123512379	123512586	123512401	123512566	MYLK	NM_053025	1	34	4	-	123512524	123512691
332144757	chr3	123512545	123512762	123512567	123512741	MYLK	NM_053025	1	34	4	-	123512524	123512691
332109008	chr3	123471059	123471282	123471082	123471261	MYLK	NM_053025	1	34	5	-	123471178	123471385
332120790	chr3	123471241	123471415	123471262	123471388	MYLK	NM_053025	1	34	5	-	123471178	123471385
332099627	chr3	123458680	123458880	123458700	123458853	MYLK	NM_053025	1	34	6	-	123458800	123458848
332069291	chr3	123457706	123457929	123457725	123457903	MYLK	NM_053025	1	34	7	-	123457744	123457909
332098042	chr3	123457883	123458007	123457904	123457981	MYLK	NM_053025	1	34	7	-	123457744	123457909
332149722	chr3	123456112	123456249	123456133	123456226	MYLK	NM_053025	1	34	8	-	123456225	123456390
332160390	chr3	123456207	123456417	123456227	123456395	MYLK	NM_053025	1	34	8	-	123456225	123456390
332042675	chr3	123454104	123454326	123454130	123454298	MYLK	NM_053025	1	34	9	-	123454245	123454263
332143448	chr3	123452950	123453170	123452971	123453148	MYLK	NM_053025	1	34	10	-	123452534	123453069
332157135	chr3	123452498	123452675	123452520	123452655	MYLK	NM_053025	1	34	10	-	123452534	123453069
332162496	chr3	123452633	123452828	123452655	123452805	MYLK	NM_053025	1	34	10	-	123452534	123453069
332165709	chr3	123452773	123452995	123452794	123452975	MYLK	NM_053025	1	34	10	-	123452534	123453069
332043088	chr3	123451667	123451887	123451688	123451863	MYLK	NM_053025	1	34	11	-	123451743	123451949
332071990	chr3	123451843	123451985	123451864	123451961	MYLK	NM_053025	1	34	11	-	123451743	123451949
332124095	chr3	123444662	123444885	123444684	123444865	MYLK	NM_053025	1	34	12	-	123444791	123444925
332138003	chr3	123444845	123444971	123444866	123444951	MYLK	NM_053025	1	34	12	-	123444791	123444925
332151484	chr3	123440935	123441155	123440956	123441136	MYLK	NM_053025	1	34	13	-	123440975	123441127
332113039	chr3	123428555	123428779	123428583	123428758	MYLK	NM_053025	1	34	14	-	123428603	123428740
332037055	chr3	123427434	123427614	123427452	123427597	MYLK	NM_053025	1	34	15	-	123427545	123427742
332054996	chr3	123427574	123427788	123427592	123427768	MYLK	NM_053025	1	34	15	-	123427545	123427742
332166520	chr3	123426544	123426733	123426567	123426712	MYLK	NM_053025	1	34	16	-	123426601	123426850
332179189	chr3	123426693	123426875	123426712	123426855	MYLK	NM_053025	1	34	16	-	123426601	123426850
332064994	chr3	123420177	123420393	123420199	123420365	MYLK	NM_053025	1	34	17	-	123420285	123420356
332032359	chr3	123419302	123419474	123419321	123419454	MYLK	NM_053025	1	34	18	-	123418867	123419852
332033567	chr3	123418826	123419013	123418846	123418990	MYLK	NM_053025	1	34	18	-	123418867	123419852
332044003	chr3	123419420	123419596	123419442	123419573	MYLK	NM_053025	1	34	18	-	123418867	123419852
332050049	chr3	123419535	123419742	123419555	123419722	MYLK	NM_053025	1	34	18	-	123418867	123419852
332056767	chr3	123418960	123419165	123418979	123419147	MYLK	NM_053025	1	34	18	-	123418867	123419852
332058255	chr3	123419679	123419900	123419696	123419880	MYLK	NM_053025	1	34	18	-	123418867	123419852

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332083699	chr3	123419126	123419349	123419148	123419325	MYLK	NM_053025	1	34	18	-	123418867	123419852
332181540	chr3	123411529	123411730	123411551	123411706	MYLK	NM_053025	1	34	19	-	123411582	123411698
332076288	chr3	123400951	123401172	123400972	123401148	MYLK	NM_053025	1	34	20	-	123401071	123401157
332088737	chr3	123401108	123401241	123401129	123401218	MYLK	NM_053025	1	34	20	-	123401071	123401157
332104370	chr3	123385878	123386102	123385899	123386076	MYLK	NM_053025	1	34	21	-	123385984	123386034
332145815	chr3	123385004	123385220	123385025	123385199	MYLK	NM_053025	1	34	22	-	123385066	123385193
332052504	chr3	123382871	123383083	123382891	123383062	MYLK	NM_053025	1	34	23	-	123382952	123383105
332060787	chr3	123382995	123383205	123383017	123383183	MYLK	NM_053025	1	34	23	-	123382952	123383105
332133101	chr3	123375931	123376147	123375955	123376127	MYLK	NM_053025	1	34	24	-	123375973	123376275
332163219	chr3	123376107	123376305	123376128	123376280	MYLK	NM_053025	1	34	24	-	123375973	123376275
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053025	1	34	25	-	123368009	123368041
332033087	chr3	123367735	123367952	123367756	123367931	MYLK	NM_053025	1	34	26	-	123367818	123367911
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053025	1	34	26	-	123367818	123367911
332050806	chr3	123365962	123366185	123365984	123366160	MYLK	NM_053025	1	34	27	-	123366071	123366274
332078517	chr3	123366139	123366303	123366161	123366279	MYLK	NM_053025	1	34	27	-	123366071	123366274
332181134	chr3	123359077	123359286	123359097	123359265	MYLK	NM_053025	1	34	28	-	123359134	123359351
332187944	chr3	123359246	123359459	123359266	123359436	MYLK	NM_053025	1	34	28	-	123359134	123359351
332114853	chr3	123356864	123357084	123356883	123357062	MYLK	NM_053025	1	34	29	-	123356918	123357041
332136240	chr3	123348283	123348500	123348306	123348480	MYLK	NM_053025	1	34	30	-	123348321	123348473
332085943	chr3	123345600	123345824	123345628	123345799	MYLK	NM_053025	1	34	31	-	123345665	123345788
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053025	1	34	32	-	123339054	123339183
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053025	1	34	33	-	123337486	123337617
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053025	1	34	34	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053025	1	34	34	-	123331143	123333196
332121800	chr3	123512379	123512586	123512401	123512566	MYLK	NM_053026	2	33	4	-	123512524	123512691
332144757	chr3	123512545	123512762	123512567	123512741	MYLK	NM_053026	2	33	4	-	123512524	123512691
332109008	chr3	123471059	123471282	123471082	123471261	MYLK	NM_053026	2	33	5	-	123471178	123471385
332120790	chr3	123471241	123471415	123471262	123471388	MYLK	NM_053026	2	33	5	-	123471178	123471385
332099627	chr3	123458680	123458880	123458700	123458853	MYLK	NM_053026	2	33	6	-	123458800	123458848
332069291	chr3	123457706	123457929	123457725	123457903	MYLK	NM_053026	2	33	7	-	123457744	123457909
332098042	chr3	123457883	123458007	123457904	123457981	MYLK	NM_053026	2	33	7	-	123457744	123457909
332149722	chr3	123456112	123456249	123456133	123456226	MYLK	NM_053026	2	33	8	-	123456225	123456390
332160390	chr3	123456207	123456417	123456227	123456395	MYLK	NM_053026	2	33	8	-	123456225	123456390
332042675	chr3	123454104	123454326	123454130	123454298	MYLK	NM_053026	2	33	9	-	123454245	123454263
332143448	chr3	123452950	123453170	123452971	123453148	MYLK	NM_053026	2	33	10	-	123452534	123453069
332157135	chr3	123452498	123452675	123452520	123452655	MYLK	NM_053026	2	33	10	-	123452534	123453069
332162496	chr3	123452633	123452828	123452655	123452805	MYLK	NM_053026	2	33	10	-	123452534	123453069
332165709	chr3	123452773	123452995	123452794	123452975	MYLK	NM_053026	2	33	10	-	123452534	123453069
332124095	chr3	123444662	123444885	123444684	123444865	MYLK	NM_053026	2	33	11	-	123444791	123444925
332138003	chr3	123444845	123444971	123444866	123444951	MYLK	NM_053026	2	33	11	-	123444791	123444925
332151484	chr3	123440935	123441155	123440956	123441136	MYLK	NM_053026	2	33	12	-	123440975	123441127

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332113039	chr3	123428555	123428779	123428583	123428758	MYLK	NM_053026	2	33	13	-	123428603	123428740
332037055	chr3	123427434	123427614	123427452	123427597	MYLK	NM_053026	2	33	14	-	123427545	123427742
332054996	chr3	123427574	123427788	123427592	123427768	MYLK	NM_053026	2	33	14	-	123427545	123427742
332166520	chr3	123426544	123426733	123426567	123426712	MYLK	NM_053026	2	33	15	-	123426601	123426850
332179189	chr3	123426693	123426875	123426712	123426855	MYLK	NM_053026	2	33	15	-	123426601	123426850
332064994	chr3	123420177	123420393	123420199	123420365	MYLK	NM_053026	2	33	16	-	123420285	123420356
332032359	chr3	123419302	123419474	123419321	123419454	MYLK	NM_053026	2	33	17	-	123418867	123419852
332033567	chr3	123418826	123419013	123418846	123418990	MYLK	NM_053026	2	33	17	-	123418867	123419852
332044003	chr3	123419420	123419596	123419442	123419573	MYLK	NM_053026	2	33	17	-	123418867	123419852
332050049	chr3	123419535	123419742	123419555	123419722	MYLK	NM_053026	2	33	17	-	123418867	123419852
332056767	chr3	123418960	123419165	123418979	123419147	MYLK	NM_053026	2	33	17	-	123418867	123419852
332058255	chr3	123419679	123419900	123419696	123419880	MYLK	NM_053026	2	33	17	-	123418867	123419852
332083699	chr3	123419126	123419349	123419148	123419325	MYLK	NM_053026	2	33	17	-	123418867	123419852
332181540	chr3	123411529	123411730	123411551	123411706	MYLK	NM_053026	2	33	18	-	123411582	123411698
332076288	chr3	123400951	123401172	123400972	123401148	MYLK	NM_053026	2	33	19	-	123401071	123401157
332088737	chr3	123401108	123401241	123401129	123401218	MYLK	NM_053026	2	33	19	-	123401071	123401157
332104370	chr3	123385878	123386102	123385899	123386076	MYLK	NM_053026	2	33	20	-	123385984	123386034
332145815	chr3	123385004	123385220	123385025	123385199	MYLK	NM_053026	2	33	21	-	123385066	123385193
332052504	chr3	123382871	123383083	123382891	123383062	MYLK	NM_053026	2	33	22	-	123382952	123383105
332060787	chr3	123382995	123383205	123383017	123383183	MYLK	NM_053026	2	33	22	-	123382952	123383105
332133101	chr3	123375931	123376147	123375955	123376127	MYLK	NM_053026	2	33	23	-	123375973	123376275
332163219	chr3	123376107	123376305	123376128	123376280	MYLK	NM_053026	2	33	23	-	123375973	123376275
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053026	2	33	24	-	123368009	123368041
332033087	chr3	123367735	123367952	123367756	123367931	MYLK	NM_053026	2	33	25	-	123367818	123367911
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053026	2	33	25	-	123367818	123367911
332050806	chr3	123365962	123366185	123365984	123366160	MYLK	NM_053026	2	33	26	-	123366071	123366274
332078517	chr3	123366139	123366303	123366161	123366279	MYLK	NM_053026	2	33	26	-	123366071	123366274
332181134	chr3	123359077	123359286	123359097	123359265	MYLK	NM_053026	2	33	27	-	123359134	123359351
332187944	chr3	123359246	123359459	123359266	123359436	MYLK	NM_053026	2	33	27	-	123359134	123359351
332114853	chr3	123356864	123357084	123356883	123357062	MYLK	NM_053026	2	33	28	-	123356918	123357041
332136240	chr3	123348283	123348500	123348306	123348480	MYLK	NM_053026	2	33	29	-	123348321	123348473
332085943	chr3	123345600	123345824	123345628	123345799	MYLK	NM_053026	2	33	30	-	123345665	123345788
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053026	2	33	31	-	123339054	123339183
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053026	2	33	32	-	123337486	123337617
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053026	2	33	33	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053026	2	33	33	-	123331143	123333196
332121800	chr3	123512379	123512586	123512401	123512566	MYLK	NM_053027	3	33	4	-	123512524	123512691
332144757	chr3	123512545	123512762	123512567	123512741	MYLK	NM_053027	3	33	4	-	123512524	123512691
332109008	chr3	123471059	123471282	123471082	123471261	MYLK	NM_053027	3	33	5	-	123471178	123471385
332120790	chr3	123471241	123471415	123471262	123471388	MYLK	NM_053027	3	33	5	-	123471178	123471385
332099627	chr3	123458680	123458880	123458700	123458853	MYLK	NM_053027	3	33	6	-	123458800	123458848

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332069291	chr3	123457706	123457929	123457725	123457903	MYLK	NM_053027	3	33	7	-	123457744	123457909
332098042	chr3	123457883	123458007	123457904	123457981	MYLK	NM_053027	3	33	7	-	123457744	123457909
332149722	chr3	123456112	123456249	123456133	123456226	MYLK	NM_053027	3	33	8	-	123456225	123456390
332160390	chr3	123456207	123456417	123456227	123456395	MYLK	NM_053027	3	33	8	-	123456225	123456390
332042675	chr3	123454104	123454326	123454130	123454298	MYLK	NM_053027	3	33	9	-	123454245	123454263
332143448	chr3	123452950	123453170	123452971	123453148	MYLK	NM_053027	3	33	10	-	123452534	123453069
332157135	chr3	123452498	123452675	123452520	123452655	MYLK	NM_053027	3	33	10	-	123452534	123453069
332162496	chr3	123452633	123452828	123452655	123452805	MYLK	NM_053027	3	33	10	-	123452534	123453069
332165709	chr3	123452773	123452995	123452794	123452975	MYLK	NM_053027	3	33	10	-	123452534	123453069
332043088	chr3	123451667	123451887	123451688	123451863	MYLK	NM_053027	3	33	11	-	123451743	123451949
332071990	chr3	123451843	123451985	123451864	123451961	MYLK	NM_053027	3	33	11	-	123451743	123451949
332124095	chr3	123444662	123444885	123444684	123444865	MYLK	NM_053027	3	33	12	-	123444791	123444925
332138003	chr3	123444845	123444971	123444866	123444951	MYLK	NM_053027	3	33	12	-	123444791	123444925
332151484	chr3	123440935	123441155	123440956	123441136	MYLK	NM_053027	3	33	13	-	123440975	123441127
332113039	chr3	123428555	123428779	123428583	123428758	MYLK	NM_053027	3	33	14	-	123428603	123428740
332037055	chr3	123427434	123427614	123427452	123427597	MYLK	NM_053027	3	33	15	-	123427545	123427742
332054996	chr3	123427574	123427788	123427592	123427768	MYLK	NM_053027	3	33	15	-	123427545	123427742
332166520	chr3	123426544	123426733	123426567	123426712	MYLK	NM_053027	3	33	16	-	123426601	123426850
332179189	chr3	123426693	123426875	123426712	123426855	MYLK	NM_053027	3	33	16	-	123426601	123426850
332064994	chr3	123420177	123420393	123420199	123420365	MYLK	NM_053027	3	33	17	-	123420285	123420356
332032359	chr3	123419302	123419474	123419321	123419454	MYLK	NM_053027	3	33	18	-	123418867	123419852
332033567	chr3	123418826	123419013	123418846	123418990	MYLK	NM_053027	3	33	18	-	123418867	123419852
332044003	chr3	123419420	123419596	123419442	123419573	MYLK	NM_053027	3	33	18	-	123418867	123419852
332050049	chr3	123419535	123419742	123419555	123419722	MYLK	NM_053027	3	33	18	-	123418867	123419852
332056767	chr3	123418960	123419165	123418979	123419147	MYLK	NM_053027	3	33	18	-	123418867	123419852
332058255	chr3	123419679	123419900	123419696	123419880	MYLK	NM_053027	3	33	18	-	123418867	123419852
332083699	chr3	123419126	123419349	123419148	123419325	MYLK	NM_053027	3	33	18	-	123418867	123419852
332181540	chr3	123411529	123411730	123411551	123411706	MYLK	NM_053027	3	33	19	-	123411582	123411698
332076288	chr3	123400951	123401172	123400972	123401148	MYLK	NM_053027	3	33	20	-	123401071	123401157
332088737	chr3	123401108	123401241	123401129	123401218	MYLK	NM_053027	3	33	20	-	123401071	123401157
332104370	chr3	123385878	123386102	123385899	123386076	MYLK	NM_053027	3	33	21	-	123385984	123386034
332145815	chr3	123385004	123385220	123385025	123385199	MYLK	NM_053027	3	33	22	-	123385066	123385193
332052504	chr3	123382871	123383083	123382891	123383062	MYLK	NM_053027	3	33	23	-	123382952	123383105
332060787	chr3	123382995	123383205	123383017	123383183	MYLK	NM_053027	3	33	23	-	123382952	123383105
332133101	chr3	123375931	123376147	123375955	123376127	MYLK	NM_053027	3	33	24	-	123375973	123376275
332163219	chr3	123376107	123376305	123376128	123376280	MYLK	NM_053027	3	33	24	-	123375973	123376275
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053027	3	33	25	-	123368009	123368041
332033087	chr3	123367735	123367952	123367756	123367931	MYLK	NM_053027	3	33	26	-	123367818	123367911
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053027	3	33	26	-	123367818	123367911
332050806	chr3	123365962	123366185	123365984	123366160	MYLK	NM_053027	3	33	27	-	123366071	123366274
332078517	chr3	123366139	123366303	123366161	123366279	MYLK	NM_053027	3	33	27	-	123366071	123366274

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332181134	chr3	123359077	123359286	123359097	123359265	MYLK	NM_053027	3	33	28	-	123359134	123359351
332187944	chr3	123359246	123359459	123359266	123359436	MYLK	NM_053027	3	33	28	-	123359134	123359351
332114853	chr3	123356864	123357084	123356883	123357062	MYLK	NM_053027	3	33	29	-	123356918	123357041
332085943	chr3	123345600	123345824	123345628	123345799	MYLK	NM_053027	3	33	30	-	123345665	123345788
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053027	3	33	31	-	123339054	123339183
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053027	3	33	32	-	123337486	123337617
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053027	3	33	33	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053027	3	33	33	-	123331143	123333196
332121800	chr3	123512379	123512586	123512401	123512566	MYLK	NM_053028	4	32	4	-	123512524	123512691
332144757	chr3	123512545	123512762	123512567	123512741	MYLK	NM_053028	4	32	4	-	123512524	123512691
332109008	chr3	123471059	123471282	123471082	123471261	MYLK	NM_053028	4	32	5	-	123471178	123471385
332120790	chr3	123471241	123471415	123471262	123471388	MYLK	NM_053028	4	32	5	-	123471178	123471385
332099627	chr3	123458680	123458880	123458700	123458853	MYLK	NM_053028	4	32	6	-	123458800	123458848
332069291	chr3	123457706	123457929	123457725	123457903	MYLK	NM_053028	4	32	7	-	123457744	123457909
332098042	chr3	123457883	123458007	123457904	123457981	MYLK	NM_053028	4	32	7	-	123457744	123457909
332149722	chr3	123456112	123456249	123456133	123456226	MYLK	NM_053028	4	32	8	-	123456225	123456390
332160390	chr3	123456207	123456417	123456227	123456395	MYLK	NM_053028	4	32	8	-	123456225	123456390
332042675	chr3	123454104	123454326	123454130	123454298	MYLK	NM_053028	4	32	9	-	123454245	123454263
332143448	chr3	123452950	123453170	123452971	123453148	MYLK	NM_053028	4	32	10	-	123452534	123453069
332157135	chr3	123452498	123452675	123452520	123452655	MYLK	NM_053028	4	32	10	-	123452534	123453069
332162496	chr3	123452633	123452828	123452655	123452805	MYLK	NM_053028	4	32	10	-	123452534	123453069
332165709	chr3	123452773	123452995	123452794	123452975	MYLK	NM_053028	4	32	10	-	123452534	123453069
332124095	chr3	123444662	123444885	123444684	123444865	MYLK	NM_053028	4	32	11	-	123444791	123444925
332138003	chr3	123444845	123444971	123444866	123444951	MYLK	NM_053028	4	32	11	-	123444791	123444925
332151484	chr3	123440935	123441155	123440956	123441136	MYLK	NM_053028	4	32	12	-	123440975	123441127
332113039	chr3	123428555	123428779	123428583	123428758	MYLK	NM_053028	4	32	13	-	123428603	123428740
332037055	chr3	123427434	123427614	123427452	123427597	MYLK	NM_053028	4	32	14	-	123427545	123427742
332054996	chr3	123427574	123427788	123427592	123427768	MYLK	NM_053028	4	32	14	-	123427545	123427742
332166520	chr3	123426544	123426733	123426567	123426712	MYLK	NM_053028	4	32	15	-	123426601	123426850
332179189	chr3	123426693	123426875	123426712	123426855	MYLK	NM_053028	4	32	15	-	123426601	123426850
332064994	chr3	123420177	123420393	123420199	123420365	MYLK	NM_053028	4	32	16	-	123420285	123420356
332032359	chr3	123419302	123419474	123419321	123419454	MYLK	NM_053028	4	32	17	-	123418867	123419852
332033567	chr3	123418826	123419013	123418846	123418990	MYLK	NM_053028	4	32	17	-	123418867	123419852
332044003	chr3	123419420	123419596	123419442	123419573	MYLK	NM_053028	4	32	17	-	123418867	123419852
332050049	chr3	123419535	123419742	123419555	123419722	MYLK	NM_053028	4	32	17	-	123418867	123419852
332056767	chr3	123418960	123419165	123418979	123419147	MYLK	NM_053028	4	32	17	-	123418867	123419852
332058255	chr3	123419679	123419900	123419696	123419880	MYLK	NM_053028	4	32	17	-	123418867	123419852
332083699	chr3	123419126	123419349	123419148	123419325	MYLK	NM_053028	4	32	17	-	123418867	123419852
332181540	chr3	123411529	123411730	123411551	123411706	MYLK	NM_053028	4	32	18	-	123411582	123411698
332076288	chr3	123400951	123401172	123400972	123401148	MYLK	NM_053028	4	32	19	-	123401071	123401157
332088737	chr3	123401108	123401241	123401129	123401218	MYLK	NM_053028	4	32	19	-	123401071	123401157

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332104370	chr3	123385878	123386102	123385899	123386076	MYLK	NM_053028	4	32	20	-	123385984	123386034
332145815	chr3	123385004	123385220	123385025	123385199	MYLK	NM_053028	4	32	21	-	123385066	123385193
332052504	chr3	123382871	123383083	123382891	123383062	MYLK	NM_053028	4	32	22	-	123382952	123383105
332060787	chr3	123382995	123383205	123383017	123383183	MYLK	NM_053028	4	32	22	-	123382952	123383105
332133101	chr3	123375931	123376147	123375955	123376127	MYLK	NM_053028	4	32	23	-	123375973	123376275
332163219	chr3	123376107	123376305	123376128	123376280	MYLK	NM_053028	4	32	23	-	123375973	123376275
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053028	4	32	24	-	123368009	123368041
332033087	chr3	123367735	123367952	123367756	123367931	MYLK	NM_053028	4	32	25	-	123367818	123367911
332038796	chr3	123367864	123368086	123367889	123368062	MYLK	NM_053028	4	32	25	-	123367818	123367911
332050806	chr3	123365962	123366185	123365984	123366160	MYLK	NM_053028	4	32	26	-	123366071	123366274
332078517	chr3	123366139	123366303	123366161	123366279	MYLK	NM_053028	4	32	26	-	123366071	123366274
332181134	chr3	123359077	123359286	123359097	123359265	MYLK	NM_053028	4	32	27	-	123359134	123359351
332187944	chr3	123359246	123359459	123359266	123359436	MYLK	NM_053028	4	32	27	-	123359134	123359351
332114853	chr3	123356864	123357084	123356883	123357062	MYLK	NM_053028	4	32	28	-	123356918	123357041
332085943	chr3	123345600	123345824	123345628	123345799	MYLK	NM_053028	4	32	29	-	123345665	123345788
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053028	4	32	30	-	123339054	123339183
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053028	4	32	31	-	123337486	123337617
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053028	4	32	32	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053028	4	32	32	-	123331143	123333196
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053031	5	3	1	-	123339054	123339530
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053031	5	3	2	-	123337486	123337614
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053031	5	3	3	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053031	5	3	3	-	123331143	123333196
332052854	chr3	123339008	123339211	123339029	123339188	MYLK	NM_053032	6	3	1	-	123339054	123339530
332062351	chr3	123337427	123337646	123337448	123337622	MYLK	NM_053032	6	3	2	-	123337486	123337617
332107773	chr3	123332837	123333061	123332864	123333041	MYLK	NM_053032	6	3	3	-	123331143	123333196
332132264	chr3	123333019	123333242	123333040	123333215	MYLK	NM_053032	6	3	3	-	123331143	123333196
313904219	chr11	76841603	76841771	76841625	76841749	MYO7A	NM_000260	1	49	2	+	76841635	76841698
314196251	chr11	76853595	76853778	76853618	76853758	MYO7A	NM_000260	1	49	3	+	76853755	76853868
314207076	chr11	76853733	76853956	76853755	76853934	MYO7A	NM_000260	1	49	3	+	76853755	76853868
313767211	chr11	76858812	76858996	76858830	76858975	MYO7A	NM_000260	1	49	4	+	76858844	76858996
313769556	chr11	76858954	76859129	76858974	76859109	MYO7A	NM_000260	1	49	4	+	76858844	76858996
313765951	chr11	76866822	76867043	76866843	76867020	MYO7A	NM_000260	1	49	5	+	76866953	76867137
313779405	chr11	76867001	76867194	76867021	76867170	MYO7A	NM_000260	1	49	5	+	76866953	76867137
313100712	chr11	76867634	76867851	76867654	76867832	MYO7A	NM_000260	1	49	6	+	76867706	76867827
314531267	chr11	76867877	76868086	76867898	76868065	MYO7A	NM_000260	1	49	7	+	76867908	76868050
314671686	chr11	76868214	76868359	76868235	76868335	MYO7A	NM_000260	1	49	8	+	76868325	76868438
314682901	chr11	76868315	76868502	76868336	76868479	MYO7A	NM_000260	1	49	8	+	76868325	76868438
313025492	chr11	76869274	76869427	76869294	76869406	MYO7A	NM_000260	1	49	9	+	76869323	76869476
313030842	chr11	76869384	76869569	76869407	76869546	MYO7A	NM_000260	1	49	9	+	76869323	76869476
314427248	chr11	76870406	76870613	76870427	76870591	MYO7A	NM_000260	1	49	10	+	76870493	76870569

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312663544	chr11	76871047	76871244	76871069	76871224	MYO7A	NM_000260	1	49	11	+	76871209	76871328
312668405	chr11	76871193	76871389	76871214	76871368	MYO7A	NM_000260	1	49	11	+	76871209	76871328
312927719	chr11	76871898	76872076	76871918	76872051	MYO7A	NM_000260	1	49	12	+	76872019	76872161
312941121	chr11	76872032	76872236	76872052	76872211	MYO7A	NM_000260	1	49	12	+	76872019	76872161
313381050	chr11	76873124	76873347	76873145	76873325	MYO7A	NM_000260	1	49	13	+	76873166	76873376
313393635	chr11	76873299	76873520	76873319	76873497	MYO7A	NM_000260	1	49	13	+	76873166	76873376
314982983	chr11	76873797	76874021	76873819	76873999	MYO7A	NM_000260	1	49	14	+	76873899	76874034
314986629	chr11	76873978	76874114	76874000	76874090	MYO7A	NM_000260	1	49	14	+	76873899	76874034
315128252	chr11	76877070	76877213	76877092	76877194	MYO7A	NM_000260	1	49	15	+	76877102	76877208
315135328	chr11	76877168	76877336	76877194	76877312	MYO7A	NM_000260	1	49	15	+	76877102	76877208
315394787	chr11	76883710	76883856	76883728	76883838	MYO7A	NM_000260	1	49	16	+	76883794	76883931
315397942	chr11	76883818	76884008	76883839	76883982	MYO7A	NM_000260	1	49	16	+	76883794	76883931
315492628	chr11	76885707	76885869	76885729	76885849	MYO7A	NM_000260	1	49	17	+	76885802	76885960
315497374	chr11	76885830	76886040	76885850	76886014	MYO7A	NM_000260	1	49	17	+	76885802	76885960
314347826	chr11	76886376	76886574	76886397	76886552	MYO7A	NM_000260	1	49	18	+	76886418	76886510
314588051	chr11	76888539	76888750	76888560	76888727	MYO7A	NM_000260	1	49	19	+	76888595	76888689
313229490	chr11	76890049	76890222	76890067	76890202	MYO7A	NM_000260	1	49	20	+	76890091	76890175
314673980	chr11	76890721	76890908	76890741	76890889	MYO7A	NM_000260	1	49	21	+	76890781	76890999
314676616	chr11	76890855	76891066	76890874	76891046	MYO7A	NM_000260	1	49	21	+	76890781	76890999
312683397	chr11	76891357	76891571	76891378	76891550	MYO7A	NM_000260	1	49	22	+	76891420	76891527
313228209	chr11	76892397	76892574	76892419	76892550	MYO7A	NM_000260	1	49	23	+	76892426	76892635
313234671	chr11	76892529	76892692	76892550	76892672	MYO7A	NM_000260	1	49	23	+	76892426	76892635
313095561	chr11	76892969	76893109	76892990	76893087	MYO7A	NM_000260	1	49	24	+	76892997	76893200
313101276	chr11	76893066	76893232	76893088	76893211	MYO7A	NM_000260	1	49	24	+	76892997	76893200
313532772	chr11	76893401	76893568	76893423	76893546	MYO7A	NM_000260	1	49	25	+	76893469	76893645
313545040	chr11	76893525	76893736	76893547	76893715	MYO7A	NM_000260	1	49	25	+	76893469	76893645
313337983	chr11	76893995	76894200	76894015	76894177	MYO7A	NM_000260	1	49	26	+	76894113	76894202
313343920	chr11	76894156	76894365	76894178	76894343	MYO7A	NM_000260	1	49	26	+	76894113	76894202
312741249	chr11	76895586	76895744	76895608	76895723	MYO7A	NM_000260	1	49	27	+	76895633	76895760
312744435	chr11	76895704	76895829	76895724	76895809	MYO7A	NM_000260	1	49	27	+	76895633	76895760
313719834	chr11	76900268	76900424	76900288	76900404	MYO7A	NM_000260	1	49	28	+	76900389	76900515
313722590	chr11	76900384	76900604	76900404	76900584	MYO7A	NM_000260	1	49	28	+	76900389	76900515
315382889	chr11	76901002	76901148	76901023	76901124	MYO7A	NM_000260	1	49	29	+	76901065	76901184
315384735	chr11	76901100	76901304	76901119	76901280	MYO7A	NM_000260	1	49	29	+	76901065	76901184
313359217	chr11	76901586	76901801	76901607	76901779	MYO7A	NM_000260	1	49	30	+	76901742	76901915
313364852	chr11	76901760	76901925	76901780	76901904	MYO7A	NM_000260	1	49	30	+	76901742	76901915
313373280	chr11	76901879	76902065	76901902	76902044	MYO7A	NM_000260	1	49	30	+	76901742	76901915
313281817	chr11	76903007	76903231	76903029	76903211	MYO7A	NM_000260	1	49	31	+	76903096	76903323
313294319	chr11	76903190	76903395	76903209	76903376	MYO7A	NM_000260	1	49	31	+	76903096	76903323
313623648	chr11	76905251	76905464	76905272	76905440	MYO7A	NM_000260	1	49	32	+	76905399	76905569
313629226	chr11	76905420	76905604	76905441	76905581	MYO7A	NM_000260	1	49	32	+	76905399	76905569

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314686828	chr11	76908455	76908649	76908480	76908625	MYO7A	NM_000260	1	49	33	+	76908526	76908643
314326256	chr11	76909375	76909595	76909396	76909575	MYO7A	NM_000260	1	49	34	+	76909540	76909666
314344339	chr11	76909552	76909761	76909572	76909738	MYO7A	NM_000260	1	49	34	+	76909540	76909666
312669050	chr11	76910546	76910751	76910568	76910730	MYO7A	NM_000260	1	49	35	+	76910580	76910863
312686439	chr11	76910670	76910842	76910690	76910816	MYO7A	NM_000260	1	49	35	+	76910580	76910863
312697333	chr11	76910787	76910922	76910808	76910900	MYO7A	NM_000260	1	49	35	+	76910580	76910863
314640556	chr11	76912436	76912650	76912458	76912629	MYO7A	NM_000260	1	49	36	+	76912493	76912683
314651728	chr11	76912592	76912816	76912615	76912792	MYO7A	NM_000260	1	49	36	+	76912493	76912683
312998982	chr11	76913258	76913477	76913280	76913453	MYO7A	NM_000260	1	49	37	+	76913345	76913469
313012870	chr11	76913433	76913626	76913454	76913604	MYO7A	NM_000260	1	49	37	+	76913345	76913469
313236816	chr11	76913992	76914199	76914012	76914181	MYO7A	NM_000260	1	49	38	+	76914105	76914262
313238505	chr11	76914125	76914332	76914144	76914313	MYO7A	NM_000260	1	49	38	+	76914105	76914262
314966637	chr11	76915079	76915275	76915099	76915254	MYO7A	NM_000260	1	49	39	+	76915121	76915274
314977521	chr11	76915228	76915387	76915251	76915366	MYO7A	NM_000260	1	49	39	+	76915121	76915274
315072685	chr11	76916449	76916670	76916468	76916650	MYO7A	NM_000260	1	49	40	+	76916507	76916662
315073379	chr11	76916593	76916800	76916612	76916779	MYO7A	NM_000260	1	49	40	+	76916507	76916662
312810287	chr11	76917122	76917273	76917139	76917253	MYO7A	NM_000260	1	49	41	+	76917142	76917247
313372832	chr11	76918241	76918442	76918262	76918418	MYO7A	NM_000260	1	49	42	+	76918334	76918447
313381720	chr11	76918397	76918589	76918419	76918567	MYO7A	NM_000260	1	49	42	+	76918334	76918447
313283616	chr11	76919405	76919595	76919426	76919575	MYO7A	NM_000260	1	49	43	+	76919475	76919562
313075487	chr11	76919683	76919886	76919701	76919866	MYO7A	NM_000260	1	49	44	+	76919742	76919848
313650595	chr11	76922171	76922385	76922190	76922366	MYO7A	NM_000260	1	49	45	+	76922197	76922382
313659010	chr11	76922346	76922561	76922366	76922540	MYO7A	NM_000260	1	49	45	+	76922197	76922382
313398219	chr11	76922714	76922898	76922735	76922877	MYO7A	NM_000260	1	49	46	+	76922866	76922982
313402171	chr11	76922854	76923073	76922875	76923052	MYO7A	NM_000260	1	49	46	+	76922866	76922982
315057820	chr11	76923924	76924135	76923946	76924113	MYO7A	NM_000260	1	49	47	+	76923997	76924080
313002431	chr11	76924837	76925052	76924856	76925033	MYO7A	NM_000260	1	49	48	+	76924905	76925024
313239648	chr11	76925613	76925811	76925632	76925791	MYO7A	NM_000260	1	49	49	+	76925652	76926286
313904219	chr11	76841603	76841771	76841625	76841749	MYO7A	NM_001127179	2	27	2	+	76841635	76841698
314196251	chr11	76853595	76853778	76853618	76853758	MYO7A	NM_001127179	2	27	3	+	76853755	76853868
314207076	chr11	76853733	76853956	76853755	76853934	MYO7A	NM_001127179	2	27	3	+	76853755	76853868
313767211	chr11	76858812	76858996	76858830	76858975	MYO7A	NM_001127179	2	27	4	+	76858844	76858996
313769556	chr11	76858954	76859129	76858974	76859109	MYO7A	NM_001127179	2	27	4	+	76858844	76858996
313765951	chr11	76866822	76867043	76866843	76867020	MYO7A	NM_001127179	2	27	5	+	76866953	76867137
313779405	chr11	76867001	76867194	76867021	76867170	MYO7A	NM_001127179	2	27	5	+	76866953	76867137
313100712	chr11	76867634	76867851	76867654	76867832	MYO7A	NM_001127179	2	27	6	+	76867706	76867827
314531267	chr11	76867877	76868086	76867898	76868065	MYO7A	NM_001127179	2	27	7	+	76867908	76868050
314671686	chr11	76868214	76868359	76868235	76868335	MYO7A	NM_001127179	2	27	8	+	76868325	76868438
314682901	chr11	76868315	76868502	76868336	76868479	MYO7A	NM_001127179	2	27	8	+	76868325	76868438
313025492	chr11	76869274	76869427	76869294	76869406	MYO7A	NM_001127179	2	27	9	+	76869323	76869476
313030842	chr11	76869384	76869569	76869407	76869546	MYO7A	NM_001127179	2	27	9	+	76869323	76869476

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314427248	chr11	76870406	76870613	76870427	76870591	MYO7A	NM_001127179	2	27	10	+	76870493	76870569
312663544	chr11	76871047	76871244	76871069	76871224	MYO7A	NM_001127179	2	27	11	+	76871209	76871328
312668405	chr11	76871193	76871389	76871214	76871368	MYO7A	NM_001127179	2	27	11	+	76871209	76871328
312927719	chr11	76871898	76872076	76871918	76872051	MYO7A	NM_001127179	2	27	12	+	76872019	76872161
312941121	chr11	76872032	76872236	76872052	76872211	MYO7A	NM_001127179	2	27	12	+	76872019	76872161
313381050	chr11	76873124	76873347	76873145	76873325	MYO7A	NM_001127179	2	27	13	+	76873166	76873376
313393635	chr11	76873299	76873520	76873319	76873497	MYO7A	NM_001127179	2	27	13	+	76873166	76873376
314982983	chr11	76873797	76874021	76873819	76873999	MYO7A	NM_001127179	2	27	14	+	76873899	76874034
314986629	chr11	76873978	76874114	76874000	76874090	MYO7A	NM_001127179	2	27	14	+	76873899	76874034
315128252	chr11	76877070	76877213	76877092	76877194	MYO7A	NM_001127179	2	27	15	+	76877102	76877208
315135328	chr11	76877168	76877336	76877194	76877312	MYO7A	NM_001127179	2	27	15	+	76877102	76877208
315394787	chr11	76883710	76883856	76883728	76883838	MYO7A	NM_001127179	2	27	16	+	76883794	76883931
315397942	chr11	76883818	76884008	76883839	76883982	MYO7A	NM_001127179	2	27	16	+	76883794	76883931
315492628	chr11	76885707	76885869	76885729	76885849	MYO7A	NM_001127179	2	27	17	+	76885802	76885960
315497374	chr11	76885830	76886040	76885850	76886014	MYO7A	NM_001127179	2	27	17	+	76885802	76885960
314347826	chr11	76886376	76886574	76886397	76886552	MYO7A	NM_001127179	2	27	18	+	76886418	76886510
314588051	chr11	76888539	76888750	76888560	76888727	MYO7A	NM_001127179	2	27	19	+	76888595	76888689
313229490	chr11	76890049	76890222	76890067	76890202	MYO7A	NM_001127179	2	27	20	+	76890091	76890175
314673980	chr11	76890721	76890908	76890741	76890889	MYO7A	NM_001127179	2	27	21	+	76890781	76890999
314676616	chr11	76890855	76891066	76890874	76891046	MYO7A	NM_001127179	2	27	21	+	76890781	76890999
312683397	chr11	76891357	76891571	76891378	76891550	MYO7A	NM_001127179	2	27	22	+	76891420	76891527
313228209	chr11	76892397	76892574	76892419	76892550	MYO7A	NM_001127179	2	27	23	+	76892426	76892635
313234671	chr11	76892529	76892692	76892550	76892672	MYO7A	NM_001127179	2	27	23	+	76892426	76892635
313095561	chr11	76892969	76893109	76892990	76893087	MYO7A	NM_001127179	2	27	24	+	76892997	76893200
313101276	chr11	76893066	76893232	76893088	76893211	MYO7A	NM_001127179	2	27	24	+	76892997	76893200
313532772	chr11	76893401	76893568	76893423	76893546	MYO7A	NM_001127179	2	27	25	+	76893469	76893645
313545040	chr11	76893525	76893736	76893547	76893715	MYO7A	NM_001127179	2	27	25	+	76893469	76893645
313337983	chr11	76893995	76894200	76894015	76894177	MYO7A	NM_001127179	2	27	26	+	76894113	76894202
313343920	chr11	76894156	76894365	76894178	76894343	MYO7A	NM_001127179	2	27	26	+	76894113	76894202
312741249	chr11	76895586	76895744	76895608	76895723	MYO7A	NM_001127179	2	27	27	+	76895633	76896041
312744435	chr11	76895704	76895829	76895724	76895809	MYO7A	NM_001127179	2	27	27	+	76895633	76896041
313904219	chr11	76841603	76841771	76841625	76841749	MYO7A	NM_001127180	3	49	2	+	76841635	76841698
314196251	chr11	76853595	76853778	76853618	76853758	MYO7A	NM_001127180	3	49	3	+	76853755	76853868
314207076	chr11	76853733	76853956	76853755	76853934	MYO7A	NM_001127180	3	49	3	+	76853755	76853868
313767211	chr11	76858812	76858996	76858830	76858975	MYO7A	NM_001127180	3	49	4	+	76858844	76858996
313769556	chr11	76858954	76859129	76858974	76859109	MYO7A	NM_001127180	3	49	4	+	76858844	76858996
313765951	chr11	76866822	76867043	76866843	76867020	MYO7A	NM_001127180	3	49	5	+	76866953	76867137
313779405	chr11	76867001	76867194	76867021	76867170	MYO7A	NM_001127180	3	49	5	+	76866953	76867137
313100712	chr11	76867634	76867851	76867654	76867832	MYO7A	NM_001127180	3	49	6	+	76867706	76867827
314531267	chr11	76867877	76868086	76867898	76868065	MYO7A	NM_001127180	3	49	7	+	76867908	76868050
314671686	chr11	76868214	76868359	76868235	76868335	MYO7A	NM_001127180	3	49	8	+	76868325	76868438

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
314682901	chr11	76868315	76868502	76868336	76868479	MYO7A	NM_001127180	3	49	8	+	76868325	76868438
313025492	chr11	76869274	76869427	76869294	76869406	MYO7A	NM_001127180	3	49	9	+	76869323	76869476
313030842	chr11	76869384	76869569	76869407	76869546	MYO7A	NM_001127180	3	49	9	+	76869323	76869476
314427248	chr11	76870406	76870613	76870427	76870591	MYO7A	NM_001127180	3	49	10	+	76870493	76870569
312663544	chr11	76871047	76871244	76871069	76871224	MYO7A	NM_001127180	3	49	11	+	76871209	76871328
312668405	chr11	76871193	76871389	76871214	76871368	MYO7A	NM_001127180	3	49	11	+	76871209	76871328
312927719	chr11	76871898	76872076	76871918	76872051	MYO7A	NM_001127180	3	49	12	+	76872019	76872161
312941121	chr11	76872032	76872236	76872052	76872211	MYO7A	NM_001127180	3	49	12	+	76872019	76872161
313381050	chr11	76873124	76873347	76873145	76873325	MYO7A	NM_001127180	3	49	13	+	76873166	76873376
313393635	chr11	76873299	76873520	76873319	76873497	MYO7A	NM_001127180	3	49	13	+	76873166	76873376
314982983	chr11	76873797	76874021	76873819	76873999	MYO7A	NM_001127180	3	49	14	+	76873899	76874034
314986629	chr11	76873978	76874114	76874000	76874090	MYO7A	NM_001127180	3	49	14	+	76873899	76874034
315128252	chr11	76877070	76877213	76877092	76877194	MYO7A	NM_001127180	3	49	15	+	76877102	76877208
315135328	chr11	76877168	76877336	76877194	76877312	MYO7A	NM_001127180	3	49	15	+	76877102	76877208
315394787	chr11	76883710	76883856	76883728	76883838	MYO7A	NM_001127180	3	49	16	+	76883794	76883931
315397942	chr11	76883818	76884008	76883839	76883982	MYO7A	NM_001127180	3	49	16	+	76883794	76883931
315492628	chr11	76885707	76885869	76885729	76885849	MYO7A	NM_001127180	3	49	17	+	76885802	76885960
315497374	chr11	76885830	76886040	76885850	76886014	MYO7A	NM_001127180	3	49	17	+	76885802	76885960
314347826	chr11	76886376	76886574	76886397	76886552	MYO7A	NM_001127180	3	49	18	+	76886418	76886510
314588051	chr11	76888539	76888750	76888560	76888727	MYO7A	NM_001127180	3	49	19	+	76888595	76888689
313229490	chr11	76890049	76890222	76890067	76890202	MYO7A	NM_001127180	3	49	20	+	76890091	76890175
314673980	chr11	76890721	76890908	76890741	76890889	MYO7A	NM_001127180	3	49	21	+	76890781	76890999
314676616	chr11	76890855	76891066	76890874	76891046	MYO7A	NM_001127180	3	49	21	+	76890781	76890999
312683397	chr11	76891357	76891571	76891378	76891550	MYO7A	NM_001127180	3	49	22	+	76891420	76891527
313228209	chr11	76892397	76892574	76892419	76892550	MYO7A	NM_001127180	3	49	23	+	76892426	76892635
313234671	chr11	76892529	76892692	76892550	76892672	MYO7A	NM_001127180	3	49	23	+	76892426	76892635
313095561	chr11	76892969	76893109	76892990	76893087	MYO7A	NM_001127180	3	49	24	+	76892997	76893200
313101276	chr11	76893066	76893232	76893088	76893211	MYO7A	NM_001127180	3	49	24	+	76892997	76893200
313532772	chr11	76893401	76893568	76893423	76893546	MYO7A	NM_001127180	3	49	25	+	76893469	76893645
313545040	chr11	76893525	76893736	76893547	76893715	MYO7A	NM_001127180	3	49	25	+	76893469	76893645
313337983	chr11	76893995	76894200	76894015	76894177	MYO7A	NM_001127180	3	49	26	+	76894113	76894202
313343920	chr11	76894156	76894365	76894178	76894343	MYO7A	NM_001127180	3	49	26	+	76894113	76894202
312741249	chr11	76895586	76895744	76895608	76895723	MYO7A	NM_001127180	3	49	27	+	76895633	76895760
312744435	chr11	76895704	76895829	76895724	76895809	MYO7A	NM_001127180	3	49	27	+	76895633	76895760
313719834	chr11	76900268	76900424	76900288	76900404	MYO7A	NM_001127180	3	49	28	+	76900389	76900515
313722590	chr11	76900384	76900604	76900404	76900584	MYO7A	NM_001127180	3	49	28	+	76900389	76900515
315382889	chr11	76901002	76901148	76901023	76901124	MYO7A	NM_001127180	3	49	29	+	76901065	76901184
315384735	chr11	76901100	76901304	76901119	76901280	MYO7A	NM_001127180	3	49	29	+	76901065	76901184
313359217	chr11	76901586	76901801	76901607	76901779	MYO7A	NM_001127180	3	49	30	+	76901742	76901915
313364852	chr11	76901760	76901925	76901780	76901904	MYO7A	NM_001127180	3	49	30	+	76901742	76901915
313373280	chr11	76901879	76902065	76901902	76902044	MYO7A	NM_001127180	3	49	30	+	76901742	76901915

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
313281817	chr11	76903007	76903231	76903029	76903211	MYO7A	NM_001127180	3	49	31	+	76903096	76903323
313294319	chr11	76903190	76903395	76903209	76903376	MYO7A	NM_001127180	3	49	31	+	76903096	76903323
313623648	chr11	76905251	76905464	76905272	76905440	MYO7A	NM_001127180	3	49	32	+	76905399	76905569
313629226	chr11	76905420	76905604	76905441	76905581	MYO7A	NM_001127180	3	49	32	+	76905399	76905569
314686828	chr11	76908455	76908649	76908480	76908625	MYO7A	NM_001127180	3	49	33	+	76908526	76908643
314326256	chr11	76909375	76909595	76909396	76909575	MYO7A	NM_001127180	3	49	34	+	76909540	76909666
314344339	chr11	76909552	76909761	76909572	76909738	MYO7A	NM_001127180	3	49	34	+	76909540	76909666
312669050	chr11	76910546	76910751	76910568	76910730	MYO7A	NM_001127180	3	49	35	+	76910694	76910863
312686439	chr11	76910670	76910842	76910690	76910816	MYO7A	NM_001127180	3	49	35	+	76910694	76910863
312697333	chr11	76910787	76910922	76910808	76910900	MYO7A	NM_001127180	3	49	35	+	76910694	76910863
314640556	chr11	76912436	76912650	76912458	76912629	MYO7A	NM_001127180	3	49	36	+	76912493	76912683
314651728	chr11	76912592	76912816	76912615	76912792	MYO7A	NM_001127180	3	49	36	+	76912493	76912683
312998982	chr11	76913258	76913477	76913280	76913453	MYO7A	NM_001127180	3	49	37	+	76913345	76913469
313012870	chr11	76913433	76913626	76913454	76913604	MYO7A	NM_001127180	3	49	37	+	76913345	76913469
313236816	chr11	76913992	76914199	76914012	76914181	MYO7A	NM_001127180	3	49	38	+	76914105	76914262
313238505	chr11	76914125	76914332	76914144	76914313	MYO7A	NM_001127180	3	49	38	+	76914105	76914262
314966637	chr11	76915079	76915275	76915099	76915254	MYO7A	NM_001127180	3	49	39	+	76915121	76915274
314977521	chr11	76915228	76915387	76915251	76915366	MYO7A	NM_001127180	3	49	39	+	76915121	76915274
315072685	chr11	76916449	76916670	76916468	76916650	MYO7A	NM_001127180	3	49	40	+	76916507	76916662
315073379	chr11	76916593	76916800	76916612	76916779	MYO7A	NM_001127180	3	49	40	+	76916507	76916662
312810287	chr11	76917122	76917273	76917139	76917253	MYO7A	NM_001127180	3	49	41	+	76917142	76917247
313372832	chr11	76918241	76918442	76918262	76918418	MYO7A	NM_001127180	3	49	42	+	76918334	76918447
313381720	chr11	76918397	76918589	76918419	76918567	MYO7A	NM_001127180	3	49	42	+	76918334	76918447
313283616	chr11	76919405	76919595	76919426	76919575	MYO7A	NM_001127180	3	49	43	+	76919475	76919562
313075487	chr11	76919683	76919886	76919701	76919866	MYO7A	NM_001127180	3	49	44	+	76919742	76919848
313650595	chr11	76922171	76922385	76922190	76922366	MYO7A	NM_001127180	3	49	45	+	76922197	76922382
313659010	chr11	76922346	76922561	76922366	76922540	MYO7A	NM_001127180	3	49	45	+	76922197	76922382
313398219	chr11	76922714	76922898	76922735	76922877	MYO7A	NM_001127180	3	49	46	+	76922866	76922976
313402171	chr11	76922854	76923073	76922875	76923052	MYO7A	NM_001127180	3	49	46	+	76922866	76922976
315057820	chr11	76923924	76924135	76923946	76924113	MYO7A	NM_001127180	3	49	47	+	76923997	76924080
313002431	chr11	76924837	76925052	76924856	76925033	MYO7A	NM_001127180	3	49	48	+	76924905	76925024
313239648	chr11	76925613	76925811	76925632	76925791	MYO7A	NM_001127180	3	49	49	+	76925652	76926286
333547171	chr4	120057610	120057796	120057637	120057768	MYOZ2	NM_016599	1	6	2	+	120057667	120057756
332482968	chr4	120072017	120072234	120072043	120072206	MYOZ2	NM_016599	1	6	3	+	120072027	120072196
333229829	chr4	120079004	120079221	120079025	120079196	MYOZ2	NM_016599	1	6	4	+	120079177	120079306
333236271	chr4	120079173	120079370	120079197	120079343	MYOZ2	NM_016599	1	6	4	+	120079177	120079306
333698143	chr4	120085207	120085420	120085230	120085395	MYOZ2	NM_016599	1	6	5	+	120085366	120085549
333720225	chr4	120085373	120085590	120085396	120085568	MYOZ2	NM_016599	1	6	5	+	120085366	120085549
332891056	chr4	120106935	120107154	120106963	120107128	MYOZ2	NM_016599	1	6	6	+	120107121	120108944
332893125	chr4	120107109	120107255	120107129	120107235	MYOZ2	NM_016599	1	6	6	+	120107121	120108944
332905452	chr4	120107211	120107434	120107236	120107407	MYOZ2	NM_016599	1	6	6	+	120107121	120108944

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258118639	chr17	29422203	29422381	29422221	29422364	NF1	NM_000267	1	57	1	+	29421945	29422387
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_000267	1	57	1	+	29421945	29422387
237186614	chr17	29482878	29483049	29482905	29483023	NF1	NM_000267	1	57	2	+	29483001	29483144
237193452	chr17	29483000	29483182	29483024	29483156	NF1	NM_000267	1	57	2	+	29483001	29483144
236388202	chr17	29485947	29486145	29485975	29486116	NF1	NM_000267	1	57	3	+	29486028	29486111
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_000267	1	57	4	+	29490204	29490394
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_000267	1	57	4	+	29490204	29490394
235554636	chr17	29496923	29497118	29496951	29497090	NF1	NM_000267	1	57	5	+	29496909	29497015
240265478	chr17	29508340	29508520	29508370	29508493	NF1	NM_000267	1	57	6	+	29508440	29508507
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_000267	1	57	6	+	29508440	29508507
238570302	chr17	29508726	29508936	29508751	29508908	NF1	NM_000267	1	57	7	+	29508728	29508803
237436422	chr17	29509430	29509587	29509455	29509564	NF1	NM_000267	1	57	8	+	29509526	29509683
237442947	chr17	29509539	29509746	29509565	29509717	NF1	NM_000267	1	57	8	+	29509526	29509683
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_000267	1	57	9	+	29527440	29527613
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_000267	1	57	9	+	29527440	29527613
235109655	chr17	29527519	29527743	29527546	29527715	NF1	NM_000267	1	57	9	+	29527440	29527613
258490074	chr17	29527941	29528141	29527963	29528116	NF1	NM_000267	1	57	10	+	29528055	29528177
258513162	chr17	29528067	29528192	29528093	29528167	NF1	NM_000267	1	57	10	+	29528055	29528177
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_000267	1	57	10	+	29528055	29528177
236497505	chr17	29528340	29528517	29528368	29528489	NF1	NM_000267	1	57	11	+	29528429	29528503
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_000267	1	57	11	+	29528429	29528503
236050823	chr17	29533129	29533288	29533151	29533264	NF1	NM_000267	1	57	12	+	29533258	29533389
236066944	chr17	29533239	29533424	29533265	29533397	NF1	NM_000267	1	57	12	+	29533258	29533389
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_000267	1	57	13	+	29541469	29541603
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_000267	1	57	14	+	29546023	29546136
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_000267	1	57	14	+	29546023	29546136
237408995	chr17	29548873	29549072	29548901	29549042	NF1	NM_000267	1	57	15	+	29548868	29548947
237780540	chr17	29550452	29550640	29550474	29550611	NF1	NM_000267	1	57	16	+	29550462	29550585
237215961	chr17	29552023	29552209	29552049	29552182	NF1	NM_000267	1	57	17	+	29552113	29552268
237229091	chr17	29552153	29552292	29552180	29552265	NF1	NM_000267	1	57	17	+	29552113	29552268
236044556	chr17	29553417	29553556	29553444	29553536	NF1	NM_000267	1	57	18	+	29553453	29553702
236052142	chr17	29553506	29553693	29553530	29553668	NF1	NM_000267	1	57	18	+	29553453	29553702
236073609	chr17	29553633	29553764	29553659	29553739	NF1	NM_000267	1	57	18	+	29553453	29553702
241781507	chr17	29554147	29554370	29554169	29554348	NF1	NM_000267	1	57	19	+	29554236	29554309
237283484	chr17	29554496	29554708	29554524	29554680	NF1	NM_000267	1	57	20	+	29554541	29554624
236361235	chr17	29555952	29556131	29555980	29556105	NF1	NM_000267	1	57	21	+	29556043	29556483
236362724	chr17	29556043	29556235	29556065	29556215	NF1	NM_000267	1	57	21	+	29556043	29556483
236382711	chr17	29556186	29556393	29556208	29556365	NF1	NM_000267	1	57	21	+	29556043	29556483
236390839	chr17	29556292	29556496	29556315	29556472	NF1	NM_000267	1	57	21	+	29556043	29556483
236397974	chr17	29556411	29556546	29556439	29556516	NF1	NM_000267	1	57	21	+	29556043	29556483
257885353	chr17	29556743	29556967	29556763	29556944	NF1	NM_000267	1	57	22	+	29556853	29556992

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257902551	chr17	29556918	29557102	29556945	29557080	NF1	NM_000267	1	57	22	+	29556853	29556992
235501936	chr17	29557215	29557366	29557248	29557338	NF1	NM_000267	1	57	23	+	29557278	29557400
235504478	chr17	29557301	29557498	29557329	29557474	NF1	NM_000267	1	57	23	+	29557278	29557400
239102154	chr17	29557800	29557937	29557823	29557910	NF1	NM_000267	1	57	24	+	29557860	29557943
236461306	chr17	29559024	29559203	29559051	29559175	NF1	NM_000267	1	57	25	+	29559091	29559207
236466777	chr17	29559153	29559298	29559176	29559271	NF1	NM_000267	1	57	25	+	29559091	29559207
236201515	chr17	29559619	29559783	29559644	29559759	NF1	NM_000267	1	57	26	+	29559718	29559899
236226704	chr17	29559735	29559959	29559760	29559933	NF1	NM_000267	1	57	26	+	29559718	29559899
237068798	chr17	29559933	29560140	29559960	29560115	NF1	NM_000267	1	57	27	+	29560020	29560231
237111695	chr17	29560092	29560262	29560116	29560236	NF1	NM_000267	1	57	27	+	29560020	29560231
239127311	chr17	29562500	29562670	29562527	29562645	NF1	NM_000267	1	57	28	+	29562629	29562790
239153785	chr17	29562622	29562828	29562646	29562803	NF1	NM_000267	1	57	28	+	29562629	29562790
236743239	chr17	29562809	29563028	29562832	29563004	NF1	NM_000267	1	57	29	+	29562936	29563039
236762074	chr17	29562963	29563133	29562991	29563112	NF1	NM_000267	1	57	29	+	29562936	29563039
242686025	chr17	29575883	29576048	29575906	29576028	NF1	NM_000267	1	57	30	+	29576002	29576137
242714582	chr17	29576008	29576223	29576029	29576195	NF1	NM_000267	1	57	30	+	29576002	29576137
235370590	chr17	29585286	29585505	29585314	29585483	NF1	NM_000267	1	57	31	+	29585362	29585520
235374615	chr17	29585435	29585650	29585458	29585622	NF1	NM_000267	1	57	31	+	29585362	29585520
237203098	chr17	29585942	29586104	29585975	29586080	NF1	NM_000267	1	57	32	+	29586050	29586147
237203200	chr17	29586052	29586176	29586080	29586152	NF1	NM_000267	1	57	32	+	29586050	29586147
235093821	chr17	29587340	29587562	29587368	29587538	NF1	NM_000267	1	57	33	+	29587387	29587533
236391839	chr17	29588613	29588793	29588639	29588771	NF1	NM_000267	1	57	34	+	29588729	29588875
236401270	chr17	29588747	29588939	29588772	29588918	NF1	NM_000267	1	57	34	+	29588729	29588875
235389989	chr17	29592193	29592318	29592222	29592292	NF1	NM_000267	1	57	35	+	29592247	29592357
235390517	chr17	29592245	29592462	29592273	29592435	NF1	NM_000267	1	57	35	+	29592247	29592357
239268603	chr17	29652823	29653030	29652851	29653010	NF1	NM_000267	1	57	36	+	29652838	29653270
239297691	chr17	29652987	29653143	29653011	29653117	NF1	NM_000267	1	57	36	+	29652838	29653270
239322145	chr17	29653096	29653303	29653118	29653276	NF1	NM_000267	1	57	36	+	29652838	29653270
239696614	chr17	29654434	29654653	29654456	29654626	NF1	NM_000267	1	57	37	+	29654517	29654857
239800318	chr17	29654602	29654801	29654627	29654779	NF1	NM_000267	1	57	37	+	29654517	29654857
239859185	chr17	29654758	29654982	29654780	29654959	NF1	NM_000267	1	57	37	+	29654517	29654857
242446520	chr17	29657203	29657353	29657236	29657325	NF1	NM_000267	1	57	38	+	29657314	29657516
242447158	chr17	29657290	29657418	29657318	29657393	NF1	NM_000267	1	57	38	+	29657314	29657516
242466922	chr17	29657460	29657624	29657483	29657593	NF1	NM_000267	1	57	38	+	29657314	29657516
257426404	chr17	29657370	29657511	29657394	29657482	NF1	NM_000267	1	57	38	+	29657314	29657516
258359458	chr17	29661724	29661938	29661746	29661910	NF1	NM_000267	1	57	39	+	29661856	29662049
258376739	chr17	29661887	29662063	29661911	29662041	NF1	NM_000267	1	57	39	+	29661856	29662049
238333700	chr17	29663234	29663445	29663261	29663421	NF1	NM_000267	1	57	40	+	29663351	29663491
238335871	chr17	29663401	29663615	29663422	29663589	NF1	NM_000267	1	57	40	+	29663351	29663491
240003548	chr17	29663591	29663793	29663617	29663768	NF1	NM_000267	1	57	41	+	29663653	29663932
240026382	chr17	29663749	29663968	29663769	29663941	NF1	NM_000267	1	57	41	+	29663653	29663932

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239206598	chr17	29664348	29664479	29664381	29664455	NF1	NM_000267	1	57	42	+	29664386	29664600
239213676	chr17	29664413	29664618	29664441	29664591	NF1	NM_000267	1	57	42	+	29664386	29664600
239661439	chr17	29664720	29664894	29664744	29664872	NF1	NM_000267	1	57	43	+	29664837	29664898
239663032	chr17	29664844	29665028	29664869	29665000	NF1	NM_000267	1	57	43	+	29664837	29664898
241493432	chr17	29665047	29665177	29665074	29665158	NF1	NM_000267	1	57	44	+	29665043	29665157
237076660	chr17	29665705	29665870	29665732	29665844	NF1	NM_000267	1	57	45	+	29665722	29665823
237656672	chr17	29667478	29667699	29667507	29667673	NF1	NM_000267	1	57	46	+	29667523	29667663
235870627	chr17	29669965	29670139	29669991	29670111	NF1	NM_000267	1	57	47	+	29670027	29670153
235874055	chr17	29670071	29670283	29670093	29670253	NF1	NM_000267	1	57	47	+	29670027	29670153
235988966	chr17	29676022	29676227	29676050	29676199	NF1	NM_000267	1	57	48	+	29676138	29676269
235997238	chr17	29676158	29676376	29676184	29676359	NF1	NM_000267	1	57	48	+	29676138	29676269
239676973	chr17	29677090	29677231	29677118	29677203	NF1	NM_000267	1	57	49	+	29677201	29677336
239688556	chr17	29677182	29677406	29677204	29677378	NF1	NM_000267	1	57	49	+	29677201	29677336
237984418	chr17	29679200	29679422	29679222	29679399	NF1	NM_000267	1	57	50	+	29679275	29679432
237994918	chr17	29679373	29679557	29679395	29679530	NF1	NM_000267	1	57	50	+	29679275	29679432
235934655	chr17	29683349	29683556	29683376	29683530	NF1	NM_000267	1	57	51	+	29683478	29683600
235938675	chr17	29683507	29683654	29683531	29683625	NF1	NM_000267	1	57	51	+	29683478	29683600
241766339	chr17	29683921	29684085	29683947	29684057	NF1	NM_000267	1	57	52	+	29683978	29684108
241777431	chr17	29684030	29684174	29684058	29684146	NF1	NM_000267	1	57	52	+	29683978	29684108
241696389	chr17	29684203	29684424	29684228	29684396	NF1	NM_000267	1	57	53	+	29684287	29684387
238959215	chr17	29685379	29685583	29685406	29685556	NF1	NM_000267	1	57	54	+	29685498	29685640
238972679	chr17	29685529	29685674	29685557	29685645	NF1	NM_000267	1	57	54	+	29685498	29685640
236222301	chr17	29685975	29686114	29686003	29686086	NF1	NM_000267	1	57	55	+	29685987	29686033
235180428	chr17	29687492	29687617	29687520	29687594	NF1	NM_000267	1	57	56	+	29687505	29687721
235197865	chr17	29687571	29687771	29687595	29687743	NF1	NM_000267	1	57	56	+	29687505	29687721
258078851	chr17	29700997	29701221	29701025	29701194	NF1	NM_000267	1	57	57	+	29701031	29704695
258118639	chr17	29422203	29422381	29422221	29422364	NF1	NM_001042492	2	58	1	+	29421945	29422387
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_001042492	2	58	1	+	29421945	29422387
237186614	chr17	29482878	29483049	29482905	29483023	NF1	NM_001042492	2	58	2	+	29483001	29483144
237193452	chr17	29483000	29483182	29483024	29483156	NF1	NM_001042492	2	58	2	+	29483001	29483144
236388202	chr17	29485947	29486145	29485975	29486116	NF1	NM_001042492	2	58	3	+	29486028	29486111
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_001042492	2	58	4	+	29490204	29490394
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_001042492	2	58	4	+	29490204	29490394
235554636	chr17	29496923	29497118	29496951	29497090	NF1	NM_001042492	2	58	5	+	29496909	29497015
240265478	chr17	29508340	29508520	29508370	29508493	NF1	NM_001042492	2	58	6	+	29508440	29508507
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_001042492	2	58	6	+	29508440	29508507
238570302	chr17	29508726	29508936	29508751	29508908	NF1	NM_001042492	2	58	7	+	29508728	29508803
237436422	chr17	29509430	29509587	29509455	29509564	NF1	NM_001042492	2	58	8	+	29509526	29509683
237442947	chr17	29509539	29509746	29509565	29509717	NF1	NM_001042492	2	58	8	+	29509526	29509683
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_001042492	2	58	9	+	29527440	29527613
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_001042492	2	58	9	+	29527440	29527613

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235109655	chr17	29527519	29527743	29527546	29527715	NF1	NM_001042492	2	58	9	+	29527440	29527613
258490074	chr17	29527941	29528141	29527963	29528116	NF1	NM_001042492	2	58	10	+	29528055	29528177
258513162	chr17	29528067	29528192	29528093	29528167	NF1	NM_001042492	2	58	10	+	29528055	29528177
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_001042492	2	58	10	+	29528055	29528177
236497505	chr17	29528340	29528517	29528368	29528489	NF1	NM_001042492	2	58	11	+	29528429	29528503
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_001042492	2	58	11	+	29528429	29528503
236050823	chr17	29533129	29533288	29533151	29533264	NF1	NM_001042492	2	58	12	+	29533258	29533389
236066944	chr17	29533239	29533424	29533265	29533397	NF1	NM_001042492	2	58	12	+	29533258	29533389
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_001042492	2	58	13	+	29541469	29541603
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_001042492	2	58	14	+	29546023	29546136
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_001042492	2	58	14	+	29546023	29546136
237408995	chr17	29548873	29549072	29548901	29549042	NF1	NM_001042492	2	58	15	+	29548868	29548947
237780540	chr17	29550452	29550640	29550474	29550611	NF1	NM_001042492	2	58	16	+	29550462	29550585
237215961	chr17	29552023	29552209	29552049	29552182	NF1	NM_001042492	2	58	17	+	29552113	29552268
237229091	chr17	29552153	29552292	29552180	29552265	NF1	NM_001042492	2	58	17	+	29552113	29552268
236044556	chr17	29553417	29553556	29553444	29553536	NF1	NM_001042492	2	58	18	+	29553453	29553702
236052142	chr17	29553506	29553693	29553530	29553668	NF1	NM_001042492	2	58	18	+	29553453	29553702
236073609	chr17	29553633	29553764	29553659	29553739	NF1	NM_001042492	2	58	18	+	29553453	29553702
241781507	chr17	29554147	29554370	29554169	29554348	NF1	NM_001042492	2	58	19	+	29554236	29554309
237283484	chr17	29554496	29554708	29554524	29554680	NF1	NM_001042492	2	58	20	+	29554541	29554624
236361235	chr17	29555952	29556131	29555980	29556105	NF1	NM_001042492	2	58	21	+	29556043	29556483
236362724	chr17	29556043	29556235	29556065	29556215	NF1	NM_001042492	2	58	21	+	29556043	29556483
236382711	chr17	29556186	29556393	29556208	29556365	NF1	NM_001042492	2	58	21	+	29556043	29556483
236390839	chr17	29556292	29556496	29556315	29556472	NF1	NM_001042492	2	58	21	+	29556043	29556483
236397974	chr17	29556411	29556546	29556439	29556516	NF1	NM_001042492	2	58	21	+	29556043	29556483
257885353	chr17	29556743	29556967	29556763	29556944	NF1	NM_001042492	2	58	22	+	29556853	29556992
257902551	chr17	29556918	29557102	29556945	29557080	NF1	NM_001042492	2	58	22	+	29556853	29556992
235501936	chr17	29557215	29557366	29557248	29557338	NF1	NM_001042492	2	58	23	+	29557278	29557400
235504478	chr17	29557301	29557498	29557329	29557474	NF1	NM_001042492	2	58	23	+	29557278	29557400
239102154	chr17	29557800	29557937	29557823	29557910	NF1	NM_001042492	2	58	24	+	29557860	29557943
236461306	chr17	29559024	29559203	29559051	29559175	NF1	NM_001042492	2	58	25	+	29559091	29559207
236466777	chr17	29559153	29559298	29559176	29559271	NF1	NM_001042492	2	58	25	+	29559091	29559207
236201515	chr17	29559619	29559783	29559644	29559759	NF1	NM_001042492	2	58	26	+	29559718	29559899
236226704	chr17	29559735	29559959	29559760	29559933	NF1	NM_001042492	2	58	26	+	29559718	29559899
237068798	chr17	29559933	29560140	29559960	29560115	NF1	NM_001042492	2	58	27	+	29560020	29560231
237111695	chr17	29560092	29560262	29560116	29560236	NF1	NM_001042492	2	58	27	+	29560020	29560231
239127311	chr17	29562500	29562670	29562527	29562645	NF1	NM_001042492	2	58	28	+	29562629	29562790
239153785	chr17	29562622	29562828	29562646	29562803	NF1	NM_001042492	2	58	28	+	29562629	29562790
236743239	chr17	29562809	29563028	29562832	29563004	NF1	NM_001042492	2	58	29	+	29562936	29563039
236762074	chr17	29562963	29563133	29562991	29563112	NF1	NM_001042492	2	58	29	+	29562936	29563039
242686025	chr17	29575883	29576048	29575906	29576028	NF1	NM_001042492	2	58	30	+	29576002	29576137

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242714582	chr17	29576008	29576223	29576029	29576195	NF1	NM_001042492	2	58	30	+	29576002	29576137
257710522	chr17	29579895	29580119	29579921	29580093	NF1	NM_001042492	2	58	31	+	29579956	29580018
235370590	chr17	29585286	29585505	29585314	29585483	NF1	NM_001042492	2	58	32	+	29585362	29585520
235374615	chr17	29585435	29585650	29585458	29585622	NF1	NM_001042492	2	58	32	+	29585362	29585520
237203098	chr17	29585942	29586104	29585975	29586080	NF1	NM_001042492	2	58	33	+	29586050	29586147
237203200	chr17	29586052	29586176	29586080	29586152	NF1	NM_001042492	2	58	33	+	29586050	29586147
235093821	chr17	29587340	29587562	29587368	29587538	NF1	NM_001042492	2	58	34	+	29587387	29587533
236391839	chr17	29588613	29588793	29588639	29588771	NF1	NM_001042492	2	58	35	+	29588729	29588875
236401270	chr17	29588747	29588939	29588772	29588918	NF1	NM_001042492	2	58	35	+	29588729	29588875
235389989	chr17	29592193	29592318	29592222	29592292	NF1	NM_001042492	2	58	36	+	29592247	29592357
235390517	chr17	29592245	29592462	29592273	29592435	NF1	NM_001042492	2	58	36	+	29592247	29592357
239268603	chr17	29652823	29653030	29652851	29653010	NF1	NM_001042492	2	58	37	+	29652838	29653270
239297691	chr17	29652987	29653143	29653011	29653117	NF1	NM_001042492	2	58	37	+	29652838	29653270
239322145	chr17	29653096	29653303	29653118	29653276	NF1	NM_001042492	2	58	37	+	29652838	29653270
239696614	chr17	29654434	29654653	29654456	29654626	NF1	NM_001042492	2	58	38	+	29654517	29654857
239800318	chr17	29654602	29654801	29654627	29654779	NF1	NM_001042492	2	58	38	+	29654517	29654857
239859185	chr17	29654758	29654982	29654780	29654959	NF1	NM_001042492	2	58	38	+	29654517	29654857
242446520	chr17	29657203	29657353	29657236	29657325	NF1	NM_001042492	2	58	39	+	29657314	29657516
242447158	chr17	29657290	29657418	29657318	29657393	NF1	NM_001042492	2	58	39	+	29657314	29657516
242466922	chr17	29657460	29657624	29657483	29657593	NF1	NM_001042492	2	58	39	+	29657314	29657516
257426404	chr17	29657370	29657511	29657394	29657482	NF1	NM_001042492	2	58	39	+	29657314	29657516
258359458	chr17	29661724	29661938	29661746	29661910	NF1	NM_001042492	2	58	40	+	29661856	29662049
258376739	chr17	29661887	29662063	29661911	29662041	NF1	NM_001042492	2	58	40	+	29661856	29662049
238333700	chr17	29663234	29663445	29663261	29663421	NF1	NM_001042492	2	58	41	+	29663351	29663491
238335871	chr17	29663401	29663615	29663422	29663589	NF1	NM_001042492	2	58	41	+	29663351	29663491
240003548	chr17	29663591	29663793	29663617	29663768	NF1	NM_001042492	2	58	42	+	29663653	29663932
240026382	chr17	29663749	29663968	29663769	29663941	NF1	NM_001042492	2	58	42	+	29663653	29663932
239206598	chr17	29664348	29664479	29664381	29664455	NF1	NM_001042492	2	58	43	+	29664386	29664600
239213676	chr17	29664413	29664618	29664441	29664591	NF1	NM_001042492	2	58	43	+	29664386	29664600
239661439	chr17	29664720	29664894	29664744	29664872	NF1	NM_001042492	2	58	44	+	29664837	29664898
239663032	chr17	29664844	29665028	29664869	29665000	NF1	NM_001042492	2	58	44	+	29664837	29664898
241493432	chr17	29665047	29665177	29665074	29665158	NF1	NM_001042492	2	58	45	+	29665043	29665157
237076660	chr17	29665705	29665870	29665732	29665844	NF1	NM_001042492	2	58	46	+	29665722	29665823
237656672	chr17	29667478	29667699	29667507	29667673	NF1	NM_001042492	2	58	47	+	29667523	29667663
235870627	chr17	29669965	29670139	29669991	29670111	NF1	NM_001042492	2	58	48	+	29670027	29670153
235874055	chr17	29670071	29670283	29670093	29670253	NF1	NM_001042492	2	58	48	+	29670027	29670153
235988966	chr17	29676022	29676227	29676050	29676199	NF1	NM_001042492	2	58	49	+	29676138	29676269
235997238	chr17	29676158	29676376	29676184	29676359	NF1	NM_001042492	2	58	49	+	29676138	29676269
239676973	chr17	29677090	29677231	29677118	29677203	NF1	NM_001042492	2	58	50	+	29677201	29677336
239688556	chr17	29677182	29677406	29677204	29677378	NF1	NM_001042492	2	58	50	+	29677201	29677336
237984418	chr17	29679200	29679422	29679222	29679399	NF1	NM_001042492	2	58	51	+	29679275	29679432

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237994918	chr17	29679373	29679557	29679395	29679530	NF1	NM_001042492	2	58	51	+	29679275	29679432
235934655	chr17	29683349	29683556	29683376	29683530	NF1	NM_001042492	2	58	52	+	29683478	29683600
235938675	chr17	29683507	29683654	29683531	29683625	NF1	NM_001042492	2	58	52	+	29683478	29683600
241766339	chr17	29683921	29684085	29683947	29684057	NF1	NM_001042492	2	58	53	+	29683978	29684108
241777431	chr17	29684030	29684174	29684058	29684146	NF1	NM_001042492	2	58	53	+	29683978	29684108
241696389	chr17	29684203	29684424	29684228	29684396	NF1	NM_001042492	2	58	54	+	29684287	29684387
238959215	chr17	29685379	29685583	29685406	29685556	NF1	NM_001042492	2	58	55	+	29685498	29685640
238972679	chr17	29685529	29685674	29685557	29685645	NF1	NM_001042492	2	58	55	+	29685498	29685640
236222301	chr17	29685975	29686114	29686003	29686086	NF1	NM_001042492	2	58	56	+	29685987	29686033
235180428	chr17	29687492	29687617	29687520	29687594	NF1	NM_001042492	2	58	57	+	29687505	29687721
235197865	chr17	29687571	29687771	29687595	29687743	NF1	NM_001042492	2	58	57	+	29687505	29687721
258078851	chr17	29700997	29701221	29701025	29701194	NF1	NM_001042492	2	58	58	+	29701031	29704695
258118639	chr17	29422203	29422381	29422221	29422364	NF1	NM_001128147	3	15	1	+	29421945	29422387
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_001128147	3	15	1	+	29421945	29422387
237186614	chr17	29482878	29483049	29482905	29483023	NF1	NM_001128147	3	15	2	+	29483001	29483144
237193452	chr17	29483000	29483182	29483024	29483156	NF1	NM_001128147	3	15	2	+	29483001	29483144
236388202	chr17	29485947	29486145	29485975	29486116	NF1	NM_001128147	3	15	3	+	29486028	29486111
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_001128147	3	15	4	+	29490204	29490394
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_001128147	3	15	4	+	29490204	29490394
235554636	chr17	29496923	29497118	29496951	29497090	NF1	NM_001128147	3	15	5	+	29496909	29497015
240265478	chr17	29508340	29508520	29508370	29508493	NF1	NM_001128147	3	15	6	+	29508440	29508507
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_001128147	3	15	6	+	29508440	29508507
238570302	chr17	29508726	29508936	29508751	29508908	NF1	NM_001128147	3	15	7	+	29508728	29508803
237436422	chr17	29509430	29509587	29509455	29509564	NF1	NM_001128147	3	15	8	+	29509526	29509683
237442947	chr17	29509539	29509746	29509565	29509717	NF1	NM_001128147	3	15	8	+	29509526	29509683
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_001128147	3	15	9	+	29527440	29527613
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_001128147	3	15	9	+	29527440	29527613
235109655	chr17	29527519	29527743	29527546	29527715	NF1	NM_001128147	3	15	9	+	29527440	29527613
258490074	chr17	29527941	29528141	29527963	29528116	NF1	NM_001128147	3	15	10	+	29528055	29528177
258513162	chr17	29528067	29528192	29528093	29528167	NF1	NM_001128147	3	15	10	+	29528055	29528177
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_001128147	3	15	10	+	29528055	29528177
236497505	chr17	29528340	29528517	29528368	29528489	NF1	NM_001128147	3	15	11	+	29528429	29528503
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_001128147	3	15	11	+	29528429	29528503
236050823	chr17	29533129	29533288	29533151	29533264	NF1	NM_001128147	3	15	12	+	29533258	29533389
236066944	chr17	29533239	29533424	29533265	29533397	NF1	NM_001128147	3	15	12	+	29533258	29533389
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_001128147	3	15	13	+	29541469	29541603
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_001128147	3	15	14	+	29546023	29546136
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_001128147	3	15	14	+	29546023	29546136
237408995	chr17	29548873	29549072	29548901	29549042	NF1	NM_001128147	3	15	15	+	29548868	29549782
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_000268	1	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_000268	1	16	1	+	29999545	30000101

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_000268	1	16	2	+	30032740	30032865
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_000268	1	16	3	+	30035079	30035201
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_000268	1	16	4	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_000268	1	16	5	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_000268	1	16	6	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_000268	1	16	7	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_000268	1	16	8	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_000268	1	16	9	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_000268	1	16	10	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_000268	1	16	11	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_000268	1	16	12	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_000268	1	16	12	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_000268	1	16	13	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_000268	1	16	14	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_000268	1	16	15	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_000268	1	16	15	+	30077428	30077590
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_000268	1	16	16	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_016418	2	17	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_016418	2	17	1	+	29999545	30000101
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_016418	2	17	2	+	30032740	30032865
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_016418	2	17	3	+	30035079	30035201
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_016418	2	17	4	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_016418	2	17	5	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_016418	2	17	6	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_016418	2	17	7	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_016418	2	17	8	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_016418	2	17	9	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_016418	2	17	10	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_016418	2	17	11	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_016418	2	17	12	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_016418	2	17	12	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_016418	2	17	13	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_016418	2	17	14	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_016418	2	17	15	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_016418	2	17	15	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_016418	2	17	16	+	30079009	30079053
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_016418	2	17	17	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181825	3	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181825	3	16	1	+	29999545	30000101
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_181825	3	16	2	+	30032740	30032865
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_181825	3	16	3	+	30035079	30035201

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181825	3	16	4	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181825	3	16	5	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181825	3	16	6	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181825	3	16	7	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181825	3	16	8	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181825	3	16	9	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181825	3	16	10	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181825	3	16	11	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181825	3	16	12	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181825	3	16	12	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181825	3	16	13	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181825	3	16	14	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181825	3	16	15	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181825	3	16	15	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181825	3	16	16	+	30079009	30079904
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181828	4	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181828	4	16	1	+	29999545	30000101
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_181828	4	16	2	+	30035079	30035201
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181828	4	16	3	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181828	4	16	4	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181828	4	16	5	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181828	4	16	6	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181828	4	16	7	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181828	4	16	8	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181828	4	16	9	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181828	4	16	10	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181828	4	16	11	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181828	4	16	11	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181828	4	16	12	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181828	4	16	13	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181828	4	16	14	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181828	4	16	14	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181828	4	16	15	+	30079009	30079053
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_181828	4	16	16	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181829	5	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181829	5	16	1	+	29999545	30000101
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_181829	5	16	2	+	30032740	30032865
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181829	5	16	3	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181829	5	16	4	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181829	5	16	5	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181829	5	16	6	+	30054178	30054253

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181829	5	16	7	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181829	5	16	8	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181829	5	16	9	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181829	5	16	10	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181829	5	16	11	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181829	5	16	11	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181829	5	16	12	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181829	5	16	13	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181829	5	16	14	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181829	5	16	14	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181829	5	16	15	+	30079009	30079053
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_181829	5	16	16	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181830	6	15	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181830	6	15	1	+	29999545	30000101
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181830	6	15	2	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181830	6	15	3	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181830	6	15	4	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181830	6	15	5	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181830	6	15	6	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181830	6	15	7	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181830	6	15	8	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181830	6	15	9	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181830	6	15	10	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181830	6	15	10	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181830	6	15	11	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181830	6	15	12	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181830	6	15	13	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181830	6	15	13	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181830	6	15	14	+	30079009	30079053
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_181830	6	15	15	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181831	7	15	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181831	7	15	1	+	29999545	30000101
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181831	7	15	2	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181831	7	15	3	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181831	7	15	4	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181831	7	15	5	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181831	7	15	6	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181831	7	15	7	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181831	7	15	8	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181831	7	15	9	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181831	7	15	10	+	30069258	30069475

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181831	7	15	10	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181831	7	15	11	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181831	7	15	12	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181831	7	15	13	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181831	7	15	13	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181831	7	15	14	+	30079009	30079053
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181832	8	17	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181832	8	17	1	+	29999545	30000101
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_181832	8	17	2	+	30032740	30032865
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_181832	8	17	3	+	30035079	30035201
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181832	8	17	4	+	30038191	30038274
236008296	chr22	30050553	30050752	30050575	30050726	NF2	NM_181832	8	17	5	+	30050646	30050714
235099002	chr22	30051521	30051705	30051550	30051677	NF2	NM_181832	8	17	6	+	30051583	30051665
235133367	chr22	30054069	30054281	30054089	30054258	NF2	NM_181832	8	17	7	+	30054178	30054253
237942095	chr22	30057153	30057357	30057173	30057335	NF2	NM_181832	8	17	8	+	30057194	30057328
257979284	chr22	30060938	30061149	30060958	30061121	NF2	NM_181832	8	17	9	+	30060979	30061053
236021889	chr22	30064259	30064472	30064280	30064444	NF2	NM_181832	8	17	10	+	30064322	30064435
237089025	chr22	30067768	30067989	30067789	30067968	NF2	NM_181832	8	17	11	+	30067815	30067937
238703788	chr22	30069179	30069402	30069202	30069384	NF2	NM_181832	8	17	12	+	30069258	30069475
238729728	chr22	30069354	30069574	30069374	30069552	NF2	NM_181832	8	17	12	+	30069258	30069475
241506017	chr22	30070760	30070979	30070781	30070957	NF2	NM_181832	8	17	13	+	30070825	30070930
239329642	chr22	30074148	30074369	30074169	30074345	NF2	NM_181832	8	17	14	+	30074185	30074312
241339762	chr22	30077321	30077508	30077341	30077484	NF2	NM_181832	8	17	15	+	30077428	30077590
241362258	chr22	30077462	30077623	30077485	30077596	NF2	NM_181832	8	17	15	+	30077428	30077590
235167895	chr22	30078899	30079079	30078922	30079055	NF2	NM_181832	8	17	16	+	30079009	30079068
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_181832	8	17	17	+	30090741	30094589
238604713	chr22	30000022	30000202	30000044	30000181	NF2	NM_181833	9	5	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181833	9	5	1	+	29999545	30000101
240856033	chr22	30032704	30032895	30032725	30032872	NF2	NM_181833	9	5	2	+	30032740	30032865
239063375	chr22	30035025	30035249	30035049	30035228	NF2	NM_181833	9	5	3	+	30035079	30035201
237136482	chr22	30038110	30038320	30038131	30038294	NF2	NM_181833	9	5	4	+	30038191	30038274
239403415	chr22	30090647	30090870	30090668	30090846	NF2	NM_181833	9	5	5	+	30090741	30094589
292194284	chr5	36953700	36953848	36953723	36953828	NIPBL	NM_015384	1	46	2	+	36953720	36953862
292200777	chr5	36953808	36953989	36953829	36953963	NIPBL	NM_015384	1	46	2	+	36953720	36953862
293612979	chr5	36955585	36955798	36955608	36955769	NIPBL	NM_015384	1	46	3	+	36955574	36955739
320045944	chr5	36955408	36955632	36955435	36955607	NIPBL	NM_015384	1	46	3	+	36955574	36955739
292834591	chr5	36958104	36958238	36958129	36958217	NIPBL	NM_015384	1	46	4	+	36958206	36958333
292839446	chr5	36958192	36958412	36958218	36958385	NIPBL	NM_015384	1	46	4	+	36958206	36958333
293544498	chr5	36961443	36961659	36961471	36961632	NIPBL	NM_015384	1	46	5	+	36961586	36961685
293544600	chr5	36961608	36961741	36961633	36961714	NIPBL	NM_015384	1	46	5	+	36961586	36961685
290321328	chr5	36962133	36962283	36962158	36962258	NIPBL	NM_015384	1	46	6	+	36962225	36962376

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
290330615	chr5	36962238	36962411	36962259	36962384	NIPBL	NM_015384	1	46	6	+	36962225	36962376
292884085	chr5	36970975	36971136	36970998	36971115	NIPBL	NM_015384	1	46	7	+	36970978	36971138
320259656	chr5	36970808	36971022	36970834	36970997	NIPBL	NM_015384	1	46	7	+	36970978	36971138
320278301	chr5	36971103	36971324	36971125	36971304	NIPBL	NM_015384	1	46	7	+	36970978	36971138
292277995	chr5	36971930	36972138	36971958	36972116	NIPBL	NM_015384	1	46	8	+	36972047	36972143
318844082	chr5	36972093	36972297	36972114	36972276	NIPBL	NM_015384	1	46	8	+	36972047	36972143
290963202	chr5	36975840	36976034	36975866	36976010	NIPBL	NM_015384	1	46	9	+	36975878	36976504
290973786	chr5	36975984	36976148	36976011	36976122	NIPBL	NM_015384	1	46	9	+	36975878	36976504
290986824	chr5	36976099	36976259	36976123	36976234	NIPBL	NM_015384	1	46	9	+	36975878	36976504
291007794	chr5	36976208	36976396	36976235	36976368	NIPBL	NM_015384	1	46	9	+	36975878	36976504
293179375	chr5	36976347	36976542	36976369	36976514	NIPBL	NM_015384	1	46	9	+	36975878	36976504
289949500	chr5	36984795	36984963	36984822	36984936	NIPBL	NM_015384	1	46	10	+	36984778	36986403
289950371	chr5	36986181	36986371	36986208	36986344	NIPBL	NM_015384	1	46	10	+	36984778	36986403
289962110	chr5	36984915	36985114	36984937	36985088	NIPBL	NM_015384	1	46	10	+	36984778	36986403
289972831	chr5	36985061	36985280	36985088	36985256	NIPBL	NM_015384	1	46	10	+	36984778	36986403
290130494	chr5	36985226	36985448	36985255	36985426	NIPBL	NM_015384	1	46	10	+	36984778	36986403
290142525	chr5	36985373	36985582	36985394	36985560	NIPBL	NM_015384	1	46	10	+	36984778	36986403
290161568	chr5	36985533	36985694	36985554	36985671	NIPBL	NM_015384	1	46	10	+	36984778	36986403
290172613	chr5	36985646	36985847	36985672	36985818	NIPBL	NM_015384	1	46	10	+	36984778	36986403
292651550	chr5	36985795	36985952	36985819	36985927	NIPBL	NM_015384	1	46	10	+	36984778	36986403
292654591	chr5	36985906	36986090	36985928	36986063	NIPBL	NM_015384	1	46	10	+	36984778	36986403
292658099	chr5	36986036	36986231	36986064	36986207	NIPBL	NM_015384	1	46	10	+	36984778	36986403
321290947	chr5	36984604	36984827	36984632	36984809	NIPBL	NM_015384	1	46	10	+	36984778	36986403
292709286	chr5	36995758	36995973	36995780	36995945	NIPBL	NM_015384	1	46	11	+	36995724	36995906
319806304	chr5	36995569	36995793	36995602	36995771	NIPBL	NM_015384	1	46	11	+	36995724	36995906
291675384	chr5	37000351	37000558	37000379	37000534	NIPBL	NM_015384	1	46	12	+	37000475	37000672
291682201	chr5	37000511	37000709	37000535	37000680	NIPBL	NM_015384	1	46	12	+	37000475	37000672
289993971	chr5	37000875	37001056	37000898	37001027	NIPBL	NM_015384	1	46	13	+	37000919	37000990
289996078	chr5	37000963	37001134	37000991	37001105	NIPBL	NM_015384	1	46	14	+	37001091	37001180
291147755	chr5	37001080	37001271	37001106	37001243	NIPBL	NM_015384	1	46	14	+	37001091	37001180
290302847	chr5	37002621	37002830	37002650	37002805	NIPBL	NM_015384	1	46	15	+	37002764	37002867
290303826	chr5	37002783	37003001	37002809	37002973	NIPBL	NM_015384	1	46	15	+	37002764	37002867
291409220	chr5	37003242	37003437	37003270	37003415	NIPBL	NM_015384	1	46	16	+	37003363	37003449
290463323	chr5	37006349	37006528	37006375	37006500	NIPBL	NM_015384	1	46	17	+	37006459	37006690
290464475	chr5	37006464	37006590	37006493	37006564	NIPBL	NM_015384	1	46	17	+	37006459	37006690
290465592	chr5	37006523	37006689	37006547	37006661	NIPBL	NM_015384	1	46	17	+	37006459	37006690
290375708	chr5	37007310	37007530	37007338	37007502	NIPBL	NM_015384	1	46	18	+	37007425	37007576
290376636	chr5	37007455	37007662	37007484	37007635	NIPBL	NM_015384	1	46	18	+	37007425	37007576
290959075	chr5	37007999	37008189	37008029	37008163	NIPBL	NM_015384	1	46	19	+	37008110	37008190
290959087	chr5	37008138	37008301	37008165	37008272	NIPBL	NM_015384	1	46	19	+	37008110	37008190
289406381	chr5	37008596	37008820	37008625	37008795	NIPBL	NM_015384	1	46	20	+	37008725	37008825

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289406398	chr5	37008776	37008955	37008801	37008927	NIPBL	NM_015384	1	46	20	+	37008725	37008825
289898789	chr5	37010095	37010317	37010119	37010289	NIPBL	NM_015384	1	46	21	+	37010189	37010327
293499012	chr5	37014781	37014965	37014809	37014937	NIPBL	NM_015384	1	46	22	+	37014785	37014867
319675139	chr5	37014623	37014835	37014648	37014808	NIPBL	NM_015384	1	46	22	+	37014785	37014867
291067092	chr5	37016124	37016347	37016151	37016319	NIPBL	NM_015384	1	46	23	+	37016140	37016272
318820643	chr5	37015954	37016175	37015982	37016150	NIPBL	NM_015384	1	46	23	+	37016140	37016272
292446429	chr5	37016978	37017170	37017006	37017146	NIPBL	NM_015384	1	46	24	+	37017121	37017264
292446611	chr5	37017120	37017339	37017147	37017311	NIPBL	NM_015384	1	46	24	+	37017121	37017264
290675367	chr5	37019423	37019579	37019451	37019552	NIPBL	NM_015384	1	46	25	+	37019413	37019502
292180921	chr5	37020519	37020708	37020546	37020686	NIPBL	NM_015384	1	46	26	+	37020561	37020775
292191379	chr5	37020661	37020885	37020687	37020857	NIPBL	NM_015384	1	46	26	+	37020561	37020775
292193542	chr5	37020691	37020913	37020714	37020886	NIPBL	NM_015384	1	46	26	+	37020561	37020775
292193542	chr5	37020691	37020913	37020714	37020886	NIPBL	NM_015384	1	46	27	+	37020877	37020979
293148558	chr5	37020861	37021040	37020887	37021012	NIPBL	NM_015384	1	46	27	+	37020877	37020979
292325885	chr5	37022130	37022260	37022155	37022234	NIPBL	NM_015384	1	46	28	+	37022153	37022251
292328437	chr5	37022186	37022391	37022209	37022364	NIPBL	NM_015384	1	46	28	+	37022153	37022251
318895717	chr5	37021958	37022178	37021985	37022154	NIPBL	NM_015384	1	46	28	+	37022153	37022251
291776449	chr5	37022340	37022555	37022365	37022527	NIPBL	NM_015384	1	46	29	+	37022346	37022492
292328437	chr5	37022186	37022391	37022209	37022364	NIPBL	NM_015384	1	46	29	+	37022346	37022492
292085560	chr5	37024636	37024770	37024664	37024742	NIPBL	NM_015384	1	46	30	+	37024687	37024821
292086400	chr5	37024691	37024844	37024719	37024812	NIPBL	NM_015384	1	46	30	+	37024687	37024821
289949692	chr5	37026242	37026464	37026264	37026443	NIPBL	NM_015384	1	46	31	+	37026331	37026429
289607975	chr5	37027372	37027542	37027398	37027515	NIPBL	NM_015384	1	46	32	+	37027461	37027514
318870861	chr5	37027489	37027705	37027511	37027676	NIPBL	NM_015384	1	46	32	+	37027461	37027514
292477743	chr5	37036353	37036544	37036386	37036516	NIPBL	NM_015384	1	46	33	+	37036481	37036589
292477909	chr5	37036485	37036702	37036511	37036675	NIPBL	NM_015384	1	46	33	+	37036481	37036589
291330162	chr5	37038590	37038740	37038615	37038714	NIPBL	NM_015384	1	46	34	+	37038704	37038840
291330442	chr5	37038687	37038822	37038715	37038795	NIPBL	NM_015384	1	46	34	+	37038704	37038840
291335296	chr5	37038772	37038913	37038796	37038885	NIPBL	NM_015384	1	46	34	+	37038704	37038840
290410937	chr5	37044371	37044595	37044395	37044567	NIPBL	NM_015384	1	46	35	+	37044449	37044589
318084297	chr5	37044561	37044785	37044588	37044757	NIPBL	NM_015384	1	46	35	+	37044449	37044589
320155732	chr5	37044537	37044761	37044566	37044738	NIPBL	NM_015384	1	46	35	+	37044449	37044589
292026713	chr5	37044731	37044879	37044758	37044851	NIPBL	NM_015384	1	46	36	+	37044738	37044831
318084297	chr5	37044561	37044785	37044588	37044757	NIPBL	NM_015384	1	46	36	+	37044738	37044831
320155732	chr5	37044537	37044761	37044566	37044738	NIPBL	NM_015384	1	46	36	+	37044738	37044831
293045069	chr5	37045572	37045756	37045597	37045728	NIPBL	NM_015384	1	46	37	+	37045545	37045699
289465955	chr5	37046176	37046303	37046204	37046275	NIPBL	NM_015384	1	46	38	+	37046211	37046301
289466104	chr5	37046187	37046352	37046214	37046325	NIPBL	NM_015384	1	46	38	+	37046211	37046301
293229192	chr5	37048582	37048783	37048607	37048759	NIPBL	NM_015384	1	46	39	+	37048604	37048777
320935596	chr5	37048424	37048631	37048448	37048606	NIPBL	NM_015384	1	46	39	+	37048604	37048777
289853661	chr5	37049092	37049276	37049116	37049251	NIPBL	NM_015384	1	46	40	+	37049213	37049403

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289875093	chr5	37049223	37049440	37049252	37049414	NIPBL	NM_015384	1	46	40	+	37049213	37049403
291781287	chr5	37051877	37052069	37051902	37052044	NIPBL	NM_015384	1	46	41	+	37051881	37051988
320084568	chr5	37051691	37051915	37051716	37051897	NIPBL	NM_015384	1	46	41	+	37051881	37051988
290296928	chr5	37052370	37052513	37052398	37052487	NIPBL	NM_015384	1	46	42	+	37052468	37052668
290304877	chr5	37052465	37052666	37052488	37052639	NIPBL	NM_015384	1	46	42	+	37052468	37052668
321459287	chr5	37052615	37052835	37052640	37052808	NIPBL	NM_015384	1	46	42	+	37052468	37052668
289609294	chr5	37057190	37057340	37057211	37057312	NIPBL	NM_015384	1	46	43	+	37057288	37057434
289619978	chr5	37057288	37057481	37057313	37057452	NIPBL	NM_015384	1	46	43	+	37057288	37057434
291052209	chr5	37058912	37059084	37058937	37059061	NIPBL	NM_015384	1	46	44	+	37058993	37059267
291053541	chr5	37059039	37059223	37059062	37059194	NIPBL	NM_015384	1	46	44	+	37058993	37059267
291057339	chr5	37059161	37059292	37059189	37059265	NIPBL	NM_015384	1	46	44	+	37058993	37059267
289583846	chr5	37060882	37061104	37060909	37061076	NIPBL	NM_015384	1	46	45	+	37060946	37061120
289588316	chr5	37061057	37061234	37061085	37061203	NIPBL	NM_015384	1	46	45	+	37060946	37061120
290491925	chr5	37063759	37063953	37063783	37063930	NIPBL	NM_015384	1	46	46	+	37063892	37065921
290512899	chr5	37063907	37064111	37063931	37064088	NIPBL	NM_015384	1	46	46	+	37063892	37065921
290520387	chr5	37064056	37064181	37064079	37064148	NIPBL	NM_015384	1	46	46	+	37063892	37065921
292824856	chr5	37064536	37064753	37064559	37064727	NIPBL	NM_015384	1	46	46	+	37063892	37065921
292841039	chr5	37064706	37064929	37064728	37064901	NIPBL	NM_015384	1	46	46	+	37063892	37065921
292868571	chr5	37064863	37065024	37064891	37064999	NIPBL	NM_015384	1	46	46	+	37063892	37065921
292194284	chr5	36953700	36953848	36953723	36953828	NIPBL	NM_133433	2	47	2	+	36953720	36953862
292200777	chr5	36953808	36953989	36953829	36953963	NIPBL	NM_133433	2	47	2	+	36953720	36953862
293612979	chr5	36955585	36955798	36955608	36955769	NIPBL	NM_133433	2	47	3	+	36955574	36955739
320045944	chr5	36955408	36955632	36955435	36955607	NIPBL	NM_133433	2	47	3	+	36955574	36955739
292834591	chr5	36958104	36958238	36958129	36958217	NIPBL	NM_133433	2	47	4	+	36958206	36958333
292839446	chr5	36958192	36958412	36958218	36958385	NIPBL	NM_133433	2	47	4	+	36958206	36958333
293544498	chr5	36961443	36961659	36961471	36961632	NIPBL	NM_133433	2	47	5	+	36961586	36961685
293544600	chr5	36961608	36961741	36961633	36961714	NIPBL	NM_133433	2	47	5	+	36961586	36961685
290321328	chr5	36962133	36962283	36962158	36962258	NIPBL	NM_133433	2	47	6	+	36962225	36962376
290330615	chr5	36962238	36962411	36962259	36962384	NIPBL	NM_133433	2	47	6	+	36962225	36962376
292884085	chr5	36970975	36971136	36970998	36971115	NIPBL	NM_133433	2	47	7	+	36970978	36971138
320259656	chr5	36970808	36971022	36970834	36970997	NIPBL	NM_133433	2	47	7	+	36970978	36971138
320278301	chr5	36971103	36971324	36971125	36971304	NIPBL	NM_133433	2	47	7	+	36970978	36971138
292277995	chr5	36971930	36972138	36971958	36972116	NIPBL	NM_133433	2	47	8	+	36972047	36972143
318844082	chr5	36972093	36972297	36972114	36972276	NIPBL	NM_133433	2	47	8	+	36972047	36972143
290963202	chr5	36975840	36976034	36975866	36976010	NIPBL	NM_133433	2	47	9	+	36975878	36976504
290973786	chr5	36975984	36976148	36976011	36976122	NIPBL	NM_133433	2	47	9	+	36975878	36976504
290986824	chr5	36976099	36976259	36976123	36976234	NIPBL	NM_133433	2	47	9	+	36975878	36976504
291007794	chr5	36976208	36976396	36976235	36976368	NIPBL	NM_133433	2	47	9	+	36975878	36976504
293179375	chr5	36976347	36976542	36976369	36976514	NIPBL	NM_133433	2	47	9	+	36975878	36976504
289949500	chr5	36984795	36984963	36984822	36984936	NIPBL	NM_133433	2	47	10	+	36984778	36986403
289950371	chr5	36986181	36986371	36986208	36986344	NIPBL	NM_133433	2	47	10	+	36984778	36986403

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289962110	chr5	36984915	36985114	36984937	36985088	NIPBL	NM_133433	2	47	10	+	36984778	36986403
289972831	chr5	36985061	36985280	36985088	36985256	NIPBL	NM_133433	2	47	10	+	36984778	36986403
290130494	chr5	36985226	36985448	36985255	36985426	NIPBL	NM_133433	2	47	10	+	36984778	36986403
290142525	chr5	36985373	36985582	36985394	36985560	NIPBL	NM_133433	2	47	10	+	36984778	36986403
290161568	chr5	36985533	36985694	36985554	36985671	NIPBL	NM_133433	2	47	10	+	36984778	36986403
290172613	chr5	36985646	36985847	36985672	36985818	NIPBL	NM_133433	2	47	10	+	36984778	36986403
292651550	chr5	36985795	36985952	36985819	36985927	NIPBL	NM_133433	2	47	10	+	36984778	36986403
292654591	chr5	36985906	36986090	36985928	36986063	NIPBL	NM_133433	2	47	10	+	36984778	36986403
292658099	chr5	36986036	36986231	36986064	36986207	NIPBL	NM_133433	2	47	10	+	36984778	36986403
321290947	chr5	36984604	36984827	36984632	36984809	NIPBL	NM_133433	2	47	10	+	36984778	36986403
292709286	chr5	36995758	36995973	36995780	36995945	NIPBL	NM_133433	2	47	11	+	36995724	36995906
319806304	chr5	36995569	36995793	36995602	36995771	NIPBL	NM_133433	2	47	11	+	36995724	36995906
291675384	chr5	37000351	37000558	37000379	37000534	NIPBL	NM_133433	2	47	12	+	37000475	37000672
291682201	chr5	37000511	37000709	37000535	37000680	NIPBL	NM_133433	2	47	12	+	37000475	37000672
289993971	chr5	37000875	37001056	37000898	37001027	NIPBL	NM_133433	2	47	13	+	37000919	37000990
289996078	chr5	37000963	37001134	37000991	37001105	NIPBL	NM_133433	2	47	14	+	37001091	37001180
291147755	chr5	37001080	37001271	37001106	37001243	NIPBL	NM_133433	2	47	14	+	37001091	37001180
290302847	chr5	37002621	37002830	37002650	37002805	NIPBL	NM_133433	2	47	15	+	37002764	37002867
290303826	chr5	37002783	37003001	37002809	37002973	NIPBL	NM_133433	2	47	15	+	37002764	37002867
291409220	chr5	37003242	37003437	37003270	37003415	NIPBL	NM_133433	2	47	16	+	37003363	37003449
290463323	chr5	37006349	37006528	37006375	37006500	NIPBL	NM_133433	2	47	17	+	37006459	37006690
290464475	chr5	37006464	37006590	37006493	37006564	NIPBL	NM_133433	2	47	17	+	37006459	37006690
290465592	chr5	37006523	37006689	37006547	37006661	NIPBL	NM_133433	2	47	17	+	37006459	37006690
290375708	chr5	37007310	37007530	37007338	37007502	NIPBL	NM_133433	2	47	18	+	37007425	37007576
290376636	chr5	37007455	37007662	37007484	37007635	NIPBL	NM_133433	2	47	18	+	37007425	37007576
290959075	chr5	37007999	37008189	37008029	37008163	NIPBL	NM_133433	2	47	19	+	37008110	37008190
290959087	chr5	37008138	37008301	37008165	37008272	NIPBL	NM_133433	2	47	19	+	37008110	37008190
289406381	chr5	37008596	37008820	37008625	37008795	NIPBL	NM_133433	2	47	20	+	37008725	37008825
289406398	chr5	37008776	37008955	37008801	37008927	NIPBL	NM_133433	2	47	20	+	37008725	37008825
289898789	chr5	37010095	37010317	37010119	37010289	NIPBL	NM_133433	2	47	21	+	37010189	37010327
293499012	chr5	37014781	37014965	37014809	37014937	NIPBL	NM_133433	2	47	22	+	37014785	37014867
319675139	chr5	37014623	37014835	37014648	37014808	NIPBL	NM_133433	2	47	22	+	37014785	37014867
291067092	chr5	37016124	37016347	37016151	37016319	NIPBL	NM_133433	2	47	23	+	37016140	37016272
318820643	chr5	37015954	37016175	37015982	37016150	NIPBL	NM_133433	2	47	23	+	37016140	37016272
292446429	chr5	37016978	37017170	37017006	37017146	NIPBL	NM_133433	2	47	24	+	37017121	37017264
292446611	chr5	37017120	37017339	37017147	37017311	NIPBL	NM_133433	2	47	24	+	37017121	37017264
290675367	chr5	37019423	37019579	37019451	37019552	NIPBL	NM_133433	2	47	25	+	37019413	37019502
292180921	chr5	37020519	37020708	37020546	37020686	NIPBL	NM_133433	2	47	26	+	37020561	37020775
292191379	chr5	37020661	37020885	37020687	37020857	NIPBL	NM_133433	2	47	26	+	37020561	37020775
292193542	chr5	37020691	37020913	37020714	37020886	NIPBL	NM_133433	2	47	26	+	37020561	37020775
292193542	chr5	37020691	37020913	37020714	37020886	NIPBL	NM_133433	2	47	27	+	37020877	37020979

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293148558	chr5	37020861	37021040	37020887	37021012	NIPBL	NM_133433	2	47	27	+	37020877	37020979
292325885	chr5	37022130	37022260	37022155	37022234	NIPBL	NM_133433	2	47	28	+	37022153	37022251
292328437	chr5	37022186	37022391	37022209	37022364	NIPBL	NM_133433	2	47	28	+	37022153	37022251
318895717	chr5	37021958	37022178	37021985	37022154	NIPBL	NM_133433	2	47	28	+	37022153	37022251
291776449	chr5	37022340	37022555	37022365	37022527	NIPBL	NM_133433	2	47	29	+	37022346	37022492
292328437	chr5	37022186	37022391	37022209	37022364	NIPBL	NM_133433	2	47	29	+	37022346	37022492
292085560	chr5	37024636	37024770	37024664	37024742	NIPBL	NM_133433	2	47	30	+	37024687	37024821
292086400	chr5	37024691	37024844	37024719	37024812	NIPBL	NM_133433	2	47	30	+	37024687	37024821
289949692	chr5	37026242	37026464	37026264	37026443	NIPBL	NM_133433	2	47	31	+	37026331	37026429
289607975	chr5	37027372	37027542	37027398	37027515	NIPBL	NM_133433	2	47	32	+	37027461	37027514
318870861	chr5	37027489	37027705	37027511	37027676	NIPBL	NM_133433	2	47	32	+	37027461	37027514
292477743	chr5	37036353	37036544	37036386	37036516	NIPBL	NM_133433	2	47	33	+	37036481	37036589
292477909	chr5	37036485	37036702	37036511	37036675	NIPBL	NM_133433	2	47	33	+	37036481	37036589
291330162	chr5	37038590	37038740	37038615	37038714	NIPBL	NM_133433	2	47	34	+	37038704	37038840
291330442	chr5	37038687	37038822	37038715	37038795	NIPBL	NM_133433	2	47	34	+	37038704	37038840
291335296	chr5	37038772	37038913	37038796	37038885	NIPBL	NM_133433	2	47	34	+	37038704	37038840
290410937	chr5	37044371	37044595	37044395	37044567	NIPBL	NM_133433	2	47	35	+	37044449	37044589
318084297	chr5	37044561	37044785	37044588	37044757	NIPBL	NM_133433	2	47	35	+	37044449	37044589
320155732	chr5	37044537	37044761	37044566	37044738	NIPBL	NM_133433	2	47	35	+	37044449	37044589
292026713	chr5	37044731	37044879	37044758	37044851	NIPBL	NM_133433	2	47	36	+	37044738	37044831
318084297	chr5	37044561	37044785	37044588	37044757	NIPBL	NM_133433	2	47	36	+	37044738	37044831
320155732	chr5	37044537	37044761	37044566	37044738	NIPBL	NM_133433	2	47	36	+	37044738	37044831
293045069	chr5	37045572	37045756	37045597	37045728	NIPBL	NM_133433	2	47	37	+	37045545	37045699
289465955	chr5	37046176	37046303	37046204	37046275	NIPBL	NM_133433	2	47	38	+	37046211	37046301
289466104	chr5	37046187	37046352	37046214	37046325	NIPBL	NM_133433	2	47	38	+	37046211	37046301
293229192	chr5	37048582	37048783	37048607	37048759	NIPBL	NM_133433	2	47	39	+	37048604	37048777
320935596	chr5	37048424	37048631	37048448	37048606	NIPBL	NM_133433	2	47	39	+	37048604	37048777
289853661	chr5	37049092	37049276	37049116	37049251	NIPBL	NM_133433	2	47	40	+	37049213	37049403
289875093	chr5	37049223	37049440	37049252	37049414	NIPBL	NM_133433	2	47	40	+	37049213	37049403
291781287	chr5	37051877	37052069	37051902	37052044	NIPBL	NM_133433	2	47	41	+	37051881	37051988
320084568	chr5	37051691	37051915	37051716	37051897	NIPBL	NM_133433	2	47	41	+	37051881	37051988
290296928	chr5	37052370	37052513	37052398	37052487	NIPBL	NM_133433	2	47	42	+	37052468	37052668
290304877	chr5	37052465	37052666	37052488	37052639	NIPBL	NM_133433	2	47	42	+	37052468	37052668
321459287	chr5	37052615	37052835	37052640	37052808	NIPBL	NM_133433	2	47	42	+	37052468	37052668
289609294	chr5	37057190	37057340	37057211	37057312	NIPBL	NM_133433	2	47	43	+	37057288	37057434
289619978	chr5	37057288	37057481	37057313	37057452	NIPBL	NM_133433	2	47	43	+	37057288	37057434
291052209	chr5	37058912	37059084	37058937	37059061	NIPBL	NM_133433	2	47	44	+	37058993	37059267
291053541	chr5	37059039	37059223	37059062	37059194	NIPBL	NM_133433	2	47	44	+	37058993	37059267
291057339	chr5	37059161	37059292	37059189	37059265	NIPBL	NM_133433	2	47	44	+	37058993	37059267
289583846	chr5	37060882	37061104	37060909	37061076	NIPBL	NM_133433	2	47	45	+	37060946	37061120
289588316	chr5	37061057	37061234	37061085	37061203	NIPBL	NM_133433	2	47	45	+	37060946	37061120

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
290491925	chr5	37063759	37063953	37063783	37063930	NIPBL	NM_133433	2	47	46	+	37063892	37064080
290512899	chr5	37063907	37064111	37063931	37064088	NIPBL	NM_133433	2	47	46	+	37063892	37064080
290520387	chr5	37064056	37064181	37064079	37064148	NIPBL	NM_133433	2	47	46	+	37063892	37064080
292824856	chr5	37064536	37064753	37064559	37064727	NIPBL	NM_133433	2	47	47	+	37064629	37065921
292841039	chr5	37064706	37064929	37064728	37064901	NIPBL	NM_133433	2	47	47	+	37064629	37065921
292868571	chr5	37064863	37065024	37064891	37064999	NIPBL	NM_133433	2	47	47	+	37064629	37065921
332031410	chr5	172661606	172661815	172661628	172661793	NKX2-5	NM_001166175	1	2	1	-	172661753	172662315
332036992	chr5	172661769	172661960	172661786	172661943	NKX2-5	NM_001166175	1	2	1	-	172661753	172662315
332039213	chr5	172661919	172662115	172661939	172662098	NKX2-5	NM_001166175	1	2	1	-	172661753	172662315
332031468	chr5	172660368	172660577	172660385	172660557	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332081297	chr5	172659526	172659685	172659545	172659662	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332085869	chr5	172659631	172659807	172659652	172659785	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332087631	chr5	172659766	172659982	172659784	172659964	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332089059	chr5	172659930	172660109	172659949	172660091	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332093136	chr5	172660060	172660266	172660079	172660246	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332117288	chr5	172660230	172660409	172660250	172660384	NKX2-5	NM_001166175	1	2	2	-	172659107	172660504
332031410	chr5	172661606	172661815	172661628	172661793	NKX2-5	NM_001166176	2	2	1	-	172661753	172662315
332036992	chr5	172661769	172661960	172661786	172661943	NKX2-5	NM_001166176	2	2	1	-	172661753	172662315
332039213	chr5	172661919	172662115	172661939	172662098	NKX2-5	NM_001166176	2	2	1	-	172661753	172662315
332031468	chr5	172660368	172660577	172660385	172660557	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332081297	chr5	172659526	172659685	172659545	172659662	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332085869	chr5	172659631	172659807	172659652	172659785	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332087631	chr5	172659766	172659982	172659784	172659964	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332089059	chr5	172659930	172660109	172659949	172660091	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332093136	chr5	172660060	172660266	172660079	172660246	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332117288	chr5	172660230	172660409	172660250	172660384	NKX2-5	NM_001166176	2	2	2	-	172659107	172660467
332031410	chr5	172661606	172661815	172661628	172661793	NKX2-5	NM_004387	3	2	1	-	172661753	172662315
332036992	chr5	172661769	172661960	172661786	172661943	NKX2-5	NM_004387	3	2	1	-	172661753	172662315
332039213	chr5	172661919	172662115	172661939	172662098	NKX2-5	NM_004387	3	2	1	-	172661753	172662315
332081297	chr5	172659526	172659685	172659545	172659662	NKX2-5	NM_004387	3	2	2	-	172659107	172660212
332085869	chr5	172659631	172659807	172659652	172659785	NKX2-5	NM_004387	3	2	2	-	172659107	172660212
332087631	chr5	172659766	172659982	172659784	172659964	NKX2-5	NM_004387	3	2	2	-	172659107	172660212
332089059	chr5	172659930	172660109	172659949	172660091	NKX2-5	NM_004387	3	2	2	-	172659107	172660212
332093136	chr5	172660060	172660266	172660079	172660246	NKX2-5	NM_004387	3	2	2	-	172659107	172660212
331254012	chr18	21166115	21166286	21166135	21166268	NPC1	NM_000271	1	25	1	-	21166251	21166581
331254345	chr18	21166250	21166423	21166268	21166406	NPC1	NM_000271	1	25	1	-	21166251	21166581
330761759	chr18	21153359	21153575	21153385	21153551	NPC1	NM_000271	1	25	2	-	21153416	21153538
330845783	chr18	21151972	21152195	21151995	21152170	NPC1	NM_000271	1	25	3	-	21152038	21152144
330993546	chr18	21148620	21148844	21148643	21148815	NPC1	NM_000271	1	25	4	-	21148787	21148962
331006229	chr18	21148792	21149010	21148816	21148983	NPC1	NM_000271	1	25	4	-	21148787	21148962
330347502	chr18	21141259	21141398	21141280	21141373	NPC1	NM_000271	1	25	5	-	21141324	21141491

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
330358295	chr18	21141351	21141527	21141374	21141502	NPC1	NM_000271	1	25	5	-	21141324	21141491
330741971	chr18	21140158	21140382	21140179	21140360	NPC1	NM_000271	1	25	6	-	21140195	21140444
330751961	chr18	21140332	21140550	21140355	21140522	NPC1	NM_000271	1	25	6	-	21140195	21140444
330680615	chr18	21137004	21137200	21137025	21137171	NPC1	NM_000271	1	25	7	-	21137081	21137154
330409011	chr18	21136096	21136300	21136121	21136280	NPC1	NM_000271	1	25	8	-	21136207	21136577
330432418	chr18	21136258	21136475	21136281	21136450	NPC1	NM_000271	1	25	8	-	21136207	21136577
330446161	chr18	21136432	21136622	21136451	21136599	NPC1	NM_000271	1	25	8	-	21136207	21136577
330921969	chr18	21134647	21134843	21134670	21134815	NPC1	NM_000271	1	25	9	-	21134722	21134948
330946890	chr18	21134795	21134990	21134816	21134966	NPC1	NM_000271	1	25	9	-	21134722	21134948
331298112	chr18	21131522	21131728	21131547	21131700	NPC1	NM_000271	1	25	10	-	21131591	21131691
330997353	chr18	21127907	21128113	21127927	21128085	NPC1	NM_000271	1	25	11	-	21127970	21128072
331431860	chr18	21124867	21125032	21124888	21125006	NPC1	NM_000271	1	25	12	-	21124924	21125113
331437922	chr18	21124982	21125199	21125007	21125171	NPC1	NM_000271	1	25	12	-	21124924	21125113
331413397	chr18	21124146	21124354	21124170	21124334	NPC1	NM_000271	1	25	13	-	21124308	21124490
331431503	chr18	21124314	21124530	21124335	21124502	NPC1	NM_000271	1	25	13	-	21124308	21124490
330715430	chr18	21123375	21123597	21123396	21123569	NPC1	NM_000271	1	25	14	-	21123419	21123533
330284358	chr18	21121128	21121352	21121150	21121332	NPC1	NM_000271	1	25	15	-	21121270	21121397
330270456	chr18	21121006	21121204	21121032	21121178	NPC1	NM_000271	1	25	16	-	21121032	21121172
330284358	chr18	21121128	21121352	21121150	21121332	NPC1	NM_000271	1	25	16	-	21121032	21121172
330602192	chr18	21120314	21120537	21120335	21120508	NPC1	NM_000271	1	25	17	-	21120412	21120501
331384272	chr18	21119744	21119966	21119769	21119938	NPC1	NM_000271	1	25	18	-	21119775	21119965
331394083	chr18	21119917	21120060	21119939	21120039	NPC1	NM_000271	1	25	18	-	21119775	21119965
331329371	chr18	21119140	21119350	21119164	21119324	NPC1	NM_000271	1	25	19	-	21119319	21119434
331345609	chr18	21119297	21119474	21119325	21119454	NPC1	NM_000271	1	25	19	-	21119319	21119434
330750501	chr18	21118456	21118666	21118481	21118644	NPC1	NM_000271	1	25	20	-	21118506	21118635
331113069	chr18	21116496	21116706	21116519	21116681	NPC1	NM_000271	1	25	21	-	21116637	21116840
331126238	chr18	21116662	21116870	21116682	21116845	NPC1	NM_000271	1	25	21	-	21116637	21116840
330490272	chr18	21115396	21115620	21115419	21115597	NPC1	NM_000271	1	25	22	-	21115433	21115664
330503740	chr18	21115579	21115740	21115598	21115718	NPC1	NM_000271	1	25	22	-	21115433	21115664
331203591	chr18	21114330	21114553	21114353	21114530	NPC1	NM_000271	1	25	23	-	21114410	21114523
331159939	chr18	21113236	21113368	21113265	21113345	NPC1	NM_000271	1	25	24	-	21113319	21113481
331165143	chr18	21113318	21113522	21113346	21113495	NPC1	NM_000271	1	25	24	-	21113319	21113481
330715219	chr18	21112100	21112295	21112120	21112271	NPC1	NM_000271	1	25	25	-	21111463	21112248
330253474	chr14	74959751	74959965	74959772	74959944	NPC2	NM_006432	1	5	1	-	74959896	74960084
330255003	chr14	74959891	74960048	74959911	74960027	NPC2	NM_006432	1	5	1	-	74959896	74960084
330848026	chr14	74952856	74953063	74952877	74953040	NPC2	NM_006432	1	5	2	-	74953032	74953139
330861969	chr14	74953020	74953191	74953041	74953163	NPC2	NM_006432	1	5	2	-	74953032	74953139
330330120	chr14	74950991	74951214	74951013	74951188	NPC2	NM_006432	1	5	3	-	74951118	74951290
330345784	chr14	74951164	74951380	74951189	74951352	NPC2	NM_006432	1	5	3	-	74951118	74951290
330399475	chr14	74947337	74947547	74947363	74947518	NPC2	NM_006432	1	5	4	-	74947405	74947482
331174334	chr14	74946795	74947019	74946818	74946997	NPC2	NM_006432	1	5	5	-	74946643	74946991

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320416008	chr15	72103001	72103213	72103023	72103192	NR2E3	NM_014249	1	9	1	+	72102894	72103201
320430844	chr15	72103158	72103374	72103179	72103351	NR2E3	NM_014249	1	9	1	+	72102894	72103201
318337847	chr15	72103725	72103932	72103745	72103910	NR2E3	NM_014249	1	9	2	+	72103823	72103949
318339087	chr15	72103869	72104055	72103891	72104033	NR2E3	NM_014249	1	9	2	+	72103823	72103949
319717318	chr15	72104032	72104256	72104053	72104237	NR2E3	NM_014249	1	9	3	+	72104106	72104209
319186976	chr15	72104258	72104482	72104275	72104458	NR2E3	NM_014249	1	9	4	+	72104295	72104516
319190726	chr15	72104420	72104634	72104437	72104614	NR2E3	NM_014249	1	9	4	+	72104295	72104516
319374393	chr15	72104639	72104860	72104660	72104838	NR2E3	NM_014249	1	9	5	+	72104676	72104851
319391181	chr15	72104808	72105010	72104830	72104989	NR2E3	NM_014249	1	9	5	+	72104676	72104851
318469799	chr15	72105593	72105795	72105615	72105775	NR2E3	NM_014249	1	9	6	+	72105729	72105928
318473728	chr15	72105746	72105956	72105768	72105936	NR2E3	NM_014249	1	9	6	+	72105729	72105928
318476194	chr15	72105888	72106086	72105912	72106063	NR2E3	NM_014249	1	9	6	+	72105729	72105928
318473728	chr15	72105746	72105956	72105768	72105936	NR2E3	NM_014249	1	9	7	+	72105930	72105976
318476194	chr15	72105888	72106086	72105912	72106063	NR2E3	NM_014249	1	9	7	+	72105930	72105976
319953695	chr15	72106285	72106502	72106307	72106480	NR2E3	NM_014249	1	9	8	+	72106353	72106458
320242989	chr15	72109847	72110035	72109871	72110012	NR2E3	NM_014249	1	9	9	+	72109893	72110597
320416008	chr15	72103001	72103213	72103023	72103192	NR2E3	NM_016346	2	8	1	+	72102894	72103201
320430844	chr15	72103158	72103374	72103179	72103351	NR2E3	NM_016346	2	8	1	+	72102894	72103201
318337847	chr15	72103725	72103932	72103745	72103910	NR2E3	NM_016346	2	8	2	+	72103823	72103949
318339087	chr15	72103869	72104055	72103891	72104033	NR2E3	NM_016346	2	8	2	+	72103823	72103949
319717318	chr15	72104032	72104256	72104053	72104237	NR2E3	NM_016346	2	8	3	+	72104106	72104209
319186976	chr15	72104258	72104482	72104275	72104458	NR2E3	NM_016346	2	8	4	+	72104295	72104516
319190726	chr15	72104420	72104634	72104437	72104614	NR2E3	NM_016346	2	8	4	+	72104295	72104516
319374393	chr15	72104639	72104860	72104660	72104838	NR2E3	NM_016346	2	8	5	+	72104676	72104851
319391181	chr15	72104808	72105010	72104830	72104989	NR2E3	NM_016346	2	8	5	+	72104676	72104851
318469799	chr15	72105593	72105795	72105615	72105775	NR2E3	NM_016346	2	8	6	+	72105729	72105928
318473728	chr15	72105746	72105956	72105768	72105936	NR2E3	NM_016346	2	8	6	+	72105729	72105928
318476194	chr15	72105888	72106086	72105912	72106063	NR2E3	NM_016346	2	8	6	+	72105729	72105928
318473728	chr15	72105746	72105956	72105768	72105936	NR2E3	NM_016346	2	8	7	+	72105930	72105976
318476194	chr15	72105888	72106086	72105912	72106063	NR2E3	NM_016346	2	8	7	+	72105930	72105976
319953695	chr15	72106285	72106502	72106307	72106480	NR2E3	NM_016346	2	8	8	+	72106353	72107270
237217145	chr1	115258600	115258811	115258627	115258789	NRAS	NM_002524	1	7	2	-	115258671	115258798
257578871	chr1	115256326	115256523	115256353	115256501	NRAS	NM_002524	1	7	3	-	115256421	115256599
257613650	chr1	115256481	115256675	115256502	115256647	NRAS	NM_002524	1	7	3	-	115256421	115256599
237210293	chr1	115252119	115252243	115252147	115252222	NRAS	NM_002524	1	7	4	-	115252190	115252349
237229810	chr1	115252199	115252402	115252223	115252374	NRAS	NM_002524	1	7	4	-	115252190	115252349
239846069	chr1	115251132	115251333	115251156	115251310	NRAS	NM_002524	1	7	5	-	115251152	115251275
235784231	chr5	176562620	176562841	176562642	176562813	NSD1	NM_022455	1	23	2	+	176562088	176563031
235816566	chr5	176562792	176562994	176562814	176562965	NSD1	NM_022455	1	23	2	+	176562088	176563031
235830815	chr5	176562941	176563102	176562966	176563074	NSD1	NM_022455	1	23	2	+	176562088	176563031
237768419	chr5	176561974	176562177	176561996	176562151	NSD1	NM_022455	1	23	2	+	176562088	176563031

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237834154	chr5	176562129	176562320	176562152	176562293	NSD1	NM_022455	1	23	2	+	176562088	176563031
240548045	chr5	176562268	176562492	176562294	176562468	NSD1	NM_022455	1	23	2	+	176562088	176563031
240608097	chr5	176562448	176562669	176562469	176562641	NSD1	NM_022455	1	23	2	+	176562088	176563031
238371345	chr5	176618848	176619059	176618875	176619031	NSD1	NM_022455	1	23	3	+	176618885	176619020
236741594	chr5	176630992	176631174	176631014	176631152	NSD1	NM_022455	1	23	4	+	176631121	176631293
236772532	chr5	176631133	176631346	176631153	176631318	NSD1	NM_022455	1	23	4	+	176631121	176631293
237611217	chr5	176637180	176637373	176637202	176637350	NSD1	NM_022455	1	23	5	+	176636637	176639196
237633876	chr5	176637330	176637541	176637351	176637515	NSD1	NM_022455	1	23	5	+	176636637	176639196
237660713	chr5	176637491	176637715	176637516	176637691	NSD1	NM_022455	1	23	5	+	176636637	176639196
242511339	chr5	176636560	176636714	176636586	176636691	NSD1	NM_022455	1	23	5	+	176636637	176639196
242556489	chr5	176638555	176638757	176638581	176638730	NSD1	NM_022455	1	23	5	+	176636637	176639196
242566923	chr5	176639054	176639264	176639078	176639236	NSD1	NM_022455	1	23	5	+	176636637	176639196
242577814	chr5	176637668	176637892	176637692	176637868	NSD1	NM_022455	1	23	5	+	176636637	176639196
242586924	chr5	176638305	176638526	176638326	176638501	NSD1	NM_022455	1	23	5	+	176636637	176639196
242674594	chr5	176638014	176638199	176638038	176638176	NSD1	NM_022455	1	23	5	+	176636637	176639196
257512191	chr5	176638151	176638346	176638176	176638326	NSD1	NM_022455	1	23	5	+	176636637	176639196
257523308	chr5	176636670	176636894	176636692	176636873	NSD1	NM_022455	1	23	5	+	176636637	176639196
257563826	chr5	176638704	176638926	176638731	176638905	NSD1	NM_022455	1	23	5	+	176636637	176639196
257600958	chr5	176636848	176637072	176636874	176637045	NSD1	NM_022455	1	23	5	+	176636637	176639196
257613968	chr5	176638884	176639098	176638906	176639077	NSD1	NM_022455	1	23	5	+	176636637	176639196
257621059	chr5	176637845	176638066	176637869	176638038	NSD1	NM_022455	1	23	5	+	176636637	176639196
257634097	chr5	176637020	176637227	176637046	176637201	NSD1	NM_022455	1	23	5	+	176636637	176639196
257653064	chr5	176638477	176638604	176638502	176638580	NSD1	NM_022455	1	23	5	+	176636637	176639196
238520908	chr5	176662765	176662982	176662788	176662957	NSD1	NM_022455	1	23	6	+	176662822	176662946
236182186	chr5	176665194	176665399	176665218	176665378	NSD1	NM_022455	1	23	7	+	176665238	176665508
236199775	chr5	176665350	176665563	176665371	176665537	NSD1	NM_022455	1	23	7	+	176665238	176665508
235404750	chr5	176666707	176666854	176666733	176666835	NSD1	NM_022455	1	23	8	+	176666757	176666866
235405510	chr5	176666809	176666993	176666836	176666968	NSD1	NM_022455	1	23	8	+	176666757	176666866
235724513	chr5	176671103	176671327	176671125	176671299	NSD1	NM_022455	1	23	9	+	176671196	176671271
258602616	chr5	176673631	176673852	176673654	176673825	NSD1	NM_022455	1	23	10	+	176673679	176673797
238129827	chr5	176675059	176675257	176675081	176675237	NSD1	NM_022455	1	23	11	+	176675182	176675325
238156460	chr5	176675216	176675357	176675238	176675332	NSD1	NM_022455	1	23	11	+	176675182	176675325
238236245	chr5	176678736	176678885	176678758	176678860	NSD1	NM_022455	1	23	12	+	176678731	176678854
240318875	chr5	176683823	176684033	176683845	176684009	NSD1	NM_022455	1	23	13	+	176683952	176684152
240344689	chr5	176683985	176684193	176684010	176684165	NSD1	NM_022455	1	23	13	+	176683952	176684152
238539831	chr5	176686958	176687106	176686983	176687077	NSD1	NM_022455	1	23	14	+	176686990	176687169
238549363	chr5	176687052	176687185	176687074	176687157	NSD1	NM_022455	1	23	14	+	176686990	176687169
238549388	chr5	176687133	176687264	176687159	176687233	NSD1	NM_022455	1	23	14	+	176686990	176687169
237703933	chr5	176694514	176694641	176694540	176694614	NSD1	NM_022455	1	23	15	+	176694563	176694719
237718489	chr5	176694592	176694760	176694615	176694732	NSD1	NM_022455	1	23	15	+	176694563	176694719
236712556	chr5	176696474	176696674	176696500	176696646	NSD1	NM_022455	1	23	16	+	176696603	176696808

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236728899	chr5	176696627	176696846	176696647	176696823	NSD1	NM_022455	1	23	16	+	176696603	176696808
257727566	chr5	176700628	176700841	176700652	176700814	NSD1	NM_022455	1	23	17	+	176700673	176700785
235819819	chr5	176707525	176707708	176707550	176707688	NSD1	NM_022455	1	23	18	+	176707566	176707835
235847659	chr5	176707666	176707884	176707688	176707859	NSD1	NM_022455	1	23	18	+	176707566	176707835
235147797	chr5	176709403	176709615	176709430	176709588	NSD1	NM_022455	1	23	19	+	176709466	176709582
235232485	chr5	176710741	176710959	176710763	176710934	NSD1	NM_022455	1	23	20	+	176710788	176710929
258741128	chr5	176715732	176715954	176715756	176715931	NSD1	NM_022455	1	23	21	+	176715820	176715926
240578276	chr5	176718867	176719073	176718892	176719047	NSD1	NM_022455	1	23	22	+	176718955	176719159
240627522	chr5	176719026	176719212	176719048	176719185	NSD1	NM_022455	1	23	22	+	176718955	176719159
235239700	chr5	176722306	176722493	176722326	176722468	NSD1	NM_022455	1	23	23	+	176720833	176727214
235270946	chr5	176721237	176721461	176721261	176721438	NSD1	NM_022455	1	23	23	+	176720833	176727214
235281148	chr5	176721406	176721597	176721427	176721574	NSD1	NM_022455	1	23	23	+	176720833	176727214
235296279	chr5	176721546	176721766	176721570	176721744	NSD1	NM_022455	1	23	23	+	176720833	176727214
235330795	chr5	176721723	176721904	176721745	176721882	NSD1	NM_022455	1	23	23	+	176720833	176727214
239727885	chr5	176720742	176720960	176720764	176720934	NSD1	NM_022455	1	23	23	+	176720833	176727214
239764859	chr5	176721863	176722054	176721883	176722033	NSD1	NM_022455	1	23	23	+	176720833	176727214
239795618	chr5	176720911	176721124	176720935	176721102	NSD1	NM_022455	1	23	23	+	176720833	176727214
239820611	chr5	176722003	176722226	176722029	176722200	NSD1	NM_022455	1	23	23	+	176720833	176727214
239847401	chr5	176722154	176722348	176722178	176722328	NSD1	NM_022455	1	23	23	+	176720833	176727214
239855743	chr5	176721080	176721302	176721102	176721279	NSD1	NM_022455	1	23	23	+	176720833	176727214
237768419	chr5	176561974	176562177	176561996	176562151	NSD1	NM_172349	2	24	2	+	176562088	176562201
237834154	chr5	176562129	176562320	176562152	176562293	NSD1	NM_172349	2	24	2	+	176562088	176562201
235816566	chr5	176562792	176562994	176562814	176562965	NSD1	NM_172349	2	24	3	+	176562942	176563031
235830815	chr5	176562941	176563102	176562966	176563074	NSD1	NM_172349	2	24	3	+	176562942	176563031
238371345	chr5	176618848	176619059	176618875	176619031	NSD1	NM_172349	2	24	4	+	176618885	176619020
236741594	chr5	176630992	176631174	176631014	176631152	NSD1	NM_172349	2	24	5	+	176631121	176631293
236772532	chr5	176631133	176631346	176631153	176631318	NSD1	NM_172349	2	24	5	+	176631121	176631293
237611217	chr5	176637180	176637373	176637202	176637350	NSD1	NM_172349	2	24	6	+	176636637	176639196
237633876	chr5	176637330	176637541	176637351	176637515	NSD1	NM_172349	2	24	6	+	176636637	176639196
237660713	chr5	176637491	176637715	176637516	176637691	NSD1	NM_172349	2	24	6	+	176636637	176639196
242511339	chr5	176636560	176636714	176636586	176636691	NSD1	NM_172349	2	24	6	+	176636637	176639196
242556489	chr5	176638555	176638757	176638581	176638730	NSD1	NM_172349	2	24	6	+	176636637	176639196
242566923	chr5	176639054	176639264	176639078	176639236	NSD1	NM_172349	2	24	6	+	176636637	176639196
242577814	chr5	176637668	176637892	176637692	176637868	NSD1	NM_172349	2	24	6	+	176636637	176639196
242586924	chr5	176638305	176638526	176638326	176638501	NSD1	NM_172349	2	24	6	+	176636637	176639196
242674594	chr5	176638014	176638199	176638038	176638176	NSD1	NM_172349	2	24	6	+	176636637	176639196
257512191	chr5	176638151	176638346	176638176	176638326	NSD1	NM_172349	2	24	6	+	176636637	176639196
257523308	chr5	176636670	176636894	176636692	176636873	NSD1	NM_172349	2	24	6	+	176636637	176639196
257563826	chr5	176638704	176638926	176638731	176638905	NSD1	NM_172349	2	24	6	+	176636637	176639196
257600958	chr5	176636848	176637072	176636874	176637045	NSD1	NM_172349	2	24	6	+	176636637	176639196
257613968	chr5	176638884	176639098	176638906	176639077	NSD1	NM_172349	2	24	6	+	176636637	176639196

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257621059	chr5	176637845	176638066	176637869	176638038	NSD1	NM_172349	2	24	6	+	176636637	176639196
257634097	chr5	176637020	176637227	176637046	176637201	NSD1	NM_172349	2	24	6	+	176636637	176639196
257653064	chr5	176638477	176638604	176638502	176638580	NSD1	NM_172349	2	24	6	+	176636637	176639196
238520908	chr5	176662765	176662982	176662788	176662957	NSD1	NM_172349	2	24	7	+	176662822	176662946
236182186	chr5	176665194	176665399	176665218	176665378	NSD1	NM_172349	2	24	8	+	176665238	176665508
236199775	chr5	176665350	176665563	176665371	176665537	NSD1	NM_172349	2	24	8	+	176665238	176665508
235404750	chr5	176666707	176666854	176666733	176666835	NSD1	NM_172349	2	24	9	+	176666757	176666866
235405510	chr5	176666809	176666993	176666836	176666968	NSD1	NM_172349	2	24	9	+	176666757	176666866
235724513	chr5	176671103	176671327	176671125	176671299	NSD1	NM_172349	2	24	10	+	176671196	176671271
258602616	chr5	176673631	176673852	176673654	176673825	NSD1	NM_172349	2	24	11	+	176673679	176673797
238129827	chr5	176675059	176675257	176675081	176675237	NSD1	NM_172349	2	24	12	+	176675182	176675325
238156460	chr5	176675216	176675357	176675238	176675332	NSD1	NM_172349	2	24	12	+	176675182	176675325
238236245	chr5	176678736	176678885	176678758	176678860	NSD1	NM_172349	2	24	13	+	176678731	176678854
240318875	chr5	176683823	176684033	176683845	176684009	NSD1	NM_172349	2	24	14	+	176683952	176684152
240344689	chr5	176683985	176684193	176684010	176684165	NSD1	NM_172349	2	24	14	+	176683952	176684152
238539831	chr5	176686958	176687106	176686983	176687077	NSD1	NM_172349	2	24	15	+	176686990	176687169
238549363	chr5	176687052	176687185	176687074	176687157	NSD1	NM_172349	2	24	15	+	176686990	176687169
238549388	chr5	176687133	176687264	176687159	176687233	NSD1	NM_172349	2	24	15	+	176686990	176687169
237703933	chr5	176694514	176694641	176694540	176694614	NSD1	NM_172349	2	24	16	+	176694563	176694719
237718489	chr5	176694592	176694760	176694615	176694732	NSD1	NM_172349	2	24	16	+	176694563	176694719
236712556	chr5	176696474	176696674	176696500	176696646	NSD1	NM_172349	2	24	17	+	176696603	176696808
236728899	chr5	176696627	176696846	176696647	176696823	NSD1	NM_172349	2	24	17	+	176696603	176696808
257727566	chr5	176700628	176700841	176700652	176700814	NSD1	NM_172349	2	24	18	+	176700673	176700785
235819819	chr5	176707525	176707708	176707550	176707688	NSD1	NM_172349	2	24	19	+	176707566	176707835
235847659	chr5	176707666	176707884	176707688	176707859	NSD1	NM_172349	2	24	19	+	176707566	176707835
235147797	chr5	176709403	176709615	176709430	176709588	NSD1	NM_172349	2	24	20	+	176709466	176709582
235232485	chr5	176710741	176710959	176710763	176710934	NSD1	NM_172349	2	24	21	+	176710788	176710929
258741128	chr5	176715732	176715954	176715756	176715931	NSD1	NM_172349	2	24	22	+	176715820	176715926
240578276	chr5	176718867	176719073	176718892	176719047	NSD1	NM_172349	2	24	23	+	176718955	176719159
240627522	chr5	176719026	176719212	176719048	176719185	NSD1	NM_172349	2	24	23	+	176718955	176719159
235239700	chr5	176722306	176722493	176722326	176722468	NSD1	NM_172349	2	24	24	+	176720833	176727214
235270946	chr5	176721237	176721461	176721261	176721438	NSD1	NM_172349	2	24	24	+	176720833	176727214
235281148	chr5	176721406	176721597	176721427	176721574	NSD1	NM_172349	2	24	24	+	176720833	176727214
235296279	chr5	176721546	176721766	176721570	176721744	NSD1	NM_172349	2	24	24	+	176720833	176727214
235330795	chr5	176721723	176721904	176721745	176721882	NSD1	NM_172349	2	24	24	+	176720833	176727214
239727885	chr5	176720742	176720960	176720764	176720934	NSD1	NM_172349	2	24	24	+	176720833	176727214
239764859	chr5	176721863	176722054	176721883	176722033	NSD1	NM_172349	2	24	24	+	176720833	176727214
239795618	chr5	176720911	176721124	176720935	176721102	NSD1	NM_172349	2	24	24	+	176720833	176727214
239820611	chr5	176722003	176722226	176722029	176722200	NSD1	NM_172349	2	24	24	+	176720833	176727214
239847401	chr5	176722154	176722348	176722178	176722328	NSD1	NM_172349	2	24	24	+	176720833	176727214
239855743	chr5	176721080	176721302	176721102	176721279	NSD1	NM_172349	2	24	24	+	176720833	176727214

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319910724	chr19	33183422	33183634	33183441	33183616	NUDT19	NM_001105570	1	3	1	+	33182867	33183580
321489236	chr19	33182838	33183038	33182857	33183020	NUDT19	NM_001105570	1	3	1	+	33182867	33183580
321489318	chr19	33183047	33183209	33183064	33183187	NUDT19	NM_001105570	1	3	1	+	33182867	33183580
321489824	chr19	33183089	33183248	33183106	33183230	NUDT19	NM_001105570	1	3	1	+	33182867	33183580
321490032	chr19	33183216	33183433	33183233	33183415	NUDT19	NM_001105570	1	3	1	+	33182867	33183580
321058046	chr19	33200006	33200191	33200031	33200167	NUDT19	NM_001105570	1	3	2	+	33200091	33200298
321081441	chr19	33200147	33200341	33200168	33200313	NUDT19	NM_001105570	1	3	2	+	33200091	33200298
320908213	chr19	33202524	33202742	33202557	33202715	NUDT19	NM_001105570	1	3	3	+	33202658	33204702
320908469	chr19	33202716	33202897	33202743	33202869	NUDT19	NM_001105570	1	3	3	+	33202658	33204702
320085158	chr15	28326727	28326943	28326749	28326923	OCA2	NM_000275	1	24	2	-	28326794	28327041
320089779	chr15	28326903	28327122	28326920	28327099	OCA2	NM_000275	1	24	2	-	28326794	28327041
320204494	chr15	28277130	28277339	28277151	28277314	OCA2	NM_000275	1	24	3	-	28277211	28277309
318198318	chr15	28272923	28273131	28272944	28273109	OCA2	NM_000275	1	24	4	-	28273017	28273205
318217950	chr15	28273066	28273289	28273086	28273266	OCA2	NM_000275	1	24	4	-	28273017	28273205
319050987	chr15	28269861	28270080	28269883	28270057	OCA2	NM_000275	1	24	5	-	28269991	28270048
320914379	chr15	28267528	28267752	28267549	28267726	OCA2	NM_000275	1	24	6	-	28267647	28267719
319439923	chr15	28263394	28263613	28263422	28263594	OCA2	NM_000275	1	24	7	-	28263543	28263703
319446198	chr15	28263576	28263734	28263594	28263713	OCA2	NM_000275	1	24	7	-	28263543	28263703
319072146	chr15	28261160	28261367	28261180	28261343	OCA2	NM_000275	1	24	8	-	28261250	28261332
318017518	chr15	28259738	28259946	28259764	28259922	OCA2	NM_000275	1	24	9	-	28259922	28260075
318047352	chr15	28259901	28260105	28259923	28260080	OCA2	NM_000275	1	24	9	-	28259922	28260075
321423536	chr15	28235600	28235820	28235621	28235798	OCA2	NM_000275	1	24	10	-	28235722	28235793
319531252	chr15	28234637	28234845	28234657	28234817	OCA2	NM_000275	1	24	11	-	28234747	28234812
321046025	chr15	28231592	28231800	28231613	28231772	OCA2	NM_000275	1	24	12	-	28231733	28231789
321051868	chr15	28231741	28231952	28231769	28231928	OCA2	NM_000275	1	24	12	-	28231733	28231789
320053325	chr15	28230102	28230235	28230125	28230215	OCA2	NM_000275	1	24	13	-	28230210	28230334
320059855	chr15	28230192	28230409	28230215	28230386	OCA2	NM_000275	1	24	13	-	28230210	28230334
319702317	chr15	28228445	28228664	28228466	28228638	OCA2	NM_000275	1	24	14	-	28228491	28228629
321205672	chr15	28211796	28212000	28211822	28211977	OCA2	NM_000275	1	24	15	-	28211836	28211968
321506639	chr15	28202695	28202908	28202715	28202887	OCA2	NM_000275	1	24	16	-	28202734	28202881
319094271	chr15	28200190	28200401	28200218	28200378	OCA2	NM_000275	1	24	17	-	28200304	28200361
319466773	chr15	28196859	28197069	28196881	28197043	OCA2	NM_000275	1	24	18	-	28196930	28197038
320943836	chr15	28171186	28171380	28171213	28171352	OCA2	NM_000275	1	24	19	-	28171273	28171400
320944997	chr15	28171315	28171478	28171343	28171452	OCA2	NM_000275	1	24	19	-	28171273	28171400
320914543	chr15	28116883	28117098	28116908	28117073	OCA2	NM_000275	1	24	20	-	28117009	28117068
318399623	chr15	28116211	28116434	28116233	28116413	OCA2	NM_000275	1	24	21	-	28116300	28116404
319917974	chr15	28096445	28096649	28096472	28096627	OCA2	NM_000275	1	24	22	-	28096528	28096621
320063024	chr15	28089930	28090153	28089958	28090129	OCA2	NM_000275	1	24	23	-	28090105	28090198
320070153	chr15	28090104	28090253	28090130	28090228	OCA2	NM_000275	1	24	23	-	28090105	28090198
319934182	chr15	28000432	28000653	28000457	28000625	OCA2	NM_000275	1	24	24	-	28000023	28000618
319533247	chrX	128674300	128674486	128674317	128674467	OCRL	NM_000276	1	24	1	+	128674252	128674455

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321424353	chrX	128674687	128674827	128674707	128674805	OCRL	NM_000276	1	24	2	+	128674721	128674800
320899375	chrX	128678805	128679025	128678828	128678997	OCRL	NM_000276	1	24	3	+	128678935	128679014
319365186	chrX	128682476	128682700	128682503	128682671	OCRL	NM_000276	1	24	4	+	128682540	128682578
318273188	chrX	128691134	128691338	128691157	128691318	OCRL	NM_000276	1	24	5	+	128691302	128691412
318279457	chrX	128691296	128691460	128691319	128691433	OCRL	NM_000276	1	24	5	+	128691302	128691412
320735979	chrX	128691749	128691970	128691775	128691946	OCRL	NM_000276	1	24	6	+	128691838	128691927
318483094	chrX	128692544	128692768	128692573	128692740	OCRL	NM_000276	1	24	7	+	128692610	128692730
318493251	chrX	128692702	128692910	128692723	128692887	OCRL	NM_000276	1	24	7	+	128692610	128692730
318493251	chrX	128692702	128692910	128692723	128692887	OCRL	NM_000276	1	24	8	+	128692817	128692978
318776572	chrX	128692868	128693055	128692888	128693028	OCRL	NM_000276	1	24	8	+	128692817	128692978
320308769	chrX	128694440	128694659	128694467	128694634	OCRL	NM_000276	1	24	9	+	128694527	128694628
318195952	chrX	128695097	128695321	128695123	128695293	OCRL	NM_000276	1	24	10	+	128695156	128695270
319556599	chrX	128696416	128696636	128696442	128696613	OCRL	NM_000276	1	24	11	+	128696361	128696477
321106207	chrX	128696329	128696538	128696354	128696510	OCRL	NM_000276	1	24	11	+	128696361	128696477
319556599	chrX	128696416	128696636	128696442	128696613	OCRL	NM_000276	1	24	12	+	128696576	128696763
319582263	chrX	128696589	128696792	128696614	128696768	OCRL	NM_000276	1	24	12	+	128696576	128696763
319423358	chrX	128699707	128699911	128699736	128699883	OCRL	NM_000276	1	24	13	+	128699749	128699860
318467709	chrX	128701191	128701385	128701220	128701360	OCRL	NM_000276	1	24	14	+	128701231	128701340
318686705	chrX	128703104	128703306	128703127	128703279	OCRL	NM_000276	1	24	15	+	128703241	128703376
318713589	chrX	128703260	128703466	128703280	128703437	OCRL	NM_000276	1	24	15	+	128703241	128703376
320258380	chrX	128709057	128709274	128709081	128709251	OCRL	NM_000276	1	24	16	+	128709117	128709227
319968798	chrX	128709682	128709901	128709705	128709874	OCRL	NM_000276	1	24	17	+	128709874	128710039
320010519	chrX	128709852	128710069	128709875	128710044	OCRL	NM_000276	1	24	17	+	128709874	128710039
318369081	chrX	128710201	128710397	128710229	128710370	OCRL	NM_000276	1	24	18	+	128710294	128710529
318392298	chrX	128710346	128710564	128710371	128710536	OCRL	NM_000276	1	24	18	+	128710294	128710529
321463395	chrX	128718280	128718406	128718308	128718379	OCRL	NM_000276	1	24	19	+	128718321	128718344
318412149	chrX	128720931	128721128	128720959	128721102	OCRL	NM_000276	1	24	20	+	128720979	128721095
318637327	chrX	128722067	128722290	128722089	128722262	OCRL	NM_000276	1	24	21	+	128722156	128722240
318632361	chrX	128722821	128723017	128722843	128722995	OCRL	NM_000276	1	24	22	+	128722863	128722990
319201703	chrX	128723759	128723967	128723786	128723949	OCRL	NM_000276	1	24	23	+	128723822	128723933
319013656	chrX	128724058	128724282	128724080	128724254	OCRL	NM_000276	1	24	24	+	128724123	128726530
319533247	chrX	128674300	128674486	128674317	128674467	OCRL	NM_001587	2	23	1	+	128674252	128674455
321424353	chrX	128674687	128674827	128674707	128674805	OCRL	NM_001587	2	23	2	+	128674721	128674800
320899375	chrX	128678805	128679025	128678828	128678997	OCRL	NM_001587	2	23	3	+	128678935	128679014
319365186	chrX	128682476	128682700	128682503	128682671	OCRL	NM_001587	2	23	4	+	128682540	128682578
318273188	chrX	128691134	128691338	128691157	128691318	OCRL	NM_001587	2	23	5	+	128691302	128691412
318279457	chrX	128691296	128691460	128691319	128691433	OCRL	NM_001587	2	23	5	+	128691302	128691412
320735979	chrX	128691749	128691970	128691775	128691946	OCRL	NM_001587	2	23	6	+	128691838	128691927
318483094	chrX	128692544	128692768	128692573	128692740	OCRL	NM_001587	2	23	7	+	128692610	128692730
318493251	chrX	128692702	128692910	128692723	128692887	OCRL	NM_001587	2	23	7	+	128692610	128692730
318493251	chrX	128692702	128692910	128692723	128692887	OCRL	NM_001587	2	23	8	+	128692817	128692978

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318776572	chrX	128692868	128693055	128692888	128693028	OCRL	NM_001587	2	23	8	+	128692817	128692978
320308769	chrX	128694440	128694659	128694467	128694634	OCRL	NM_001587	2	23	9	+	128694527	128694628
318195952	chrX	128695097	128695321	128695123	128695293	OCRL	NM_001587	2	23	10	+	128695156	128695270
319556599	chrX	128696416	128696636	128696442	128696613	OCRL	NM_001587	2	23	11	+	128696361	128696477
321106207	chrX	128696329	128696538	128696354	128696510	OCRL	NM_001587	2	23	11	+	128696361	128696477
319556599	chrX	128696416	128696636	128696442	128696613	OCRL	NM_001587	2	23	12	+	128696576	128696763
319582263	chrX	128696589	128696792	128696614	128696768	OCRL	NM_001587	2	23	12	+	128696576	128696763
319423358	chrX	128699707	128699911	128699736	128699883	OCRL	NM_001587	2	23	13	+	128699749	128699860
318467709	chrX	128701191	128701385	128701220	128701360	OCRL	NM_001587	2	23	14	+	128701231	128701340
318686705	chrX	128703104	128703306	128703127	128703279	OCRL	NM_001587	2	23	15	+	128703241	128703376
318713589	chrX	128703260	128703466	128703280	128703437	OCRL	NM_001587	2	23	15	+	128703241	128703376
320258380	chrX	128709057	128709274	128709081	128709251	OCRL	NM_001587	2	23	16	+	128709117	128709227
319968798	chrX	128709682	128709901	128709705	128709874	OCRL	NM_001587	2	23	17	+	128709874	128710039
320010519	chrX	128709852	128710069	128709875	128710044	OCRL	NM_001587	2	23	17	+	128709874	128710039
318369081	chrX	128710201	128710397	128710229	128710370	OCRL	NM_001587	2	23	18	+	128710294	128710529
318392298	chrX	128710346	128710564	128710371	128710536	OCRL	NM_001587	2	23	18	+	128710294	128710529
318412149	chrX	128720931	128721128	128720959	128721102	OCRL	NM_001587	2	23	19	+	128720979	128721095
318637327	chrX	128722067	128722290	128722089	128722262	OCRL	NM_001587	2	23	20	+	128722156	128722240
318632361	chrX	128722821	128723017	128722843	128722995	OCRL	NM_001587	2	23	21	+	128722863	128722990
319201703	chrX	128723759	128723967	128723786	128723949	OCRL	NM_001587	2	23	22	+	128723822	128723933
319013656	chrX	128724058	128724282	128724080	128724254	OCRL	NM_001587	2	23	23	+	128724123	128726530
318809334	chrX	38211839	38212054	38211860	38212031	OTC	NM_000531	1	10	1	+	38211736	38212026
319486861	chrX	38226474	38226656	38226502	38226630	OTC	NM_000531	1	10	2	+	38226544	38226682
319490800	chrX	38226582	38226753	38226603	38226730	OTC	NM_000531	1	10	2	+	38226544	38226682
318960536	chrX	38229048	38229175	38229074	38229150	OTC	NM_000531	1	10	3	+	38229049	38229130
321470476	chrX	38240499	38240722	38240526	38240694	OTC	NM_000531	1	10	4	+	38240595	38240682
318434158	chrX	38260391	38260595	38260418	38260569	OTC	NM_000531	1	10	5	+	38260528	38260681
318441443	chrX	38260547	38260736	38260570	38260709	OTC	NM_000531	1	10	5	+	38260528	38260681
320178500	chrX	38262834	38263058	38262856	38263030	OTC	NM_000531	1	10	6	+	38262871	38262993
320223673	chrX	38267873	38268093	38267894	38268065	OTC	NM_000531	1	10	7	+	38267995	38268048
318895855	chrX	38268091	38268314	38268116	38268286	OTC	NM_000531	1	10	8	+	38268129	38268278
319554819	chrX	38271082	38271295	38271108	38271268	OTC	NM_000531	1	10	9	+	38271115	38271252
319267652	chrX	38280172	38280392	38280194	38280364	OTC	NM_000531	1	10	10	+	38280276	38280703
320109858	chr14	23790631	23790854	23790648	23790835	PABPN1	NM_004643	1	7	1	+	23789397	23791029
320131477	chr14	23790818	23791037	23790835	23791020	PABPN1	NM_004643	1	7	1	+	23789397	23791029
320132837	chr14	23790985	23791198	23791003	23791180	PABPN1	NM_004643	1	7	1	+	23789397	23791029
318494077	chr14	23791363	23791584	23791384	23791563	PABPN1	NM_004643	1	7	2	+	23791390	23791504
318776496	chr14	23792135	23792358	23792159	23792330	PABPN1	NM_004643	1	7	3	+	23792208	23792275
321616064	chr14	23792426	23792634	23792447	23792612	PABPN1	NM_004643	1	7	4	+	23792586	23792692
321634505	chr14	23792590	23792788	23792613	23792760	PABPN1	NM_004643	1	7	4	+	23792586	23792692
319102287	chr14	23793156	23793292	23793182	23793266	PABPN1	NM_004643	1	7	5	+	23793174	23793261

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320550392	chr14	23793291	23793514	23793316	23793490	PABPN1	NM_004643	1	7	6	+	23793347	23793498
320577065	chr14	23793451	23793655	23793477	23793634	PABPN1	NM_004643	1	7	6	+	23793347	23793498
321357106	chr14	23794319	23794527	23794343	23794500	PABPN1	NM_004643	1	7	7	+	23794456	23795394
318188499	chr17	2541531	2541702	2541554	2541674	PAFAH1B1	NM_000430	1	11	2	+	2541393	2541614
319526003	chr17	2568487	2568703	2568510	2568677	PAFAH1B1	NM_000430	1	11	3	+	2568666	2568750
319526073	chr17	2568670	2568845	2568697	2568817	PAFAH1B1	NM_000430	1	11	3	+	2568666	2568750
318833954	chr17	2570187	2570344	2570217	2570318	PAFAH1B1	NM_000430	1	11	5	+	2570286	2570492
318835170	chr17	2570325	2570526	2570349	2570501	PAFAH1B1	NM_000430	1	11	5	+	2570286	2570492
319592558	chr17	2573390	2573614	2573416	2573590	PAFAH1B1	NM_000430	1	11	6	+	2573457	2573625
319614117	chr17	2573563	2573750	2573591	2573722	PAFAH1B1	NM_000430	1	11	6	+	2573457	2573625
318341084	chr17	2575867	2576082	2575894	2576056	PAFAH1B1	NM_000430	1	11	7	+	2575949	2576051
320293791	chr17	2577293	2577482	2577316	2577459	PAFAH1B1	NM_000430	1	11	8	+	2577354	2577582
320318386	chr17	2577440	2577664	2577460	2577636	PAFAH1B1	NM_000430	1	11	8	+	2577354	2577582
321368275	chr17	2579747	2579942	2579773	2579913	PAFAH1B1	NM_000430	1	11	9	+	2579799	2579900
320507702	chr17	2583456	2583660	2583478	2583633	PAFAH1B1	NM_000430	1	11	10	+	2583458	2583614
321018493	chr17	2584975	2585142	2585002	2585120	PAFAH1B1	NM_000430	1	11	11	+	2585023	2588909
321173910	chr12	103310722	103310945	103310746	103310922	PAH	NM_000277	1	13	1	-	103310849	103311381
319678362	chr12	103306513	103306734	103306538	103306706	PAH	NM_000277	1	13	2	-	103306569	103306676
319993348	chr12	103288451	103288600	103288479	103288574	PAH	NM_000277	1	13	3	-	103288513	103288696
320004105	chr12	103288554	103288747	103288575	103288725	PAH	NM_000277	1	13	3	-	103288513	103288696
319553261	chr12	103271140	103271360	103271165	103271338	PAH	NM_000277	1	13	4	-	103271240	103271328
318294422	chr12	103260256	103260474	103260278	103260448	PAH	NM_000277	1	13	5	-	103260374	103260441
318989511	chr12	103248806	103249019	103248828	103248991	PAH	NM_000277	1	13	6	-	103248914	103249110
319021658	chr12	103248966	103249141	103248992	103249115	PAH	NM_000277	1	13	6	-	103248914	103249110
318836986	chr12	103246564	103246767	103246584	103246739	PAH	NM_000277	1	13	7	-	103246593	103246728
318406251	chr12	103245338	103245562	103245364	103245541	PAH	NM_000277	1	13	8	-	103245465	103245534
319557445	chr12	103240595	103240798	103240621	103240773	PAH	NM_000277	1	13	9	-	103240673	103240729
319281563	chr12	103238048	103238239	103238074	103238214	PAH	NM_000277	1	13	10	-	103238114	103238209
319474050	chr12	103237390	103237612	103237410	103237584	PAH	NM_000277	1	13	11	-	103237424	103237557
318663839	chr12	103234103	103234319	103234125	103234298	PAH	NM_000277	1	13	12	-	103234178	103234293
319065409	chr12	103232823	103233028	103232851	103233005	PAH	NM_000277	1	13	13	-	103232104	103232996
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_000438	1	4	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_000438	1	4	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_000438	1	4	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_000438	1	4	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_000438	1	4	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_000438	1	4	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_000438	1	4	4	-	223158349	223159020
237541899	chr2	223158301	223158523	223158322	223158495	PAX3	NM_000438	1	4	4	-	223158349	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_000438	1	4	4	-	223158349	223159020
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_001127366	2	9	1	-	223163250	223163715

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_001127366	2	9	3	-	223160247	223160373
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_001127366	2	9	3	-	223160247	223160373
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_001127366	2	9	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_001127366	2	9	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_001127366	2	9	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_001127366	2	9	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_001127366	2	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_001127366	2	9	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_001127366	2	9	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_001127366	2	9	7	-	223084859	223085073
235189691	chr2	223066562	223066756	223066587	223066733	PAX3	NM_001127366	2	9	8	-	223066663	223066909
235208252	chr2	223066713	223066937	223066734	223066914	PAX3	NM_001127366	2	9	8	-	223066663	223066909
238348183	chr2	223065782	223065994	223065806	223065966	PAX3	NM_001127366	2	9	9	-	223064606	223066161
240912438	chr2	223065967	223066190	223065995	223066167	PAX3	NM_001127366	2	9	9	-	223064606	223066161
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_013942	3	5	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_013942	3	5	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_013942	3	5	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_013942	3	5	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_013942	3	5	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_013942	3	5	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_013942	3	5	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_013942	3	5	4	-	223158886	223159020
237541899	chr2	223158301	223158523	223158322	223158495	PAX3	NM_013942	3	5	5	-	223158349	223158476
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_181457	4	8	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_181457	4	8	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_181457	4	8	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_181457	4	8	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_181457	4	8	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_181457	4	8	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_181457	4	8	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_181457	4	8	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_181457	4	8	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_181457	4	8	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_181457	4	8	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181457	4	8	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_181457	4	8	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_181457	4	8	7	-	223084859	223085073
235189691	chr2	223066562	223066756	223066587	223066733	PAX3	NM_181457	4	8	8	-	223066432	223066909

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235208252	chr2	223066713	223066937	223066734	223066914	PAX3	NM_181457	4	8	8	-	223066432	223066909
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_181458	5	9	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_181458	5	9	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_181458	5	9	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_181458	5	9	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_181458	5	9	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_181458	5	9	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_181458	5	9	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_181458	5	9	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_181458	5	9	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_181458	5	9	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_181458	5	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181458	5	9	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_181458	5	9	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_181458	5	9	7	-	223084859	223085073
235189691	chr2	223066562	223066756	223066587	223066733	PAX3	NM_181458	5	9	8	-	223066663	223066909
235208252	chr2	223066713	223066937	223066734	223066914	PAX3	NM_181458	5	9	8	-	223066663	223066909
238348183	chr2	223065782	223065994	223065806	223065966	PAX3	NM_181458	5	9	9	-	223064606	223066161
240912438	chr2	223065967	223066190	223065995	223066167	PAX3	NM_181458	5	9	9	-	223064606	223066161
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_181459	6	10	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_181459	6	10	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_181459	6	10	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_181459	6	10	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_181459	6	10	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_181459	6	10	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_181459	6	10	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_181459	6	10	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_181459	6	10	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_181459	6	10	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_181459	6	10	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181459	6	10	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_181459	6	10	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_181459	6	10	7	-	223084859	223085073
235189691	chr2	223066562	223066756	223066587	223066733	PAX3	NM_181459	6	10	8	-	223066663	223066909
235208252	chr2	223066713	223066937	223066734	223066914	PAX3	NM_181459	6	10	8	-	223066663	223066909
240912438	chr2	223065967	223066190	223065995	223066167	PAX3	NM_181459	6	10	9	-	223066131	223066161
238348183	chr2	223065782	223065994	223065806	223065966	PAX3	NM_181459	6	10	10	-	223064606	223065959
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_181460	7	9	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_181460	7	9	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_181460	7	9	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_181460	7	9	2	-	223161697	223161932

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_181460	7	9	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_181460	7	9	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_181460	7	9	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_181460	7	9	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_181460	7	9	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_181460	7	9	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_181460	7	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181460	7	9	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_181460	7	9	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_181460	7	9	7	-	223084859	223085073
240912438	chr2	223065967	223066190	223065995	223066167	PAX3	NM_181460	7	9	8	-	223066131	223066161
238348183	chr2	223065782	223065994	223065806	223065966	PAX3	NM_181460	7	9	9	-	223064606	223065959
236712630	chr2	223163149	223163367	223163169	223163342	PAX3	NM_181461	8	8	1	-	223163250	223163715
235285155	chr2	223161575	223161766	223161603	223161745	PAX3	NM_181461	8	8	2	-	223161697	223161932
235289854	chr2	223161724	223161900	223161744	223161880	PAX3	NM_181461	8	8	2	-	223161697	223161932
235298457	chr2	223161842	223162051	223161862	223162031	PAX3	NM_181461	8	8	2	-	223161697	223161932
235247006	chr2	223160138	223160310	223160163	223160288	PAX3	NM_181461	8	8	3	-	223160247	223160376
235252282	chr2	223160270	223160491	223160289	223160471	PAX3	NM_181461	8	8	3	-	223160247	223160376
237358806	chr2	223158880	223159075	223158899	223159054	PAX3	NM_181461	8	8	4	-	223158886	223159020
237580324	chr2	223158711	223158916	223158734	223158898	PAX3	NM_181461	8	8	4	-	223158886	223159020
239878384	chr2	223096671	223096879	223096693	223096851	PAX3	NM_181461	8	8	5	-	223096797	223097002
239908636	chr2	223096829	223097026	223096852	223097000	PAX3	NM_181461	8	8	5	-	223096797	223097002
234923091	chr2	223085887	223086095	223085910	223086077	PAX3	NM_181461	8	8	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181461	8	8	6	-	223085941	223086106
236031729	chr2	223084779	223084956	223084802	223084934	PAX3	NM_181461	8	8	7	-	223084859	223085073
236045805	chr2	223084914	223085116	223084935	223085087	PAX3	NM_181461	8	8	7	-	223084859	223085073
238348183	chr2	223065782	223065994	223065806	223065966	PAX3	NM_181461	8	8	8	-	223064606	223066161
240912438	chr2	223065967	223066190	223065995	223066167	PAX3	NM_181461	8	8	8	-	223064606	223066161
320028156	chr11	31827867	31828025	31827884	31827999	PAX6	NM_000280	1	13	4	-	31827950	31828010
321097146	chr11	31824178	31824396	31824203	31824375	PAX6	NM_000280	1	13	5	-	31824252	31824382
321108379	chr11	31824351	31824558	31824371	31824536	PAX6	NM_000280	1	13	5	-	31824252	31824382
318206826	chr11	31822961	31823174	31822983	31823152	PAX6	NM_000280	1	13	6	-	31823109	31823324
318239177	chr11	31823132	31823352	31823153	31823329	PAX6	NM_000280	1	13	6	-	31823109	31823324
319939087	chr11	31823289	31823512	31823313	31823483	PAX6	NM_000280	1	13	6	-	31823109	31823324
319795090	chr11	31822130	31822348	31822151	31822323	PAX6	NM_000280	1	13	7	-	31822239	31822404
319826801	chr11	31822304	31822442	31822324	31822414	PAX6	NM_000280	1	13	7	-	31822239	31822404
318496369	chr11	31816024	31816225	31816051	31816197	PAX6	NM_000280	1	13	8	-	31816178	31816336
318503495	chr11	31816177	31816388	31816198	31816360	PAX6	NM_000280	1	13	8	-	31816178	31816336
318911728	chr11	31815498	31815700	31815522	31815672	PAX6	NM_000280	1	13	9	-	31815580	31815662
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_000280	1	13	10	-	31815200	31815350
319105812	chr11	31815186	31815393	31815211	31815371	PAX6	NM_000280	1	13	10	-	31815200	31815350

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318495733	chr11	31814924	31815140	31814945	31815113	PAX6	NM_000280	1	13	11	-	31814986	31815101
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_000280	1	13	11	-	31814986	31815101
320119938	chr11	31812169	31812388	31812192	31812367	PAX6	NM_000280	1	13	12	-	31812258	31812408
320148161	chr11	31812345	31812526	31812364	31812499	PAX6	NM_000280	1	13	12	-	31812258	31812408
319066981	chr11	31811405	31811625	31811426	31811597	PAX6	NM_000280	1	13	13	-	31806340	31811567
320028156	chr11	31827867	31828025	31827884	31827999	PAX6	NM_001127612	2	13	4	-	31827950	31828010
321097146	chr11	31824178	31824396	31824203	31824375	PAX6	NM_001127612	2	13	5	-	31824252	31824382
321108379	chr11	31824351	31824558	31824371	31824536	PAX6	NM_001127612	2	13	5	-	31824252	31824382
318206826	chr11	31822961	31823174	31822983	31823152	PAX6	NM_001127612	2	13	6	-	31823109	31823324
318239177	chr11	31823132	31823352	31823153	31823329	PAX6	NM_001127612	2	13	6	-	31823109	31823324
319939087	chr11	31823289	31823512	31823313	31823483	PAX6	NM_001127612	2	13	6	-	31823109	31823324
319795090	chr11	31822130	31822348	31822151	31822323	PAX6	NM_001127612	2	13	7	-	31822239	31822404
319826801	chr11	31822304	31822442	31822324	31822414	PAX6	NM_001127612	2	13	7	-	31822239	31822404
318496369	chr11	31816024	31816225	31816051	31816197	PAX6	NM_001127612	2	13	8	-	31816178	31816336
318503495	chr11	31816177	31816388	31816198	31816360	PAX6	NM_001127612	2	13	8	-	31816178	31816336
318911728	chr11	31815498	31815700	31815522	31815672	PAX6	NM_001127612	2	13	9	-	31815580	31815662
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_001127612	2	13	10	-	31815200	31815350
319105812	chr11	31815186	31815393	31815211	31815371	PAX6	NM_001127612	2	13	10	-	31815200	31815350
318495733	chr11	31814924	31815140	31814945	31815113	PAX6	NM_001127612	2	13	11	-	31814986	31815101
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_001127612	2	13	11	-	31814986	31815101
320119938	chr11	31812169	31812388	31812192	31812367	PAX6	NM_001127612	2	13	12	-	31812258	31812408
320148161	chr11	31812345	31812526	31812364	31812499	PAX6	NM_001127612	2	13	12	-	31812258	31812408
319066981	chr11	31811405	31811625	31811426	31811597	PAX6	NM_001127612	2	13	13	-	31806340	31811567
320028156	chr11	31827867	31828025	31827884	31827999	PAX6	NM_001604	3	14	4	-	31827950	31828010
321097146	chr11	31824178	31824396	31824203	31824375	PAX6	NM_001604	3	14	5	-	31824252	31824382
321108379	chr11	31824351	31824558	31824371	31824536	PAX6	NM_001604	3	14	5	-	31824252	31824382
319939087	chr11	31823289	31823512	31823313	31823483	PAX6	NM_001604	3	14	6	-	31823419	31823460
318206826	chr11	31822961	31823174	31822983	31823152	PAX6	NM_001604	3	14	7	-	31823109	31823324
318239177	chr11	31823132	31823352	31823153	31823329	PAX6	NM_001604	3	14	7	-	31823109	31823324
319939087	chr11	31823289	31823512	31823313	31823483	PAX6	NM_001604	3	14	7	-	31823109	31823324
319795090	chr11	31822130	31822348	31822151	31822323	PAX6	NM_001604	3	14	8	-	31822239	31822404
319826801	chr11	31822304	31822442	31822324	31822414	PAX6	NM_001604	3	14	8	-	31822239	31822404
318496369	chr11	31816024	31816225	31816051	31816197	PAX6	NM_001604	3	14	9	-	31816178	31816336
318503495	chr11	31816177	31816388	31816198	31816360	PAX6	NM_001604	3	14	9	-	31816178	31816336
318911728	chr11	31815498	31815700	31815522	31815672	PAX6	NM_001604	3	14	10	-	31815580	31815662
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_001604	3	14	11	-	31815200	31815350
319105812	chr11	31815186	31815393	31815211	31815371	PAX6	NM_001604	3	14	11	-	31815200	31815350
318495733	chr11	31814924	31815140	31814945	31815113	PAX6	NM_001604	3	14	12	-	31814986	31815101
318509514	chr11	31815030	31815234	31815050	31815210	PAX6	NM_001604	3	14	12	-	31814986	31815101
320119938	chr11	31812169	31812388	31812192	31812367	PAX6	NM_001604	3	14	13	-	31812258	31812408
320148161	chr11	31812345	31812526	31812364	31812499	PAX6	NM_001604	3	14	13	-	31812258	31812408

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319066981	chr11	31811405	31811625	31811426	31811597	PAX6	NM_001604	3	14	14	-	31806340	31811567
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142763	1	35	2	-	56423932	56424050
320223276	chr10	56288089	56288215	56288112	56288187	PCDH15	NM_001142763	1	35	3	-	56288148	56288162
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142763	1	35	4	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142763	1	35	5	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142763	1	35	5	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142763	1	35	6	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142763	1	35	6	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142763	1	35	7	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142763	1	35	7	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142763	1	35	8	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142763	1	35	8	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142763	1	35	9	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142763	1	35	9	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142763	1	35	10	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142763	1	35	10	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142763	1	35	11	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142763	1	35	11	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142763	1	35	12	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142763	1	35	12	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142763	1	35	12	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142763	1	35	13	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142763	1	35	13	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142763	1	35	14	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142763	1	35	14	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142763	1	35	15	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142763	1	35	15	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142763	1	35	16	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142763	1	35	16	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142763	1	35	17	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142763	1	35	18	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142763	1	35	18	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142763	1	35	19	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142763	1	35	19	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142763	1	35	20	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142763	1	35	20	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142763	1	35	20	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142763	1	35	21	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142763	1	35	21	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142763	1	35	22	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142763	1	35	22	-	55755409	55755525

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142763	1	35	23	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142763	1	35	23	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142763	1	35	24	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142763	1	35	25	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142763	1	35	26	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142763	1	35	26	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142763	1	35	27	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142763	1	35	27	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142763	1	35	28	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142763	1	35	28	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142763	1	35	29	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142763	1	35	30	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142763	1	35	30	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142763	1	35	31	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142763	1	35	31	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142763	1	35	32	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142763	1	35	33	-	55587152	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142763	1	35	33	-	55587152	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142763	1	35	34	-	55583189	55583193
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142763	1	35	35	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142764	2	34	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142764	2	34	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142764	2	34	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142764	2	34	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142764	2	34	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142764	2	34	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142764	2	34	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142764	2	34	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142764	2	34	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142764	2	34	7	-	56089356	56089466

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142764	2	34	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142764	2	34	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142764	2	34	9	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142764	2	34	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142764	2	34	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142764	2	34	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142764	2	34	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142764	2	34	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142764	2	34	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142764	2	34	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142764	2	34	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142764	2	34	13	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142764	2	34	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142764	2	34	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142764	2	34	14	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142764	2	34	15	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142764	2	34	15	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142764	2	34	16	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142764	2	34	17	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142764	2	34	17	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142764	2	34	18	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142764	2	34	18	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142764	2	34	19	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142764	2	34	19	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142764	2	34	19	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142764	2	34	20	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142764	2	34	20	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142764	2	34	21	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142764	2	34	21	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142764	2	34	22	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142764	2	34	22	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142764	2	34	23	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142764	2	34	24	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142764	2	34	25	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142764	2	34	25	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142764	2	34	26	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142764	2	34	26	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142764	2	34	27	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142764	2	34	27	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142764	2	34	28	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142764	2	34	29	-	55600080	55600256

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142764	2	34	29	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142764	2	34	30	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142764	2	34	30	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142764	2	34	31	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142764	2	34	32	-	55587152	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142764	2	34	32	-	55587152	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142764	2	34	33	-	55583189	55583193
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142764	2	34	34	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142765	3	32	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142765	3	32	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142765	3	32	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142765	3	32	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142765	3	32	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142765	3	32	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142765	3	32	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142765	3	32	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142765	3	32	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142765	3	32	7	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142765	3	32	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142765	3	32	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142765	3	32	9	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142765	3	32	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142765	3	32	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142765	3	32	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142765	3	32	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142765	3	32	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142765	3	32	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142765	3	32	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142765	3	32	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142765	3	32	13	-	55943204	55943353

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142765	3	32	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142765	3	32	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142765	3	32	14	-	55912860	55913053
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142765	3	32	15	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142765	3	32	15	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142765	3	32	16	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142765	3	32	16	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142765	3	32	17	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142765	3	32	17	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142765	3	32	17	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142765	3	32	18	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142765	3	32	18	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142765	3	32	19	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142765	3	32	19	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142765	3	32	20	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142765	3	32	20	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142765	3	32	21	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142765	3	32	22	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142765	3	32	23	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142765	3	32	23	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142765	3	32	24	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142765	3	32	24	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142765	3	32	25	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142765	3	32	25	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142765	3	32	26	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142765	3	32	27	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142765	3	32	27	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142765	3	32	28	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142765	3	32	28	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142765	3	32	29	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142765	3	32	30	-	55587152	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142765	3	32	30	-	55587152	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142765	3	32	31	-	55583189	55583193
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142765	3	32	32	-	55580860	55583118

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142765	3	32	32	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142766	4	32	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142766	4	32	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142766	4	32	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142766	4	32	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142766	4	32	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142766	4	32	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142766	4	32	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142766	4	32	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142766	4	32	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142766	4	32	7	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142766	4	32	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142766	4	32	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142766	4	32	9	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142766	4	32	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142766	4	32	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142766	4	32	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142766	4	32	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142766	4	32	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142766	4	32	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142766	4	32	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142766	4	32	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142766	4	32	13	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142766	4	32	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142766	4	32	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142766	4	32	14	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142766	4	32	15	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142766	4	32	15	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142766	4	32	16	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142766	4	32	17	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142766	4	32	17	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142766	4	32	18	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142766	4	32	18	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142766	4	32	19	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142766	4	32	19	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142766	4	32	19	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142766	4	32	20	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142766	4	32	20	-	55779952	55780176

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142766	4	32	21	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142766	4	32	21	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142766	4	32	22	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142766	4	32	22	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142766	4	32	23	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142766	4	32	24	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142766	4	32	25	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142766	4	32	25	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142766	4	32	26	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142766	4	32	26	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142766	4	32	27	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142766	4	32	27	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142766	4	32	28	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142766	4	32	29	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142766	4	32	29	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142766	4	32	30	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142766	4	32	30	-	55591075	55591293
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142766	4	32	31	-	55587153	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142766	4	32	31	-	55587153	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142766	4	32	32	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142767	5	31	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142767	5	31	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142767	5	31	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142767	5	31	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142767	5	31	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142767	5	31	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142767	5	31	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142767	5	31	6	-	56106125	56106244
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142767	5	31	7	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142767	5	31	7	-	56077031	56077201

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142767	5	31	8	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142767	5	31	8	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142767	5	31	9	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142767	5	31	9	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142767	5	31	10	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142767	5	31	10	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142767	5	31	10	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142767	5	31	11	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142767	5	31	11	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142767	5	31	12	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142767	5	31	12	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142767	5	31	13	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142767	5	31	13	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142767	5	31	14	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142767	5	31	14	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142767	5	31	15	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142767	5	31	16	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142767	5	31	16	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142767	5	31	17	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142767	5	31	17	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142767	5	31	18	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142767	5	31	18	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142767	5	31	18	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142767	5	31	19	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142767	5	31	19	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142767	5	31	20	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142767	5	31	20	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142767	5	31	21	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142767	5	31	21	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142767	5	31	22	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142767	5	31	23	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142767	5	31	24	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142767	5	31	24	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142767	5	31	25	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142767	5	31	25	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142767	5	31	26	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142767	5	31	26	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142767	5	31	27	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142767	5	31	28	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142767	5	31	28	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142767	5	31	29	-	55591075	55591293

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142767	5	31	29	-	55591075	55591293
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142767	5	31	30	-	55587153	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142767	5	31	30	-	55587153	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142767	5	31	31	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142768	6	33	2	-	56423932	56424050
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142768	6	33	3	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142768	6	33	3	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142768	6	33	4	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142768	6	33	4	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142768	6	33	5	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142768	6	33	5	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142768	6	33	6	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142768	6	33	6	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142768	6	33	7	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142768	6	33	7	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142768	6	33	8	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142768	6	33	8	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142768	6	33	9	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142768	6	33	9	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142768	6	33	10	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142768	6	33	10	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142768	6	33	10	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142768	6	33	11	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142768	6	33	11	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142768	6	33	12	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142768	6	33	12	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142768	6	33	13	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142768	6	33	13	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142768	6	33	14	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142768	6	33	14	-	55892635	55892767

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142768	6	33	15	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142768	6	33	16	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142768	6	33	16	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142768	6	33	17	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142768	6	33	17	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142768	6	33	18	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142768	6	33	18	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142768	6	33	18	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142768	6	33	19	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142768	6	33	19	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142768	6	33	20	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142768	6	33	20	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142768	6	33	21	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142768	6	33	21	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142768	6	33	22	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142768	6	33	23	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142768	6	33	24	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142768	6	33	24	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142768	6	33	25	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142768	6	33	25	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142768	6	33	26	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142768	6	33	26	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142768	6	33	27	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142768	6	33	28	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142768	6	33	28	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142768	6	33	29	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142768	6	33	29	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142768	6	33	30	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142768	6	33	31	-	55587152	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142768	6	33	31	-	55587152	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142768	6	33	32	-	55583189	55583193
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142768	6	33	33	-	55580860	55583118

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142768	6	33	33	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142769	7	36	2	-	56423932	56424050
320223276	chr10	56288089	56288215	56288112	56288187	PCDH15	NM_001142769	7	36	3	-	56288148	56288162
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142769	7	36	4	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142769	7	36	5	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142769	7	36	5	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142769	7	36	6	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142769	7	36	6	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142769	7	36	7	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142769	7	36	7	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142769	7	36	8	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142769	7	36	8	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142769	7	36	9	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142769	7	36	9	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142769	7	36	10	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142769	7	36	10	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142769	7	36	11	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142769	7	36	11	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142769	7	36	12	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142769	7	36	12	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142769	7	36	12	-	55955443	55955649
319026265	chr10	55949072	55949209	55949101	55949181	PCDH15	NM_001142769	7	36	13	-	55949124	55949144
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142769	7	36	14	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142769	7	36	14	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142769	7	36	15	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142769	7	36	15	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142769	7	36	16	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142769	7	36	16	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142769	7	36	17	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142769	7	36	17	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142769	7	36	18	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142769	7	36	19	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142769	7	36	19	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142769	7	36	20	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142769	7	36	20	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142769	7	36	21	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142769	7	36	21	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142769	7	36	21	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142769	7	36	22	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142769	7	36	22	-	55779952	55780176

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142769	7	36	23	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142769	7	36	23	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142769	7	36	24	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142769	7	36	24	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142769	7	36	25	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142769	7	36	26	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142769	7	36	27	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142769	7	36	27	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142769	7	36	28	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142769	7	36	28	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142769	7	36	29	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142769	7	36	29	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142769	7	36	30	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142769	7	36	31	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142769	7	36	31	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142769	7	36	32	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142769	7	36	32	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142769	7	36	33	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142769	7	36	34	-	55587149	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142769	7	36	34	-	55587149	55587308
318422602	chr10	55570143	55570367	55570166	55570344	PCDH15	NM_001142769	7	36	35	-	55570316	55570426
318439218	chr10	55570320	55570485	55570345	55570457	PCDH15	NM_001142769	7	36	35	-	55570316	55570426
319630186	chr10	55568349	55568544	55568375	55568525	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
319692890	chr10	55568502	55568698	55568526	55568675	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
319725248	chr10	55568650	55568873	55568676	55568846	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
319758795	chr10	55568815	55569031	55568841	55569007	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
321358122	chr10	55568982	55569186	55569008	55569159	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
321388708	chr10	55569123	55569344	55569151	55569321	PCDH15	NM_001142769	7	36	36	-	55568452	55569306
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142770	8	35	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142770	8	35	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142770	8	35	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142770	8	35	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142770	8	35	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142770	8	35	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142770	8	35	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142770	8	35	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142770	8	35	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142770	8	35	7	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142770	8	35	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142770	8	35	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142770	8	35	9	-	55996583	55996691

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142770	8	35	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142770	8	35	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142770	8	35	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142770	8	35	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142770	8	35	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142770	8	35	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142770	8	35	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142770	8	35	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142770	8	35	13	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142770	8	35	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142770	8	35	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142770	8	35	14	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142770	8	35	15	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142770	8	35	15	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142770	8	35	16	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142770	8	35	17	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142770	8	35	17	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142770	8	35	18	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142770	8	35	18	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142770	8	35	19	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142770	8	35	19	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142770	8	35	19	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142770	8	35	20	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142770	8	35	20	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142770	8	35	21	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142770	8	35	21	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142770	8	35	22	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142770	8	35	22	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142770	8	35	23	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142770	8	35	24	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142770	8	35	25	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142770	8	35	25	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142770	8	35	26	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142770	8	35	26	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142770	8	35	27	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142770	8	35	27	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142770	8	35	28	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142770	8	35	29	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142770	8	35	29	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142770	8	35	30	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142770	8	35	30	-	55591075	55591293

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142770	8	35	31	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142770	8	35	32	-	55587149	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142770	8	35	32	-	55587149	55587308
320217912	chr10	55571182	55571351	55571212	55571325	PCDH15	NM_001142770	8	35	33	-	55571309	55571381
320219085	chr10	55571299	55571437	55571326	55571410	PCDH15	NM_001142770	8	35	33	-	55571309	55571381
318422602	chr10	55570143	55570367	55570166	55570344	PCDH15	NM_001142770	8	35	34	-	55570316	55570424
318439218	chr10	55570320	55570485	55570345	55570457	PCDH15	NM_001142770	8	35	34	-	55570316	55570424
319630186	chr10	55568349	55568544	55568375	55568525	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
319692890	chr10	55568502	55568698	55568526	55568675	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
319725248	chr10	55568650	55568873	55568676	55568846	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
319758795	chr10	55568815	55569031	55568841	55569007	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
321358122	chr10	55568982	55569186	55569008	55569159	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
321388708	chr10	55569123	55569344	55569151	55569321	PCDH15	NM_001142770	8	35	35	-	55568452	55569306
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142771	9	35	2	-	56423932	56424050
320223276	chr10	56288089	56288215	56288112	56288187	PCDH15	NM_001142771	9	35	3	-	56288148	56288162
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142771	9	35	4	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142771	9	35	5	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142771	9	35	5	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142771	9	35	6	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142771	9	35	6	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142771	9	35	7	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142771	9	35	7	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142771	9	35	8	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142771	9	35	8	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142771	9	35	9	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142771	9	35	9	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142771	9	35	10	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142771	9	35	10	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142771	9	35	11	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142771	9	35	11	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142771	9	35	12	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142771	9	35	12	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142771	9	35	12	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142771	9	35	13	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142771	9	35	13	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142771	9	35	14	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142771	9	35	14	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142771	9	35	15	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142771	9	35	15	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142771	9	35	16	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142771	9	35	16	-	55892635	55892767

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142771	9	35	17	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142771	9	35	18	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142771	9	35	18	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142771	9	35	19	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142771	9	35	19	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142771	9	35	20	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142771	9	35	20	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142771	9	35	20	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142771	9	35	21	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142771	9	35	21	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142771	9	35	22	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142771	9	35	22	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142771	9	35	23	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142771	9	35	23	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142771	9	35	24	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142771	9	35	25	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142771	9	35	26	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142771	9	35	26	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142771	9	35	27	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142771	9	35	27	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142771	9	35	28	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142771	9	35	28	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142771	9	35	29	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142771	9	35	30	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142771	9	35	30	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142771	9	35	31	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142771	9	35	31	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142771	9	35	32	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142771	9	35	33	-	55587149	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142771	9	35	33	-	55587149	55587308
318422602	chr10	55570143	55570367	55570166	55570344	PCDH15	NM_001142771	9	35	34	-	55570316	55570426
318439218	chr10	55570320	55570485	55570345	55570457	PCDH15	NM_001142771	9	35	34	-	55570316	55570426
319444996	chr10	55566584	55566808	55566610	55566786	PCDH15	NM_001142771	9	35	35	-	55562533	55566890
319462880	chr10	55566759	55566972	55566787	55566944	PCDH15	NM_001142771	9	35	35	-	55562533	55566890
321216885	chr10	55566167	55566378	55566195	55566357	PCDH15	NM_001142771	9	35	35	-	55562533	55566890
321219523	chr10	55566330	55566468	55566358	55566442	PCDH15	NM_001142771	9	35	35	-	55562533	55566890
321234883	chr10	55566417	55566632	55566443	55566609	PCDH15	NM_001142771	9	35	35	-	55562533	55566890
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142772	10	34	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_001142772	10	34	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142772	10	34	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142772	10	34	4	-	56138542	56138702

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142772	10	34	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142772	10	34	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142772	10	34	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142772	10	34	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142772	10	34	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142772	10	34	7	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142772	10	34	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142772	10	34	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142772	10	34	9	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142772	10	34	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142772	10	34	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142772	10	34	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142772	10	34	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142772	10	34	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142772	10	34	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142772	10	34	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142772	10	34	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142772	10	34	13	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142772	10	34	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142772	10	34	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142772	10	34	14	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142772	10	34	15	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142772	10	34	15	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142772	10	34	16	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142772	10	34	17	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142772	10	34	17	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142772	10	34	18	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142772	10	34	18	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142772	10	34	19	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142772	10	34	19	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142772	10	34	19	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142772	10	34	20	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142772	10	34	20	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142772	10	34	21	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142772	10	34	21	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142772	10	34	22	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142772	10	34	22	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142772	10	34	23	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142772	10	34	24	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142772	10	34	25	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142772	10	34	25	-	55698575	55698715

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142772	10	34	26	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142772	10	34	26	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142772	10	34	27	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142772	10	34	27	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142772	10	34	28	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142772	10	34	29	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142772	10	34	29	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142772	10	34	30	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142772	10	34	30	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_001142772	10	34	31	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142772	10	34	32	-	55587149	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142772	10	34	32	-	55587149	55587308
318422602	chr10	55570143	55570367	55570166	55570344	PCDH15	NM_001142772	10	34	33	-	55570316	55570426
318439218	chr10	55570320	55570485	55570345	55570457	PCDH15	NM_001142772	10	34	33	-	55570316	55570426
319444996	chr10	55566584	55566808	55566610	55566786	PCDH15	NM_001142772	10	34	34	-	55562533	55566890
319462880	chr10	55566759	55566972	55566787	55566944	PCDH15	NM_001142772	10	34	34	-	55562533	55566890
321216885	chr10	55566167	55566378	55566195	55566357	PCDH15	NM_001142772	10	34	34	-	55562533	55566890
321219523	chr10	55566330	55566468	55566358	55566442	PCDH15	NM_001142772	10	34	34	-	55562533	55566890
321234883	chr10	55566417	55566632	55566443	55566609	PCDH15	NM_001142772	10	34	34	-	55562533	55566890
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_001142773	11	32	2	-	56423932	56424050
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_001142773	11	32	3	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_001142773	11	32	3	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_001142773	11	32	4	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_001142773	11	32	4	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_001142773	11	32	5	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_001142773	11	32	5	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_001142773	11	32	6	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_001142773	11	32	6	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_001142773	11	32	7	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_001142773	11	32	7	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_001142773	11	32	8	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_001142773	11	32	8	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_001142773	11	32	9	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_001142773	11	32	9	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_001142773	11	32	10	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_001142773	11	32	10	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_001142773	11	32	10	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_001142773	11	32	11	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_001142773	11	32	11	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_001142773	11	32	12	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_001142773	11	32	12	-	55943204	55943353

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_001142773	11	32	13	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_001142773	11	32	13	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_001142773	11	32	14	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_001142773	11	32	14	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_001142773	11	32	15	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_001142773	11	32	16	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_001142773	11	32	16	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_001142773	11	32	17	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_001142773	11	32	17	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_001142773	11	32	18	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_001142773	11	32	18	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_001142773	11	32	18	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_001142773	11	32	19	-	55779952	55780176
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_001142773	11	32	19	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_001142773	11	32	20	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_001142773	11	32	20	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_001142773	11	32	21	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_001142773	11	32	21	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_001142773	11	32	22	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_001142773	11	32	23	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_001142773	11	32	24	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_001142773	11	32	24	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_001142773	11	32	25	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_001142773	11	32	25	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_001142773	11	32	26	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_001142773	11	32	26	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_001142773	11	32	27	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_001142773	11	32	28	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_001142773	11	32	28	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_001142773	11	32	29	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_001142773	11	32	29	-	55591075	55591293
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_001142773	11	32	30	-	55587152	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_001142773	11	32	30	-	55587152	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142773	11	32	31	-	55583189	55583193
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_001142773	11	32	32	-	55580860	55583118

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_001142773	11	32	32	-	55580860	55583118
320125880	chr10	56423889	56424054	56423911	56424028	PCDH15	NM_033056	12	33	2	-	56423932	56424050
319541789	chr10	56287455	56287679	56287478	56287652	PCDH15	NM_033056	12	33	3	-	56287572	56287637
320008395	chr10	56138409	56138608	56138438	56138584	PCDH15	NM_033056	12	33	4	-	56138542	56138702
320012399	chr10	56138563	56138781	56138585	56138757	PCDH15	NM_033056	12	33	4	-	56138542	56138702
318980098	chr10	56128875	56129044	56128896	56129024	PCDH15	NM_033056	12	33	5	-	56128880	56129035
318995958	chr10	56129002	56129126	56129024	56129099	PCDH15	NM_033056	12	33	5	-	56128880	56129035
319173951	chr10	56106013	56106176	56106044	56106149	PCDH15	NM_033056	12	33	6	-	56106125	56106244
319174054	chr10	56106111	56106310	56106139	56106286	PCDH15	NM_033056	12	33	6	-	56106125	56106244
320721143	chr10	56089238	56089411	56089260	56089383	PCDH15	NM_033056	12	33	7	-	56089356	56089466
320728526	chr10	56089356	56089566	56089384	56089538	PCDH15	NM_033056	12	33	7	-	56089356	56089466
318694875	chr10	56076876	56077082	56076904	56077059	PCDH15	NM_033056	12	33	8	-	56077031	56077201
318699500	chr10	56077038	56077261	56077060	56077233	PCDH15	NM_033056	12	33	8	-	56077031	56077201
320129169	chr10	55996398	55996621	55996423	55996595	PCDH15	NM_033056	12	33	9	-	55996583	55996691
320129797	chr10	55996567	55996726	55996596	55996699	PCDH15	NM_033056	12	33	9	-	55996583	55996691
318040006	chr10	55973617	55973774	55973639	55973750	PCDH15	NM_033056	12	33	10	-	55973696	55973808
318045340	chr10	55973729	55973891	55973751	55973864	PCDH15	NM_033056	12	33	10	-	55973696	55973808
320090567	chr10	55955319	55955475	55955350	55955449	PCDH15	NM_033056	12	33	11	-	55955443	55955649
320090606	chr10	55955437	55955611	55955465	55955583	PCDH15	NM_033056	12	33	11	-	55955443	55955649
320097618	chr10	55955551	55955715	55955579	55955689	PCDH15	NM_033056	12	33	11	-	55955443	55955649
319789889	chr10	55944812	55945027	55944838	55945004	PCDH15	NM_033056	12	33	12	-	55944894	55945028
319793577	chr10	55945002	55945224	55945025	55945196	PCDH15	NM_033056	12	33	12	-	55944894	55945028
318844220	chr10	55943150	55943312	55943178	55943284	PCDH15	NM_033056	12	33	13	-	55943204	55943353
318852192	chr10	55943264	55943470	55943285	55943442	PCDH15	NM_033056	12	33	13	-	55943204	55943353
318208047	chr10	55912777	55912985	55912800	55912956	PCDH15	NM_033056	12	33	14	-	55912860	55913053
318223999	chr10	55912937	55913092	55912957	55913064	PCDH15	NM_033056	12	33	14	-	55912860	55913053
318603209	chr10	55892454	55892669	55892477	55892646	PCDH15	NM_033056	12	33	15	-	55892635	55892767
318636198	chr10	55892618	55892801	55892647	55892773	PCDH15	NM_033056	12	33	15	-	55892635	55892767
318957561	chr10	55849653	55849877	55849678	55849856	PCDH15	NM_033056	12	33	16	-	55849744	55849823
320336205	chr10	55838943	55839156	55838968	55839136	PCDH15	NM_033056	12	33	17	-	55839091	55839184
320336820	chr10	55839148	55839370	55839169	55839342	PCDH15	NM_033056	12	33	17	-	55839091	55839184
318328749	chr10	55826389	55826555	55826417	55826534	PCDH15	NM_033056	12	33	18	-	55826517	55826645
318329566	chr10	55826508	55826682	55826535	55826656	PCDH15	NM_033056	12	33	18	-	55826517	55826645
319349113	chr10	55782459	55782679	55782483	55782658	PCDH15	NM_033056	12	33	19	-	55782652	55782957
319359146	chr10	55782635	55782830	55782659	55782804	PCDH15	NM_033056	12	33	19	-	55782652	55782957
319388006	chr10	55782784	55783007	55782805	55782981	PCDH15	NM_033056	12	33	19	-	55782652	55782957
319871167	chr10	55779921	55780062	55779944	55780036	PCDH15	NM_033056	12	33	20	-	55779952	55780176

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319898229	chr10	55780011	55780234	55780037	55780206	PCDH15	NM_033056	12	33	20	-	55779952	55780176
318737966	chr10	55755240	55755442	55755268	55755416	PCDH15	NM_033056	12	33	21	-	55755409	55755525
318744058	chr10	55755394	55755574	55755417	55755546	PCDH15	NM_033056	12	33	21	-	55755409	55755525
320945675	chr10	55721432	55721596	55721455	55721569	PCDH15	NM_033056	12	33	22	-	55721512	55721652
320948168	chr10	55721541	55721711	55721570	55721683	PCDH15	NM_033056	12	33	22	-	55721512	55721652
318643730	chr10	55719455	55719664	55719483	55719638	PCDH15	NM_033056	12	33	23	-	55719492	55719604
318928238	chr10	55700589	55700758	55700616	55700732	PCDH15	NM_033056	12	33	24	-	55700626	55700735
319884877	chr10	55698404	55698620	55698430	55698598	PCDH15	NM_033056	12	33	25	-	55698575	55698715
319889945	chr10	55698574	55698762	55698599	55698734	PCDH15	NM_033056	12	33	25	-	55698575	55698715
318022350	chr10	55662877	55663050	55662900	55663021	PCDH15	NM_033056	12	33	26	-	55663003	55663130
318039413	chr10	55662997	55663180	55663022	55663153	PCDH15	NM_033056	12	33	26	-	55663003	55663130
321411143	chr10	55626357	55626581	55626383	55626553	PCDH15	NM_033056	12	33	27	-	55626402	55626617
321426053	chr10	55626527	55626682	55626554	55626654	PCDH15	NM_033056	12	33	27	-	55626402	55626617
319828875	chr10	55616957	55617145	55616981	55617116	PCDH15	NM_033056	12	33	28	-	55616935	55617023
318985270	chr10	55599932	55600133	55599960	55600111	PCDH15	NM_033056	12	33	29	-	55600080	55600256
318996586	chr10	55600087	55600290	55600112	55600261	PCDH15	NM_033056	12	33	29	-	55600080	55600256
318875963	chr10	55590974	55591196	55591001	55591168	PCDH15	NM_033056	12	33	30	-	55591075	55591293
318902721	chr10	55591147	55591343	55591169	55591314	PCDH15	NM_033056	12	33	30	-	55591075	55591293
320170811	chr10	55588266	55588484	55588294	55588452	PCDH15	NM_033056	12	33	31	-	55588325	55588333
319492634	chr10	55587095	55587300	55587123	55587277	PCDH15	NM_033056	12	33	32	-	55587153	55587308
319506268	chr10	55587259	55587390	55587278	55587362	PCDH15	NM_033056	12	33	32	-	55587153	55587308
318457353	chr10	55583016	55583240	55583044	55583212	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321127906	chr10	55581579	55581761	55581601	55581734	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321137555	chr10	55581707	55581926	55581735	55581902	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321143403	chr10	55582399	55582567	55582421	55582542	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321147998	chr10	55582806	55582997	55582831	55582972	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321154978	chr10	55581879	55582101	55581903	55582077	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321157382	chr10	55582945	55583168	55582973	55583140	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321182585	chr10	55582516	55582729	55582543	55582702	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321191559	chr10	55582075	55582274	55582097	55582252	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321193691	chr10	55582078	55582289	55582103	55582265	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321195711	chr10	55582253	55582448	55582275	55582420	PCDH15	NM_033056	12	33	33	-	55580860	55583118
321212922	chr10	55582682	55582858	55582703	55582830	PCDH15	NM_033056	12	33	33	-	55580860	55583118
320207465	chr7	92157578	92157787	92157597	92157770	PEX1	NM_000466	1	24	1	-	92157621	92157845
321106450	chr7	92151311	92151469	92151335	92151442	PEX1	NM_000466	1	24	2	-	92151416	92151559
321110893	chr7	92151420	92151556	92151443	92151531	PEX1	NM_000466	1	24	2	-	92151416	92151559
321112524	chr7	92151512	92151735	92151532	92151707	PEX1	NM_000466	1	24	2	-	92151416	92151559
318263228	chr7	92148176	92148343	92148203	92148323	PEX1	NM_000466	1	24	3	-	92148309	92148392
318263604	chr7	92148296	92148520	92148324	92148497	PEX1	NM_000466	1	24	3	-	92148309	92148392
318814857	chr7	92147283	92147507	92147305	92147484	PEX1	NM_000466	1	24	4	-	92147455	92147569
318819838	chr7	92147381	92147601	92147408	92147574	PEX1	NM_000466	1	24	4	-	92147455	92147569

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318814857	chr7	92147283	92147507	92147305	92147484	PEX1	NM_000466	1	24	5	-	92146590	92147356
319146607	chr7	92147107	92147326	92147134	92147304	PEX1	NM_000466	1	24	5	-	92146590	92147356
321088780	chr7	92146465	92146687	92146488	92146664	PEX1	NM_000466	1	24	5	-	92146590	92147356
321093564	chr7	92146638	92146854	92146665	92146830	PEX1	NM_000466	1	24	5	-	92146590	92147356
321113959	chr7	92146802	92147000	92146830	92146972	PEX1	NM_000466	1	24	5	-	92146590	92147356
321121259	chr7	92146945	92147161	92146973	92147133	PEX1	NM_000466	1	24	5	-	92146590	92147356
318392721	chr7	92143094	92143278	92143125	92143250	PEX1	NM_000466	1	24	6	-	92143162	92143281
318454139	chr7	92140801	92140972	92140827	92140950	PEX1	NM_000466	1	24	7	-	92140894	92141017
318457844	chr7	92140924	92141122	92140951	92141094	PEX1	NM_000466	1	24	7	-	92140894	92141017
321487983	chr7	92140160	92140301	92140185	92140275	PEX1	NM_000466	1	24	8	-	92140258	92140361
321489868	chr7	92140256	92140410	92140283	92140382	PEX1	NM_000466	1	24	8	-	92140258	92140361
318351722	chr7	92138608	92138738	92138634	92138713	PEX1	NM_000466	1	24	9	-	92138643	92138725
318353146	chr7	92138685	92138893	92138714	92138866	PEX1	NM_000466	1	24	9	-	92138643	92138725
319459898	chr7	92136167	92136359	92136195	92136335	PEX1	NM_000466	1	24	10	-	92136308	92136440
319464000	chr7	92136313	92136527	92136336	92136503	PEX1	NM_000466	1	24	10	-	92136308	92136440
319776597	chr7	92135541	92135728	92135570	92135703	PEX1	NM_000466	1	24	11	-	92135562	92135658
320163526	chr7	92133993	92134151	92134020	92134130	PEX1	NM_000466	1	24	12	-	92134046	92134216
320172954	chr7	92134109	92134311	92134130	92134283	PEX1	NM_000466	1	24	12	-	92134046	92134216
321171784	chr7	92132203	92132395	92132225	92132371	PEX1	NM_000466	1	24	13	-	92132355	92132509
321180668	chr7	92132345	92132547	92132372	92132518	PEX1	NM_000466	1	24	13	-	92132355	92132509
319378884	chr7	92131042	92131266	92131070	92131244	PEX1	NM_000466	1	24	14	-	92131204	92131393
321598717	chr7	92130712	92130917	92130735	92130892	PEX1	NM_000466	1	24	15	-	92130821	92130987
321628759	chr7	92130872	92131068	92130893	92131040	PEX1	NM_000466	1	24	15	-	92130821	92130987
318425291	chr7	92129047	92129219	92129068	92129190	PEX1	NM_000466	1	24	16	-	92129018	92129152
318283880	chr7	92125880	92126091	92125903	92126072	PEX1	NM_000466	1	24	17	-	92126027	92126091
318722120	chr7	92123631	92123846	92123656	92123822	PEX1	NM_000466	1	24	18	-	92123801	92123943
320968536	chr7	92123800	92123994	92123823	92123967	PEX1	NM_000466	1	24	18	-	92123801	92123943
318701824	chr7	92123465	92123658	92123487	92123636	PEX1	NM_000466	1	24	19	-	92123607	92123710
318721613	chr7	92123611	92123820	92123637	92123792	PEX1	NM_000466	1	24	19	-	92123607	92123710
318722120	chr7	92123631	92123846	92123656	92123822	PEX1	NM_000466	1	24	19	-	92123607	92123710
318212758	chr7	92122094	92122314	92122119	92122293	PEX1	NM_000466	1	24	20	-	92122267	92122443
318217340	chr7	92122274	92122410	92122294	92122386	PEX1	NM_000466	1	24	20	-	92122267	92122443
318223008	chr7	92122363	92122586	92122387	92122558	PEX1	NM_000466	1	24	20	-	92122267	92122443
319651668	chr7	92120498	92120682	92120520	92120654	PEX1	NM_000466	1	24	21	-	92120586	92120816
319696036	chr7	92120629	92120851	92120655	92120823	PEX1	NM_000466	1	24	21	-	92120586	92120816
320109763	chr7	92118893	92119112	92118919	92119085	PEX1	NM_000466	1	24	22	-	92119028	92119225
320122315	chr7	92119061	92119266	92119086	92119238	PEX1	NM_000466	1	24	22	-	92119028	92119225
319201979	chr7	92118427	92118638	92118454	92118611	PEX1	NM_000466	1	24	23	-	92118607	92118737
319202713	chr7	92118575	92118747	92118603	92118719	PEX1	NM_000466	1	24	23	-	92118607	92118737
319209283	chr7	92118697	92118892	92118720	92118865	PEX1	NM_000466	1	24	23	-	92118607	92118737
320482786	chr7	92116769	92116933	92116799	92116905	PEX1	NM_000466	1	24	24	-	92116337	92116855

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320489080	chr7	92116602	92116810	92116635	92116787	PEX1	NM_000466	1	24	24	-	92116337	92116855
319798464	chr1	2343870	2344020	2343888	2344000	PEX10	NM_002617	1	6	1	-	2343830	2344010
318267065	chr1	2341709	2341921	2341730	2341898	PEX10	NM_002617	1	6	2	-	2341810	2341890
319371252	chr1	2339750	2339972	2339771	2339952	PEX10	NM_002617	1	6	3	-	2339891	2340297
319379396	chr1	2339928	2340147	2339951	2340130	PEX10	NM_002617	1	6	3	-	2339891	2340297
319382399	chr1	2340111	2340326	2340128	2340304	PEX10	NM_002617	1	6	3	-	2339891	2340297
318167710	chr1	2338092	2338295	2338114	2338275	PEX10	NM_002617	1	6	4	-	2338159	2338334
318173480	chr1	2338252	2338436	2338272	2338415	PEX10	NM_002617	1	6	4	-	2338159	2338334
318672195	chr1	2337738	2337962	2337760	2337942	PEX10	NM_002617	1	6	5	-	2337923	2338058
318678325	chr1	2337921	2338118	2337938	2338097	PEX10	NM_002617	1	6	5	-	2337923	2338058
321495290	chr1	2337141	2337364	2337164	2337337	PEX10	NM_002617	1	6	6	-	2336241	2337273
319798464	chr1	2343870	2344020	2343888	2344000	PEX10	NM_153818	2	6	1	-	2343830	2344010
318267065	chr1	2341709	2341921	2341730	2341898	PEX10	NM_153818	2	6	2	-	2341810	2341890
319371252	chr1	2339750	2339972	2339771	2339952	PEX10	NM_153818	2	6	3	-	2339891	2340297
319379396	chr1	2339928	2340147	2339951	2340130	PEX10	NM_153818	2	6	3	-	2339891	2340297
319382399	chr1	2340111	2340326	2340128	2340304	PEX10	NM_153818	2	6	3	-	2339891	2340297
318167710	chr1	2338092	2338295	2338114	2338275	PEX10	NM_153818	2	6	4	-	2338159	2338394
318173480	chr1	2338252	2338436	2338272	2338415	PEX10	NM_153818	2	6	4	-	2338159	2338394
318672195	chr1	2337738	2337962	2337760	2337942	PEX10	NM_153818	2	6	5	-	2337923	2338058
318678325	chr1	2337921	2338118	2337938	2338097	PEX10	NM_153818	2	6	5	-	2337923	2338058
321495290	chr1	2337141	2337364	2337164	2337337	PEX10	NM_153818	2	6	6	-	2336241	2337273
320297825	chr2	61244802	61245014	61244823	61244993	PEX13	NM_002618	1	4	1	+	61244812	61244986
320118125	chr2	61258447	61258662	61258474	61258641	PEX13	NM_002618	1	4	2	+	61258554	61259248
320137099	chr2	61258619	61258819	61258642	61258792	PEX13	NM_002618	1	4	2	+	61258554	61259248
320163697	chr2	61258774	61258951	61258793	61258925	PEX13	NM_002618	1	4	2	+	61258554	61259248
320194660	chr2	61258902	61259117	61258926	61259095	PEX13	NM_002618	1	4	2	+	61258554	61259248
321525241	chr2	61259070	61259283	61259093	61259258	PEX13	NM_002618	1	4	2	+	61258554	61259248
318236073	chr2	61272751	61272968	61272775	61272948	PEX13	NM_002618	1	4	3	+	61272861	61272986
318243446	chr2	61272922	61273146	61272947	61273119	PEX13	NM_002618	1	4	3	+	61272861	61272986
320457042	chr2	61275541	61275761	61275568	61275735	PEX13	NM_002618	1	4	4	+	61275607	61279125
320495266	chr2	61275709	61275933	61275736	61275911	PEX13	NM_002618	1	4	4	+	61275607	61279125
319829812	chr1	10534991	10535133	10535010	10535114	PEX14	NM_004565	1	9	1	+	10535003	10535059
319532258	chr1	10555206	10555430	10555233	10555402	PEX14	NM_004565	1	9	2	+	10555331	10555378
319280642	chr1	10596180	10596369	10596202	10596345	PEX14	NM_004565	1	9	3	+	10596270	10596354
319288430	chr1	10596324	10596469	10596346	10596449	PEX14	NM_004565	1	9	3	+	10596270	10596354
320923398	chr1	10659237	10659461	10659259	10659435	PEX14	NM_004565	1	9	4	+	10659295	10659423
318603316	chr1	10678345	10678545	10678365	10678523	PEX14	NM_004565	1	9	5	+	10678389	10678474
320538881	chr1	10683000	10683208	10683022	10683183	PEX14	NM_004565	1	9	6	+	10683076	10683178
318461291	chr1	10684344	10684559	10684365	10684538	PEX14	NM_004565	1	9	7	+	10684397	10684494
318057940	chr1	10687300	10687449	10687317	10687429	PEX14	NM_004565	1	9	8	+	10687329	10687420
318579630	chr1	10689441	10689660	10689460	10689641	PEX14	NM_004565	1	9	9	+	10689588	10690815

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318584283	chr1	10689619	10689831	10689639	10689813	PEX14	NM_004565	1	9	9	+	10689588	10690815
318590158	chr1	10689764	10689986	10689783	10689967	PEX14	NM_004565	1	9	9	+	10689588	10690815
318592384	chr1	10689898	10690089	10689921	10690067	PEX14	NM_004565	1	9	9	+	10689588	10690815
320100123	chr1	160254717	160254939	160254737	160254919	PEX19	NM_001193644	1	8	1	-	160254845	160254941
318841018	chr1	160253283	160253457	160253303	160253434	PEX19	NM_001193644	1	8	2	-	160253320	160253429
320188415	chr1	160252660	160252883	160252684	160252857	PEX19	NM_001193644	1	8	3	-	160252734	160252899
320214627	chr1	160252837	160252978	160252858	160252956	PEX19	NM_001193644	1	8	3	-	160252734	160252899
319825472	chr1	160252108	160252329	160252133	160252306	PEX19	NM_001193644	1	8	4	-	160252207	160252292
319601926	chr1	160251801	160252024	160251829	160251998	PEX19	NM_001193644	1	8	5	-	160251829	160251990
321494908	chr1	160249730	160249911	160249756	160249888	PEX19	NM_001193644	1	8	6	-	160249860	160250036
321519402	chr1	160249865	160250080	160249889	160250052	PEX19	NM_001193644	1	8	6	-	160249860	160250036
319540480	chr1	160249462	160249678	160249489	160249650	PEX19	NM_001193644	1	8	7	-	160249591	160249635
318157466	chr1	160249266	160249458	160249287	160249433	PEX19	NM_001193644	1	8	8	-	160246599	160249372
320100123	chr1	160254717	160254939	160254737	160254919	PEX19	NM_002857	2	8	1	-	160254845	160254941
318841018	chr1	160253283	160253457	160253303	160253434	PEX19	NM_002857	2	8	2	-	160253320	160253429
320188415	chr1	160252660	160252883	160252684	160252857	PEX19	NM_002857	2	8	3	-	160252734	160252899
320214627	chr1	160252837	160252978	160252858	160252956	PEX19	NM_002857	2	8	3	-	160252734	160252899
319825472	chr1	160252108	160252329	160252133	160252306	PEX19	NM_002857	2	8	4	-	160252207	160252292
319601926	chr1	160251801	160252024	160251829	160251998	PEX19	NM_002857	2	8	5	-	160251829	160251990
321494908	chr1	160249730	160249911	160249756	160249888	PEX19	NM_002857	2	8	6	-	160249860	160250036
321519402	chr1	160249865	160250080	160249889	160250052	PEX19	NM_002857	2	8	6	-	160249860	160250036
319540480	chr1	160249462	160249678	160249489	160249650	PEX19	NM_002857	2	8	7	-	160249591	160249635
318157466	chr1	160249266	160249458	160249287	160249433	PEX19	NM_002857	2	8	8	-	160246599	160249424
320100123	chr1	160254717	160254939	160254737	160254919	PEX19	NR_036492	3	7	1	-	160254845	160254941
320188415	chr1	160252660	160252883	160252684	160252857	PEX19	NR_036492	3	7	2	-	160252734	160252899
320214627	chr1	160252837	160252978	160252858	160252956	PEX19	NR_036492	3	7	2	-	160252734	160252899
319825472	chr1	160252108	160252329	160252133	160252306	PEX19	NR_036492	3	7	3	-	160252207	160252292
319601926	chr1	160251801	160252024	160251829	160251998	PEX19	NR_036492	3	7	4	-	160251829	160251990
321494908	chr1	160249730	160249911	160249756	160249888	PEX19	NR_036492	3	7	5	-	160249860	160250036
321519402	chr1	160249865	160250080	160249889	160250052	PEX19	NR_036492	3	7	5	-	160249860	160250036
319540480	chr1	160249462	160249678	160249489	160249650	PEX19	NR_036492	3	7	6	-	160249591	160249635
318157466	chr1	160249266	160249458	160249287	160249433	PEX19	NR_036492	3	7	7	-	160246599	160249424
320100123	chr1	160254717	160254939	160254737	160254919	PEX19	NR_036493	4	7	1	-	160254845	160254941
318841018	chr1	160253283	160253457	160253303	160253434	PEX19	NR_036493	4	7	2	-	160253320	160253429
320188415	chr1	160252660	160252883	160252684	160252857	PEX19	NR_036493	4	7	3	-	160252734	160252899
320214627	chr1	160252837	160252978	160252858	160252956	PEX19	NR_036493	4	7	3	-	160252734	160252899
319601926	chr1	160251801	160252024	160251829	160251998	PEX19	NR_036493	4	7	4	-	160251829	160251990
321494908	chr1	160249730	160249911	160249756	160249888	PEX19	NR_036493	4	7	5	-	160249860	160250036
321519402	chr1	160249865	160250080	160249889	160250052	PEX19	NR_036493	4	7	5	-	160249860	160250036
319540480	chr1	160249462	160249678	160249489	160249650	PEX19	NR_036493	4	7	6	-	160249591	160249635
318157466	chr1	160249266	160249458	160249287	160249433	PEX19	NR_036493	4	7	7	-	160246599	160249424

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318362480	chr22	18560959	18561165	18560980	18561143	PEX26	NM_001127649	1	5	1	+	18560760	18561372
318366309	chr22	18561125	18561321	18561144	18561304	PEX26	NM_001127649	1	5	1	+	18560760	18561372
318382506	chr22	18561277	18561487	18561296	18561465	PEX26	NM_001127649	1	5	1	+	18560760	18561372
320206574	chr22	18562530	18562749	18562551	18562725	PEX26	NM_001127649	1	5	2	+	18562640	18562780
320228202	chr22	18562696	18562891	18562716	18562869	PEX26	NM_001127649	1	5	2	+	18562640	18562780
320054968	chr22	18566144	18566367	18566169	18566347	PEX26	NM_001127649	1	5	3	+	18566203	18566498
320077084	chr22	18566306	18566530	18566327	18566507	PEX26	NM_001127649	1	5	3	+	18566203	18566498
319044033	chr22	18567782	18567983	18567803	18567960	PEX26	NM_001127649	1	5	4	+	18567878	18568024
319063598	chr22	18567938	18568121	18567961	18568099	PEX26	NM_001127649	1	5	4	+	18567878	18568024
318765799	chr22	18570700	18570919	18570719	18570899	PEX26	NM_001127649	1	5	5	+	18570738	18573797
318362480	chr22	18560959	18561165	18560980	18561143	PEX26	NM_001199319	2	5	2	+	18561062	18561372
318366309	chr22	18561125	18561321	18561144	18561304	PEX26	NM_001199319	2	5	2	+	18561062	18561372
318382506	chr22	18561277	18561487	18561296	18561465	PEX26	NM_001199319	2	5	2	+	18561062	18561372
320206574	chr22	18562530	18562749	18562551	18562725	PEX26	NM_001199319	2	5	3	+	18562640	18562780
320228202	chr22	18562696	18562891	18562716	18562869	PEX26	NM_001199319	2	5	3	+	18562640	18562780
320054968	chr22	18566144	18566367	18566169	18566347	PEX26	NM_001199319	2	5	4	+	18566203	18566498
320077084	chr22	18566306	18566530	18566327	18566507	PEX26	NM_001199319	2	5	4	+	18566203	18566498
318765799	chr22	18570700	18570919	18570719	18570899	PEX26	NM_001199319	2	5	5	+	18570738	18573797
318362480	chr22	18560959	18561165	18560980	18561143	PEX26	NM_017929	3	6	2	+	18561062	18561372
318366309	chr22	18561125	18561321	18561144	18561304	PEX26	NM_017929	3	6	2	+	18561062	18561372
318382506	chr22	18561277	18561487	18561296	18561465	PEX26	NM_017929	3	6	2	+	18561062	18561372
320206574	chr22	18562530	18562749	18562551	18562725	PEX26	NM_017929	3	6	3	+	18562640	18562780
320228202	chr22	18562696	18562891	18562716	18562869	PEX26	NM_017929	3	6	3	+	18562640	18562780
320054968	chr22	18566144	18566367	18566169	18566347	PEX26	NM_017929	3	6	4	+	18566203	18566498
320077084	chr22	18566306	18566530	18566327	18566507	PEX26	NM_017929	3	6	4	+	18566203	18566498
319044033	chr22	18567782	18567983	18567803	18567960	PEX26	NM_017929	3	6	5	+	18567878	18568024
319063598	chr22	18567938	18568121	18567961	18568099	PEX26	NM_017929	3	6	5	+	18567878	18568024
318765799	chr22	18570700	18570919	18570719	18570899	PEX26	NM_017929	3	6	6	+	18570738	18573797
319380256	chr6	143772104	143772277	143772126	143772257	PEX3	NM_003630	1	12	1	+	143771918	143772252
320690799	chr6	143780059	143780283	143780084	143780259	PEX3	NM_003630	1	12	2	+	143780222	143780353
320691598	chr6	143780236	143780400	143780263	143780372	PEX3	NM_003630	1	12	2	+	143780222	143780353
320908342	chr6	143783988	143784174	143784011	143784147	PEX3	NM_003630	1	12	3	+	143784053	143784134
320664297	chr6	143789124	143789340	143789146	143789312	PEX3	NM_003630	1	12	4	+	143789259	143789302
319226234	chr6	143792064	143792268	143792092	143792244	PEX3	NM_003630	1	12	5	+	143792098	143792222
319918256	chr6	143792535	143792712	143792562	143792683	PEX3	NM_003630	1	12	6	+	143792520	143792586
321280697	chr6	143792423	143792586	143792451	143792561	PEX3	NM_003630	1	12	6	+	143792520	143792586
321289888	chr6	143792570	143792782	143792597	143792753	PEX3	NM_003630	1	12	7	+	143792694	143792748
318273153	chr6	143793154	143793372	143793180	143793344	PEX3	NM_003630	1	12	8	+	143793297	143793465
318276391	chr6	143793319	143793482	143793341	143793457	PEX3	NM_003630	1	12	8	+	143793297	143793465
318277408	chr6	143793431	143793568	143793458	143793540	PEX3	NM_003630	1	12	8	+	143793297	143793465
320678652	chr6	143795865	143796083	143795892	143796055	PEX3	NM_003630	1	12	9	+	143795923	143795993

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320977483	chr6	143800101	143800318	143800130	143800295	PEX3	NM_003630	1	12	10	+	143800213	143800335
320981925	chr6	143800270	143800494	143800296	143800466	PEX3	NM_003630	1	12	10	+	143800213	143800335
321165432	chr6	143806273	143806403	143806303	143806377	PEX3	NM_003630	1	12	11	+	143806289	143806385
321173401	chr6	143806352	143806480	143806378	143806452	PEX3	NM_003630	1	12	11	+	143806289	143806385
319424031	chr6	143810182	143810323	143810209	143810297	PEX3	NM_003630	1	12	12	+	143810280	143811751
319426569	chr6	143810271	143810396	143810297	143810368	PEX3	NM_003630	1	12	12	+	143810280	143811751
319426816	chr12	7342865	7343089	7342882	7343072	PEX5	NM_000319	1	15	1	+	7342958	7343120
319435431	chr12	7343060	7343260	7343078	7343241	PEX5	NM_000319	1	15	1	+	7342958	7343120
321394286	chr12	7343344	7343553	7343367	7343527	PEX5	NM_000319	1	15	2	+	7343484	7343519
321401034	chr12	7343779	7343983	7343801	7343962	PEX5	NM_000319	1	15	3	+	7343822	7343954
319541620	chr12	7344045	7344269	7344067	7344241	PEX5	NM_000319	1	15	4	+	7344165	7344296
319556922	chr12	7344221	7344357	7344242	7344329	PEX5	NM_000319	1	15	4	+	7344165	7344296
318413942	chr12	7351515	7351738	7351538	7351714	PEX5	NM_000319	1	15	5	+	7351607	7351709
319975348	chr12	7354297	7354498	7354318	7354473	PEX5	NM_000319	1	15	6	+	7354347	7354437
319733970	chr12	7354760	7354976	7354780	7354953	PEX5	NM_000319	1	15	7	+	7354837	7354947
318956483	chr12	7355122	7355329	7355144	7355307	PEX5	NM_000319	1	15	8	+	7355208	7355300
318640981	chr12	7355978	7356194	7356000	7356167	PEX5	NM_000319	1	15	9	+	7356052	7356147
320127738	chr12	7360216	7360428	7360237	7360403	PEX5	NM_000319	1	15	10	+	7360255	7360398
320047732	chr12	7360489	7360703	7360511	7360681	PEX5	NM_000319	1	15	11	+	7360606	7360676
318475162	chr12	7360993	7361204	7361014	7361183	PEX5	NM_000319	1	15	12	+	7361053	7361265
318504412	chr12	7361161	7361378	7361181	7361355	PEX5	NM_000319	1	15	12	+	7361053	7361265
319406049	chr12	7361544	7361703	7361569	7361682	PEX5	NM_000319	1	15	13	+	7361601	7361766
319422726	chr12	7361662	7361802	7361683	7361778	PEX5	NM_000319	1	15	13	+	7361601	7361766
318948137	chr12	7362116	7362308	7362137	7362287	PEX5	NM_000319	1	15	14	+	7362279	7362436
318975984	chr12	7362264	7362482	7362288	7362454	PEX5	NM_000319	1	15	14	+	7362279	7362436
319331269	chr12	7362561	7362742	7362584	7362718	PEX5	NM_000319	1	15	15	+	7362618	7364079
319347340	chr12	7362689	7362888	7362710	7362866	PEX5	NM_000319	1	15	15	+	7362618	7364079
319426816	chr12	7342865	7343089	7342882	7343072	PEX5	NM_001131023	2	16	2	+	7342958	7343165
319435431	chr12	7343060	7343260	7343078	7343241	PEX5	NM_001131023	2	16	2	+	7342958	7343165
321394286	chr12	7343344	7343553	7343367	7343527	PEX5	NM_001131023	2	16	3	+	7343484	7343519
321401034	chr12	7343779	7343983	7343801	7343962	PEX5	NM_001131023	2	16	4	+	7343822	7343954
319541620	chr12	7344045	7344269	7344067	7344241	PEX5	NM_001131023	2	16	5	+	7344165	7344296
319556922	chr12	7344221	7344357	7344242	7344329	PEX5	NM_001131023	2	16	5	+	7344165	7344296
318413942	chr12	7351515	7351738	7351538	7351714	PEX5	NM_001131023	2	16	6	+	7351607	7351709
319975348	chr12	7354297	7354498	7354318	7354473	PEX5	NM_001131023	2	16	7	+	7354347	7354437
319733970	chr12	7354760	7354976	7354780	7354953	PEX5	NM_001131023	2	16	8	+	7354837	7354947
318956483	chr12	7355122	7355329	7355144	7355307	PEX5	NM_001131023	2	16	9	+	7355208	7355300
318640981	chr12	7355978	7356194	7356000	7356167	PEX5	NM_001131023	2	16	10	+	7356028	7356147
320127738	chr12	7360216	7360428	7360237	7360403	PEX5	NM_001131023	2	16	11	+	7360255	7360398
320047732	chr12	7360489	7360703	7360511	7360681	PEX5	NM_001131023	2	16	12	+	7360606	7360676
318475162	chr12	7360993	7361204	7361014	7361183	PEX5	NM_001131023	2	16	13	+	7361053	7361265

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318504412	chr12	7361161	7361378	7361181	7361355	PEX5	NM_001131023	2	16	13	+	7361053	7361265
319406049	chr12	7361544	7361703	7361569	7361682	PEX5	NM_001131023	2	16	14	+	7361601	7361766
319422726	chr12	7361662	7361802	7361683	7361778	PEX5	NM_001131023	2	16	14	+	7361601	7361766
318948137	chr12	7362116	7362308	7362137	7362287	PEX5	NM_001131023	2	16	15	+	7362279	7362436
318975984	chr12	7362264	7362482	7362288	7362454	PEX5	NM_001131023	2	16	15	+	7362279	7362436
319331269	chr12	7362561	7362742	7362584	7362718	PEX5	NM_001131023	2	16	16	+	7362618	7364079
319347340	chr12	7362689	7362888	7362710	7362866	PEX5	NM_001131023	2	16	16	+	7362618	7364079
319426816	chr12	7342865	7343089	7342882	7343072	PEX5	NM_001131024	3	15	2	+	7342958	7343120
319435431	chr12	7343060	7343260	7343078	7343241	PEX5	NM_001131024	3	15	2	+	7342958	7343120
321394286	chr12	7343344	7343553	7343367	7343527	PEX5	NM_001131024	3	15	3	+	7343484	7343519
321401034	chr12	7343779	7343983	7343801	7343962	PEX5	NM_001131024	3	15	4	+	7343822	7343954
319541620	chr12	7344045	7344269	7344067	7344241	PEX5	NM_001131024	3	15	5	+	7344165	7344296
319556922	chr12	7344221	7344357	7344242	7344329	PEX5	NM_001131024	3	15	5	+	7344165	7344296
318413942	chr12	7351515	7351738	7351538	7351714	PEX5	NM_001131024	3	15	6	+	7351607	7351709
319975348	chr12	7354297	7354498	7354318	7354473	PEX5	NM_001131024	3	15	7	+	7354347	7354437
318956483	chr12	7355122	7355329	7355144	7355307	PEX5	NM_001131024	3	15	8	+	7355208	7355300
318640981	chr12	7355978	7356194	7356000	7356167	PEX5	NM_001131024	3	15	9	+	7356028	7356147
320127738	chr12	7360216	7360428	7360237	7360403	PEX5	NM_001131024	3	15	10	+	7360255	7360398
320047732	chr12	7360489	7360703	7360511	7360681	PEX5	NM_001131024	3	15	11	+	7360606	7360676
318475162	chr12	7360993	7361204	7361014	7361183	PEX5	NM_001131024	3	15	12	+	7361053	7361265
318504412	chr12	7361161	7361378	7361181	7361355	PEX5	NM_001131024	3	15	12	+	7361053	7361265
319406049	chr12	7361544	7361703	7361569	7361682	PEX5	NM_001131024	3	15	13	+	7361601	7361766
319422726	chr12	7361662	7361802	7361683	7361778	PEX5	NM_001131024	3	15	13	+	7361601	7361766
318948137	chr12	7362116	7362308	7362137	7362287	PEX5	NM_001131024	3	15	14	+	7362279	7362436
318975984	chr12	7362264	7362482	7362288	7362454	PEX5	NM_001131024	3	15	14	+	7362279	7362436
319331269	chr12	7362561	7362742	7362584	7362718	PEX5	NM_001131024	3	15	15	+	7362618	7364079
319347340	chr12	7362689	7362888	7362710	7362866	PEX5	NM_001131024	3	15	15	+	7362618	7364079
319426816	chr12	7342865	7343089	7342882	7343072	PEX5	NM_001131025	4	16	2	+	7342958	7343120
319435431	chr12	7343060	7343260	7343078	7343241	PEX5	NM_001131025	4	16	2	+	7342958	7343120
321394286	chr12	7343344	7343553	7343367	7343527	PEX5	NM_001131025	4	16	3	+	7343484	7343519
321401034	chr12	7343779	7343983	7343801	7343962	PEX5	NM_001131025	4	16	4	+	7343822	7343954
319541620	chr12	7344045	7344269	7344067	7344241	PEX5	NM_001131025	4	16	5	+	7344165	7344296
319556922	chr12	7344221	7344357	7344242	7344329	PEX5	NM_001131025	4	16	5	+	7344165	7344296
318413942	chr12	7351515	7351738	7351538	7351714	PEX5	NM_001131025	4	16	6	+	7351607	7351709
319975348	chr12	7354297	7354498	7354318	7354473	PEX5	NM_001131025	4	16	7	+	7354347	7354437
319733970	chr12	7354760	7354976	7354780	7354953	PEX5	NM_001131025	4	16	8	+	7354837	7354947
318956483	chr12	7355122	7355329	7355144	7355307	PEX5	NM_001131025	4	16	9	+	7355208	7355300
318640981	chr12	7355978	7356194	7356000	7356167	PEX5	NM_001131025	4	16	10	+	7356028	7356147
320127738	chr12	7360216	7360428	7360237	7360403	PEX5	NM_001131025	4	16	11	+	7360255	7360398
320047732	chr12	7360489	7360703	7360511	7360681	PEX5	NM_001131025	4	16	12	+	7360606	7360676
318475162	chr12	7360993	7361204	7361014	7361183	PEX5	NM_001131025	4	16	13	+	7361053	7361265

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318504412	chr12	7361161	7361378	7361181	7361355	PEX5	NM_001131025	4	16	13	+	7361053	7361265
319406049	chr12	7361544	7361703	7361569	7361682	PEX5	NM_001131025	4	16	14	+	7361601	7361766
319422726	chr12	7361662	7361802	7361683	7361778	PEX5	NM_001131025	4	16	14	+	7361601	7361766
318948137	chr12	7362116	7362308	7362137	7362287	PEX5	NM_001131025	4	16	15	+	7362279	7362436
318975984	chr12	7362264	7362482	7362288	7362454	PEX5	NM_001131025	4	16	15	+	7362279	7362436
319331269	chr12	7362561	7362742	7362584	7362718	PEX5	NM_001131025	4	16	16	+	7362618	7364079
319347340	chr12	7362689	7362888	7362710	7362866	PEX5	NM_001131025	4	16	16	+	7362618	7364079
319426816	chr12	7342865	7343089	7342882	7343072	PEX5	NM_001131026	5	18	3	+	7342958	7343120
319435431	chr12	7343060	7343260	7343078	7343241	PEX5	NM_001131026	5	18	3	+	7342958	7343120
321394286	chr12	7343344	7343553	7343367	7343527	PEX5	NM_001131026	5	18	4	+	7343484	7343519
321401034	chr12	7343779	7343983	7343801	7343962	PEX5	NM_001131026	5	18	5	+	7343822	7343954
319541620	chr12	7344045	7344269	7344067	7344241	PEX5	NM_001131026	5	18	6	+	7344165	7344296
319556922	chr12	7344221	7344357	7344242	7344329	PEX5	NM_001131026	5	18	6	+	7344165	7344296
318413942	chr12	7351515	7351738	7351538	7351714	PEX5	NM_001131026	5	18	7	+	7351607	7351709
319975348	chr12	7354297	7354498	7354318	7354473	PEX5	NM_001131026	5	18	8	+	7354347	7354437
319733970	chr12	7354760	7354976	7354780	7354953	PEX5	NM_001131026	5	18	9	+	7354837	7354947
318956483	chr12	7355122	7355329	7355144	7355307	PEX5	NM_001131026	5	18	10	+	7355208	7355300
318640981	chr12	7355978	7356194	7356000	7356167	PEX5	NM_001131026	5	18	11	+	7356028	7356147
320127738	chr12	7360216	7360428	7360237	7360403	PEX5	NM_001131026	5	18	12	+	7360255	7360398
320047732	chr12	7360489	7360703	7360511	7360681	PEX5	NM_001131026	5	18	13	+	7360606	7360676
318475162	chr12	7360993	7361204	7361014	7361183	PEX5	NM_001131026	5	18	14	+	7361053	7361265
318504412	chr12	7361161	7361378	7361181	7361355	PEX5	NM_001131026	5	18	14	+	7361053	7361265
319406049	chr12	7361544	7361703	7361569	7361682	PEX5	NM_001131026	5	18	15	+	7361601	7361766
319422726	chr12	7361662	7361802	7361683	7361778	PEX5	NM_001131026	5	18	15	+	7361601	7361766
318948137	chr12	7362116	7362308	7362137	7362287	PEX5	NM_001131026	5	18	16	+	7362279	7362436
318975984	chr12	7362264	7362482	7362288	7362454	PEX5	NM_001131026	5	18	16	+	7362279	7362436
319331269	chr12	7362561	7362742	7362584	7362718	PEX5	NM_001131026	5	18	17	+	7362618	7362838
319347340	chr12	7362689	7362888	7362710	7362866	PEX5	NM_001131026	5	18	17	+	7362618	7362838
319709989	chr1	20960090	20960296	20960107	20960279	PINK1	NM_032409	1	8	1	+	20959948	20960428
319712797	chr1	20960245	20960460	20960263	20960443	PINK1	NM_032409	1	8	1	+	20959948	20960428
319300319	chr1	20964306	20964507	20964328	20964485	PINK1	NM_032409	1	8	2	+	20964335	20964622
319318090	chr1	20964459	20964681	20964481	20964658	PINK1	NM_032409	1	8	2	+	20964335	20964622
319078457	chr1	20966262	20966485	20966286	20966461	PINK1	NM_032409	1	8	3	+	20966385	20966485
319100426	chr1	20966407	20966630	20966430	20966603	PINK1	NM_032409	1	8	3	+	20966385	20966485
320889198	chr1	20970941	20971165	20970965	20971142	PINK1	NM_032409	1	8	4	+	20970983	20971165
320895704	chr1	20971083	20971294	20971104	20971272	PINK1	NM_032409	1	8	4	+	20970983	20971165
318507325	chr1	20971993	20972193	20972017	20972170	PINK1	NM_032409	1	8	5	+	20972053	20972216
318529612	chr1	20972147	20972346	20972168	20972322	PINK1	NM_032409	1	8	5	+	20972053	20972216
318415853	chr1	20974962	20975153	20974985	20975134	PINK1	NM_032409	1	8	6	+	20974998	20975125
318352283	chr1	20975381	20975600	20975403	20975578	PINK1	NM_032409	1	8	7	+	20975488	20975724
318370646	chr1	20975554	20975777	20975578	20975754	PINK1	NM_032409	1	8	7	+	20975488	20975724

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320394068	chr1	20976897	20977108	20976920	20977081	PINK1	NM_032409	1	8	8	+	20976927	20978004
320438365	chr1	20977060	20977212	20977082	20977189	PINK1	NM_032409	1	8	8	+	20976927	20978004
318729651	chr16	2169172	2169396	2169198	2169376	PKD1	NM_000296	1	46	2	-	2169308	2169379
318730842	chr16	2169357	2169546	2169375	2169520	PKD1	NM_000296	1	46	2	-	2169308	2169379
318285537	chr16	2167385	2167581	2167403	2167564	PKD1	NM_000296	1	46	6	-	2167490	2167673
318747592	chr16	2166372	2166583	2166394	2166566	PKD1	NM_000296	1	46	8	-	2166530	2166645
319572261	chr16	2165999	2166204	2166017	2166183	PKD1	NM_000296	1	46	9	-	2165993	2166119
320138881	chr16	2164155	2164358	2164176	2164336	PKD1	NM_000296	1	46	11	-	2164171	2164926
320142422	chr16	2164301	2164480	2164318	2164461	PKD1	NM_000296	1	46	11	-	2164171	2164926
320145887	chr16	2164396	2164609	2164417	2164590	PKD1	NM_000296	1	46	11	-	2164171	2164926
321596469	chr16	2164573	2164792	2164592	2164775	PKD1	NM_000296	1	46	11	-	2164171	2164926
318212534	chr16	2162739	2162938	2162758	2162916	PKD1	NM_000296	1	46	13	-	2162789	2162964
318215092	chr16	2162869	2163090	2162889	2163070	PKD1	NM_000296	1	46	13	-	2162789	2162964
320685808	chr16	2162348	2162508	2162368	2162490	PKD1	NM_000296	1	46	14	-	2162341	2162474
319583375	chr16	2158964	2159144	2158981	2159126	PKD1	NM_000296	1	46	15	-	2158253	2161872
319588125	chr16	2161678	2161881	2161701	2161862	PKD1	NM_000296	1	46	15	-	2158253	2161872
319590329	chr16	2161851	2162053	2161870	2162035	PKD1	NM_000296	1	46	15	-	2158253	2161872
319646083	chr16	2160177	2160389	2160197	2160365	PKD1	NM_000296	1	46	15	-	2158253	2161872
319654006	chr16	2160323	2160517	2160347	2160498	PKD1	NM_000296	1	46	15	-	2158253	2161872
319660137	chr16	2160362	2160553	2160385	2160532	PKD1	NM_000296	1	46	15	-	2158253	2161872
319665578	chr16	2160497	2160622	2160515	2160600	PKD1	NM_000296	1	46	15	-	2158253	2161872
321329675	chr16	2159408	2159598	2159426	2159580	PKD1	NM_000296	1	46	15	-	2158253	2161872
321331118	chr16	2159563	2159766	2159581	2159747	PKD1	NM_000296	1	46	15	-	2158253	2161872
321331286	chr16	2159564	2159788	2159582	2159768	PKD1	NM_000296	1	46	15	-	2158253	2161872
321335555	chr16	2158421	2158617	2158441	2158597	PKD1	NM_000296	1	46	15	-	2158253	2161872
321335563	chr16	2160794	2160975	2160813	2160958	PKD1	NM_000296	1	46	15	-	2158253	2161872
321335934	chr16	2161179	2161398	2161201	2161379	PKD1	NM_000296	1	46	15	-	2158253	2161872
321337344	chr16	2161373	2161528	2161395	2161508	PKD1	NM_000296	1	46	15	-	2158253	2161872
321337364	chr16	2159863	2160046	2159882	2160029	PKD1	NM_000296	1	46	15	-	2158253	2161872
321337923	chr16	2161431	2161642	2161452	2161623	PKD1	NM_000296	1	46	15	-	2158253	2161872
321339346	chr16	2158478	2158683	2158497	2158664	PKD1	NM_000296	1	46	15	-	2158253	2161872
321340389	chr16	2161645	2161849	2161663	2161826	PKD1	NM_000296	1	46	15	-	2158253	2161872
321340424	chr16	2160013	2160195	2160032	2160175	PKD1	NM_000296	1	46	15	-	2158253	2161872
321341008	chr16	2160016	2160215	2160035	2160198	PKD1	NM_000296	1	46	15	-	2158253	2161872
321342301	chr16	2158646	2158843	2158664	2158826	PKD1	NM_000296	1	46	15	-	2158253	2161872
321342930	chr16	2160988	2161200	2161008	2161177	PKD1	NM_000296	1	46	15	-	2158253	2161872
321344666	chr16	2161041	2161205	2161063	2161186	PKD1	NM_000296	1	46	15	-	2158253	2161872
318179402	chr16	2156395	2156562	2156414	2156542	PKD1	NM_000296	1	46	18	-	2156399	2156678
318741691	chr16	2156009	2156211	2156029	2156194	PKD1	NM_000296	1	46	19	-	2156092	2156305
321313879	chr16	2155770	2155954	2155788	2155937	PKD1	NM_000296	1	46	20	-	2155866	2156025
321033512	chr16	2155410	2155589	2155427	2155570	PKD1	NM_000296	1	46	21	-	2155323	2155475

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320592366	chr16	2153367	2153510	2153385	2153489	PKD1	NM_000296	1	46	23	-	2153267	2153896
320593826	chr16	2153369	2153576	2153387	2153555	PKD1	NM_000296	1	46	23	-	2153267	2153896
320595115	chr16	2153704	2153922	2153721	2153905	PKD1	NM_000296	1	46	23	-	2153267	2153896
318018128	chr16	2152676	2152893	2152696	2152874	PKD1	NM_000296	1	46	24	-	2152815	2152971
318025066	chr16	2152847	2152981	2152865	2152964	PKD1	NM_000296	1	46	24	-	2152815	2152971
318030018	chr16	2152946	2153088	2152969	2153067	PKD1	NM_000296	1	46	24	-	2152815	2152971
320080970	chr16	2152367	2152536	2152387	2152515	PKD1	NM_000296	1	46	25	-	2152382	2152634
320082882	chr16	2152499	2152712	2152517	2152694	PKD1	NM_000296	1	46	25	-	2152382	2152634
319532704	chr16	2150384	2150579	2150404	2150560	PKD1	NM_000296	1	46	27	-	2150397	2150567
319536438	chr16	2150527	2150669	2150548	2150651	PKD1	NM_000296	1	46	27	-	2150397	2150567
319432069	chr16	2149954	2150081	2149973	2150064	PKD1	NM_000296	1	46	29	-	2149862	2150072
321101293	chr16	2149567	2149713	2149584	2149692	PKD1	NM_000296	1	46	30	-	2149645	2149771
320244116	chr16	2147782	2147953	2147803	2147936	PKD1	NM_000296	1	46	31	-	2147869	2147985
320241834	chr16	2147746	2147878	2147772	2147860	PKD1	NM_000296	1	46	32	-	2147729	2147778
318148914	chr16	2147222	2147445	2147246	2147423	PKD1	NM_000296	1	46	33	-	2147320	2147504
318153238	chr16	2147333	2147550	2147353	2147529	PKD1	NM_000296	1	46	33	-	2147320	2147504
320319320	chr16	2147103	2147269	2147121	2147249	PKD1	NM_000296	1	46	34	-	2147149	2147242
320216886	chr16	2144027	2144242	2144047	2144218	PKD1	NM_000296	1	46	35	-	2144093	2144211
318280831	chr16	2143661	2143884	2143681	2143866	PKD1	NM_000296	1	46	36	-	2143812	2144014
320074095	chr16	2143821	2144044	2143840	2144023	PKD1	NM_000296	1	46	36	-	2143812	2144014
318275733	chr16	2143410	2143607	2143431	2143587	PKD1	NM_000296	1	46	37	-	2143545	2143739
318279392	chr16	2143570	2143791	2143588	2143772	PKD1	NM_000296	1	46	37	-	2143545	2143739
318280831	chr16	2143661	2143884	2143681	2143866	PKD1	NM_000296	1	46	37	-	2143545	2143739
318251179	chr16	2142891	2143083	2142913	2143059	PKD1	NM_000296	1	46	38	-	2142955	2143094
318255154	chr16	2143028	2143240	2143047	2143220	PKD1	NM_000296	1	46	38	-	2142955	2143094
318582247	chr16	2142416	2142622	2142437	2142602	PKD1	NM_000296	1	46	39	-	2142481	2142593
320503303	chr16	2141983	2142107	2142004	2142086	PKD1	NM_000296	1	46	40	-	2142048	2142189
320508000	chr16	2142054	2142249	2142073	2142225	PKD1	NM_000296	1	46	40	-	2142048	2142189
321283310	chr16	2141680	2141892	2141697	2141872	PKD1	NM_000296	1	46	41	-	2141782	2141907
321284910	chr16	2141848	2142025	2141865	2142007	PKD1	NM_000296	1	46	41	-	2141782	2141907
318857151	chr16	2141418	2141634	2141435	2141616	PKD1	NM_000296	1	46	42	-	2141424	2141598
319908012	chr16	2140809	2141005	2140829	2140986	PKD1	NM_000296	1	46	43	-	2140885	2141175
320111961	chr16	2140948	2141163	2140968	2141146	PKD1	NM_000296	1	46	43	-	2140885	2141175
319902349	chr16	2140617	2140841	2140635	2140821	PKD1	NM_000296	1	46	44	-	2140675	2140809
319900999	chr16	2140480	2140684	2140499	2140664	PKD1	NM_000296	1	46	45	-	2140286	2140591
319919866	chr16	2140179	2140395	2140198	2140376	PKD1	NM_000296	1	46	45	-	2140286	2140591
319922384	chr16	2140331	2140520	2140354	2140500	PKD1	NM_000296	1	46	45	-	2140286	2140591
321558308	chr16	2139618	2139800	2139638	2139783	PKD1	NM_000296	1	46	46	-	2138711	2140195
321558950	chr16	2139749	2139968	2139768	2139947	PKD1	NM_000296	1	46	46	-	2138711	2140195
321559349	chr16	2139925	2140134	2139945	2140114	PKD1	NM_000296	1	46	46	-	2138711	2140195
321561028	chr16	2140059	2140231	2140076	2140214	PKD1	NM_000296	1	46	46	-	2138711	2140195

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318729651	chr16	2169172	2169396	2169198	2169376	PKD1	NM_001009944	2	46	2	-	2169308	2169379
318730842	chr16	2169357	2169546	2169375	2169520	PKD1	NM_001009944	2	46	2	-	2169308	2169379
318285537	chr16	2167385	2167581	2167403	2167564	PKD1	NM_001009944	2	46	6	-	2167490	2167673
318747592	chr16	2166372	2166583	2166394	2166566	PKD1	NM_001009944	2	46	8	-	2166530	2166645
319572261	chr16	2165999	2166204	2166017	2166183	PKD1	NM_001009944	2	46	9	-	2165993	2166119
320138881	chr16	2164155	2164358	2164176	2164336	PKD1	NM_001009944	2	46	11	-	2164171	2164926
320142422	chr16	2164301	2164480	2164318	2164461	PKD1	NM_001009944	2	46	11	-	2164171	2164926
320145887	chr16	2164396	2164609	2164417	2164590	PKD1	NM_001009944	2	46	11	-	2164171	2164926
321596469	chr16	2164573	2164792	2164592	2164775	PKD1	NM_001009944	2	46	11	-	2164171	2164926
318212534	chr16	2162739	2162938	2162758	2162916	PKD1	NM_001009944	2	46	13	-	2162789	2162964
318215092	chr16	2162869	2163090	2162889	2163070	PKD1	NM_001009944	2	46	13	-	2162789	2162964
320685808	chr16	2162348	2162508	2162368	2162490	PKD1	NM_001009944	2	46	14	-	2162341	2162474
319583375	chr16	2158964	2159144	2158981	2159126	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319588125	chr16	2161678	2161881	2161701	2161862	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319590329	chr16	2161851	2162053	2161870	2162035	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319646083	chr16	2160177	2160389	2160197	2160365	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319654006	chr16	2160323	2160517	2160347	2160498	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319660137	chr16	2160362	2160553	2160385	2160532	PKD1	NM_001009944	2	46	15	-	2158253	2161872
319665578	chr16	2160497	2160622	2160515	2160600	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321329675	chr16	2159408	2159598	2159426	2159580	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321331118	chr16	2159563	2159766	2159581	2159747	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321331286	chr16	2159564	2159788	2159582	2159768	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321335555	chr16	2158421	2158617	2158441	2158597	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321335563	chr16	2160794	2160975	2160813	2160958	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321335934	chr16	2161179	2161398	2161201	2161379	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321337344	chr16	2161373	2161528	2161395	2161508	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321337364	chr16	2159863	2160046	2159882	2160029	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321337923	chr16	2161431	2161642	2161452	2161623	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321339346	chr16	2158478	2158683	2158497	2158664	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321340389	chr16	2161645	2161849	2161663	2161826	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321340424	chr16	2160013	2160195	2160032	2160175	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321341008	chr16	2160016	2160215	2160035	2160198	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321342301	chr16	2158646	2158843	2158664	2158826	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321342930	chr16	2160988	2161200	2161008	2161177	PKD1	NM_001009944	2	46	15	-	2158253	2161872
321344666	chr16	2161041	2161205	2161063	2161186	PKD1	NM_001009944	2	46	15	-	2158253	2161872
318179402	chr16	2156395	2156562	2156414	2156542	PKD1	NM_001009944	2	46	18	-	2156399	2156678
318741691	chr16	2156009	2156211	2156029	2156194	PKD1	NM_001009944	2	46	19	-	2156092	2156305
321313879	chr16	2155770	2155954	2155788	2155937	PKD1	NM_001009944	2	46	20	-	2155866	2156025
321033512	chr16	2155410	2155589	2155427	2155570	PKD1	NM_001009944	2	46	21	-	2155323	2155475
320592366	chr16	2153367	2153510	2153385	2153489	PKD1	NM_001009944	2	46	23	-	2153267	2153896
320593826	chr16	2153369	2153576	2153387	2153555	PKD1	NM_001009944	2	46	23	-	2153267	2153896

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320595115	chr16	2153704	2153922	2153721	2153905	PKD1	NM_001009944	2	46	23	-	2153267	2153896
318018128	chr16	2152676	2152893	2152696	2152874	PKD1	NM_001009944	2	46	24	-	2152815	2152971
318025066	chr16	2152847	2152981	2152865	2152964	PKD1	NM_001009944	2	46	24	-	2152815	2152971
318030018	chr16	2152946	2153088	2152969	2153067	PKD1	NM_001009944	2	46	24	-	2152815	2152971
320080970	chr16	2152367	2152536	2152387	2152515	PKD1	NM_001009944	2	46	25	-	2152382	2152634
320082882	chr16	2152499	2152712	2152517	2152694	PKD1	NM_001009944	2	46	25	-	2152382	2152634
319532704	chr16	2150384	2150579	2150404	2150560	PKD1	NM_001009944	2	46	27	-	2150397	2150567
319536438	chr16	2150527	2150669	2150548	2150651	PKD1	NM_001009944	2	46	27	-	2150397	2150567
319432069	chr16	2149954	2150081	2149973	2150064	PKD1	NM_001009944	2	46	29	-	2149862	2150072
321101293	chr16	2149567	2149713	2149584	2149692	PKD1	NM_001009944	2	46	30	-	2149645	2149771
320244116	chr16	2147782	2147953	2147803	2147936	PKD1	NM_001009944	2	46	31	-	2147869	2147985
320241834	chr16	2147746	2147878	2147772	2147860	PKD1	NM_001009944	2	46	32	-	2147729	2147781
318148914	chr16	2147222	2147445	2147246	2147423	PKD1	NM_001009944	2	46	33	-	2147320	2147504
318153238	chr16	2147333	2147550	2147353	2147529	PKD1	NM_001009944	2	46	33	-	2147320	2147504
320319320	chr16	2147103	2147269	2147121	2147249	PKD1	NM_001009944	2	46	34	-	2147149	2147242
320216886	chr16	2144027	2144242	2144047	2144218	PKD1	NM_001009944	2	46	35	-	2144093	2144211
318280831	chr16	2143661	2143884	2143681	2143866	PKD1	NM_001009944	2	46	36	-	2143812	2144014
320074095	chr16	2143821	2144044	2143840	2144023	PKD1	NM_001009944	2	46	36	-	2143812	2144014
318275733	chr16	2143410	2143607	2143431	2143587	PKD1	NM_001009944	2	46	37	-	2143545	2143739
318279392	chr16	2143570	2143791	2143588	2143772	PKD1	NM_001009944	2	46	37	-	2143545	2143739
318280831	chr16	2143661	2143884	2143681	2143866	PKD1	NM_001009944	2	46	37	-	2143545	2143739
318251179	chr16	2142891	2143083	2142913	2143059	PKD1	NM_001009944	2	46	38	-	2142955	2143094
318255154	chr16	2143028	2143240	2143047	2143220	PKD1	NM_001009944	2	46	38	-	2142955	2143094
318582247	chr16	2142416	2142622	2142437	2142602	PKD1	NM_001009944	2	46	39	-	2142481	2142593
320503303	chr16	2141983	2142107	2142004	2142086	PKD1	NM_001009944	2	46	40	-	2142048	2142189
320508000	chr16	2142054	2142249	2142073	2142225	PKD1	NM_001009944	2	46	40	-	2142048	2142189
321283310	chr16	2141680	2141892	2141697	2141872	PKD1	NM_001009944	2	46	41	-	2141782	2141907
321284910	chr16	2141848	2142025	2141865	2142007	PKD1	NM_001009944	2	46	41	-	2141782	2141907
318857151	chr16	2141418	2141634	2141435	2141616	PKD1	NM_001009944	2	46	42	-	2141424	2141598
319908012	chr16	2140809	2141005	2140829	2140986	PKD1	NM_001009944	2	46	43	-	2140885	2141175
320111961	chr16	2140948	2141163	2140968	2141146	PKD1	NM_001009944	2	46	43	-	2140885	2141175
319902349	chr16	2140617	2140841	2140635	2140821	PKD1	NM_001009944	2	46	44	-	2140675	2140809
319900999	chr16	2140480	2140684	2140499	2140664	PKD1	NM_001009944	2	46	45	-	2140286	2140591
319919866	chr16	2140179	2140395	2140198	2140376	PKD1	NM_001009944	2	46	45	-	2140286	2140591
319922384	chr16	2140331	2140520	2140354	2140500	PKD1	NM_001009944	2	46	45	-	2140286	2140591
321558308	chr16	2139618	2139800	2139638	2139783	PKD1	NM_001009944	2	46	46	-	2138711	2140195
321558950	chr16	2139749	2139968	2139768	2139947	PKD1	NM_001009944	2	46	46	-	2138711	2140195
321559349	chr16	2139925	2140134	2139945	2140114	PKD1	NM_001009944	2	46	46	-	2138711	2140195
321561028	chr16	2140059	2140231	2140076	2140214	PKD1	NM_001009944	2	46	46	-	2138711	2140195
320737185	chr4	88928873	88929061	88928890	88929042	PKD2	NM_000297	1	15	1	+	88928799	88929480
320737470	chr4	88928878	88929065	88928896	88929048	PKD2	NM_000297	1	15	1	+	88928799	88929480

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320738020	chr4	88929035	88929244	88929053	88929227	PKD2	NM_000297	1	15	1	+	88928799	88929480
320739802	chr4	88929214	88929421	88929234	88929404	PKD2	NM_000297	1	15	1	+	88928799	88929480
320740006	chr4	88929452	88929658	88929469	88929639	PKD2	NM_000297	1	15	1	+	88928799	88929480
320178736	chr4	88940540	88940763	88940566	88940737	PKD2	NM_000297	1	15	2	+	88940610	88940723
319994420	chr4	88957239	88957398	88957261	88957376	PKD2	NM_000297	1	15	3	+	88957372	88957505
320009385	chr4	88957353	88957577	88957377	88957550	PKD2	NM_000297	1	15	3	+	88957372	88957505
320695289	chr4	88959303	88959508	88959327	88959481	PKD2	NM_000297	1	15	4	+	88959403	88959653
320718954	chr4	88959460	88959681	88959482	88959659	PKD2	NM_000297	1	15	4	+	88959403	88959653
318222579	chr4	88964313	88964491	88964336	88964463	PKD2	NM_000297	1	15	5	+	88964385	88964609
318236687	chr4	88964440	88964636	88964464	88964614	PKD2	NM_000297	1	15	5	+	88964385	88964609
318277281	chr4	88967737	88967961	88967762	88967932	PKD2	NM_000297	1	15	6	+	88967794	88968022
318294266	chr4	88967894	88968118	88967919	88968092	PKD2	NM_000297	1	15	6	+	88967794	88968022
320963416	chr4	88972972	88973196	88972997	88973168	PKD2	NM_000297	1	15	7	+	88973143	88973310
320968133	chr4	88973141	88973271	88973169	88973246	PKD2	NM_000297	1	15	7	+	88973143	88973310
320970142	chr4	88973221	88973421	88973247	88973398	PKD2	NM_000297	1	15	7	+	88973143	88973310
319950349	chr4	88977215	88977362	88977242	88977334	PKD2	NM_000297	1	15	8	+	88977238	88977419
319958557	chr4	88977308	88977475	88977335	88977447	PKD2	NM_000297	1	15	8	+	88977238	88977419
318283397	chr4	88979003	88979206	88979028	88979181	PKD2	NM_000297	1	15	9	+	88979135	88979255
318289946	chr4	88979159	88979337	88979182	88979308	PKD2	NM_000297	1	15	9	+	88979135	88979255
319028640	chr4	88982961	88983118	88982990	88983095	PKD2	NM_000297	1	15	10	+	88983058	88983156
319029606	chr4	88983094	88983222	88983118	88983195	PKD2	NM_000297	1	15	10	+	88983058	88983156
320088692	chr4	88986473	88986677	88986501	88986652	PKD2	NM_000297	1	15	11	+	88986526	88986647
320105349	chr4	88986845	88987069	88986868	88987042	PKD2	NM_000297	1	15	12	+	88986914	88987031
319704002	chr4	88989023	88989246	88989043	88989218	PKD2	NM_000297	1	15	13	+	88989050	88989213
321606176	chr4	88995924	88996139	88995946	88996116	PKD2	NM_000297	1	15	14	+	88995964	88996111
320184783	chr4	88996505	88996710	88996530	88996691	PKD2	NM_000297	1	15	15	+	88996610	88998931
320233200	chr4	88996671	88996890	88996692	88996862	PKD2	NM_000297	1	15	15	+	88996610	88998931
270222529	chr6	51949668	51949801	51949694	51949774	PKHD1	NM_138694	1	67	2	-	51949680	51949815
320101654	chr6	51949499	51949720	51949524	51949693	PKHD1	NM_138694	1	67	2	-	51949680	51949815
269582037	chr6	51947911	51948108	51947938	51948083	PKHD1	NM_138694	1	67	3	-	51947976	51948053
272542877	chr6	51947151	51947375	51947176	51947350	PKHD1	NM_138694	1	67	4	-	51947190	51947340
269483210	chr6	51944636	51944860	51944662	51944832	PKHD1	NM_138694	1	67	5	-	51944698	51944806
269773966	chr6	51940984	51941164	51941008	51941137	PKHD1	NM_138694	1	67	6	-	51941074	51941131
270751504	chr6	51938269	51938450	51938298	51938424	PKHD1	NM_138694	1	67	7	-	51938261	51938339
318780644	chr6	51938113	51938326	51938134	51938297	PKHD1	NM_138694	1	67	7	-	51938261	51938339
270485156	chr6	51936832	51937042	51936858	51937014	PKHD1	NM_138694	1	67	8	-	51936913	51936987
271522375	chr6	51935712	51935902	51935737	51935873	PKHD1	NM_138694	1	67	9	-	51935804	51935868
272038156	chr6	51935127	51935276	51935156	51935248	PKHD1	NM_138694	1	67	10	-	51935204	51935243
271383285	chr6	51934202	51934402	51934223	51934380	PKHD1	NM_138694	1	67	11	-	51934255	51934325
270170044	chr6	51930782	51931000	51930806	51930972	PKHD1	NM_138694	1	67	12	-	51930774	51930875
321443960	chr6	51930613	51930834	51930635	51930805	PKHD1	NM_138694	1	67	12	-	51930774	51930875

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271086981	chr6	51929639	51929863	51929668	51929836	PKHD1	NM_138694	1	67	13	-	51929753	51929848
319473951	chr6	51929822	51930025	51929848	51930006	PKHD1	NM_138694	1	67	13	-	51929753	51929848
271832752	chr6	51927281	51927494	51927302	51927469	PKHD1	NM_138694	1	67	14	-	51927317	51927458
270978201	chr6	51924678	51924875	51924700	51924846	PKHD1	NM_138694	1	67	15	-	51924726	51924840
271455878	chr6	51923092	51923289	51923113	51923268	PKHD1	NM_138694	1	67	16	-	51923121	51923399
271468275	chr6	51923248	51923450	51923269	51923426	PKHD1	NM_138694	1	67	16	-	51923121	51923399
271186670	chr6	51921627	51921815	51921648	51921789	PKHD1	NM_138694	1	67	17	-	51921688	51921777
269656496	chr6	51921486	51921693	51921507	51921667	PKHD1	NM_138694	1	67	18	-	51921496	51921586
318539449	chr6	51921349	51921526	51921371	51921506	PKHD1	NM_138694	1	67	18	-	51921496	51921586
272734737	chr6	51920368	51920561	51920393	51920534	PKHD1	NM_138694	1	67	19	-	51920385	51920527
320167961	chr6	51920206	51920414	51920227	51920392	PKHD1	NM_138694	1	67	19	-	51920385	51920527
271842756	chr6	51918784	51919008	51918805	51918981	PKHD1	NM_138694	1	67	20	-	51918836	51918963
269601864	chr6	51917842	51918057	51917864	51918034	PKHD1	NM_138694	1	67	21	-	51917874	51918049
318484912	chr6	51918014	51918228	51918035	51918204	PKHD1	NM_138694	1	67	21	-	51917874	51918049
270363964	chr6	51914851	51915046	51914874	51915024	PKHD1	NM_138694	1	67	22	-	51914955	51915093
270371161	chr6	51914997	51915214	51915018	51915186	PKHD1	NM_138694	1	67	22	-	51914955	51915093
269580192	chr6	51913232	51913455	51913258	51913427	PKHD1	NM_138694	1	67	23	-	51913290	51913417
270907385	chr6	51910749	51910892	51910771	51910865	PKHD1	NM_138694	1	67	24	-	51910802	51910986
270924784	chr6	51910845	51911055	51910866	51911027	PKHD1	NM_138694	1	67	24	-	51910802	51910986
269691508	chr6	51909736	51909925	51909755	51909897	PKHD1	NM_138694	1	67	25	-	51909764	51909886
270818306	chr6	51908393	51908614	51908414	51908586	PKHD1	NM_138694	1	67	26	-	51908423	51908528
271957249	chr6	51907637	51907860	51907658	51907833	PKHD1	NM_138694	1	67	27	-	51907657	51907932
271971206	chr6	51907807	51908025	51907834	51907997	PKHD1	NM_138694	1	67	27	-	51907657	51907932
319731311	chr6	51907463	51907678	51907489	51907657	PKHD1	NM_138694	1	67	27	-	51907657	51907932
272501880	chr6	51900330	51900554	51900357	51900527	PKHD1	NM_138694	1	67	28	-	51900389	51900519
272123659	chr6	51897749	51897902	51897773	51897874	PKHD1	NM_138694	1	67	29	-	51897828	51897963
272127084	chr6	51897849	51898032	51897875	51898004	PKHD1	NM_138694	1	67	29	-	51897828	51897963
271373443	chr6	51892835	51893004	51892863	51892978	PKHD1	NM_138694	1	67	30	-	51892954	51893149
271383849	chr6	51892958	51893180	51892979	51893154	PKHD1	NM_138694	1	67	30	-	51892954	51893149
270735979	chr6	51892533	51892757	51892558	51892729	PKHD1	NM_138694	1	67	31	-	51892627	51892694
270073156	chr6	51890868	51891048	51890888	51891020	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271878907	chr6	51890272	51890495	51890293	51890468	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271881009	chr6	51889303	51889512	51889326	51889493	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271882226	chr6	51889916	51890140	51889943	51890119	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271900199	chr6	51889450	51889656	51889472	51889630	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271900712	chr6	51890094	51890316	51890117	51890292	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271910033	chr6	51890443	51890573	51890465	51890553	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271925528	chr6	51889604	51889809	51889631	51889788	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271928257	chr6	51890530	51890729	51890552	51890708	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271936438	chr6	51889768	51889971	51889789	51889948	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271944854	chr6	51890685	51890909	51890706	51890887	PKHD1	NM_138694	1	67	32	-	51889372	51890979

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270334169	chr6	51887582	51887797	51887605	51887770	PKHD1	NM_138694	1	67	33	-	51887599	51887742
320253687	chr6	51887422	51887646	51887445	51887622	PKHD1	NM_138694	1	67	33	-	51887599	51887742
269708801	chr6	51882073	51882288	51882094	51882267	PKHD1	NM_138694	1	67	34	-	51882208	51882427
269732805	chr6	51882247	51882460	51882268	51882434	PKHD1	NM_138694	1	67	34	-	51882208	51882427
271401003	chr6	51875119	51875297	51875138	51875271	PKHD1	NM_138694	1	67	35	-	51875107	51875257
320172451	chr6	51874950	51875163	51874978	51875137	PKHD1	NM_138694	1	67	35	-	51875107	51875257
269482626	chr6	51824586	51824785	51824609	51824763	PKHD1	NM_138694	1	67	36	-	51824668	51824824
269506866	chr6	51824738	51824949	51824758	51824922	PKHD1	NM_138694	1	67	36	-	51824668	51824824
269965409	chr6	51798776	51798979	51798801	51798955	PKHD1	NM_138694	1	67	37	-	51798908	51799120
269980447	chr6	51798935	51799155	51798956	51799133	PKHD1	NM_138694	1	67	37	-	51798908	51799120
271336549	chr6	51777123	51777325	51777149	51777303	PKHD1	NM_138694	1	67	38	-	51777164	51777374
271364675	chr6	51777282	51777478	51777304	51777450	PKHD1	NM_138694	1	67	38	-	51777164	51777374
269928230	chr6	51776456	51776680	51776480	51776652	PKHD1	NM_138694	1	67	39	-	51776597	51776754
269947043	chr6	51776630	51776802	51776653	51776774	PKHD1	NM_138694	1	67	39	-	51776597	51776754
271087417	chr6	51773980	51774128	51774008	51774104	PKHD1	NM_138694	1	67	40	-	51774081	51774272
271108217	chr6	51774084	51774306	51774105	51774277	PKHD1	NM_138694	1	67	40	-	51774081	51774272
269700141	chr6	51770970	51771193	51770997	51771167	PKHD1	NM_138694	1	67	41	-	51771013	51771138
270619807	chr6	51768686	51768903	51768714	51768874	PKHD1	NM_138694	1	67	42	-	51768784	51768840
272626675	chr6	51768331	51768554	51768359	51768530	PKHD1	NM_138694	1	67	43	-	51768395	51768525
270527593	chr6	51751895	51752109	51751922	51752081	PKHD1	NM_138694	1	67	44	-	51751931	51752043
271043537	chr6	51750686	51750890	51750708	51750862	PKHD1	NM_138694	1	67	45	-	51750665	51750770
318817528	chr6	51750515	51750730	51750540	51750707	PKHD1	NM_138694	1	67	45	-	51750665	51750770
269791332	chr6	51747833	51748057	51747861	51748031	PKHD1	NM_138694	1	67	46	-	51747891	51748025
269750958	chr6	51735261	51735388	51735288	51735362	PKHD1	NM_138694	1	67	47	-	51735302	51735437
269753164	chr6	51735333	51735489	51735356	51735460	PKHD1	NM_138694	1	67	47	-	51735302	51735437
272215900	chr6	51732586	51732796	51732611	51732769	PKHD1	NM_138694	1	67	48	-	51732661	51732907
272237046	chr6	51732744	51732963	51732770	51732935	PKHD1	NM_138694	1	67	48	-	51732661	51732907
271508805	chr6	51720592	51720813	51720616	51720786	PKHD1	NM_138694	1	67	49	-	51720691	51720868
271521218	chr6	51720766	51720939	51720787	51720911	PKHD1	NM_138694	1	67	49	-	51720691	51720868
271315665	chr6	51712450	51712643	51712472	51712622	PKHD1	NM_138694	1	67	50	-	51712573	51712768
271354238	chr6	51712599	51712815	51712623	51712787	PKHD1	NM_138694	1	67	50	-	51712573	51712768
272693807	chr6	51701087	51701301	51701110	51701276	PKHD1	NM_138694	1	67	51	-	51701202	51701267
271896987	chr6	51695597	51695745	51695621	51695721	PKHD1	NM_138694	1	67	52	-	51695659	51695787
271904592	chr6	51695701	51695880	51695722	51695854	PKHD1	NM_138694	1	67	52	-	51695659	51695787
272539402	chr6	51656055	51656241	51656076	51656214	PKHD1	NM_138694	1	67	53	-	51656034	51656171
319267128	chr6	51655889	51656098	51655912	51656075	PKHD1	NM_138694	1	67	53	-	51656034	51656171
270895342	chr6	51640549	51640695	51640573	51640667	PKHD1	NM_138694	1	67	54	-	51640606	51640719
270897277	chr6	51640646	51640849	51640668	51640821	PKHD1	NM_138694	1	67	54	-	51640606	51640719
270767888	chr6	51637432	51637650	51637456	51637626	PKHD1	NM_138694	1	67	55	-	51637500	51637587
271907968	chr6	51619566	51619778	51619591	51619751	PKHD1	NM_138694	1	67	56	-	51619582	51619736
319506337	chr6	51619426	51619613	51619450	51619590	PKHD1	NM_138694	1	67	56	-	51619582	51619736

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272647951	chr6	51617868	51618087	51617896	51618059	PKHD1	NM_138694	1	67	57	-	51617999	51618151
272657385	chr6	51618037	51618220	51618060	51618195	PKHD1	NM_138694	1	67	57	-	51617999	51618151
270536070	chr6	51613110	51613321	51613132	51613294	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270552425	chr6	51613271	51613495	51613293	51613469	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272257534	chr6	51612471	51612690	51612493	51612666	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272269557	chr6	51612645	51612854	51612667	51612829	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272302150	chr6	51612805	51612987	51612830	51612963	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272335301	chr6	51612939	51613152	51612964	51613131	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270380019	chr6	51611452	51611607	51611478	51611582	PKHD1	NM_138694	1	67	59	-	51611519	51611687
270381671	chr6	51611555	51611749	51611583	51611721	PKHD1	NM_138694	1	67	59	-	51611519	51611687
269837079	chr6	51609165	51609386	51609192	51609358	PKHD1	NM_138694	1	67	60	-	51609183	51609340
318776201	chr6	51608997	51609213	51609024	51609191	PKHD1	NM_138694	1	67	60	-	51609183	51609340
271069298	chr6	51524175	51524372	51524203	51524348	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271076114	chr6	51523711	51523931	51523735	51523908	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271078092	chr6	51524324	51524538	51524349	51524515	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271103854	chr6	51523884	51524057	51523909	51524032	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271111052	chr6	51524491	51524683	51524516	51524661	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271127300	chr6	51524009	51524230	51524033	51524202	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271139524	chr6	51524634	51524849	51524662	51524821	PKHD1	NM_138694	1	67	61	-	51523750	51524767
269731439	chr6	51513863	51514080	51513889	51514052	PKHD1	NM_138694	1	67	62	-	51513883	51514018
318725640	chr6	51513713	51513913	51513736	51513888	PKHD1	NM_138694	1	67	62	-	51513883	51514018
270055012	chr6	51512744	51512953	51512769	51512928	PKHD1	NM_138694	1	67	63	-	51512829	51512916
270999842	chr6	51503645	51503823	51503669	51503796	PKHD1	NM_138694	1	67	64	-	51503647	51503754
319029122	chr6	51503468	51503692	51503496	51503668	PKHD1	NM_138694	1	67	64	-	51503647	51503754
271522863	chr6	51497249	51497471	51497277	51497448	PKHD1	NM_138694	1	67	65	-	51497363	51497521
271523537	chr6	51497373	51497531	51497396	51497512	PKHD1	NM_138694	1	67	65	-	51497363	51497521
271272952	chr6	51491744	51491967	51491764	51491941	PKHD1	NM_138694	1	67	66	-	51491795	51491914
270533001	chr6	51484075	51484271	51484098	51484246	PKHD1	NM_138694	1	67	67	-	51480145	51484318
270540959	chr6	51484226	51484401	51484247	51484372	PKHD1	NM_138694	1	67	67	-	51480145	51484318
272203438	chr6	51483772	51483994	51483796	51483972	PKHD1	NM_138694	1	67	67	-	51480145	51484318
272221889	chr6	51483945	51484122	51483968	51484100	PKHD1	NM_138694	1	67	67	-	51480145	51484318
270222529	chr6	51949668	51949801	51949694	51949774	PKHD1	NM_170724	2	61	2	-	51949680	51949815
320101654	chr6	51949499	51949720	51949524	51949693	PKHD1	NM_170724	2	61	2	-	51949680	51949815
269582037	chr6	51947911	51948108	51947938	51948083	PKHD1	NM_170724	2	61	3	-	51947976	51948053
272542877	chr6	51947151	51947375	51947176	51947350	PKHD1	NM_170724	2	61	4	-	51947190	51947340
269483210	chr6	51944636	51944860	51944662	51944832	PKHD1	NM_170724	2	61	5	-	51944698	51944806
269773966	chr6	51940984	51941164	51941008	51941137	PKHD1	NM_170724	2	61	6	-	51941074	51941131
270751504	chr6	51938269	51938450	51938298	51938424	PKHD1	NM_170724	2	61	7	-	51938261	51938339
318780644	chr6	51938113	51938326	51938134	51938297	PKHD1	NM_170724	2	61	7	-	51938261	51938339
270485156	chr6	51936832	51937042	51936858	51937014	PKHD1	NM_170724	2	61	8	-	51936913	51936987
271522375	chr6	51935712	51935902	51935737	51935873	PKHD1	NM_170724	2	61	9	-	51935804	51935868

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272038156	chr6	51935127	51935276	51935156	51935248	PKHD1	NM_170724	2	61	10	-	51935204	51935243
271383285	chr6	51934202	51934402	51934223	51934380	PKHD1	NM_170724	2	61	11	-	51934255	51934325
270170044	chr6	51930782	51931000	51930806	51930972	PKHD1	NM_170724	2	61	12	-	51930774	51930875
321443960	chr6	51930613	51930834	51930635	51930805	PKHD1	NM_170724	2	61	12	-	51930774	51930875
271086981	chr6	51929639	51929863	51929668	51929836	PKHD1	NM_170724	2	61	13	-	51929753	51929848
319473951	chr6	51929822	51930025	51929848	51930006	PKHD1	NM_170724	2	61	13	-	51929753	51929848
271832752	chr6	51927281	51927494	51927302	51927469	PKHD1	NM_170724	2	61	14	-	51927317	51927458
270978201	chr6	51924678	51924875	51924700	51924846	PKHD1	NM_170724	2	61	15	-	51924726	51924840
271455878	chr6	51923092	51923289	51923113	51923268	PKHD1	NM_170724	2	61	16	-	51923121	51923399
271468275	chr6	51923248	51923450	51923269	51923426	PKHD1	NM_170724	2	61	16	-	51923121	51923399
271186670	chr6	51921627	51921815	51921648	51921789	PKHD1	NM_170724	2	61	17	-	51921688	51921777
269656496	chr6	51921486	51921693	51921507	51921667	PKHD1	NM_170724	2	61	18	-	51921496	51921586
318539449	chr6	51921349	51921526	51921371	51921506	PKHD1	NM_170724	2	61	18	-	51921496	51921586
272734737	chr6	51920368	51920561	51920393	51920534	PKHD1	NM_170724	2	61	19	-	51920385	51920527
320167961	chr6	51920206	51920414	51920227	51920392	PKHD1	NM_170724	2	61	19	-	51920385	51920527
271842756	chr6	51918784	51919008	51918805	51918981	PKHD1	NM_170724	2	61	20	-	51918836	51918963
269601864	chr6	51917842	51918057	51917864	51918034	PKHD1	NM_170724	2	61	21	-	51917874	51918049
318484912	chr6	51918014	51918228	51918035	51918204	PKHD1	NM_170724	2	61	21	-	51917874	51918049
270363964	chr6	51914851	51915046	51914874	51915024	PKHD1	NM_170724	2	61	22	-	51914955	51915093
270371161	chr6	51914997	51915214	51915018	51915186	PKHD1	NM_170724	2	61	22	-	51914955	51915093
269580192	chr6	51913232	51913455	51913258	51913427	PKHD1	NM_170724	2	61	23	-	51913290	51913417
270907385	chr6	51910749	51910892	51910771	51910865	PKHD1	NM_170724	2	61	24	-	51910802	51910986
270924784	chr6	51910845	51911055	51910866	51911027	PKHD1	NM_170724	2	61	24	-	51910802	51910986
269691508	chr6	51909736	51909925	51909755	51909897	PKHD1	NM_170724	2	61	25	-	51909764	51909886
270818306	chr6	51908393	51908614	51908414	51908586	PKHD1	NM_170724	2	61	26	-	51908423	51908528
271957249	chr6	51907637	51907860	51907658	51907833	PKHD1	NM_170724	2	61	27	-	51907657	51907932
271971206	chr6	51907807	51908025	51907834	51907997	PKHD1	NM_170724	2	61	27	-	51907657	51907932
319731311	chr6	51907463	51907678	51907489	51907657	PKHD1	NM_170724	2	61	27	-	51907657	51907932
272501880	chr6	51900330	51900554	51900357	51900527	PKHD1	NM_170724	2	61	28	-	51900389	51900519
272123659	chr6	51897749	51897902	51897773	51897874	PKHD1	NM_170724	2	61	29	-	51897828	51897963
272127084	chr6	51897849	51898032	51897875	51898004	PKHD1	NM_170724	2	61	29	-	51897828	51897963
271373443	chr6	51892835	51893004	51892863	51892978	PKHD1	NM_170724	2	61	30	-	51892954	51893149
271383849	chr6	51892958	51893180	51892979	51893154	PKHD1	NM_170724	2	61	30	-	51892954	51893149
270735979	chr6	51892533	51892757	51892558	51892729	PKHD1	NM_170724	2	61	31	-	51892627	51892694
270073156	chr6	51890868	51891048	51890888	51891020	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271878907	chr6	51890272	51890495	51890293	51890468	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271881009	chr6	51889303	51889512	51889326	51889493	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271882226	chr6	51889916	51890140	51889943	51890119	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271900199	chr6	51889450	51889656	51889472	51889630	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271900712	chr6	51890094	51890316	51890117	51890292	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271910033	chr6	51890443	51890573	51890465	51890553	PKHD1	NM_170724	2	61	32	-	51889372	51890979

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271925528	chr6	51889604	51889809	51889631	51889788	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271928257	chr6	51890530	51890729	51890552	51890708	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271936438	chr6	51889768	51889971	51889789	51889948	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271944854	chr6	51890685	51890909	51890706	51890887	PKHD1	NM_170724	2	61	32	-	51889372	51890979
270334169	chr6	51887582	51887797	51887605	51887770	PKHD1	NM_170724	2	61	33	-	51887599	51887742
320253687	chr6	51887422	51887646	51887445	51887622	PKHD1	NM_170724	2	61	33	-	51887599	51887742
269708801	chr6	51882073	51882288	51882094	51882267	PKHD1	NM_170724	2	61	34	-	51882208	51882427
269732805	chr6	51882247	51882460	51882268	51882434	PKHD1	NM_170724	2	61	34	-	51882208	51882427
271401003	chr6	51875119	51875297	51875138	51875271	PKHD1	NM_170724	2	61	35	-	51875107	51875257
320172451	chr6	51874950	51875163	51874978	51875137	PKHD1	NM_170724	2	61	35	-	51875107	51875257
269482626	chr6	51824586	51824785	51824609	51824763	PKHD1	NM_170724	2	61	36	-	51824668	51824824
269506866	chr6	51824738	51824949	51824758	51824922	PKHD1	NM_170724	2	61	36	-	51824668	51824824
269965409	chr6	51798776	51798979	51798801	51798955	PKHD1	NM_170724	2	61	37	-	51798908	51799120
269980447	chr6	51798935	51799155	51798956	51799133	PKHD1	NM_170724	2	61	37	-	51798908	51799120
271336549	chr6	51777123	51777325	51777149	51777303	PKHD1	NM_170724	2	61	38	-	51777164	51777374
271364675	chr6	51777282	51777478	51777304	51777450	PKHD1	NM_170724	2	61	38	-	51777164	51777374
269928230	chr6	51776456	51776680	51776480	51776652	PKHD1	NM_170724	2	61	39	-	51776597	51776754
269947043	chr6	51776630	51776802	51776653	51776774	PKHD1	NM_170724	2	61	39	-	51776597	51776754
271087417	chr6	51773980	51774128	51774008	51774104	PKHD1	NM_170724	2	61	40	-	51774081	51774272
271108217	chr6	51774084	51774306	51774105	51774277	PKHD1	NM_170724	2	61	40	-	51774081	51774272
269700141	chr6	51770970	51771193	51770997	51771167	PKHD1	NM_170724	2	61	41	-	51771013	51771138
270619807	chr6	51768686	51768903	51768714	51768874	PKHD1	NM_170724	2	61	42	-	51768784	51768840
272626675	chr6	51768331	51768554	51768359	51768530	PKHD1	NM_170724	2	61	43	-	51768395	51768525
270527593	chr6	51751895	51752109	51751922	51752081	PKHD1	NM_170724	2	61	44	-	51751931	51752043
271043537	chr6	51750686	51750890	51750708	51750862	PKHD1	NM_170724	2	61	45	-	51750665	51750770
318817528	chr6	51750515	51750730	51750540	51750707	PKHD1	NM_170724	2	61	45	-	51750665	51750770
269791332	chr6	51747833	51748057	51747861	51748031	PKHD1	NM_170724	2	61	46	-	51747891	51748025
269750958	chr6	51735261	51735388	51735288	51735362	PKHD1	NM_170724	2	61	47	-	51735302	51735437
269753164	chr6	51735333	51735489	51735356	51735460	PKHD1	NM_170724	2	61	47	-	51735302	51735437
272215900	chr6	51732586	51732796	51732611	51732769	PKHD1	NM_170724	2	61	48	-	51732661	51732907
272237046	chr6	51732744	51732963	51732770	51732935	PKHD1	NM_170724	2	61	48	-	51732661	51732907
271508805	chr6	51720592	51720813	51720616	51720786	PKHD1	NM_170724	2	61	49	-	51720691	51720868
271521218	chr6	51720766	51720939	51720787	51720911	PKHD1	NM_170724	2	61	49	-	51720691	51720868
271315665	chr6	51712450	51712643	51712472	51712622	PKHD1	NM_170724	2	61	50	-	51712573	51712768
271354238	chr6	51712599	51712815	51712623	51712787	PKHD1	NM_170724	2	61	50	-	51712573	51712768
272693807	chr6	51701087	51701301	51701110	51701276	PKHD1	NM_170724	2	61	51	-	51701202	51701267
271896987	chr6	51695597	51695745	51695621	51695721	PKHD1	NM_170724	2	61	52	-	51695659	51695787
271904592	chr6	51695701	51695880	51695722	51695854	PKHD1	NM_170724	2	61	52	-	51695659	51695787
272539402	chr6	51656055	51656241	51656076	51656214	PKHD1	NM_170724	2	61	53	-	51656034	51656171
319267128	chr6	51655889	51656098	51655912	51656075	PKHD1	NM_170724	2	61	53	-	51656034	51656171
270895342	chr6	51640549	51640695	51640573	51640667	PKHD1	NM_170724	2	61	54	-	51640606	51640719

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270897277	chr6	51640646	51640849	51640668	51640821	PKHD1	NM_170724	2	61	54	-	51640606	51640719
270767888	chr6	51637432	51637650	51637456	51637626	PKHD1	NM_170724	2	61	55	-	51637500	51637587
271907968	chr6	51619566	51619778	51619591	51619751	PKHD1	NM_170724	2	61	56	-	51619582	51619736
319506337	chr6	51619426	51619613	51619450	51619590	PKHD1	NM_170724	2	61	56	-	51619582	51619736
272647951	chr6	51617868	51618087	51617896	51618059	PKHD1	NM_170724	2	61	57	-	51617999	51618151
272657385	chr6	51618037	51618220	51618060	51618195	PKHD1	NM_170724	2	61	57	-	51617999	51618151
270536070	chr6	51613110	51613321	51613132	51613294	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270552425	chr6	51613271	51613495	51613293	51613469	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272257534	chr6	51612471	51612690	51612493	51612666	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272269557	chr6	51612645	51612854	51612667	51612829	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272302150	chr6	51612805	51612987	51612830	51612963	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272335301	chr6	51612939	51613152	51612964	51613131	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270380019	chr6	51611452	51611607	51611478	51611582	PKHD1	NM_170724	2	61	59	-	51611519	51611687
270381671	chr6	51611555	51611749	51611583	51611721	PKHD1	NM_170724	2	61	59	-	51611519	51611687
269837079	chr6	51609165	51609386	51609192	51609358	PKHD1	NM_170724	2	61	60	-	51609183	51609340
318776201	chr6	51608997	51609213	51609024	51609191	PKHD1	NM_170724	2	61	60	-	51609183	51609340
272476013	chr6	51586633	51586857	51586659	51586829	PKHD1	NM_170724	2	61	61	-	51585647	51586818
319924933	chr12	33049375	33049567	33049394	33049549	PKP2	NM_001005242	1	13	1	-	33049443	33049780
319925799	chr12	33049503	33049647	33049523	33049628	PKP2	NM_001005242	1	13	1	-	33049443	33049780
319917167	chr12	33031685	33031909	33031711	33031885	PKP2	NM_001005242	1	13	2	-	33031854	33031966
319918108	chr12	33031884	33032093	33031905	33032065	PKP2	NM_001005242	1	13	2	-	33031854	33031966
321573367	chr12	33031318	33031499	33031338	33031474	PKP2	NM_001005242	1	13	3	-	33030780	33031477
321575933	chr12	33030728	33030944	33030749	33030923	PKP2	NM_001005242	1	13	3	-	33030780	33031477
321583993	chr12	33030900	33031061	33030917	33031040	PKP2	NM_001005242	1	13	3	-	33030780	33031477
321586104	chr12	33031449	33031604	33031472	33031583	PKP2	NM_001005242	1	13	3	-	33030780	33031477
321591682	chr12	33031021	33031236	33031041	33031214	PKP2	NM_001005242	1	13	3	-	33030780	33031477
321604004	chr12	33031151	33031372	33031177	33031350	PKP2	NM_001005242	1	13	3	-	33030780	33031477
319266356	chr12	33021813	33022034	33021835	33022010	PKP2	NM_001005242	1	13	4	-	33021861	33021996
318464518	chr12	33003579	33003794	33003604	33003771	PKP2	NM_001005242	1	13	5	-	33003700	33003907
318478911	chr12	33003752	33003970	33003772	33003948	PKP2	NM_001005242	1	13	5	-	33003700	33003907
318852574	chr12	32993877	32994029	32993904	32994004	PKP2	NM_001005242	1	13	6	-	32993962	32994139
318871063	chr12	32993977	32994170	32994005	32994144	PKP2	NM_001005242	1	13	6	-	32993962	32994139
318606677	chr12	32976855	32977016	32976881	32976992	PKP2	NM_001005242	1	13	7	-	32976979	32977096
318610792	chr12	32976967	32977147	32976993	32977119	PKP2	NM_001005242	1	13	7	-	32976979	32977096
321397670	chr12	32975340	32975561	32975366	32975538	PKP2	NM_001005242	1	13	8	-	32975401	32975565
321415391	chr12	32975516	32975646	32975539	32975622	PKP2	NM_001005242	1	13	8	-	32975401	32975565
318080912	chr12	32974131	32974351	32974152	32974327	PKP2	NM_001005242	1	13	9	-	32974290	32974463
318103135	chr12	32974307	32974497	32974328	32974469	PKP2	NM_001005242	1	13	9	-	32974290	32974463
318960929	chr12	32955206	32955414	32955229	32955390	PKP2	NM_001005242	1	13	10	-	32955337	32955490
318986715	chr12	32955369	32955580	32955390	32955552	PKP2	NM_001005242	1	13	10	-	32955337	32955490
318545099	chr12	32949016	32949236	32949035	32949213	PKP2	NM_001005242	1	13	11	-	32949043	32949232

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318712518	chr12	32945494	32945697	32945515	32945671	PKP2	NM_001005242	1	13	12	-	32945578	32945665
319636228	chr12	32945238	32945461	32945266	32945433	PKP2	NM_001005242	1	13	13	-	32943680	32945426
319924933	chr12	33049375	33049567	33049394	33049549	PKP2	NM_004572	2	14	1	-	33049443	33049780
319925799	chr12	33049503	33049647	33049523	33049628	PKP2	NM_004572	2	14	1	-	33049443	33049780
319917167	chr12	33031685	33031909	33031711	33031885	PKP2	NM_004572	2	14	2	-	33031854	33031966
319918108	chr12	33031884	33032093	33031905	33032065	PKP2	NM_004572	2	14	2	-	33031854	33031966
321573367	chr12	33031318	33031499	33031338	33031474	PKP2	NM_004572	2	14	3	-	33030780	33031477
321575933	chr12	33030728	33030944	33030749	33030923	PKP2	NM_004572	2	14	3	-	33030780	33031477
321583993	chr12	33030900	33031061	33030917	33031040	PKP2	NM_004572	2	14	3	-	33030780	33031477
321586104	chr12	33031449	33031604	33031472	33031583	PKP2	NM_004572	2	14	3	-	33030780	33031477
321591682	chr12	33031021	33031236	33031041	33031214	PKP2	NM_004572	2	14	3	-	33030780	33031477
321604004	chr12	33031151	33031372	33031177	33031350	PKP2	NM_004572	2	14	3	-	33030780	33031477
319266356	chr12	33021813	33022034	33021835	33022010	PKP2	NM_004572	2	14	4	-	33021861	33021996
318464518	chr12	33003579	33003794	33003604	33003771	PKP2	NM_004572	2	14	5	-	33003700	33003907
318478911	chr12	33003752	33003970	33003772	33003948	PKP2	NM_004572	2	14	5	-	33003700	33003907
319751979	chr12	32996210	32996336	32996230	32996314	PKP2	NM_004572	2	14	6	-	32996116	32996247
318852574	chr12	32993877	32994029	32993904	32994004	PKP2	NM_004572	2	14	7	-	32993962	32994139
318871063	chr12	32993977	32994170	32994005	32994144	PKP2	NM_004572	2	14	7	-	32993962	32994139
318606677	chr12	32976855	32977016	32976881	32976992	PKP2	NM_004572	2	14	8	-	32976979	32977096
318610792	chr12	32976967	32977147	32976993	32977119	PKP2	NM_004572	2	14	8	-	32976979	32977096
321397670	chr12	32975340	32975561	32975366	32975538	PKP2	NM_004572	2	14	9	-	32975401	32975565
321415391	chr12	32975516	32975646	32975539	32975622	PKP2	NM_004572	2	14	9	-	32975401	32975565
318080912	chr12	32974131	32974351	32974152	32974327	PKP2	NM_004572	2	14	10	-	32974290	32974463
318103135	chr12	32974307	32974497	32974328	32974469	PKP2	NM_004572	2	14	10	-	32974290	32974463
318960929	chr12	32955206	32955414	32955229	32955390	PKP2	NM_004572	2	14	11	-	32955337	32955490
318986715	chr12	32955369	32955580	32955390	32955552	PKP2	NM_004572	2	14	11	-	32955337	32955490
318545099	chr12	32949016	32949236	32949035	32949213	PKP2	NM_004572	2	14	12	-	32949043	32949232
318712518	chr12	32945494	32945697	32945515	32945671	PKP2	NM_004572	2	14	13	-	32945578	32945665
319636228	chr12	32945238	32945461	32945266	32945433	PKP2	NM_004572	2	14	14	-	32943680	32945426
321041065	chr8	145049284	145049508	145049304	145049482	PLEC	NM_000445	1	33	2	-	145049345	145049543
321049913	chr8	145049426	145049644	145049446	145049621	PLEC	NM_000445	1	33	2	-	145049345	145049543
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_000445	1	33	3	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_000445	1	33	4	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_000445	1	33	5	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_000445	1	33	5	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_000445	1	33	6	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_000445	1	33	6	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_000445	1	33	7	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_000445	1	33	7	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_000445	1	33	8	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_000445	1	33	8	-	145009366	145009481

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_000445	1	33	9	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_000445	1	33	9	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_000445	1	33	9	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_000445	1	33	10	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_000445	1	33	10	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_000445	1	33	10	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_000445	1	33	11	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_000445	1	33	11	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_000445	1	33	12	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_000445	1	33	13	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_000445	1	33	13	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_000445	1	33	14	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_000445	1	33	15	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_000445	1	33	15	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_000445	1	33	15	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_000445	1	33	15	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_000445	1	33	16	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_000445	1	33	16	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_000445	1	33	17	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_000445	1	33	17	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_000445	1	33	18	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_000445	1	33	18	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_000445	1	33	19	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_000445	1	33	19	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_000445	1	33	20	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_000445	1	33	20	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_000445	1	33	21	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_000445	1	33	21	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_000445	1	33	22	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_000445	1	33	22	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_000445	1	33	23	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_000445	1	33	24	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_000445	1	33	24	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_000445	1	33	25	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_000445	1	33	25	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_000445	1	33	25	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_000445	1	33	26	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_000445	1	33	26	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_000445	1	33	27	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_000445	1	33	27	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_000445	1	33	28	-	145001578	145001934

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_000445	1	33	28	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_000445	1	33	28	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_000445	1	33	28	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_000445	1	33	29	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_000445	1	33	30	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_000445	1	33	31	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_000445	1	33	32	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_000445	1	33	32	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_000445	1	33	32	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_000445	1	33	32	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_000445	1	33	32	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_000445	1	33	32	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_000445	1	33	32	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_000445	1	33	32	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_000445	1	33	32	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_000445	1	33	32	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_000445	1	33	32	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_000445	1	33	32	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_000445	1	33	32	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_000445	1	33	32	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_000445	1	33	32	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_000445	1	33	32	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_000445	1	33	32	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_000445	1	33	32	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_000445	1	33	32	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_000445	1	33	32	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_000445	1	33	32	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_000445	1	33	32	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_000445	1	33	32	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_000445	1	33	32	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_000445	1	33	33	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_000445	1	33	33	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_000445	1	33	33	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_000445	1	33	33	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_000445	1	33	33	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_000445	1	33	33	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_000445	1	33	33	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_000445	1	33	33	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_000445	1	33	33	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_000445	1	33	33	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_000445	1	33	33	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_000445	1	33	33	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_000445	1	33	33	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_000445	1	33	33	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_000445	1	33	33	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_000445	1	33	33	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_000445	1	33	33	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_000445	1	33	33	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_000445	1	33	33	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_000445	1	33	33	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_000445	1	33	33	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_000445	1	33	33	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_000445	1	33	33	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_000445	1	33	33	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_000445	1	33	33	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_000445	1	33	33	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_000445	1	33	33	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_000445	1	33	33	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_000445	1	33	33	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_000445	1	33	33	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_000445	1	33	33	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_000445	1	33	33	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_000445	1	33	33	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_000445	1	33	33	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_000445	1	33	33	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_000445	1	33	33	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_000445	1	33	33	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_000445	1	33	33	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_000445	1	33	33	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_000445	1	33	33	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_000445	1	33	33	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_000445	1	33	33	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_000445	1	33	33	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_000445	1	33	33	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_000445	1	33	33	-	144989321	144996563
318573674	chr8	145047404	145047624	145047423	145047604	PLEC	NM_201378	2	32	1	-	145047571	145047697
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201378	2	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201378	2	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201378	2	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201378	2	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201378	2	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201378	2	32	5	-	145011147	145011239

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201378	2	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201378	2	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201378	2	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201378	2	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201378	2	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201378	2	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201378	2	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201378	2	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201378	2	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201378	2	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201378	2	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201378	2	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201378	2	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201378	2	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201378	2	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201378	2	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201378	2	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201378	2	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201378	2	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201378	2	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201378	2	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201378	2	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201378	2	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201378	2	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201378	2	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201378	2	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201378	2	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201378	2	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201378	2	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201378	2	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201378	2	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201378	2	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201378	2	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201378	2	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201378	2	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201378	2	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201378	2	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201378	2	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201378	2	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201378	2	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201378	2	32	25	-	145003271	145003449

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201378	2	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201378	2	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201378	2	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201378	2	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201378	2	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201378	2	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201378	2	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201378	2	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201378	2	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201378	2	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201378	2	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201378	2	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201378	2	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201378	2	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201378	2	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201378	2	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201378	2	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201378	2	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201378	2	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201378	2	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201378	2	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201378	2	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201378	2	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201378	2	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201378	2	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201378	2	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201378	2	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201378	2	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201378	2	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201378	2	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201378	2	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201378	2	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201378	2	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201378	2	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201378	2	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201378	2	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201378	2	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201378	2	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201378	2	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201378	2	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201378	2	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201378	2	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201378	2	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201378	2	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201378	2	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201378	2	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201378	2	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201378	2	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201378	2	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201378	2	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201378	2	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201378	2	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201378	2	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201378	2	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201378	2	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201378	2	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201378	2	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201378	2	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201378	2	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201378	2	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201378	2	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201378	2	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201378	2	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201378	2	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201378	2	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201378	2	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201378	2	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201378	2	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201378	2	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201378	2	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201378	2	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201378	2	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201378	2	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201378	2	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201378	2	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201378	2	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201378	2	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201378	2	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201378	2	32	32	-	144989321	144996563
321491808	chr8	145027770	145027987	145027788	145027969	PLEC	NM_201379	3	32	1	-	145027894	145028088
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201379	3	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201379	3	32	3	-	145012319	145012408

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201379	3	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201379	3	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201379	3	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201379	3	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201379	3	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201379	3	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201379	3	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201379	3	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201379	3	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201379	3	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201379	3	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201379	3	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201379	3	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201379	3	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201379	3	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201379	3	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201379	3	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201379	3	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201379	3	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201379	3	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201379	3	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201379	3	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201379	3	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201379	3	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201379	3	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201379	3	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201379	3	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201379	3	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201379	3	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201379	3	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201379	3	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201379	3	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201379	3	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201379	3	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201379	3	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201379	3	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201379	3	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201379	3	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201379	3	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201379	3	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201379	3	32	23	-	145003814	145003997

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201379	3	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201379	3	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201379	3	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201379	3	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201379	3	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201379	3	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201379	3	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201379	3	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201379	3	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201379	3	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201379	3	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201379	3	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201379	3	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201379	3	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201379	3	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201379	3	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201379	3	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201379	3	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201379	3	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201379	3	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201379	3	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201379	3	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201379	3	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201379	3	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201379	3	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201379	3	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201379	3	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201379	3	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201379	3	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201379	3	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201379	3	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201379	3	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201379	3	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201379	3	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201379	3	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201379	3	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201379	3	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201379	3	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201379	3	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201379	3	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201379	3	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201379	3	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201379	3	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201379	3	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201379	3	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201379	3	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201379	3	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201379	3	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201379	3	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201379	3	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201379	3	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201379	3	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201379	3	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201379	3	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201379	3	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201379	3	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201379	3	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201379	3	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201379	3	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201379	3	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201379	3	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201379	3	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201379	3	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201379	3	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201379	3	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201379	3	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201379	3	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201379	3	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201379	3	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201379	3	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201379	3	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201379	3	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201379	3	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201379	3	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201379	3	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201379	3	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201379	3	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201379	3	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201379	3	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201379	3	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201379	3	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201379	3	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201379	3	32	32	-	144989321	144996563
318550723	chr8	145024309	145024461	145024332	145024442	PLEC	NM_201380	4	32	1	-	145024352	145025044
318551435	chr8	145024421	145024635	145024442	145024618	PLEC	NM_201380	4	32	1	-	145024352	145025044
318552755	chr8	145024599	145024771	145024616	145024754	PLEC	NM_201380	4	32	1	-	145024352	145025044
318556506	chr8	145024718	145024940	145024736	145024923	PLEC	NM_201380	4	32	1	-	145024352	145025044
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201380	4	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201380	4	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201380	4	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201380	4	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201380	4	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201380	4	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201380	4	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201380	4	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201380	4	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201380	4	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201380	4	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201380	4	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201380	4	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201380	4	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201380	4	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201380	4	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201380	4	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201380	4	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201380	4	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201380	4	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201380	4	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201380	4	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201380	4	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201380	4	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201380	4	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201380	4	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201380	4	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201380	4	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201380	4	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201380	4	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201380	4	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201380	4	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201380	4	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201380	4	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201380	4	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201380	4	32	19	-	145005702	145005827

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201380	4	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201380	4	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201380	4	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201380	4	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201380	4	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201380	4	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201380	4	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201380	4	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201380	4	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201380	4	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201380	4	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201380	4	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201380	4	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201380	4	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201380	4	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201380	4	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201380	4	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201380	4	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201380	4	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201380	4	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201380	4	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201380	4	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201380	4	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201380	4	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201380	4	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201380	4	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201380	4	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201380	4	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201380	4	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201380	4	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201380	4	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201380	4	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201380	4	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201380	4	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201380	4	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201380	4	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201380	4	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201380	4	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201380	4	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201380	4	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201380	4	32	31	-	144996672	145000052

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201380	4	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201380	4	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201380	4	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201380	4	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201380	4	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201380	4	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201380	4	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201380	4	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201380	4	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201380	4	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201380	4	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201380	4	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201380	4	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201380	4	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201380	4	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201380	4	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201380	4	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201380	4	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201380	4	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201380	4	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201380	4	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201380	4	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201380	4	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201380	4	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201380	4	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201380	4	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201380	4	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201380	4	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201380	4	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201380	4	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201380	4	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201380	4	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201380	4	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201380	4	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201380	4	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201380	4	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201380	4	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201380	4	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201380	4	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201380	4	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201380	4	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201380	4	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201380	4	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201380	4	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201380	4	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201380	4	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201380	4	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201380	4	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201380	4	32	32	-	144989321	144996563
321305154	chr8	145018776	145018978	145018797	145018959	PLEC	NM_201381	5	32	1	-	145018816	145018905
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201381	5	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201381	5	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201381	5	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201381	5	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201381	5	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201381	5	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201381	5	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201381	5	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201381	5	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201381	5	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201381	5	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201381	5	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201381	5	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201381	5	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201381	5	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201381	5	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201381	5	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201381	5	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201381	5	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201381	5	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201381	5	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201381	5	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201381	5	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201381	5	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201381	5	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201381	5	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201381	5	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201381	5	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201381	5	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201381	5	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201381	5	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201381	5	32	17	-	145006298	145006402

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201381	5	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201381	5	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201381	5	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201381	5	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201381	5	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201381	5	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201381	5	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201381	5	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201381	5	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201381	5	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201381	5	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201381	5	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201381	5	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201381	5	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201381	5	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201381	5	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201381	5	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201381	5	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201381	5	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201381	5	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201381	5	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201381	5	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201381	5	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201381	5	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201381	5	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201381	5	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201381	5	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201381	5	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201381	5	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201381	5	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201381	5	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201381	5	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201381	5	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201381	5	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201381	5	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201381	5	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201381	5	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201381	5	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201381	5	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201381	5	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201381	5	32	31	-	144996672	145000052

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201381	5	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201381	5	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201381	5	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201381	5	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201381	5	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201381	5	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201381	5	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201381	5	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201381	5	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201381	5	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201381	5	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201381	5	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201381	5	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201381	5	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201381	5	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201381	5	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201381	5	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201381	5	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201381	5	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201381	5	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201381	5	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201381	5	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201381	5	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201381	5	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201381	5	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201381	5	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201381	5	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201381	5	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201381	5	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201381	5	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201381	5	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201381	5	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201381	5	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201381	5	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201381	5	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201381	5	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201381	5	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201381	5	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201381	5	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201381	5	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201381	5	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201381	5	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201381	5	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201381	5	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201381	5	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201381	5	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201381	5	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201381	5	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201381	5	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201381	5	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201381	5	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201381	5	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201381	5	32	32	-	144989321	144996563
318017587	chr8	145017820	145018041	145017840	145018022	PLEC	NM_201382	6	32	1	-	145017947	145018110
318020797	chr8	145018003	145018128	145018023	145018111	PLEC	NM_201382	6	32	1	-	145017947	145018110
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201382	6	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201382	6	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201382	6	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201382	6	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201382	6	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201382	6	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201382	6	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201382	6	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201382	6	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201382	6	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201382	6	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201382	6	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201382	6	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201382	6	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201382	6	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201382	6	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201382	6	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201382	6	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201382	6	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201382	6	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201382	6	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201382	6	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201382	6	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201382	6	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201382	6	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201382	6	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201382	6	32	15	-	145006803	145006880

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201382	6	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201382	6	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201382	6	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201382	6	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201382	6	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201382	6	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201382	6	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201382	6	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201382	6	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201382	6	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201382	6	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201382	6	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201382	6	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201382	6	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201382	6	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201382	6	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201382	6	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201382	6	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201382	6	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201382	6	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201382	6	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201382	6	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201382	6	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201382	6	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201382	6	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201382	6	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201382	6	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201382	6	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201382	6	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201382	6	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201382	6	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201382	6	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201382	6	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201382	6	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201382	6	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201382	6	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201382	6	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201382	6	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201382	6	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201382	6	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201382	6	32	31	-	144996672	145000052

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201382	6	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201382	6	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201382	6	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201382	6	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201382	6	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201382	6	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201382	6	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201382	6	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201382	6	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201382	6	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201382	6	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201382	6	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201382	6	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201382	6	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201382	6	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201382	6	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201382	6	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201382	6	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201382	6	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201382	6	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201382	6	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201382	6	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201382	6	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201382	6	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201382	6	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201382	6	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201382	6	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201382	6	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201382	6	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201382	6	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201382	6	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201382	6	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201382	6	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201382	6	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201382	6	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201382	6	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201382	6	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201382	6	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201382	6	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201382	6	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201382	6	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201382	6	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201382	6	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201382	6	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201382	6	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201382	6	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201382	6	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201382	6	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201382	6	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201382	6	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201382	6	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201382	6	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201382	6	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201382	6	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201382	6	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201382	6	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201382	6	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201382	6	32	32	-	144989321	144996563
318376529	chr8	145016495	145016652	145016514	145016633	PLEC	NM_201383	7	32	1	-	145016560	145016692
318376855	chr8	145016568	145016766	145016588	145016749	PLEC	NM_201383	7	32	1	-	145016560	145016692
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201383	7	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201383	7	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201383	7	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201383	7	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201383	7	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201383	7	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201383	7	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201383	7	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201383	7	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201383	7	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201383	7	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201383	7	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201383	7	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201383	7	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201383	7	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201383	7	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201383	7	32	10	-	145008803	145008898
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201383	7	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201383	7	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201383	7	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201383	7	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201383	7	32	13	-	145007365	145007519

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201383	7	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201383	7	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201383	7	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201383	7	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201383	7	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201383	7	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201383	7	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201383	7	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201383	7	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201383	7	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201383	7	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201383	7	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201383	7	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201383	7	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201383	7	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201383	7	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201383	7	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201383	7	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201383	7	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201383	7	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201383	7	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201383	7	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201383	7	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201383	7	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201383	7	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201383	7	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201383	7	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201383	7	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201383	7	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201383	7	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201383	7	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201383	7	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201383	7	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201383	7	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201383	7	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201383	7	32	31	-	144996672	145000052
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201383	7	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201383	7	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201383	7	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201383	7	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201383	7	32	31	-	144996672	145000052

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201383	7	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201383	7	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201383	7	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201383	7	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201383	7	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201383	7	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201383	7	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201383	7	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201383	7	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201383	7	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201383	7	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201383	7	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201383	7	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201383	7	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201383	7	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201383	7	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201383	7	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201383	7	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201383	7	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201383	7	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201383	7	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201383	7	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201383	7	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201383	7	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201383	7	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201383	7	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201383	7	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201383	7	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201383	7	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201383	7	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201383	7	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201383	7	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201383	7	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201383	7	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201383	7	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201383	7	32	32	-	144989321	144996563
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201383	7	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201383	7	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201383	7	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201383	7	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201383	7	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201383	7	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201383	7	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201383	7	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201383	7	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201383	7	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201383	7	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201383	7	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201383	7	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201383	7	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201383	7	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201383	7	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201383	7	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201383	7	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201383	7	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201383	7	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201383	7	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201383	7	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201383	7	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201383	7	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201383	7	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201383	7	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201383	7	32	32	-	144989321	144996563
319787490	chr8	145013395	145013565	145013414	145013545	PLEC	NM_201384	8	32	1	-	145013518	145013758
319789605	chr8	145013505	145013681	145013526	145013664	PLEC	NM_201384	8	32	1	-	145013518	145013758
318181312	chr8	145012679	145012888	145012702	145012866	PLEC	NM_201384	8	32	2	-	145012799	145012860
320197921	chr8	145012260	145012470	145012278	145012451	PLEC	NM_201384	8	32	3	-	145012319	145012408
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201384	8	32	4	-	145011333	145011410
320341086	chr8	145011345	145011549	145011366	145011529	PLEC	NM_201384	8	32	4	-	145011333	145011410
319031808	chr8	145011052	145011239	145011073	145011217	PLEC	NM_201384	8	32	5	-	145011147	145011239
319034902	chr8	145011198	145011388	145011218	145011365	PLEC	NM_201384	8	32	5	-	145011147	145011239
318686539	chr8	145009936	145010160	145009957	145010141	PLEC	NM_201384	8	32	6	-	145010016	145010182
318694931	chr8	145010119	145010285	145010139	145010267	PLEC	NM_201384	8	32	6	-	145010016	145010182
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201384	8	32	7	-	145009366	145009481
318914242	chr8	145009444	145009618	145009464	145009593	PLEC	NM_201384	8	32	7	-	145009366	145009481
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201384	8	32	8	-	145009179	145009285
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201384	8	32	8	-	145009179	145009285
318906410	chr8	145009239	145009457	145009263	145009438	PLEC	NM_201384	8	32	8	-	145009179	145009285
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201384	8	32	9	-	145008978	145009097
318300600	chr8	145009030	145009247	145009050	145009227	PLEC	NM_201384	8	32	9	-	145008978	145009097
318302503	chr8	145009059	145009283	145009077	145009265	PLEC	NM_201384	8	32	9	-	145008978	145009097
318294686	chr8	145008852	145009076	145008872	145009058	PLEC	NM_201384	8	32	10	-	145008803	145008898

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321184283	chr8	145008733	145008895	145008753	145008872	PLEC	NM_201384	8	32	10	-	145008803	145008898
319966208	chr8	145008422	145008646	145008442	145008626	PLEC	NM_201384	8	32	11	-	145008486	145008613
320713379	chr8	145008081	145008263	145008099	145008244	PLEC	NM_201384	8	32	12	-	145008166	145008259
320714729	chr8	145008221	145008388	145008241	145008369	PLEC	NM_201384	8	32	12	-	145008166	145008259
319394198	chr8	145007323	145007546	145007341	145007527	PLEC	NM_201384	8	32	13	-	145007365	145007519
318021112	chr8	145006883	145007017	145006904	145006997	PLEC	NM_201384	8	32	14	-	145006961	145007279
318024056	chr8	145006979	145007152	145006998	145007132	PLEC	NM_201384	8	32	14	-	145006961	145007279
318030589	chr8	145007111	145007279	145007129	145007260	PLEC	NM_201384	8	32	14	-	145006961	145007279
318034458	chr8	145007218	145007380	145007239	145007361	PLEC	NM_201384	8	32	14	-	145006961	145007279
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201384	8	32	15	-	145006803	145006880
318148558	chr8	145006715	145006906	145006735	145006885	PLEC	NM_201384	8	32	15	-	145006803	145006880
318144050	chr8	145006482	145006674	145006503	145006653	PLEC	NM_201384	8	32	16	-	145006568	145006729
318147128	chr8	145006628	145006827	145006651	145006809	PLEC	NM_201384	8	32	16	-	145006568	145006729
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201384	8	32	17	-	145006298	145006402
321585115	chr8	145006343	145006511	145006363	145006492	PLEC	NM_201384	8	32	17	-	145006298	145006402
318321136	chr8	145006009	145006209	145006028	145006192	PLEC	NM_201384	8	32	18	-	145006105	145006200
318323320	chr8	145006162	145006386	145006180	145006362	PLEC	NM_201384	8	32	18	-	145006105	145006200
319850440	chr8	145005640	145005780	145005657	145005762	PLEC	NM_201384	8	32	19	-	145005702	145005827
319855583	chr8	145005742	145005934	145005763	145005913	PLEC	NM_201384	8	32	19	-	145005702	145005827
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201384	8	32	20	-	145004552	145004704
318025163	chr8	145004546	145004740	145004565	145004721	PLEC	NM_201384	8	32	20	-	145004552	145004704
318020525	chr8	145004389	145004581	145004407	145004564	PLEC	NM_201384	8	32	21	-	145004312	145004466
321423191	chr8	145004240	145004424	145004258	145004407	PLEC	NM_201384	8	32	21	-	145004312	145004466
321420896	chr8	145004042	145004264	145004060	145004245	PLEC	NM_201384	8	32	22	-	145004104	145004230
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201384	8	32	23	-	145003814	145003997
318201371	chr8	145003842	145004021	145003861	145004004	PLEC	NM_201384	8	32	23	-	145003814	145003997
318198054	chr8	145003679	145003881	145003699	145003863	PLEC	NM_201384	8	32	24	-	145003582	145003739
319113940	chr8	145003464	145003678	145003484	145003660	PLEC	NM_201384	8	32	24	-	145003582	145003739
319115673	chr8	145003615	145003768	145003633	145003750	PLEC	NM_201384	8	32	24	-	145003582	145003739
320078896	chr8	145003192	145003317	145003210	145003299	PLEC	NM_201384	8	32	25	-	145003271	145003449
320082493	chr8	145003272	145003485	145003293	145003466	PLEC	NM_201384	8	32	25	-	145003271	145003449
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201384	8	32	26	-	145002022	145002160
320275634	chr8	145001996	145002209	145002015	145002189	PLEC	NM_201384	8	32	26	-	145002022	145002160
320274646	chr8	145001896	145002041	145001913	145002023	PLEC	NM_201384	8	32	27	-	145001578	145001934
320498829	chr8	145001506	145001701	145001525	145001683	PLEC	NM_201384	8	32	27	-	145001578	145001934
320499473	chr8	145001623	145001826	145001641	145001809	PLEC	NM_201384	8	32	27	-	145001578	145001934
320499907	chr8	145001771	145001951	145001789	145001932	PLEC	NM_201384	8	32	27	-	145001578	145001934
320209737	chr8	145001374	145001531	145001391	145001513	PLEC	NM_201384	8	32	28	-	145001420	145001503
320756515	chr8	145001109	145001329	145001128	145001308	PLEC	NM_201384	8	32	29	-	145001145	145001249
320896261	chr8	145000894	145001086	145000915	145001068	PLEC	NM_201384	8	32	30	-	145000952	145001050
318016810	chr8	144999618	144999743	144999635	144999726	PLEC	NM_201384	8	32	31	-	144996672	145000052

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318016816	chr8	144998579	144998782	144998597	144998763	PLEC	NM_201384	8	32	31	-	144996672	145000052
318016839	chr8	144997672	144997882	144997689	144997865	PLEC	NM_201384	8	32	31	-	144996672	145000052
318016947	chr8	144997866	144998080	144997883	144998063	PLEC	NM_201384	8	32	31	-	144996672	145000052
318017000	chr8	144998824	144999038	144998841	144999020	PLEC	NM_201384	8	32	31	-	144996672	145000052
318017104	chr8	144999838	145000055	144999857	145000038	PLEC	NM_201384	8	32	31	-	144996672	145000052
318017395	chr8	144998835	144999039	144998853	144999022	PLEC	NM_201384	8	32	31	-	144996672	145000052
318018149	chr8	144998038	144998261	144998058	144998244	PLEC	NM_201384	8	32	31	-	144996672	145000052
318019482	chr8	144999936	145000153	144999953	145000136	PLEC	NM_201384	8	32	31	-	144996672	145000052
320337968	chr8	144996645	144996809	144996662	144996789	PLEC	NM_201384	8	32	31	-	144996672	145000052
320338849	chr8	144998110	144998312	144998127	144998295	PLEC	NM_201384	8	32	31	-	144996672	145000052
320339232	chr8	144998289	144998437	144998309	144998417	PLEC	NM_201384	8	32	31	-	144996672	145000052
320339654	chr8	144997109	144997318	144997127	144997299	PLEC	NM_201384	8	32	31	-	144996672	145000052
320340695	chr8	144998382	144998600	144998399	144998583	PLEC	NM_201384	8	32	31	-	144996672	145000052
320341693	chr8	144996758	144996972	144996777	144996954	PLEC	NM_201384	8	32	31	-	144996672	145000052
320344350	chr8	144999091	144999315	144999112	144999296	PLEC	NM_201384	8	32	31	-	144996672	145000052
320344628	chr8	144996953	144997175	144996971	144997151	PLEC	NM_201384	8	32	31	-	144996672	145000052
320344732	chr8	144999168	144999359	144999185	144999342	PLEC	NM_201384	8	32	31	-	144996672	145000052
320345125	chr8	144999287	144999411	144999305	144999393	PLEC	NM_201384	8	32	31	-	144996672	145000052
320345969	chr8	144997267	144997417	144997288	144997398	PLEC	NM_201384	8	32	31	-	144996672	145000052
320347530	chr8	144997330	144997543	144997349	144997523	PLEC	NM_201384	8	32	31	-	144996672	145000052
320349721	chr8	144997482	144997609	144997502	144997590	PLEC	NM_201384	8	32	31	-	144996672	145000052
320350249	chr8	144997566	144997749	144997589	144997730	PLEC	NM_201384	8	32	31	-	144996672	145000052
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201384	8	32	31	-	144996672	145000052
318156048	chr8	144992301	144992511	144992322	144992490	PLEC	NM_201384	8	32	32	-	144989321	144996563
318157455	chr8	144992471	144992681	144992489	144992662	PLEC	NM_201384	8	32	32	-	144989321	144996563
318160656	chr8	144992637	144992861	144992658	144992840	PLEC	NM_201384	8	32	32	-	144989321	144996563
318310998	chr8	144990811	144990969	144990831	144990948	PLEC	NM_201384	8	32	32	-	144989321	144996563
318315971	chr8	144990926	144991149	144990945	144991131	PLEC	NM_201384	8	32	32	-	144989321	144996563
318323604	chr8	144991111	144991317	144991130	144991299	PLEC	NM_201384	8	32	32	-	144989321	144996563
318325376	chr8	144991279	144991420	144991298	144991398	PLEC	NM_201384	8	32	32	-	144989321	144996563
318325793	chr8	144992785	144992919	144992803	144992901	PLEC	NM_201384	8	32	32	-	144989321	144996563
318329266	chr8	144992860	144993035	144992881	144993014	PLEC	NM_201384	8	32	32	-	144989321	144996563
318334464	chr8	144992993	144993148	144993015	144993124	PLEC	NM_201384	8	32	32	-	144989321	144996563
318341315	chr8	144993098	144993322	144993125	144993300	PLEC	NM_201384	8	32	32	-	144989321	144996563
320606658	chr8	144990254	144990451	144990278	144990426	PLEC	NM_201384	8	32	32	-	144989321	144996563
320607951	chr8	144990407	144990582	144990426	144990561	PLEC	NM_201384	8	32	32	-	144989321	144996563
320611654	chr8	144990541	144990701	144990558	144990679	PLEC	NM_201384	8	32	32	-	144989321	144996563
320615834	chr8	144990647	144990867	144990675	144990845	PLEC	NM_201384	8	32	32	-	144989321	144996563
320617787	chr8	144991744	144991939	144991766	144991916	PLEC	NM_201384	8	32	32	-	144989321	144996563
320624529	chr8	144991364	144991537	144991386	144991515	PLEC	NM_201384	8	32	32	-	144989321	144996563
320625284	chr8	144993277	144993501	144993301	144993482	PLEC	NM_201384	8	32	32	-	144989321	144996563

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320626599	chr8	144993747	144993920	144993764	144993903	PLEC	NM_201384	8	32	32	-	144989321	144996563
320629917	chr8	144991883	144992068	144991905	144992046	PLEC	NM_201384	8	32	32	-	144989321	144996563
320629976	chr8	144994240	144994458	144994258	144994440	PLEC	NM_201384	8	32	32	-	144989321	144996563
320630592	chr8	144993875	144994012	144993897	144993992	PLEC	NM_201384	8	32	32	-	144989321	144996563
320631809	chr8	144994402	144994619	144994419	144994601	PLEC	NM_201384	8	32	32	-	144989321	144996563
320632599	chr8	144994836	144995016	144994857	144994997	PLEC	NM_201384	8	32	32	-	144989321	144996563
320632667	chr8	144993964	144994150	144993984	144994126	PLEC	NM_201384	8	32	32	-	144989321	144996563
320634004	chr8	144994573	144994722	144994590	144994697	PLEC	NM_201384	8	32	32	-	144989321	144996563
320634553	chr8	144995259	144995478	144995279	144995459	PLEC	NM_201384	8	32	32	-	144989321	144996563
320635498	chr8	144993457	144993664	144993474	144993644	PLEC	NM_201384	8	32	32	-	144989321	144996563
320635554	chr8	144991485	144991679	144991507	144991656	PLEC	NM_201384	8	32	32	-	144989321	144996563
320636979	chr8	144994672	144994886	144994693	144994862	PLEC	NM_201384	8	32	32	-	144989321	144996563
320640040	chr8	144995423	144995640	144995444	144995618	PLEC	NM_201384	8	32	32	-	144989321	144996563
320640056	chr8	144994956	144995144	144994974	144995122	PLEC	NM_201384	8	32	32	-	144989321	144996563
320640783	chr8	144993617	144993782	144993636	144993764	PLEC	NM_201384	8	32	32	-	144989321	144996563
320640785	chr8	144994105	144994290	144994127	144994268	PLEC	NM_201384	8	32	32	-	144989321	144996563
320641148	chr8	144992025	144992229	144992044	144992206	PLEC	NM_201384	8	32	32	-	144989321	144996563
320644730	chr8	144995597	144995747	144995616	144995729	PLEC	NM_201384	8	32	32	-	144989321	144996563
320645884	chr8	144991620	144991784	144991639	144991767	PLEC	NM_201384	8	32	32	-	144989321	144996563
320645950	chr8	144995847	144996037	144995870	144996017	PLEC	NM_201384	8	32	32	-	144989321	144996563
320646460	chr8	144992161	144992348	144992179	144992330	PLEC	NM_201384	8	32	32	-	144989321	144996563
320647373	chr8	144995100	144995310	144995123	144995289	PLEC	NM_201384	8	32	32	-	144989321	144996563
320648533	chr8	144996294	144996518	144996311	144996498	PLEC	NM_201384	8	32	32	-	144989321	144996563
320648864	chr8	144995985	144996165	144996003	144996148	PLEC	NM_201384	8	32	32	-	144989321	144996563
320649773	chr8	144995711	144995887	144995730	144995869	PLEC	NM_201384	8	32	32	-	144989321	144996563
320651300	chr8	144996129	144996347	144996146	144996330	PLEC	NM_201384	8	32	32	-	144989321	144996563
320655542	chr8	144996477	144996699	144996499	144996678	PLEC	NM_201384	8	32	32	-	144989321	144996563
333190531	chr6	118880041	118880261	118880067	118880236	PLN	NM_002667	1	2	2	+	118879988	118881587
333211379	chr6	118880213	118880434	118880237	118880407	PLN	NM_002667	1	2	2	+	118879988	118881587
318410723	chr1	11994769	11994929	11994786	11994912	PLOD1	NM_000302	1	19	1	+	11994724	11994912
318183714	chr1	12007988	12008189	12008010	12008166	PLOD1	NM_000302	1	19	2	+	12008033	12008124
318923451	chr1	12009791	12009969	12009815	12009946	PLOD1	NM_000302	1	19	3	+	12009830	12009963
318932681	chr1	12009926	12010143	12009947	12010118	PLOD1	NM_000302	1	19	3	+	12009830	12009963
318921884	chr1	12010256	12010468	12010277	12010449	PLOD1	NM_000302	1	19	4	+	12010414	12010577
318930990	chr1	12010413	12010630	12010434	12010610	PLOD1	NM_000302	1	19	4	+	12010414	12010577
318777703	chr1	12012635	12012859	12012656	12012842	PLOD1	NM_000302	1	19	5	+	12012680	12012792
319649825	chr1	12014780	12015000	12014801	12014977	PLOD1	NM_000302	1	19	6	+	12014887	12014950
318129195	chr1	12016947	12017134	12016967	12017109	PLOD1	NM_000302	1	19	7	+	12016974	12017071
319605708	chr1	12017869	12018073	12017889	12018052	PLOD1	NM_000302	1	19	8	+	12017899	12018000
319814535	chr1	12018530	12018753	12018550	12018733	PLOD1	NM_000302	1	19	9	+	12018573	12018704
319141628	chr1	12020632	12020849	12020652	12020829	PLOD1	NM_000302	1	19	10	+	12020703	12020824

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319461015	chr1	12023525	12023736	12023545	12023718	PLOD1	NM_000302	1	19	11	+	12023589	12023693
320987407	chr1	12024196	12024411	12024214	12024390	PLOD1	NM_000302	1	19	12	+	12024232	12024357
320775030	chr1	12024674	12024879	12024692	12024862	PLOD1	NM_000302	1	19	13	+	12024701	12024842
319904258	chr1	12025522	12025685	12025540	12025667	PLOD1	NM_000302	1	19	14	+	12025537	12025650
320184951	chr1	12026188	12026402	12026209	12026382	PLOD1	NM_000302	1	19	15	+	12026308	12026373
319988948	chr1	12026901	12027121	12026924	12027100	PLOD1	NM_000302	1	19	16	+	12027044	12027148
320001269	chr1	12027053	12027276	12027078	12027256	PLOD1	NM_000302	1	19	16	+	12027044	12027148
319348565	chr1	12030698	12030908	12030720	12030890	PLOD1	NM_000302	1	19	17	+	12030727	12030873
318846445	chr1	12032872	12033055	12032896	12033035	PLOD1	NM_000302	1	19	18	+	12032929	12033054
318873190	chr1	12033014	12033236	12033034	12033214	PLOD1	NM_000302	1	19	18	+	12032929	12033054
320312817	chr1	12034682	12034898	12034703	12034875	PLOD1	NM_000302	1	19	19	+	12034710	12035599
319241012	chr16	8891697	8891888	8891717	8891867	PMM2	NM_000303	1	8	1	+	8891670	8891805
318378972	chr16	8895575	8895715	8895603	8895689	PMM2	NM_000303	1	8	2	+	8895656	8895767
318387781	chr16	8895662	8895843	8895690	8895816	PMM2	NM_000303	1	8	2	+	8895656	8895767
319765516	chr16	8898570	8898785	8898598	8898757	PMM2	NM_000303	1	8	3	+	8898624	8898700
319214786	chr16	8900080	8900294	8900100	8900269	PMM2	NM_000303	1	8	4	+	8900173	8900264
320904924	chr16	8904862	8905070	8904889	8905042	PMM2	NM_000303	1	8	5	+	8904936	8905035
318947269	chr16	8905407	8905604	8905431	8905578	PMM2	NM_000303	1	8	6	+	8905495	8905570
319216006	chr16	8906779	8906997	8906807	8906973	PMM2	NM_000303	1	8	7	+	8906848	8906963
320800879	chr16	8941549	8941733	8941571	8941713	PMM2	NM_000303	1	8	8	+	8941581	8943194
319368270	chr17	15163850	15164074	15163873	15164054	PMP22	NM_000304	1	5	2	-	15163967	15164078
318200263	chr17	15162320	15162544	15162344	15162516	PMP22	NM_000304	1	5	3	-	15162411	15162510
318178248	chr17	15142752	15142958	15142773	15142933	PMP22	NM_000304	1	5	4	-	15142788	15142928
320074088	chr17	15134164	15134348	15134188	15134325	PMP22	NM_000304	1	5	5	-	15133097	15134397
320092947	chr17	15134305	15134523	15134326	15134498	PMP22	NM_000304	1	5	5	-	15133097	15134397
319368270	chr17	15163850	15164074	15163873	15164054	PMP22	NM_153321	2	5	2	-	15163967	15164078
318200263	chr17	15162320	15162544	15162344	15162516	PMP22	NM_153321	2	5	3	-	15162411	15162510
318178248	chr17	15142752	15142958	15142773	15142933	PMP22	NM_153321	2	5	4	-	15142788	15142928
320074088	chr17	15134164	15134348	15134188	15134325	PMP22	NM_153321	2	5	5	-	15133096	15134397
320092947	chr17	15134305	15134523	15134326	15134498	PMP22	NM_153321	2	5	5	-	15133096	15134397
319368270	chr17	15163850	15164074	15163873	15164054	PMP22	NM_153322	3	4	1	-	15163967	15164093
318200263	chr17	15162320	15162544	15162344	15162516	PMP22	NM_153322	3	4	2	-	15162411	15162510
318178248	chr17	15142752	15142958	15142773	15142933	PMP22	NM_153322	3	4	3	-	15142788	15142928
320074088	chr17	15134164	15134348	15134188	15134325	PMP22	NM_153322	3	4	4	-	15133097	15134397
320092947	chr17	15134305	15134523	15134326	15134498	PMP22	NM_153322	3	4	4	-	15133097	15134397
320161102	chr15	89876788	89876986	89876808	89876969	POLG	NM_001126131	1	23	2	-	89876327	89877144
321587869	chr15	89876286	89876435	89876305	89876418	POLG	NM_001126131	1	23	2	-	89876327	89877144
321588710	chr15	89876381	89876588	89876400	89876568	POLG	NM_001126131	1	23	2	-	89876327	89877144
321589186	chr15	89876536	89876741	89876555	89876721	POLG	NM_001126131	1	23	2	-	89876327	89877144
321590973	chr15	89876699	89876913	89876718	89876896	POLG	NM_001126131	1	23	2	-	89876327	89877144
318942452	chr15	89873232	89873392	89873254	89873371	POLG	NM_001126131	1	23	3	-	89873312	89873507

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318948868	chr15	89873340	89873554	89873363	89873528	POLG	NM_001126131	1	23	3	-	89873312	89873507
319538716	chr15	89872129	89872341	89872149	89872324	POLG	NM_001126131	1	23	4	-	89872174	89872341
319555963	chr15	89872300	89872504	89872321	89872478	POLG	NM_001126131	1	23	4	-	89872174	89872341
319167269	chr15	89871746	89871948	89871766	89871927	POLG	NM_001126131	1	23	5	-	89871916	89872062
319252384	chr15	89871905	89872097	89871927	89872076	POLG	NM_001126131	1	23	5	-	89871916	89872062
319158871	chr15	89871607	89871830	89871627	89871808	POLG	NM_001126131	1	23	6	-	89871687	89871766
319167269	chr15	89871746	89871948	89871766	89871927	POLG	NM_001126131	1	23	6	-	89871687	89871766
319919197	chr15	89870291	89870466	89870314	89870445	POLG	NM_001126131	1	23	7	-	89870398	89870580
319949057	chr15	89870422	89870630	89870445	89870607	POLG	NM_001126131	1	23	7	-	89870398	89870580
319888334	chr15	89870046	89870258	89870067	89870232	POLG	NM_001126131	1	23	8	-	89870143	89870294
319914155	chr15	89870208	89870415	89870233	89870394	POLG	NM_001126131	1	23	8	-	89870143	89870294
320359122	chr15	89869780	89870002	89869801	89869981	POLG	NM_001126131	1	23	9	-	89869843	89869969
318297780	chr15	89868582	89868804	89868607	89868783	POLG	NM_001126131	1	23	10	-	89868681	89868917
318310811	chr15	89868762	89868964	89868781	89868943	POLG	NM_001126131	1	23	10	-	89868681	89868917
318667906	chr15	89867272	89867486	89867292	89867465	POLG	NM_001126131	1	23	11	-	89867338	89867458
319272110	chr15	89866941	89867162	89866964	89867138	POLG	NM_001126131	1	23	12	-	89867046	89867132
319294092	chr15	89866550	89866774	89866572	89866753	POLG	NM_001126131	1	23	13	-	89866635	89866742
319442294	chr15	89865886	89866032	89865908	89866008	POLG	NM_001126131	1	23	14	-	89865973	89866133
319460633	chr15	89865987	89866209	89866009	89866188	POLG	NM_001126131	1	23	14	-	89865973	89866133
320361836	chr15	89865051	89865273	89865073	89865253	POLG	NM_001126131	1	23	15	-	89865193	89865246
320361836	chr15	89865051	89865273	89865073	89865253	POLG	NM_001126131	1	23	16	-	89864967	89865084
320970723	chr15	89864897	89865120	89864918	89865098	POLG	NM_001126131	1	23	16	-	89864967	89865084
318097663	chr15	89864262	89864473	89864286	89864452	POLG	NM_001126131	1	23	17	-	89864356	89864491
318115999	chr15	89864404	89864627	89864425	89864605	POLG	NM_001126131	1	23	17	-	89864356	89864491
319654530	chr15	89863882	89864099	89863903	89864076	POLG	NM_001126131	1	23	18	-	89863997	89864243
319682942	chr15	89864056	89864272	89864077	89864250	POLG	NM_001126131	1	23	18	-	89863997	89864243
320021523	chr15	89862420	89862612	89862441	89862588	POLG	NM_001126131	1	23	19	-	89862459	89862581
321540650	chr15	89862133	89862357	89862153	89862336	POLG	NM_001126131	1	23	20	-	89862162	89862330
319119617	chr15	89861671	89861872	89861695	89861851	POLG	NM_001126131	1	23	21	-	89861772	89861980
319137988	chr15	89861833	89862048	89861852	89862024	POLG	NM_001126131	1	23	21	-	89861772	89861980
321197685	chr15	89860453	89860661	89860476	89860638	POLG	NM_001126131	1	23	22	-	89860607	89860767
321227027	chr15	89860617	89860797	89860639	89860772	POLG	NM_001126131	1	23	22	-	89860607	89860767
319741581	chr15	89859890	89860091	89859912	89860068	POLG	NM_001126131	1	23	23	-	89859536	89860058
320161102	chr15	89876788	89876986	89876808	89876969	POLG	NM_002693	2	23	2	-	89876327	89877144
321587869	chr15	89876286	89876435	89876305	89876418	POLG	NM_002693	2	23	2	-	89876327	89877144
321588710	chr15	89876381	89876588	89876400	89876568	POLG	NM_002693	2	23	2	-	89876327	89877144
321589186	chr15	89876536	89876741	89876555	89876721	POLG	NM_002693	2	23	2	-	89876327	89877144
321590973	chr15	89876699	89876913	89876718	89876896	POLG	NM_002693	2	23	2	-	89876327	89877144
318942452	chr15	89873232	89873392	89873254	89873371	POLG	NM_002693	2	23	3	-	89873312	89873507
318948868	chr15	89873340	89873554	89873363	89873528	POLG	NM_002693	2	23	3	-	89873312	89873507
319538716	chr15	89872129	89872341	89872149	89872324	POLG	NM_002693	2	23	4	-	89872174	89872341

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319555963	chr15	89872300	89872504	89872321	89872478	POLG	NM_002693	2	23	4	-	89872174	89872341
319167269	chr15	89871746	89871948	89871766	89871927	POLG	NM_002693	2	23	5	-	89871916	89872062
319252384	chr15	89871905	89872097	89871927	89872076	POLG	NM_002693	2	23	5	-	89871916	89872062
319158871	chr15	89871607	89871830	89871627	89871808	POLG	NM_002693	2	23	6	-	89871687	89871766
319167269	chr15	89871746	89871948	89871766	89871927	POLG	NM_002693	2	23	6	-	89871687	89871766
319919197	chr15	89870291	89870466	89870314	89870445	POLG	NM_002693	2	23	7	-	89870398	89870580
319949057	chr15	89870422	89870630	89870445	89870607	POLG	NM_002693	2	23	7	-	89870398	89870580
319888334	chr15	89870046	89870258	89870067	89870232	POLG	NM_002693	2	23	8	-	89870143	89870294
319914155	chr15	89870208	89870415	89870233	89870394	POLG	NM_002693	2	23	8	-	89870143	89870294
320359122	chr15	89869780	89870002	89869801	89869981	POLG	NM_002693	2	23	9	-	89869843	89869969
318297780	chr15	89868582	89868804	89868607	89868783	POLG	NM_002693	2	23	10	-	89868681	89868917
318310811	chr15	89868762	89868964	89868781	89868943	POLG	NM_002693	2	23	10	-	89868681	89868917
318667906	chr15	89867272	89867486	89867292	89867465	POLG	NM_002693	2	23	11	-	89867338	89867458
319272110	chr15	89866941	89867162	89866964	89867138	POLG	NM_002693	2	23	12	-	89867046	89867132
319294092	chr15	89866550	89866774	89866572	89866753	POLG	NM_002693	2	23	13	-	89866635	89866742
319442294	chr15	89865886	89866032	89865908	89866008	POLG	NM_002693	2	23	14	-	89865973	89866133
319460633	chr15	89865987	89866209	89866009	89866188	POLG	NM_002693	2	23	14	-	89865973	89866133
320361836	chr15	89865051	89865273	89865073	89865253	POLG	NM_002693	2	23	15	-	89865193	89865246
320361836	chr15	89865051	89865273	89865073	89865253	POLG	NM_002693	2	23	16	-	89864967	89865084
320970723	chr15	89864897	89865120	89864918	89865098	POLG	NM_002693	2	23	16	-	89864967	89865084
318097663	chr15	89864262	89864473	89864286	89864452	POLG	NM_002693	2	23	17	-	89864356	89864491
318115999	chr15	89864404	89864627	89864425	89864605	POLG	NM_002693	2	23	17	-	89864356	89864491
319654530	chr15	89863882	89864099	89863903	89864076	POLG	NM_002693	2	23	18	-	89863997	89864243
319682942	chr15	89864056	89864272	89864077	89864250	POLG	NM_002693	2	23	18	-	89863997	89864243
320021523	chr15	89862420	89862612	89862441	89862588	POLG	NM_002693	2	23	19	-	89862459	89862581
321540650	chr15	89862133	89862357	89862153	89862336	POLG	NM_002693	2	23	20	-	89862162	89862330
319119617	chr15	89861671	89861872	89861695	89861851	POLG	NM_002693	2	23	21	-	89861772	89861980
319137988	chr15	89861833	89862048	89861852	89862024	POLG	NM_002693	2	23	21	-	89861772	89861980
321197685	chr15	89860453	89860661	89860476	89860638	POLG	NM_002693	2	23	22	-	89860607	89860767
321227027	chr15	89860617	89860797	89860639	89860772	POLG	NM_002693	2	23	22	-	89860607	89860767
319741581	chr15	89859890	89860091	89859912	89860068	POLG	NM_002693	2	23	23	-	89859536	89860058
321426061	chr1	40562737	40562933	40562761	40562915	PPT1	NM_000310	1	9	1	-	40562787	40563142
318430951	chr1	40558018	40558214	40558043	40558186	PPT1	NM_000310	1	9	2	-	40558070	40558179
318136926	chr1	40557568	40557775	40557595	40557751	PPT1	NM_000310	1	9	3	-	40557717	40557844
318140068	chr1	40557730	40557874	40557752	40557850	PPT1	NM_000310	1	9	3	-	40557717	40557844
319933196	chr1	40556880	40557104	40556905	40557080	PPT1	NM_000310	1	9	4	-	40557001	40557071
319825293	chr1	40554978	40555153	40555005	40555129	PPT1	NM_000310	1	9	5	-	40555082	40555184
319858249	chr1	40555108	40555328	40555130	40555301	PPT1	NM_000310	1	9	5	-	40555082	40555184
319678866	chr1	40545974	40546198	40545998	40546171	PPT1	NM_000310	1	9	6	-	40546069	40546159
319244094	chr1	40544169	40544369	40544190	40544344	PPT1	NM_000310	1	9	7	-	40544232	40544330
318547694	chr1	40542395	40542616	40542418	40542591	PPT1	NM_000310	1	9	8	-	40542514	40542585

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320769670	chr1	40539650	40539872	40539670	40539852	PPT1	NM_000310	1	9	9	-	40538382	40539855
320776974	chr1	40539819	40539975	40539844	40539945	PPT1	NM_000310	1	9	9	-	40538382	40539855
321426061	chr1	40562737	40562933	40562761	40562915	PPT1	NM_001142604	2	6	1	-	40562787	40563142
319825293	chr1	40554978	40555153	40555005	40555129	PPT1	NM_001142604	2	6	2	-	40555082	40555184
319858249	chr1	40555108	40555328	40555130	40555301	PPT1	NM_001142604	2	6	2	-	40555082	40555184
319678866	chr1	40545974	40546198	40545998	40546171	PPT1	NM_001142604	2	6	3	-	40546069	40546159
319244094	chr1	40544169	40544369	40544190	40544344	PPT1	NM_001142604	2	6	4	-	40544232	40544330
318547694	chr1	40542395	40542616	40542418	40542591	PPT1	NM_001142604	2	6	5	-	40542514	40542585
320769670	chr1	40539650	40539872	40539670	40539852	PPT1	NM_001142604	2	6	6	-	40538382	40539855
320776974	chr1	40539819	40539975	40539844	40539945	PPT1	NM_001142604	2	6	6	-	40538382	40539855
318628566	chr17	74536175	74536321	74536195	74536302	PRCD	NM_001077620	1	5	1	+	74536121	74536297
318622343	chr17	74536552	74536766	74536576	74536748	PRCD	NM_001077620	1	5	2	+	74536587	74536655
318902301	chr17	74538603	74538820	74538624	74538798	PRCD	NM_001077620	1	5	3	+	74538635	74538715
318622343	chr17	74536552	74536766	74536576	74536748	PRCD	NR_033357	2	5	2	+	74536587	74536655
318902301	chr17	74538603	74538820	74538624	74538798	PRCD	NR_033357	2	5	3	+	74538635	74538715
319206655	chr7	151483511	151483706	151483532	151483684	PRKAG2	NM_001040633	1	16	2	-	151483556	151483627
318781225	chr7	151478201	151478398	151478223	151478377	PRKAG2	NM_001040633	1	16	3	-	151478238	151478517
318791036	chr7	151478332	151478548	151478352	151478525	PRKAG2	NM_001040633	1	16	3	-	151478238	151478517
321150664	chr7	151372326	151372533	151372347	151372513	PRKAG2	NM_001040633	1	16	4	-	151372506	151372723
321163015	chr7	151372494	151372644	151372514	151372623	PRKAG2	NM_001040633	1	16	4	-	151372506	151372723
321173344	chr7	151372603	151372751	151372624	151372729	PRKAG2	NM_001040633	1	16	4	-	151372506	151372723
319516774	chr7	151329144	151329268	151329161	151329251	PRKAG2	NM_001040633	1	16	5	-	151329155	151329224
318892240	chr7	151292346	151292546	151292373	151292518	PRKAG2	NM_001040633	1	16	6	-	151292431	151292540
320712099	chr7	151273365	151273564	151273389	151273536	PRKAG2	NM_001040633	1	16	7	-	151273457	151273538
319638117	chr7	151271840	151272040	151271863	151272011	PRKAG2	NM_001040633	1	16	8	-	151271977	151272035
319641360	chr7	151271965	151272131	151271991	151272102	PRKAG2	NM_001040633	1	16	8	-	151271977	151272035
321173230	chr7	151269655	151269799	151269682	151269769	PRKAG2	NM_001040633	1	16	9	-	151269750	151269795
321177698	chr7	151269743	151269918	151269770	151269894	PRKAG2	NM_001040633	1	16	9	-	151269750	151269795
320312448	chr7	151267147	151267360	151267169	151267332	PRKAG2	NM_001040633	1	16	10	-	151267257	151267311
321437801	chr7	151265647	151265837	151265675	151265812	PRKAG2	NM_001040633	1	16	11	-	151265802	151265928
321442983	chr7	151265785	151265972	151265813	151265946	PRKAG2	NM_001040633	1	16	11	-	151265802	151265928
320652276	chr7	151262670	151262839	151262691	151262816	PRKAG2	NM_001040633	1	16	12	-	151262806	151262971
320668694	chr7	151262793	151263004	151262817	151262978	PRKAG2	NM_001040633	1	16	12	-	151262806	151262971
319584973	chr7	151261086	151261219	151261109	151261193	PRKAG2	NM_001040633	1	16	14	-	151261164	151261310
319591782	chr7	151261169	151261390	151261194	151261361	PRKAG2	NM_001040633	1	16	14	-	151261164	151261310
319250236	chr7	151257517	151257739	151257543	151257712	PRKAG2	NM_001040633	1	16	15	-	151257610	151257703
319928146	chr7	151254191	151254363	151254214	151254335	PRKAG2	NM_001040633	1	16	16	-	151253201	151254318
319485331	chr7	151573512	151573696	151573531	151573671	PRKAG2	NM_016203	2	16	1	-	151573592	151574316
319490696	chr7	151573617	151573821	151573640	151573800	PRKAG2	NM_016203	2	16	1	-	151573592	151574316
319206655	chr7	151483511	151483706	151483532	151483684	PRKAG2	NM_016203	2	16	2	-	151483556	151483627
318781225	chr7	151478201	151478398	151478223	151478377	PRKAG2	NM_016203	2	16	3	-	151478238	151478517

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318791036	chr7	151478332	151478548	151478352	151478525	PRKAG2	NM_016203	2	16	3	-	151478238	151478517
321150664	chr7	151372326	151372533	151372347	151372513	PRKAG2	NM_016203	2	16	4	-	151372506	151372723
321163015	chr7	151372494	151372644	151372514	151372623	PRKAG2	NM_016203	2	16	4	-	151372506	151372723
321173344	chr7	151372603	151372751	151372624	151372729	PRKAG2	NM_016203	2	16	4	-	151372506	151372723
319516774	chr7	151329144	151329268	151329161	151329251	PRKAG2	NM_016203	2	16	5	-	151329155	151329224
318892240	chr7	151292346	151292546	151292373	151292518	PRKAG2	NM_016203	2	16	6	-	151292431	151292540
320712099	chr7	151273365	151273564	151273389	151273536	PRKAG2	NM_016203	2	16	7	-	151273457	151273538
319638117	chr7	151271840	151272040	151271863	151272011	PRKAG2	NM_016203	2	16	8	-	151271977	151272035
319641360	chr7	151271965	151272131	151271991	151272102	PRKAG2	NM_016203	2	16	8	-	151271977	151272035
321173230	chr7	151269655	151269799	151269682	151269769	PRKAG2	NM_016203	2	16	9	-	151269750	151269795
321177698	chr7	151269743	151269918	151269770	151269894	PRKAG2	NM_016203	2	16	9	-	151269750	151269795
320312448	chr7	151267147	151267360	151267169	151267332	PRKAG2	NM_016203	2	16	10	-	151267257	151267311
321437801	chr7	151265647	151265837	151265675	151265812	PRKAG2	NM_016203	2	16	11	-	151265802	151265928
321442983	chr7	151265785	151265972	151265813	151265946	PRKAG2	NM_016203	2	16	11	-	151265802	151265928
320652276	chr7	151262670	151262839	151262691	151262816	PRKAG2	NM_016203	2	16	12	-	151262806	151262971
320668694	chr7	151262793	151263004	151262817	151262978	PRKAG2	NM_016203	2	16	12	-	151262806	151262971
319584973	chr7	151261086	151261219	151261109	151261193	PRKAG2	NM_016203	2	16	14	-	151261164	151261310
319591782	chr7	151261169	151261390	151261194	151261361	PRKAG2	NM_016203	2	16	14	-	151261164	151261310
319250236	chr7	151257517	151257739	151257543	151257712	PRKAG2	NM_016203	2	16	15	-	151257610	151257703
319928146	chr7	151254191	151254363	151254214	151254335	PRKAG2	NM_016203	2	16	16	-	151253201	151254318
319516774	chr7	151329144	151329268	151329161	151329251	PRKAG2	NM_024429	3	12	1	-	151329155	151329344
318892240	chr7	151292346	151292546	151292373	151292518	PRKAG2	NM_024429	3	12	2	-	151292431	151292540
320712099	chr7	151273365	151273564	151273389	151273536	PRKAG2	NM_024429	3	12	3	-	151273457	151273538
319638117	chr7	151271840	151272040	151271863	151272011	PRKAG2	NM_024429	3	12	4	-	151271977	151272035
319641360	chr7	151271965	151272131	151271991	151272102	PRKAG2	NM_024429	3	12	4	-	151271977	151272035
321173230	chr7	151269655	151269799	151269682	151269769	PRKAG2	NM_024429	3	12	5	-	151269750	151269795
321177698	chr7	151269743	151269918	151269770	151269894	PRKAG2	NM_024429	3	12	5	-	151269750	151269795
320312448	chr7	151267147	151267360	151267169	151267332	PRKAG2	NM_024429	3	12	6	-	151267257	151267311
321437801	chr7	151265647	151265837	151265675	151265812	PRKAG2	NM_024429	3	12	7	-	151265802	151265928
321442983	chr7	151265785	151265972	151265813	151265946	PRKAG2	NM_024429	3	12	7	-	151265802	151265928
320652276	chr7	151262670	151262839	151262691	151262816	PRKAG2	NM_024429	3	12	8	-	151262806	151262971
320668694	chr7	151262793	151263004	151262817	151262978	PRKAG2	NM_024429	3	12	8	-	151262806	151262971
319584973	chr7	151261086	151261219	151261109	151261193	PRKAG2	NM_024429	3	12	10	-	151261164	151261310
319591782	chr7	151261169	151261390	151261194	151261361	PRKAG2	NM_024429	3	12	10	-	151261164	151261310
319250236	chr7	151257517	151257739	151257543	151257712	PRKAG2	NM_024429	3	12	11	-	151257610	151257703
319928146	chr7	151254191	151254363	151254214	151254335	PRKAG2	NM_024429	3	12	12	-	151253201	151254318
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145847	1	27	2	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145847	1	27	2	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145847	1	27	3	-	16040569	16040624
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145847	1	27	4	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145847	1	27	4	-	16034927	16035132

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145847	1	27	5	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145847	1	27	6	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145847	1	27	7	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145847	1	27	8	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145847	1	27	8	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145847	1	27	9	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145847	1	27	10	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145847	1	27	11	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145847	1	27	11	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145847	1	27	12	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145847	1	27	13	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145847	1	27	13	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145847	1	27	14	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145847	1	27	14	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145847	1	27	15	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145847	1	27	16	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145847	1	27	16	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145847	1	27	17	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145847	1	27	18	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145847	1	27	19	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145847	1	27	20	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145847	1	27	21	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145847	1	27	22	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145847	1	27	23	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145847	1	27	23	-	15982045	15982160
320321779	chr4	15981373	15981597	15981396	15981569	PROM1	NM_001145847	1	27	24	-	15981504	15981527
320313515	chr4	15980993	15981133	15981016	15981102	PROM1	NM_001145847	1	27	25	-	15981018	15981086
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145847	1	27	26	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145848	2	27	2	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145848	2	27	2	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145848	2	27	3	-	16040569	16040624
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145848	2	27	4	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145848	2	27	4	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145848	2	27	5	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145848	2	27	6	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145848	2	27	7	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145848	2	27	8	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145848	2	27	8	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145848	2	27	9	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145848	2	27	10	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145848	2	27	11	-	16010572	16010731

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145848	2	27	11	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145848	2	27	12	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145848	2	27	13	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145848	2	27	13	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145848	2	27	14	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145848	2	27	14	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145848	2	27	15	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145848	2	27	16	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145848	2	27	16	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145848	2	27	17	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145848	2	27	18	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145848	2	27	19	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145848	2	27	20	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145848	2	27	21	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145848	2	27	22	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145848	2	27	23	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145848	2	27	23	-	15982045	15982160
320321779	chr4	15981373	15981597	15981396	15981569	PROM1	NM_001145848	2	27	24	-	15981504	15981527
320313515	chr4	15980993	15981133	15981016	15981102	PROM1	NM_001145848	2	27	25	-	15981018	15981086
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145848	2	27	26	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145849	3	26	1	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145849	3	26	1	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145849	3	26	2	-	16040569	16040624
319847665	chr4	16037243	16037412	16037271	16037390	PROM1	NM_001145849	3	26	3	-	16037358	16037384
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145849	3	26	4	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145849	3	26	4	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145849	3	26	5	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145849	3	26	6	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145849	3	26	7	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145849	3	26	8	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145849	3	26	8	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145849	3	26	9	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145849	3	26	10	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145849	3	26	11	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145849	3	26	11	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145849	3	26	12	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145849	3	26	13	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145849	3	26	13	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145849	3	26	14	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145849	3	26	14	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145849	3	26	15	-	15995610	15995694

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145849	3	26	16	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145849	3	26	16	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145849	3	26	17	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145849	3	26	18	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145849	3	26	19	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145849	3	26	20	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145849	3	26	21	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145849	3	26	22	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145849	3	26	23	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145849	3	26	23	-	15982045	15982160
320321779	chr4	15981373	15981597	15981396	15981569	PROM1	NM_001145849	3	26	24	-	15981504	15981527
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145849	3	26	25	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145850	4	25	1	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145850	4	25	1	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145850	4	25	2	-	16040569	16040624
319847665	chr4	16037243	16037412	16037271	16037390	PROM1	NM_001145850	4	25	3	-	16037358	16037384
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145850	4	25	4	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145850	4	25	4	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145850	4	25	5	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145850	4	25	6	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145850	4	25	7	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145850	4	25	8	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145850	4	25	8	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145850	4	25	9	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145850	4	25	10	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145850	4	25	11	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145850	4	25	11	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145850	4	25	12	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145850	4	25	13	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145850	4	25	13	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145850	4	25	14	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145850	4	25	14	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145850	4	25	15	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145850	4	25	16	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145850	4	25	16	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145850	4	25	17	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145850	4	25	18	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145850	4	25	19	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145850	4	25	20	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145850	4	25	21	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145850	4	25	22	-	15985886	15985978

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145850	4	25	23	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145850	4	25	23	-	15982045	15982160
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145850	4	25	24	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145851	5	25	1	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145851	5	25	1	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145851	5	25	2	-	16040569	16040624
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145851	5	25	3	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145851	5	25	3	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145851	5	25	4	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145851	5	25	5	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145851	5	25	6	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145851	5	25	7	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145851	5	25	7	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145851	5	25	8	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145851	5	25	9	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145851	5	25	10	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145851	5	25	10	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145851	5	25	11	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145851	5	25	12	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145851	5	25	12	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145851	5	25	13	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145851	5	25	13	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145851	5	25	14	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145851	5	25	15	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145851	5	25	15	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145851	5	25	16	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145851	5	25	17	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145851	5	25	18	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145851	5	25	19	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145851	5	25	20	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145851	5	25	21	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145851	5	25	22	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145851	5	25	22	-	15982045	15982160
320321779	chr4	15981373	15981597	15981396	15981569	PROM1	NM_001145851	5	25	23	-	15981504	15981527
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145851	5	25	24	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_001145852	6	24	1	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_001145852	6	24	1	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_001145852	6	24	2	-	16040569	16040624
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_001145852	6	24	3	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_001145852	6	24	3	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_001145852	6	24	4	-	16026815	16026935

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_001145852	6	24	5	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_001145852	6	24	6	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_001145852	6	24	7	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_001145852	6	24	7	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_001145852	6	24	8	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_001145852	6	24	9	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_001145852	6	24	10	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_001145852	6	24	10	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_001145852	6	24	11	-	16008161	16008313
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_001145852	6	24	12	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_001145852	6	24	12	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_001145852	6	24	13	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_001145852	6	24	13	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_001145852	6	24	14	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_001145852	6	24	15	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_001145852	6	24	15	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_001145852	6	24	16	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_001145852	6	24	17	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_001145852	6	24	18	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_001145852	6	24	19	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_001145852	6	24	20	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_001145852	6	24	21	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_001145852	6	24	22	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_001145852	6	24	22	-	15982045	15982160
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_001145852	6	24	23	-	15972666	15972705
320879421	chr4	16077177	16077395	16077200	16077373	PROM1	NM_006017	7	27	1	-	16077310	16077741
320897773	chr4	16077346	16077570	16077374	16077546	PROM1	NM_006017	7	27	1	-	16077310	16077741
318734378	chr4	16040579	16040800	16040610	16040772	PROM1	NM_006017	7	27	2	-	16040569	16040624
319847665	chr4	16037243	16037412	16037271	16037390	PROM1	NM_006017	7	27	3	-	16037358	16037384
318526120	chr4	16034868	16035055	16034893	16035026	PROM1	NM_006017	7	27	4	-	16034927	16035132
318537329	chr4	16035004	16035172	16035027	16035144	PROM1	NM_006017	7	27	4	-	16034927	16035132
319961499	chr4	16026770	16026966	16026796	16026941	PROM1	NM_006017	7	27	5	-	16026815	16026935
321302139	chr4	16025787	16026011	16025811	16025986	PROM1	NM_006017	7	27	6	-	16025918	16025981
319611118	chr4	16024854	16025070	16024875	16025045	PROM1	NM_006017	7	27	7	-	16024949	16025038
320764309	chr4	16019830	16020027	16019852	16020005	PROM1	NM_006017	7	27	8	-	16019946	16020163
320803977	chr4	16019984	16020204	16020006	16020181	PROM1	NM_006017	7	27	8	-	16019946	16020163
319202196	chr4	16017654	16017866	16017680	16017848	PROM1	NM_006017	7	27	9	-	16017789	16017863
321277528	chr4	16014821	16015044	16014845	16015017	PROM1	NM_006017	7	27	10	-	16014898	16014961
318025165	chr4	16010442	16010613	16010467	16010584	PROM1	NM_006017	7	27	11	-	16010572	16010731
318043211	chr4	16010559	16010772	16010585	16010744	PROM1	NM_006017	7	27	11	-	16010572	16010731
319855306	chr4	16008124	16008345	16008144	16008319	PROM1	NM_006017	7	27	12	-	16008161	16008313

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
320227876	chr4	16002017	16002167	16002042	16002142	PROM1	NM_006017	7	27	13	-	16002119	16002242
320235247	chr4	16002119	16002342	16002143	16002314	PROM1	NM_006017	7	27	13	-	16002119	16002242
321239138	chr4	15999882	16000100	15999908	16000073	PROM1	NM_006017	7	27	14	-	16000008	16000111
321240057	chr4	16000059	16000256	16000087	16000225	PROM1	NM_006017	7	27	14	-	16000008	16000111
318304844	chr4	15995546	15995739	15995573	15995712	PROM1	NM_006017	7	27	15	-	15995610	15995694
318037170	chr4	15993801	15993925	15993828	15993900	PROM1	NM_006017	7	27	16	-	15993871	15994014
318050204	chr4	15993873	15994076	15993901	15994051	PROM1	NM_006017	7	27	16	-	15993871	15994014
318153174	chr4	15992767	15992980	15992789	15992952	PROM1	NM_006017	7	27	17	-	15992845	15992916
320280678	chr4	15991275	15991499	15991298	15991471	PROM1	NM_006017	7	27	18	-	15991355	15991447
318758766	chr4	15989215	15989400	15989240	15989375	PROM1	NM_006017	7	27	19	-	15989286	15989339
320693421	chr4	15987521	15987687	15987546	15987665	PROM1	NM_006017	7	27	20	-	15987580	15987660
319401936	chr4	15987319	15987498	15987345	15987469	PROM1	NM_006017	7	27	21	-	15987383	15987451
318984015	chr4	15985832	15986040	15985860	15986014	PROM1	NM_006017	7	27	22	-	15985886	15985978
318354462	chr4	15981958	15982150	15981985	15982125	PROM1	NM_006017	7	27	23	-	15982045	15982160
318361107	chr4	15982098	15982316	15982126	15982288	PROM1	NM_006017	7	27	23	-	15982045	15982160
320321779	chr4	15981373	15981597	15981396	15981569	PROM1	NM_006017	7	27	24	-	15981504	15981527
320313515	chr4	15980993	15981133	15981016	15981102	PROM1	NM_006017	7	27	25	-	15981018	15981086
318022765	chr4	15972552	15972762	15972579	15972741	PROM1	NM_006017	7	27	26	-	15972666	15972705
319404570	chr19	54621767	54621941	54621790	54621918	PRPF31	NM_015629	1	14	2	+	54621651	54621835
320974199	chr19	54621617	54621817	54621640	54621796	PRPF31	NM_015629	1	14	2	+	54621651	54621835
319411377	chr19	54621892	54622108	54621915	54622084	PRPF31	NM_015629	1	14	3	+	54621953	54622013
320003837	chr19	54625101	54625314	54625122	54625293	PRPF31	NM_015629	1	14	4	+	54625239	54625322
320024696	chr19	54625274	54625435	54625294	54625414	PRPF31	NM_015629	1	14	4	+	54625239	54625322
319435806	chr19	54625849	54625974	54625870	54625953	PRPF31	NM_015629	1	14	5	+	54625876	54625973
319447212	chr19	54625928	54626080	54625948	54626059	PRPF31	NM_015629	1	14	5	+	54625876	54625973
318299565	chr19	54626769	54626993	54626790	54626971	PRPF31	NM_015629	1	14	6	+	54626833	54626939
319635440	chr19	54626982	54627206	54627002	54627188	PRPF31	NM_015629	1	14	7	+	54627128	54627297
319640980	chr19	54627164	54627384	54627181	54627360	PRPF31	NM_015629	1	14	7	+	54627128	54627297
318629426	chr19	54627823	54628008	54627845	54627987	PRPF31	NM_015629	1	14	8	+	54627878	54628035
318633785	chr19	54627955	54628150	54627974	54628131	PRPF31	NM_015629	1	14	8	+	54627878	54628035
320186403	chr19	54629850	54630074	54629872	54630056	PRPF31	NM_015629	1	14	9	+	54629903	54629992
318626197	chr19	54631541	54631763	54631561	54631743	PRPF31	NM_015629	1	14	10	+	54631448	54631575
319384802	chr19	54631439	54631627	54631456	54631608	PRPF31	NM_015629	1	14	10	+	54631448	54631575
318626197	chr19	54631541	54631763	54631561	54631743	PRPF31	NM_015629	1	14	11	+	54631680	54631752
318627342	chr19	54631724	54631919	54631743	54631898	PRPF31	NM_015629	1	14	11	+	54631680	54631752
319123277	chr19	54632390	54632575	54632407	54632557	PRPF31	NM_015629	1	14	12	+	54632432	54632560
319127177	chr19	54632532	54632754	54632551	54632736	PRPF31	NM_015629	1	14	12	+	54632432	54632560
319127177	chr19	54632532	54632754	54632551	54632736	PRPF31	NM_015629	1	14	13	+	54632647	54632745
321180560	chr19	54632719	54632935	54632736	54632918	PRPF31	NM_015629	1	14	13	+	54632647	54632745
319405720	chr19	54634691	54634913	54634713	54634892	PRPF31	NM_015629	1	14	14	+	54634738	54635150
318753060	chr17	1587637	1587849	1587665	1587829	PRPF8	NM_006445	1	43	2	-	1587766	1587876

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
318761886	chr17	1587785	1587919	1587806	1587897	PRPF8	NM_006445	1	43	2	-	1587766	1587876
318064126	chr17	1586653	1586854	1586675	1586833	PRPF8	NM_006445	1	43	3	-	1586827	1586995
318091399	chr17	1586811	1587022	1586834	1587000	PRPF8	NM_006445	1	43	3	-	1586827	1586995
318202874	chr17	1585266	1585472	1585286	1585449	PRPF8	NM_006445	1	43	4	-	1585423	1585587
318239298	chr17	1585427	1585627	1585450	1585599	PRPF8	NM_006445	1	43	4	-	1585423	1585587
318202874	chr17	1585266	1585472	1585286	1585449	PRPF8	NM_006445	1	43	5	-	1585114	1585332
320003570	chr17	1585020	1585243	1585044	1585219	PRPF8	NM_006445	1	43	5	-	1585114	1585332
320043137	chr17	1585199	1585362	1585220	1585338	PRPF8	NM_006445	1	43	5	-	1585114	1585332
319687694	chr17	1584666	1584853	1584693	1584830	PRPF8	NM_006445	1	43	6	-	1584772	1584984
319708397	chr17	1584810	1585014	1584831	1584991	PRPF8	NM_006445	1	43	6	-	1584772	1584984
319480291	chr17	1584170	1584378	1584192	1584351	PRPF8	NM_006445	1	43	7	-	1584223	1584348
319082608	chr17	1583932	1584155	1583952	1584130	PRPF8	NM_006445	1	43	8	-	1584020	1584125
320271054	chr17	1582827	1583029	1582848	1583005	PRPF8	NM_006445	1	43	9	-	1582903	1583093
320290333	chr17	1582984	1583126	1583006	1583102	PRPF8	NM_006445	1	43	9	-	1582903	1583093
319948837	chr17	1582512	1582732	1582535	1582709	PRPF8	NM_006445	1	43	10	-	1582585	1582704
318078023	chr17	1582140	1582353	1582162	1582329	PRPF8	NM_006445	1	43	11	-	1582311	1582500
318315422	chr17	1582310	1582530	1582330	1582506	PRPF8	NM_006445	1	43	11	-	1582311	1582500
318030160	chr17	1581907	1582119	1581932	1582095	PRPF8	NM_006445	1	43	12	-	1582056	1582175
318060725	chr17	1582077	1582230	1582096	1582207	PRPF8	NM_006445	1	43	12	-	1582056	1582175
318078023	chr17	1582140	1582353	1582162	1582329	PRPF8	NM_006445	1	43	12	-	1582056	1582175
318030160	chr17	1581907	1582119	1581932	1582095	PRPF8	NM_006445	1	43	13	-	1581812	1581946
321438788	chr17	1581784	1581909	1581812	1581889	PRPF8	NM_006445	1	43	13	-	1581812	1581946
321452339	chr17	1581863	1582065	1581889	1582040	PRPF8	NM_006445	1	43	13	-	1581812	1581946
318234482	chr17	1580698	1580922	1580726	1580901	PRPF8	NM_006445	1	43	14	-	1580859	1580988
318248551	chr17	1580882	1581059	1580902	1581032	PRPF8	NM_006445	1	43	14	-	1580859	1580988
318055494	chr17	1580179	1580390	1580199	1580365	PRPF8	NM_006445	1	43	15	-	1580270	1580466
318086271	chr17	1580345	1580495	1580366	1580471	PRPF8	NM_006445	1	43	15	-	1580270	1580466
318827300	chr17	1579675	1579893	1579698	1579871	PRPF8	NM_006445	1	43	16	-	1579799	1580005
318860805	chr17	1579851	1580035	1579872	1580012	PRPF8	NM_006445	1	43	16	-	1579799	1580005
320351029	chr17	1579471	1579692	1579495	1579669	PRPF8	NM_006445	1	43	17	-	1579501	1579664
320895759	chr17	1579156	1579376	1579178	1579353	PRPF8	NM_006445	1	43	18	-	1579222	1579348
318407716	chr17	1578809	1579027	1578833	1579005	PRPF8	NM_006445	1	43	19	-	1578914	1579106
318457206	chr17	1578987	1579147	1579006	1579125	PRPF8	NM_006445	1	43	19	-	1578914	1579106
321484757	chr17	1578369	1578502	1578393	1578480	PRPF8	NM_006445	1	43	20	-	1578446	1578633
321510429	chr17	1578460	1578673	1578481	1578650	PRPF8	NM_006445	1	43	20	-	1578446	1578633
321598982	chr17	1577634	1577842	1577656	1577818	PRPF8	NM_006445	1	43	21	-	1577736	1577974
321626283	chr17	1577797	1578018	1577819	1577997	PRPF8	NM_006445	1	43	21	-	1577736	1577974
319188277	chr17	1576989	1577213	1577010	1577192	PRPF8	NM_006445	1	43	22	-	1577040	1577186
319134033	chr17	1576504	1576715	1576528	1576695	PRPF8	NM_006445	1	43	23	-	1576651	1576861
319164898	chr17	1576675	1576889	1576696	1576867	PRPF8	NM_006445	1	43	23	-	1576651	1576861
321286193	chr17	1576312	1576522	1576333	1576497	PRPF8	NM_006445	1	43	24	-	1576375	1576491

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
319867433	chr17	1565148	1565333	1565169	1565307	PRPF8	NM_006445	1	43	25	-	1565200	1565447
319898707	chr17	1565288	1565491	1565308	1565463	PRPF8	NM_006445	1	43	25	-	1565200	1565447
318058943	chr17	1564797	1565006	1564820	1564984	PRPF8	NM_006445	1	43	26	-	1564905	1565084
318085370	chr17	1564962	1565172	1564985	1565151	PRPF8	NM_006445	1	43	26	-	1564905	1565084
318320195	chr17	1564540	1564745	1564565	1564717	PRPF8	NM_006445	1	43	27	-	1564565	1564700
318692467	chr17	1564130	1564333	1564152	1564308	PRPF8	NM_006445	1	43	28	-	1564287	1564456
318727677	chr17	1564289	1564500	1564309	1564478	PRPF8	NM_006445	1	43	28	-	1564287	1564456
318741462	chr17	1564369	1564592	1564394	1564564	PRPF8	NM_006445	1	43	28	-	1564287	1564456
319231566	chr17	1563938	1564154	1563959	1564130	PRPF8	NM_006445	1	43	29	-	1563992	1564121
319982261	chr17	1563652	1563790	1563673	1563769	PRPF8	NM_006445	1	43	30	-	1563726	1563872
320002099	chr17	1563748	1563916	1563770	1563889	PRPF8	NM_006445	1	43	30	-	1563726	1563872
318387000	chr17	1562980	1563200	1563004	1563177	PRPF8	NM_006445	1	43	31	-	1563135	1563295
318429298	chr17	1563157	1563336	1563178	1563308	PRPF8	NM_006445	1	43	31	-	1563135	1563295
318126732	chr17	1562614	1562746	1562637	1562725	PRPF8	NM_006445	1	43	32	-	1562651	1562842
318133270	chr17	1562701	1562924	1562725	1562898	PRPF8	NM_006445	1	43	32	-	1562651	1562842
320994062	chr17	1561696	1561920	1561718	1561893	PRPF8	NM_006445	1	43	33	-	1561820	1562057
321036026	chr17	1561873	1562095	1561894	1562067	PRPF8	NM_006445	1	43	33	-	1561820	1562057
318708359	chr17	1561491	1561713	1561515	1561690	PRPF8	NM_006445	1	43	34	-	1561547	1561675
318404636	chr17	1559885	1560109	1559908	1560082	PRPF8	NM_006445	1	43	35	-	1559942	1560055
318161567	chr17	1559512	1559716	1559533	1559691	PRPF8	NM_006445	1	43	36	-	1559686	1559859
318192843	chr17	1559671	1559891	1559692	1559864	PRPF8	NM_006445	1	43	36	-	1559686	1559859
318562222	chr17	1558545	1558690	1558569	1558668	PRPF8	NM_006445	1	43	37	-	1558644	1558837
318580060	chr17	1558648	1558868	1558669	1558844	PRPF8	NM_006445	1	43	37	-	1558644	1558837
319463310	chr17	1557008	1557223	1557028	1557202	PRPF8	NM_006445	1	43	38	-	1557071	1557310
319487133	chr17	1557183	1557345	1557203	1557318	PRPF8	NM_006445	1	43	38	-	1557071	1557310
318902701	chr17	1556810	1557010	1556830	1556991	PRPF8	NM_006445	1	43	39	-	1556836	1556977
320304743	chr17	1554889	1555113	1554909	1555091	PRPF8	NM_006445	1	43	40	-	1554942	1555082
318250571	chr17	1554514	1554737	1554536	1554713	PRPF8	NM_006445	1	43	41	-	1554708	1554847
318258992	chr17	1554672	1554878	1554693	1554852	PRPF8	NM_006445	1	43	41	-	1554708	1554847
318250571	chr17	1554514	1554737	1554536	1554713	PRPF8	NM_006445	1	43	42	-	1554402	1554604
319579861	chr17	1554344	1554563	1554366	1554544	PRPF8	NM_006445	1	43	42	-	1554402	1554604
318549845	chr17	1554005	1554227	1554027	1554204	PRPF8	NM_006445	1	43	43	-	1553923	1554250
318561205	chr17	1554180	1554367	1554203	1554345	PRPF8	NM_006445	1	43	43	-	1553923	1554250
325403774	chr6	42689892	42690097	42689919	42690077	PRPH2	NM_000322	1	3	1	-	42689492	42690358
325417354	chr6	42689433	42689618	42689456	42689595	PRPH2	NM_000322	1	3	1	-	42689492	42690358
325460483	chr6	42689574	42689774	42689596	42689750	PRPH2	NM_000322	1	3	1	-	42689492	42690358
325482640	chr6	42689727	42689938	42689751	42689918	PRPH2	NM_000322	1	3	1	-	42689492	42690358
324833544	chr6	42672033	42672252	42672054	42672230	PRPH2	NM_000322	1	3	2	-	42672103	42672349
324848408	chr6	42672211	42672379	42672231	42672357	PRPH2	NM_000322	1	3	2	-	42672103	42672349
325024465	chr6	42665974	42666187	42665997	42666166	PRPH2	NM_000322	1	3	3	-	42664333	42666245
325036814	chr6	42666098	42666318	42666122	42666295	PRPH2	NM_000322	1	3	3	-	42664333	42666245

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324531519	chr14	73614640	73614845	73614667	73614822	PSEN1	NM_000021	1	12	3	+	73614675	73614814
324543160	chr14	73637428	73637651	73637453	73637626	PSEN1	NM_000021	1	12	4	+	73637505	73637755
324552404	chr14	73637604	73637797	73637627	73637768	PSEN1	NM_000021	1	12	4	+	73637505	73637755
324536536	chr14	73640223	73640446	73640247	73640422	PSEN1	NM_000021	1	12	5	+	73640274	73640415
324104216	chr14	73653505	73653699	73653530	73653671	PSEN1	NM_000021	1	12	6	+	73653561	73653628
323640633	chr14	73659352	73659479	73659380	73659458	PSEN1	NM_000021	1	12	7	+	73659352	73659572
323655327	chr14	73659437	73659613	73659459	73659586	PSEN1	NM_000021	1	12	7	+	73659352	73659572
325942186	chr14	73664574	73664783	73664596	73664760	PSEN1	NM_000021	1	12	8	+	73664739	73664837
325954430	chr14	73664734	73664899	73664761	73664872	PSEN1	NM_000021	1	12	8	+	73664739	73664837
325618738	chr14	73672970	73673146	73672994	73673127	PSEN1	NM_000021	1	12	9	+	73673094	73673180
324102386	chr14	73678348	73678525	73678370	73678503	PSEN1	NM_000021	1	12	10	+	73678477	73678650
324123059	chr14	73678481	73678689	73678504	73678662	PSEN1	NM_000021	1	12	10	+	73678477	73678650
323316524	chr14	73683776	73684000	73683802	73683972	PSEN1	NM_000021	1	12	11	+	73683834	73683952
325480146	chr14	73685809	73686033	73685833	73686006	PSEN1	NM_000021	1	12	12	+	73685842	73690399
324531519	chr14	73614640	73614845	73614667	73614822	PSEN1	NM_007318	2	12	3	+	73614675	73614802
324543160	chr14	73637428	73637651	73637453	73637626	PSEN1	NM_007318	2	12	4	+	73637505	73637755
324552404	chr14	73637604	73637797	73637627	73637768	PSEN1	NM_007318	2	12	4	+	73637505	73637755
324536536	chr14	73640223	73640446	73640247	73640422	PSEN1	NM_007318	2	12	5	+	73640274	73640415
324104216	chr14	73653505	73653699	73653530	73653671	PSEN1	NM_007318	2	12	6	+	73653561	73653628
323640633	chr14	73659352	73659479	73659380	73659458	PSEN1	NM_007318	2	12	7	+	73659352	73659572
323655327	chr14	73659437	73659613	73659459	73659586	PSEN1	NM_007318	2	12	7	+	73659352	73659572
325942186	chr14	73664574	73664783	73664596	73664760	PSEN1	NM_007318	2	12	8	+	73664739	73664837
325954430	chr14	73664734	73664899	73664761	73664872	PSEN1	NM_007318	2	12	8	+	73664739	73664837
325618738	chr14	73672970	73673146	73672994	73673127	PSEN1	NM_007318	2	12	9	+	73673094	73673180
324102386	chr14	73678348	73678525	73678370	73678503	PSEN1	NM_007318	2	12	10	+	73678477	73678650
324123059	chr14	73678481	73678689	73678504	73678662	PSEN1	NM_007318	2	12	10	+	73678477	73678650
323316524	chr14	73683776	73684000	73683802	73683972	PSEN1	NM_007318	2	12	11	+	73683834	73683952
325480146	chr14	73685809	73686033	73685833	73686006	PSEN1	NM_007318	2	12	12	+	73685842	73690399
325623944	chr1	227069447	227069671	227069471	227069651	PSEN2	NM_000447	1	13	4	+	227069589	227069749
325643792	chr1	227069631	227069841	227069652	227069819	PSEN2	NM_000447	1	13	4	+	227069589	227069749
323878149	chr1	227071325	227071547	227071348	227071525	PSEN2	NM_000447	1	13	5	+	227071406	227071620
323884687	chr1	227071504	227071716	227071525	227071696	PSEN2	NM_000447	1	13	5	+	227071406	227071620
324573198	chr1	227073152	227073357	227073173	227073335	PSEN2	NM_000447	1	13	6	+	227073239	227073380
324586918	chr1	227073315	227073472	227073336	227073448	PSEN2	NM_000447	1	13	6	+	227073239	227073380
324264567	chr1	227075675	227075886	227075701	227075865	PSEN2	NM_000447	1	13	7	+	227075792	227075859
323386818	chr1	227076474	227076697	227076496	227076674	PSEN2	NM_000447	1	13	8	+	227076530	227076750
323407119	chr1	227076648	227076865	227076671	227076844	PSEN2	NM_000447	1	13	8	+	227076530	227076750
325321514	chr1	227077587	227077806	227077613	227077784	PSEN2	NM_000447	1	13	9	+	227077736	227077834
325332437	chr1	227077764	227077940	227077785	227077918	PSEN2	NM_000447	1	13	9	+	227077736	227077834
325827373	chr1	227078945	227079089	227078966	227079067	PSEN2	NM_000447	1	13	10	+	227078979	227079062
324177899	chr1	227079357	227079510	227079378	227079489	PSEN2	NM_000447	1	13	11	+	227079444	227079545

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324192191	chr1	227079470	227079674	227079490	227079652	PSEN2	NM_000447	1	13	11	+	227079444	227079545
324176086	chr1	227081630	227081854	227081652	227081837	PSEN2	NM_000447	1	13	12	+	227081708	227081826
324399568	chr1	227083013	227083231	227083034	227083207	PSEN2	NM_000447	1	13	13	+	227083125	227083804
324426887	chr1	227083189	227083327	227083208	227083303	PSEN2	NM_000447	1	13	13	+	227083125	227083804
325623944	chr1	227069447	227069671	227069471	227069651	PSEN2	NM_012486	2	13	4	+	227069589	227069749
325643792	chr1	227069631	227069841	227069652	227069819	PSEN2	NM_012486	2	13	4	+	227069589	227069749
323878149	chr1	227071325	227071547	227071348	227071525	PSEN2	NM_012486	2	13	5	+	227071406	227071620
323884687	chr1	227071504	227071716	227071525	227071696	PSEN2	NM_012486	2	13	5	+	227071406	227071620
324573198	chr1	227073152	227073357	227073173	227073335	PSEN2	NM_012486	2	13	6	+	227073239	227073380
324586918	chr1	227073315	227073472	227073336	227073448	PSEN2	NM_012486	2	13	6	+	227073239	227073380
324264567	chr1	227075675	227075886	227075701	227075865	PSEN2	NM_012486	2	13	7	+	227075792	227075859
323386818	chr1	227076474	227076697	227076496	227076674	PSEN2	NM_012486	2	13	8	+	227076530	227076750
323407119	chr1	227076648	227076865	227076671	227076844	PSEN2	NM_012486	2	13	8	+	227076530	227076750
325321514	chr1	227077587	227077806	227077613	227077784	PSEN2	NM_012486	2	13	9	+	227077736	227077834
325332437	chr1	227077764	227077940	227077785	227077918	PSEN2	NM_012486	2	13	9	+	227077736	227077834
325827373	chr1	227078945	227079089	227078966	227079067	PSEN2	NM_012486	2	13	10	+	227078979	227079062
324177899	chr1	227079357	227079510	227079378	227079489	PSEN2	NM_012486	2	13	11	+	227079447	227079545
324192191	chr1	227079470	227079674	227079490	227079652	PSEN2	NM_012486	2	13	11	+	227079447	227079545
324176086	chr1	227081630	227081854	227081652	227081837	PSEN2	NM_012486	2	13	12	+	227081708	227081826
324399568	chr1	227083013	227083231	227083034	227083207	PSEN2	NM_012486	2	13	13	+	227083125	227083804
324426887	chr1	227083189	227083327	227083208	227083303	PSEN2	NM_012486	2	13	13	+	227083125	227083804
235585662	chr9	98270413	98270594	98270436	98270577	PTCH1	NM_000264	1	24	1	-	98270443	98270831
235586852	chr9	98270486	98270643	98270504	98270625	PTCH1	NM_000264	1	24	1	-	98270443	98270831
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_000264	1	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_000264	1	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_000264	1	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_000264	1	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_000264	1	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_000264	1	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_000264	1	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_000264	1	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_000264	1	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_000264	1	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_000264	1	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_000264	1	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_000264	1	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_000264	1	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_000264	1	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_000264	1	24	14	-	98231033	98231435

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_000264	1	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_000264	1	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_000264	1	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_000264	1	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_000264	1	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_000264	1	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_000264	1	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_000264	1	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_000264	1	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_000264	1	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_000264	1	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_000264	1	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_000264	1	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_000264	1	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_000264	1	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237339958	chr9	98278866	98279086	98278886	98279061	PTCH1	NM_001083602	2	24	1	-	98278751	98279247
237350243	chr9	98278992	98279216	98279019	98279190	PTCH1	NM_001083602	2	24	1	-	98278751	98279247
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083602	2	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083602	2	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083602	2	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083602	2	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083602	2	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083602	2	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083602	2	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083602	2	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083602	2	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083602	2	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083602	2	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083602	2	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083602	2	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083602	2	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083602	2	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083602	2	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083602	2	24	15	-	98229398	98229707

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083602	2	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083602	2	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083602	2	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083602	2	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083602	2	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083602	2	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083602	2	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083602	2	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083602	2	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083602	2	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083602	2	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083602	2	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083602	2	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237339958	chr9	98278866	98279086	98278886	98279061	PTCH1	NM_001083603	3	24	1	-	98278905	98279247
237350243	chr9	98278992	98279216	98279019	98279190	PTCH1	NM_001083603	3	24	1	-	98278905	98279247
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083603	3	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083603	3	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083603	3	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083603	3	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083603	3	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083603	3	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083603	3	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083603	3	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083603	3	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083603	3	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083603	3	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083603	3	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083603	3	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083603	3	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083603	3	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083603	3	24	16	-	98224138	98224280

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083603	3	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083603	3	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083603	3	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083603	3	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083603	3	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083603	3	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083603	3	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083603	3	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083603	3	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083603	3	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083603	3	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083604	4	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083604	4	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083604	4	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083604	4	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083604	4	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083604	4	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083604	4	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083604	4	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083604	4	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083604	4	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083604	4	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083604	4	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083604	4	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083604	4	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083604	4	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083604	4	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083604	4	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083604	4	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083604	4	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083604	4	24	18	-	98220295	98220575

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083604	4	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083604	4	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083604	4	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083604	4	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083604	4	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083604	4	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083604	4	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083605	5	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083605	5	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083605	5	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083605	5	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083605	5	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083605	5	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083605	5	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083605	5	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083605	5	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083605	5	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083605	5	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083605	5	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083605	5	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083605	5	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083605	5	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083605	5	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083605	5	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083605	5	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083605	5	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083605	5	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083605	5	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083605	5	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083605	5	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083605	5	24	20	-	98215760	98215902

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083605	5	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083605	5	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083605	5	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083606	6	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083606	6	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083606	6	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083606	6	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083606	6	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083606	6	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083606	6	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083606	6	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083606	6	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083606	6	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083606	6	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083606	6	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083606	6	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083606	6	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083606	6	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083606	6	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083606	6	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083606	6	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083606	6	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083606	6	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083606	6	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083606	6	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083606	6	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083606	6	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083606	6	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083606	6	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083606	6	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083606	6	24	23	-	98209193	98209733

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083607	7	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083607	7	24	2	-	98268689	98268881
236992287	chr9	98247843	98248055	98247869	98248033	PTCH1	NM_001083607	7	24	3	-	98247967	98248156
237018918	chr9	98248014	98248209	98248034	98248181	PTCH1	NM_001083607	7	24	3	-	98247967	98248156
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083607	7	24	4	-	98244416	98244485
235564482	chr9	98244143	98244361	98244172	98244339	PTCH1	NM_001083607	7	24	5	-	98244231	98244322
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083607	7	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083607	7	24	6	-	98242672	98242870
237864243	chr9	98242202	98242422	98242227	98242395	PTCH1	NM_001083607	7	24	7	-	98242251	98242372
237010380	chr9	98241254	98241478	98241272	98241454	PTCH1	NM_001083607	7	24	8	-	98241282	98241429
236664964	chr9	98240282	98240496	98240308	98240474	PTCH1	NM_001083607	7	24	9	-	98240337	98240468
235832485	chr9	98239789	98240012	98239811	98239992	PTCH1	NM_001083607	7	24	10	-	98239829	98239984
237901478	chr9	98238950	98239174	98238976	98239151	PTCH1	NM_001083607	7	24	11	-	98239041	98239139
237667013	chr9	98238289	98238483	98238310	98238463	PTCH1	NM_001083607	7	24	12	-	98238316	98238441
237942590	chr9	98232030	98232251	98232054	98232226	PTCH1	NM_001083607	7	24	13	-	98232095	98232213
235315358	chr9	98230952	98231164	98230980	98231145	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235328531	chr9	98231123	98231336	98231142	98231315	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235339049	chr9	98231296	98231475	98231316	98231447	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235661651	chr9	98229309	98229475	98229337	98229447	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
235686237	chr9	98229425	98229625	98229448	98229604	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
235708085	chr9	98229578	98229733	98229605	98229712	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
236779679	chr9	98224026	98224236	98224047	98224208	PTCH1	NM_001083607	7	24	16	-	98224138	98224280
236794396	chr9	98224188	98224321	98224209	98224293	PTCH1	NM_001083607	7	24	16	-	98224138	98224280
236304261	chr9	98221787	98221916	98221806	98221895	PTCH1	NM_001083607	7	24	17	-	98221882	98222065
236320880	chr9	98221872	98222091	98221896	98222070	PTCH1	NM_001083607	7	24	17	-	98221882	98222065
234949708	chr9	98220260	98220484	98220284	98220462	PTCH1	NM_001083607	7	24	18	-	98220295	98220575
234957680	chr9	98220444	98220602	98220463	98220581	PTCH1	NM_001083607	7	24	18	-	98220295	98220575
236557004	chr9	98218462	98218615	98218483	98218594	PTCH1	NM_001083607	7	24	19	-	98218558	98218695
236582605	chr9	98218574	98218795	98218595	98218772	PTCH1	NM_001083607	7	24	19	-	98218558	98218695
239396236	chr9	98215721	98215936	98215749	98215912	PTCH1	NM_001083607	7	24	20	-	98215760	98215902
235857677	chr9	98212032	98212250	98212053	98212227	PTCH1	NM_001083607	7	24	21	-	98212123	98212222
235184774	chr9	98211301	98211506	98211321	98211486	PTCH1	NM_001083607	7	24	22	-	98211351	98211605
235195980	chr9	98211463	98211653	98211487	98211625	PTCH1	NM_001083607	7	24	22	-	98211351	98211605
237357245	chr9	98209127	98209274	98209150	98209253	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237365822	chr9	98209232	98209451	98209251	98209433	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237371796	chr9	98209415	98209584	98209434	98209562	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237376621	chr9	98209542	98209763	98209563	98209743	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
239363589	chr12	112856739	112856935	112856756	112856918	PTPN11	NM_002834	1	16	1	+	112856536	112856929

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236445412	chr12	112884011	112884233	112884035	112884207	PTPN11	NM_002834	1	16	2	+	112884080	112884202
235863556	chr12	112888004	112888177	112888028	112888149	PTPN11	NM_002834	1	16	3	+	112888122	112888316
326782141	chr12	112888129	112888351	112888150	112888324	PTPN11	NM_002834	1	16	3	+	112888122	112888316
235141692	chr12	112890936	112891146	112890963	112891125	PTPN11	NM_002834	1	16	4	+	112890999	112891191
235156587	chr12	112891102	112891227	112891126	112891203	PTPN11	NM_002834	1	16	4	+	112890999	112891191
235035551	chr12	112892359	112892509	112892386	112892487	PTPN11	NM_002834	1	16	5	+	112892368	112892484
241315625	chr12	112893628	112893783	112893649	112893759	PTPN11	NM_002834	1	16	6	+	112893754	112893867
241322262	chr12	112893740	112893937	112893760	112893910	PTPN11	NM_002834	1	16	6	+	112893754	112893867
237505086	chr12	112910667	112910882	112910692	112910854	PTPN11	NM_002834	1	16	7	+	112910748	112910844
236206807	chr12	112915353	112915566	112915379	112915540	PTPN11	NM_002834	1	16	8	+	112915455	112915534
235517465	chr12	112915539	112915713	112915563	112915685	PTPN11	NM_002834	1	16	9	+	112915661	112915819
235527038	chr12	112915661	112915883	112915686	112915855	PTPN11	NM_002834	1	16	9	+	112915661	112915819
240073649	chr12	112919759	112919914	112919781	112919890	PTPN11	NM_002834	1	16	10	+	112919878	112920009
240092527	chr12	112919863	112920045	112919891	112920017	PTPN11	NM_002834	1	16	10	+	112919878	112920009
237934046	chr12	112924184	112924408	112924211	112924387	PTPN11	NM_002834	1	16	11	+	112924279	112924433
237941495	chr12	112924368	112924512	112924388	112924490	PTPN11	NM_002834	1	16	11	+	112924279	112924433
235678543	chr12	112926140	112926339	112926167	112926319	PTPN11	NM_002834	1	16	12	+	112926247	112926314
238240105	chr12	112926726	112926853	112926754	112926830	PTPN11	NM_002834	1	16	13	+	112926828	112926979
326872652	chr12	112926805	112927028	112926831	112927005	PTPN11	NM_002834	1	16	13	+	112926828	112926979
237759649	chr12	112939898	112940101	112939924	112940073	PTPN11	NM_002834	1	16	14	+	112939948	112940060
236449885	chr12	112942436	112942627	112942461	112942598	PTPN11	NM_002834	1	16	15	+	112942499	112942600
236777816	chr3	12659930	12660146	12659957	12660122	RAF1	NM_002880	1	17	2	-	12660014	12660246
236801214	chr3	12660102	12660304	12660123	12660276	RAF1	NM_002880	1	17	2	-	12660014	12660246
236455510	chr3	12653394	12653540	12653424	12653517	RAF1	NM_002880	1	17	3	-	12653449	12653561
236472540	chr3	12653462	12653667	12653484	12653646	RAF1	NM_002880	1	17	3	-	12653449	12653561
236823376	chr3	12650667	12650830	12650691	12650804	RAF1	NM_002880	1	17	4	-	12650732	12650834
235612037	chr3	12650164	12650315	12650189	12650289	RAF1	NM_002880	1	17	5	-	12650265	12650422
235627741	chr3	12650264	12650455	12650290	12650427	RAF1	NM_002880	1	17	5	-	12650265	12650422
237933606	chr3	12647602	12647737	12647625	12647717	RAF1	NM_002880	1	17	6	-	12647700	12647798
237940579	chr3	12647691	12647853	12647718	12647825	RAF1	NM_002880	1	17	6	-	12647700	12647798
234916217	chr3	12645569	12645705	12645597	12645685	RAF1	NM_002880	1	17	7	-	12645635	12645788
234934226	chr3	12645665	12645820	12645686	12645793	RAF1	NM_002880	1	17	7	-	12645635	12645788
235212165	chr3	12641765	12641943	12641787	12641919	RAF1	NM_002880	1	17	8	-	12641887	12641914
237416684	chr3	12641594	12641808	12641621	12641785	RAF1	NM_002880	1	17	9	-	12641651	12641778
236155884	chr3	12641083	12641226	12641104	12641199	RAF1	NM_002880	1	17	10	-	12641190	12641307
236167121	chr3	12641180	12641384	12641200	12641358	RAF1	NM_002880	1	17	10	-	12641190	12641307
235587751	chr3	12633122	12633322	12633141	12633298	RAF1	NM_002880	1	17	11	-	12633207	12633291
235042201	chr3	12632199	12632359	12632224	12632334	RAF1	NM_002880	1	17	12	-	12632297	12632473
235049836	chr3	12632314	12632531	12632335	12632509	RAF1	NM_002880	1	17	12	-	12632297	12632473
237170982	chr3	12628964	12629188	12628989	12629160	RAF1	NM_002880	1	17	13	-	12629090	12629136
237668851	chr3	12627107	12627328	12627131	12627303	RAF1	NM_002880	1	17	14	-	12627180	12627298

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235602534	chr3	12626587	12626791	12626606	12626763	RAF1	NM_002880	1	17	15	-	12626621	12626752
236239648	chr3	12626289	12626512	12626311	12626487	RAF1	NM_002880	1	17	16	-	12626346	12626480
235224752	chr3	12626003	12626216	12626027	12626192	RAF1	NM_002880	1	17	17	-	12625100	12626156
238438627	chr3	12625840	12626063	12625867	12626040	RAF1	NM_002880	1	17	17	-	12625100	12626156
332416328	chr11	36595321	36595536	36595343	36595513	RAG1	NM_000448	1	2	2	+	36594841	36601310
332436734	chr11	36595481	36595693	36595503	36595668	RAG1	NM_000448	1	2	2	+	36594841	36601310
332443457	chr11	36596285	36596480	36596306	36596458	RAG1	NM_000448	1	2	2	+	36594841	36601310
332456629	chr11	36595646	36595828	36595669	36595805	RAG1	NM_000448	1	2	2	+	36594841	36601310
332465779	chr11	36596436	36596591	36596459	36596566	RAG1	NM_000448	1	2	2	+	36594841	36601310
332491467	chr11	36596544	36596768	36596567	36596742	RAG1	NM_000448	1	2	2	+	36594841	36601310
332529902	chr11	36596718	36596942	36596743	36596921	RAG1	NM_000448	1	2	2	+	36594841	36601310
333436022	chr11	36594820	36595023	36594848	36594998	RAG1	NM_000448	1	2	2	+	36594841	36601310
333440704	chr11	36595786	36595995	36595806	36595966	RAG1	NM_000448	1	2	2	+	36594841	36601310
333450293	chr11	36597822	36598035	36597845	36598009	RAG1	NM_000448	1	2	2	+	36594841	36601310
333450699	chr11	36597360	36597547	36597380	36597522	RAG1	NM_000448	1	2	2	+	36594841	36601310
333451876	chr11	36594975	36595188	36594999	36595167	RAG1	NM_000448	1	2	2	+	36594841	36601310
333462665	chr11	36596901	36597110	36596922	36597083	RAG1	NM_000448	1	2	2	+	36594841	36601310
333468470	chr11	36595942	36596161	36595967	36596141	RAG1	NM_000448	1	2	2	+	36594841	36601310
333476252	chr11	36597500	36597723	36597523	36597702	RAG1	NM_000448	1	2	2	+	36594841	36601310
333476593	chr11	36595146	36595365	36595167	36595342	RAG1	NM_000448	1	2	2	+	36594841	36601310
333483800	chr11	36596118	36596330	36596142	36596305	RAG1	NM_000448	1	2	2	+	36594841	36601310
333500471	chr11	36597062	36597248	36597084	36597226	RAG1	NM_000448	1	2	2	+	36594841	36601310
333508729	chr11	36597680	36597871	36597703	36597844	RAG1	NM_000448	1	2	2	+	36594841	36601310
333521673	chr11	36597200	36597406	36597227	36597379	RAG1	NM_000448	1	2	2	+	36594841	36601310
333374458	chr11	36614102	36614292	36614127	36614267	RAG2	NM_000536	1	2	2	-	36613493	36615745
333379058	chr11	36614588	36614793	36614608	36614767	RAG2	NM_000536	1	2	2	-	36613493	36615745
333380863	chr11	36615096	36615318	36615122	36615294	RAG2	NM_000536	1	2	2	-	36613493	36615745
333384648	chr11	36614247	36614471	36614268	36614448	RAG2	NM_000536	1	2	2	-	36613493	36615745
333385274	chr11	36615600	36615819	36615621	36615790	RAG2	NM_000536	1	2	2	-	36613493	36615745
333395971	chr11	36614745	36614969	36614768	36614947	RAG2	NM_000536	1	2	2	-	36613493	36615745
333405365	chr11	36615273	36615472	36615295	36615448	RAG2	NM_000536	1	2	2	-	36613493	36615745
333412753	chr11	36614424	36614635	36614449	36614607	RAG2	NM_000536	1	2	2	-	36613493	36615745
333415508	chr11	36614925	36615149	36614947	36615121	RAG2	NM_000536	1	2	2	-	36613493	36615745
333424067	chr11	36615424	36615647	36615449	36615620	RAG2	NM_000536	1	2	2	-	36613493	36615745
333374458	chr11	36614102	36614292	36614127	36614267	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333379058	chr11	36614588	36614793	36614608	36614767	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333380863	chr11	36615096	36615318	36615122	36615294	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333384648	chr11	36614247	36614471	36614268	36614448	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333385274	chr11	36615600	36615819	36615621	36615790	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333395971	chr11	36614745	36614969	36614768	36614947	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333405365	chr11	36615273	36615472	36615295	36615448	RAG2	NM_001243785	2	3	3	-	36613493	36615745

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333412753	chr11	36614424	36614635	36614449	36614607	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333415508	chr11	36614925	36615149	36614947	36615121	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333424067	chr11	36615424	36615647	36615449	36615620	RAG2	NM_001243785	2	3	3	-	36613493	36615745
333374458	chr11	36614102	36614292	36614127	36614267	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333379058	chr11	36614588	36614793	36614608	36614767	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333380863	chr11	36615096	36615318	36615122	36615294	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333384648	chr11	36614247	36614471	36614268	36614448	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333385274	chr11	36615600	36615819	36615621	36615790	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333395971	chr11	36614745	36614969	36614768	36614947	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333405365	chr11	36615273	36615472	36615295	36615448	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333412753	chr11	36614424	36614635	36614449	36614607	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333415508	chr11	36614925	36615149	36614947	36615121	RAG2	NM_001243786	3	3	3	-	36613493	36615745
333424067	chr11	36615424	36615647	36615449	36615620	RAG2	NM_001243786	3	3	3	-	36613493	36615745
323644338	chr17	17701258	17701423	17701278	17701398	RAI1	NM_030665	1	6	3	+	17696247	17701827
323652176	chr17	17701376	17701500	17701398	17701481	RAI1	NM_030665	1	6	3	+	17696247	17701827
323653968	chr17	17701462	17701681	17701482	17701660	RAI1	NM_030665	1	6	3	+	17696247	17701827
323656023	chr17	17701606	17701801	17701626	17701782	RAI1	NM_030665	1	6	3	+	17696247	17701827
323682960	chr17	17696673	17696855	17696696	17696834	RAI1	NM_030665	1	6	3	+	17696247	17701827
323688664	chr17	17696812	17696985	17696833	17696961	RAI1	NM_030665	1	6	3	+	17696247	17701827
323696344	chr17	17696919	17697078	17696940	17697061	RAI1	NM_030665	1	6	3	+	17696247	17701827
323699035	chr17	17701760	17701948	17701777	17701928	RAI1	NM_030665	1	6	3	+	17696247	17701827
323702265	chr17	17697042	17697200	17697062	17697178	RAI1	NM_030665	1	6	3	+	17696247	17701827
323707775	chr17	17697653	17697866	17697674	17697846	RAI1	NM_030665	1	6	3	+	17696247	17701827
323708806	chr17	17697800	17697983	17697819	17697959	RAI1	NM_030665	1	6	3	+	17696247	17701827
323714975	chr17	17697939	17698148	17697960	17698128	RAI1	NM_030665	1	6	3	+	17696247	17701827
323722860	chr17	17698106	17698313	17698126	17698293	RAI1	NM_030665	1	6	3	+	17696247	17701827
325551448	chr17	17698687	17698901	17698708	17698881	RAI1	NM_030665	1	6	3	+	17696247	17701827
325551562	chr17	17697158	17697373	17697179	17697350	RAI1	NM_030665	1	6	3	+	17696247	17701827
325553386	chr17	17698854	17699069	17698875	17699050	RAI1	NM_030665	1	6	3	+	17696247	17701827
325554260	chr17	17698267	17698461	17698287	17698441	RAI1	NM_030665	1	6	3	+	17696247	17701827
325555024	chr17	17699151	17699354	17699169	17699334	RAI1	NM_030665	1	6	3	+	17696247	17701827
325557596	chr17	17699316	17699454	17699335	17699435	RAI1	NM_030665	1	6	3	+	17696247	17701827
325558098	chr17	17699691	17699838	17699711	17699817	RAI1	NM_030665	1	6	3	+	17696247	17701827
325560342	chr17	17699414	17699576	17699434	17699558	RAI1	NM_030665	1	6	3	+	17696247	17701827
325560557	chr17	17699028	17699201	17699046	17699182	RAI1	NM_030665	1	6	3	+	17696247	17701827
325561094	chr17	17699792	17699980	17699812	17699961	RAI1	NM_030665	1	6	3	+	17696247	17701827
325561425	chr17	17696156	17696337	17696175	17696316	RAI1	NM_030665	1	6	3	+	17696247	17701827
325561638	chr17	17697323	17697540	17697344	17697519	RAI1	NM_030665	1	6	3	+	17696247	17701827
325562343	chr17	17699533	17699732	17699551	17699710	RAI1	NM_030665	1	6	3	+	17696247	17701827
325564111	chr17	17698420	17698621	17698441	17698601	RAI1	NM_030665	1	6	3	+	17696247	17701827
325566176	chr17	17699916	17700100	17699937	17700077	RAI1	NM_030665	1	6	3	+	17696247	17701827

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325568530	chr17	17700058	17700281	17700077	17700261	RAI1	NM_030665	1	6	3	+	17696247	17701827
325569064	chr17	17700242	17700461	17700262	17700439	RAI1	NM_030665	1	6	3	+	17696247	17701827
325569229	chr17	17698581	17698732	17698601	17698713	RAI1	NM_030665	1	6	3	+	17696247	17701827
325571961	chr17	17700682	17700888	17700701	17700871	RAI1	NM_030665	1	6	3	+	17696247	17701827
325572880	chr17	17697499	17697699	17697519	17697678	RAI1	NM_030665	1	6	3	+	17696247	17701827
325576255	chr17	17700846	17701007	17700870	17700984	RAI1	NM_030665	1	6	3	+	17696247	17701827
325578363	chr17	17700967	17701129	17700985	17701112	RAI1	NM_030665	1	6	3	+	17696247	17701827
325578662	chr17	17696288	17696507	17696313	17696487	RAI1	NM_030665	1	6	3	+	17696247	17701827
325581402	chr17	17700396	17700614	17700419	17700592	RAI1	NM_030665	1	6	3	+	17696247	17701827
325582458	chr17	17696405	17696619	17696430	17696599	RAI1	NM_030665	1	6	3	+	17696247	17701827
325584270	chr17	17701086	17701308	17701110	17701288	RAI1	NM_030665	1	6	3	+	17696247	17701827
325584499	chr17	17696581	17696717	17696599	17696695	RAI1	NM_030665	1	6	3	+	17696247	17701827
325586707	chr17	17700534	17700744	17700555	17700723	RAI1	NM_030665	1	6	3	+	17696247	17701827
324979544	chr17	17707027	17707199	17707048	17707179	RAI1	NM_030665	1	6	4	+	17707070	17707163
324928207	chr17	17712580	17712780	17712600	17712759	RAI1	NM_030665	1	6	5	+	17712704	17712753
324712293	chr17	17713224	17713426	17713244	17713406	RAI1	NM_030665	1	6	6	+	17713284	17714765
324150793	chr11	47470284	47470453	47470301	47470432	RAPSN	NM_005055	1	8	1	-	47470325	47470730
324154910	chr11	47470412	47470633	47470433	47470611	RAPSN	NM_005055	1	8	1	-	47470325	47470730
323393006	chr11	47469269	47469469	47469290	47469449	RAPSN	NM_005055	1	8	2	-	47469364	47469702
323400300	chr11	47469412	47469617	47469433	47469597	RAPSN	NM_005055	1	8	2	-	47469364	47469702
323406402	chr11	47469572	47469699	47469595	47469679	RAPSN	NM_005055	1	8	2	-	47469364	47469702
323411274	chr11	47469636	47469857	47469658	47469833	RAPSN	NM_005055	1	8	2	-	47469364	47469702
326404022	chr11	47464104	47464318	47464125	47464296	RAPSN	NM_005055	1	8	3	-	47464208	47464366
326415145	chr11	47464275	47464462	47464295	47464437	RAPSN	NM_005055	1	8	3	-	47464208	47464366
323495463	chr11	47463231	47463415	47463253	47463395	RAPSN	NM_005055	1	8	4	-	47463375	47463473
323497275	chr11	47463302	47463518	47463324	47463499	RAPSN	NM_005055	1	8	4	-	47463375	47463473
323495463	chr11	47463231	47463415	47463253	47463395	RAPSN	NM_005055	1	8	5	-	47463163	47463285
325767618	chr11	47463089	47463273	47463108	47463254	RAPSN	NM_005055	1	8	5	-	47463163	47463285
324910279	chr11	47462679	47462895	47462701	47462875	RAPSN	NM_005055	1	8	6	-	47462710	47462763
324139901	chr11	47460169	47460381	47460191	47460360	RAPSN	NM_005055	1	8	7	-	47460283	47460482
324143967	chr11	47460324	47460530	47460345	47460508	RAPSN	NM_005055	1	8	7	-	47460283	47460482
323944945	chr11	47459408	47459625	47459427	47459607	RAPSN	NM_005055	1	8	8	-	47459308	47459598
324150793	chr11	47470284	47470453	47470301	47470432	RAPSN	NM_032645	2	6	1	-	47470325	47470730
324154910	chr11	47470412	47470633	47470433	47470611	RAPSN	NM_032645	2	6	1	-	47470325	47470730
323393006	chr11	47469269	47469469	47469290	47469449	RAPSN	NM_032645	2	6	2	-	47469364	47469702
323400300	chr11	47469412	47469617	47469433	47469597	RAPSN	NM_032645	2	6	2	-	47469364	47469702
323406402	chr11	47469572	47469699	47469595	47469679	RAPSN	NM_032645	2	6	2	-	47469364	47469702
323411274	chr11	47469636	47469857	47469658	47469833	RAPSN	NM_032645	2	6	2	-	47469364	47469702
326404022	chr11	47464104	47464318	47464125	47464296	RAPSN	NM_032645	2	6	3	-	47464208	47464366
326415145	chr11	47464275	47464462	47464295	47464437	RAPSN	NM_032645	2	6	3	-	47464208	47464366
323495463	chr11	47463231	47463415	47463253	47463395	RAPSN	NM_032645	2	6	4	-	47463375	47463473

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323497275	chr11	47463302	47463518	47463324	47463499	RAPSN	NM_032645	2	6	4	-	47463375	47463473
324139901	chr11	47460169	47460381	47460191	47460360	RAPSN	NM_032645	2	6	5	-	47460283	47460482
324143967	chr11	47460324	47460530	47460345	47460508	RAPSN	NM_032645	2	6	5	-	47460283	47460482
323944945	chr11	47459408	47459625	47459427	47459607	RAPSN	NM_032645	2	6	6	-	47459308	47459598
242692069	chr13	48878045	48878202	48878062	48878185	RB1	NM_000321	1	27	1	+	48877883	48878185
264234192	chr13	48881318	48881497	48881347	48881469	RB1	NM_000321	1	27	2	+	48881416	48881542
264236629	chr13	48881419	48881554	48881447	48881526	RB1	NM_000321	1	27	2	+	48881416	48881542
242616297	chr13	48916662	48916795	48916695	48916767	RB1	NM_000321	1	27	3	+	48916735	48916850
260627787	chr13	48916727	48916905	48916755	48916879	RB1	NM_000321	1	27	3	+	48916735	48916850
240121588	chr13	48919082	48919298	48919111	48919270	RB1	NM_000321	1	27	4	+	48919216	48919335
240121618	chr13	48919254	48919470	48919283	48919442	RB1	NM_000321	1	27	4	+	48919216	48919335
241362320	chr13	48921939	48922105	48921970	48922078	RB1	NM_000321	1	27	5	+	48921961	48921999
241902207	chr13	48922953	48923135	48922983	48923107	RB1	NM_000321	1	27	6	+	48923092	48923159
326771467	chr13	48923096	48923276	48923125	48923252	RB1	NM_000321	1	27	6	+	48923092	48923159
242580836	chr13	48934070	48934259	48934097	48934237	RB1	NM_000321	1	27	7	+	48934153	48934263
261119271	chr13	48936844	48937023	48936876	48937003	RB1	NM_000321	1	27	8	+	48936951	48937093
331017229	chr13	48937001	48937223	48937022	48937195	RB1	NM_000321	1	27	8	+	48936951	48937093
262539419	chr13	48939074	48939234	48939103	48939210	RB1	NM_000321	1	27	9	+	48939030	48939107
240330971	chr13	48941568	48941772	48941593	48941742	RB1	NM_000321	1	27	10	+	48941630	48941739
239977367	chr13	48942570	48942736	48942598	48942711	RB1	NM_000321	1	27	11	+	48942663	48942740
240782641	chr13	48947407	48947606	48947431	48947581	RB1	NM_000321	1	27	12	+	48947541	48947628
241480691	chr13	48951019	48951240	48951047	48951212	RB1	NM_000321	1	27	13	+	48951054	48951170
241627128	chr13	48954168	48954347	48954201	48954321	RB1	NM_000321	1	27	15	+	48954189	48954220
241627128	chr13	48954168	48954347	48954201	48954321	RB1	NM_000321	1	27	16	+	48954301	48954377
241627309	chr13	48954294	48954475	48954322	48954450	RB1	NM_000321	1	27	16	+	48954301	48954377
242315995	chr13	48955498	48955667	48955526	48955639	RB1	NM_000321	1	27	17	+	48955383	48955579
326815367	chr13	48955399	48955565	48955426	48955539	RB1	NM_000321	1	27	17	+	48955383	48955579
263342572	chr13	49027008	49027225	49027030	49027198	RB1	NM_000321	1	27	18	+	49027129	49027247
326867722	chr13	49027174	49027308	49027198	49027280	RB1	NM_000321	1	27	18	+	49027129	49027247
238045415	chr13	49030246	49030468	49030271	49030440	RB1	NM_000321	1	27	19	+	49030340	49030485
242180110	chr13	49033685	49033861	49033713	49033835	RB1	NM_000321	1	27	20	+	49033824	49033969
242181132	chr13	49033810	49034021	49033835	49033993	RB1	NM_000321	1	27	20	+	49033824	49033969
242362523	chr13	49037731	49037903	49037759	49037878	RB1	NM_000321	1	27	21	+	49037867	49037971
242362921	chr13	49037881	49038045	49037909	49038012	RB1	NM_000321	1	27	21	+	49037867	49037971
241675134	chr13	49038995	49039210	49039026	49039183	RB1	NM_000321	1	27	22	+	49039134	49039247
241676023	chr13	49039125	49039305	49039151	49039281	RB1	NM_000321	1	27	22	+	49039134	49039247
241676359	chr13	49039186	49039372	49039212	49039347	RB1	NM_000321	1	27	22	+	49039134	49039247
238907536	chr13	49039324	49039547	49039348	49039519	RB1	NM_000321	1	27	23	+	49039341	49039504
241676359	chr13	49039186	49039372	49039212	49039347	RB1	NM_000321	1	27	23	+	49039341	49039504
242609956	chr13	49047430	49047630	49047458	49047601	RB1	NM_000321	1	27	24	+	49047496	49047526
239932898	chr13	49050768	49050910	49050796	49050887	RB1	NM_000321	1	27	25	+	49050837	49050979

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239943702	chr13	49050866	49051011	49050888	49050984	RB1	NM_000321	1	27	25	+	49050837	49050979
240874670	chr13	49051393	49051606	49051421	49051577	RB1	NM_000321	1	27	26	+	49051491	49051540
262072283	chr13	49054031	49054246	49054051	49054225	RB1	NM_000321	1	27	27	+	49054134	49056026
325286954	chr14	68189332	68189467	68189354	68189439	RDH12	NM_152443	1	9	3	+	68189141	68189427
323442239	chr14	68191122	68191344	68191150	68191322	RDH12	NM_152443	1	9	4	+	68191190	68191308
325017659	chr14	68191639	68191863	68191665	68191841	RDH12	NM_152443	1	9	5	+	68191816	68191971
325048169	chr14	68191820	68192003	68191842	68191979	RDH12	NM_152443	1	9	5	+	68191816	68191971
325561249	chr14	68192723	68192926	68192745	68192898	RDH12	NM_152443	1	9	6	+	68192768	68192872
326355335	chr14	68193579	68193803	68193604	68193781	RDH12	NM_152443	1	9	7	+	68193698	68193907
326383224	chr14	68193760	68193974	68193781	68193949	RDH12	NM_152443	1	9	7	+	68193698	68193907
324138640	chr14	68195877	68196099	68195901	68196077	RDH12	NM_152443	1	9	8	+	68195908	68196097
324143270	chr14	68195997	68196220	68196019	68196200	RDH12	NM_152443	1	9	8	+	68195908	68196097
324900064	chr14	68200441	68200606	68200462	68200585	RDH12	NM_152443	1	9	9	+	68200463	68201168
240735446	chr10	43595870	43596093	43595892	43596070	RET	NM_020630	1	19	2	+	43595907	43596170
240745868	chr10	43596041	43596264	43596061	43596243	RET	NM_020630	1	19	2	+	43595907	43596170
242191185	chr10	43597763	43597919	43597784	43597896	RET	NM_020630	1	19	3	+	43597790	43598077
242208630	chr10	43597875	43598096	43597895	43598077	RET	NM_020630	1	19	3	+	43597790	43598077
242225366	chr10	43598031	43598192	43598051	43598168	RET	NM_020630	1	19	3	+	43597790	43598077
242042504	chr10	43600377	43600545	43600394	43600527	RET	NM_020630	1	19	4	+	43600400	43600641
242042835	chr10	43600475	43600685	43600495	43600664	RET	NM_020630	1	19	4	+	43600400	43600641
261489208	chr10	43601736	43601903	43601757	43601884	RET	NM_020630	1	19	5	+	43601824	43602019
261512021	chr10	43601857	43602080	43601877	43602058	RET	NM_020630	1	19	5	+	43601824	43602019
238099727	chr10	43604347	43604525	43604370	43604507	RET	NM_020630	1	19	6	+	43604479	43604678
238120409	chr10	43604486	43604708	43604507	43604687	RET	NM_020630	1	19	6	+	43604479	43604678
238688959	chr10	43606619	43606842	43606639	43606820	RET	NM_020630	1	19	7	+	43606655	43606913
238720513	chr10	43606780	43607004	43606805	43606981	RET	NM_020630	1	19	7	+	43606655	43606913
238023974	chr10	43607516	43607698	43607535	43607680	RET	NM_020630	1	19	8	+	43607547	43607672
240756507	chr10	43608222	43608444	43608242	43608421	RET	NM_020630	1	19	9	+	43608301	43608411
240421317	chr10	43608977	43609187	43608995	43609165	RET	NM_020630	1	19	10	+	43609004	43609123
264060723	chr10	43609853	43610048	43609873	43610028	RET	NM_020630	1	19	11	+	43609928	43610184
264074492	chr10	43610008	43610193	43610029	43610172	RET	NM_020630	1	19	11	+	43609928	43610184
264082246	chr10	43610150	43610317	43610170	43610298	RET	NM_020630	1	19	11	+	43609928	43610184
239566285	chr10	43611898	43612120	43611919	43612097	RET	NM_020630	1	19	12	+	43612032	43612179
239637376	chr10	43612074	43612295	43612098	43612275	RET	NM_020630	1	19	12	+	43612032	43612179
238818258	chr10	43613780	43614001	43613800	43613980	RET	NM_020630	1	19	13	+	43613821	43613928
241505630	chr10	43614913	43615126	43614931	43615109	RET	NM_020630	1	19	14	+	43614979	43615193
241510364	chr10	43615060	43615220	43615077	43615202	RET	NM_020630	1	19	14	+	43614979	43615193
241626667	chr10	43615498	43615623	43615517	43615600	RET	NM_020630	1	19	15	+	43615529	43615651
241633877	chr10	43615576	43615742	43615601	43615719	RET	NM_020630	1	19	15	+	43615529	43615651
240365924	chr10	43617278	43617502	43617301	43617481	RET	NM_020630	1	19	16	+	43617394	43617464
242440430	chr10	43619115	43619324	43619137	43619302	RET	NM_020630	1	19	17	+	43619119	43619256

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260350819	chr10	43618988	43619160	43619011	43619140	RET	NM_020630	1	19	17	+	43619119	43619256
241717895	chr10	43620266	43620469	43620286	43620447	RET	NM_020630	1	19	18	+	43620331	43620430
238886903	chr10	43621890	43622087	43621912	43622066	RET	NM_020630	1	19	19	+	43622023	43622952
238920142	chr10	43622045	43622235	43622067	43622212	RET	NM_020630	1	19	19	+	43622023	43622952
240735446	chr10	43595870	43596093	43595892	43596070	RET	NM_020975	2	20	2	+	43595907	43596170
240745868	chr10	43596041	43596264	43596061	43596243	RET	NM_020975	2	20	2	+	43595907	43596170
242191185	chr10	43597763	43597919	43597784	43597896	RET	NM_020975	2	20	3	+	43597790	43598077
242208630	chr10	43597875	43598096	43597895	43598077	RET	NM_020975	2	20	3	+	43597790	43598077
242225366	chr10	43598031	43598192	43598051	43598168	RET	NM_020975	2	20	3	+	43597790	43598077
242042504	chr10	43600377	43600545	43600394	43600527	RET	NM_020975	2	20	4	+	43600400	43600641
242042835	chr10	43600475	43600685	43600495	43600664	RET	NM_020975	2	20	4	+	43600400	43600641
261489208	chr10	43601736	43601903	43601757	43601884	RET	NM_020975	2	20	5	+	43601824	43602019
261512021	chr10	43601857	43602080	43601877	43602058	RET	NM_020975	2	20	5	+	43601824	43602019
238099727	chr10	43604347	43604525	43604370	43604507	RET	NM_020975	2	20	6	+	43604479	43604678
238120409	chr10	43604486	43604708	43604507	43604687	RET	NM_020975	2	20	6	+	43604479	43604678
238688959	chr10	43606619	43606842	43606639	43606820	RET	NM_020975	2	20	7	+	43606655	43606913
238720513	chr10	43606780	43607004	43606805	43606981	RET	NM_020975	2	20	7	+	43606655	43606913
238023974	chr10	43607516	43607698	43607535	43607680	RET	NM_020975	2	20	8	+	43607547	43607672
240756507	chr10	43608222	43608444	43608242	43608421	RET	NM_020975	2	20	9	+	43608301	43608411
240421317	chr10	43608977	43609187	43608995	43609165	RET	NM_020975	2	20	10	+	43609004	43609123
264060723	chr10	43609853	43610048	43609873	43610028	RET	NM_020975	2	20	11	+	43609928	43610184
264074492	chr10	43610008	43610193	43610029	43610172	RET	NM_020975	2	20	11	+	43609928	43610184
264082246	chr10	43610150	43610317	43610170	43610298	RET	NM_020975	2	20	11	+	43609928	43610184
239566285	chr10	43611898	43612120	43611919	43612097	RET	NM_020975	2	20	12	+	43612032	43612179
239637376	chr10	43612074	43612295	43612098	43612275	RET	NM_020975	2	20	12	+	43612032	43612179
238818258	chr10	43613780	43614001	43613800	43613980	RET	NM_020975	2	20	13	+	43613821	43613928
241505630	chr10	43614913	43615126	43614931	43615109	RET	NM_020975	2	20	14	+	43614979	43615193
241510364	chr10	43615060	43615220	43615077	43615202	RET	NM_020975	2	20	14	+	43614979	43615193
241626667	chr10	43615498	43615623	43615517	43615600	RET	NM_020975	2	20	15	+	43615529	43615651
241633877	chr10	43615576	43615742	43615601	43615719	RET	NM_020975	2	20	15	+	43615529	43615651
240365924	chr10	43617278	43617502	43617301	43617481	RET	NM_020975	2	20	16	+	43617394	43617464
242440430	chr10	43619115	43619324	43619137	43619302	RET	NM_020975	2	20	17	+	43619119	43619256
260350819	chr10	43618988	43619160	43619011	43619140	RET	NM_020975	2	20	17	+	43619119	43619256
241717895	chr10	43620266	43620469	43620286	43620447	RET	NM_020975	2	20	18	+	43620331	43620430
238886903	chr10	43621890	43622087	43621912	43622066	RET	NM_020975	2	20	19	+	43622023	43622170
238920142	chr10	43622045	43622235	43622067	43622212	RET	NM_020975	2	20	19	+	43622023	43622170
262763241	chr10	43623478	43623624	43623499	43623603	RET	NM_020975	2	20	20	+	43623560	43625797
262811156	chr10	43623582	43623759	43623604	43623734	RET	NM_020975	2	20	20	+	43623560	43625797
324627543	chr3	129247521	129247724	129247541	129247701	RHO	NM_000539	1	5	1	+	129247482	129247937
324641359	chr3	129247676	129247891	129247696	129247867	RHO	NM_000539	1	5	1	+	129247482	129247937
324665360	chr3	129247846	129248068	129247867	129248044	RHO	NM_000539	1	5	1	+	129247482	129247937

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326400261	chr3	129249624	129249803	129249645	129249783	RHO	NM_000539	1	5	2	+	129249719	129249887
326408371	chr3	129249760	129249976	129249781	129249955	RHO	NM_000539	1	5	2	+	129249719	129249887
325717688	chr3	129250965	129251187	129250989	129251159	RHO	NM_000539	1	5	3	+	129251094	129251259
325737618	chr3	129251142	129251352	129251160	129251333	RHO	NM_000539	1	5	3	+	129251094	129251259
323747558	chr3	129251333	129251540	129251352	129251519	RHO	NM_000539	1	5	4	+	129251376	129251615
323758976	chr3	129251493	129251691	129251517	129251670	RHO	NM_000539	1	5	4	+	129251376	129251615
323378341	chr3	129252373	129252592	129252393	129252569	RHO	NM_000539	1	5	5	+	129252451	129254187
297004150	chr9	94712111	94712335	94712129	94712315	ROR2	NM_004560	1	9	1	-	94712149	94712444
295876766	chr9	94537980	94538153	94538001	94538125	ROR2	NM_004560	1	9	2	-	94538023	94538100
295780780	chr9	94519499	94519694	94519520	94519671	ROR2	NM_004560	1	9	3	-	94519554	94519841
295806128	chr9	94519650	94519868	94519672	94519846	ROR2	NM_004560	1	9	3	-	94519554	94519841
296605170	chr9	94518232	94518445	94518253	94518417	ROR2	NM_004560	1	9	4	-	94518353	94518383
296625166	chr9	94499621	94499832	94499643	94499805	ROR2	NM_004560	1	9	5	-	94499673	94499800
295521631	chr9	94495326	94495549	94495347	94495530	ROR2	NM_004560	1	9	6	-	94495404	94495718
295529197	chr9	94495495	94495711	94495515	94495691	ROR2	NM_004560	1	9	6	-	94495404	94495718
295533967	chr9	94495648	94495785	94495668	94495763	ROR2	NM_004560	1	9	6	-	94495404	94495718
295994388	chr9	94493208	94493427	94493229	94493405	ROR2	NM_004560	1	9	7	-	94493192	94493437
296013136	chr9	94493386	94493519	94493406	94493492	ROR2	NM_004560	1	9	7	-	94493192	94493437
324651976	chr9	94493051	94493252	94493076	94493228	ROR2	NM_004560	1	9	7	-	94493192	94493437
297218079	chr9	94488757	94488958	94488778	94488935	ROR2	NM_004560	1	9	8	-	94488823	94489025
297236458	chr9	94488915	94489094	94488936	94489065	ROR2	NM_004560	1	9	8	-	94488823	94489025
296693859	chr9	94485908	94486117	94485927	94486100	ROR2	NM_004560	1	9	9	-	94484878	94487389
296704661	chr9	94486075	94486280	94486095	94486259	ROR2	NM_004560	1	9	9	-	94484878	94487389
296710247	chr9	94486235	94486447	94486255	94486426	ROR2	NM_004560	1	9	9	-	94484878	94487389
298408190	chr9	94486405	94486620	94486422	94486601	ROR2	NM_004560	1	9	9	-	94484878	94487389
298417192	chr9	94486926	94487136	94486945	94487116	ROR2	NM_004560	1	9	9	-	94484878	94487389
298420680	chr9	94486580	94486788	94486601	94486765	ROR2	NM_004560	1	9	9	-	94484878	94487389
298425714	chr9	94487097	94487316	94487115	94487294	ROR2	NM_004560	1	9	9	-	94484878	94487389
298436137	chr9	94487238	94487435	94487262	94487415	ROR2	NM_004560	1	9	9	-	94484878	94487389
298439996	chr9	94486743	94486966	94486766	94486945	ROR2	NM_004560	1	9	9	-	94484878	94487389
331900319	chr7	33148636	33148856	33148654	33148838	RP9	NM_203288	1	6	1	-	33148833	33149002
325541882	chr7	33140006	33140165	33140032	33140144	RP9	NM_203288	1	6	2	-	33140143	33140173
325542805	chr7	33140118	33140308	33140145	33140280	RP9	NM_203288	1	6	2	-	33140143	33140173
325672900	chr7	33138873	33139079	33138896	33139053	RP9	NM_203288	1	6	3	-	33138919	33139048
323677462	chr7	33136764	33136969	33136788	33136948	RP9	NM_203288	1	6	4	-	33136883	33136974
323686940	chr7	33136927	33137146	33136948	33137119	RP9	NM_203288	1	6	4	-	33136883	33136974
324831220	chr7	33135996	33136200	33136021	33136174	RP9	NM_203288	1	6	5	-	33136105	33136166
325787032	chr7	33134813	33135028	33134841	33135002	RP9	NM_203288	1	6	6	-	33134410	33135044
325789501	chr7	33134981	33135202	33135003	33135174	RP9	NM_203288	1	6	6	-	33134410	33135044
325276214	chr1	68915446	68915647	68915468	68915621	RPE65	NM_000329	1	14	1	-	68915578	68915642
326163334	chr1	68914216	68914419	68914236	68914394	RPE65	NM_000329	1	14	2	-	68914307	68914389

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324892414	chr1	68912351	68912571	68912373	68912548	RPE65	NM_000329	1	14	3	-	68912393	68912543
324030532	chr1	68910381	68910605	68910408	68910576	RPE65	NM_000329	1	14	4	-	68910459	68910566
324575720	chr1	68910178	68910401	68910205	68910373	RPE65	NM_000329	1	14	5	-	68910214	68910355
325251846	chr1	68906498	68906718	68906527	68906693	RPE65	NM_000329	1	14	6	-	68906536	68906683
323908246	chr1	68905159	68905360	68905186	68905333	RPE65	NM_000329	1	14	7	-	68905244	68905325
323632439	chr1	68904692	68904916	68904724	68904890	RPE65	NM_000329	1	14	8	-	68904874	68905006
323635193	chr1	68904862	68905042	68904887	68905018	RPE65	NM_000329	1	14	8	-	68904874	68905006
323500249	chr1	68904542	68904765	68904564	68904739	RPE65	NM_000329	1	14	9	-	68904625	68904764
323632439	chr1	68904692	68904916	68904724	68904890	RPE65	NM_000329	1	14	9	-	68904625	68904764
323464349	chr1	68903810	68904034	68903838	68904012	RPE65	NM_000329	1	14	10	-	68903870	68903999
323787288	chr1	68897106	68897300	68897130	68897273	RPE65	NM_000329	1	14	11	-	68897154	68897268
323892305	chr1	68896909	68897092	68896937	68897064	RPE65	NM_000329	1	14	12	-	68896965	68897059
324576087	chr1	68896563	68896772	68896592	68896748	RPE65	NM_000329	1	14	13	-	68896748	68896859
324581684	chr1	68896721	68896938	68896749	68896910	RPE65	NM_000329	1	14	13	-	68896748	68896859
326241167	chr1	68895469	68895676	68895493	68895648	RPE65	NM_000329	1	14	14	-	68894507	68895610
326246617	chr1	68895296	68895516	68895317	68895492	RPE65	NM_000329	1	14	14	-	68894507	68895610
325097346	chrX	38186428	38186645	38186448	38186628	RPGR	NM_000328	1	19	1	-	38186593	38186788
323490888	chrX	38182560	38182738	38182586	38182710	RPGR	NM_000328	1	19	2	-	38182652	38182777
323492455	chrX	38182678	38182889	38182703	38182868	RPGR	NM_000328	1	19	2	-	38182652	38182777
323366966	chrX	38181924	38182145	38181952	38182122	RPGR	NM_000328	1	19	3	-	38182106	38182198
323367417	chrX	38182096	38182279	38182121	38182252	RPGR	NM_000328	1	19	3	-	38182106	38182198
324799479	chrX	38180200	38180402	38180228	38180375	RPGR	NM_000328	1	19	4	-	38180280	38180342
326132984	chrX	38177994	38178137	38178015	38178113	RPGR	NM_000328	1	19	5	-	38178082	38178240
326148617	chrX	38178090	38178312	38178114	38178284	RPGR	NM_000328	1	19	5	-	38178082	38178240
324721853	chrX	38176414	38176615	38176441	38176588	RPGR	NM_000328	1	19	6	-	38176569	38176718
324724081	chrX	38176560	38176767	38176589	38176741	RPGR	NM_000328	1	19	6	-	38176569	38176718
324873356	chrX	38169837	38170004	38169859	38169979	RPGR	NM_000328	1	19	7	-	38169868	38170026
324883931	chrX	38169959	38170091	38169980	38170066	RPGR	NM_000328	1	19	7	-	38169868	38170026
324641253	chrX	38163762	38163978	38163790	38163951	RPGR	NM_000328	1	19	8	-	38163888	38164043
324650288	chrX	38163898	38164097	38163926	38164071	RPGR	NM_000328	1	19	8	-	38163888	38164043
325056252	chrX	38160348	38160554	38160375	38160527	RPGR	NM_000328	1	19	9	-	38160500	38160624
325058228	chrX	38160482	38160619	38160510	38160592	RPGR	NM_000328	1	19	9	-	38160500	38160624
325059115	chrX	38160565	38160789	38160589	38160766	RPGR	NM_000328	1	19	9	-	38160500	38160624
326257656	chrX	38158187	38158344	38158211	38158316	RPGR	NM_000328	1	19	10	-	38158209	38158394
326278227	chrX	38158289	38158432	38158317	38158404	RPGR	NM_000328	1	19	10	-	38158209	38158394
323590558	chrX	38156498	38156645	38156523	38156623	RPGR	NM_000328	1	19	11	-	38156537	38156705
323603975	chrX	38156599	38156821	38156624	38156792	RPGR	NM_000328	1	19	11	-	38156537	38156705
323695142	chrX	38150536	38150691	38150564	38150665	RPGR	NM_000328	1	19	12	-	38150646	38150737
323695150	chrX	38150655	38150797	38150683	38150772	RPGR	NM_000328	1	19	12	-	38150646	38150737
324247152	chrX	38150065	38150287	38150093	38150260	RPGR	NM_000328	1	19	13	-	38150212	38150277
324248910	chrX	38150236	38150454	38150267	38150426	RPGR	NM_000328	1	19	13	-	38150212	38150277

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323558458	chrX	38147057	38147278	38147082	38147258	RPGR	NM_000328	1	19	14	-	38147114	38147294
323567697	chrX	38147251	38147472	38147273	38147444	RPGR	NM_000328	1	19	14	-	38147114	38147294
323456772	chrX	38146231	38146385	38146252	38146357	RPGR	NM_000328	1	19	15	-	38146347	38146498
323467774	chrX	38146336	38146553	38146358	38146525	RPGR	NM_000328	1	19	15	-	38146347	38146498
326206620	chrX	38135734	38135926	38135758	38135898	RPGR	NM_000328	1	19	16	-	38135840	38136025
326216471	chrX	38135873	38136097	38135899	38136070	RPGR	NM_000328	1	19	16	-	38135840	38136025
324515582	chrX	38134189	38134386	38134217	38134366	RPGR	NM_000328	1	19	17	-	38134342	38134399
324712694	chrX	38132498	38132722	38132522	38132694	RPGR	NM_000328	1	19	18	-	38132639	38132730
324721468	chrX	38132667	38132793	38132695	38132766	RPGR	NM_000328	1	19	18	-	38132639	38132730
326060881	chrX	38128836	38128960	38128864	38128934	RPGR	NM_000328	1	19	19	-	38128423	38129085
326064778	chrX	38128907	38129078	38128935	38129050	RPGR	NM_000328	1	19	19	-	38128423	38129085
326068714	chrX	38129022	38129244	38129046	38129218	RPGR	NM_000328	1	19	19	-	38128423	38129085
325097346	chrX	38186428	38186645	38186448	38186628	RPGR	NM_001034853	2	15	1	-	38186593	38186788
323490888	chrX	38182560	38182738	38182586	38182710	RPGR	NM_001034853	2	15	2	-	38182652	38182777
323492455	chrX	38182678	38182889	38182703	38182868	RPGR	NM_001034853	2	15	2	-	38182652	38182777
323366966	chrX	38181924	38182145	38181952	38182122	RPGR	NM_001034853	2	15	3	-	38182106	38182198
323367417	chrX	38182096	38182279	38182121	38182252	RPGR	NM_001034853	2	15	3	-	38182106	38182198
324799479	chrX	38180200	38180402	38180228	38180375	RPGR	NM_001034853	2	15	4	-	38180280	38180342
326132984	chrX	38177994	38178137	38178015	38178113	RPGR	NM_001034853	2	15	5	-	38178082	38178240
326148617	chrX	38178090	38178312	38178114	38178284	RPGR	NM_001034853	2	15	5	-	38178082	38178240
324721853	chrX	38176414	38176615	38176441	38176588	RPGR	NM_001034853	2	15	6	-	38176569	38176718
324724081	chrX	38176560	38176767	38176589	38176741	RPGR	NM_001034853	2	15	6	-	38176569	38176718
324873356	chrX	38169837	38170004	38169859	38169979	RPGR	NM_001034853	2	15	7	-	38169868	38170026
324883931	chrX	38169959	38170091	38169980	38170066	RPGR	NM_001034853	2	15	7	-	38169868	38170026
324641253	chrX	38163762	38163978	38163790	38163951	RPGR	NM_001034853	2	15	8	-	38163888	38164043
324650288	chrX	38163898	38164097	38163926	38164071	RPGR	NM_001034853	2	15	8	-	38163888	38164043
325056252	chrX	38160348	38160554	38160375	38160527	RPGR	NM_001034853	2	15	9	-	38160500	38160624
325058228	chrX	38160482	38160619	38160510	38160592	RPGR	NM_001034853	2	15	9	-	38160500	38160624
325059115	chrX	38160565	38160789	38160589	38160766	RPGR	NM_001034853	2	15	9	-	38160500	38160624
326257656	chrX	38158187	38158344	38158211	38158316	RPGR	NM_001034853	2	15	10	-	38158209	38158394
326278227	chrX	38158289	38158432	38158317	38158404	RPGR	NM_001034853	2	15	10	-	38158209	38158394
323590558	chrX	38156498	38156645	38156523	38156623	RPGR	NM_001034853	2	15	11	-	38156537	38156705
323603975	chrX	38156599	38156821	38156624	38156792	RPGR	NM_001034853	2	15	11	-	38156537	38156705
323695142	chrX	38150536	38150691	38150564	38150665	RPGR	NM_001034853	2	15	12	-	38150646	38150737
323695150	chrX	38150655	38150797	38150683	38150772	RPGR	NM_001034853	2	15	12	-	38150646	38150737
324247152	chrX	38150065	38150287	38150093	38150260	RPGR	NM_001034853	2	15	13	-	38150212	38150277
324248910	chrX	38150236	38150454	38150267	38150426	RPGR	NM_001034853	2	15	13	-	38150212	38150277
323558458	chrX	38147057	38147278	38147082	38147258	RPGR	NM_001034853	2	15	14	-	38147114	38147294
323567697	chrX	38147251	38147472	38147273	38147444	RPGR	NM_001034853	2	15	14	-	38147114	38147294
323456772	chrX	38146231	38146385	38146252	38146357	RPGR	NM_001034853	2	15	15	-	38143702	38146498
323467774	chrX	38146336	38146553	38146358	38146525	RPGR	NM_001034853	2	15	15	-	38143702	38146498

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325386461	chrX	38144715	38144886	38144738	38144861	RPGR	NM_001034853	2	15	15	-	38143702	38146498
325393983	chrX	38144842	38145016	38144862	38144995	RPGR	NM_001034853	2	15	15	-	38143702	38146498
325399829	chrX	38144909	38145051	38144936	38145029	RPGR	NM_001034853	2	15	15	-	38143702	38146498
324213893	chr14	21756022	21756246	21756049	21756225	RPGRIP1	NM_020366	1	24	1	+	21756136	21756220
325049550	chr14	21762749	21762972	21762774	21762946	RPGRIP1	NM_020366	1	24	2	+	21762836	21762968
324857358	chr14	21769095	21769300	21769114	21769282	RPGRIP1	NM_020366	1	24	3	+	21769125	21769396
324860336	chr14	21769264	21769441	21769283	21769419	RPGRIP1	NM_020366	1	24	3	+	21769125	21769396
323593159	chr14	21770563	21770781	21770585	21770753	RPGRIP1	NM_020366	1	24	4	+	21770647	21770743
325288844	chr14	21771375	21771563	21771400	21771541	RPGRIP1	NM_020366	1	24	5	+	21771490	21771702
325294550	chr14	21771517	21771738	21771542	21771717	RPGRIP1	NM_020366	1	24	5	+	21771490	21771702
323987101	chr14	21775803	21776027	21775831	21776004	RPGRIP1	NM_020366	1	24	6	+	21775890	21775995
325625084	chr14	21778563	21778783	21778585	21778755	RPGRIP1	NM_020366	1	24	7	+	21778743	21778766
325625148	chr14	21778733	21778859	21778756	21778831	RPGRIP1	NM_020366	1	24	7	+	21778743	21778766
323848814	chr14	21779806	21780004	21779830	21779983	RPGRIP1	NM_020366	1	24	8	+	21779983	21780129
323866485	chr14	21779960	21780179	21779984	21780151	RPGRIP1	NM_020366	1	24	8	+	21779983	21780129
323675175	chr14	21780467	21780691	21780489	21780670	RPGRIP1	NM_020366	1	24	9	+	21780592	21780665
323686793	chr14	21785821	21786043	21785844	21786018	RPGRIP1	NM_020366	1	24	10	+	21785855	21786009
326339242	chr14	21788007	21788206	21788033	21788180	RPGRIP1	NM_020366	1	24	11	+	21788176	21788336
326351312	chr14	21788158	21788372	21788181	21788344	RPGRIP1	NM_020366	1	24	11	+	21788176	21788336
324321742	chr14	21789387	21789589	21789410	21789566	RPGRIP1	NM_020366	1	24	12	+	21789418	21789561
326429717	chr14	21789972	21790195	21789997	21790169	RPGRIP1	NM_020366	1	24	13	+	21790013	21790163
325241882	chr14	21792741	21792959	21792763	21792938	RPGRIP1	NM_020366	1	24	14	+	21792777	21793229
325261866	chr14	21792893	21793109	21792917	21793085	RPGRIP1	NM_020366	1	24	14	+	21792777	21793229
325294026	chr14	21793062	21793278	21793086	21793254	RPGRIP1	NM_020366	1	24	14	+	21792777	21793229
325108971	chr14	21793351	21793573	21793374	21793554	RPGRIP1	NM_020366	1	24	15	+	21793391	21793542
324854256	chr14	21793958	21794182	21793984	21794160	RPGRIP1	NM_020366	1	24	16	+	21793990	21794332
324890300	chr14	21794140	21794364	21794161	21794339	RPGRIP1	NM_020366	1	24	16	+	21793990	21794332
324216612	chr14	21795699	21795838	21795724	21795814	RPGRIP1	NM_020366	1	24	17	+	21795782	21795966
324224185	chr14	21795794	21796008	21795815	21795986	RPGRIP1	NM_020366	1	24	17	+	21795782	21795966
325826131	chr14	21796468	21796655	21796492	21796633	RPGRIP1	NM_020366	1	24	18	+	21796583	21796786
325851459	chr14	21796613	21796823	21796634	21796796	RPGRIP1	NM_020366	1	24	18	+	21796583	21796786
325703437	chr14	21798389	21798516	21798415	21798489	RPGRIP1	NM_020366	1	24	19	+	21798408	21798546
325709091	chr14	21798423	21798548	21798449	21798521	RPGRIP1	NM_020366	1	24	19	+	21798408	21798546
323354613	chr14	21802672	21802896	21802694	21802869	RPGRIP1	NM_020366	1	24	20	+	21802764	21802864
325250909	chr14	21811103	21811257	21811131	21811235	RPGRIP1	NM_020366	1	24	21	+	21811195	21811387
325258276	chr14	21811213	21811424	21811236	21811403	RPGRIP1	NM_020366	1	24	21	+	21811195	21811387
323662926	chr14	21813215	21813437	21813236	21813411	RPGRIP1	NM_020366	1	24	22	+	21813272	21813356
326097882	chr14	21816282	21816469	21816310	21816446	RPGRIP1	NM_020366	1	24	23	+	21816331	21816461
326098429	chr14	21816424	21816579	21816452	21816550	RPGRIP1	NM_020366	1	24	23	+	21816331	21816461
325109963	chr14	21819209	21819428	21819236	21819400	RPGRIP1	NM_020366	1	24	24	+	21819263	21819460
324578014	chr1	24018154	24018368	24018175	24018347	RPL11	NM_000975	1	6	1	+	24018269	24018319

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324313690	chr1	24019055	24019279	24019077	24019254	RPL11	NM_000975	1	6	2	+	24019099	24019249
325627518	chr1	24020219	24020442	24020241	24020415	RPL11	NM_000975	1	6	3	+	24020297	24020403
323980783	chr1	24021112	24021333	24021138	24021311	RPL11	NM_000975	1	6	4	+	24021150	24021281
325736282	chr1	24022210	24022433	24022235	24022405	RPL11	NM_000975	1	6	5	+	24022288	24022398
325257752	chr1	24022704	24022921	24022728	24022893	RPL11	NM_000975	1	6	6	+	24022834	24022915
324578014	chr1	24018154	24018368	24018175	24018347	RPL11	NM_001199802	2	6	1	+	24018269	24018319
324313690	chr1	24019055	24019279	24019077	24019254	RPL11	NM_001199802	2	6	2	+	24019102	24019249
325627518	chr1	24020219	24020442	24020241	24020415	RPL11	NM_001199802	2	6	3	+	24020297	24020403
323980783	chr1	24021112	24021333	24021138	24021311	RPL11	NM_001199802	2	6	4	+	24021150	24021281
325736282	chr1	24022210	24022433	24022235	24022405	RPL11	NM_001199802	2	6	5	+	24022288	24022398
325257752	chr1	24022704	24022921	24022728	24022893	RPL11	NM_001199802	2	6	6	+	24022834	24022915
325588969	chr3	197677682	197677904	197677703	197677876	RPL35A	NM_000996	1	5	2	+	197677807	197677849
323547167	chr3	197677930	197678125	197677959	197678103	RPL35A	NM_000996	1	5	3	+	197678030	197678182
323557470	chr3	197678083	197678215	197678104	197678191	RPL35A	NM_000996	1	5	3	+	197678030	197678182
324973138	chr3	197680837	197681057	197680862	197681030	RPL35A	NM_000996	1	5	4	+	197680874	197681018
324979717	chr3	197682610	197682762	197682631	197682735	RPL35A	NM_000996	1	5	5	+	197682621	197682721
324164040	chr6	34392809	34393026	34392831	34393003	RPS10	NM_001014	1	6	2	-	34392849	34392998
323319846	chr6	34392347	34392559	34392368	34392532	RPS10	NM_001014	1	6	3	-	34392446	34392617
323340017	chr6	34392511	34392661	34392533	34392633	RPS10	NM_001014	1	6	3	-	34392446	34392617
323617314	chr6	34389392	34389615	34389419	34389589	RPS10	NM_001014	1	6	4	-	34389507	34389584
324557804	chr6	34386051	34386275	34386077	34386249	RPS10	NM_001014	1	6	5	-	34386146	34386201
325925876	chr6	34385128	34385352	34385150	34385329	RPS10	NM_001014	1	6	6	-	34385231	34385324
324164040	chr6	34392809	34393026	34392831	34393003	RPS10	NM_001203245	2	6	2	-	34392849	34392998
323319846	chr6	34392347	34392559	34392368	34392532	RPS10	NM_001203245	2	6	3	-	34392446	34392617
323340017	chr6	34392511	34392661	34392533	34392633	RPS10	NM_001203245	2	6	3	-	34392446	34392617
323617314	chr6	34389392	34389615	34389419	34389589	RPS10	NM_001203245	2	6	4	-	34389507	34389584
324557804	chr6	34386051	34386275	34386077	34386249	RPS10	NM_001203245	2	6	5	-	34386146	34386201
325925876	chr6	34385128	34385352	34385150	34385329	RPS10	NM_001203245	2	6	6	-	34385231	34385324
324164040	chr6	34392809	34393026	34392831	34393003	RPS10	NM_001204091	3	6	2	-	34392849	34392998
323319846	chr6	34392347	34392559	34392368	34392532	RPS10	NM_001204091	3	6	3	-	34392446	34392617
323340017	chr6	34392511	34392661	34392533	34392633	RPS10	NM_001204091	3	6	3	-	34392446	34392617
323617314	chr6	34389392	34389615	34389419	34389589	RPS10	NM_001204091	3	6	4	-	34389507	34389584
324557804	chr6	34386051	34386275	34386077	34386249	RPS10	NM_001204091	3	6	5	-	34386146	34386201
325925876	chr6	34385128	34385352	34385150	34385329	RPS10	NM_001204091	3	6	6	-	34385231	34385324
325083100	chr19	42364812	42364951	42364833	42364931	RPS19	NM_001022	1	6	2	+	42364845	42364915
324570399	chr19	42365087	42365311	42365109	42365288	RPS19	NM_001022	1	6	3	+	42365181	42365281
324222850	chr19	42372960	42373183	42372982	42373161	RPS19	NM_001022	1	6	4	+	42373101	42373284
324235470	chr19	42373141	42373326	42373162	42373303	RPS19	NM_001022	1	6	4	+	42373101	42373284
326302357	chr19	42373676	42373897	42373697	42373873	RPS19	NM_001022	1	6	5	+	42373769	42373823
324910858	chr19	42375329	42375491	42375350	42375463	RPS19	NM_001022	1	6	6	+	42375419	42375484
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_001026	1	5	1	+	79793518	79793662

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_001026	1	5	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_001026	1	5	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_001026	1	5	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_001026	1	5	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_001026	1	5	4	+	79796952	79797062
324839755	chr10	79800279	79800415	79800308	79800393	RPS24	NM_001026	1	5	5	+	79800373	79800473
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_001142282	2	6	1	+	79793518	79793662
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_001142282	2	6	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_001142282	2	6	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_001142282	2	6	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_001142282	2	6	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_001142282	2	6	4	+	79796952	79797062
323629843	chr10	79799816	79800032	79799844	79800005	RPS24	NM_001142282	2	6	5	+	79799959	79799983
324839755	chr10	79800279	79800415	79800308	79800393	RPS24	NM_001142282	2	6	6	+	79800373	79800473
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_001142283	3	7	1	+	79793518	79793662
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_001142283	3	7	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_001142283	3	7	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_001142283	3	7	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_001142283	3	7	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_001142283	3	7	4	+	79796952	79797062
323733567	chr10	79797541	79797759	79797565	79797734	RPS24	NM_001142283	3	7	5	+	79797720	79797740
323629843	chr10	79799816	79800032	79799844	79800005	RPS24	NM_001142283	3	7	6	+	79799962	79799983
324839755	chr10	79800279	79800415	79800308	79800393	RPS24	NM_001142283	3	7	7	+	79800373	79800473
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_001142284	4	7	1	+	79793518	79793662
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_001142284	4	7	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_001142284	4	7	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_001142284	4	7	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_001142284	4	7	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_001142284	4	7	4	+	79796952	79797062
323733567	chr10	79797541	79797759	79797565	79797734	RPS24	NM_001142284	4	7	5	+	79797723	79797740
323629843	chr10	79799816	79800032	79799844	79800005	RPS24	NM_001142284	4	7	6	+	79799962	79799983
324839755	chr10	79800279	79800415	79800308	79800393	RPS24	NM_001142284	4	7	7	+	79800373	79800473
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_001142285	5	5	1	+	79793518	79793662
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_001142285	5	5	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_001142285	5	5	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_001142285	5	5	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_001142285	5	5	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_001142285	5	5	4	+	79796952	79797062
325798477	chr10	79814163	79814380	79814184	79814356	RPS24	NM_001142285	5	5	5	+	79814289	79816571
325821034	chr10	79814334	79814548	79814357	79814530	RPS24	NM_001142285	5	5	5	+	79814289	79816571
324255244	chr10	79793499	79793716	79793519	79793697	RPS24	NM_033022	6	6	1	+	79793518	79793662

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324738087	chr10	79794994	79795208	79795021	79795181	RPS24	NM_033022	6	6	2	+	79795110	79795175
324623144	chr10	79795162	79795335	79795187	79795310	RPS24	NM_033022	6	6	3	+	79795269	79795478
324631472	chr10	79795291	79795512	79795311	79795485	RPS24	NM_033022	6	6	3	+	79795269	79795478
324145309	chr10	79796873	79797069	79796895	79797046	RPS24	NM_033022	6	6	4	+	79796952	79797062
324147784	chr10	79797028	79797245	79797047	79797218	RPS24	NM_033022	6	6	4	+	79796952	79797062
323629843	chr10	79799816	79800032	79799844	79800005	RPS24	NM_033022	6	6	5	+	79799962	79799983
324839755	chr10	79800279	79800415	79800308	79800393	RPS24	NM_033022	6	6	6	+	79800373	79800473
324191260	chr12	56435815	56436022	56435843	56436001	RPS26	NM_001029	1	4	1	+	56435686	56435953
324652050	chr12	56436172	56436345	56436193	56436322	RPS26	NM_001029	1	4	2	+	56436209	56436386
324673270	chr12	56436297	56436429	56436323	56436405	RPS26	NM_001029	1	4	2	+	56436209	56436386
323353481	chr12	56437022	56437187	56437045	56437159	RPS26	NM_001029	1	4	3	+	56437147	56437277
323361128	chr12	56437132	56437341	56437160	56437315	RPS26	NM_001029	1	4	3	+	56437147	56437277
324733852	chr12	56437745	56437969	56437768	56437943	RPS26	NM_001029	1	4	4	+	56437903	56438007
325247391	chrX	20252744	20252968	20252772	20252945	RPS6KA3	NM_004586	1	22	2	-	20252876	20252932
325584775	chrX	20227284	20227432	20227310	20227407	RPS6KA3	NM_004586	1	22	3	-	20227406	20227522
325589931	chrX	20227383	20227554	20227408	20227527	RPS6KA3	NM_004586	1	22	3	-	20227406	20227522
323940311	chrX	20221976	20222196	20222001	20222172	RPS6KA3	NM_004586	1	22	4	-	20222140	20222221
323949621	chrX	20222146	20222293	20222170	20222260	RPS6KA3	NM_004586	1	22	4	-	20222140	20222221
324620555	chrX	20213130	20213346	20213153	20213319	RPS6KA3	NM_004586	1	22	5	-	20213183	20213263
323667823	chrX	20212170	20212387	20212196	20212362	RPS6KA3	NM_004586	1	22	6	-	20212307	20212386
323668436	chrX	20212335	20212546	20212363	20212516	RPS6KA3	NM_004586	1	22	6	-	20212307	20212386
324871822	chrX	20211519	20211715	20211543	20211687	RPS6KA3	NM_004586	1	22	7	-	20211605	20211711
324872997	chrX	20211669	20211890	20211697	20211858	RPS6KA3	NM_004586	1	22	7	-	20211605	20211711
324347691	chrX	20206538	20206743	20206566	20206714	RPS6KA3	NM_004586	1	22	8	-	20206615	20206652
324993310	chrX	20205875	20206099	20205901	20206077	RPS6KA3	NM_004586	1	22	9	-	20205946	20206088
326102961	chrX	20195040	20195201	20195068	20195181	RPS6KA3	NM_004586	1	22	11	-	20195114	20195202
324089359	chrX	20194429	20194629	20194451	20194605	RPS6KA3	NM_004586	1	22	12	-	20194552	20194616
324090561	chrX	20194442	20194646	20194470	20194613	RPS6KA3	NM_004586	1	22	12	-	20194552	20194616
324087316	chrX	20194282	20194479	20194308	20194452	RPS6KA3	NM_004586	1	22	13	-	20194368	20194470
324089359	chrX	20194429	20194629	20194451	20194605	RPS6KA3	NM_004586	1	22	13	-	20194368	20194470
324090561	chrX	20194442	20194646	20194470	20194613	RPS6KA3	NM_004586	1	22	13	-	20194368	20194470
323840795	chrX	20193188	20193317	20193216	20193293	RPS6KA3	NM_004586	1	22	14	-	20193282	20193406
323840888	chrX	20193270	20193473	20193294	20193445	RPS6KA3	NM_004586	1	22	14	-	20193282	20193406
326132618	chrX	20190805	20191029	20190830	20191000	RPS6KA3	NM_004586	1	22	15	-	20190864	20190989
324183703	chrX	20187411	20187571	20187435	20187544	RPS6KA3	NM_004586	1	22	16	-	20187520	20187609
324184504	chrX	20187529	20187698	20187555	20187670	RPS6KA3	NM_004586	1	22	16	-	20187520	20187609
325037960	chrX	20185571	20185754	20185598	20185725	RPS6KA3	NM_004586	1	22	17	-	20185707	20185865
325039322	chrX	20185702	20185925	20185726	20185898	RPS6KA3	NM_004586	1	22	17	-	20185707	20185865
324808662	chrX	20182984	20183139	20183011	20183114	RPS6KA3	NM_004586	1	22	18	-	20183017	20183178
324818887	chrX	20183087	20183264	20183115	20183236	RPS6KA3	NM_004586	1	22	18	-	20183017	20183178
324618966	chrX	20181026	20181150	20181052	20181127	RPS6KA3	NM_004586	1	22	19	-	20181082	20181158

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324622088	chrX	20181100	20181283	20181128	20181254	RPS6KA3	NM_004586	1	22	19	-	20181082	20181158
324489070	chrX	20179799	20180023	20179823	20179995	RPS6KA3	NM_004586	1	22	20	-	20179762	20179879
325045995	chrX	20174068	20174280	20174093	20174256	RPS6KA3	NM_004586	1	22	21	-	20174227	20174367
325087480	chrX	20174236	20174414	20174257	20174386	RPS6KA3	NM_004586	1	22	21	-	20174227	20174367
326247314	chrX	20173472	20173695	20173497	20173670	RPS6KA3	NM_004586	1	22	22	-	20168029	20173638
324983994	chr2	3623063	3623286	3623083	3623265	RPS7	NM_001011	1	7	2	+	3623182	3623274
324986890	chr2	3623216	3623418	3623237	3623395	RPS7	NM_001011	1	7	2	+	3623182	3623274
323827697	chr2	3623379	3623576	3623398	3623552	RPS7	NM_001011	1	7	3	+	3623407	3623478
323782787	chr2	3624026	3624249	3624053	3624226	RPS7	NM_001011	1	7	4	+	3624077	3624220
324026125	chr2	3625176	3625400	3625201	3625373	RPS7	NM_001011	1	7	5	+	3625300	3625364
325230427	chr2	3627663	3627887	3627690	3627859	RPS7	NM_001011	1	7	6	+	3627700	3627850
326295274	chr2	3628344	3628553	3628371	3628525	RPS7	NM_001011	1	7	7	+	3628395	3628509
324730207	chrX	18689968	18690170	18689991	18690142	RS1	NM_000330	1	6	1	-	18690137	18690223
324733521	chrX	18690115	18690239	18690143	18690217	RS1	NM_000330	1	6	1	-	18690137	18690223
324902467	chrX	18675719	18675847	18675747	18675820	RS1	NM_000330	1	6	2	-	18675760	18675785
324595974	chrX	18674700	18674924	18674724	18674902	RS1	NM_000330	1	6	3	-	18674773	18674878
324260803	chrX	18665301	18665505	18665319	18665477	RS1	NM_000330	1	6	4	-	18665311	18665452
323928176	chrX	18662420	18662596	18662441	18662573	RS1	NM_000330	1	6	5	-	18662550	18662745
323945422	chrX	18662552	18662772	18662574	18662750	RS1	NM_000330	1	6	5	-	18662550	18662745
324660013	chrX	18660024	18660248	18660047	18660229	RS1	NM_000330	1	6	6	-	18657808	18660276
324673873	chrX	18660200	18660406	18660220	18660383	RS1	NM_000330	1	6	6	-	18657808	18660276
323715581	chr6	116938118	116938342	116938139	116938317	RSPH4A	NM_001010892	1	6	1	+	116937642	116938472
323755191	chr6	116938294	116938518	116938318	116938491	RSPH4A	NM_001010892	1	6	1	+	116937642	116938472
325619256	chr6	116937697	116937915	116937719	116937895	RSPH4A	NM_001010892	1	6	1	+	116937642	116938472
325636718	chr6	116937869	116938035	116937892	116938012	RSPH4A	NM_001010892	1	6	1	+	116937642	116938472
325640801	chr6	116937979	116938161	116937999	116938139	RSPH4A	NM_001010892	1	6	1	+	116937642	116938472
323468034	chr6	116943874	116944075	116943901	116944047	RSPH4A	NM_001010892	1	6	2	+	116943931	116944165
323471596	chr6	116944012	116944229	116944035	116944207	RSPH4A	NM_001010892	1	6	2	+	116943931	116944165
325149951	chr6	116948673	116948856	116948700	116948828	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325155216	chr6	116949245	116949464	116949270	116949440	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325168258	chr6	116948803	116948994	116948829	116948966	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325178377	chr6	116949419	116949625	116949441	116949597	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325203845	chr6	116948939	116949152	116948967	116949127	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325221161	chr6	116949107	116949291	116949128	116949269	RSPH4A	NM_001010892	1	6	3	+	116948792	116949532
325371428	chr6	116950635	116950859	116950662	116950833	RSPH4A	NM_001010892	1	6	4	+	116950730	116950865
325376216	chr6	116950802	116951023	116950830	116950999	RSPH4A	NM_001010892	1	6	4	+	116950730	116950865
323711616	chr6	116951435	116951639	116951461	116951616	RSPH4A	NM_001010892	1	6	5	+	116951598	116951715
323720729	chr6	116951589	116951761	116951615	116951733	RSPH4A	NM_001010892	1	6	5	+	116951598	116951715
323810224	chr6	116953301	116953515	116953329	116953495	RSPH4A	NM_001010892	1	6	6	+	116953370	116954148
323819211	chr6	116953466	116953652	116953494	116953627	RSPH4A	NM_001010892	1	6	6	+	116953370	116954148
323715581	chr6	116938118	116938342	116938139	116938317	RSPH4A	NM_001161664	2	5	1	+	116937642	116938472

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323755191	chr6	116938294	116938518	116938318	116938491	RSPH4A	NM_001161664	2	5	1	+	116937642	116938472
325619256	chr6	116937697	116937915	116937719	116937895	RSPH4A	NM_001161664	2	5	1	+	116937642	116938472
325636718	chr6	116937869	116938035	116937892	116938012	RSPH4A	NM_001161664	2	5	1	+	116937642	116938472
325640801	chr6	116937979	116938161	116937999	116938139	RSPH4A	NM_001161664	2	5	1	+	116937642	116938472
323468034	chr6	116943874	116944075	116943901	116944047	RSPH4A	NM_001161664	2	5	2	+	116943931	116944165
323471596	chr6	116944012	116944229	116944035	116944207	RSPH4A	NM_001161664	2	5	2	+	116943931	116944165
325149951	chr6	116948673	116948856	116948700	116948828	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
325155216	chr6	116949245	116949464	116949270	116949440	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
325168258	chr6	116948803	116948994	116948829	116948966	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
325178377	chr6	116949419	116949625	116949441	116949597	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
325203845	chr6	116948939	116949152	116948967	116949127	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
325221161	chr6	116949107	116949291	116949128	116949269	RSPH4A	NM_001161664	2	5	3	+	116948792	116949532
323711616	chr6	116951435	116951639	116951461	116951616	RSPH4A	NM_001161664	2	5	4	+	116951598	116951715
323720729	chr6	116951589	116951761	116951615	116951733	RSPH4A	NM_001161664	2	5	4	+	116951598	116951715
323810224	chr6	116953301	116953515	116953329	116953495	RSPH4A	NM_001161664	2	5	5	+	116953370	116954148
323819211	chr6	116953466	116953652	116953494	116953627	RSPH4A	NM_001161664	2	5	5	+	116953370	116954148
324623989	chr6	43612800	43613021	43612817	43613000	RSPH9	NM_001193341	1	6	1	+	43612767	43613062
324628790	chr6	43612953	43613147	43612976	43613128	RSPH9	NM_001193341	1	6	1	+	43612767	43613062
326384993	chr6	43618065	43618289	43618088	43618261	RSPH9	NM_001193341	1	6	2	+	43618112	43618277
326401420	chr6	43618234	43618358	43618262	43618330	RSPH9	NM_001193341	1	6	2	+	43618112	43618277
324299616	chr6	43623286	43623487	43623307	43623461	RSPH9	NM_001193341	1	6	3	+	43623344	43623428
326195152	chr6	43624270	43624485	43624295	43624465	RSPH9	NM_001193341	1	6	4	+	43624314	43624460
325258883	chr6	43634058	43634282	43634081	43634262	RSPH9	NM_001193341	1	6	5	+	43634161	43634257
324148827	chr6	43638499	43638695	43638520	43638671	RSPH9	NM_001193341	1	6	6	+	43638526	43638748
324157291	chr6	43638650	43638788	43638672	43638760	RSPH9	NM_001193341	1	6	6	+	43638526	43638748
324623989	chr6	43612800	43613021	43612817	43613000	RSPH9	NM_152732	2	5	1	+	43612767	43613062
324628790	chr6	43612953	43613147	43612976	43613128	RSPH9	NM_152732	2	5	1	+	43612767	43613062
326384993	chr6	43618065	43618289	43618088	43618261	RSPH9	NM_152732	2	5	2	+	43618112	43618277
326401420	chr6	43618234	43618358	43618262	43618330	RSPH9	NM_152732	2	5	2	+	43618112	43618277
324294029	chr6	43623164	43623326	43623182	43623306	RSPH9	NM_152732	2	5	3	+	43623299	43623428
324299616	chr6	43623286	43623487	43623307	43623461	RSPH9	NM_152732	2	5	3	+	43623299	43623428
326195152	chr6	43624270	43624485	43624295	43624465	RSPH9	NM_152732	2	5	4	+	43624314	43624460
324148827	chr6	43638499	43638695	43638520	43638671	RSPH9	NM_152732	2	5	5	+	43638526	43638748
324157291	chr6	43638650	43638788	43638672	43638760	RSPH9	NM_152732	2	5	5	+	43638526	43638748
323496723	chr19	38924318	38924540	38924338	38924519	RYR1	NM_000540	1	106	1	+	38924340	38924514
325330745	chr19	38931228	38931441	38931249	38931421	RYR1	NM_000540	1	106	2	+	38931385	38931504
325336715	chr19	38931375	38931589	38931394	38931567	RYR1	NM_000540	1	106	2	+	38931385	38931504
326388399	chr19	38932949	38933169	38932972	38933151	RYR1	NM_000540	1	106	3	+	38932989	38933093
324609045	chr19	38934159	38934370	38934182	38934346	RYR1	NM_000540	1	106	4	+	38934198	38934272
324589668	chr19	38934330	38934548	38934350	38934526	RYR1	NM_000540	1	106	5	+	38934358	38934436
325924063	chr19	38934733	38934914	38934754	38934894	RYR1	NM_000540	1	106	6	+	38934789	38934901

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325929436	chr19	38934871	38935087	38934892	38935065	RYR1	NM_000540	1	106	6	+	38934789	38934901
323362558	chr19	38935182	38935380	38935202	38935357	RYR1	NM_000540	1	106	7	+	38935224	38935317
324818329	chr19	38937075	38937291	38937096	38937264	RYR1	NM_000540	1	106	8	+	38937112	38937205
323783226	chr19	38937263	38937485	38937289	38937463	RYR1	NM_000540	1	106	9	+	38937334	38937408
323438384	chr19	38938930	38939134	38938955	38939113	RYR1	NM_000540	1	106	10	+	38938995	38939151
323443077	chr19	38939057	38939262	38939076	38939240	RYR1	NM_000540	1	106	10	+	38938995	38939151
325262487	chr19	38939255	38939460	38939274	38939439	RYR1	NM_000540	1	106	11	+	38939289	38939453
325269072	chr19	38939385	38939597	38939406	38939578	RYR1	NM_000540	1	106	11	+	38939289	38939453
325090951	chr19	38942312	38942532	38942333	38942509	RYR1	NM_000540	1	106	12	+	38942404	38942525
325096537	chr19	38942490	38942614	38942510	38942590	RYR1	NM_000540	1	106	12	+	38942404	38942525
325923676	chr19	38943401	38943603	38943420	38943583	RYR1	NM_000540	1	106	13	+	38943459	38943654
325926226	chr19	38943542	38943763	38943564	38943744	RYR1	NM_000540	1	106	13	+	38943459	38943654
324670052	chr19	38945705	38945925	38945726	38945900	RYR1	NM_000540	1	106	14	+	38945875	38946010
324701131	chr19	38945879	38946080	38945901	38946055	RYR1	NM_000540	1	106	14	+	38945875	38946010
323881149	chr19	38946046	38946264	38946069	38946243	RYR1	NM_000540	1	106	15	+	38946091	38946186
323995581	chr19	38946238	38946443	38946258	38946422	RYR1	NM_000540	1	106	16	+	38946273	38946391
324277054	chr19	38948095	38948316	38948116	38948293	RYR1	NM_000540	1	106	17	+	38948137	38948270
324648804	chr19	38948599	38948770	38948623	38948748	RYR1	NM_000540	1	106	18	+	38948691	38948932
324663247	chr19	38948727	38948929	38948748	38948906	RYR1	NM_000540	1	106	18	+	38948691	38948932
324673749	chr19	38948885	38949009	38948907	38948981	RYR1	NM_000540	1	106	18	+	38948691	38948932
323566784	chr19	38949701	38949925	38949725	38949904	RYR1	NM_000540	1	106	19	+	38949786	38949978
323574149	chr19	38949874	38950039	38949894	38950017	RYR1	NM_000540	1	106	19	+	38949786	38949978
324568762	chr19	38950959	38951150	38950980	38951131	RYR1	NM_000540	1	106	20	+	38951015	38951231
324580408	chr19	38951109	38951264	38951132	38951243	RYR1	NM_000540	1	106	20	+	38951015	38951231
323735240	chr19	38954003	38954219	38954026	38954201	RYR1	NM_000540	1	106	21	+	38954063	38954167
326298995	chr19	38954280	38954504	38954299	38954487	RYR1	NM_000540	1	106	22	+	38954387	38954490
323815332	chr19	38955247	38955461	38955264	38955442	RYR1	NM_000540	1	106	23	+	38955279	38955362
326166543	chr19	38956704	38956892	38956722	38956874	RYR1	NM_000540	1	106	24	+	38956731	38957038
326173245	chr19	38956823	38957029	38956844	38957010	RYR1	NM_000540	1	106	24	+	38956731	38957038
326175397	chr19	38956993	38957124	38957011	38957102	RYR1	NM_000540	1	106	24	+	38956731	38957038
323524607	chr19	38958135	38958353	38958157	38958329	RYR1	NM_000540	1	106	25	+	38958250	38958452
323554948	chr19	38958294	38958516	38958317	38958494	RYR1	NM_000540	1	106	25	+	38958250	38958452
325328629	chr19	38959570	38959783	38959591	38959761	RYR1	NM_000540	1	106	26	+	38959606	38959780
325340178	chr19	38959731	38959952	38959751	38959935	RYR1	NM_000540	1	106	26	+	38959606	38959780
325148773	chr19	38959944	38960086	38959961	38960069	RYR1	NM_000540	1	106	27	+	38959945	38960153
325153981	chr19	38960044	38960214	38960064	38960192	RYR1	NM_000540	1	106	27	+	38959945	38960153
323459942	chr19	38963942	38964149	38963963	38964130	RYR1	NM_000540	1	106	28	+	38964017	38964411
323463741	chr19	38964094	38964305	38964116	38964284	RYR1	NM_000540	1	106	28	+	38964017	38964411
323466011	chr19	38964232	38964417	38964254	38964392	RYR1	NM_000540	1	106	28	+	38964017	38964411
323466270	chr19	38964369	38964573	38964391	38964546	RYR1	NM_000540	1	106	28	+	38964017	38964411
325658235	chr19	38965914	38966119	38965935	38966095	RYR1	NM_000540	1	106	29	+	38965958	38966090

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326401120	chr19	38968259	38968457	38968282	38968436	RYR1	NM_000540	1	106	30	+	38968350	38968510
326411812	chr19	38968416	38968629	38968437	38968608	RYR1	NM_000540	1	106	30	+	38968350	38968510
323315626	chr19	38969021	38969220	38969042	38969197	RYR1	NM_000540	1	106	31	+	38969075	38969240
323339414	chr19	38969177	38969309	38969198	38969284	RYR1	NM_000540	1	106	31	+	38969075	38969240
323775548	chr19	38973564	38973784	38973587	38973764	RYR1	NM_000540	1	106	32	+	38973667	38973753
323490186	chr19	38973850	38974065	38973871	38974046	RYR1	NM_000540	1	106	33	+	38973930	38974156
323495295	chr19	38974017	38974190	38974037	38974172	RYR1	NM_000540	1	106	33	+	38973930	38974156
325391912	chr19	38976685	38976900	38976702	38976877	RYR1	NM_000540	1	106	34	+	38976230	38976842
325396407	chr19	38976174	38976380	38976194	38976362	RYR1	NM_000540	1	106	34	+	38976230	38976842
325404126	chr19	38976344	38976566	38976363	38976543	RYR1	NM_000540	1	106	34	+	38976230	38976842
325411553	chr19	38976524	38976740	38976544	38976720	RYR1	NM_000540	1	106	34	+	38976230	38976842
324765917	chr19	38979683	38979862	38979703	38979834	RYR1	NM_000540	1	106	35	+	38979817	38980083
324785400	chr19	38979810	38980029	38979833	38980006	RYR1	NM_000540	1	106	35	+	38979817	38980083
324796243	chr19	38979870	38980092	38979891	38980071	RYR1	NM_000540	1	106	35	+	38979817	38980083
324801285	chr19	38980050	38980210	38980072	38980187	RYR1	NM_000540	1	106	35	+	38979817	38980083
325117755	chr19	38980666	38980887	38980688	38980867	RYR1	NM_000540	1	106	36	+	38980716	38980916
325129747	chr19	38980839	38980999	38980863	38980977	RYR1	NM_000540	1	106	36	+	38980716	38980916
323816438	chr19	38981203	38981427	38981225	38981403	RYR1	NM_000540	1	106	37	+	38981261	38981372
323869753	chr19	38983098	38983241	38983120	38983216	RYR1	NM_000540	1	106	38	+	38983130	38983276
323877630	chr19	38983190	38983405	38983213	38983383	RYR1	NM_000540	1	106	38	+	38983130	38983276
324315447	chr19	38984962	38985181	38984983	38985161	RYR1	NM_000540	1	106	39	+	38984992	38985265
324320905	chr19	38985140	38985342	38985161	38985314	RYR1	NM_000540	1	106	39	+	38984992	38985265
323692950	chr19	38986826	38987002	38986843	38986985	RYR1	NM_000540	1	106	40	+	38986855	38986969
323699665	chr19	38986919	38987140	38986939	38987120	RYR1	NM_000540	1	106	40	+	38986855	38986969
323699665	chr19	38986919	38987140	38986939	38987120	RYR1	NM_000540	1	106	41	+	38987049	38987181
325609143	chr19	38987087	38987267	38987111	38987247	RYR1	NM_000540	1	106	41	+	38987049	38987181
324106178	chr19	38987453	38987642	38987475	38987622	RYR1	NM_000540	1	106	42	+	38987500	38987594
324070619	chr19	38989710	38989934	38989731	38989911	RYR1	NM_000540	1	106	43	+	38989748	38989883
323338038	chr19	38990375	38990585	38990394	38990565	RYR1	NM_000540	1	106	44	+	38990275	38990461
324288298	chr19	38990224	38990412	38990245	38990394	RYR1	NM_000540	1	106	44	+	38990275	38990461
323338038	chr19	38990375	38990585	38990394	38990565	RYR1	NM_000540	1	106	45	+	38990548	38990656
323341206	chr19	38990476	38990668	38990496	38990646	RYR1	NM_000540	1	106	45	+	38990548	38990656
323346137	chr19	38990602	38990746	38990623	38990728	RYR1	NM_000540	1	106	45	+	38990548	38990656
325127543	chr19	38991177	38991398	38991197	38991377	RYR1	NM_000540	1	106	46	+	38991246	38991366
324359005	chr19	38991377	38991574	38991398	38991552	RYR1	NM_000540	1	106	47	+	38991461	38991630
324367140	chr19	38991528	38991745	38991549	38991717	RYR1	NM_000540	1	106	47	+	38991461	38991630
324720460	chr19	38993072	38993295	38993092	38993273	RYR1	NM_000540	1	106	48	+	38993147	38993367
324724838	chr19	38993233	38993370	38993252	38993351	RYR1	NM_000540	1	106	48	+	38993147	38993367
324726906	chr19	38993330	38993516	38993350	38993494	RYR1	NM_000540	1	106	48	+	38993147	38993367
324881683	chr19	38993489	38993635	38993513	38993615	RYR1	NM_000540	1	106	49	+	38993520	38993610
325241886	chr19	38994826	38995042	38994847	38995020	RYR1	NM_000540	1	106	50	+	38994860	38995000

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325102790	chr19	38995223	38995409	38995248	38995389	RYR1	NM_000540	1	106	51	+	38995388	38995551
325112384	chr19	38995369	38995590	38995390	38995566	RYR1	NM_000540	1	106	51	+	38995388	38995551
324697384	chr19	38995535	38995758	38995555	38995734	RYR1	NM_000540	1	106	52	+	38995643	38995721
324103423	chr19	38995819	38995977	38995840	38995952	RYR1	NM_000540	1	106	53	+	38995949	38996038
324113041	chr19	38995931	38996082	38995953	38996058	RYR1	NM_000540	1	106	53	+	38995949	38996038
324572657	chr19	38996286	38996496	38996307	38996475	RYR1	NM_000540	1	106	54	+	38996446	38996586
324598428	chr19	38996453	38996653	38996473	38996632	RYR1	NM_000540	1	106	54	+	38996446	38996586
323828744	chr19	38996937	38997161	38996962	38997144	RYR1	NM_000540	1	106	55	+	38996943	38997017
323928929	chr19	38996915	38997087	38996935	38997066	RYR1	NM_000540	1	106	55	+	38996943	38997017
323828744	chr19	38996937	38997161	38996962	38997144	RYR1	NM_000540	1	106	56	+	38997111	38997186
323839039	chr19	38997120	38997339	38997145	38997317	RYR1	NM_000540	1	106	56	+	38997111	38997186
323360728	chr19	38997394	38997592	38997415	38997571	RYR1	NM_000540	1	106	57	+	38997469	38997592
323369502	chr19	38997548	38997718	38997572	38997696	RYR1	NM_000540	1	106	57	+	38997469	38997592
323647323	chr19	38998321	38998545	38998343	38998524	RYR1	NM_000540	1	106	58	+	38998352	38998467
326281703	chr19	39001062	39001284	39001084	39001261	RYR1	NM_000540	1	106	59	+	39001138	39001205
323445502	chr19	39001268	39001489	39001289	39001465	RYR1	NM_000540	1	106	60	+	39001300	39001421
325134860	chr19	39002099	39002321	39002123	39002299	RYR1	NM_000540	1	106	61	+	39002201	39002250
325004829	chr19	39002657	39002862	39002679	39002841	RYR1	NM_000540	1	106	62	+	39002712	39002772
323853243	chr19	39002842	39003060	39002864	39003040	RYR1	NM_000540	1	106	63	+	39002885	39003123
323863633	chr19	39003023	39003238	39003041	39003212	RYR1	NM_000540	1	106	63	+	39002885	39003123
324244699	chr19	39005618	39005831	39005637	39005809	RYR1	NM_000540	1	106	64	+	39005666	39005747
323470921	chr19	39006692	39006901	39006712	39006880	RYR1	NM_000540	1	106	65	+	39006727	39006857
323811168	chr19	39007956	39008136	39007976	39008115	RYR1	NM_000540	1	106	66	+	39007999	39008331
323817799	chr19	39008092	39008291	39008111	39008263	RYR1	NM_000540	1	106	66	+	39007999	39008331
323824208	chr19	39008234	39008447	39008255	39008424	RYR1	NM_000540	1	106	66	+	39007999	39008331
323382731	chr19	39009701	39009921	39009726	39009897	RYR1	NM_000540	1	106	67	+	39009854	39010094
323393848	chr19	39009852	39010064	39009871	39010044	RYR1	NM_000540	1	106	67	+	39009854	39010094
323399556	chr19	39010020	39010233	39010041	39010210	RYR1	NM_000540	1	106	67	+	39009854	39010094
323885984	chr19	39013702	39013926	39013723	39013904	RYR1	NM_000540	1	106	68	+	39013668	39013755
326214327	chr19	39013527	39013751	39013548	39013725	RYR1	NM_000540	1	106	68	+	39013668	39013755
323885984	chr19	39013702	39013926	39013723	39013904	RYR1	NM_000540	1	106	69	+	39013857	39013949
323894448	chr19	39013824	39014015	39013843	39013993	RYR1	NM_000540	1	106	69	+	39013857	39013949
324240873	chr19	39014418	39014599	39014439	39014580	RYR1	NM_000540	1	106	70	+	39014555	39014569
325133311	chr19	39015839	39016063	39015857	39016043	RYR1	NM_000540	1	106	71	+	39015972	39016142
325138222	chr19	39016022	39016237	39016043	39016215	RYR1	NM_000540	1	106	71	+	39015972	39016142
324929983	chr19	39017519	39017721	39017542	39017698	RYR1	NM_000540	1	106	72	+	39017633	39017692
323619319	chr19	39018193	39018415	39018216	39018395	RYR1	NM_000540	1	106	73	+	39018287	39018424
323623482	chr19	39018370	39018582	39018390	39018559	RYR1	NM_000540	1	106	73	+	39018287	39018424
326337790	chr19	39018914	39019132	39018934	39019109	RYR1	NM_000540	1	106	74	+	39018946	39019058
324046920	chr19	39019107	39019320	39019128	39019299	RYR1	NM_000540	1	106	75	+	39019239	39019335
324055466	chr19	39019278	39019449	39019300	39019424	RYR1	NM_000540	1	106	75	+	39019239	39019335

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323679501	chr19	39019551	39019704	39019574	39019682	RYR1	NM_000540	1	106	76	+	39019591	39019697
323682310	chr19	39019653	39019847	39019673	39019819	RYR1	NM_000540	1	106	76	+	39019591	39019697
323791223	chr19	39023102	39023294	39023122	39023269	RYR1	NM_000540	1	106	77	+	39023130	39023181
325680639	chr19	39023157	39023378	39023180	39023356	RYR1	NM_000540	1	106	77	+	39023130	39023181
325680639	chr19	39023157	39023378	39023180	39023356	RYR1	NM_000540	1	106	78	+	39023311	39023376
325698417	chr19	39023336	39023533	39023357	39023510	RYR1	NM_000540	1	106	78	+	39023311	39023376
323971438	chr19	39025319	39025518	39025340	39025495	RYR1	NM_000540	1	106	79	+	39025360	39025459
324274710	chr19	39025669	39025893	39025693	39025870	RYR1	NM_000540	1	106	80	+	39025781	39025860
324969068	chr19	39025847	39026062	39025868	39026037	RYR1	NM_000540	1	106	81	+	39025956	39026032
323332797	chr19	39026594	39026764	39026616	39026740	RYR1	NM_000540	1	106	82	+	39026637	39026710
325310926	chr19	39027358	39027496	39027379	39027476	RYR1	NM_000540	1	106	83	+	39027390	39027407
324123774	chr19	39028467	39028681	39028486	39028658	RYR1	NM_000540	1	106	84	+	39028520	39028600
323729237	chr19	39033927	39034103	39033948	39034083	RYR1	NM_000540	1	106	85	+	39033987	39034075
323739574	chr19	39033990	39034210	39034012	39034188	RYR1	NM_000540	1	106	85	+	39033987	39034075
323739574	chr19	39033990	39034210	39034012	39034188	RYR1	NM_000540	1	106	86	+	39034172	39034300
326121562	chr19	39034168	39034368	39034189	39034346	RYR1	NM_000540	1	106	86	+	39034172	39034300
323417699	chr19	39034349	39034511	39034370	39034490	RYR1	NM_000540	1	106	87	+	39034411	39034515
323421920	chr19	39034469	39034666	39034489	39034643	RYR1	NM_000540	1	106	87	+	39034411	39034515
324935836	chr19	39037039	39037218	39037060	39037193	RYR1	NM_000540	1	106	88	+	39037085	39037166
325632787	chr19	39038823	39038961	39038842	39038935	RYR1	NM_000540	1	106	89	+	39038873	39039060
325642688	chr19	39038916	39039084	39038936	39039067	RYR1	NM_000540	1	106	89	+	39038873	39039060
324237764	chr19	39051701	39051843	39051723	39051818	RYR1	NM_000540	1	106	90	+	39051753	39052094
324241277	chr19	39051785	39051930	39051808	39051911	RYR1	NM_000540	1	106	90	+	39051753	39052094
324244483	chr19	39051875	39052071	39051893	39052049	RYR1	NM_000540	1	106	90	+	39051753	39052094
324248769	chr19	39052031	39052254	39052049	39052230	RYR1	NM_000540	1	106	90	+	39051753	39052094
326283601	chr19	39056285	39056460	39056302	39056437	RYR1	NM_000540	1	106	91	+	39055599	39056411
326284789	chr19	39055509	39055642	39055528	39055621	RYR1	NM_000540	1	106	91	+	39055599	39056411
326286850	chr19	39055604	39055738	39055622	39055721	RYR1	NM_000540	1	106	91	+	39055599	39056411
326287558	chr19	39055685	39055904	39055706	39055887	RYR1	NM_000540	1	106	91	+	39055599	39056411
326287708	chr19	39055887	39056111	39055904	39056094	RYR1	NM_000540	1	106	91	+	39055599	39056411
324774571	chr19	39057421	39057643	39057444	39057625	RYR1	NM_000540	1	106	92	+	39057551	39057627
323543241	chr19	39058379	39058595	39058399	39058573	RYR1	NM_000540	1	106	93	+	39058413	39058557
325308791	chr19	39061162	39061386	39061188	39061365	RYR1	NM_000540	1	106	94	+	39061247	39061333
323996229	chr19	39062622	39062822	39062643	39062800	RYR1	NM_000540	1	106	95	+	39062659	39062910
324007061	chr19	39062778	39062914	39062801	39062888	RYR1	NM_000540	1	106	95	+	39062659	39062910
324015835	chr19	39062869	39063089	39062889	39063068	RYR1	NM_000540	1	106	95	+	39062659	39062910
326220829	chr19	39063780	39063998	39063797	39063980	RYR1	NM_000540	1	106	96	+	39063817	39063947
324855718	chr19	39066501	39066666	39066522	39066648	RYR1	NM_000540	1	106	97	+	39066559	39066601
323484623	chr19	39068529	39068752	39068551	39068731	RYR1	NM_000540	1	106	98	+	39068558	39068688
323314946	chr19	39068730	39068912	39068751	39068892	RYR1	NM_000540	1	106	99	+	39068784	39068844
325318817	chr19	39070475	39070689	39070495	39070663	RYR1	NM_000540	1	106	100	+	39070622	39070768

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325332277	chr19	39070639	39070840	39070664	39070818	RYR1	NM_000540	1	106	100	+	39070622	39070768
325455778	chr19	39070984	39071152	39071001	39071133	RYR1	NM_000540	1	106	101	+	39071010	39071144
323863111	chr19	39075565	39075694	39075583	39075672	RYR1	NM_000540	1	106	102	+	39075583	39075739
323867845	chr19	39075591	39075732	39075613	39075711	RYR1	NM_000540	1	106	102	+	39075583	39075739
323678203	chr19	39076499	39076693	39076520	39076672	RYR1	NM_000540	1	106	103	+	39076578	39076642
324326830	chr19	39076699	39076906	39076721	39076884	RYR1	NM_000540	1	106	104	+	39076731	39076831
324108396	chr19	39077113	39077284	39077140	39077258	RYR1	NM_000540	1	106	105	+	39077165	39077216
324985108	chr19	39077911	39078116	39077936	39078092	RYR1	NM_000540	1	106	106	+	39077965	39078204
323496723	chr19	38924318	38924540	38924338	38924519	RYR1	NM_001042723	2	105	1	+	38924340	38924514
325330745	chr19	38931228	38931441	38931249	38931421	RYR1	NM_001042723	2	105	2	+	38931385	38931504
325336715	chr19	38931375	38931589	38931394	38931567	RYR1	NM_001042723	2	105	2	+	38931385	38931504
326388399	chr19	38932949	38933169	38932972	38933151	RYR1	NM_001042723	2	105	3	+	38932989	38933093
324609045	chr19	38934159	38934370	38934182	38934346	RYR1	NM_001042723	2	105	4	+	38934198	38934272
324589668	chr19	38934330	38934548	38934350	38934526	RYR1	NM_001042723	2	105	5	+	38934358	38934436
325924063	chr19	38934733	38934914	38934754	38934894	RYR1	NM_001042723	2	105	6	+	38934789	38934901
325929436	chr19	38934871	38935087	38934892	38935065	RYR1	NM_001042723	2	105	6	+	38934789	38934901
323362558	chr19	38935182	38935380	38935202	38935357	RYR1	NM_001042723	2	105	7	+	38935224	38935317
324818329	chr19	38937075	38937291	38937096	38937264	RYR1	NM_001042723	2	105	8	+	38937112	38937205
323783226	chr19	38937263	38937485	38937289	38937463	RYR1	NM_001042723	2	105	9	+	38937334	38937408
323438384	chr19	38938930	38939134	38938955	38939113	RYR1	NM_001042723	2	105	10	+	38938995	38939151
323443077	chr19	38939057	38939262	38939076	38939240	RYR1	NM_001042723	2	105	10	+	38938995	38939151
325262487	chr19	38939255	38939460	38939274	38939439	RYR1	NM_001042723	2	105	11	+	38939289	38939453
325269072	chr19	38939385	38939597	38939406	38939578	RYR1	NM_001042723	2	105	11	+	38939289	38939453
325090951	chr19	38942312	38942532	38942333	38942509	RYR1	NM_001042723	2	105	12	+	38942404	38942525
325096537	chr19	38942490	38942614	38942510	38942590	RYR1	NM_001042723	2	105	12	+	38942404	38942525
325923676	chr19	38943401	38943603	38943420	38943583	RYR1	NM_001042723	2	105	13	+	38943459	38943654
325926226	chr19	38943542	38943763	38943564	38943744	RYR1	NM_001042723	2	105	13	+	38943459	38943654
324670052	chr19	38945705	38945925	38945726	38945900	RYR1	NM_001042723	2	105	14	+	38945875	38946010
324701131	chr19	38945879	38946080	38945901	38946055	RYR1	NM_001042723	2	105	14	+	38945875	38946010
323881149	chr19	38946046	38946264	38946069	38946243	RYR1	NM_001042723	2	105	15	+	38946091	38946186
323995581	chr19	38946238	38946443	38946258	38946422	RYR1	NM_001042723	2	105	16	+	38946273	38946391
324277054	chr19	38948095	38948316	38948116	38948293	RYR1	NM_001042723	2	105	17	+	38948137	38948270
324648804	chr19	38948599	38948770	38948623	38948748	RYR1	NM_001042723	2	105	18	+	38948691	38948932
324663247	chr19	38948727	38948929	38948748	38948906	RYR1	NM_001042723	2	105	18	+	38948691	38948932
324673749	chr19	38948885	38949009	38948907	38948981	RYR1	NM_001042723	2	105	18	+	38948691	38948932
323566784	chr19	38949701	38949925	38949725	38949904	RYR1	NM_001042723	2	105	19	+	38949786	38949978
323574149	chr19	38949874	38950039	38949894	38950017	RYR1	NM_001042723	2	105	19	+	38949786	38949978
324568762	chr19	38950959	38951150	38950980	38951131	RYR1	NM_001042723	2	105	20	+	38951015	38951231
324580408	chr19	38951109	38951264	38951132	38951243	RYR1	NM_001042723	2	105	20	+	38951015	38951231
323735240	chr19	38954003	38954219	38954026	38954201	RYR1	NM_001042723	2	105	21	+	38954063	38954167
326298995	chr19	38954280	38954504	38954299	38954487	RYR1	NM_001042723	2	105	22	+	38954387	38954490

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323815332	chr19	38955247	38955461	38955264	38955442	RYR1	NM_001042723	2	105	23	+	38955279	38955362
326166543	chr19	38956704	38956892	38956722	38956874	RYR1	NM_001042723	2	105	24	+	38956731	38957038
326173245	chr19	38956823	38957029	38956844	38957010	RYR1	NM_001042723	2	105	24	+	38956731	38957038
326175397	chr19	38956993	38957124	38957011	38957102	RYR1	NM_001042723	2	105	24	+	38956731	38957038
323524607	chr19	38958135	38958353	38958157	38958329	RYR1	NM_001042723	2	105	25	+	38958250	38958452
323554948	chr19	38958294	38958516	38958317	38958494	RYR1	NM_001042723	2	105	25	+	38958250	38958452
325328629	chr19	38959570	38959783	38959591	38959761	RYR1	NM_001042723	2	105	26	+	38959606	38959780
325340178	chr19	38959731	38959952	38959751	38959935	RYR1	NM_001042723	2	105	26	+	38959606	38959780
325148773	chr19	38959944	38960086	38959961	38960069	RYR1	NM_001042723	2	105	27	+	38959945	38960153
325153981	chr19	38960044	38960214	38960064	38960192	RYR1	NM_001042723	2	105	27	+	38959945	38960153
323459942	chr19	38963942	38964149	38963963	38964130	RYR1	NM_001042723	2	105	28	+	38964017	38964411
323463741	chr19	38964094	38964305	38964116	38964284	RYR1	NM_001042723	2	105	28	+	38964017	38964411
323466011	chr19	38964232	38964417	38964254	38964392	RYR1	NM_001042723	2	105	28	+	38964017	38964411
323466270	chr19	38964369	38964573	38964391	38964546	RYR1	NM_001042723	2	105	28	+	38964017	38964411
325658235	chr19	38965914	38966119	38965935	38966095	RYR1	NM_001042723	2	105	29	+	38965958	38966090
326401120	chr19	38968259	38968457	38968282	38968436	RYR1	NM_001042723	2	105	30	+	38968350	38968510
326411812	chr19	38968416	38968629	38968437	38968608	RYR1	NM_001042723	2	105	30	+	38968350	38968510
323315626	chr19	38969021	38969220	38969042	38969197	RYR1	NM_001042723	2	105	31	+	38969075	38969240
323339414	chr19	38969177	38969309	38969198	38969284	RYR1	NM_001042723	2	105	31	+	38969075	38969240
323775548	chr19	38973564	38973784	38973587	38973764	RYR1	NM_001042723	2	105	32	+	38973667	38973753
323490186	chr19	38973850	38974065	38973871	38974046	RYR1	NM_001042723	2	105	33	+	38973930	38974156
323495295	chr19	38974017	38974190	38974037	38974172	RYR1	NM_001042723	2	105	33	+	38973930	38974156
325391912	chr19	38976685	38976900	38976702	38976877	RYR1	NM_001042723	2	105	34	+	38976230	38976842
325396407	chr19	38976174	38976380	38976194	38976362	RYR1	NM_001042723	2	105	34	+	38976230	38976842
325404126	chr19	38976344	38976566	38976363	38976543	RYR1	NM_001042723	2	105	34	+	38976230	38976842
325411553	chr19	38976524	38976740	38976544	38976720	RYR1	NM_001042723	2	105	34	+	38976230	38976842
324765917	chr19	38979683	38979862	38979703	38979834	RYR1	NM_001042723	2	105	35	+	38979817	38980083
324785400	chr19	38979810	38980029	38979833	38980006	RYR1	NM_001042723	2	105	35	+	38979817	38980083
324796243	chr19	38979870	38980092	38979891	38980071	RYR1	NM_001042723	2	105	35	+	38979817	38980083
324801285	chr19	38980050	38980210	38980072	38980187	RYR1	NM_001042723	2	105	35	+	38979817	38980083
325117755	chr19	38980666	38980887	38980688	38980867	RYR1	NM_001042723	2	105	36	+	38980716	38980916
325129747	chr19	38980839	38980999	38980863	38980977	RYR1	NM_001042723	2	105	36	+	38980716	38980916
323816438	chr19	38981203	38981427	38981225	38981403	RYR1	NM_001042723	2	105	37	+	38981261	38981372
323869753	chr19	38983098	38983241	38983120	38983216	RYR1	NM_001042723	2	105	38	+	38983130	38983276
323877630	chr19	38983190	38983405	38983213	38983383	RYR1	NM_001042723	2	105	38	+	38983130	38983276
324315447	chr19	38984962	38985181	38984983	38985161	RYR1	NM_001042723	2	105	39	+	38984992	38985265
324320905	chr19	38985140	38985342	38985161	38985314	RYR1	NM_001042723	2	105	39	+	38984992	38985265
323692950	chr19	38986826	38987002	38986843	38986985	RYR1	NM_001042723	2	105	40	+	38986855	38986969
323699665	chr19	38986919	38987140	38986939	38987120	RYR1	NM_001042723	2	105	40	+	38986855	38986969
323699665	chr19	38986919	38987140	38986939	38987120	RYR1	NM_001042723	2	105	41	+	38987049	38987181
325609143	chr19	38987087	38987267	38987111	38987247	RYR1	NM_001042723	2	105	41	+	38987049	38987181

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324106178	chr19	38987453	38987642	38987475	38987622	RYR1	NM_001042723	2	105	42	+	38987500	38987594
324070619	chr19	38989710	38989934	38989731	38989911	RYR1	NM_001042723	2	105	43	+	38989748	38989883
323338038	chr19	38990375	38990585	38990394	38990565	RYR1	NM_001042723	2	105	44	+	38990275	38990461
324288298	chr19	38990224	38990412	38990245	38990394	RYR1	NM_001042723	2	105	44	+	38990275	38990461
323338038	chr19	38990375	38990585	38990394	38990565	RYR1	NM_001042723	2	105	45	+	38990548	38990656
323341206	chr19	38990476	38990668	38990496	38990646	RYR1	NM_001042723	2	105	45	+	38990548	38990656
323346137	chr19	38990602	38990746	38990623	38990728	RYR1	NM_001042723	2	105	45	+	38990548	38990656
325127543	chr19	38991177	38991398	38991197	38991377	RYR1	NM_001042723	2	105	46	+	38991246	38991366
324359005	chr19	38991377	38991574	38991398	38991552	RYR1	NM_001042723	2	105	47	+	38991461	38991630
324367140	chr19	38991528	38991745	38991549	38991717	RYR1	NM_001042723	2	105	47	+	38991461	38991630
324720460	chr19	38993072	38993295	38993092	38993273	RYR1	NM_001042723	2	105	48	+	38993147	38993367
324724838	chr19	38993233	38993370	38993252	38993351	RYR1	NM_001042723	2	105	48	+	38993147	38993367
324726906	chr19	38993330	38993516	38993350	38993494	RYR1	NM_001042723	2	105	48	+	38993147	38993367
324881683	chr19	38993489	38993635	38993513	38993615	RYR1	NM_001042723	2	105	49	+	38993520	38993610
325241886	chr19	38994826	38995042	38994847	38995020	RYR1	NM_001042723	2	105	50	+	38994860	38995000
325102790	chr19	38995223	38995409	38995248	38995389	RYR1	NM_001042723	2	105	51	+	38995388	38995551
325112384	chr19	38995369	38995590	38995390	38995566	RYR1	NM_001042723	2	105	51	+	38995388	38995551
324697384	chr19	38995535	38995758	38995555	38995734	RYR1	NM_001042723	2	105	52	+	38995643	38995721
324103423	chr19	38995819	38995977	38995840	38995952	RYR1	NM_001042723	2	105	53	+	38995949	38996038
324113041	chr19	38995931	38996082	38995953	38996058	RYR1	NM_001042723	2	105	53	+	38995949	38996038
324572657	chr19	38996286	38996496	38996307	38996475	RYR1	NM_001042723	2	105	54	+	38996446	38996586
324598428	chr19	38996453	38996653	38996473	38996632	RYR1	NM_001042723	2	105	54	+	38996446	38996586
323828744	chr19	38996937	38997161	38996962	38997144	RYR1	NM_001042723	2	105	55	+	38996943	38997017
323928929	chr19	38996915	38997087	38996935	38997066	RYR1	NM_001042723	2	105	55	+	38996943	38997017
323828744	chr19	38996937	38997161	38996962	38997144	RYR1	NM_001042723	2	105	56	+	38997111	38997186
323839039	chr19	38997120	38997339	38997145	38997317	RYR1	NM_001042723	2	105	56	+	38997111	38997186
323360728	chr19	38997394	38997592	38997415	38997571	RYR1	NM_001042723	2	105	57	+	38997469	38997592
323369502	chr19	38997548	38997718	38997572	38997696	RYR1	NM_001042723	2	105	57	+	38997469	38997592
323647323	chr19	38998321	38998545	38998343	38998524	RYR1	NM_001042723	2	105	58	+	38998352	38998467
326281703	chr19	39001062	39001284	39001084	39001261	RYR1	NM_001042723	2	105	59	+	39001138	39001205
323445502	chr19	39001268	39001489	39001289	39001465	RYR1	NM_001042723	2	105	60	+	39001300	39001421
325134860	chr19	39002099	39002321	39002123	39002299	RYR1	NM_001042723	2	105	61	+	39002201	39002250
325004829	chr19	39002657	39002862	39002679	39002841	RYR1	NM_001042723	2	105	62	+	39002712	39002772
323853243	chr19	39002842	39003060	39002864	39003040	RYR1	NM_001042723	2	105	63	+	39002885	39003123
323863633	chr19	39003023	39003238	39003041	39003212	RYR1	NM_001042723	2	105	63	+	39002885	39003123
324244699	chr19	39005618	39005831	39005637	39005809	RYR1	NM_001042723	2	105	64	+	39005666	39005747
323470921	chr19	39006692	39006901	39006712	39006880	RYR1	NM_001042723	2	105	65	+	39006727	39006857
323811168	chr19	39007956	39008136	39007976	39008115	RYR1	NM_001042723	2	105	66	+	39007999	39008331
323817799	chr19	39008092	39008291	39008111	39008263	RYR1	NM_001042723	2	105	66	+	39007999	39008331
323824208	chr19	39008234	39008447	39008255	39008424	RYR1	NM_001042723	2	105	66	+	39007999	39008331
323382731	chr19	39009701	39009921	39009726	39009897	RYR1	NM_001042723	2	105	67	+	39009854	39010094

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323393848	chr19	39009852	39010064	39009871	39010044	RYR1	NM_001042723	2	105	67	+	39009854	39010094
323399556	chr19	39010020	39010233	39010041	39010210	RYR1	NM_001042723	2	105	67	+	39009854	39010094
323885984	chr19	39013702	39013926	39013723	39013904	RYR1	NM_001042723	2	105	68	+	39013668	39013755
326214327	chr19	39013527	39013751	39013548	39013725	RYR1	NM_001042723	2	105	68	+	39013668	39013755
323885984	chr19	39013702	39013926	39013723	39013904	RYR1	NM_001042723	2	105	69	+	39013857	39013949
323894448	chr19	39013824	39014015	39013843	39013993	RYR1	NM_001042723	2	105	69	+	39013857	39013949
325133311	chr19	39015839	39016063	39015857	39016043	RYR1	NM_001042723	2	105	70	+	39015972	39016142
325138222	chr19	39016022	39016237	39016043	39016215	RYR1	NM_001042723	2	105	70	+	39015972	39016142
324929983	chr19	39017519	39017721	39017542	39017698	RYR1	NM_001042723	2	105	71	+	39017633	39017692
323619319	chr19	39018193	39018415	39018216	39018395	RYR1	NM_001042723	2	105	72	+	39018287	39018424
323623482	chr19	39018370	39018582	39018390	39018559	RYR1	NM_001042723	2	105	72	+	39018287	39018424
326337790	chr19	39018914	39019132	39018934	39019109	RYR1	NM_001042723	2	105	73	+	39018946	39019058
324046920	chr19	39019107	39019320	39019128	39019299	RYR1	NM_001042723	2	105	74	+	39019239	39019335
324055466	chr19	39019278	39019449	39019300	39019424	RYR1	NM_001042723	2	105	74	+	39019239	39019335
323679501	chr19	39019551	39019704	39019574	39019682	RYR1	NM_001042723	2	105	75	+	39019591	39019697
323682310	chr19	39019653	39019847	39019673	39019819	RYR1	NM_001042723	2	105	75	+	39019591	39019697
323791223	chr19	39023102	39023294	39023122	39023269	RYR1	NM_001042723	2	105	76	+	39023130	39023181
325680639	chr19	39023157	39023378	39023180	39023356	RYR1	NM_001042723	2	105	76	+	39023130	39023181
325680639	chr19	39023157	39023378	39023180	39023356	RYR1	NM_001042723	2	105	77	+	39023311	39023376
325698417	chr19	39023336	39023533	39023357	39023510	RYR1	NM_001042723	2	105	77	+	39023311	39023376
323971438	chr19	39025319	39025518	39025340	39025495	RYR1	NM_001042723	2	105	78	+	39025360	39025459
324274710	chr19	39025669	39025893	39025693	39025870	RYR1	NM_001042723	2	105	79	+	39025781	39025860
324969068	chr19	39025847	39026062	39025868	39026037	RYR1	NM_001042723	2	105	80	+	39025956	39026032
323332797	chr19	39026594	39026764	39026616	39026740	RYR1	NM_001042723	2	105	81	+	39026637	39026710
325310926	chr19	39027358	39027496	39027379	39027476	RYR1	NM_001042723	2	105	82	+	39027390	39027407
324123774	chr19	39028467	39028681	39028486	39028658	RYR1	NM_001042723	2	105	83	+	39028520	39028600
323729237	chr19	39033927	39034103	39033948	39034083	RYR1	NM_001042723	2	105	84	+	39033987	39034075
323739574	chr19	39033990	39034210	39034012	39034188	RYR1	NM_001042723	2	105	84	+	39033987	39034075
323739574	chr19	39033990	39034210	39034012	39034188	RYR1	NM_001042723	2	105	85	+	39034172	39034300
326121562	chr19	39034168	39034368	39034189	39034346	RYR1	NM_001042723	2	105	85	+	39034172	39034300
323417699	chr19	39034349	39034511	39034370	39034490	RYR1	NM_001042723	2	105	86	+	39034411	39034515
323421920	chr19	39034469	39034666	39034489	39034643	RYR1	NM_001042723	2	105	86	+	39034411	39034515
324935836	chr19	39037039	39037218	39037060	39037193	RYR1	NM_001042723	2	105	87	+	39037085	39037166
325632787	chr19	39038823	39038961	39038842	39038935	RYR1	NM_001042723	2	105	88	+	39038873	39039060
325642688	chr19	39038916	39039084	39038936	39039067	RYR1	NM_001042723	2	105	88	+	39038873	39039060
324237764	chr19	39051701	39051843	39051723	39051818	RYR1	NM_001042723	2	105	89	+	39051753	39052094
324241277	chr19	39051785	39051930	39051808	39051911	RYR1	NM_001042723	2	105	89	+	39051753	39052094
324244483	chr19	39051875	39052071	39051893	39052049	RYR1	NM_001042723	2	105	89	+	39051753	39052094
324248769	chr19	39052031	39052254	39052049	39052230	RYR1	NM_001042723	2	105	89	+	39051753	39052094
326283601	chr19	39056285	39056460	39056302	39056437	RYR1	NM_001042723	2	105	90	+	39055599	39056411
326284789	chr19	39055509	39055642	39055528	39055621	RYR1	NM_001042723	2	105	90	+	39055599	39056411

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326286850	chr19	39055604	39055738	39055622	39055721	RYR1	NM_001042723	2	105	90	+	39055599	39056411
326287558	chr19	39055685	39055904	39055706	39055887	RYR1	NM_001042723	2	105	90	+	39055599	39056411
326287708	chr19	39055887	39056111	39055904	39056094	RYR1	NM_001042723	2	105	90	+	39055599	39056411
324774571	chr19	39057421	39057643	39057444	39057625	RYR1	NM_001042723	2	105	91	+	39057551	39057627
323543241	chr19	39058379	39058595	39058399	39058573	RYR1	NM_001042723	2	105	92	+	39058413	39058557
325308791	chr19	39061162	39061386	39061188	39061365	RYR1	NM_001042723	2	105	93	+	39061247	39061333
323996229	chr19	39062622	39062822	39062643	39062800	RYR1	NM_001042723	2	105	94	+	39062659	39062910
324007061	chr19	39062778	39062914	39062801	39062888	RYR1	NM_001042723	2	105	94	+	39062659	39062910
324015835	chr19	39062869	39063089	39062889	39063068	RYR1	NM_001042723	2	105	94	+	39062659	39062910
326220829	chr19	39063780	39063998	39063797	39063980	RYR1	NM_001042723	2	105	95	+	39063817	39063947
324855718	chr19	39066501	39066666	39066522	39066648	RYR1	NM_001042723	2	105	96	+	39066559	39066601
323484623	chr19	39068529	39068752	39068551	39068731	RYR1	NM_001042723	2	105	97	+	39068558	39068688
323314946	chr19	39068730	39068912	39068751	39068892	RYR1	NM_001042723	2	105	98	+	39068784	39068844
325318817	chr19	39070475	39070689	39070495	39070663	RYR1	NM_001042723	2	105	99	+	39070622	39070768
325332277	chr19	39070639	39070840	39070664	39070818	RYR1	NM_001042723	2	105	99	+	39070622	39070768
325455778	chr19	39070984	39071152	39071001	39071133	RYR1	NM_001042723	2	105	100	+	39071010	39071144
323863111	chr19	39075565	39075694	39075583	39075672	RYR1	NM_001042723	2	105	101	+	39075583	39075739
323867845	chr19	39075591	39075732	39075613	39075711	RYR1	NM_001042723	2	105	101	+	39075583	39075739
323678203	chr19	39076499	39076693	39076520	39076672	RYR1	NM_001042723	2	105	102	+	39076578	39076642
324326830	chr19	39076699	39076906	39076721	39076884	RYR1	NM_001042723	2	105	103	+	39076731	39076831
324108396	chr19	39077113	39077284	39077140	39077258	RYR1	NM_001042723	2	105	104	+	39077165	39077216
324985108	chr19	39077911	39078116	39077936	39078092	RYR1	NM_001042723	2	105	105	+	39077965	39078204
324637871	chr1	237205840	237206032	237205860	237206012	RYR2	NM_001035	1	105	1	+	237205702	237205869
323387420	chr1	237433755	237433974	237433783	237433947	RYR2	NM_001035	1	105	2	+	237433797	237433916
325080064	chr1	237494140	237494361	237494161	237494333	RYR2	NM_001035	1	105	3	+	237494178	237494282
324375674	chr1	237519136	237519343	237519165	237519319	RYR2	NM_001035	1	105	4	+	237519265	237519285
324948674	chr1	237527631	237527845	237527655	237527815	RYR2	NM_001035	1	105	5	+	237527658	237527672
324871355	chr1	237532721	237532943	237532750	237532917	RYR2	NM_001035	1	105	6	+	237532834	237532908
323956267	chr1	237537967	237538144	237537994	237538123	RYR2	NM_001035	1	105	7	+	237538017	237538095
323905570	chr1	237540545	237540769	237540573	237540742	RYR2	NM_001035	1	105	8	+	237540623	237540735
323574558	chr1	237550485	237550708	237550511	237550685	RYR2	NM_001035	1	105	9	+	237550581	237550680
325058845	chr1	237551346	237551523	237551367	237551498	RYR2	NM_001035	1	105	10	+	237551387	237551483
324813273	chr1	237580237	237580456	237580260	237580431	RYR2	NM_001035	1	105	11	+	237580349	237580423
326255301	chr1	237586303	237586429	237586330	237586406	RYR2	NM_001035	1	105	12	+	237586392	237586548
326265573	chr1	237586386	237586607	237586407	237586580	RYR2	NM_001035	1	105	12	+	237586392	237586548
326075581	chr1	237604508	237604728	237604533	237604707	RYR2	NM_001035	1	105	13	+	237604619	237604783
326080097	chr1	237604680	237604864	237604708	237604836	RYR2	NM_001035	1	105	13	+	237604619	237604783
323664586	chr1	237608640	237608863	237608668	237608835	RYR2	NM_001035	1	105	14	+	237608701	237608822
323714169	chr1	237617553	237617759	237617574	237617736	RYR2	NM_001035	1	105	15	+	237617691	237617874
323728973	chr1	237617717	237617937	237617737	237617909	RYR2	NM_001035	1	105	15	+	237617691	237617874
326428917	chr1	237619843	237620064	237619868	237620040	RYR2	NM_001035	1	105	16	+	237619900	237620035

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323305369	chr1	237632299	237632428	237632326	237632400	RYR2	NM_001035	1	105	17	+	237632392	237632487
323307261	chr1	237632379	237632546	237632401	237632518	RYR2	NM_001035	1	105	17	+	237632392	237632487
324279228	chr1	237655005	237655225	237655033	237655196	RYR2	NM_001035	1	105	18	+	237655106	237655224
324280057	chr1	237655104	237655235	237655129	237655205	RYR2	NM_001035	1	105	18	+	237655106	237655224
324206803	chr1	237656220	237656416	237656246	237656392	RYR2	NM_001035	1	105	19	+	237656254	237656387
323730907	chr1	237659778	237659921	237659803	237659899	RYR2	NM_001035	1	105	20	+	237659811	237660052
323748894	chr1	237659877	237660097	237659899	237660072	RYR2	NM_001035	1	105	20	+	237659811	237660052
323703454	chr1	237663904	237664127	237663932	237664101	RYR2	NM_001035	1	105	21	+	237664011	237664203
323716705	chr1	237664079	237664257	237664102	237664229	RYR2	NM_001035	1	105	21	+	237664011	237664203
323578188	chr1	237666468	237666669	237666495	237666644	RYR2	NM_001035	1	105	22	+	237666589	237666805
323590711	chr1	237666618	237666835	237666645	237666813	RYR2	NM_001035	1	105	22	+	237666589	237666805
326380858	chr1	237669860	237670066	237669888	237670038	RYR2	NM_001035	1	105	23	+	237670010	237670114
326385314	chr1	237670013	237670203	237670039	237670183	RYR2	NM_001035	1	105	23	+	237670010	237670114
326272051	chr1	237674906	237675130	237674932	237675102	RYR2	NM_001035	1	105	24	+	237674988	237675091
326182993	chr1	237693658	237693882	237693681	237693854	RYR2	NM_001035	1	105	25	+	237693727	237693810
325270204	chr1	237711597	237711761	237711619	237711741	RYR2	NM_001035	1	105	26	+	237711731	237711890
325278675	chr1	237711716	237711925	237711742	237711897	RYR2	NM_001035	1	105	26	+	237711731	237711890
325131247	chr1	237713699	237713898	237713721	237713874	RYR2	NM_001035	1	105	27	+	237713844	237713991
325145344	chr1	237713851	237714040	237713875	237714013	RYR2	NM_001035	1	105	27	+	237713844	237713991
325026780	chr1	237729814	237729993	237729836	237729972	RYR2	NM_001035	1	105	28	+	237729867	237730075
325050983	chr1	237729947	237730160	237729973	237730136	RYR2	NM_001035	1	105	28	+	237729867	237730075
326144412	chr1	237732332	237732553	237732358	237732530	RYR2	NM_001035	1	105	29	+	237732445	237732619
326180820	chr1	237732508	237732669	237732531	237732643	RYR2	NM_001035	1	105	29	+	237732445	237732619
325247175	chr1	237752980	237753164	237753001	237753141	RYR2	NM_001035	1	105	30	+	237753093	237753301
325254752	chr1	237753121	237753345	237753142	237753320	RYR2	NM_001035	1	105	30	+	237753093	237753301
324903793	chr1	237753831	237754011	237753851	237753985	RYR2	NM_001035	1	105	31	+	237753940	237754292
324938023	chr1	237753959	237754182	237753986	237754157	RYR2	NM_001035	1	105	31	+	237753940	237754292
324954168	chr1	237754129	237754351	237754158	237754324	RYR2	NM_001035	1	105	31	+	237753940	237754292
325449072	chr1	237754942	237755104	237754964	237755082	RYR2	NM_001035	1	105	32	+	237755039	237755153
325453947	chr1	237755061	237755185	237755083	237755159	RYR2	NM_001035	1	105	32	+	237755039	237755153
325362834	chr1	237756608	237756830	237756633	237756808	RYR2	NM_001035	1	105	33	+	237756776	237756936
325373506	chr1	237756784	237757008	237756809	237756980	RYR2	NM_001035	1	105	33	+	237756776	237756936
324069182	chr1	237758627	237758833	237758651	237758811	RYR2	NM_001035	1	105	34	+	237758798	237758957
324090186	chr1	237758790	237758993	237758812	237758965	RYR2	NM_001035	1	105	34	+	237758798	237758957
324277351	chr1	237765190	237765397	237765216	237765372	RYR2	NM_001035	1	105	35	+	237765325	237765411
324284305	chr1	237765352	237765576	237765373	237765550	RYR2	NM_001035	1	105	35	+	237765325	237765411
324702041	chr1	237773991	237774192	237774019	237774168	RYR2	NM_001035	1	105	36	+	237774062	237774288
324728411	chr1	237774149	237774331	237774169	237774310	RYR2	NM_001035	1	105	36	+	237774062	237774288
324880551	chr1	237777773	237777969	237777794	237777944	RYR2	NM_001035	1	105	37	+	237777339	237778143
324912814	chr1	237777922	237778142	237777945	237778120	RYR2	NM_001035	1	105	37	+	237777339	237778143
324933245	chr1	237778099	237778250	237778121	237778222	RYR2	NM_001035	1	105	37	+	237777339	237778143

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326265802	chr1	237777305	237777521	237777332	237777499	RYR2	NM_001035	1	105	37	+	237777339	237778143
326279953	chr1	237777477	237777640	237777500	237777620	RYR2	NM_001035	1	105	37	+	237777339	237778143
326294465	chr1	237777600	237777818	237777621	237777793	RYR2	NM_001035	1	105	37	+	237777339	237778143
326220542	chr1	237780577	237780705	237780600	237780678	RYR2	NM_001035	1	105	38	+	237780586	237780786
326231525	chr1	237780651	237780854	237780679	237780831	RYR2	NM_001035	1	105	38	+	237780586	237780786
324960132	chr1	237787028	237787252	237787056	237787224	RYR2	NM_001035	1	105	39	+	237787065	237787170
323367117	chr1	237788793	237789010	237788821	237788982	RYR2	NM_001035	1	105	40	+	237788961	237789104
323381034	chr1	237788957	237789130	237788983	237789109	RYR2	NM_001035	1	105	40	+	237788961	237789104
324995463	chr1	237791023	237791230	237791048	237791211	RYR2	NM_001035	1	105	41	+	237791107	237791380
325005792	chr1	237791189	237791351	237791211	237791328	RYR2	NM_001035	1	105	41	+	237791107	237791380
325009000	chr1	237791298	237791422	237791319	237791395	RYR2	NM_001035	1	105	41	+	237791107	237791380
323702684	chr1	237794681	237794870	237794704	237794843	RYR2	NM_001035	1	105	42	+	237794727	237794841
323454802	chr1	237796797	237797020	237796823	237796994	RYR2	NM_001035	1	105	43	+	237796878	237797010
323952673	chr1	237798132	237798337	237798158	237798309	RYR2	NM_001035	1	105	44	+	237798189	237798292
325685142	chr1	237801602	237801752	237801630	237801730	RYR2	NM_001035	1	105	45	+	237801657	237801792
325693744	chr1	237801707	237801883	237801731	237801857	RYR2	NM_001035	1	105	45	+	237801657	237801792
326127151	chr1	237802165	237802370	237802193	237802350	RYR2	NM_001035	1	105	46	+	237802315	237802501
326131598	chr1	237802328	237802533	237802351	237802506	RYR2	NM_001035	1	105	46	+	237802315	237802501
325114070	chr1	237804105	237804328	237804128	237804307	RYR2	NM_001035	1	105	47	+	237804197	237804302
324225300	chr1	237806445	237806668	237806473	237806644	RYR2	NM_001035	1	105	48	+	237806627	237806747
324228440	chr1	237806620	237806834	237806645	237806810	RYR2	NM_001035	1	105	48	+	237806627	237806747
325180848	chr1	237811626	237811834	237811653	237811811	RYR2	NM_001035	1	105	49	+	237811744	237811913
325206395	chr1	237811790	237811943	237811812	237811923	RYR2	NM_001035	1	105	49	+	237811744	237811913
323632150	chr1	237813137	237813341	237813161	237813313	RYR2	NM_001035	1	105	50	+	237813177	237813397
323649873	chr1	237813287	237813430	237813314	237813402	RYR2	NM_001035	1	105	50	+	237813177	237813397
325041013	chr1	237814545	237814736	237814578	237814713	RYR2	NM_001035	1	105	51	+	237814711	237814801
325044245	chr1	237814688	237814901	237814714	237814873	RYR2	NM_001035	1	105	51	+	237814711	237814801
324850745	chr1	237817447	237817617	237817470	237817590	RYR2	NM_001035	1	105	52	+	237817574	237817714
324856153	chr1	237817565	237817689	237817591	237817661	RYR2	NM_001035	1	105	52	+	237817574	237817714
324857841	chr1	237817641	237817830	237817662	237817806	RYR2	NM_001035	1	105	52	+	237817574	237817714
323502101	chr1	237819052	237819271	237819074	237819248	RYR2	NM_001035	1	105	53	+	237819121	237819284
323517471	chr1	237819221	237819383	237819249	237819355	RYR2	NM_001035	1	105	53	+	237819121	237819284
324388188	chr1	237821194	237821324	237821224	237821299	RYR2	NM_001035	1	105	54	+	237821244	237821322
324388193	chr1	237821273	237821400	237821301	237821372	RYR2	NM_001035	1	105	54	+	237821244	237821322
324717667	chr1	237823203	237823361	237823226	237823333	RYR2	NM_001035	1	105	55	+	237823285	237823374
324941701	chr1	237824017	237824235	237824045	237824213	RYR2	NM_001035	1	105	56	+	237824110	237824247
324947939	chr1	237824194	237824376	237824214	237824347	RYR2	NM_001035	1	105	56	+	237824110	237824247
325026334	chr1	237829766	237829972	237829791	237829944	RYR2	NM_001035	1	105	57	+	237829812	237829889
324934052	chr1	237831010	237831209	237831038	237831186	RYR2	NM_001035	1	105	58	+	237831183	237831258
324934233	chr1	237831182	237831318	237831204	237831292	RYR2	NM_001035	1	105	58	+	237831183	237831258
323626254	chr1	237837355	237837555	237837383	237837527	RYR2	NM_001035	1	105	59	+	237837396	237837519

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324383153	chr1	237837963	237838180	237837990	237838155	RYR2	NM_001035	1	105	60	+	237838031	237838146
325024345	chr1	237841265	237841483	237841293	237841454	RYR2	NM_001035	1	105	61	+	237841348	237841412
323693612	chr1	237843706	237843928	237843731	237843899	RYR2	NM_001035	1	105	62	+	237843756	237843877
323930202	chr1	237850623	237850847	237850649	237850824	RYR2	NM_001035	1	105	63	+	237850755	237850804
323305162	chr1	237862227	237862412	237862254	237862384	RYR2	NM_001035	1	105	64	+	237862265	237862325
324050313	chr1	237863493	237863698	237863518	237863669	RYR2	NM_001035	1	105	65	+	237863529	237863767
324065689	chr1	237863638	237863857	237863658	237863831	RYR2	NM_001035	1	105	65	+	237863529	237863767
325115544	chr1	237865207	237865335	237865232	237865306	RYR2	NM_001035	1	105	66	+	237865278	237865359
325116784	chr1	237865280	237865488	237865307	237865461	RYR2	NM_001035	1	105	66	+	237865278	237865359
324270182	chr1	237868471	237868681	237868499	237868657	RYR2	NM_001035	1	105	67	+	237868513	237868643
324313275	chr1	237870132	237870313	237870152	237870287	RYR2	NM_001035	1	105	68	+	237870249	237870569
324338153	chr1	237870261	237870418	237870288	237870396	RYR2	NM_001035	1	105	68	+	237870249	237870569
324357251	chr1	237870373	237870597	237870396	237870573	RYR2	NM_001035	1	105	68	+	237870249	237870569
324056773	chr1	237872183	237872345	237872208	237872324	RYR2	NM_001035	1	105	69	+	237872158	237872398
324074585	chr1	237872303	237872445	237872325	237872417	RYR2	NM_001035	1	105	69	+	237872158	237872398
325017782	chr1	237872734	237872909	237872761	237872881	RYR2	NM_001035	1	105	70	+	237872780	237872867
324560144	chr1	237874954	237875138	237874980	237875110	RYR2	NM_001035	1	105	71	+	237875045	237875137
324560567	chr1	237875061	237875251	237875088	237875223	RYR2	NM_001035	1	105	71	+	237875045	237875137
326385259	chr1	237880323	237880534	237880352	237880506	RYR2	NM_001035	1	105	72	+	237880498	237880668
326415668	chr1	237880484	237880698	237880507	237880675	RYR2	NM_001035	1	105	72	+	237880498	237880668
323342042	chr1	237881617	237881829	237881641	237881801	RYR2	NM_001035	1	105	73	+	237881762	237881821
323344384	chr1	237881777	237881966	237881802	237881939	RYR2	NM_001035	1	105	73	+	237881762	237881821
324603937	chr1	237886382	237886601	237886410	237886573	RYR2	NM_001035	1	105	74	+	237886428	237886562
323879372	chr1	237889412	237889636	237889434	237889613	RYR2	NM_001035	1	105	75	+	237889573	237889608
323352541	chr1	237890370	237890512	237890394	237890488	RYR2	NM_001035	1	105	76	+	237890387	237890499
323357127	chr1	237890469	237890599	237890489	237890571	RYR2	NM_001035	1	105	76	+	237890387	237890499
323486047	chr1	237893526	237893700	237893553	237893674	RYR2	NM_001035	1	105	77	+	237893560	237893656
325288675	chr1	237895252	237895476	237895280	237895454	RYR2	NM_001035	1	105	78	+	237895346	237895449
323924887	chr1	237896957	237897181	237896980	237897153	RYR2	NM_001035	1	105	79	+	237897005	237897056
323831924	chr1	237905512	237905646	237905541	237905620	RYR2	NM_001035	1	105	80	+	237905596	237905649
323832105	chr1	237905593	237905816	237905619	237905790	RYR2	NM_001035	1	105	80	+	237905596	237905649
324745521	chr1	237919523	237919743	237919550	237919719	RYR2	NM_001035	1	105	81	+	237919588	237919687
324655843	chr1	237920863	237921042	237920888	237921017	RYR2	NM_001035	1	105	82	+	237920997	237921076
324663254	chr1	237920992	237921216	237921018	237921190	RYR2	NM_001035	1	105	82	+	237920997	237921076
324364309	chr1	237922983	237923190	237923009	237923167	RYR2	NM_001035	1	105	83	+	237923076	237923152
323913452	chr1	237924142	237924365	237924169	237924337	RYR2	NM_001035	1	105	84	+	237924255	237924328
326227518	chr1	237934067	237934260	237934088	237934233	RYR2	NM_001035	1	105	85	+	237934107	237934187
326335480	chr1	237935235	237935458	237935262	237935430	RYR2	NM_001035	1	105	86	+	237935312	237935400
324209052	chr1	237936747	237936904	237936771	237936879	RYR2	NM_001035	1	105	87	+	237936820	237936948
324211142	chr1	237936852	237936980	237936880	237936953	RYR2	NM_001035	1	105	87	+	237936820	237936948
323394123	chr1	237941892	237942114	237941919	237942086	RYR2	NM_001035	1	105	88	+	237941966	237942070

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323977868	chr1	237944792	237945013	237944820	237944985	RYR2	NM_001035	1	105	89	+	237944865	237944946
325600362	chr1	237946852	237947054	237946879	237947030	RYR2	NM_001035	1	105	90	+	237946975	237948272
325608884	chr1	237947006	237947221	237947031	237947195	RYR2	NM_001035	1	105	90	+	237946975	237948272
325615900	chr1	237947973	237948135	237948000	237948113	RYR2	NM_001035	1	105	90	+	237946975	237948272
325626001	chr1	237947505	237947668	237947531	237947646	RYR2	NM_001035	1	105	90	+	237946975	237948272
325634749	chr1	237948091	237948308	237948114	237948284	RYR2	NM_001035	1	105	90	+	237946975	237948272
325635237	chr1	237947174	237947385	237947196	237947360	RYR2	NM_001035	1	105	90	+	237946975	237948272
325638349	chr1	237947626	237947850	237947647	237947825	RYR2	NM_001035	1	105	90	+	237946975	237948272
325666242	chr1	237947797	237948020	237947822	237947999	RYR2	NM_001035	1	105	90	+	237946975	237948272
325672966	chr1	237947340	237947551	237947361	237947530	RYR2	NM_001035	1	105	90	+	237946975	237948272
324536657	chr1	237949176	237949388	237949201	237949360	RYR2	NM_001035	1	105	91	+	237949269	237949336
324483010	chr1	237951189	237951380	237951217	237951357	RYR2	NM_001035	1	105	92	+	237951288	237951435
324493297	chr1	237951335	237951498	237951358	237951470	RYR2	NM_001035	1	105	92	+	237951288	237951435
325026183	chr1	237954683	237954904	237954705	237954876	RYR2	NM_001035	1	105	93	+	237954729	237954815
325679520	chr1	237955257	237955480	237955285	237955457	RYR2	NM_001035	1	105	94	+	237955405	237955623
325722046	chr1	237955437	237955652	237955458	237955628	RYR2	NM_001035	1	105	94	+	237955405	237955623
323682244	chr1	237956992	237957213	237957016	237957190	RYR2	NM_001035	1	105	95	+	237957167	237957297
323688646	chr1	237957165	237957370	237957191	237957342	RYR2	NM_001035	1	105	95	+	237957167	237957297
325681096	chr1	237958459	237958672	237958487	237958642	RYR2	NM_001035	1	105	96	+	237958589	237958631
323315041	chr1	237961285	237961505	237961313	237961479	RYR2	NM_001035	1	105	97	+	237961337	237961470
323596230	chr1	237965053	237965277	237965077	237965249	RYR2	NM_001035	1	105	98	+	237965156	237965216
324800155	chr1	237969390	237969563	237969415	237969535	RYR2	NM_001035	1	105	99	+	237969437	237969583
324808397	chr1	237969511	237969722	237969536	237969700	RYR2	NM_001035	1	105	99	+	237969437	237969583
326331347	chr1	237972158	237972382	237972186	237972354	RYR2	NM_001035	1	105	100	+	237972201	237972335
323914125	chr1	237982299	237982521	237982322	237982497	RYR2	NM_001035	1	105	101	+	237982336	237982492
325796899	chr1	237991552	237991776	237991575	237991750	RYR2	NM_001035	1	105	102	+	237991681	237991745
325173321	chr1	237993736	237993957	237993761	237993935	RYR2	NM_001035	1	105	103	+	237993830	237993930
324149676	chr1	237994771	237994949	237994799	237994921	RYR2	NM_001035	1	105	104	+	237994814	237994865
325709609	chr1	237995757	237995979	237995783	237995953	RYR2	NM_001035	1	105	105	+	237995852	237997288
325454224	chr20	50418753	50418961	50418771	50418943	SALL4	NM_020436	1	4	1	-	50418818	50419048
325457557	chr20	50418896	50419111	50418917	50419090	SALL4	NM_020436	1	4	1	-	50418818	50419048
324438661	chr20	50406499	50406723	50406523	50406700	SALL4	NM_020436	1	4	2	-	50406561	50408891
324477316	chr20	50406681	50406835	50406701	50406813	SALL4	NM_020436	1	4	2	-	50406561	50408891
324491411	chr20	50406784	50406980	50406804	50406954	SALL4	NM_020436	1	4	2	-	50406561	50408891
324501516	chr20	50406932	50407120	50406955	50407098	SALL4	NM_020436	1	4	2	-	50406561	50408891
326019651	chr20	50408040	50408262	50408059	50408242	SALL4	NM_020436	1	4	2	-	50406561	50408891
326028187	chr20	50407525	50407649	50407547	50407626	SALL4	NM_020436	1	4	2	-	50406561	50408891
326032331	chr20	50408499	50408681	50408525	50408660	SALL4	NM_020436	1	4	2	-	50406561	50408891
326037165	chr20	50408209	50408407	50408228	50408389	SALL4	NM_020436	1	4	2	-	50406561	50408891
326044496	chr20	50407075	50407294	50407098	50407272	SALL4	NM_020436	1	4	2	-	50406561	50408891
326047460	chr20	50407597	50407809	50407623	50407789	SALL4	NM_020436	1	4	2	-	50406561	50408891

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326051928	chr20	50408361	50408569	50408383	50408544	SALL4	NM_020436	1	4	2	-	50406561	50408891
326053279	chr20	50408612	50408788	50408636	50408767	SALL4	NM_020436	1	4	2	-	50406561	50408891
326067361	chr20	50407762	50407975	50407782	50407955	SALL4	NM_020436	1	4	2	-	50406561	50408891
326071530	chr20	50408740	50408926	50408768	50408903	SALL4	NM_020436	1	4	2	-	50406561	50408891
326078923	chr20	50407254	50407442	50407273	50407419	SALL4	NM_020436	1	4	2	-	50406561	50408891
326082035	chr20	50407934	50408094	50407955	50408074	SALL4	NM_020436	1	4	2	-	50406561	50408891
326089428	chr20	50407360	50407579	50407381	50407554	SALL4	NM_020436	1	4	2	-	50406561	50408891
324657805	chr20	50405326	50405542	50405348	50405523	SALL4	NM_020436	1	4	3	-	50405400	50405680
324695579	chr20	50405503	50405724	50405524	50405698	SALL4	NM_020436	1	4	3	-	50405400	50405680
325586375	chr20	50401090	50401281	50401113	50401255	SALL4	NM_020436	1	4	4	-	50400583	50401223
325596197	chr20	50400755	50400957	50400782	50400936	SALL4	NM_020436	1	4	4	-	50400583	50401223
325611736	chr20	50400912	50401135	50400933	50401112	SALL4	NM_020436	1	4	4	-	50400583	50401223
332516827	chr19	35521729	35521911	35521746	35521888	SCN1B	NM_001037	1	6	1	+	35521592	35521764
332644003	chr19	35523370	35523521	35523390	35523495	SCN1B	NM_001037	1	6	2	+	35523432	35523598
332645936	chr19	35523476	35523685	35523496	35523664	SCN1B	NM_001037	1	6	2	+	35523432	35523598
333214446	chr19	35524330	35524536	35524351	35524508	SCN1B	NM_001037	1	6	3	+	35524403	35524643
333233574	chr19	35524488	35524701	35524509	35524682	SCN1B	NM_001037	1	6	3	+	35524403	35524643
333664496	chr19	35529987	35530133	35530006	35530112	SCN1B	NM_001037	1	6	4	+	35530021	35530162
333670829	chr19	35530091	35530225	35530113	35530204	SCN1B	NM_001037	1	6	4	+	35530021	35530162
332989606	chr19	35530486	35530628	35530506	35530610	SCN1B	NM_001037	1	6	5	+	35530539	35530610
332516827	chr19	35521729	35521911	35521746	35521888	SCN1B	NM_199037	2	3	1	+	35521592	35521764
332644003	chr19	35523370	35523521	35523390	35523495	SCN1B	NM_199037	2	3	2	+	35523432	35523598
332645936	chr19	35523476	35523685	35523496	35523664	SCN1B	NM_199037	2	3	2	+	35523432	35523598
333214446	chr19	35524330	35524536	35524351	35524508	SCN1B	NM_199037	2	3	3	+	35524403	35525174
333233574	chr19	35524488	35524701	35524509	35524682	SCN1B	NM_199037	2	3	3	+	35524403	35525174
333810181	chr19	35524822	35525045	35524839	35525025	SCN1B	NM_199037	2	3	3	+	35524403	35525174
333845075	chr19	35524663	35524860	35524681	35524841	SCN1B	NM_199037	2	3	3	+	35524403	35525174
333266825	chr11	123524326	123524550	123524346	123524526	SCN3B	NM_001040151	1	7	2	-	123524455	123524534
333588414	chr11	123516267	123516491	123516287	123516469	SCN3B	NM_001040151	1	7	3	-	123516295	123516458
332313655	chr11	123513059	123513282	123513081	123513261	SCN3B	NM_001040151	1	7	4	-	123513154	123513379
332336451	chr11	123513242	123513408	123513262	123513384	SCN3B	NM_001040151	1	7	4	-	123513154	123513379
332663389	chr11	123508878	123509073	123508899	123509046	SCN3B	NM_001040151	1	7	5	-	123508894	123509032
332777874	chr11	123504717	123504941	123504739	123504919	SCN3B	NM_001040151	1	7	6	-	123504829	123504914
333266825	chr11	123524326	123524550	123524346	123524526	SCN3B	NM_018400	2	6	1	-	123524455	123525315
333588414	chr11	123516267	123516491	123516287	123516469	SCN3B	NM_018400	2	6	2	-	123516295	123516458
332313655	chr11	123513059	123513282	123513081	123513261	SCN3B	NM_018400	2	6	3	-	123513154	123513379
332336451	chr11	123513242	123513408	123513262	123513384	SCN3B	NM_018400	2	6	3	-	123513154	123513379
332663389	chr11	123508878	123509073	123508899	123509046	SCN3B	NM_018400	2	6	4	-	123508894	123509032
332777874	chr11	123504717	123504941	123504739	123504919	SCN3B	NM_018400	2	6	5	-	123504829	123504914
333417972	chr11	118023242	118023444	118023264	118023424	SCN4B	NM_001142348	1	3	1	-	118023328	118023630
333146316	chr11	118011895	118012084	118011916	118012063	SCN4B	NM_001142348	1	3	2	-	118011922	118012051

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
332793434	chr11	118007676	118007885	118007697	118007862	SCN4B	NM_001142348	1	3	3	-	118004092	118007835
333277358	chr11	118015742	118015957	118015764	118015936	SCN4B	NM_001142349	2	4	1	-	118015772	118016184
333290794	chr11	118015909	118016103	118015928	118016082	SCN4B	NM_001142349	2	4	1	-	118015772	118016184
332273515	chr11	118014452	118014673	118014474	118014651	SCN4B	NM_001142349	2	4	2	-	118014548	118014776
332303025	chr11	118014623	118014836	118014642	118014815	SCN4B	NM_001142349	2	4	2	-	118014548	118014776
333146316	chr11	118011895	118012084	118011916	118012063	SCN4B	NM_001142349	2	4	3	-	118011922	118012051
332793434	chr11	118007676	118007885	118007697	118007862	SCN4B	NM_001142349	2	4	4	-	118004092	118007835
333417972	chr11	118023242	118023444	118023264	118023424	SCN4B	NM_174934	3	5	1	-	118023328	118023630
333277358	chr11	118015742	118015957	118015764	118015936	SCN4B	NM_174934	3	5	2	-	118015772	118015944
333290794	chr11	118015909	118016103	118015928	118016082	SCN4B	NM_174934	3	5	2	-	118015772	118015944
332273515	chr11	118014452	118014673	118014474	118014651	SCN4B	NM_174934	3	5	3	-	118014548	118014776
332303025	chr11	118014623	118014836	118014642	118014815	SCN4B	NM_174934	3	5	3	-	118014548	118014776
333146316	chr11	118011895	118012084	118011916	118012063	SCN4B	NM_174934	3	5	4	-	118011922	118012051
332793434	chr11	118007676	118007885	118007697	118007862	SCN4B	NM_174934	3	5	5	-	118004092	118007835
333277358	chr11	118015742	118015957	118015764	118015936	SCN4B	NR_024527	4	4	1	-	118015772	118016184
333290794	chr11	118015909	118016103	118015928	118016082	SCN4B	NR_024527	4	4	1	-	118015772	118016184
332303025	chr11	118014623	118014836	118014642	118014815	SCN4B	NR_024527	4	4	2	-	118014702	118014776
333146316	chr11	118011895	118012084	118011916	118012063	SCN4B	NR_024527	4	4	3	-	118011922	118012051
332793434	chr11	118007676	118007885	118007697	118007862	SCN4B	NR_024527	4	4	4	-	118004092	118007835
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_000335	1	28	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_000335	1	28	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_000335	1	28	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_000335	1	28	3	-	38671802	38671920
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_000335	1	28	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_000335	1	28	5	-	38662334	38662462
325020162	chr3	38655191	38655353	38655212	38655330	SCN5A	NM_000335	1	28	6	-	38655234	38655325
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_000335	1	28	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_000335	1	28	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_000335	1	28	7	-	38651225	38651455
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_000335	1	28	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_000335	1	28	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_000335	1	28	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_000335	1	28	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_000335	1	28	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_000335	1	28	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_000335	1	28	12	-	38645203	38645574
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_000335	1	28	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_000335	1	28	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_000335	1	28	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_000335	1	28	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_000335	1	28	14	-	38639220	38639458

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_000335	1	28	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_000335	1	28	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_000335	1	28	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_000335	1	28	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_000335	1	28	16	-	38627182	38627532
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_000335	1	28	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_000335	1	28	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_000335	1	28	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_000335	1	28	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_000335	1	28	17	-	38622422	38622862
325131456	chr3	38620684	38620889	38620703	38620871	SCN5A	NM_000335	1	28	18	-	38620825	38620983
325137978	chr3	38620807	38621024	38620830	38621003	SCN5A	NM_000335	1	28	18	-	38620825	38620983
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_000335	1	28	19	-	38618152	38618272
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_000335	1	28	19	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_000335	1	28	20	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_000335	1	28	20	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_000335	1	28	21	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_000335	1	28	21	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_000335	1	28	22	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_000335	1	28	22	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_000335	1	28	23	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_000335	1	28	23	-	38601638	38601919
324266860	chr3	38598627	38598830	38598648	38598802	SCN5A	NM_000335	1	28	24	-	38598722	38598775
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_000335	1	28	25	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_000335	1	28	25	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_000335	1	28	26	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_000335	1	28	27	-	38595770	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_000335	1	28	27	-	38595770	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_000335	1	28	28	-	38589553	38593049
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_000335	1	28	28	-	38589553	38593049
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_001099404	2	28	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_001099404	2	28	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_001099404	2	28	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_001099404	2	28	3	-	38671802	38671920

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_001099404	2	28	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_001099404	2	28	5	-	38662334	38662462
326355654	chr3	38655412	38655595	38655437	38655567	SCN5A	NM_001099404	2	28	6	-	38655466	38655557
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_001099404	2	28	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_001099404	2	28	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_001099404	2	28	7	-	38651225	38651455
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_001099404	2	28	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_001099404	2	28	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_001099404	2	28	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_001099404	2	28	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_001099404	2	28	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_001099404	2	28	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_001099404	2	28	12	-	38645203	38645574
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_001099404	2	28	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_001099404	2	28	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_001099404	2	28	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_001099404	2	28	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_001099404	2	28	14	-	38639220	38639458
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_001099404	2	28	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_001099404	2	28	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_001099404	2	28	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_001099404	2	28	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_001099404	2	28	16	-	38627182	38627532
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_001099404	2	28	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_001099404	2	28	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_001099404	2	28	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_001099404	2	28	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_001099404	2	28	17	-	38622422	38622862
325131456	chr3	38620684	38620889	38620703	38620871	SCN5A	NM_001099404	2	28	18	-	38620825	38620986
325137978	chr3	38620807	38621024	38620830	38621003	SCN5A	NM_001099404	2	28	18	-	38620825	38620986
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_001099404	2	28	19	-	38618152	38618272
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_001099404	2	28	19	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_001099404	2	28	20	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_001099404	2	28	20	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_001099404	2	28	21	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_001099404	2	28	21	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_001099404	2	28	22	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_001099404	2	28	22	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_001099404	2	28	23	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_001099404	2	28	23	-	38601638	38601919
324266860	chr3	38598627	38598830	38598648	38598802	SCN5A	NM_001099404	2	28	24	-	38598722	38598775

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_001099404	2	28	25	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_001099404	2	28	25	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_001099404	2	28	26	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_001099404	2	28	27	-	38595770	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_001099404	2	28	27	-	38595770	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_001099404	2	28	28	-	38589553	38593049
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_001099405	3	27	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_001099405	3	27	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_001099405	3	27	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_001099405	3	27	3	-	38671802	38671920
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_001099405	3	27	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_001099405	3	27	5	-	38662334	38662462
326355654	chr3	38655412	38655595	38655437	38655567	SCN5A	NM_001099405	3	27	6	-	38655466	38655557
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_001099405	3	27	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_001099405	3	27	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_001099405	3	27	7	-	38651225	38651455
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_001099405	3	27	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_001099405	3	27	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_001099405	3	27	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_001099405	3	27	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_001099405	3	27	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_001099405	3	27	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_001099405	3	27	12	-	38645203	38645574
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_001099405	3	27	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_001099405	3	27	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_001099405	3	27	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_001099405	3	27	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_001099405	3	27	14	-	38639220	38639458
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_001099405	3	27	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_001099405	3	27	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_001099405	3	27	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_001099405	3	27	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_001099405	3	27	16	-	38627182	38627532

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_001099405	3	27	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_001099405	3	27	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_001099405	3	27	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_001099405	3	27	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_001099405	3	27	17	-	38622422	38622862
325131456	chr3	38620684	38620889	38620703	38620871	SCN5A	NM_001099405	3	27	18	-	38620825	38620986
325137978	chr3	38620807	38621024	38620830	38621003	SCN5A	NM_001099405	3	27	18	-	38620825	38620986
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_001099405	3	27	19	-	38618152	38618272
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_001099405	3	27	19	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_001099405	3	27	20	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_001099405	3	27	20	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_001099405	3	27	21	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_001099405	3	27	21	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_001099405	3	27	22	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_001099405	3	27	22	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_001099405	3	27	23	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_001099405	3	27	23	-	38601638	38601919
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_001099405	3	27	24	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_001099405	3	27	24	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_001099405	3	27	25	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_001099405	3	27	26	-	38595770	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_001099405	3	27	26	-	38595770	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_001099405	3	27	27	-	38589553	38593049
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_001160160	4	28	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_001160160	4	28	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_001160160	4	28	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_001160160	4	28	3	-	38671802	38671920
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_001160160	4	28	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_001160160	4	28	5	-	38662334	38662462
326355654	chr3	38655412	38655595	38655437	38655567	SCN5A	NM_001160160	4	28	6	-	38655466	38655557
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_001160160	4	28	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_001160160	4	28	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_001160160	4	28	7	-	38651225	38651455

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_001160160	4	28	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_001160160	4	28	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_001160160	4	28	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_001160160	4	28	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_001160160	4	28	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_001160160	4	28	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_001160160	4	28	12	-	38645203	38645574
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_001160160	4	28	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_001160160	4	28	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_001160160	4	28	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_001160160	4	28	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_001160160	4	28	14	-	38639220	38639458
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_001160160	4	28	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_001160160	4	28	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_001160160	4	28	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_001160160	4	28	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_001160160	4	28	16	-	38627182	38627532
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_001160160	4	28	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_001160160	4	28	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_001160160	4	28	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_001160160	4	28	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_001160160	4	28	17	-	38622422	38622862
325131456	chr3	38620684	38620889	38620703	38620871	SCN5A	NM_001160160	4	28	18	-	38620825	38620983
325137978	chr3	38620807	38621024	38620830	38621003	SCN5A	NM_001160160	4	28	18	-	38620825	38620983
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_001160160	4	28	19	-	38618152	38618272
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_001160160	4	28	19	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_001160160	4	28	20	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_001160160	4	28	20	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_001160160	4	28	21	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_001160160	4	28	21	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_001160160	4	28	22	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_001160160	4	28	22	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_001160160	4	28	23	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_001160160	4	28	23	-	38601638	38601919
324266860	chr3	38598627	38598830	38598648	38598802	SCN5A	NM_001160160	4	28	24	-	38598722	38598775
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_001160160	4	28	25	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_001160160	4	28	25	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_001160160	4	28	26	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_001160160	4	28	27	-	38595866	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_001160160	4	28	27	-	38595866	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_001160160	4	28	28	-	38589553	38593049

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_001160160	4	28	28	-	38589553	38593049
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_001160161	5	27	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_001160161	5	27	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_001160161	5	27	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_001160161	5	27	3	-	38671802	38671920
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_001160161	5	27	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_001160161	5	27	5	-	38662334	38662462
326355654	chr3	38655412	38655595	38655437	38655567	SCN5A	NM_001160161	5	27	6	-	38655466	38655557
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_001160161	5	27	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_001160161	5	27	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_001160161	5	27	7	-	38651225	38651455
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_001160161	5	27	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_001160161	5	27	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_001160161	5	27	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_001160161	5	27	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_001160161	5	27	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_001160161	5	27	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_001160161	5	27	12	-	38645203	38645574
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_001160161	5	27	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_001160161	5	27	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_001160161	5	27	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_001160161	5	27	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_001160161	5	27	14	-	38639220	38639458
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_001160161	5	27	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_001160161	5	27	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_001160161	5	27	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_001160161	5	27	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_001160161	5	27	16	-	38627182	38627532
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_001160161	5	27	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_001160161	5	27	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_001160161	5	27	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_001160161	5	27	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_001160161	5	27	17	-	38622422	38622862
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_001160161	5	27	18	-	38618152	38618272

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_001160161	5	27	18	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_001160161	5	27	19	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_001160161	5	27	19	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_001160161	5	27	20	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_001160161	5	27	20	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_001160161	5	27	21	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_001160161	5	27	21	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_001160161	5	27	22	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_001160161	5	27	22	-	38601638	38601919
324266860	chr3	38598627	38598830	38598648	38598802	SCN5A	NM_001160161	5	27	23	-	38598722	38598775
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_001160161	5	27	24	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_001160161	5	27	24	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_001160161	5	27	25	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_001160161	5	27	26	-	38595770	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_001160161	5	27	26	-	38595770	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_001160161	5	27	27	-	38589553	38593049
324307190	chr3	38674470	38674694	38674492	38674674	SCN5A	NM_198056	6	28	2	-	38674526	38674850
324311970	chr3	38674597	38674813	38674620	38674790	SCN5A	NM_198056	6	28	2	-	38674526	38674850
324323875	chr3	38674770	38674895	38674791	38674873	SCN5A	NM_198056	6	28	2	-	38674526	38674850
323525729	chr3	38671770	38671947	38671795	38671925	SCN5A	NM_198056	6	28	3	-	38671802	38671920
324915915	chr3	38663828	38664010	38663851	38663990	SCN5A	NM_198056	6	28	4	-	38663891	38663980
326317956	chr3	38662303	38662505	38662328	38662484	SCN5A	NM_198056	6	28	5	-	38662334	38662462
325020162	chr3	38655191	38655353	38655212	38655330	SCN5A	NM_198056	6	28	6	-	38655234	38655325
324412591	chr3	38651066	38651256	38651088	38651234	SCN5A	NM_198056	6	28	7	-	38651225	38651455
324432916	chr3	38651214	38651423	38651235	38651401	SCN5A	NM_198056	6	28	7	-	38651225	38651455
324451676	chr3	38651380	38651587	38651402	38651565	SCN5A	NM_198056	6	28	7	-	38651225	38651455
326201849	chr3	38649547	38649765	38649576	38649744	SCN5A	NM_198056	6	28	8	-	38649642	38649705
324053321	chr3	38648126	38648333	38648146	38648309	SCN5A	NM_198056	6	28	9	-	38648160	38648301
324427562	chr3	38647391	38647608	38647413	38647582	SCN5A	NM_198056	6	28	10	-	38647442	38647639
324459827	chr3	38647559	38647762	38647581	38647740	SCN5A	NM_198056	6	28	10	-	38647442	38647639
323618335	chr3	38646041	38646258	38646063	38646236	SCN5A	NM_198056	6	28	11	-	38646220	38646399
323630372	chr3	38646214	38646427	38646237	38646407	SCN5A	NM_198056	6	28	11	-	38646220	38646399
323592784	chr3	38645129	38645337	38645150	38645316	SCN5A	NM_198056	6	28	12	-	38645203	38645574

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323598150	chr3	38645280	38645485	38645303	38645462	SCN5A	NM_198056	6	28	12	-	38645203	38645574
323607070	chr3	38645440	38645617	38645463	38645596	SCN5A	NM_198056	6	28	12	-	38645203	38645574
325090199	chr3	38640359	38640571	38640378	38640550	SCN5A	NM_198056	6	28	13	-	38640409	38640541
324434167	chr3	38639095	38639319	38639118	38639295	SCN5A	NM_198056	6	28	14	-	38639220	38639458
324475741	chr3	38639276	38639493	38639296	38639466	SCN5A	NM_198056	6	28	14	-	38639220	38639458
325818729	chr3	38628789	38628982	38628814	38628959	SCN5A	NM_198056	6	28	15	-	38628891	38629064
325838581	chr3	38628939	38629096	38628960	38629074	SCN5A	NM_198056	6	28	15	-	38628891	38629064
323845966	chr3	38627012	38627212	38627039	38627189	SCN5A	NM_198056	6	28	16	-	38627182	38627532
323863971	chr3	38627169	38627336	38627190	38627314	SCN5A	NM_198056	6	28	16	-	38627182	38627532
323880478	chr3	38627292	38627450	38627315	38627430	SCN5A	NM_198056	6	28	16	-	38627182	38627532
323888893	chr3	38627406	38627623	38627430	38627601	SCN5A	NM_198056	6	28	16	-	38627182	38627532
323746002	chr3	38622368	38622494	38622390	38622471	SCN5A	NM_198056	6	28	17	-	38622422	38622862
323749503	chr3	38622449	38622639	38622472	38622620	SCN5A	NM_198056	6	28	17	-	38622422	38622862
323756160	chr3	38622590	38622808	38622609	38622789	SCN5A	NM_198056	6	28	17	-	38622422	38622862
323768230	chr3	38622767	38622892	38622789	38622872	SCN5A	NM_198056	6	28	17	-	38622422	38622862
325131456	chr3	38620684	38620889	38620703	38620871	SCN5A	NM_198056	6	28	18	-	38620825	38620986
325137978	chr3	38620807	38621024	38620830	38621003	SCN5A	NM_198056	6	28	18	-	38620825	38620986
323496961	chr3	38618023	38618188	38618046	38618167	SCN5A	NM_198056	6	28	19	-	38618152	38618272
323505894	chr3	38618144	38618368	38618167	38618347	SCN5A	NM_198056	6	28	19	-	38618152	38618272
325322157	chr3	38616618	38616839	38616641	38616813	SCN5A	NM_198056	6	28	20	-	38616788	38616942
325335866	chr3	38616792	38617003	38616814	38616980	SCN5A	NM_198056	6	28	20	-	38616788	38616942
325052525	chr3	38607855	38608021	38607878	38607998	SCN5A	NM_198056	6	28	21	-	38607900	38608073
325068734	chr3	38607977	38608107	38607999	38608085	SCN5A	NM_198056	6	28	21	-	38607900	38608073
326366317	chr3	38603790	38603941	38603809	38603920	SCN5A	NM_198056	6	28	22	-	38603906	38604028
326374658	chr3	38603898	38604057	38603921	38604035	SCN5A	NM_198056	6	28	22	-	38603906	38604028
324704084	chr3	38601604	38601771	38601625	38601749	SCN5A	NM_198056	6	28	23	-	38601638	38601919
324728742	chr3	38601727	38601948	38601750	38601926	SCN5A	NM_198056	6	28	23	-	38601638	38601919
324266860	chr3	38598627	38598830	38598648	38598802	SCN5A	NM_198056	6	28	24	-	38598722	38598775
325681420	chr3	38597758	38597963	38597780	38597936	SCN5A	NM_198056	6	28	25	-	38597932	38598069
325696998	chr3	38597913	38598096	38597937	38598074	SCN5A	NM_198056	6	28	25	-	38597932	38598069
325694022	chr3	38597074	38597279	38597094	38597256	SCN5A	NM_198056	6	28	26	-	38597147	38597251
324076684	chr3	38595742	38595944	38595763	38595921	SCN5A	NM_198056	6	28	27	-	38595770	38596040
324116439	chr3	38595898	38596069	38595922	38596047	SCN5A	NM_198056	6	28	27	-	38595770	38596040
325186083	chr3	38592069	38592251	38592089	38592226	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325194809	chr3	38591730	38591952	38591752	38591930	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325203620	chr3	38592196	38592402	38592219	38592382	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325214841	chr3	38591910	38592114	38591931	38592093	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325217530	chr3	38592528	38592686	38592546	38592668	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325225995	chr3	38592645	38592847	38592664	38592825	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325228091	chr3	38592348	38592572	38592373	38592547	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325234871	chr3	38592803	38593006	38592824	38592986	SCN5A	NM_198056	6	28	28	-	38589553	38593049

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325244501	chr3	38592957	38593164	38592977	38593143	SCN5A	NM_198056	6	28	28	-	38589553	38593049
325026777	chr2	167167970	167168189	167167992	167168162	SCN9A	NM_002977	1	27	2	-	167168009	167168316
325047986	chr2	167168129	167168331	167168158	167168309	SCN9A	NM_002977	1	27	2	-	167168009	167168316
323637245	chr2	167163361	167163547	167163384	167163521	SCN9A	NM_002977	1	27	3	-	167163466	167163584
323642558	chr2	167163496	167163671	167163522	167163642	SCN9A	NM_002977	1	27	3	-	167163466	167163584
324310621	chr2	167162921	167163142	167162949	167163114	SCN9A	NM_002977	1	27	4	-	167163020	167163109
324224846	chr2	167162243	167162463	167162264	167162435	SCN9A	NM_002977	1	27	5	-	167162302	167162430
324163484	chr2	167160696	167160910	167160723	167160882	SCN9A	NM_002977	1	27	6	-	167160748	167160839
324512769	chr2	167159461	167159639	167159485	167159610	SCN9A	NM_002977	1	27	7	-	167159600	167159812
324513019	chr2	167159611	167159748	167159640	167159725	SCN9A	NM_002977	1	27	7	-	167159600	167159812
324514451	chr2	167159701	167159858	167159726	167159830	SCN9A	NM_002977	1	27	7	-	167159600	167159812
324339837	chr2	167151057	167151281	167151085	167151253	SCN9A	NM_002977	1	27	8	-	167151109	167151172
324008426	chr2	167149661	167149790	167149689	167149763	SCN9A	NM_002977	1	27	9	-	167149741	167149882
324022723	chr2	167149740	167149924	167149764	167149896	SCN9A	NM_002977	1	27	9	-	167149741	167149882
323802044	chr2	167144886	167145108	167144910	167145079	SCN9A	NM_002977	1	27	10	-	167144947	167145153
323813376	chr2	167145058	167145238	167145080	167145216	SCN9A	NM_002977	1	27	10	-	167144947	167145153
323516841	chr2	167142748	167142965	167142771	167142939	SCN9A	NM_002977	1	27	11	-	167142846	167143133
323542366	chr2	167142915	167143079	167142940	167143055	SCN9A	NM_002977	1	27	11	-	167142846	167143133
323556112	chr2	167143030	167143203	167143056	167143181	SCN9A	NM_002977	1	27	11	-	167142846	167143133
326349768	chr2	167140899	167141121	167140921	167141101	SCN9A	NM_002977	1	27	12	-	167140996	167141334
326373021	chr2	167141078	167141294	167141099	167141268	SCN9A	NM_002977	1	27	12	-	167140996	167141334
326388590	chr2	167141242	167141378	167141269	167141357	SCN9A	NM_002977	1	27	12	-	167140996	167141334
324878848	chr2	167138109	167138323	167138135	167138298	SCN9A	NM_002977	1	27	13	-	167138189	167138318
324554315	chr2	167136705	167136927	167136733	167136907	SCN9A	NM_002977	1	27	14	-	167136867	167137105
324555503	chr2	167136880	167137076	167136908	167137053	SCN9A	NM_002977	1	27	14	-	167136867	167137105
324558130	chr2	167137027	167137183	167137054	167137156	SCN9A	NM_002977	1	27	14	-	167136867	167137105
324500199	chr2	167134480	167134679	167134510	167134654	SCN9A	NM_002977	1	27	15	-	167134650	167134823
324500208	chr2	167134628	167134814	167134656	167134786	SCN9A	NM_002977	1	27	15	-	167134650	167134823
324504168	chr2	167134695	167134822	167134723	167134797	SCN9A	NM_002977	1	27	15	-	167134650	167134823
324505753	chr2	167134794	167135009	167134819	167134988	SCN9A	NM_002977	1	27	15	-	167134650	167134823
323841117	chr2	167133330	167133518	167133357	167133495	SCN9A	NM_002977	1	27	16	-	167133493	167133849
323841591	chr2	167133468	167133688	167133495	167133661	SCN9A	NM_002977	1	27	16	-	167133493	167133849
323851764	chr2	167133644	167133860	167133662	167133836	SCN9A	NM_002977	1	27	16	-	167133493	167133849
324715800	chr2	167128748	167128950	167128773	167128926	SCN9A	NM_002977	1	27	17	-	167128909	167129385
324723743	chr2	167128899	167129027	167128927	167129002	SCN9A	NM_002977	1	27	17	-	167128909	167129385
324730801	chr2	167128983	167129194	167129003	167129166	SCN9A	NM_002977	1	27	17	-	167128909	167129385
324742862	chr2	167129120	167129330	167129148	167129306	SCN9A	NM_002977	1	27	17	-	167128909	167129385
324751539	chr2	167129284	167129425	167129307	167129401	SCN9A	NM_002977	1	27	17	-	167128909	167129385
323853033	chr2	167108192	167108416	167108219	167108392	SCN9A	NM_002977	1	27	18	-	167108275	167108395
324101447	chr2	167098869	167099087	167098896	167099061	SCN9A	NM_002977	1	27	19	-	167099012	167099166
324114459	chr2	167099036	167099259	167099062	167099234	SCN9A	NM_002977	1	27	19	-	167099012	167099166

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323506360	chr2	167094426	167094636	167094452	167094618	SCN9A	NM_002977	1	27	20	-	167094604	167094777
323506845	chr2	167094602	167094824	167094628	167094796	SCN9A	NM_002977	1	27	20	-	167094604	167094777
326312239	chr2	167089762	167089908	167089792	167089884	SCN9A	NM_002977	1	27	21	-	167089850	167089972
326312313	chr2	167089850	167090072	167089878	167090046	SCN9A	NM_002977	1	27	21	-	167089850	167089972
324770570	chr2	167085169	167085380	167085194	167085354	SCN9A	NM_002977	1	27	22	-	167085201	167085482
324800297	chr2	167085334	167085556	167085355	167085529	SCN9A	NM_002977	1	27	22	-	167085201	167085482
324723265	chr2	167084044	167084233	167084069	167084209	SCN9A	NM_002977	1	27	23	-	167084180	167084233
324727999	chr2	167084184	167084367	167084210	167084338	SCN9A	NM_002977	1	27	23	-	167084180	167084233
324389327	chr2	167083090	167083313	167083118	167083286	SCN9A	NM_002977	1	27	24	-	167083077	167083214
323670865	chr2	167060689	167060896	167060715	167060874	SCN9A	NM_002977	1	27	25	-	167060870	167060974
323671082	chr2	167060896	167061027	167060917	167060997	SCN9A	NM_002977	1	27	25	-	167060870	167060974
323670865	chr2	167060689	167060896	167060715	167060874	SCN9A	NM_002977	1	27	26	-	167060465	167060735
324942385	chr2	167060382	167060570	167060411	167060544	SCN9A	NM_002977	1	27	26	-	167060465	167060735
324945265	chr2	167060520	167060743	167060545	167060715	SCN9A	NM_002977	1	27	26	-	167060465	167060735
323921298	chr2	167055676	167055897	167055698	167055871	SCN9A	NM_002977	1	27	27	-	167051697	167056374
323950467	chr2	167055836	167056045	167055864	167056017	SCN9A	NM_002977	1	27	27	-	167051697	167056374
323964401	chr2	167055969	167056166	167055996	167056140	SCN9A	NM_002977	1	27	27	-	167051697	167056374
323979169	chr2	167056084	167056285	167056110	167056262	SCN9A	NM_002977	1	27	27	-	167051697	167056374
325773827	chr2	167055097	167055297	167055122	167055275	SCN9A	NM_002977	1	27	27	-	167051697	167056374
325779223	chr2	167055249	167055472	167055276	167055448	SCN9A	NM_002977	1	27	27	-	167051697	167056374
325783872	chr2	167056229	167056447	167056253	167056419	SCN9A	NM_002977	1	27	27	-	167051697	167056374
325788907	chr2	167055427	167055571	167055449	167055545	SCN9A	NM_002977	1	27	27	-	167051697	167056374
325819058	chr2	167055521	167055723	167055545	167055697	SCN9A	NM_002977	1	27	27	-	167051697	167056374
324526574	chr1	156124343	156124551	156124363	156124527	SEMA4A	NM_001193300	1	15	2	+	156124341	156124508
325311918	chr1	156126169	156126393	156126195	156126370	SEMA4A	NM_001193300	1	15	3	+	156126205	156126365
324451513	chr1	156127737	156127960	156127759	156127938	SEMA4A	NM_001193300	1	15	4	+	156127861	156127923
325665109	chr1	156128124	156128343	156128146	156128318	SEMA4A	NM_001193300	1	15	5	+	156128179	156128277
325289495	chr1	156128425	156128645	156128447	156128623	SEMA4A	NM_001193300	1	15	6	+	156128510	156128615
323419489	chr1	156130193	156130406	156130215	156130383	SEMA4A	NM_001193300	1	15	7	+	156130234	156130350
325647178	chr1	156130661	156130872	156130682	156130847	SEMA4A	NM_001193300	1	15	8	+	156130696	156130820
323504700	chr1	156130988	156131199	156131006	156131181	SEMA4A	NM_001193300	1	15	9	+	156131137	156131309
323508967	chr1	156131152	156131365	156131174	156131346	SEMA4A	NM_001193300	1	15	9	+	156131137	156131309
324367833	chr1	156132701	156132925	156132723	156132901	SEMA4A	NM_001193300	1	15	10	+	156132735	156132885
323981816	chr1	156142502	156142680	156142525	156142656	SEMA4A	NM_001193300	1	15	11	+	156142617	156142797
323989970	chr1	156142635	156142823	156142657	156142802	SEMA4A	NM_001193300	1	15	11	+	156142617	156142797
324590176	chr1	156144550	156144769	156144572	156144748	SEMA4A	NM_001193300	1	15	12	+	156144613	156144731
326218480	chr1	156144735	156144947	156144756	156144923	SEMA4A	NM_001193300	1	15	13	+	156144877	156145034
326226941	chr1	156144890	156145111	156144911	156145088	SEMA4A	NM_001193300	1	15	13	+	156144877	156145034
324879397	chr1	156145284	156145501	156145307	156145478	SEMA4A	NM_001193300	1	15	14	+	156145347	156145447
325152553	chr1	156146710	156146883	156146731	156146860	SEMA4A	NM_001193300	1	15	15	+	156146196	156147542
325158714	chr1	156146143	156146351	156146167	156146328	SEMA4A	NM_001193300	1	15	15	+	156146196	156147542

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325190135	chr1	156146300	156146426	156146324	156146404	SEMA4A	NM_001193300	1	15	15	+	156146196	156147542
325202046	chr1	156146380	156146599	156146405	156146578	SEMA4A	NM_001193300	1	15	15	+	156146196	156147542
325221920	chr1	156146551	156146750	156146576	156146730	SEMA4A	NM_001193300	1	15	15	+	156146196	156147542
324526574	chr1	156124343	156124551	156124363	156124527	SEMA4A	NM_001193301	2	15	2	+	156124341	156124508
325311918	chr1	156126169	156126393	156126195	156126370	SEMA4A	NM_001193301	2	15	3	+	156126205	156126365
324451513	chr1	156127737	156127960	156127759	156127938	SEMA4A	NM_001193301	2	15	4	+	156127861	156127923
325665109	chr1	156128124	156128343	156128146	156128318	SEMA4A	NM_001193301	2	15	5	+	156128179	156128277
325289495	chr1	156128425	156128645	156128447	156128623	SEMA4A	NM_001193301	2	15	6	+	156128510	156128615
323419489	chr1	156130193	156130406	156130215	156130383	SEMA4A	NM_001193301	2	15	7	+	156130234	156130350
325647178	chr1	156130661	156130872	156130682	156130847	SEMA4A	NM_001193301	2	15	8	+	156130696	156130820
323504700	chr1	156130988	156131199	156131006	156131181	SEMA4A	NM_001193301	2	15	9	+	156131137	156131309
323508967	chr1	156131152	156131365	156131174	156131346	SEMA4A	NM_001193301	2	15	9	+	156131137	156131309
324367833	chr1	156132701	156132925	156132723	156132901	SEMA4A	NM_001193301	2	15	10	+	156132735	156132885
323981816	chr1	156142502	156142680	156142525	156142656	SEMA4A	NM_001193301	2	15	11	+	156142617	156142797
323989970	chr1	156142635	156142823	156142657	156142802	SEMA4A	NM_001193301	2	15	11	+	156142617	156142797
324590176	chr1	156144550	156144769	156144572	156144748	SEMA4A	NM_001193301	2	15	12	+	156144613	156144731
326218480	chr1	156144735	156144947	156144756	156144923	SEMA4A	NM_001193301	2	15	13	+	156144877	156145034
326226941	chr1	156144890	156145111	156144911	156145088	SEMA4A	NM_001193301	2	15	13	+	156144877	156145034
324879397	chr1	156145284	156145501	156145307	156145478	SEMA4A	NM_001193301	2	15	14	+	156145347	156145447
325152553	chr1	156146710	156146883	156146731	156146860	SEMA4A	NM_001193301	2	15	15	+	156146196	156147542
325158714	chr1	156146143	156146351	156146167	156146328	SEMA4A	NM_001193301	2	15	15	+	156146196	156147542
325190135	chr1	156146300	156146426	156146324	156146404	SEMA4A	NM_001193301	2	15	15	+	156146196	156147542
325202046	chr1	156146380	156146599	156146405	156146578	SEMA4A	NM_001193301	2	15	15	+	156146196	156147542
325221920	chr1	156146551	156146750	156146576	156146730	SEMA4A	NM_001193301	2	15	15	+	156146196	156147542
325311918	chr1	156126169	156126393	156126195	156126370	SEMA4A	NM_001193302	3	13	2	+	156126205	156126365
324451513	chr1	156127737	156127960	156127759	156127938	SEMA4A	NM_001193302	3	13	3	+	156127861	156127923
325289495	chr1	156128425	156128645	156128447	156128623	SEMA4A	NM_001193302	3	13	4	+	156128510	156128615
323419489	chr1	156130193	156130406	156130215	156130383	SEMA4A	NM_001193302	3	13	5	+	156130234	156130350
325647178	chr1	156130661	156130872	156130682	156130847	SEMA4A	NM_001193302	3	13	6	+	156130696	156130820
323504700	chr1	156130988	156131199	156131006	156131181	SEMA4A	NM_001193302	3	13	7	+	156131137	156131309
323508967	chr1	156131152	156131365	156131174	156131346	SEMA4A	NM_001193302	3	13	7	+	156131137	156131309
324367833	chr1	156132701	156132925	156132723	156132901	SEMA4A	NM_001193302	3	13	8	+	156132735	156132885
323981816	chr1	156142502	156142680	156142525	156142656	SEMA4A	NM_001193302	3	13	9	+	156142617	156142797
323989970	chr1	156142635	156142823	156142657	156142802	SEMA4A	NM_001193302	3	13	9	+	156142617	156142797
324590176	chr1	156144550	156144769	156144572	156144748	SEMA4A	NM_001193302	3	13	10	+	156144613	156144731
326218480	chr1	156144735	156144947	156144756	156144923	SEMA4A	NM_001193302	3	13	11	+	156144877	156145034
326226941	chr1	156144890	156145111	156144911	156145088	SEMA4A	NM_001193302	3	13	11	+	156144877	156145034
324879397	chr1	156145284	156145501	156145307	156145478	SEMA4A	NM_001193302	3	13	12	+	156145347	156145447
325152553	chr1	156146710	156146883	156146731	156146860	SEMA4A	NM_001193302	3	13	13	+	156146196	156147542
325158714	chr1	156146143	156146351	156146167	156146328	SEMA4A	NM_001193302	3	13	13	+	156146196	156147542
325190135	chr1	156146300	156146426	156146324	156146404	SEMA4A	NM_001193302	3	13	13	+	156146196	156147542

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325202046	chr1	156146380	156146599	156146405	156146578	SEMA4A	NM_001193302	3	13	13	+	156146196	156147542
325221920	chr1	156146551	156146750	156146576	156146730	SEMA4A	NM_001193302	3	13	13	+	156146196	156147542
324526574	chr1	156124343	156124551	156124363	156124527	SEMA4A	NM_022367	4	15	2	+	156124341	156124508
325311918	chr1	156126169	156126393	156126195	156126370	SEMA4A	NM_022367	4	15	3	+	156126205	156126365
324451513	chr1	156127737	156127960	156127759	156127938	SEMA4A	NM_022367	4	15	4	+	156127861	156127923
325665109	chr1	156128124	156128343	156128146	156128318	SEMA4A	NM_022367	4	15	5	+	156128179	156128277
325289495	chr1	156128425	156128645	156128447	156128623	SEMA4A	NM_022367	4	15	6	+	156128510	156128615
323419489	chr1	156130193	156130406	156130215	156130383	SEMA4A	NM_022367	4	15	7	+	156130234	156130350
325647178	chr1	156130661	156130872	156130682	156130847	SEMA4A	NM_022367	4	15	8	+	156130696	156130820
323504700	chr1	156130988	156131199	156131006	156131181	SEMA4A	NM_022367	4	15	9	+	156131137	156131309
323508967	chr1	156131152	156131365	156131174	156131346	SEMA4A	NM_022367	4	15	9	+	156131137	156131309
324367833	chr1	156132701	156132925	156132723	156132901	SEMA4A	NM_022367	4	15	10	+	156132735	156132885
323981816	chr1	156142502	156142680	156142525	156142656	SEMA4A	NM_022367	4	15	11	+	156142617	156142797
323989970	chr1	156142635	156142823	156142657	156142802	SEMA4A	NM_022367	4	15	11	+	156142617	156142797
324590176	chr1	156144550	156144769	156144572	156144748	SEMA4A	NM_022367	4	15	12	+	156144613	156144731
326218480	chr1	156144735	156144947	156144756	156144923	SEMA4A	NM_022367	4	15	13	+	156144877	156145034
326226941	chr1	156144890	156145111	156144911	156145088	SEMA4A	NM_022367	4	15	13	+	156144877	156145034
324879397	chr1	156145284	156145501	156145307	156145478	SEMA4A	NM_022367	4	15	14	+	156145347	156145447
325152553	chr1	156146710	156146883	156146731	156146860	SEMA4A	NM_022367	4	15	15	+	156146196	156147542
325158714	chr1	156146143	156146351	156146167	156146328	SEMA4A	NM_022367	4	15	15	+	156146196	156147542
325190135	chr1	156146300	156146426	156146324	156146404	SEMA4A	NM_022367	4	15	15	+	156146196	156147542
325202046	chr1	156146380	156146599	156146405	156146578	SEMA4A	NM_022367	4	15	15	+	156146196	156147542
325221920	chr1	156146551	156146750	156146576	156146730	SEMA4A	NM_022367	4	15	15	+	156146196	156147542
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_000295	1	5	2	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_000295	1	5	2	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_000295	1	5	2	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_000295	1	5	2	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_000295	1	5	2	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_000295	1	5	3	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_000295	1	5	3	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_000295	1	5	4	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_000295	1	5	5	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_000295	1	5	5	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001002235	2	5	2	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001002235	2	5	2	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001002235	2	5	2	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001002235	2	5	2	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001002235	2	5	2	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001002235	2	5	3	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001002235	2	5	3	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001002235	2	5	4	-	94845801	94845948

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001002235	2	5	5	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001002235	2	5	5	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001002236	3	7	4	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001002236	3	7	4	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001002236	3	7	4	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001002236	3	7	4	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001002236	3	7	4	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001002236	3	7	5	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001002236	3	7	5	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001002236	3	7	6	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001002236	3	7	7	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001002236	3	7	7	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127700	4	5	2	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127700	4	5	2	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127700	4	5	2	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127700	4	5	2	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127700	4	5	2	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127700	4	5	3	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127700	4	5	3	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127700	4	5	4	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127700	4	5	5	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127700	4	5	5	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127701	5	7	4	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127701	5	7	4	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127701	5	7	4	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127701	5	7	4	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127701	5	7	4	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127701	5	7	5	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127701	5	7	5	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127701	5	7	6	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127701	5	7	7	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127701	5	7	7	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127702	6	6	3	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127702	6	6	3	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127702	6	6	3	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127702	6	6	3	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127702	6	6	3	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127702	6	6	4	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127702	6	6	4	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127702	6	6	5	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127702	6	6	6	-	94843084	94844977

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127702	6	6	6	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127703	7	7	4	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127703	7	7	4	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127703	7	7	4	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127703	7	7	4	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127703	7	7	4	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127703	7	7	5	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127703	7	7	5	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127703	7	7	6	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127703	7	7	7	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127703	7	7	7	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127704	8	7	4	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127704	8	7	4	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127704	8	7	4	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127704	8	7	4	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127704	8	7	4	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127704	8	7	5	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127704	8	7	5	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127704	8	7	6	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127704	8	7	7	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127704	8	7	7	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127705	9	7	4	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127705	9	7	4	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127705	9	7	4	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127705	9	7	4	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127705	9	7	4	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127705	9	7	5	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127705	9	7	5	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127705	9	7	6	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127705	9	7	7	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127705	9	7	7	-	94843084	94844977
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127706	10	6	3	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127706	10	6	3	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127706	10	6	3	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127706	10	6	3	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127706	10	6	3	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127706	10	6	4	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127706	10	6	4	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127706	10	6	5	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127706	10	6	6	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127706	10	6	6	-	94843084	94844977

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324404925	chr14	94848792	94848965	94848817	94848937	SERPINA1	NM_001127707	11	6	3	-	94848929	94849578
324441121	chr14	94848912	94849128	94848938	94849101	SERPINA1	NM_001127707	11	6	3	-	94848929	94849578
324476988	chr14	94849075	94849299	94849102	94849278	SERPINA1	NM_001127707	11	6	3	-	94848929	94849578
324493652	chr14	94849257	94849470	94849279	94849445	SERPINA1	NM_001127707	11	6	3	-	94848929	94849578
326045363	chr14	94849422	94849646	94849445	94849624	SERPINA1	NM_001127707	11	6	3	-	94848929	94849578
326167778	chr14	94847177	94847381	94847198	94847358	SERPINA1	NM_001127707	11	6	4	-	94847208	94847478
326194668	chr14	94847338	94847538	94847359	94847514	SERPINA1	NM_001127707	11	6	4	-	94847208	94847478
323755345	chr14	94845758	94845982	94845780	94845957	SERPINA1	NM_001127707	11	6	5	-	94845801	94845948
325823198	chr14	94844622	94844835	94844643	94844814	SERPINA1	NM_001127707	11	6	6	-	94843084	94844977
325844610	chr14	94844793	94845009	94844815	94844985	SERPINA1	NM_001127707	11	6	6	-	94843084	94844977
323670108	chr11	57365599	57365822	57365621	57365804	SERPING1	NM_000062	1	8	2	+	57365722	57365794
324764340	chr11	57367280	57367504	57367307	57367485	SERPING1	NM_000062	1	8	3	+	57367352	57367850
324793672	chr11	57367466	57367684	57367486	57367663	SERPING1	NM_000062	1	8	3	+	57367352	57367850
324794663	chr11	57367479	57367701	57367498	57367677	SERPING1	NM_000062	1	8	3	+	57367352	57367850
324813501	chr11	57367649	57367793	57367669	57367770	SERPING1	NM_000062	1	8	3	+	57367352	57367850
324825940	chr11	57367751	57367884	57367771	57367859	SERPING1	NM_000062	1	8	3	+	57367352	57367850
324656304	chr11	57369462	57369675	57369482	57369655	SERPING1	NM_000062	1	8	4	+	57369508	57369642
324507163	chr11	57373366	57373590	57373389	57373568	SERPING1	NM_000062	1	8	5	+	57373483	57373686
324525034	chr11	57373542	57373730	57373566	57373707	SERPING1	NM_000062	1	8	5	+	57373483	57373686
324704078	chr11	57373840	57374061	57373862	57374034	SERPING1	NM_000062	1	8	6	+	57373881	57374020
323502649	chr11	57379052	57379270	57379073	57379245	SERPING1	NM_000062	1	8	7	+	57379190	57379409
323538800	chr11	57379225	57379436	57379246	57379414	SERPING1	NM_000062	1	8	7	+	57379190	57379409
325725465	chr11	57381759	57381977	57381781	57381957	SERPING1	NM_000062	1	8	8	+	57381801	57382326
325738554	chr11	57381887	57382087	57381908	57382069	SERPING1	NM_000062	1	8	8	+	57381801	57382326
323670108	chr11	57365599	57365822	57365621	57365804	SERPING1	NM_001032295	2	7	1	+	57365705	57365794
324764340	chr11	57367280	57367504	57367307	57367485	SERPING1	NM_001032295	2	7	2	+	57367352	57367850
324793672	chr11	57367466	57367684	57367486	57367663	SERPING1	NM_001032295	2	7	2	+	57367352	57367850
324794663	chr11	57367479	57367701	57367498	57367677	SERPING1	NM_001032295	2	7	2	+	57367352	57367850
324813501	chr11	57367649	57367793	57367669	57367770	SERPING1	NM_001032295	2	7	2	+	57367352	57367850
324825940	chr11	57367751	57367884	57367771	57367859	SERPING1	NM_001032295	2	7	2	+	57367352	57367850
324656304	chr11	57369462	57369675	57369482	57369655	SERPING1	NM_001032295	2	7	3	+	57369508	57369642
324507163	chr11	57373366	57373590	57373389	57373568	SERPING1	NM_001032295	2	7	4	+	57373483	57373686
324525034	chr11	57373542	57373730	57373566	57373707	SERPING1	NM_001032295	2	7	4	+	57373483	57373686
324704078	chr11	57373840	57374061	57373862	57374034	SERPING1	NM_001032295	2	7	5	+	57373881	57374020
323502649	chr11	57379052	57379270	57379073	57379245	SERPING1	NM_001032295	2	7	6	+	57379190	57379409
323538800	chr11	57379225	57379436	57379246	57379414	SERPING1	NM_001032295	2	7	6	+	57379190	57379409
325725465	chr11	57381759	57381977	57381781	57381957	SERPING1	NM_001032295	2	7	7	+	57381801	57382326
325738554	chr11	57381887	57382087	57381908	57382069	SERPING1	NM_001032295	2	7	7	+	57381801	57382326
325104581	chr5	155756414	155756613	155756436	155756594	SGCD	NM_000337	1	9	2	+	155756544	155756589
323870453	chr5	155771441	155771635	155771468	155771606	SGCD	NM_000337	1	9	3	+	155771499	155771687
323884495	chr5	155771585	155771724	155771607	155771696	SGCD	NM_000337	1	9	3	+	155771499	155771687

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
324571073	chr5	155935544	155935751	155935570	155935726	SGCD	NM_000337	1	9	4	+	155935611	155935712
324753141	chr5	156016135	156016359	156016159	156016333	SGCD	NM_000337	1	9	5	+	156016241	156016328
324994415	chr5	156021850	156022048	156021876	156022020	SGCD	NM_000337	1	9	6	+	156021942	156022061
325000666	chr5	156021996	156022121	156022021	156022093	SGCD	NM_000337	1	9	6	+	156021942	156022061
324248731	chr5	156074366	156074581	156074387	156074553	SGCD	NM_000337	1	9	7	+	156074474	156074546
323739178	chr5	156184437	156184657	156184463	156184634	SGCD	NM_000337	1	9	8	+	156184592	156184715
323774690	chr5	156184614	156184820	156184635	156184792	SGCD	NM_000337	1	9	8	+	156184592	156184715
325958154	chr5	156186137	156186278	156186165	156186256	SGCD	NM_000337	1	9	9	+	156186228	156194798
325969284	chr5	156186236	156186430	156186257	156186407	SGCD	NM_000337	1	9	9	+	156186228	156194798
323870453	chr5	155771441	155771635	155771468	155771606	SGCD	NM_001128209	2	8	2	+	155771499	155771687
323884495	chr5	155771585	155771724	155771607	155771696	SGCD	NM_001128209	2	8	2	+	155771499	155771687
324571073	chr5	155935544	155935751	155935570	155935726	SGCD	NM_001128209	2	8	3	+	155935611	155935712
324753141	chr5	156016135	156016359	156016159	156016333	SGCD	NM_001128209	2	8	4	+	156016241	156016328
324994415	chr5	156021850	156022048	156021876	156022020	SGCD	NM_001128209	2	8	5	+	156021942	156022061
325000666	chr5	156021996	156022121	156022021	156022093	SGCD	NM_001128209	2	8	5	+	156021942	156022061
324248731	chr5	156074366	156074581	156074387	156074553	SGCD	NM_001128209	2	8	6	+	156074474	156074546
323739178	chr5	156184437	156184657	156184463	156184634	SGCD	NM_001128209	2	8	7	+	156184592	156184715
323774690	chr5	156184614	156184820	156184635	156184792	SGCD	NM_001128209	2	8	7	+	156184592	156184715
325958154	chr5	156186137	156186278	156186165	156186256	SGCD	NM_001128209	2	8	8	+	156186228	156194798
325969284	chr5	156186236	156186430	156186257	156186407	SGCD	NM_001128209	2	8	8	+	156186228	156194798
325104581	chr5	155756414	155756613	155756436	155756594	SGCD	NM_172244	3	8	2	+	155756544	155756589
323870453	chr5	155771441	155771635	155771468	155771606	SGCD	NM_172244	3	8	3	+	155771499	155771687
323884495	chr5	155771585	155771724	155771607	155771696	SGCD	NM_172244	3	8	3	+	155771499	155771687
324571073	chr5	155935544	155935751	155935570	155935726	SGCD	NM_172244	3	8	4	+	155935611	155935712
324753141	chr5	156016135	156016359	156016159	156016333	SGCD	NM_172244	3	8	5	+	156016241	156016328
324994415	chr5	156021850	156022048	156021876	156022020	SGCD	NM_172244	3	8	6	+	156021942	156022061
325000666	chr5	156021996	156022121	156022021	156022093	SGCD	NM_172244	3	8	6	+	156021942	156022061
324248731	chr5	156074366	156074581	156074387	156074553	SGCD	NM_172244	3	8	7	+	156074474	156074546
323739178	chr5	156184437	156184657	156184463	156184634	SGCD	NM_172244	3	8	8	+	156184592	156185070
323774690	chr5	156184614	156184820	156184635	156184792	SGCD	NM_172244	3	8	8	+	156184592	156185070
326422178	chr4	2822314	2822516	2822335	2822496	SH3BP2	NM_001122681	1	13	2	+	2822341	2822480
323309072	chr4	2824529	2824709	2824550	2824686	SH3BP2	NM_001122681	1	13	3	+	2824662	2824764
323325797	chr4	2824666	2824880	2824687	2824858	SH3BP2	NM_001122681	1	13	3	+	2824662	2824764
323512216	chr4	2826279	2826417	2826300	2826394	SH3BP2	NM_001122681	1	13	4	+	2826340	2826457
323517385	chr4	2826370	2826594	2826394	2826573	SH3BP2	NM_001122681	1	13	4	+	2826340	2826457
325140686	chr4	2826740	2826960	2826759	2826942	SH3BP2	NM_001122681	1	13	5	+	2826853	2826923
323332802	chr4	2828890	2829071	2828911	2829050	SH3BP2	NM_001122681	1	13	6	+	2828957	2829045
324843744	chr4	2829246	2829455	2829264	2829436	SH3BP2	NM_001122681	1	13	7	+	2829333	2829401
325530790	chr4	2831149	2831369	2831169	2831351	SH3BP2	NM_001122681	1	13	8	+	2831220	2831874
325533232	chr4	2831703	2831925	2831729	2831907	SH3BP2	NM_001122681	1	13	8	+	2831220	2831874
325534561	chr4	2831300	2831493	2831320	2831475	SH3BP2	NM_001122681	1	13	8	+	2831220	2831874

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325536675	chr4	2831455	2831652	2831474	2831629	SH3BP2	NM_001122681	1	13	8	+	2831220	2831874
325539928	chr4	2831609	2831766	2831629	2831747	SH3BP2	NM_001122681	1	13	8	+	2831220	2831874
324614909	chr4	2833247	2833461	2833267	2833441	SH3BP2	NM_001122681	1	13	9	+	2833298	2833406
323633981	chr4	2833604	2833781	2833624	2833759	SH3BP2	NM_001122681	1	13	10	+	2833650	2833705
325237849	chr4	2834020	2834229	2834039	2834206	SH3BP2	NM_001122681	1	13	11	+	2834058	2834139
325034502	chr4	2834676	2834859	2834696	2834837	SH3BP2	NM_001122681	1	13	12	+	2834717	2834776
325838886	chr4	2835396	2835603	2835415	2835585	SH3BP2	NM_001122681	1	13	13	+	2835424	2842823
324545151	chr4	2814072	2814267	2814092	2814245	SH3BP2	NM_001145855	2	13	1	+	2813946	2814204
326422178	chr4	2822314	2822516	2822335	2822496	SH3BP2	NM_001145855	2	13	2	+	2822341	2822480
323309072	chr4	2824529	2824709	2824550	2824686	SH3BP2	NM_001145855	2	13	3	+	2824662	2824764
323325797	chr4	2824666	2824880	2824687	2824858	SH3BP2	NM_001145855	2	13	3	+	2824662	2824764
323512216	chr4	2826279	2826417	2826300	2826394	SH3BP2	NM_001145855	2	13	4	+	2826340	2826457
323517385	chr4	2826370	2826594	2826394	2826573	SH3BP2	NM_001145855	2	13	4	+	2826340	2826457
325140686	chr4	2826740	2826960	2826759	2826942	SH3BP2	NM_001145855	2	13	5	+	2826853	2826923
323332802	chr4	2828890	2829071	2828911	2829050	SH3BP2	NM_001145855	2	13	6	+	2828957	2829045
324843744	chr4	2829246	2829455	2829264	2829436	SH3BP2	NM_001145855	2	13	7	+	2829333	2829401
325530790	chr4	2831149	2831369	2831169	2831351	SH3BP2	NM_001145855	2	13	8	+	2831220	2831874
325533232	chr4	2831703	2831925	2831729	2831907	SH3BP2	NM_001145855	2	13	8	+	2831220	2831874
325534561	chr4	2831300	2831493	2831320	2831475	SH3BP2	NM_001145855	2	13	8	+	2831220	2831874
325536675	chr4	2831455	2831652	2831474	2831629	SH3BP2	NM_001145855	2	13	8	+	2831220	2831874
325539928	chr4	2831609	2831766	2831629	2831747	SH3BP2	NM_001145855	2	13	8	+	2831220	2831874
324614909	chr4	2833247	2833461	2833267	2833441	SH3BP2	NM_001145855	2	13	9	+	2833298	2833406
323633981	chr4	2833604	2833781	2833624	2833759	SH3BP2	NM_001145855	2	13	10	+	2833650	2833705
325237849	chr4	2834020	2834229	2834039	2834206	SH3BP2	NM_001145855	2	13	11	+	2834058	2834139
325034502	chr4	2834676	2834859	2834696	2834837	SH3BP2	NM_001145855	2	13	12	+	2834717	2834776
325838886	chr4	2835396	2835603	2835415	2835585	SH3BP2	NM_001145855	2	13	13	+	2835424	2842823
326422178	chr4	2822314	2822516	2822335	2822496	SH3BP2	NM_001145856	3	13	2	+	2822341	2822480
323309072	chr4	2824529	2824709	2824550	2824686	SH3BP2	NM_001145856	3	13	3	+	2824662	2824764
323325797	chr4	2824666	2824880	2824687	2824858	SH3BP2	NM_001145856	3	13	3	+	2824662	2824764
323512216	chr4	2826279	2826417	2826300	2826394	SH3BP2	NM_001145856	3	13	4	+	2826340	2826457
323517385	chr4	2826370	2826594	2826394	2826573	SH3BP2	NM_001145856	3	13	4	+	2826340	2826457
325140686	chr4	2826740	2826960	2826759	2826942	SH3BP2	NM_001145856	3	13	5	+	2826853	2826923
323332802	chr4	2828890	2829071	2828911	2829050	SH3BP2	NM_001145856	3	13	6	+	2828957	2829045
324843744	chr4	2829246	2829455	2829264	2829436	SH3BP2	NM_001145856	3	13	7	+	2829333	2829401
325530790	chr4	2831149	2831369	2831169	2831351	SH3BP2	NM_001145856	3	13	8	+	2831220	2831874
325533232	chr4	2831703	2831925	2831729	2831907	SH3BP2	NM_001145856	3	13	8	+	2831220	2831874
325534561	chr4	2831300	2831493	2831320	2831475	SH3BP2	NM_001145856	3	13	8	+	2831220	2831874
325536675	chr4	2831455	2831652	2831474	2831629	SH3BP2	NM_001145856	3	13	8	+	2831220	2831874
325539928	chr4	2831609	2831766	2831629	2831747	SH3BP2	NM_001145856	3	13	8	+	2831220	2831874
324614909	chr4	2833247	2833461	2833267	2833441	SH3BP2	NM_001145856	3	13	9	+	2833298	2833406
323633981	chr4	2833604	2833781	2833624	2833759	SH3BP2	NM_001145856	3	13	10	+	2833650	2833705

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325237849	chr4	2834020	2834229	2834039	2834206	SH3BP2	NM_001145856	3	13	11	+	2834058	2834139
325034502	chr4	2834676	2834859	2834696	2834837	SH3BP2	NM_001145856	3	13	12	+	2834717	2834776
325838886	chr4	2835396	2835603	2835415	2835585	SH3BP2	NM_001145856	3	13	13	+	2835424	2842823
326422178	chr4	2822314	2822516	2822335	2822496	SH3BP2	NM_003023	4	13	2	+	2822341	2822480
323309072	chr4	2824529	2824709	2824550	2824686	SH3BP2	NM_003023	4	13	3	+	2824662	2824764
323325797	chr4	2824666	2824880	2824687	2824858	SH3BP2	NM_003023	4	13	3	+	2824662	2824764
323512216	chr4	2826279	2826417	2826300	2826394	SH3BP2	NM_003023	4	13	4	+	2826340	2826457
323517385	chr4	2826370	2826594	2826394	2826573	SH3BP2	NM_003023	4	13	4	+	2826340	2826457
325140686	chr4	2826740	2826960	2826759	2826942	SH3BP2	NM_003023	4	13	5	+	2826853	2826923
323332802	chr4	2828890	2829071	2828911	2829050	SH3BP2	NM_003023	4	13	6	+	2828957	2829045
324843744	chr4	2829246	2829455	2829264	2829436	SH3BP2	NM_003023	4	13	7	+	2829333	2829401
325530790	chr4	2831149	2831369	2831169	2831351	SH3BP2	NM_003023	4	13	8	+	2831220	2831874
325533232	chr4	2831703	2831925	2831729	2831907	SH3BP2	NM_003023	4	13	8	+	2831220	2831874
325534561	chr4	2831300	2831493	2831320	2831475	SH3BP2	NM_003023	4	13	8	+	2831220	2831874
325536675	chr4	2831455	2831652	2831474	2831629	SH3BP2	NM_003023	4	13	8	+	2831220	2831874
325539928	chr4	2831609	2831766	2831629	2831747	SH3BP2	NM_003023	4	13	8	+	2831220	2831874
324614909	chr4	2833247	2833461	2833267	2833441	SH3BP2	NM_003023	4	13	9	+	2833298	2833406
323633981	chr4	2833604	2833781	2833624	2833759	SH3BP2	NM_003023	4	13	10	+	2833650	2833705
325237849	chr4	2834020	2834229	2834039	2834206	SH3BP2	NM_003023	4	13	11	+	2834058	2834139
325034502	chr4	2834676	2834859	2834696	2834837	SH3BP2	NM_003023	4	13	12	+	2834717	2834776
325838886	chr4	2835396	2835603	2835415	2835585	SH3BP2	NM_003023	4	13	13	+	2835424	2842823
325004254	chr14	61115293	61115488	61115314	61115469	SIX1	NM_005982	1	2	1	-	61115348	61116155
325007354	chr14	61115445	61115650	61115462	61115631	SIX1	NM_005982	1	2	1	-	61115348	61116155
325010512	chr14	61115553	61115777	61115573	61115754	SIX1	NM_005982	1	2	1	-	61115348	61116155
325013498	chr14	61115694	61115904	61115718	61115886	SIX1	NM_005982	1	2	1	-	61115348	61116155
326324485	chr14	61115865	61116029	61115885	61116008	SIX1	NM_005982	1	2	1	-	61115348	61116155
326391633	chr14	61112850	61113061	61112878	61113040	SIX1	NM_005982	1	2	2	-	61111417	61113295
326401633	chr14	61112997	61113202	61113018	61113180	SIX1	NM_005982	1	2	2	-	61111417	61113295
326410373	chr14	61113158	61113382	61113179	61113360	SIX1	NM_005982	1	2	2	-	61111417	61113295
325911350	chr19	46271159	46271379	46271177	46271361	SIX5	NM_175875	1	3	1	-	46271300	46272497
325911476	chr19	46271981	46272118	46272000	46272096	SIX5	NM_175875	1	3	1	-	46271300	46272497
325912004	chr19	46272081	46272273	46272098	46272253	SIX5	NM_175875	1	3	1	-	46271300	46272497
325914051	chr19	46271340	46271560	46271359	46271540	SIX5	NM_175875	1	3	1	-	46271300	46272497
325916493	chr19	46271472	46271677	46271494	46271657	SIX5	NM_175875	1	3	1	-	46271300	46272497
325917851	chr19	46271582	46271786	46271599	46271769	SIX5	NM_175875	1	3	1	-	46271300	46272497
325917996	chr19	46271656	46271849	46271676	46271832	SIX5	NM_175875	1	3	1	-	46271300	46272497
323670726	chr19	46270016	46270218	46270034	46270199	SIX5	NM_175875	1	3	2	-	46269608	46270413
323672232	chr19	46270171	46270394	46270190	46270375	SIX5	NM_175875	1	3	2	-	46269608	46270413
323677497	chr19	46270352	46270538	46270373	46270516	SIX5	NM_175875	1	3	2	-	46269608	46270413
325600212	chr19	46269583	46269804	46269601	46269782	SIX5	NM_175875	1	3	2	-	46269608	46270413
325602292	chr19	46269756	46269915	46269774	46269896	SIX5	NM_175875	1	3	2	-	46269608	46270413

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325602536	chr19	46269845	46270063	46269863	46270044	SIX5	NM_175875	1	3	2	-	46269608	46270413
323840494	chr19	46268663	46268821	46268683	46268801	SIX5	NM_175875	1	3	3	-	46268043	46269369
323841675	chr19	46268766	46268984	46268784	46268964	SIX5	NM_175875	1	3	3	-	46268043	46269369
325754060	chr19	46268943	46269160	46268961	46269142	SIX5	NM_175875	1	3	3	-	46268043	46269369
325758102	chr19	46269111	46269333	46269129	46269315	SIX5	NM_175875	1	3	3	-	46268043	46269369
325764356	chr19	46269285	46269447	46269305	46269426	SIX5	NM_175875	1	3	3	-	46268043	46269369
324867973	chr7	95951144	95951355	95951162	95951337	SLC25A13	NM_001160210	1	18	1	-	95951254	95951459
325105793	chr7	95926089	95926264	95926111	95926242	SLC25A13	NM_001160210	1	18	2	-	95926210	95926263
325106475	chr7	95926231	95926394	95926251	95926366	SLC25A13	NM_001160210	1	18	2	-	95926210	95926263
325458727	chr7	95906430	95906646	95906456	95906619	SLC25A13	NM_001160210	1	18	3	-	95906508	95906650
325466744	chr7	95906584	95906808	95906611	95906781	SLC25A13	NM_001160210	1	18	3	-	95906508	95906650
326145898	chr7	95864057	95864274	95864081	95864247	SLC25A13	NM_001160210	1	18	4	-	95864114	95864229
325622737	chr7	95838111	95838309	95838138	95838281	SLC25A13	NM_001160210	1	18	5	-	95838150	95838289
325626749	chr7	95838259	95838449	95838282	95838421	SLC25A13	NM_001160210	1	18	5	-	95838150	95838289
325065061	chr7	95822313	95822437	95822340	95822417	SLC25A13	NM_001160210	1	18	6	-	95822349	95822495
325069488	chr7	95822397	95822615	95822418	95822587	SLC25A13	NM_001160210	1	18	6	-	95822349	95822495
324499214	chr7	95820375	95820571	95820396	95820546	SLC25A13	NM_001160210	1	18	7	-	95820421	95820559
324504100	chr7	95820521	95820744	95820547	95820717	SLC25A13	NM_001160210	1	18	7	-	95820421	95820559
323733372	chr7	95818821	95819034	95818841	95819006	SLC25A13	NM_001160210	1	18	8	-	95818893	95818986
323304496	chr7	95818482	95818670	95818510	95818649	SLC25A13	NM_001160210	1	18	9	-	95818606	95818690
323324994	chr7	95818627	95818810	95818650	95818782	SLC25A13	NM_001160210	1	18	9	-	95818606	95818690
323331968	chr7	95814133	95814354	95814160	95814332	SLC25A13	NM_001160210	1	18	10	-	95814239	95814326
324123358	chr7	95813478	95813692	95813504	95813669	SLC25A13	NM_001160210	1	18	11	-	95813589	95813747
324144145	chr7	95813642	95813831	95813670	95813803	SLC25A13	NM_001160210	1	18	11	-	95813589	95813747
323830510	chr7	95800700	95800912	95800727	95800884	SLC25A13	NM_001160210	1	18	12	-	95800784	95800836
323487446	chr7	95799219	95799439	95799239	95799411	SLC25A13	NM_001160210	1	18	13	-	95799357	95799437
323492972	chr7	95799389	95799565	95799412	95799533	SLC25A13	NM_001160210	1	18	13	-	95799357	95799437
326345688	chr7	95775733	95775942	95775754	95775920	SLC25A13	NM_001160210	1	18	14	-	95775868	95776008
326350340	chr7	95775900	95776057	95775921	95776029	SLC25A13	NM_001160210	1	18	14	-	95775868	95776008
325309676	chr7	95761012	95761225	95761034	95761198	SLC25A13	NM_001160210	1	18	15	-	95761055	95761193
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NM_001160210	1	18	16	-	95751151	95751309
324507598	chr7	95751134	95751355	95751160	95751330	SLC25A13	NM_001160210	1	18	16	-	95751151	95751309
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NM_001160210	1	18	17	-	95750967	95751057
326192282	chr7	95750802	95750995	95750826	95750968	SLC25A13	NM_001160210	1	18	17	-	95750967	95751057
326202653	chr7	95750942	95751157	95750969	95751129	SLC25A13	NM_001160210	1	18	17	-	95750967	95751057
325758100	chr7	95750457	95750671	95750479	95750647	SLC25A13	NM_001160210	1	18	18	-	95749532	95750689
325772016	chr7	95750615	95750819	95750636	95750794	SLC25A13	NM_001160210	1	18	18	-	95749532	95750689
324867973	chr7	95951144	95951355	95951162	95951337	SLC25A13	NM_014251	2	18	1	-	95951254	95951459
325105793	chr7	95926089	95926264	95926111	95926242	SLC25A13	NM_014251	2	18	2	-	95926210	95926263
325106475	chr7	95926231	95926394	95926251	95926366	SLC25A13	NM_014251	2	18	2	-	95926210	95926263
325458727	chr7	95906430	95906646	95906456	95906619	SLC25A13	NM_014251	2	18	3	-	95906508	95906650

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
325466744	chr7	95906584	95906808	95906611	95906781	SLC25A13	NM_014251	2	18	3	-	95906508	95906650
326145898	chr7	95864057	95864274	95864081	95864247	SLC25A13	NM_014251	2	18	4	-	95864114	95864229
325622737	chr7	95838111	95838309	95838138	95838281	SLC25A13	NM_014251	2	18	5	-	95838150	95838289
325626749	chr7	95838259	95838449	95838282	95838421	SLC25A13	NM_014251	2	18	5	-	95838150	95838289
325065061	chr7	95822313	95822437	95822340	95822417	SLC25A13	NM_014251	2	18	6	-	95822349	95822495
325069488	chr7	95822397	95822615	95822418	95822587	SLC25A13	NM_014251	2	18	6	-	95822349	95822495
324499214	chr7	95820375	95820571	95820396	95820546	SLC25A13	NM_014251	2	18	7	-	95820421	95820559
324504100	chr7	95820521	95820744	95820547	95820717	SLC25A13	NM_014251	2	18	7	-	95820421	95820559
323733372	chr7	95818821	95819034	95818841	95819006	SLC25A13	NM_014251	2	18	8	-	95818893	95818986
323304496	chr7	95818482	95818670	95818510	95818649	SLC25A13	NM_014251	2	18	9	-	95818606	95818690
323324994	chr7	95818627	95818810	95818650	95818782	SLC25A13	NM_014251	2	18	9	-	95818606	95818690
323331968	chr7	95814133	95814354	95814160	95814332	SLC25A13	NM_014251	2	18	10	-	95814239	95814323
324123358	chr7	95813478	95813692	95813504	95813669	SLC25A13	NM_014251	2	18	11	-	95813589	95813747
324144145	chr7	95813642	95813831	95813670	95813803	SLC25A13	NM_014251	2	18	11	-	95813589	95813747
323830510	chr7	95800700	95800912	95800727	95800884	SLC25A13	NM_014251	2	18	12	-	95800784	95800836
323487446	chr7	95799219	95799439	95799239	95799411	SLC25A13	NM_014251	2	18	13	-	95799357	95799437
323492972	chr7	95799389	95799565	95799412	95799533	SLC25A13	NM_014251	2	18	13	-	95799357	95799437
326345688	chr7	95775733	95775942	95775754	95775920	SLC25A13	NM_014251	2	18	14	-	95775868	95776008
326350340	chr7	95775900	95776057	95775921	95776029	SLC25A13	NM_014251	2	18	14	-	95775868	95776008
325309676	chr7	95761012	95761225	95761034	95761198	SLC25A13	NM_014251	2	18	15	-	95761055	95761193
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NM_014251	2	18	16	-	95751151	95751309
324507598	chr7	95751134	95751355	95751160	95751330	SLC25A13	NM_014251	2	18	16	-	95751151	95751309
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NM_014251	2	18	17	-	95750967	95751057
326192282	chr7	95750802	95750995	95750826	95750968	SLC25A13	NM_014251	2	18	17	-	95750967	95751057
326202653	chr7	95750942	95751157	95750969	95751129	SLC25A13	NM_014251	2	18	17	-	95750967	95751057
325758100	chr7	95750457	95750671	95750479	95750647	SLC25A13	NM_014251	2	18	18	-	95749532	95750689
325772016	chr7	95750615	95750819	95750636	95750794	SLC25A13	NM_014251	2	18	18	-	95749532	95750689
324867973	chr7	95951144	95951355	95951162	95951337	SLC25A13	NR_027662	3	17	1	-	95951254	95951459
325105793	chr7	95926089	95926264	95926111	95926242	SLC25A13	NR_027662	3	17	2	-	95926210	95926263
325106475	chr7	95926231	95926394	95926251	95926366	SLC25A13	NR_027662	3	17	2	-	95926210	95926263
325458727	chr7	95906430	95906646	95906456	95906619	SLC25A13	NR_027662	3	17	3	-	95906508	95906650
325466744	chr7	95906584	95906808	95906611	95906781	SLC25A13	NR_027662	3	17	3	-	95906508	95906650
325622737	chr7	95838111	95838309	95838138	95838281	SLC25A13	NR_027662	3	17	4	-	95838150	95838289
325626749	chr7	95838259	95838449	95838282	95838421	SLC25A13	NR_027662	3	17	4	-	95838150	95838289
325065061	chr7	95822313	95822437	95822340	95822417	SLC25A13	NR_027662	3	17	5	-	95822349	95822495
325069488	chr7	95822397	95822615	95822418	95822587	SLC25A13	NR_027662	3	17	5	-	95822349	95822495
324499214	chr7	95820375	95820571	95820396	95820546	SLC25A13	NR_027662	3	17	6	-	95820421	95820559
324504100	chr7	95820521	95820744	95820547	95820717	SLC25A13	NR_027662	3	17	6	-	95820421	95820559
323733372	chr7	95818821	95819034	95818841	95819006	SLC25A13	NR_027662	3	17	7	-	95818893	95818986
323304496	chr7	95818482	95818670	95818510	95818649	SLC25A13	NR_027662	3	17	8	-	95818606	95818690
323324994	chr7	95818627	95818810	95818650	95818782	SLC25A13	NR_027662	3	17	8	-	95818606	95818690

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323331968	chr7	95814133	95814354	95814160	95814332	SLC25A13	NR_027662	3	17	9	-	95814239	95814323
324123358	chr7	95813478	95813692	95813504	95813669	SLC25A13	NR_027662	3	17	10	-	95813589	95813747
324144145	chr7	95813642	95813831	95813670	95813803	SLC25A13	NR_027662	3	17	10	-	95813589	95813747
323830510	chr7	95800700	95800912	95800727	95800884	SLC25A13	NR_027662	3	17	11	-	95800784	95800836
323487446	chr7	95799219	95799439	95799239	95799411	SLC25A13	NR_027662	3	17	12	-	95799357	95799437
323492972	chr7	95799389	95799565	95799412	95799533	SLC25A13	NR_027662	3	17	12	-	95799357	95799437
326345688	chr7	95775733	95775942	95775754	95775920	SLC25A13	NR_027662	3	17	13	-	95775868	95776008
326350340	chr7	95775900	95776057	95775921	95776029	SLC25A13	NR_027662	3	17	13	-	95775868	95776008
325309676	chr7	95761012	95761225	95761034	95761198	SLC25A13	NR_027662	3	17	14	-	95761055	95761193
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NR_027662	3	17	15	-	95751151	95751309
324507598	chr7	95751134	95751355	95751160	95751330	SLC25A13	NR_027662	3	17	15	-	95751151	95751309
324497331	chr7	95750966	95751181	95750994	95751159	SLC25A13	NR_027662	3	17	16	-	95750967	95751057
326192282	chr7	95750802	95750995	95750826	95750968	SLC25A13	NR_027662	3	17	16	-	95750967	95751057
326202653	chr7	95750942	95751157	95750969	95751129	SLC25A13	NR_027662	3	17	16	-	95750967	95751057
325758100	chr7	95750457	95750671	95750479	95750647	SLC25A13	NR_027662	3	17	17	-	95749532	95750689
325772016	chr7	95750615	95750819	95750636	95750794	SLC25A13	NR_027662	3	17	17	-	95749532	95750689
324302644	chr4	186064502	186064641	186064519	186064623	SLC25A4	NM_001151	1	4	1	+	186064417	186064637
324304978	chr4	186064606	186064748	186064624	186064730	SLC25A4	NM_001151	1	4	1	+	186064417	186064637
323961816	chr4	186065858	186066081	186065881	186066059	SLC25A4	NM_001151	1	4	2	+	186065918	186066404
323984536	chr4	186066031	186066230	186066052	186066208	SLC25A4	NM_001151	1	4	2	+	186065918	186066404
323999787	chr4	186066182	186066387	186066204	186066365	SLC25A4	NM_001151	1	4	2	+	186065918	186066404
324023169	chr4	186066341	186066481	186066366	186066453	SLC25A4	NM_001151	1	4	2	+	186065918	186066404
323789503	chr4	186066877	186067088	186066898	186067060	SLC25A4	NM_001151	1	4	3	+	186066913	186067053
323471876	chr4	186067814	186068030	186067836	186068008	SLC25A4	NM_001151	1	4	4	+	186067968	186071538
323480265	chr4	186067988	186068193	186068009	186068165	SLC25A4	NM_001151	1	4	4	+	186067968	186071538
323753502	chr7	107301986	107302193	107302007	107302174	SLC26A4	NM_000441	1	21	2	+	107302084	107302250
323757613	chr7	107302136	107302291	107302154	107302272	SLC26A4	NM_000441	1	21	2	+	107302084	107302250
325930680	chr7	107303685	107303909	107303710	107303885	SLC26A4	NM_000441	1	21	3	+	107303741	107303880
323434511	chr7	107312526	107312694	107312554	107312667	SLC26A4	NM_000441	1	21	4	+	107312583	107312693
324358145	chr7	107314471	107314654	107314492	107314628	SLC26A4	NM_000441	1	21	5	+	107314609	107314793
324366515	chr7	107314608	107314792	107314629	107314766	SLC26A4	NM_000441	1	21	5	+	107314609	107314793
324373678	chr7	107314743	107314963	107314765	107314935	SLC26A4	NM_000441	1	21	5	+	107314609	107314793
326099105	chr7	107315264	107315436	107315289	107315412	SLC26A4	NM_000441	1	21	6	+	107315390	107315554
326104575	chr7	107315388	107315597	107315413	107315575	SLC26A4	NM_000441	1	21	6	+	107315390	107315554
324624609	chr7	107323719	107323943	107323742	107323918	SLC26A4	NM_000441	1	21	7	+	107323647	107323799
325916697	chr7	107323513	107323730	107323540	107323707	SLC26A4	NM_000441	1	21	7	+	107323647	107323799
325923054	chr7	107323685	107323850	107323708	107323822	SLC26A4	NM_000441	1	21	7	+	107323647	107323799
324624609	chr7	107323719	107323943	107323742	107323918	SLC26A4	NM_000441	1	21	8	+	107323900	107323982
324628239	chr7	107323894	107324087	107323919	107324060	SLC26A4	NM_000441	1	21	8	+	107323900	107323982
324816963	chr7	107329362	107329536	107329388	107329515	SLC26A4	NM_000441	1	21	9	+	107329498	107329645
324824489	chr7	107329492	107329692	107329516	107329668	SLC26A4	NM_000441	1	21	9	+	107329498	107329645

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
323664757	chr7	107330495	107330715	107330519	107330687	SLC26A4	NM_000441	1	21	10	+	107330569	107330682
323425717	chr7	107334746	107334964	107334768	107334937	SLC26A4	NM_000441	1	21	11	+	107334848	107334925
325843828	chr7	107335006	107335222	107335032	107335195	SLC26A4	NM_000441	1	21	12	+	107335066	107335161
323907837	chr7	107336373	107336535	107336398	107336507	SLC26A4	NM_000441	1	21	13	+	107336378	107336484
324498891	chr7	107338361	107338585	107338389	107338561	SLC26A4	NM_000441	1	21	14	+	107338487	107338556
323710419	chr7	107340422	107340596	107340444	107340569	SLC26A4	NM_000441	1	21	15	+	107340528	107340620
326352937	chr7	107341487	107341698	107341512	107341670	SLC26A4	NM_000441	1	21	16	+	107341546	107341641
323429259	chr7	107342174	107342377	107342197	107342348	SLC26A4	NM_000441	1	21	17	+	107342272	107342502
323443564	chr7	107342322	107342544	107342349	107342515	SLC26A4	NM_000441	1	21	17	+	107342272	107342502
325280261	chr7	107344686	107344873	107344714	107344846	SLC26A4	NM_000441	1	21	18	+	107344776	107344830
324019268	chr7	107350460	107350589	107350488	107350563	SLC26A4	NM_000441	1	21	19	+	107350499	107350644
324021685	chr7	107350537	107350728	107350564	107350700	SLC26A4	NM_000441	1	21	19	+	107350499	107350644
325369510	chr7	107352849	107353069	107352877	107353045	SLC26A4	NM_000441	1	21	20	+	107352984	107353067
325381086	chr7	107353017	107353209	107353046	107353185	SLC26A4	NM_000441	1	21	20	+	107352984	107353067
324783843	chr7	107355748	107355917	107355774	107355896	SLC26A4	NM_000441	1	21	21	+	107355868	107358252
270068977	chr15	67457176	67457389	67457200	67457365	SMAD3	NM_001145102	1	9	2	+	67457233	67457426
332478151	chr15	67457346	67457569	67457366	67457550	SMAD3	NM_001145102	1	9	2	+	67457233	67457426
272300790	chr15	67457541	67457728	67457560	67457705	SMAD3	NM_001145102	1	9	3	+	67457591	67457722
333561970	chr15	67457663	67457887	67457688	67457867	SMAD3	NM_001145102	1	9	3	+	67457591	67457722
272425910	chr15	67459002	67459220	67459022	67459196	SMAD3	NM_001145102	1	9	4	+	67459117	67459191
270145662	chr15	67462767	67462970	67462788	67462947	SMAD3	NM_001145102	1	9	5	+	67462892	67462942
272480187	chr15	67473540	67473760	67473561	67473737	SMAD3	NM_001145102	1	9	6	+	67473579	67473791
272494146	chr15	67473708	67473905	67473727	67473884	SMAD3	NM_001145102	1	9	6	+	67473579	67473791
270319919	chr15	67477031	67477249	67477051	67477230	SMAD3	NM_001145102	1	9	7	+	67477065	67477202
271277460	chr15	67479674	67479874	67479695	67479853	SMAD3	NM_001145102	1	9	8	+	67479703	67479847
271742204	chr15	67482685	67482900	67482706	67482879	SMAD3	NM_001145102	1	9	9	+	67482751	67487533
270385364	chr15	67430300	67430524	67430328	67430504	SMAD3	NM_001145103	2	9	1	+	67430359	67430438
270068977	chr15	67457176	67457389	67457200	67457365	SMAD3	NM_001145103	2	9	2	+	67457233	67457426
332478151	chr15	67457346	67457569	67457366	67457550	SMAD3	NM_001145103	2	9	2	+	67457233	67457426
272300790	chr15	67457541	67457728	67457560	67457705	SMAD3	NM_001145103	2	9	3	+	67457591	67457722
333561970	chr15	67457663	67457887	67457688	67457867	SMAD3	NM_001145103	2	9	3	+	67457591	67457722
272425910	chr15	67459002	67459220	67459022	67459196	SMAD3	NM_001145103	2	9	4	+	67459117	67459191
270145662	chr15	67462767	67462970	67462788	67462947	SMAD3	NM_001145103	2	9	5	+	67462892	67462942
272480187	chr15	67473540	67473760	67473561	67473737	SMAD3	NM_001145103	2	9	6	+	67473579	67473791
272494146	chr15	67473708	67473905	67473727	67473884	SMAD3	NM_001145103	2	9	6	+	67473579	67473791
270319919	chr15	67477031	67477249	67477051	67477230	SMAD3	NM_001145103	2	9	7	+	67477065	67477202
271277460	chr15	67479674	67479874	67479695	67479853	SMAD3	NM_001145103	2	9	8	+	67479703	67479847
271742204	chr15	67482685	67482900	67482706	67482879	SMAD3	NM_001145103	2	9	9	+	67482751	67487533
272425910	chr15	67459002	67459220	67459022	67459196	SMAD3	NM_001145104	3	7	2	+	67459117	67459191
270145662	chr15	67462767	67462970	67462788	67462947	SMAD3	NM_001145104	3	7	3	+	67462892	67462942
272480187	chr15	67473540	67473760	67473561	67473737	SMAD3	NM_001145104	3	7	4	+	67473579	67473791

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272494146	chr15	67473708	67473905	67473727	67473884	SMAD3	NM_001145104	3	7	4	+	67473579	67473791
270319919	chr15	67477031	67477249	67477051	67477230	SMAD3	NM_001145104	3	7	5	+	67477065	67477202
271277460	chr15	67479674	67479874	67479695	67479853	SMAD3	NM_001145104	3	7	6	+	67479703	67479847
271742204	chr15	67482685	67482900	67482706	67482879	SMAD3	NM_001145104	3	7	7	+	67482751	67487533
272700216	chr15	67358365	67358536	67358385	67358519	SMAD3	NM_005902	4	9	1	+	67358195	67358698
272703644	chr15	67358492	67358618	67358513	67358595	SMAD3	NM_005902	4	9	1	+	67358195	67358698
272706670	chr15	67358570	67358794	67358592	67358773	SMAD3	NM_005902	4	9	1	+	67358195	67358698
270068977	chr15	67457176	67457389	67457200	67457365	SMAD3	NM_005902	4	9	2	+	67457233	67457426
332478151	chr15	67457346	67457569	67457366	67457550	SMAD3	NM_005902	4	9	2	+	67457233	67457426
272300790	chr15	67457541	67457728	67457560	67457705	SMAD3	NM_005902	4	9	3	+	67457591	67457722
333561970	chr15	67457663	67457887	67457688	67457867	SMAD3	NM_005902	4	9	3	+	67457591	67457722
272425910	chr15	67459002	67459220	67459022	67459196	SMAD3	NM_005902	4	9	4	+	67459117	67459191
270145662	chr15	67462767	67462970	67462788	67462947	SMAD3	NM_005902	4	9	5	+	67462892	67462942
272480187	chr15	67473540	67473760	67473561	67473737	SMAD3	NM_005902	4	9	6	+	67473579	67473791
272494146	chr15	67473708	67473905	67473727	67473884	SMAD3	NM_005902	4	9	6	+	67473579	67473791
270319919	chr15	67477031	67477249	67477051	67477230	SMAD3	NM_005902	4	9	7	+	67477065	67477202
271277460	chr15	67479674	67479874	67479695	67479853	SMAD3	NM_005902	4	9	8	+	67479703	67479847
271742204	chr15	67482685	67482900	67482706	67482879	SMAD3	NM_005902	4	9	9	+	67482751	67487533
260738028	chr18	48573313	48573533	48573338	48573506	SMAD4	NM_005359	1	12	2	+	48573290	48573665
260793641	chr18	48573485	48573706	48573507	48573679	SMAD4	NM_005359	1	12	2	+	48573290	48573665
261778730	chr18	48575051	48575203	48575069	48575177	SMAD4	NM_005359	1	12	3	+	48575056	48575230
261793982	chr18	48575150	48575334	48575178	48575306	SMAD4	NM_005359	1	12	3	+	48575056	48575230
263539942	chr18	48575531	48575704	48575557	48575677	SMAD4	NM_005359	1	12	4	+	48575665	48575694
263540385	chr18	48575663	48575787	48575689	48575770	SMAD4	NM_005359	1	12	4	+	48575665	48575694
240139242	chr18	48581162	48581331	48581189	48581308	SMAD4	NM_005359	1	12	5	+	48581151	48581363
240170708	chr18	48581289	48581414	48581309	48581386	SMAD4	NM_005359	1	12	5	+	48581151	48581363
238060087	chr18	48584366	48584562	48584389	48584542	SMAD4	NM_005359	1	12	6	+	48584495	48584614
238074839	chr18	48584519	48584742	48584542	48584720	SMAD4	NM_005359	1	12	6	+	48584495	48584614
264277681	chr18	48584581	48584770	48584603	48584745	SMAD4	NM_005359	1	12	6	+	48584495	48584614
238074839	chr18	48584519	48584742	48584542	48584720	SMAD4	NM_005359	1	12	7	+	48584710	48584826
264277681	chr18	48584581	48584770	48584603	48584745	SMAD4	NM_005359	1	12	7	+	48584710	48584826
264300513	chr18	48584725	48584853	48584746	48584828	SMAD4	NM_005359	1	12	7	+	48584710	48584826
239527302	chr18	48586112	48586267	48586143	48586247	SMAD4	NM_005359	1	12	8	+	48586236	48586286
239529723	chr18	48586224	48586348	48586248	48586321	SMAD4	NM_005359	1	12	8	+	48586236	48586286
326808571	chr18	48591713	48591902	48591736	48591877	SMAD4	NM_005359	1	12	9	+	48591793	48591976
326977243	chr18	48591857	48592059	48591878	48592030	SMAD4	NM_005359	1	12	9	+	48591793	48591976
239063567	chr18	48593381	48593506	48593405	48593479	SMAD4	NM_005359	1	12	10	+	48593389	48593557
239080634	chr18	48593460	48593630	48593480	48593602	SMAD4	NM_005359	1	12	10	+	48593389	48593557
238601985	chr18	48603006	48603138	48603029	48603114	SMAD4	NM_005359	1	12	11	+	48603008	48603146
326795490	chr18	48603091	48603233	48603110	48603207	SMAD4	NM_005359	1	12	11	+	48603008	48603146
261601407	chr18	48604501	48604703	48604528	48604679	SMAD4	NM_005359	1	12	12	+	48604626	48611411

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261673372	chr18	48604657	48604863	48604680	48604842	SMAD4	NM_005359	1	12	12	+	48604626	48611411
326803474	chr4	90756639	90756850	90756667	90756824	SNCA	NM_000345	1	6	2	-	90756698	90756843
326920174	chr4	90749216	90749374	90749239	90749347	SNCA	NM_000345	1	6	3	-	90749294	90749335
326442863	chr4	90743288	90743433	90743308	90743411	SNCA	NM_000345	1	6	4	-	90743397	90743539
326463773	chr4	90743391	90743578	90743412	90743554	SNCA	NM_000345	1	6	4	-	90743397	90743539
327878942	chr4	90650224	90650415	90650249	90650394	SNCA	NM_000345	1	6	5	-	90650345	90650428
326882904	chr4	90647622	90647846	90647647	90647819	SNCA	NM_000345	1	6	6	-	90645250	90647811
326803474	chr4	90756639	90756850	90756667	90756824	SNCA	NM_001146054	2	6	2	-	90756698	90756843
326920174	chr4	90749216	90749374	90749239	90749347	SNCA	NM_001146054	2	6	3	-	90749294	90749335
326442863	chr4	90743288	90743433	90743308	90743411	SNCA	NM_001146054	2	6	4	-	90743397	90743539
326463773	chr4	90743391	90743578	90743412	90743554	SNCA	NM_001146054	2	6	4	-	90743397	90743539
327878942	chr4	90650224	90650415	90650249	90650394	SNCA	NM_001146054	2	6	5	-	90650345	90650428
326882904	chr4	90647622	90647846	90647647	90647819	SNCA	NM_001146054	2	6	6	-	90645250	90647811
326803474	chr4	90756639	90756850	90756667	90756824	SNCA	NM_001146055	3	6	2	-	90756698	90756843
326920174	chr4	90749216	90749374	90749239	90749347	SNCA	NM_001146055	3	6	3	-	90749294	90749335
326442863	chr4	90743288	90743433	90743308	90743411	SNCA	NM_001146055	3	6	4	-	90743397	90743539
326463773	chr4	90743391	90743578	90743412	90743554	SNCA	NM_001146055	3	6	4	-	90743397	90743539
327878942	chr4	90650224	90650415	90650249	90650394	SNCA	NM_001146055	3	6	5	-	90650345	90650428
326882904	chr4	90647622	90647846	90647647	90647819	SNCA	NM_001146055	3	6	6	-	90645250	90647811
326803474	chr4	90756639	90756850	90756667	90756824	SNCA	NM_007308	4	5	2	-	90756698	90756843
326920174	chr4	90749216	90749374	90749239	90749347	SNCA	NM_007308	4	5	3	-	90749294	90749335
326442863	chr4	90743288	90743433	90743308	90743411	SNCA	NM_007308	4	5	4	-	90743397	90743539
326463773	chr4	90743391	90743578	90743412	90743554	SNCA	NM_007308	4	5	4	-	90743397	90743539
326882904	chr4	90647622	90647846	90647647	90647819	SNCA	NM_007308	4	5	5	-	90645250	90647811
326843536	chr2	96971092	96971302	96971113	96971280	SNRNP200	NM_014014	1	45	1	-	96971131	96971307
326594820	chr2	96970393	96970608	96970418	96970584	SNRNP200	NM_014014	1	45	2	-	96970443	96970606
326606272	chr2	96970563	96970777	96970585	96970753	SNRNP200	NM_014014	1	45	2	-	96970443	96970606
327952545	chr2	96968889	96969109	96968908	96969082	SNRNP200	NM_014014	1	45	3	-	96968897	96969068
326631235	chr2	96967097	96967319	96967121	96967296	SNRNP200	NM_014014	1	45	4	-	96967262	96967454
326638244	chr2	96967270	96967485	96967297	96967459	SNRNP200	NM_014014	1	45	4	-	96967262	96967454
326585640	chr2	96966599	96966823	96966621	96966796	SNRNP200	NM_014014	1	45	5	-	96966736	96966791
327756644	chr2	96965006	96965200	96965031	96965178	SNRNP200	NM_014014	1	45	6	-	96965067	96965165
327324458	chr2	96964396	96964581	96964419	96964553	SNRNP200	NM_014014	1	45	7	-	96964553	96964705
327342051	chr2	96964528	96964735	96964554	96964710	SNRNP200	NM_014014	1	45	7	-	96964553	96964705
327324458	chr2	96964396	96964581	96964419	96964553	SNRNP200	NM_014014	1	45	8	-	96964341	96964440
328453742	chr2	96964245	96964469	96964270	96964445	SNRNP200	NM_014014	1	45	8	-	96964341	96964440
326951826	chr2	96963968	96964189	96963990	96964163	SNRNP200	NM_014014	1	45	9	-	96964022	96964158
328050634	chr2	96963334	96963555	96963356	96963528	SNRNP200	NM_014014	1	45	10	-	96963375	96963458
327802232	chr2	96963019	96963223	96963044	96963201	SNRNP200	NM_014014	1	45	11	-	96963101	96963274
327819667	chr2	96963182	96963345	96963202	96963320	SNRNP200	NM_014014	1	45	11	-	96963101	96963274
326585576	chr2	96962619	96962843	96962646	96962815	SNRNP200	NM_014014	1	45	12	-	96962671	96962808

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327635592	chr2	96962242	96962465	96962268	96962443	SNRNP200	NM_014014	1	45	13	-	96962274	96962429
327540452	chr2	96961205	96961429	96961226	96961405	SNRNP200	NM_014014	1	45	14	-	96961226	96961396
326725229	chr2	96958900	96959123	96958923	96959096	SNRNP200	NM_014014	1	45	15	-	96959054	96959247
326755922	chr2	96959077	96959280	96959097	96959252	SNRNP200	NM_014014	1	45	15	-	96959054	96959247
328188628	chr2	96958650	96958864	96958678	96958838	SNRNP200	NM_014014	1	45	16	-	96958710	96958833
328093668	chr2	96957447	96957671	96957469	96957649	SNRNP200	NM_014014	1	45	17	-	96957489	96957638
327496820	chr2	96957046	96957267	96957068	96957245	SNRNP200	NM_014014	1	45	18	-	96957130	96957240
327973964	chr2	96956368	96956591	96956392	96956563	SNRNP200	NM_014014	1	45	19	-	96956422	96956553
327007949	chr2	96955887	96956104	96955916	96956079	SNRNP200	NM_014014	1	45	20	-	96956064	96956252
327015684	chr2	96956059	96956281	96956080	96956259	SNRNP200	NM_014014	1	45	20	-	96956064	96956252
326841953	chr2	96955378	96955590	96955403	96955567	SNRNP200	NM_014014	1	45	21	-	96955537	96955734
326863627	chr2	96955546	96955762	96955568	96955739	SNRNP200	NM_014014	1	45	21	-	96955537	96955734
326972989	chr2	96954939	96955146	96954958	96955122	SNRNP200	NM_014014	1	45	22	-	96954965	96955117
327501185	chr2	96954659	96954882	96954682	96954860	SNRNP200	NM_014014	1	45	23	-	96954775	96954855
327597765	chr2	96954337	96954536	96954359	96954512	SNRNP200	NM_014014	1	45	24	-	96954401	96954484
327521445	chr2	96953524	96953735	96953545	96953713	SNRNP200	NM_014014	1	45	25	-	96953601	96953707
328423245	chr2	96953101	96953324	96953127	96953304	SNRNP200	NM_014014	1	45	26	-	96953177	96953295
327183513	chr2	96952707	96952927	96952727	96952904	SNRNP200	NM_014014	1	45	27	-	96952744	96952898
328205962	chr2	96952350	96952564	96952371	96952539	SNRNP200	NM_014014	1	45	28	-	96952426	96952615
328218034	chr2	96952519	96952645	96952540	96952621	SNRNP200	NM_014014	1	45	28	-	96952426	96952615
326769030	chr2	96951883	96952107	96951909	96952079	SNRNP200	NM_014014	1	45	29	-	96952049	96952222
326785535	chr2	96952054	96952260	96952080	96952236	SNRNP200	NM_014014	1	45	29	-	96952049	96952222
326943221	chr2	96950813	96951024	96950837	96951003	SNRNP200	NM_014014	1	45	30	-	96950918	96951078
326956622	chr2	96950983	96951199	96951003	96951177	SNRNP200	NM_014014	1	45	30	-	96950918	96951078
327764358	chr2	96950009	96950229	96950030	96950204	SNRNP200	NM_014014	1	45	31	-	96950096	96950323
327780312	chr2	96950180	96950369	96950204	96950347	SNRNP200	NM_014014	1	45	31	-	96950096	96950323
328386826	chr2	96949479	96949698	96949501	96949679	SNRNP200	NM_014014	1	45	32	-	96949551	96949742
328399616	chr2	96949657	96949881	96949678	96949857	SNRNP200	NM_014014	1	45	32	-	96949551	96949742
328267528	chr2	96949181	96949396	96949201	96949374	SNRNP200	NM_014014	1	45	33	-	96949273	96949451
328280450	chr2	96949352	96949557	96949374	96949536	SNRNP200	NM_014014	1	45	33	-	96949273	96949451
327211833	chr2	96948837	96949060	96948863	96949038	SNRNP200	NM_014014	1	45	34	-	96948939	96949090
327219980	chr2	96949019	96949147	96949039	96949122	SNRNP200	NM_014014	1	45	34	-	96948939	96949090
327585373	chr2	96947502	96947716	96947528	96947697	SNRNP200	NM_014014	1	45	35	-	96947552	96947660
327666104	chr2	96945131	96945339	96945158	96945317	SNRNP200	NM_014014	1	45	36	-	96945189	96945297
327412461	chr2	96944412	96944634	96944433	96944613	SNRNP200	NM_014014	1	45	37	-	96944547	96944736
327425123	chr2	96944591	96944772	96944614	96944743	SNRNP200	NM_014014	1	45	37	-	96944547	96944736
327412461	chr2	96944412	96944634	96944433	96944613	SNRNP200	NM_014014	1	45	38	-	96944285	96944449
327602107	chr2	96944107	96944325	96944134	96944302	SNRNP200	NM_014014	1	45	38	-	96944285	96944449
327611050	chr2	96944280	96944504	96944303	96944483	SNRNP200	NM_014014	1	45	38	-	96944285	96944449
327167423	chr2	96943919	96944133	96943939	96944105	SNRNP200	NM_014014	1	45	39	-	96943975	96944096
326833773	chr2	96943497	96943720	96943520	96943693	SNRNP200	NM_014014	1	45	40	-	96943545	96943688

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328078763	chr2	96943124	96943316	96943145	96943290	SNRNP200	NM_014014	1	45	41	-	96943277	96943453
328092151	chr2	96943271	96943486	96943291	96943461	SNRNP200	NM_014014	1	45	41	-	96943277	96943453
327790026	chr2	96942764	96942961	96942785	96942936	SNRNP200	NM_014014	1	45	42	-	96942819	96942979
327796932	chr2	96942919	96943050	96942937	96943027	SNRNP200	NM_014014	1	45	42	-	96942819	96942979
326959844	chr2	96942575	96942799	96942597	96942776	SNRNP200	NM_014014	1	45	43	-	96942642	96942723
327963939	chr2	96940899	96941119	96940923	96941092	SNRNP200	NM_014014	1	45	44	-	96940995	96941087
327260656	chr2	96940700	96940922	96940724	96940898	SNRNP200	NM_014014	1	45	45	-	96940074	96940893
333237526	chr20	32030971	32031192	32030990	32031174	SNTA1	NM_003098	1	8	1	-	32031117	32031698
333239432	chr20	32031110	32031316	32031130	32031298	SNTA1	NM_003098	1	8	1	-	32031117	32031698
333239578	chr20	32031177	32031339	32031194	32031322	SNTA1	NM_003098	1	8	1	-	32031117	32031698
333239591	chr20	32031311	32031441	32031328	32031423	SNTA1	NM_003098	1	8	1	-	32031117	32031698
332633812	chr20	32026583	32026743	32026605	32026722	SNTA1	NM_003098	1	8	2	-	32026647	32026832
332640477	chr20	32026701	32026881	32026723	32026855	SNTA1	NM_003098	1	8	2	-	32026647	32026832
332827450	chr20	32005453	32005596	32005474	32005575	SNTA1	NM_003098	1	8	3	-	32005525	32005729
332835623	chr20	32005551	32005757	32005576	32005736	SNTA1	NM_003098	1	8	3	-	32005525	32005729
333687139	chr20	32000345	32000540	32000367	32000521	SNTA1	NM_003098	1	8	4	-	32000381	32000588
333700445	chr20	32000479	32000691	32000501	32000670	SNTA1	NM_003098	1	8	4	-	32000381	32000588
333674495	chr20	32000051	32000262	32000072	32000238	SNTA1	NM_003098	1	8	5	-	32000102	32000232
332992865	chr20	31997895	31998102	31997919	31998079	SNTA1	NM_003098	1	8	6	-	31997941	31998137
332998152	chr20	31998033	31998257	31998054	31998233	SNTA1	NM_003098	1	8	6	-	31997941	31998137
332560050	chr20	31996367	31996587	31996391	31996566	SNTA1	NM_003098	1	8	7	-	31996507	31996694
332568150	chr20	31996547	31996729	31996567	31996708	SNTA1	NM_003098	1	8	7	-	31996507	31996694
332560050	chr20	31996367	31996587	31996391	31996566	SNTA1	NM_003098	1	8	8	-	31995763	31996405
333227533	chr20	31996268	31996434	31996289	31996412	SNTA1	NM_003098	1	8	8	-	31995763	31996405
327372200	chr21	33032039	33032234	33032058	33032215	SOD1	NM_000454	1	5	1	+	33031935	33032154
328348940	chr21	33036044	33036233	33036072	33036212	SOD1	NM_000454	1	5	2	+	33036103	33036199
328436905	chr21	33038650	33038869	33038671	33038840	SOD1	NM_000454	1	5	3	+	33038762	33038831
326583644	chr21	33039401	33039613	33039426	33039591	SOD1	NM_000454	1	5	4	+	33039571	33039688
326598555	chr21	33039571	33039768	33039592	33039740	SOD1	NM_000454	1	5	4	+	33039571	33039688
326593555	chr21	33040716	33040917	33040738	33040896	SOD1	NM_000454	1	5	5	+	33040784	33041243
327099904	chr2	39347341	39347554	39347358	39347537	SOS1	NM_005633	1	23	1	-	39347477	39347604
326795337	chr2	39294682	39294886	39294707	39294862	SOS1	NM_005633	1	23	2	-	39294769	39294894
328260389	chr2	39285784	39285960	39285807	39285934	SOS1	NM_005633	1	23	3	-	39285814	39285945
327115349	chr2	39283725	39283875	39283752	39283848	SOS1	NM_005633	1	23	4	-	39283843	39284007
327115631	chr2	39283823	39284021	39283849	39283994	SOS1	NM_005633	1	23	4	-	39283843	39284007
327119937	chr2	39283965	39284145	39283992	39284117	SOS1	NM_005633	1	23	4	-	39283843	39284007
327704910	chr2	39281691	39281895	39281718	39281868	SOS1	NM_005633	1	23	5	-	39281755	39281964
327707968	chr2	39281837	39282046	39281865	39282017	SOS1	NM_005633	1	23	5	-	39281755	39281964
328381294	chr2	39278243	39278462	39278268	39278436	SOS1	NM_005633	1	23	6	-	39278285	39278428
326580108	chr2	39262396	39262590	39262418	39262563	SOS1	NM_005633	1	23	7	-	39262531	39262641
326792555	chr2	39262544	39262713	39262564	39262686	SOS1	NM_005633	1	23	7	-	39262531	39262641

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326577220	chr2	39262246	39262443	39262270	39262415	SOS1	NM_005633	1	23	8	-	39262353	39262451
326579927	chr2	39262395	39262549	39262416	39262521	SOS1	NM_005633	1	23	8	-	39262353	39262451
326580108	chr2	39262396	39262590	39262418	39262563	SOS1	NM_005633	1	23	8	-	39262353	39262451
327656602	chr2	39250994	39251214	39251020	39251186	SOS1	NM_005633	1	23	9	-	39251151	39251278
327663718	chr2	39251149	39251309	39251172	39251284	SOS1	NM_005633	1	23	9	-	39251151	39251278
326444458	chr2	39249642	39249866	39249666	39249843	SOS1	NM_005633	1	23	10	-	39249711	39250366
326459959	chr2	39249822	39249988	39249844	39249965	SOS1	NM_005633	1	23	10	-	39249711	39250366
326471280	chr2	39249935	39250157	39249963	39250133	SOS1	NM_005633	1	23	10	-	39249711	39250366
327847006	chr2	39250113	39250318	39250134	39250291	SOS1	NM_005633	1	23	10	-	39249711	39250366
327850624	chr2	39250265	39250420	39250292	39250391	SOS1	NM_005633	1	23	10	-	39249711	39250366
327591588	chr2	39241827	39241985	39241857	39241958	SOS1	NM_005633	1	23	11	-	39241906	39241987
327592995	chr2	39241933	39242115	39241959	39242087	SOS1	NM_005633	1	23	11	-	39241906	39241987
327411283	chr2	39240900	39241064	39240928	39241035	SOS1	NM_005633	1	23	12	-	39241008	39241130
327414092	chr2	39241009	39241213	39241036	39241189	SOS1	NM_005633	1	23	12	-	39241008	39241130
327577734	chr2	39240535	39240737	39240562	39240708	SOS1	NM_005633	1	23	13	-	39240601	39240704
328113147	chr2	39239105	39239327	39239129	39239301	SOS1	NM_005633	1	23	14	-	39239267	39239489
328117454	chr2	39239282	39239429	39239307	39239401	SOS1	NM_005633	1	23	14	-	39239267	39239489
328121251	chr2	39239378	39239577	39239402	39239549	SOS1	NM_005633	1	23	14	-	39239267	39239489
326685074	chr2	39237710	39237842	39237738	39237816	SOS1	NM_005633	1	23	15	-	39237725	39237844
326685386	chr2	39237791	39237975	39237817	39237947	SOS1	NM_005633	1	23	15	-	39237725	39237844
327595942	chr2	39234052	39234202	39234085	39234177	SOS1	NM_005633	1	23	16	-	39234172	39234334
327595952	chr2	39234152	39234297	39234181	39234270	SOS1	NM_005633	1	23	16	-	39234172	39234334
327597525	chr2	39234183	39234309	39234211	39234285	SOS1	NM_005633	1	23	16	-	39234172	39234334
327598740	chr2	39234274	39234477	39234300	39234450	SOS1	NM_005633	1	23	16	-	39234172	39234334
326608397	chr2	39233438	39233639	39233466	39233611	SOS1	NM_005633	1	23	17	-	39233553	39233670
326610423	chr2	39233572	39233753	39233601	39233732	SOS1	NM_005633	1	23	17	-	39233553	39233670
326500861	chr2	39224401	39224531	39224429	39224510	SOS1	NM_005633	1	23	18	-	39224394	39224566
326502962	chr2	39224463	39224686	39224490	39224661	SOS1	NM_005633	1	23	18	-	39224394	39224566
327047005	chr2	39223913	39224114	39223940	39224086	SOS1	NM_005633	1	23	19	-	39224063	39224179
327047268	chr2	39224150	39224358	39224176	39224325	SOS1	NM_005633	1	23	19	-	39224063	39224179
326858187	chr2	39222147	39222323	39222175	39222300	SOS1	NM_005633	1	23	20	-	39222264	39222528
326863295	chr2	39222276	39222495	39222301	39222473	SOS1	NM_005633	1	23	20	-	39222264	39222528
326875592	chr2	39222453	39222617	39222474	39222589	SOS1	NM_005633	1	23	20	-	39222264	39222528
328248981	chr2	39216271	39216475	39216294	39216449	SOS1	NM_005633	1	23	21	-	39216411	39216455
328253885	chr2	39216423	39216575	39216450	39216545	SOS1	NM_005633	1	23	21	-	39216411	39216455
327621392	chr2	39214533	39214738	39214558	39214710	SOS1	NM_005633	1	23	22	-	39214614	39214732
327622864	chr2	39214685	39214815	39214711	39214787	SOS1	NM_005633	1	23	22	-	39214614	39214732
327747089	chr2	39213103	39213304	39213126	39213280	SOS1	NM_005633	1	23	23	-	39208690	39213456
327759137	chr2	39213259	39213438	39213281	39213420	SOS1	NM_005633	1	23	23	-	39208690	39213456
327760808	chr2	39212930	39213147	39212955	39213125	SOS1	NM_005633	1	23	23	-	39208690	39213456
327763202	chr2	39213403	39213543	39213423	39213512	SOS1	NM_005633	1	23	23	-	39208690	39213456

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327267923	chr17	70117360	70117574	70117377	70117554	SOX9	NM_000346	1	3	1	+	70117161	70117963
327268429	chr17	70117534	70117739	70117555	70117718	SOX9	NM_000346	1	3	1	+	70117161	70117963
328200390	chr17	70117699	70117862	70117718	70117844	SOX9	NM_000346	1	3	1	+	70117161	70117963
328202880	chr17	70117815	70118037	70117834	70118018	SOX9	NM_000346	1	3	1	+	70117161	70117963
327148602	chr17	70118809	70119026	70118829	70119007	SOX9	NM_000346	1	3	2	+	70118860	70119113
327151160	chr17	70118960	70119157	70118981	70119137	SOX9	NM_000346	1	3	2	+	70118860	70119113
327619077	chr17	70119642	70119865	70119664	70119842	SOX9	NM_000346	1	3	3	+	70119684	70122560
327621967	chr17	70119820	70120020	70119837	70120002	SOX9	NM_000346	1	3	3	+	70119684	70122560
327622743	chr17	70119946	70120155	70119964	70120138	SOX9	NM_000346	1	3	3	+	70119684	70122560
327622945	chr17	70119993	70120198	70120012	70120178	SOX9	NM_000346	1	3	3	+	70119684	70122560
328404063	chr17	70120141	70120341	70120158	70120321	SOX9	NM_000346	1	3	3	+	70119684	70122560
328404591	chr17	70120303	70120527	70120321	70120507	SOX9	NM_000346	1	3	3	+	70119684	70122560
328409032	chr17	70120487	70120611	70120508	70120588	SOX9	NM_000346	1	3	3	+	70119684	70122560
326822151	chr14	88851982	88852197	88852004	88852176	SPATA7	NM_001040428	1	11	1	+	88851988	88852181
326825655	chr14	88852144	88852363	88852165	88852343	SPATA7	NM_001040428	1	11	1	+	88851988	88852181
328032802	chr14	88857552	88857760	88857578	88857738	SPATA7	NM_001040428	1	11	2	+	88857725	88857799
328034782	chr14	88857712	88857860	88857739	88857832	SPATA7	NM_001040428	1	11	2	+	88857725	88857799
327171849	chr14	88862404	88862547	88862425	88862524	SPATA7	NM_001040428	1	11	3	+	88862500	88862547
328124724	chr14	88882966	88883142	88882999	88883114	SPATA7	NM_001040428	1	11	4	+	88883055	88883188
328028310	chr14	88892541	88892765	88892567	88892744	SPATA7	NM_001040428	1	11	5	+	88892576	88893048
328048248	chr14	88892713	88892927	88892736	88892898	SPATA7	NM_001040428	1	11	5	+	88892576	88893048
328060106	chr14	88892871	88893078	88892899	88893053	SPATA7	NM_001040428	1	11	5	+	88892576	88893048
326742469	chr14	88893790	88894008	88893817	88893985	SPATA7	NM_001040428	1	11	6	+	88893974	88894040
326742589	chr14	88893990	88894148	88894013	88894123	SPATA7	NM_001040428	1	11	6	+	88893974	88894040
327851640	chr14	88895621	88895786	88895650	88895758	SPATA7	NM_001040428	1	11	7	+	88895692	88895807
327852569	chr14	88895734	88895924	88895759	88895898	SPATA7	NM_001040428	1	11	7	+	88895692	88895807
326524325	chr14	88897509	88897633	88897535	88897602	SPATA7	NM_001040428	1	11	8	+	88897516	88897569
328115065	chr14	88899464	88899598	88899490	88899567	SPATA7	NM_001040428	1	11	9	+	88899479	88899556
326512440	chr14	88903741	88903953	88903768	88903927	SPATA7	NM_001040428	1	11	10	+	88903887	88903941
326512754	chr14	88903898	88904088	88903926	88904067	SPATA7	NM_001040428	1	11	10	+	88903887	88903941
328072276	chr14	88904072	88904254	88904096	88904231	SPATA7	NM_001040428	1	11	11	+	88904182	88904804
328073082	chr14	88904642	88904804	88904666	88904777	SPATA7	NM_001040428	1	11	11	+	88904182	88904804
328074755	chr14	88904208	88904429	88904232	88904403	SPATA7	NM_001040428	1	11	11	+	88904182	88904804
328080766	chr14	88904379	88904601	88904404	88904573	SPATA7	NM_001040428	1	11	11	+	88904182	88904804
328085618	chr14	88904548	88904688	88904574	88904665	SPATA7	NM_001040428	1	11	11	+	88904182	88904804
326822151	chr14	88851982	88852197	88852004	88852176	SPATA7	NM_018418	2	12	1	+	88851988	88852181
326825655	chr14	88852144	88852363	88852165	88852343	SPATA7	NM_018418	2	12	1	+	88851988	88852181
328032802	chr14	88857552	88857760	88857578	88857738	SPATA7	NM_018418	2	12	2	+	88857725	88857799
328034782	chr14	88857712	88857860	88857739	88857832	SPATA7	NM_018418	2	12	2	+	88857725	88857799
327537853	chr14	88859666	88859864	88859692	88859837	SPATA7	NM_018418	2	12	3	+	88859737	88859832
327171849	chr14	88862404	88862547	88862425	88862524	SPATA7	NM_018418	2	12	4	+	88862500	88862547

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328124724	chr14	88882966	88883142	88882999	88883114	SPATA7	NM_018418	2	12	5	+	88883055	88883188
328028310	chr14	88892541	88892765	88892567	88892744	SPATA7	NM_018418	2	12	6	+	88892576	88893048
328048248	chr14	88892713	88892927	88892736	88892898	SPATA7	NM_018418	2	12	6	+	88892576	88893048
328060106	chr14	88892871	88893078	88892899	88893053	SPATA7	NM_018418	2	12	6	+	88892576	88893048
326742469	chr14	88893790	88894008	88893817	88893985	SPATA7	NM_018418	2	12	7	+	88893974	88894040
326742589	chr14	88893990	88894148	88894013	88894123	SPATA7	NM_018418	2	12	7	+	88893974	88894040
327851640	chr14	88895621	88895786	88895650	88895758	SPATA7	NM_018418	2	12	8	+	88895692	88895807
327852569	chr14	88895734	88895924	88895759	88895898	SPATA7	NM_018418	2	12	8	+	88895692	88895807
326524325	chr14	88897509	88897633	88897535	88897602	SPATA7	NM_018418	2	12	9	+	88897516	88897569
328115065	chr14	88899464	88899598	88899490	88899567	SPATA7	NM_018418	2	12	10	+	88899479	88899556
326512440	chr14	88903741	88903953	88903768	88903927	SPATA7	NM_018418	2	12	11	+	88903887	88903941
326512754	chr14	88903898	88904088	88903926	88904067	SPATA7	NM_018418	2	12	11	+	88903887	88903941
328072276	chr14	88904072	88904254	88904096	88904231	SPATA7	NM_018418	2	12	12	+	88904182	88904804
328073082	chr14	88904642	88904804	88904666	88904777	SPATA7	NM_018418	2	12	12	+	88904182	88904804
328074755	chr14	88904208	88904429	88904232	88904403	SPATA7	NM_018418	2	12	12	+	88904182	88904804
328080766	chr14	88904379	88904601	88904404	88904573	SPATA7	NM_018418	2	12	12	+	88904182	88904804
328085618	chr14	88904548	88904688	88904574	88904665	SPATA7	NM_018418	2	12	12	+	88904182	88904804
327101725	chr16	89576821	89577031	89576847	89577005	SPG7	NM_003119	1	17	2	+	89576898	89577000
328175871	chr16	89579262	89579480	89579291	89579456	SPG7	NM_003119	1	17	3	+	89579356	89579445
327377723	chr16	89590363	89590564	89590388	89590545	SPG7	NM_003119	1	17	4	+	89590414	89590655
327382209	chr16	89590524	89590744	89590544	89590724	SPG7	NM_003119	1	17	4	+	89590414	89590655
327416676	chr16	89592703	89592920	89592725	89592892	SPG7	NM_003119	1	17	5	+	89592737	89592876
327053934	chr16	89595837	89596056	89595856	89596028	SPG7	NM_003119	1	17	6	+	89595885	89595987
327919818	chr16	89597059	89597282	89597079	89597262	SPG7	NM_003119	1	17	7	+	89597091	89597216
327592651	chr16	89598267	89598491	89598291	89598471	SPG7	NM_003119	1	17	8	+	89598312	89598474
327596939	chr16	89598450	89598604	89598472	89598581	SPG7	NM_003119	1	17	8	+	89598312	89598474
327846959	chr16	89598836	89599046	89598859	89599022	SPG7	NM_003119	1	17	9	+	89598871	89599044
327849976	chr16	89598980	89599116	89599000	89599092	SPG7	NM_003119	1	17	9	+	89598871	89599044
327187703	chr16	89610903	89611114	89610924	89611092	SPG7	NM_003119	1	17	10	+	89611056	89611180
327196640	chr16	89611066	89611281	89611087	89611260	SPG7	NM_003119	1	17	10	+	89611056	89611180
327674430	chr16	89613027	89613172	89613048	89613150	SPG7	NM_003119	1	17	11	+	89613066	89613168
327678005	chr16	89613112	89613330	89613133	89613309	SPG7	NM_003119	1	17	11	+	89613066	89613168
327855147	chr16	89614350	89614571	89614374	89614550	SPG7	NM_003119	1	17	12	+	89614411	89614521
328203623	chr16	89616875	89617073	89616894	89617054	SPG7	NM_003119	1	17	13	+	89616902	89617017
328299450	chr16	89619310	89619530	89619332	89619509	SPG7	NM_003119	1	17	14	+	89619387	89619543
328316074	chr16	89619471	89619656	89619491	89619628	SPG7	NM_003119	1	17	14	+	89619387	89619543
326914028	chr16	89620054	89620274	89620074	89620255	SPG7	NM_003119	1	17	15	+	89620202	89620368
326917212	chr16	89620233	89620443	89620255	89620423	SPG7	NM_003119	1	17	15	+	89620202	89620368
327651181	chr16	89620804	89621016	89620825	89620997	SPG7	NM_003119	1	17	16	+	89620894	89620971
328354219	chr16	89623224	89623432	89623246	89623410	SPG7	NM_003119	1	17	17	+	89623295	89624174
328361867	chr16	89623377	89623586	89623398	89623563	SPG7	NM_003119	1	17	17	+	89623295	89624174

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327101725	chr16	89576821	89577031	89576847	89577005	SPG7	NM_199367	2	10	2	+	89576898	89577000
328175871	chr16	89579262	89579480	89579291	89579456	SPG7	NM_199367	2	10	3	+	89579356	89579445
327377723	chr16	89590363	89590564	89590388	89590545	SPG7	NM_199367	2	10	4	+	89590414	89590655
327382209	chr16	89590524	89590744	89590544	89590724	SPG7	NM_199367	2	10	4	+	89590414	89590655
327416676	chr16	89592703	89592920	89592725	89592892	SPG7	NM_199367	2	10	5	+	89592737	89592876
327053934	chr16	89595837	89596056	89595856	89596028	SPG7	NM_199367	2	10	6	+	89595885	89595987
327919818	chr16	89597059	89597282	89597079	89597262	SPG7	NM_199367	2	10	7	+	89597091	89597216
327592651	chr16	89598267	89598491	89598291	89598471	SPG7	NM_199367	2	10	8	+	89598312	89598474
327596939	chr16	89598450	89598604	89598472	89598581	SPG7	NM_199367	2	10	8	+	89598312	89598474
327846959	chr16	89598836	89599046	89598859	89599022	SPG7	NM_199367	2	10	9	+	89598871	89599044
327849976	chr16	89598980	89599116	89599000	89599092	SPG7	NM_199367	2	10	9	+	89598871	89599044
327810584	chr16	89603129	89603352	89603151	89603329	SPG7	NM_199367	2	10	10	+	89603173	89604129
332512861	chr17	37809698	37809922	37809719	37809903	STARD3	NM_001165937	1	15	2	+	37809734	37810003
332515512	chr17	37809872	37810079	37809889	37810058	STARD3	NM_001165937	1	15	2	+	37809734	37810003
332276267	chr17	37813222	37813411	37813243	37813388	STARD3	NM_001165937	1	15	3	+	37813261	37813338
333062855	chr17	37813984	37814185	37814004	37814164	STARD3	NM_001165937	1	15	4	+	37814028	37814092
332907122	chr17	37814162	37814332	37814183	37814310	STARD3	NM_001165937	1	15	5	+	37814226	37814279
332619575	chr17	37814571	37814782	37814593	37814760	STARD3	NM_001165937	1	15	6	+	37814658	37814775
332630622	chr17	37814738	37814948	37814761	37814926	STARD3	NM_001165937	1	15	6	+	37814658	37814775
333306636	chr17	37814931	37815135	37814951	37815114	STARD3	NM_001165937	1	15	7	+	37814962	37815073
333353601	chr17	37815266	37815466	37815287	37815444	STARD3	NM_001165937	1	15	8	+	37815304	37815359
332678808	chr17	37815624	37815848	37815651	37815828	STARD3	NM_001165937	1	15	9	+	37815714	37815806
332770768	chr17	37816288	37816512	37816313	37816491	STARD3	NM_001165937	1	15	10	+	37816464	37816526
332777909	chr17	37816471	37816637	37816492	37816616	STARD3	NM_001165937	1	15	10	+	37816464	37816526
332292146	chr17	37816617	37816819	37816638	37816798	STARD3	NM_001165937	1	15	11	+	37816684	37816779
333462205	chr17	37817024	37817184	37817044	37817162	STARD3	NM_001165937	1	15	12	+	37817063	37817142
332341030	chr17	37817187	37817410	37817208	37817389	STARD3	NM_001165937	1	15	13	+	37817234	37817338
333358745	chr17	37818457	37818674	37818479	37818653	STARD3	NM_001165937	1	15	14	+	37818504	37818597
332679607	chr17	37819019	37819224	37819041	37819203	STARD3	NM_001165937	1	15	15	+	37819057	37820454
332512861	chr17	37809698	37809922	37809719	37809903	STARD3	NM_001165938	2	14	2	+	37809734	37810003
332515512	chr17	37809872	37810079	37809889	37810058	STARD3	NM_001165938	2	14	2	+	37809734	37810003
332276267	chr17	37813222	37813411	37813243	37813388	STARD3	NM_001165938	2	14	3	+	37813261	37813338
333062855	chr17	37813984	37814185	37814004	37814164	STARD3	NM_001165938	2	14	4	+	37814028	37814105
332619575	chr17	37814571	37814782	37814593	37814760	STARD3	NM_001165938	2	14	5	+	37814658	37814775
332630622	chr17	37814738	37814948	37814761	37814926	STARD3	NM_001165938	2	14	5	+	37814658	37814775
333306636	chr17	37814931	37815135	37814951	37815114	STARD3	NM_001165938	2	14	6	+	37814975	37815073
333353601	chr17	37815266	37815466	37815287	37815444	STARD3	NM_001165938	2	14	7	+	37815304	37815359
332678808	chr17	37815624	37815848	37815651	37815828	STARD3	NM_001165938	2	14	8	+	37815714	37815806
332770768	chr17	37816288	37816512	37816313	37816491	STARD3	NM_001165938	2	14	9	+	37816464	37816526
332777909	chr17	37816471	37816637	37816492	37816616	STARD3	NM_001165938	2	14	9	+	37816464	37816526
332292146	chr17	37816617	37816819	37816638	37816798	STARD3	NM_001165938	2	14	10	+	37816684	37816779

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333462205	chr17	37817024	37817184	37817044	37817162	STARD3	NM_001165938	2	14	11	+	37817063	37817142
332341030	chr17	37817187	37817410	37817208	37817389	STARD3	NM_001165938	2	14	12	+	37817234	37817338
333358745	chr17	37818457	37818674	37818479	37818653	STARD3	NM_001165938	2	14	13	+	37818504	37818597
332679607	chr17	37819019	37819224	37819041	37819203	STARD3	NM_001165938	2	14	14	+	37819057	37820454
332512861	chr17	37809698	37809922	37809719	37809903	STARD3	NM_006804	3	15	2	+	37809734	37810003
332515512	chr17	37809872	37810079	37809889	37810058	STARD3	NM_006804	3	15	2	+	37809734	37810003
332276267	chr17	37813222	37813411	37813243	37813388	STARD3	NM_006804	3	15	3	+	37813261	37813338
333062855	chr17	37813984	37814185	37814004	37814164	STARD3	NM_006804	3	15	4	+	37814028	37814105
332907122	chr17	37814162	37814332	37814183	37814310	STARD3	NM_006804	3	15	5	+	37814226	37814279
332619575	chr17	37814571	37814782	37814593	37814760	STARD3	NM_006804	3	15	6	+	37814658	37814775
332630622	chr17	37814738	37814948	37814761	37814926	STARD3	NM_006804	3	15	6	+	37814658	37814775
333306636	chr17	37814931	37815135	37814951	37815114	STARD3	NM_006804	3	15	7	+	37814975	37815073
333353601	chr17	37815266	37815466	37815287	37815444	STARD3	NM_006804	3	15	8	+	37815304	37815359
332678808	chr17	37815624	37815848	37815651	37815828	STARD3	NM_006804	3	15	9	+	37815714	37815806
332770768	chr17	37816288	37816512	37816313	37816491	STARD3	NM_006804	3	15	10	+	37816464	37816526
332777909	chr17	37816471	37816637	37816492	37816616	STARD3	NM_006804	3	15	10	+	37816464	37816526
332292146	chr17	37816617	37816819	37816638	37816798	STARD3	NM_006804	3	15	11	+	37816684	37816779
333462205	chr17	37817024	37817184	37817044	37817162	STARD3	NM_006804	3	15	12	+	37817063	37817142
332341030	chr17	37817187	37817410	37817208	37817389	STARD3	NM_006804	3	15	13	+	37817234	37817338
333358745	chr17	37818457	37818674	37818479	37818653	STARD3	NM_006804	3	15	14	+	37818504	37818597
332679607	chr17	37819019	37819224	37819041	37819203	STARD3	NM_006804	3	15	15	+	37819057	37820454
303250199	chrX	70586115	70586307	70586138	70586282	TAF1	NM_004606	1	38	1	+	70586114	70586344
303260558	chrX	70586259	70586405	70586280	70586384	TAF1	NM_004606	1	38	1	+	70586114	70586344
305043659	chrX	70587292	70587514	70587314	70587494	TAF1	NM_004606	1	38	2	+	70587349	70587463
301334729	chrX	70587839	70588053	70587863	70588028	TAF1	NM_004606	1	38	3	+	70587904	70588020
305593159	chrX	70594949	70595169	70594970	70595142	TAF1	NM_004606	1	38	4	+	70595017	70595136
300421279	chrX	70596848	70597070	70596870	70597046	TAF1	NM_004606	1	38	5	+	70596800	70597041
327060657	chrX	70596673	70596894	70596695	70596869	TAF1	NM_004606	1	38	5	+	70596800	70597041
302165306	chrX	70597509	70597708	70597530	70597680	TAF1	NM_004606	1	38	6	+	70597453	70597671
326870162	chrX	70597325	70597549	70597349	70597529	TAF1	NM_004606	1	38	6	+	70597453	70597671
303966711	chrX	70598025	70598242	70598047	70598220	TAF1	NM_004606	1	38	7	+	70598085	70598303
303987357	chrX	70598198	70598349	70598221	70598322	TAF1	NM_004606	1	38	7	+	70598085	70598303
305123392	chrX	70598702	70598926	70598727	70598900	TAF1	NM_004606	1	38	8	+	70598674	70598881
327896849	chrX	70598523	70598747	70598548	70598726	TAF1	NM_004606	1	38	8	+	70598674	70598881
304880539	chrX	70601593	70601803	70601615	70601781	TAF1	NM_004606	1	38	9	+	70601593	70601769
327807418	chrX	70601447	70601640	70601472	70601614	TAF1	NM_004606	1	38	9	+	70601593	70601769
301125178	chrX	70602325	70602549	70602351	70602525	TAF1	NM_004606	1	38	10	+	70602386	70602513
304840692	chrX	70602531	70602753	70602553	70602726	TAF1	NM_004606	1	38	11	+	70602611	70602718
301091682	chrX	70602747	70602936	70602768	70602915	TAF1	NM_004606	1	38	12	+	70602841	70603014
301108376	chrX	70602896	70603032	70602916	70603005	TAF1	NM_004606	1	38	12	+	70602841	70603014
305878252	chrX	70603722	70603932	70603749	70603903	TAF1	NM_004606	1	38	13	+	70603812	70603985

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305895735	chrX	70603878	70604096	70603904	70604071	TAF1	NM_004606	1	38	13	+	70603812	70603985
300777167	chrX	70604721	70604892	70604750	70604870	TAF1	NM_004606	1	38	14	+	70604795	70604899
300780414	chrX	70604844	70604968	70604870	70604946	TAF1	NM_004606	1	38	14	+	70604795	70604899
300417938	chrX	70607014	70607237	70607042	70607209	TAF1	NM_004606	1	38	15	+	70607111	70607311
300435889	chrX	70607184	70607346	70607210	70607325	TAF1	NM_004606	1	38	15	+	70607111	70607311
305646670	chrX	70607975	70608128	70607998	70608104	TAF1	NM_004606	1	38	16	+	70608087	70608228
305661224	chrX	70608082	70608260	70608105	70608233	TAF1	NM_004606	1	38	16	+	70608087	70608228
301932849	chrX	70608528	70608749	70608555	70608723	TAF1	NM_004606	1	38	17	+	70608588	70608718
299798177	chrX	70612385	70612560	70612406	70612534	TAF1	NM_004606	1	38	19	+	70612419	70612568
299810576	chrX	70612512	70612644	70612535	70612620	TAF1	NM_004606	1	38	19	+	70612419	70612568
303122675	chrX	70612678	70612901	70612706	70612873	TAF1	NM_004606	1	38	20	+	70612725	70612844
302844782	chrX	70613034	70613219	70613057	70613197	TAF1	NM_004606	1	38	21	+	70613151	70613326
302867539	chrX	70613177	70613355	70613198	70613331	TAF1	NM_004606	1	38	21	+	70613151	70613326
300514363	chrX	70613961	70614162	70613986	70614139	TAF1	NM_004606	1	38	22	+	70613917	70614095
327221449	chrX	70613790	70614013	70613811	70613985	TAF1	NM_004606	1	38	22	+	70613917	70614095
303450337	chrX	70617116	70617340	70617138	70617312	TAF1	NM_004606	1	38	23	+	70617103	70617316
326446463	chrX	70616983	70617159	70617011	70617137	TAF1	NM_004606	1	38	23	+	70617103	70617316
301154193	chrX	70618406	70618620	70618427	70618592	TAF1	NM_004606	1	38	24	+	70618422	70618587
327600008	chrX	70618250	70618453	70618271	70618426	TAF1	NM_004606	1	38	24	+	70618422	70618587
304783742	chrX	70621313	70621463	70621340	70621438	TAF1	NM_004606	1	38	25	+	70621378	70621589
304806866	chrX	70621416	70621618	70621439	70621595	TAF1	NM_004606	1	38	25	+	70621378	70621589
299452347	chrX	70626433	70626628	70626456	70626602	TAF1	NM_004606	1	38	26	+	70626488	70626596
304409966	chrX	70627381	70627565	70627406	70627537	TAF1	NM_004606	1	38	27	+	70627424	70627522
302929735	chrX	70627811	70628034	70627832	70628010	TAF1	NM_004606	1	38	28	+	70627824	70628001
327517050	chrX	70627678	70627853	70627703	70627831	TAF1	NM_004606	1	38	28	+	70627824	70628001
302694084	chrX	70641044	70641258	70641066	70641232	TAF1	NM_004606	1	38	29	+	70641159	70641226
300534542	chrX	70642908	70643119	70642934	70643095	TAF1	NM_004606	1	38	30	+	70642967	70643089
305583006	chrX	70643747	70643965	70643770	70643938	TAF1	NM_004606	1	38	31	+	70643824	70643916
299944276	chrX	70643907	70644131	70643934	70644102	TAF1	NM_004606	1	38	32	+	70644004	70644088
305743957	chrX	70673893	70674116	70673916	70674092	TAF1	NM_004606	1	38	33	+	70674020	70674087
300286979	chrX	70674594	70674784	70674622	70674758	TAF1	NM_004606	1	38	34	+	70674591	70674707
301385793	chrX	70678047	70678265	70678075	70678237	TAF1	NM_004606	1	38	35	+	70678091	70678216
303062026	chrX	70679385	70679607	70679408	70679580	TAF1	NM_004606	1	38	36	+	70679402	70679558
327588995	chrX	70679208	70679431	70679229	70679407	TAF1	NM_004606	1	38	36	+	70679402	70679558
301986569	chrX	70680486	70680709	70680510	70680686	TAF1	NM_004606	1	38	37	+	70680476	70680653
327935040	chrX	70680312	70680532	70680334	70680509	TAF1	NM_004606	1	38	37	+	70680476	70680653
300066940	chrX	70683615	70683838	70683638	70683818	TAF1	NM_004606	1	38	38	+	70683674	70685855
300094167	chrX	70683799	70683951	70683819	70683930	TAF1	NM_004606	1	38	38	+	70683674	70685855
303250199	chrX	70586115	70586307	70586138	70586282	TAF1	NM_138923	2	38	1	+	70586114	70586344
303260558	chrX	70586259	70586405	70586280	70586384	TAF1	NM_138923	2	38	1	+	70586114	70586344
305043659	chrX	70587292	70587514	70587314	70587494	TAF1	NM_138923	2	38	2	+	70587349	70587463

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
301334729	chrX	70587839	70588053	70587863	70588028	TAF1	NM_138923	2	38	3	+	70587904	70588020
305593159	chrX	70594949	70595169	70594970	70595142	TAF1	NM_138923	2	38	4	+	70595017	70595136
300421279	chrX	70596848	70597070	70596870	70597046	TAF1	NM_138923	2	38	5	+	70596863	70597041
327060657	chrX	70596673	70596894	70596695	70596869	TAF1	NM_138923	2	38	5	+	70596863	70597041
302165306	chrX	70597509	70597708	70597530	70597680	TAF1	NM_138923	2	38	6	+	70597453	70597671
326870162	chrX	70597325	70597549	70597349	70597529	TAF1	NM_138923	2	38	6	+	70597453	70597671
303966711	chrX	70598025	70598242	70598047	70598220	TAF1	NM_138923	2	38	7	+	70598085	70598303
303987357	chrX	70598198	70598349	70598221	70598322	TAF1	NM_138923	2	38	7	+	70598085	70598303
305123392	chrX	70598702	70598926	70598727	70598900	TAF1	NM_138923	2	38	8	+	70598674	70598881
327896849	chrX	70598523	70598747	70598548	70598726	TAF1	NM_138923	2	38	8	+	70598674	70598881
304880539	chrX	70601593	70601803	70601615	70601781	TAF1	NM_138923	2	38	9	+	70601593	70601769
327807418	chrX	70601447	70601640	70601472	70601614	TAF1	NM_138923	2	38	9	+	70601593	70601769
301125178	chrX	70602325	70602549	70602351	70602525	TAF1	NM_138923	2	38	10	+	70602386	70602513
304840692	chrX	70602531	70602753	70602553	70602726	TAF1	NM_138923	2	38	11	+	70602611	70602718
301091682	chrX	70602747	70602936	70602768	70602915	TAF1	NM_138923	2	38	12	+	70602841	70603014
301108376	chrX	70602896	70603032	70602916	70603005	TAF1	NM_138923	2	38	12	+	70602841	70603014
305878252	chrX	70603722	70603932	70603749	70603903	TAF1	NM_138923	2	38	13	+	70603812	70603985
305895735	chrX	70603878	70604096	70603904	70604071	TAF1	NM_138923	2	38	13	+	70603812	70603985
300777167	chrX	70604721	70604892	70604750	70604870	TAF1	NM_138923	2	38	14	+	70604795	70604899
300780414	chrX	70604844	70604968	70604870	70604946	TAF1	NM_138923	2	38	14	+	70604795	70604899
300417938	chrX	70607014	70607237	70607042	70607209	TAF1	NM_138923	2	38	15	+	70607111	70607311
300435889	chrX	70607184	70607346	70607210	70607325	TAF1	NM_138923	2	38	15	+	70607111	70607311
305646670	chrX	70607975	70608128	70607998	70608104	TAF1	NM_138923	2	38	16	+	70608087	70608228
305661224	chrX	70608082	70608260	70608105	70608233	TAF1	NM_138923	2	38	16	+	70608087	70608228
301932849	chrX	70608528	70608749	70608555	70608723	TAF1	NM_138923	2	38	17	+	70608588	70608718
299798177	chrX	70612385	70612560	70612406	70612534	TAF1	NM_138923	2	38	19	+	70612419	70612568
299810576	chrX	70612512	70612644	70612535	70612620	TAF1	NM_138923	2	38	19	+	70612419	70612568
303122675	chrX	70612678	70612901	70612706	70612873	TAF1	NM_138923	2	38	20	+	70612725	70612844
302844782	chrX	70613034	70613219	70613057	70613197	TAF1	NM_138923	2	38	21	+	70613151	70613326
302867539	chrX	70613177	70613355	70613198	70613331	TAF1	NM_138923	2	38	21	+	70613151	70613326
300514363	chrX	70613961	70614162	70613986	70614139	TAF1	NM_138923	2	38	22	+	70613917	70614095
327221449	chrX	70613790	70614013	70613811	70613985	TAF1	NM_138923	2	38	22	+	70613917	70614095
303450337	chrX	70617116	70617340	70617138	70617312	TAF1	NM_138923	2	38	23	+	70617103	70617316
326446463	chrX	70616983	70617159	70617011	70617137	TAF1	NM_138923	2	38	23	+	70617103	70617316
301154193	chrX	70618406	70618620	70618427	70618592	TAF1	NM_138923	2	38	24	+	70618422	70618587
327600008	chrX	70618250	70618453	70618271	70618426	TAF1	NM_138923	2	38	24	+	70618422	70618587
304783742	chrX	70621313	70621463	70621340	70621438	TAF1	NM_138923	2	38	25	+	70621378	70621589
304806866	chrX	70621416	70621618	70621439	70621595	TAF1	NM_138923	2	38	25	+	70621378	70621589
299452347	chrX	70626433	70626628	70626456	70626602	TAF1	NM_138923	2	38	26	+	70626488	70626596
304409966	chrX	70627381	70627565	70627406	70627537	TAF1	NM_138923	2	38	27	+	70627424	70627522
302929735	chrX	70627811	70628034	70627832	70628010	TAF1	NM_138923	2	38	28	+	70627824	70628001

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327517050	chrX	70627678	70627853	70627703	70627831	TAF1	NM_138923	2	38	28	+	70627824	70628001
302694084	chrX	70641044	70641258	70641066	70641232	TAF1	NM_138923	2	38	29	+	70641159	70641226
300534542	chrX	70642908	70643119	70642934	70643095	TAF1	NM_138923	2	38	30	+	70642967	70643089
305583006	chrX	70643747	70643965	70643770	70643938	TAF1	NM_138923	2	38	31	+	70643824	70643916
299944276	chrX	70643907	70644131	70643934	70644102	TAF1	NM_138923	2	38	32	+	70644004	70644088
305743957	chrX	70673893	70674116	70673916	70674092	TAF1	NM_138923	2	38	33	+	70674020	70674087
300286979	chrX	70674594	70674784	70674622	70674758	TAF1	NM_138923	2	38	34	+	70674591	70674707
301385793	chrX	70678047	70678265	70678075	70678237	TAF1	NM_138923	2	38	35	+	70678091	70678216
303062026	chrX	70679385	70679607	70679408	70679580	TAF1	NM_138923	2	38	36	+	70679402	70679558
327588995	chrX	70679208	70679431	70679229	70679407	TAF1	NM_138923	2	38	36	+	70679402	70679558
301986569	chrX	70680486	70680709	70680510	70680686	TAF1	NM_138923	2	38	37	+	70680476	70680653
327935040	chrX	70680312	70680532	70680334	70680509	TAF1	NM_138923	2	38	37	+	70680476	70680653
300066940	chrX	70683615	70683838	70683638	70683818	TAF1	NM_138923	2	38	38	+	70683674	70685855
300094167	chrX	70683799	70683951	70683819	70683930	TAF1	NM_138923	2	38	38	+	70683674	70685855
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_000116	1	11	1	+	153639877	153640289
333619592	chrX	153640104	153640296	153640123	153640276	TAZ	NM_000116	1	11	1	+	153639877	153640289
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_000116	1	11	2	+	153640423	153640551
333551238	chrX	153640394	153640602	153640411	153640583	TAZ	NM_000116	1	11	2	+	153640423	153640551
332500768	chrX	153641455	153641663	153641477	153641643	TAZ	NM_000116	1	11	3	+	153641544	153641589
332260270	chrX	153641787	153641994	153641809	153641973	TAZ	NM_000116	1	11	4	+	153641819	153641904
333093464	chrX	153642257	153642479	153642282	153642456	TAZ	NM_000116	1	11	5	+	153642438	153642527
332562165	chrX	153647836	153648055	153647855	153648032	TAZ	NM_000116	1	11	6	+	153647882	153647962
332599021	chrX	153647989	153648203	153648008	153648182	TAZ	NM_000116	1	11	7	+	153648044	153648085
333803255	chrX	153648262	153648471	153648286	153648450	TAZ	NM_000116	1	11	8	+	153648371	153648433
332264606	chrX	153648523	153648746	153648543	153648722	TAZ	NM_000116	1	11	9	+	153648551	153648603
333671748	chrX	153648946	153649169	153648963	153649151	TAZ	NM_000116	1	11	10	+	153648997	153649074
333144239	chrX	153649058	153649274	153649078	153649253	TAZ	NM_000116	1	11	11	+	153649242	153650063
333151698	chrX	153649229	153649444	153649250	153649418	TAZ	NM_000116	1	11	11	+	153649242	153650063
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181311	2	10	1	+	153639877	153640289
333619592	chrX	153640104	153640296	153640123	153640276	TAZ	NM_181311	2	10	1	+	153639877	153640289
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181311	2	10	2	+	153640423	153640551
333551238	chrX	153640394	153640602	153640411	153640583	TAZ	NM_181311	2	10	2	+	153640423	153640551
332500768	chrX	153641455	153641663	153641477	153641643	TAZ	NM_181311	2	10	3	+	153641544	153641589
332260270	chrX	153641787	153641994	153641809	153641973	TAZ	NM_181311	2	10	4	+	153641819	153641904
332562165	chrX	153647836	153648055	153647855	153648032	TAZ	NM_181311	2	10	5	+	153647882	153647962
332599021	chrX	153647989	153648203	153648008	153648182	TAZ	NM_181311	2	10	6	+	153648044	153648085
333803255	chrX	153648262	153648471	153648286	153648450	TAZ	NM_181311	2	10	7	+	153648371	153648433
332264606	chrX	153648523	153648746	153648543	153648722	TAZ	NM_181311	2	10	8	+	153648551	153648603
333671748	chrX	153648946	153649169	153648963	153649151	TAZ	NM_181311	2	10	9	+	153648997	153649074
333144239	chrX	153649058	153649274	153649078	153649253	TAZ	NM_181311	2	10	10	+	153649242	153650063
333151698	chrX	153649229	153649444	153649250	153649418	TAZ	NM_181311	2	10	10	+	153649242	153650063

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181312	3	10	1	+	153639877	153640289
333619592	chrX	153640104	153640296	153640123	153640276	TAZ	NM_181312	3	10	1	+	153639877	153640289
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181312	3	10	2	+	153640423	153640551
333551238	chrX	153640394	153640602	153640411	153640583	TAZ	NM_181312	3	10	2	+	153640423	153640551
332500768	chrX	153641455	153641663	153641477	153641643	TAZ	NM_181312	3	10	3	+	153641544	153641589
332260270	chrX	153641787	153641994	153641809	153641973	TAZ	NM_181312	3	10	4	+	153641819	153641904
333093464	chrX	153642257	153642479	153642282	153642456	TAZ	NM_181312	3	10	5	+	153642438	153642527
332562165	chrX	153647836	153648055	153647855	153648032	TAZ	NM_181312	3	10	6	+	153647882	153647962
333803255	chrX	153648262	153648471	153648286	153648450	TAZ	NM_181312	3	10	7	+	153648371	153648433
332264606	chrX	153648523	153648746	153648543	153648722	TAZ	NM_181312	3	10	8	+	153648551	153648603
333671748	chrX	153648946	153649169	153648963	153649151	TAZ	NM_181312	3	10	9	+	153648997	153649074
333144239	chrX	153649058	153649274	153649078	153649253	TAZ	NM_181312	3	10	10	+	153649242	153650063
333151698	chrX	153649229	153649444	153649250	153649418	TAZ	NM_181312	3	10	10	+	153649242	153650063
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181313	4	9	1	+	153639877	153640289
333619592	chrX	153640104	153640296	153640123	153640276	TAZ	NM_181313	4	9	1	+	153639877	153640289
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NM_181313	4	9	2	+	153640423	153640551
333551238	chrX	153640394	153640602	153640411	153640583	TAZ	NM_181313	4	9	2	+	153640423	153640551
332500768	chrX	153641455	153641663	153641477	153641643	TAZ	NM_181313	4	9	3	+	153641544	153641589
332260270	chrX	153641787	153641994	153641809	153641973	TAZ	NM_181313	4	9	4	+	153641819	153641904
332562165	chrX	153647836	153648055	153647855	153648032	TAZ	NM_181313	4	9	5	+	153647882	153647962
333803255	chrX	153648262	153648471	153648286	153648450	TAZ	NM_181313	4	9	6	+	153648371	153648433
332264606	chrX	153648523	153648746	153648543	153648722	TAZ	NM_181313	4	9	7	+	153648551	153648603
333671748	chrX	153648946	153649169	153648963	153649151	TAZ	NM_181313	4	9	8	+	153648997	153649074
333144239	chrX	153649058	153649274	153649078	153649253	TAZ	NM_181313	4	9	9	+	153649242	153650063
333151698	chrX	153649229	153649444	153649250	153649418	TAZ	NM_181313	4	9	9	+	153649242	153650063
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NR_024048	5	10	1	+	153639877	153640289
333619592	chrX	153640104	153640296	153640123	153640276	TAZ	NR_024048	5	10	1	+	153639877	153640289
333549607	chrX	153640246	153640469	153640264	153640451	TAZ	NR_024048	5	10	2	+	153640423	153640551
333551238	chrX	153640394	153640602	153640411	153640583	TAZ	NR_024048	5	10	2	+	153640423	153640551
332500768	chrX	153641455	153641663	153641477	153641643	TAZ	NR_024048	5	10	3	+	153641544	153641695
332260270	chrX	153641787	153641994	153641809	153641973	TAZ	NR_024048	5	10	4	+	153641819	153641904
332562165	chrX	153647836	153648055	153647855	153648032	TAZ	NR_024048	5	10	5	+	153647882	153647962
332599021	chrX	153647989	153648203	153648008	153648182	TAZ	NR_024048	5	10	6	+	153648044	153648085
333803255	chrX	153648262	153648471	153648286	153648450	TAZ	NR_024048	5	10	7	+	153648371	153648433
332264606	chrX	153648523	153648746	153648543	153648722	TAZ	NR_024048	5	10	8	+	153648551	153648603
333671748	chrX	153648946	153649169	153648963	153649151	TAZ	NR_024048	5	10	9	+	153648997	153649074
333144239	chrX	153649058	153649274	153649078	153649253	TAZ	NR_024048	5	10	10	+	153649242	153650063
333151698	chrX	153649229	153649444	153649250	153649418	TAZ	NR_024048	5	10	10	+	153649242	153650063
327448268	chr12	114841419	114841641	114841444	114841622	TBX5	NM_000192	1	9	2	-	114841557	114841741
327450582	chr12	114841549	114841751	114841570	114841729	TBX5	NM_000192	1	9	2	-	114841557	114841741
326993127	chr12	114839605	114839785	114839631	114839765	TBX5	NM_000192	1	9	3	-	114839631	114839725

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328108510	chr12	114837256	114837393	114837281	114837365	TBX5	NM_000192	1	9	4	-	114837318	114837437
328114021	chr12	114837345	114837501	114837366	114837475	TBX5	NM_000192	1	9	4	-	114837318	114837437
326627708	chr12	114836355	114836561	114836373	114836541	TBX5	NM_000192	1	9	5	-	114836378	114836525
326751580	chr12	114832382	114832594	114832404	114832569	TBX5	NM_000192	1	9	6	-	114832546	114832698
326774766	chr12	114832546	114832763	114832570	114832737	TBX5	NM_000192	1	9	6	-	114832546	114832698
327518261	chr12	114823213	114823402	114823234	114823377	TBX5	NM_000192	1	9	7	-	114823281	114823372
327435031	chr12	114803788	114804008	114803815	114803982	TBX5	NM_000192	1	9	8	-	114803970	114804196
327438482	chr12	114803961	114804118	114803983	114804097	TBX5	NM_000192	1	9	8	-	114803970	114804196
327444577	chr12	114804075	114804238	114804098	114804217	TBX5	NM_000192	1	9	8	-	114803970	114804196
326443437	chr12	114793668	114793888	114793688	114793863	TBX5	NM_000192	1	9	9	-	114791735	114793911
326463416	chr12	114793839	114793972	114793864	114793951	TBX5	NM_000192	1	9	9	-	114791735	114793911
327810400	chr12	114793192	114793414	114793214	114793390	TBX5	NM_000192	1	9	9	-	114791735	114793911
327831356	chr12	114793372	114793564	114793391	114793546	TBX5	NM_000192	1	9	9	-	114791735	114793911
327835478	chr12	114793523	114793715	114793544	114793694	TBX5	NM_000192	1	9	9	-	114791735	114793911
326993127	chr12	114839605	114839785	114839631	114839765	TBX5	NM_080717	2	8	2	-	114839631	114839725
328108510	chr12	114837256	114837393	114837281	114837365	TBX5	NM_080717	2	8	3	-	114837318	114837437
328114021	chr12	114837345	114837501	114837366	114837475	TBX5	NM_080717	2	8	3	-	114837318	114837437
326627708	chr12	114836355	114836561	114836373	114836541	TBX5	NM_080717	2	8	4	-	114836378	114836525
326751580	chr12	114832382	114832594	114832404	114832569	TBX5	NM_080717	2	8	5	-	114832546	114832698
326774766	chr12	114832546	114832763	114832570	114832737	TBX5	NM_080717	2	8	5	-	114832546	114832698
327518261	chr12	114823213	114823402	114823234	114823377	TBX5	NM_080717	2	8	6	-	114823281	114823372
327435031	chr12	114803788	114804008	114803815	114803982	TBX5	NM_080717	2	8	7	-	114803970	114804196
327438482	chr12	114803961	114804118	114803983	114804097	TBX5	NM_080717	2	8	7	-	114803970	114804196
327444577	chr12	114804075	114804238	114804098	114804217	TBX5	NM_080717	2	8	7	-	114803970	114804196
326443437	chr12	114793668	114793888	114793688	114793863	TBX5	NM_080717	2	8	8	-	114791735	114793911
326463416	chr12	114793839	114793972	114793864	114793951	TBX5	NM_080717	2	8	8	-	114791735	114793911
327810400	chr12	114793192	114793414	114793214	114793390	TBX5	NM_080717	2	8	8	-	114791735	114793911
327831356	chr12	114793372	114793564	114793391	114793546	TBX5	NM_080717	2	8	8	-	114791735	114793911
327835478	chr12	114793523	114793715	114793544	114793694	TBX5	NM_080717	2	8	8	-	114791735	114793911
327448268	chr12	114841419	114841641	114841444	114841622	TBX5	NM_080718	3	7	1	-	114841557	114841703
327450582	chr12	114841549	114841751	114841570	114841729	TBX5	NM_080718	3	7	1	-	114841557	114841703
326993127	chr12	114839605	114839785	114839631	114839765	TBX5	NM_080718	3	7	2	-	114839631	114839725
328108510	chr12	114837256	114837393	114837281	114837365	TBX5	NM_080718	3	7	3	-	114837318	114837437
328114021	chr12	114837345	114837501	114837366	114837475	TBX5	NM_080718	3	7	3	-	114837318	114837437
326627708	chr12	114836355	114836561	114836373	114836541	TBX5	NM_080718	3	7	4	-	114836378	114836525
326751580	chr12	114832382	114832594	114832404	114832569	TBX5	NM_080718	3	7	5	-	114832546	114832698
326774766	chr12	114832546	114832763	114832570	114832737	TBX5	NM_080718	3	7	5	-	114832546	114832698
327518261	chr12	114823213	114823402	114823234	114823377	TBX5	NM_080718	3	7	6	-	114823281	114823372
327435031	chr12	114803788	114804008	114803815	114803982	TBX5	NM_080718	3	7	7	-	114803902	114804196
327438482	chr12	114803961	114804118	114803983	114804097	TBX5	NM_080718	3	7	7	-	114803902	114804196
327444577	chr12	114804075	114804238	114804098	114804217	TBX5	NM_080718	3	7	7	-	114803902	114804196

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327448268	chr12	114841419	114841641	114841444	114841622	TBX5	NM_181486	4	9	2	-	114841557	114841741
327450582	chr12	114841549	114841751	114841570	114841729	TBX5	NM_181486	4	9	2	-	114841557	114841741
326993127	chr12	114839605	114839785	114839631	114839765	TBX5	NM_181486	4	9	3	-	114839631	114839725
328108510	chr12	114837256	114837393	114837281	114837365	TBX5	NM_181486	4	9	4	-	114837318	114837437
328114021	chr12	114837345	114837501	114837366	114837475	TBX5	NM_181486	4	9	4	-	114837318	114837437
326627708	chr12	114836355	114836561	114836373	114836541	TBX5	NM_181486	4	9	5	-	114836378	114836525
326751580	chr12	114832382	114832594	114832404	114832569	TBX5	NM_181486	4	9	6	-	114832546	114832698
326774766	chr12	114832546	114832763	114832570	114832737	TBX5	NM_181486	4	9	6	-	114832546	114832698
327518261	chr12	114823213	114823402	114823234	114823377	TBX5	NM_181486	4	9	7	-	114823281	114823372
327435031	chr12	114803788	114804008	114803815	114803982	TBX5	NM_181486	4	9	8	-	114803970	114804196
327438482	chr12	114803961	114804118	114803983	114804097	TBX5	NM_181486	4	9	8	-	114803970	114804196
327444577	chr12	114804075	114804238	114804098	114804217	TBX5	NM_181486	4	9	8	-	114803970	114804196
326443437	chr12	114793668	114793888	114793688	114793863	TBX5	NM_181486	4	9	9	-	114791735	114793911
326463416	chr12	114793839	114793972	114793864	114793951	TBX5	NM_181486	4	9	9	-	114791735	114793911
327810400	chr12	114793192	114793414	114793214	114793390	TBX5	NM_181486	4	9	9	-	114791735	114793911
327831356	chr12	114793372	114793564	114793391	114793546	TBX5	NM_181486	4	9	9	-	114791735	114793911
327835478	chr12	114793523	114793715	114793544	114793694	TBX5	NM_181486	4	9	9	-	114791735	114793911
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_000356	1	26	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_000356	1	26	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_000356	1	26	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_000356	1	26	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_000356	1	26	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_000356	1	26	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_000356	1	26	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_000356	1	26	6	+	149749092	149749165
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_000356	1	26	7	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_000356	1	26	7	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_000356	1	26	8	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_000356	1	26	8	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_000356	1	26	9	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_000356	1	26	9	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_000356	1	26	10	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_000356	1	26	10	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_000356	1	26	11	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_000356	1	26	11	+	149755284	149755472
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_000356	1	26	12	+	149755645	149755893
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_000356	1	26	12	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_000356	1	26	13	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_000356	1	26	13	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_000356	1	26	14	+	149758468	149758605
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_000356	1	26	15	+	149758792	149758971

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_000356	1	26	15	+	149758792	149758971
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_000356	1	26	16	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_000356	1	26	16	+	149759095	149759295
327011905	chr5	149767364	149767508	149767387	149767483	TCOF1	NM_000356	1	26	17	+	149767465	149767651
327016505	chr5	149767461	149767681	149767484	149767661	TCOF1	NM_000356	1	26	17	+	149767465	149767651
326890108	chr5	149769359	149769572	149769379	149769550	TCOF1	NM_000356	1	26	18	+	149769450	149769586
326896751	chr5	149769530	149769656	149769551	149769631	TCOF1	NM_000356	1	26	18	+	149769450	149769586
327714086	chr5	149771021	149771217	149771040	149771198	TCOF1	NM_000356	1	26	19	+	149771107	149771220
328212748	chr5	149771462	149771684	149771484	149771663	TCOF1	NM_000356	1	26	20	+	149771520	149771739
328223626	chr5	149771640	149771850	149771663	149771825	TCOF1	NM_000356	1	26	20	+	149771520	149771739
327098252	chr5	149772239	149772436	149772261	149772416	TCOF1	NM_000356	1	26	21	+	149772271	149772353
327555510	chr5	149772813	149773017	149772835	149772996	TCOF1	NM_000356	1	26	22	+	149772935	149773115
327565369	chr5	149772975	149773161	149772996	149773140	TCOF1	NM_000356	1	26	22	+	149772935	149773115
328316775	chr5	149775722	149775886	149775744	149775866	TCOF1	NM_000356	1	26	23	+	149775845	149776405
328317921	chr5	149776279	149776426	149776297	149776408	TCOF1	NM_000356	1	26	23	+	149775845	149776405
328332408	chr5	149775844	149776051	149775865	149776027	TCOF1	NM_000356	1	26	23	+	149775845	149776405
328336428	chr5	149776005	149776228	149776026	149776209	TCOF1	NM_000356	1	26	23	+	149775845	149776405
328340290	chr5	149776186	149776337	149776209	149776316	TCOF1	NM_000356	1	26	23	+	149775845	149776405
326646235	chr5	149777841	149778054	149777861	149778032	TCOF1	NM_000356	1	26	24	+	149777917	149778014
328086852	chr5	149778436	149778653	149778458	149778631	TCOF1	NM_000356	1	26	25	+	149778585	149778633
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_001008657	2	18	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_001008657	2	18	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_001008657	2	18	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_001008657	2	18	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_001008657	2	18	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_001008657	2	18	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_001008657	2	18	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_001008657	2	18	6	+	149749092	149749165
327518127	chr5	149751577	149751778	149751598	149751757	TCOF1	NM_001008657	2	18	7	+	149751569	149751799
327528223	chr5	149751735	149751928	149751758	149751903	TCOF1	NM_001008657	2	18	7	+	149751569	149751799
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_001008657	2	18	8	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_001008657	2	18	8	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_001008657	2	18	9	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_001008657	2	18	9	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_001008657	2	18	10	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_001008657	2	18	10	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_001008657	2	18	11	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_001008657	2	18	11	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_001008657	2	18	12	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_001008657	2	18	12	+	149755284	149755472
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_001008657	2	18	13	+	149755645	149755893

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_001008657	2	18	13	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_001008657	2	18	14	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_001008657	2	18	14	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_001008657	2	18	15	+	149758468	149758605
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_001008657	2	18	16	+	149758792	149758971
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_001008657	2	18	16	+	149758792	149758971
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_001008657	2	18	17	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_001008657	2	18	17	+	149759095	149759295
326566219	chr5	149763284	149763468	149763310	149763443	TCOF1	NM_001008657	2	18	18	+	149763301	149764195
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_001135243	3	27	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_001135243	3	27	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_001135243	3	27	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_001135243	3	27	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_001135243	3	27	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_001135243	3	27	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_001135243	3	27	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_001135243	3	27	6	+	149749092	149749165
327518127	chr5	149751577	149751778	149751598	149751757	TCOF1	NM_001135243	3	27	7	+	149751569	149751799
327528223	chr5	149751735	149751928	149751758	149751903	TCOF1	NM_001135243	3	27	7	+	149751569	149751799
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_001135243	3	27	8	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_001135243	3	27	8	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_001135243	3	27	9	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_001135243	3	27	9	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_001135243	3	27	10	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_001135243	3	27	10	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_001135243	3	27	11	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_001135243	3	27	11	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_001135243	3	27	12	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_001135243	3	27	12	+	149755284	149755472
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_001135243	3	27	13	+	149755645	149755893
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_001135243	3	27	13	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_001135243	3	27	14	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_001135243	3	27	14	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_001135243	3	27	15	+	149758468	149758605
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_001135243	3	27	16	+	149758792	149758971
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_001135243	3	27	16	+	149758792	149758971
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_001135243	3	27	17	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_001135243	3	27	17	+	149759095	149759295
327011905	chr5	149767364	149767508	149767387	149767483	TCOF1	NM_001135243	3	27	18	+	149767465	149767651
327016505	chr5	149767461	149767681	149767484	149767661	TCOF1	NM_001135243	3	27	18	+	149767465	149767651
326890108	chr5	149769359	149769572	149769379	149769550	TCOF1	NM_001135243	3	27	19	+	149769450	149769586

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326896751	chr5	149769530	149769656	149769551	149769631	TCOF1	NM_001135243	3	27	19	+	149769450	149769586
327714086	chr5	149771021	149771217	149771040	149771198	TCOF1	NM_001135243	3	27	20	+	149771107	149771220
328212748	chr5	149771462	149771684	149771484	149771663	TCOF1	NM_001135243	3	27	21	+	149771520	149771739
328223626	chr5	149771640	149771850	149771663	149771825	TCOF1	NM_001135243	3	27	21	+	149771520	149771739
327098252	chr5	149772239	149772436	149772261	149772416	TCOF1	NM_001135243	3	27	22	+	149772271	149772353
327555510	chr5	149772813	149773017	149772835	149772996	TCOF1	NM_001135243	3	27	23	+	149772935	149773115
327565369	chr5	149772975	149773161	149772996	149773140	TCOF1	NM_001135243	3	27	23	+	149772935	149773115
328316775	chr5	149775722	149775886	149775744	149775866	TCOF1	NM_001135243	3	27	24	+	149775845	149776405
328317921	chr5	149776279	149776426	149776297	149776408	TCOF1	NM_001135243	3	27	24	+	149775845	149776405
328332408	chr5	149775844	149776051	149775865	149776027	TCOF1	NM_001135243	3	27	24	+	149775845	149776405
328336428	chr5	149776005	149776228	149776026	149776209	TCOF1	NM_001135243	3	27	24	+	149775845	149776405
328340290	chr5	149776186	149776337	149776209	149776316	TCOF1	NM_001135243	3	27	24	+	149775845	149776405
326646235	chr5	149777841	149778054	149777861	149778032	TCOF1	NM_001135243	3	27	25	+	149777917	149778014
328086852	chr5	149778436	149778653	149778458	149778631	TCOF1	NM_001135243	3	27	26	+	149778585	149778633
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_001135244	4	26	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_001135244	4	26	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_001135244	4	26	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_001135244	4	26	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_001135244	4	26	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_001135244	4	26	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_001135244	4	26	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_001135244	4	26	6	+	149749092	149749165
327518127	chr5	149751577	149751778	149751598	149751757	TCOF1	NM_001135244	4	26	7	+	149751569	149751799
327528223	chr5	149751735	149751928	149751758	149751903	TCOF1	NM_001135244	4	26	7	+	149751569	149751799
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_001135244	4	26	8	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_001135244	4	26	8	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_001135244	4	26	9	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_001135244	4	26	9	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_001135244	4	26	10	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_001135244	4	26	10	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_001135244	4	26	11	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_001135244	4	26	11	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_001135244	4	26	12	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_001135244	4	26	12	+	149755284	149755472
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_001135244	4	26	13	+	149755645	149755893
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_001135244	4	26	13	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_001135244	4	26	14	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_001135244	4	26	14	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_001135244	4	26	15	+	149758468	149758605
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_001135244	4	26	16	+	149758792	149758971
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_001135244	4	26	16	+	149758792	149758971

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_001135244	4	26	17	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_001135244	4	26	17	+	149759095	149759295
327011905	chr5	149767364	149767508	149767387	149767483	TCOF1	NM_001135244	4	26	18	+	149767465	149767651
327016505	chr5	149767461	149767681	149767484	149767661	TCOF1	NM_001135244	4	26	18	+	149767465	149767651
326890108	chr5	149769359	149769572	149769379	149769550	TCOF1	NM_001135244	4	26	19	+	149769450	149769586
326896751	chr5	149769530	149769656	149769551	149769631	TCOF1	NM_001135244	4	26	19	+	149769450	149769586
328212748	chr5	149771462	149771684	149771484	149771663	TCOF1	NM_001135244	4	26	20	+	149771520	149771739
328223626	chr5	149771640	149771850	149771663	149771825	TCOF1	NM_001135244	4	26	20	+	149771520	149771739
327098252	chr5	149772239	149772436	149772261	149772416	TCOF1	NM_001135244	4	26	21	+	149772268	149772353
327555510	chr5	149772813	149773017	149772835	149772996	TCOF1	NM_001135244	4	26	22	+	149772935	149773115
327565369	chr5	149772975	149773161	149772996	149773140	TCOF1	NM_001135244	4	26	22	+	149772935	149773115
328316775	chr5	149775722	149775886	149775744	149775866	TCOF1	NM_001135244	4	26	23	+	149775845	149776405
328317921	chr5	149776279	149776426	149776297	149776408	TCOF1	NM_001135244	4	26	23	+	149775845	149776405
328332408	chr5	149775844	149776051	149775865	149776027	TCOF1	NM_001135244	4	26	23	+	149775845	149776405
328336428	chr5	149776005	149776228	149776026	149776209	TCOF1	NM_001135244	4	26	23	+	149775845	149776405
328340290	chr5	149776186	149776337	149776209	149776316	TCOF1	NM_001135244	4	26	23	+	149775845	149776405
326646235	chr5	149777841	149778054	149777861	149778032	TCOF1	NM_001135244	4	26	24	+	149777917	149778014
328086852	chr5	149778436	149778653	149778458	149778631	TCOF1	NM_001135244	4	26	25	+	149778585	149778633
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_001135245	5	26	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_001135245	5	26	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_001135245	5	26	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_001135245	5	26	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_001135245	5	26	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_001135245	5	26	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_001135245	5	26	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_001135245	5	26	6	+	149749092	149749165
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_001135245	5	26	7	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_001135245	5	26	7	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_001135245	5	26	8	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_001135245	5	26	8	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_001135245	5	26	9	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_001135245	5	26	9	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_001135245	5	26	10	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_001135245	5	26	10	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_001135245	5	26	11	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_001135245	5	26	11	+	149755284	149755472
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_001135245	5	26	12	+	149755645	149755893
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_001135245	5	26	12	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_001135245	5	26	13	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_001135245	5	26	13	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_001135245	5	26	14	+	149758468	149758605

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_001135245	5	26	15	+	149758792	149758971
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_001135245	5	26	15	+	149758792	149758971
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_001135245	5	26	16	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_001135245	5	26	16	+	149759095	149759295
327011905	chr5	149767364	149767508	149767387	149767483	TCOF1	NM_001135245	5	26	17	+	149767465	149767651
327016505	chr5	149767461	149767681	149767484	149767661	TCOF1	NM_001135245	5	26	17	+	149767465	149767651
326890108	chr5	149769359	149769572	149769379	149769550	TCOF1	NM_001135245	5	26	18	+	149769450	149769586
326896751	chr5	149769530	149769656	149769551	149769631	TCOF1	NM_001135245	5	26	18	+	149769450	149769586
327714086	chr5	149771021	149771217	149771040	149771198	TCOF1	NM_001135245	5	26	19	+	149771107	149771220
328212748	chr5	149771462	149771684	149771484	149771663	TCOF1	NM_001135245	5	26	20	+	149771520	149771739
328223626	chr5	149771640	149771850	149771663	149771825	TCOF1	NM_001135245	5	26	20	+	149771520	149771739
327098252	chr5	149772239	149772436	149772261	149772416	TCOF1	NM_001135245	5	26	21	+	149772268	149772353
327555510	chr5	149772813	149773017	149772835	149772996	TCOF1	NM_001135245	5	26	22	+	149772935	149773115
327565369	chr5	149772975	149773161	149772996	149773140	TCOF1	NM_001135245	5	26	22	+	149772935	149773115
328316775	chr5	149775722	149775886	149775744	149775866	TCOF1	NM_001135245	5	26	23	+	149775845	149776405
328317921	chr5	149776279	149776426	149776297	149776408	TCOF1	NM_001135245	5	26	23	+	149775845	149776405
328332408	chr5	149775844	149776051	149775865	149776027	TCOF1	NM_001135245	5	26	23	+	149775845	149776405
328336428	chr5	149776005	149776228	149776026	149776209	TCOF1	NM_001135245	5	26	23	+	149775845	149776405
328340290	chr5	149776186	149776337	149776209	149776316	TCOF1	NM_001135245	5	26	23	+	149775845	149776405
326646235	chr5	149777841	149778054	149777861	149778032	TCOF1	NM_001135245	5	26	24	+	149777917	149778014
328086852	chr5	149778436	149778653	149778458	149778631	TCOF1	NM_001135245	5	26	25	+	149778585	149778633
326598924	chr5	149737224	149737369	149737241	149737351	TCOF1	NM_001195141	6	26	1	+	149737202	149737417
326599028	chr5	149737331	149737473	149737351	149737452	TCOF1	NM_001195141	6	26	1	+	149737202	149737417
326495748	chr5	149740683	149740841	149740710	149740817	TCOF1	NM_001195141	6	26	2	+	149740719	149740774
327073920	chr5	149743634	149743857	149743658	149743830	TCOF1	NM_001195141	6	26	3	+	149743676	149743815
326927060	chr5	149747361	149747522	149747383	149747495	TCOF1	NM_001195141	6	26	4	+	149747407	149747480
327249067	chr5	149748243	149748404	149748269	149748381	TCOF1	NM_001195141	6	26	5	+	149748279	149748465
327254004	chr5	149748360	149748584	149748381	149748562	TCOF1	NM_001195141	6	26	5	+	149748279	149748465
328147900	chr5	149748997	149749198	149749019	149749177	TCOF1	NM_001195141	6	26	6	+	149749092	149749165
327518127	chr5	149751577	149751778	149751598	149751757	TCOF1	NM_001195141	6	26	7	+	149751569	149751799
327528223	chr5	149751735	149751928	149751758	149751903	TCOF1	NM_001195141	6	26	7	+	149751569	149751799
326701016	chr5	149753708	149753926	149753729	149753906	TCOF1	NM_001195141	6	26	8	+	149753737	149753949
326705869	chr5	149753888	149754024	149753907	149754001	TCOF1	NM_001195141	6	26	8	+	149753737	149753949
327866619	chr5	149754111	149754335	149754131	149754318	TCOF1	NM_001195141	6	26	9	+	149754180	149754374
327868677	chr5	149754274	149754472	149754292	149754452	TCOF1	NM_001195141	6	26	9	+	149754180	149754374
327580185	chr5	149754487	149754711	149754507	149754694	TCOF1	NM_001195141	6	26	10	+	149754517	149754726
327584030	chr5	149754674	149754872	149754694	149754849	TCOF1	NM_001195141	6	26	10	+	149754517	149754726
327385898	chr5	149754847	149755071	149754871	149755047	TCOF1	NM_001195141	6	26	11	+	149754902	149755117
327391044	chr5	149755003	149755213	149755020	149755190	TCOF1	NM_001195141	6	26	11	+	149754902	149755117
327231801	chr5	149755190	149755411	149755212	149755391	TCOF1	NM_001195141	6	26	12	+	149755284	149755472
327240472	chr5	149755368	149755570	149755389	149755550	TCOF1	NM_001195141	6	26	12	+	149755284	149755472

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328174911	chr5	149755609	149755829	149755632	149755808	TCOF1	NM_001195141	6	26	13	+	149755645	149755893
328182079	chr5	149755767	149755954	149755788	149755933	TCOF1	NM_001195141	6	26	13	+	149755645	149755893
326926125	chr5	149755941	149756143	149755962	149756120	TCOF1	NM_001195141	6	26	14	+	149755986	149756183
326937436	chr5	149756099	149756269	149756121	149756248	TCOF1	NM_001195141	6	26	14	+	149755986	149756183
326689926	chr5	149758432	149758654	149758457	149758634	TCOF1	NM_001195141	6	26	15	+	149758468	149758605
326527027	chr5	149758647	149758864	149758669	149758844	TCOF1	NM_001195141	6	26	16	+	149758792	149758971
326532605	chr5	149758813	149759031	149758833	149759009	TCOF1	NM_001195141	6	26	16	+	149758792	149758971
326695897	chr5	149759062	149759270	149759085	149759249	TCOF1	NM_001195141	6	26	17	+	149759095	149759295
326700454	chr5	149759224	149759355	149759243	149759335	TCOF1	NM_001195141	6	26	17	+	149759095	149759295
327011905	chr5	149767364	149767508	149767387	149767483	TCOF1	NM_001195141	6	26	18	+	149767465	149767651
327016505	chr5	149767461	149767681	149767484	149767661	TCOF1	NM_001195141	6	26	18	+	149767465	149767651
326890108	chr5	149769359	149769572	149769379	149769550	TCOF1	NM_001195141	6	26	19	+	149769450	149769586
326896751	chr5	149769530	149769656	149769551	149769631	TCOF1	NM_001195141	6	26	19	+	149769450	149769586
328212748	chr5	149771462	149771684	149771484	149771663	TCOF1	NM_001195141	6	26	20	+	149771520	149771739
328223626	chr5	149771640	149771850	149771663	149771825	TCOF1	NM_001195141	6	26	20	+	149771520	149771739
327098252	chr5	149772239	149772436	149772261	149772416	TCOF1	NM_001195141	6	26	21	+	149772271	149772353
327555510	chr5	149772813	149773017	149772835	149772996	TCOF1	NM_001195141	6	26	22	+	149772935	149773115
327565369	chr5	149772975	149773161	149772996	149773140	TCOF1	NM_001195141	6	26	22	+	149772935	149773115
328316775	chr5	149775722	149775886	149775744	149775866	TCOF1	NM_001195141	6	26	23	+	149775845	149776405
328317921	chr5	149776279	149776426	149776297	149776408	TCOF1	NM_001195141	6	26	23	+	149775845	149776405
328332408	chr5	149775844	149776051	149775865	149776027	TCOF1	NM_001195141	6	26	23	+	149775845	149776405
328336428	chr5	149776005	149776228	149776026	149776209	TCOF1	NM_001195141	6	26	23	+	149775845	149776405
328340290	chr5	149776186	149776337	149776209	149776316	TCOF1	NM_001195141	6	26	23	+	149775845	149776405
326646235	chr5	149777841	149778054	149777861	149778032	TCOF1	NM_001195141	6	26	24	+	149777917	149778014
328086852	chr5	149778436	149778653	149778458	149778631	TCOF1	NM_001195141	6	26	25	+	149778585	149778633
327463360	chr9	101891011	101891195	101891038	101891167	TGFBR1	NM_001130916	1	8	2	+	101891137	101891382
327467470	chr9	101891145	101891356	101891168	101891333	TGFBR1	NM_001130916	1	8	2	+	101891137	101891382
327475805	chr9	101891331	101891552	101891354	101891524	TGFBR1	NM_001130916	1	8	2	+	101891137	101891382
327519579	chr9	101900057	101900231	101900081	101900206	TGFBR1	NM_001130916	1	8	3	+	101900141	101900371
327522542	chr9	101900181	101900346	101900207	101900318	TGFBR1	NM_001130916	1	8	3	+	101900141	101900371
327525115	chr9	101900294	101900504	101900319	101900475	TGFBR1	NM_001130916	1	8	3	+	101900141	101900371
327879215	chr9	101904706	101904929	101904732	101904900	TGFBR1	NM_001130916	1	8	4	+	101904818	101904985
327882446	chr9	101904861	101905064	101904888	101905040	TGFBR1	NM_001130916	1	8	4	+	101904818	101904985
326648955	chr9	101906885	101907106	101906908	101907085	TGFBR1	NM_001130916	1	8	5	+	101907014	101907170
326663583	chr9	101907058	101907270	101907086	101907243	TGFBR1	NM_001130916	1	8	5	+	101907014	101907170
327905701	chr9	101908688	101908864	101908714	101908838	TGFBR1	NM_001130916	1	8	6	+	101908767	101908891
327910931	chr9	101908815	101908942	101908839	101908915	TGFBR1	NM_001130916	1	8	6	+	101908767	101908891
327957333	chr9	101909784	101910005	101909811	101909979	TGFBR1	NM_001130916	1	8	7	+	101909936	101910066
327961160	chr9	101909952	101910113	101909980	101910085	TGFBR1	NM_001130916	1	8	7	+	101909936	101910066
327702045	chr9	101911407	101911613	101911430	101911592	TGFBR1	NM_001130916	1	8	8	+	101911462	101916473
327463360	chr9	101891011	101891195	101891038	101891167	TGFBR1	NM_004612	2	9	2	+	101891137	101891382

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327467470	chr9	101891145	101891356	101891168	101891333	TGFBR1	NM_004612	2	9	2	+	101891137	101891382
327475805	chr9	101891331	101891552	101891354	101891524	TGFBR1	NM_004612	2	9	2	+	101891137	101891382
327779218	chr9	101894728	101894951	101894748	101894928	TGFBR1	NM_004612	2	9	3	+	101894791	101895021
327786149	chr9	101894906	101895124	101894929	101895096	TGFBR1	NM_004612	2	9	3	+	101894791	101895021
327519579	chr9	101900057	101900231	101900081	101900206	TGFBR1	NM_004612	2	9	4	+	101900141	101900371
327522542	chr9	101900181	101900346	101900207	101900318	TGFBR1	NM_004612	2	9	4	+	101900141	101900371
327525115	chr9	101900294	101900504	101900319	101900475	TGFBR1	NM_004612	2	9	4	+	101900141	101900371
327879215	chr9	101904706	101904929	101904732	101904900	TGFBR1	NM_004612	2	9	5	+	101904818	101904985
327882446	chr9	101904861	101905064	101904888	101905040	TGFBR1	NM_004612	2	9	5	+	101904818	101904985
326648955	chr9	101906885	101907106	101906908	101907085	TGFBR1	NM_004612	2	9	6	+	101907014	101907170
326663583	chr9	101907058	101907270	101907086	101907243	TGFBR1	NM_004612	2	9	6	+	101907014	101907170
327905701	chr9	101908688	101908864	101908714	101908838	TGFBR1	NM_004612	2	9	7	+	101908767	101908891
327910931	chr9	101908815	101908942	101908839	101908915	TGFBR1	NM_004612	2	9	7	+	101908767	101908891
327957333	chr9	101909784	101910005	101909811	101909979	TGFBR1	NM_004612	2	9	8	+	101909936	101910066
327961160	chr9	101909952	101910113	101909980	101910085	TGFBR1	NM_004612	2	9	8	+	101909936	101910066
327702045	chr9	101911407	101911613	101911430	101911592	TGFBR1	NM_004612	2	9	9	+	101911462	101916473
272552166	chr3	30648343	30648556	30648361	30648539	TGFBR2	NM_001024847	1	8	1	+	30647994	30648469
328197893	chr3	30664731	30664921	30664753	30664898	TGFBR2	NM_001024847	1	8	2	+	30664691	30664765
270338714	chr3	30686190	30686350	30686211	30686327	TGFBR2	NM_001024847	1	8	3	+	30686239	30686407
270342389	chr3	30686303	30686514	30686328	30686486	TGFBR2	NM_001024847	1	8	3	+	30686239	30686407
271958165	chr3	30691760	30691982	30691788	30691957	TGFBR2	NM_001024847	1	8	4	+	30691762	30691952
328357382	chr3	30691587	30691809	30691609	30691787	TGFBR2	NM_001024847	1	8	4	+	30691762	30691952
272296489	chr3	30713628	30713850	30713651	30713827	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272298050	chr3	30713057	30713245	30713079	30713220	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272311872	chr3	30713807	30713999	30713828	30713973	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272340910	chr3	30713199	30713399	30713221	30713377	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272362046	chr3	30713359	30713512	30713378	30713488	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272373477	chr3	30713466	30713683	30713489	30713661	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
269565559	chr3	30715555	30715764	30715580	30715743	TGFBR2	NM_001024847	1	8	6	+	30715597	30715738
270825483	chr3	30729827	30730047	30729848	30730020	TGFBR2	NM_001024847	1	8	7	+	30729876	30730003
272489774	chr3	30732875	30733080	30732896	30733059	TGFBR2	NM_001024847	1	8	8	+	30732912	30735633
272508592	chr3	30733039	30733193	30733060	30733169	TGFBR2	NM_001024847	1	8	8	+	30732912	30735633
272552166	chr3	30648343	30648556	30648361	30648539	TGFBR2	NM_003242	2	7	1	+	30647994	30648469
270338714	chr3	30686190	30686350	30686211	30686327	TGFBR2	NM_003242	2	7	2	+	30686239	30686407
270342389	chr3	30686303	30686514	30686328	30686486	TGFBR2	NM_003242	2	7	2	+	30686239	30686407
271958165	chr3	30691760	30691982	30691788	30691957	TGFBR2	NM_003242	2	7	3	+	30691762	30691952
328357382	chr3	30691587	30691809	30691609	30691787	TGFBR2	NM_003242	2	7	3	+	30691762	30691952
272296489	chr3	30713628	30713850	30713651	30713827	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272298050	chr3	30713057	30713245	30713079	30713220	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272311872	chr3	30713807	30713999	30713828	30713973	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272340910	chr3	30713199	30713399	30713221	30713377	TGFBR2	NM_003242	2	7	4	+	30713130	30713929

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272362046	chr3	30713359	30713512	30713378	30713488	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272373477	chr3	30713466	30713683	30713489	30713661	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
269565559	chr3	30715555	30715764	30715580	30715743	TGFBR2	NM_003242	2	7	5	+	30715597	30715738
270825483	chr3	30729827	30730047	30729848	30730020	TGFBR2	NM_003242	2	7	6	+	30729876	30730003
272489774	chr3	30732875	30733080	30732896	30733059	TGFBR2	NM_003242	2	7	7	+	30732912	30735633
272508592	chr3	30733039	30733193	30733060	30733169	TGFBR2	NM_003242	2	7	7	+	30732912	30735633
332602491	chr3	14166572	14166792	14166590	14166771	TMEM43	NM_024334	1	12	1	+	14166440	14166705
333586429	chr3	14170905	14171099	14170931	14171078	TMEM43	NM_024334	1	12	2	+	14170912	14171061
333175151	chr3	14172257	14172446	14172279	14172426	TMEM43	NM_024334	1	12	3	+	14172322	14172456
333184245	chr3	14172405	14172531	14172427	14172507	TMEM43	NM_024334	1	12	3	+	14172322	14172456
333212703	chr3	14173018	14173210	14173039	14173186	TMEM43	NM_024334	1	12	4	+	14173080	14173174
333524168	chr3	14173912	14174130	14173934	14174110	TMEM43	NM_024334	1	12	5	+	14174046	14174095
332783221	chr3	14174271	14174476	14174292	14174454	TMEM43	NM_024334	1	12	6	+	14174366	14174435
333145512	chr3	14175208	14175420	14175230	14175398	TMEM43	NM_024334	1	12	7	+	14175239	14175309
332337870	chr3	14176231	14176433	14176252	14176410	TMEM43	NM_024334	1	12	8	+	14176270	14176391
333344055	chr3	14176612	14176797	14176632	14176775	TMEM43	NM_024334	1	12	9	+	14176658	14176732
332264093	chr3	14177268	14177443	14177288	14177422	TMEM43	NM_024334	1	12	10	+	14177307	14177408
333134564	chr3	14180512	14180719	14180533	14180694	TMEM43	NM_024334	1	12	11	+	14180680	14180797
333138999	chr3	14180673	14180882	14180695	14180861	TMEM43	NM_024334	1	12	11	+	14180680	14180797
332395205	chr3	14183061	14183270	14183082	14183250	TMEM43	NM_024334	1	12	12	+	14183093	14185180
332401799	chr3	14183197	14183414	14183217	14183391	TMEM43	NM_024334	1	12	12	+	14183093	14185180
328366316	chr3	52487929	52488096	52487950	52488074	TNNC1	NM_003280	1	6	1	-	52488008	52488057
327939946	chr3	52486466	52486599	52486487	52486577	TNNC1	NM_003280	1	6	2	-	52486499	52486529
326947322	chr3	52486115	52486310	52486132	52486290	TNNC1	NM_003280	1	6	3	-	52486122	52486268
327068995	chr3	52485702	52485916	52485721	52485895	TNNC1	NM_003280	1	6	4	-	52485760	52485874
326893324	chr3	52485262	52485466	52485283	52485444	TNNC1	NM_003280	1	6	5	-	52485407	52485543
326896156	chr3	52485304	52485528	52485328	52485506	TNNC1	NM_003280	1	6	5	-	52485407	52485543
326903239	chr3	52485486	52485698	52485507	52485676	TNNC1	NM_003280	1	6	5	-	52485407	52485543
326893324	chr3	52485262	52485466	52485283	52485444	TNNC1	NM_003280	1	6	6	-	52485107	52485322
327507705	chr19	55668806	55669025	55668826	55669005	TNNI3	NM_000363	1	7	1	-	55668936	55669100
327409402	chr19	55668355	55668568	55668375	55668550	TNNI3	NM_000363	1	7	2	-	55668418	55668502
328035709	chr19	55667830	55668047	55667851	55668025	TNNI3	NM_000363	1	7	3	-	55667971	55668012
326980262	chr19	55667535	55667758	55667557	55667736	TNNI3	NM_000363	1	7	4	-	55667569	55667700
327002068	chr19	55666066	55666224	55666086	55666204	TNNI3	NM_000363	1	7	5	-	55666109	55666198
326832868	chr19	55665365	55665577	55665386	55665551	TNNI3	NM_000363	1	7	6	-	55665398	55665574
326850537	chr19	55665527	55665680	55665552	55665656	TNNI3	NM_000363	1	7	6	-	55665398	55665574
327748260	chr19	55663100	55663314	55663122	55663291	TNNI3	NM_000363	1	7	7	-	55663136	55663285
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_001126132	1	14	2	-	55658494	55658536
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_001126132	1	14	3	-	55658376	55658389
326487987	chr19	55657916	55658112	55657937	55658090	TNNT1	NM_001126132	1	14	4	-	55658049	55658075
328333121	chr19	55657710	55657930	55657731	55657908	TNNT1	NM_001126132	1	14	5	-	55657802	55657834

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327289738	chr19	55656783	55656988	55656805	55656961	TNNT1	NM_001126132	1	14	6	-	55656912	55656933
327322132	chr19	55653207	55653345	55653231	55653328	TNNT1	NM_001126132	1	14	7	-	55653225	55653288
327479124	chr19	55652422	55652632	55652443	55652610	TNNT1	NM_001126132	1	14	8	-	55652554	55652670
327483196	chr19	55652590	55652765	55652611	55652743	TNNT1	NM_001126132	1	14	8	-	55652554	55652670
327629406	chr19	55652197	55652354	55652217	55652333	TNNT1	NM_001126132	1	14	9	-	55652251	55652328
326733169	chr19	55649309	55649473	55649327	55649448	TNNT1	NM_001126132	1	14	10	-	55649329	55649442
326657638	chr19	55648395	55648619	55648418	55648599	TNNT1	NM_001126132	1	14	11	-	55648471	55648580
327645260	chr19	55645276	55645492	55645298	55645471	TNNT1	NM_001126132	1	14	12	-	55645434	55645524
327647478	chr19	55645448	55645663	55645468	55645642	TNNT1	NM_001126132	1	14	12	-	55645434	55645524
326954561	chr19	55645187	55645327	55645207	55645306	TNNT1	NM_001126132	1	14	13	-	55645255	55645295
326535274	chr19	55644151	55644365	55644172	55644344	TNNT1	NM_001126132	1	14	14	-	55644161	55644328
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_001126133	2	13	2	-	55658494	55658536
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_001126133	2	13	3	-	55658376	55658389
326487987	chr19	55657916	55658112	55657937	55658090	TNNT1	NM_001126133	2	13	4	-	55658049	55658075
327289738	chr19	55656783	55656988	55656805	55656961	TNNT1	NM_001126133	2	13	5	-	55656912	55656933
327322132	chr19	55653207	55653345	55653231	55653328	TNNT1	NM_001126133	2	13	6	-	55653225	55653288
327479124	chr19	55652422	55652632	55652443	55652610	TNNT1	NM_001126133	2	13	7	-	55652554	55652670
327483196	chr19	55652590	55652765	55652611	55652743	TNNT1	NM_001126133	2	13	7	-	55652554	55652670
327629406	chr19	55652197	55652354	55652217	55652333	TNNT1	NM_001126133	2	13	8	-	55652251	55652328
326733169	chr19	55649309	55649473	55649327	55649448	TNNT1	NM_001126133	2	13	9	-	55649329	55649442
326657638	chr19	55648395	55648619	55648418	55648599	TNNT1	NM_001126133	2	13	10	-	55648471	55648580
327645260	chr19	55645276	55645492	55645298	55645471	TNNT1	NM_001126133	2	13	11	-	55645434	55645524
327647478	chr19	55645448	55645663	55645468	55645642	TNNT1	NM_001126133	2	13	11	-	55645434	55645524
326954561	chr19	55645187	55645327	55645207	55645306	TNNT1	NM_001126133	2	13	12	-	55645255	55645295
326535274	chr19	55644151	55644365	55644172	55644344	TNNT1	NM_001126133	2	13	13	-	55644161	55644328
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_003283	3	14	2	-	55658494	55658536
326601957	chr19	55658335	55658559	55658354	55658536	TNNT1	NM_003283	3	14	3	-	55658376	55658389
326487987	chr19	55657916	55658112	55657937	55658090	TNNT1	NM_003283	3	14	4	-	55658049	55658075
328333121	chr19	55657710	55657930	55657731	55657908	TNNT1	NM_003283	3	14	5	-	55657802	55657834
327289738	chr19	55656783	55656988	55656805	55656961	TNNT1	NM_003283	3	14	6	-	55656912	55656933
327322132	chr19	55653207	55653345	55653231	55653328	TNNT1	NM_003283	3	14	7	-	55653225	55653288
327479124	chr19	55652422	55652632	55652443	55652610	TNNT1	NM_003283	3	14	8	-	55652554	55652670
327483196	chr19	55652590	55652765	55652611	55652743	TNNT1	NM_003283	3	14	8	-	55652554	55652670
327629406	chr19	55652197	55652354	55652217	55652333	TNNT1	NM_003283	3	14	9	-	55652251	55652328
326733169	chr19	55649309	55649473	55649327	55649448	TNNT1	NM_003283	3	14	10	-	55649329	55649442
326657638	chr19	55648395	55648619	55648418	55648599	TNNT1	NM_003283	3	14	11	-	55648471	55648580
327645260	chr19	55645276	55645492	55645298	55645471	TNNT1	NM_003283	3	14	12	-	55645434	55645572
327647478	chr19	55645448	55645663	55645468	55645642	TNNT1	NM_003283	3	14	12	-	55645434	55645572
326954561	chr19	55645187	55645327	55645207	55645306	TNNT1	NM_003283	3	14	13	-	55645255	55645295
326535274	chr19	55644151	55644365	55644172	55644344	TNNT1	NM_003283	3	14	14	-	55644161	55644328
327139431	chr1	201342222	201342434	201342247	201342410	TNNT2	NM_000364	1	16	2	-	201342342	201342396

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_000364	1	16	3	-	201341273	201341283
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_000364	1	16	4	-	201341155	201341169
326700286	chr1	201338809	201339033	201338830	201339012	TNNT2	NM_000364	1	16	5	-	201338944	201338973
326730134	chr1	201337168	201337385	201337191	201337360	TNNT2	NM_000364	1	16	6	-	201337290	201337355
327936273	chr1	201336746	201336965	201336767	201336939	TNNT2	NM_000364	1	16	7	-	201336899	201336934
326488359	chr1	201335872	201336026	201335892	201336004	TNNT2	NM_000364	1	16	8	-	201335966	201335999
326657558	chr1	201334628	201334827	201334649	201334803	TNNT2	NM_000364	1	16	9	-	201334738	201334798
327099126	chr1	201334271	201334490	201334292	201334467	TNNT2	NM_000364	1	16	10	-	201334319	201334435
326922495	chr1	201333306	201333528	201333329	201333508	TNNT2	NM_000364	1	16	11	-	201333426	201333503
326679253	chr1	201332363	201332582	201332384	201332557	TNNT2	NM_000364	1	16	12	-	201332424	201332534
327489580	chr1	201330908	201331100	201330930	201331078	TNNT2	NM_000364	1	16	13	-	201331041	201331150
327491650	chr1	201331047	201331187	201331072	201331164	TNNT2	NM_000364	1	16	13	-	201331041	201331150
327491932	chr1	201331078	201331277	201331100	201331252	TNNT2	NM_000364	1	16	13	-	201331041	201331150
326518431	chr1	201330320	201330534	201330341	201330512	TNNT2	NM_000364	1	16	14	-	201330407	201330497
327558657	chr1	201328616	201328820	201328637	201328796	TNNT2	NM_000364	1	16	15	-	201328751	201328791
327630659	chr1	201328304	201328525	201328325	201328504	TNNT2	NM_000364	1	16	16	-	201328142	201328383
327139431	chr1	201342222	201342434	201342247	201342410	TNNT2	NM_001001430	2	16	2	-	201342342	201342396
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_001001430	2	16	3	-	201341273	201341283
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_001001430	2	16	4	-	201341155	201341169
326730134	chr1	201337168	201337385	201337191	201337360	TNNT2	NM_001001430	2	16	5	-	201337290	201337355
327936273	chr1	201336746	201336965	201336767	201336939	TNNT2	NM_001001430	2	16	6	-	201336899	201336934
326488359	chr1	201335872	201336026	201335892	201336004	TNNT2	NM_001001430	2	16	7	-	201335966	201335999
326657558	chr1	201334628	201334827	201334649	201334803	TNNT2	NM_001001430	2	16	8	-	201334738	201334798
327099126	chr1	201334271	201334490	201334292	201334467	TNNT2	NM_001001430	2	16	9	-	201334319	201334435
326922495	chr1	201333306	201333528	201333329	201333508	TNNT2	NM_001001430	2	16	10	-	201333426	201333503
326679253	chr1	201332363	201332582	201332384	201332557	TNNT2	NM_001001430	2	16	11	-	201332424	201332534
327491932	chr1	201331078	201331277	201331100	201331252	TNNT2	NM_001001430	2	16	12	-	201331238	201331243
327489580	chr1	201330908	201331100	201330930	201331078	TNNT2	NM_001001430	2	16	13	-	201331041	201331153
327491650	chr1	201331047	201331187	201331072	201331164	TNNT2	NM_001001430	2	16	13	-	201331041	201331153
327491932	chr1	201331078	201331277	201331100	201331252	TNNT2	NM_001001430	2	16	13	-	201331041	201331153
326518431	chr1	201330320	201330534	201330341	201330512	TNNT2	NM_001001430	2	16	14	-	201330407	201330497
327558657	chr1	201328616	201328820	201328637	201328796	TNNT2	NM_001001430	2	16	15	-	201328751	201328791
327630659	chr1	201328304	201328525	201328325	201328504	TNNT2	NM_001001430	2	16	16	-	201328142	201328383
327139431	chr1	201342222	201342434	201342247	201342410	TNNT2	NM_001001431	3	15	2	-	201342342	201342396
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_001001431	3	15	3	-	201341273	201341283
326645897	chr1	201341088	201341312	201341109	201341288	TNNT2	NM_001001431	3	15	4	-	201341155	201341169
326730134	chr1	201337168	201337385	201337191	201337360	TNNT2	NM_001001431	3	15	5	-	201337290	201337355
327936273	chr1	201336746	201336965	201336767	201336939	TNNT2	NM_001001431	3	15	6	-	201336899	201336934
326488359	chr1	201335872	201336026	201335892	201336004	TNNT2	NM_001001431	3	15	7	-	201335966	201335999
326657558	chr1	201334628	201334827	201334649	201334803	TNNT2	NM_001001431	3	15	8	-	201334738	201334798
327099126	chr1	201334271	201334490	201334292	201334467	TNNT2	NM_001001431	3	15	9	-	201334319	201334435

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326922495	chr1	201333306	201333528	201333329	201333508	TNNT2	NM_001001431	3	15	10	-	201333426	201333503
326679253	chr1	201332363	201332582	201332384	201332557	TNNT2	NM_001001431	3	15	11	-	201332424	201332534
327489580	chr1	201330908	201331100	201330930	201331078	TNNT2	NM_001001431	3	15	12	-	201331041	201331150
327491650	chr1	201331047	201331187	201331072	201331164	TNNT2	NM_001001431	3	15	12	-	201331041	201331150
327491932	chr1	201331078	201331277	201331100	201331252	TNNT2	NM_001001431	3	15	12	-	201331041	201331150
326518431	chr1	201330320	201330534	201330341	201330512	TNNT2	NM_001001431	3	15	13	-	201330407	201330497
327558657	chr1	201328616	201328820	201328637	201328796	TNNT2	NM_001001431	3	15	14	-	201328751	201328791
327630659	chr1	201328304	201328525	201328325	201328504	TNNT2	NM_001001431	3	15	15	-	201328142	201328383
327139431	chr1	201342222	201342434	201342247	201342410	TNNT2	NM_001001432	4	14	2	-	201342341	201342396
327216385	chr1	201338401	201338597	201338420	201338578	TNNT2	NM_001001432	4	14	3	-	201338461	201338470
326730134	chr1	201337168	201337385	201337191	201337360	TNNT2	NM_001001432	4	14	4	-	201337290	201337355
327936273	chr1	201336746	201336965	201336767	201336939	TNNT2	NM_001001432	4	14	5	-	201336899	201336934
326488359	chr1	201335872	201336026	201335892	201336004	TNNT2	NM_001001432	4	14	6	-	201335966	201335999
326657558	chr1	201334628	201334827	201334649	201334803	TNNT2	NM_001001432	4	14	7	-	201334738	201334798
327099126	chr1	201334271	201334490	201334292	201334467	TNNT2	NM_001001432	4	14	8	-	201334319	201334435
326922495	chr1	201333306	201333528	201333329	201333508	TNNT2	NM_001001432	4	14	9	-	201333426	201333503
326679253	chr1	201332363	201332582	201332384	201332557	TNNT2	NM_001001432	4	14	10	-	201332423	201332534
327489580	chr1	201330908	201331100	201330930	201331078	TNNT2	NM_001001432	4	14	11	-	201331041	201331155
327491650	chr1	201331047	201331187	201331072	201331164	TNNT2	NM_001001432	4	14	11	-	201331041	201331155
327491932	chr1	201331078	201331277	201331100	201331252	TNNT2	NM_001001432	4	14	11	-	201331041	201331155
326518431	chr1	201330320	201330534	201330341	201330512	TNNT2	NM_001001432	4	14	12	-	201330407	201330497
327558657	chr1	201328616	201328820	201328637	201328796	TNNT2	NM_001001432	4	14	13	-	201328751	201328791
327630659	chr1	201328304	201328525	201328325	201328504	TNNT2	NM_001001432	4	14	14	-	201328142	201328383
331862460	chr6	32065545	32065695	32065567	32065673	TNXB	NM_019105	1	44	2	-	32065573	32065983
331863230	chr6	32065648	32065818	32065669	32065797	TNXB	NM_019105	1	44	2	-	32065573	32065983
331864985	chr6	32065779	32065978	32065798	32065956	TNXB	NM_019105	1	44	2	-	32065573	32065983
331867630	chr6	32065933	32066064	32065954	32066043	TNXB	NM_019105	1	44	2	-	32065573	32065983
331572195	chr6	32064300	32064480	32064317	32064461	TNXB	NM_019105	1	44	3	-	32063388	32065226
331572274	chr6	32064447	32064632	32064466	32064615	TNXB	NM_019105	1	44	3	-	32063388	32065226
331572326	chr6	32064604	32064816	32064621	32064797	TNXB	NM_019105	1	44	3	-	32063388	32065226
331572439	chr6	32064765	32064916	32064782	32064899	TNXB	NM_019105	1	44	3	-	32063388	32065226
331887722	chr6	32063327	32063522	32063349	32063501	TNXB	NM_019105	1	44	3	-	32063388	32065226
331888575	chr6	32063473	32063644	32063493	32063626	TNXB	NM_019105	1	44	3	-	32063388	32065226
331888875	chr6	32063596	32063814	32063614	32063793	TNXB	NM_019105	1	44	3	-	32063388	32065226
331889263	chr6	32063774	32063933	32063793	32063916	TNXB	NM_019105	1	44	3	-	32063388	32065226
331834414	chr6	32062774	32062997	32062795	32062973	TNXB	NM_019105	1	44	4	-	32062853	32062968
331559281	chr6	32056936	32057106	32056960	32057084	TNXB	NM_019105	1	44	5	-	32057000	32057156
331560405	chr6	32057058	32057278	32057079	32057255	TNXB	NM_019105	1	44	5	-	32057000	32057156
331551700	chr6	32053494	32053710	32053520	32053690	TNXB	NM_019105	1	44	7	-	32053527	32053895
331552461	chr6	32053647	32053871	32053667	32053851	TNXB	NM_019105	1	44	7	-	32053527	32053895
331552983	chr6	32053824	32054026	32053841	32054004	TNXB	NM_019105	1	44	7	-	32053527	32053895

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
331711245	chr6	32052158	32052375	32052178	32052353	TNXB	NM_019105	1	44	8	-	32052190	32052486
331712772	chr6	32052333	32052518	32052354	32052494	TNXB	NM_019105	1	44	8	-	32052190	32052486
331826550	chr6	32049740	32049897	32049761	32049873	TNXB	NM_019105	1	44	9	-	32049813	32050103
331827649	chr6	32049850	32049997	32049874	32049975	TNXB	NM_019105	1	44	9	-	32049813	32050103
331829649	chr6	32049954	32050177	32049975	32050154	TNXB	NM_019105	1	44	9	-	32049813	32050103
331646492	chr6	32049022	32049231	32049043	32049210	TNXB	NM_019105	1	44	10	-	32049145	32049450
331647540	chr6	32049190	32049330	32049211	32049309	TNXB	NM_019105	1	44	10	-	32049145	32049450
331648140	chr6	32049287	32049476	32049308	32049456	TNXB	NM_019105	1	44	10	-	32049145	32049450
331755677	chr6	32046673	32046886	32046698	32046862	TNXB	NM_019105	1	44	11	-	32046810	32047142
331756060	chr6	32046797	32046995	32046816	32046975	TNXB	NM_019105	1	44	11	-	32046810	32047142
331756947	chr6	32046955	32047172	32046976	32047147	TNXB	NM_019105	1	44	11	-	32046810	32047142
331857530	chr6	32041384	32041534	32041407	32041513	TNXB	NM_019105	1	44	12	-	32041424	32041729
331858283	chr6	32041487	32041656	32041514	32041635	TNXB	NM_019105	1	44	12	-	32041424	32041729
331858935	chr6	32041581	32041764	32041608	32041740	TNXB	NM_019105	1	44	12	-	32041424	32041729
331666340	chr6	32039734	32039953	32039753	32039930	TNXB	NM_019105	1	44	13	-	32039767	32040075
331668881	chr6	32039910	32040106	32039931	32040080	TNXB	NM_019105	1	44	13	-	32039767	32040075
331775666	chr6	32037877	32038083	32037896	32038060	TNXB	NM_019105	1	44	14	-	32037904	32038191
331776293	chr6	32038041	32038243	32038061	32038218	TNXB	NM_019105	1	44	14	-	32037904	32038191
331789693	chr6	32037296	32037511	32037314	32037487	TNXB	NM_019105	1	44	15	-	32037330	32037638
331790827	chr6	32037469	32037676	32037487	32037657	TNXB	NM_019105	1	44	15	-	32037330	32037638
331785469	chr6	32036482	32036684	32036504	32036663	TNXB	NM_019105	1	44	16	-	32036599	32036913
331782916	chr6	32036002	32036199	32036023	32036181	TNXB	NM_019105	1	44	17	-	32036167	32036484
331783328	chr6	32036165	32036354	32036182	32036333	TNXB	NM_019105	1	44	17	-	32036167	32036484
331783922	chr6	32036308	32036519	32036330	32036496	TNXB	NM_019105	1	44	17	-	32036167	32036484
331759750	chr6	32035300	32035495	32035321	32035477	TNXB	NM_019105	1	44	18	-	32035438	32035761
331761672	chr6	32035418	32035622	32035437	32035603	TNXB	NM_019105	1	44	18	-	32035438	32035761
331761805	chr6	32035580	32035786	32035600	32035762	TNXB	NM_019105	1	44	18	-	32035438	32035761
331762124	chr6	32035660	32035822	32035682	32035802	TNXB	NM_019105	1	44	18	-	32035438	32035761
331875093	chr6	32032438	32032662	32032461	32032641	TNXB	NM_019105	1	44	19	-	32032598	32032894
331876278	chr6	32032592	32032787	32032615	32032766	TNXB	NM_019105	1	44	19	-	32032598	32032894
331878143	chr6	32032743	32032937	32032767	32032912	TNXB	NM_019105	1	44	19	-	32032598	32032894
331682870	chr6	32029774	32029998	32029796	32029977	TNXB	NM_019105	1	44	20	-	32029934	32030260
331683853	chr6	32029928	32030130	32029947	32030110	TNXB	NM_019105	1	44	20	-	32029934	32030260
331685849	chr6	32030084	32030290	32030109	32030266	TNXB	NM_019105	1	44	20	-	32029934	32030260
331637833	chr6	32029143	32029356	32029163	32029337	TNXB	NM_019105	1	44	21	-	32029174	32029497
331638475	chr6	32029316	32029526	32029336	32029505	TNXB	NM_019105	1	44	21	-	32029174	32029497
331600001	chr6	32025785	32026005	32025809	32025985	TNXB	NM_019105	1	44	22	-	32025835	32026167
331600281	chr6	32025926	32026057	32025946	32026037	TNXB	NM_019105	1	44	22	-	32025835	32026167
331600621	chr6	32025996	32026220	32026017	32026197	TNXB	NM_019105	1	44	22	-	32025835	32026167
331561127	chr6	32024188	32024393	32024206	32024376	TNXB	NM_019105	1	44	23	-	32024363	32024680
331562527	chr6	32024360	32024572	32024378	32024555	TNXB	NM_019105	1	44	23	-	32024363	32024680

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
331563423	chr6	32024525	32024705	32024547	32024686	TNXB	NM_019105	1	44	23	-	32024363	32024680
331814080	chr6	32023600	32023813	32023622	32023793	TNXB	NM_019105	1	44	24	-	32023628	32023951
331814878	chr6	32023773	32023987	32023794	32023965	TNXB	NM_019105	1	44	24	-	32023628	32023951
331983550	chr6	32021007	32021229	32021029	32021208	TNXB	NM_019105	1	44	25	-	32021165	32021482
331984323	chr6	32021166	32021380	32021188	32021361	TNXB	NM_019105	1	44	25	-	32021165	32021482
331984550	chr6	32021307	32021529	32021327	32021509	TNXB	NM_019105	1	44	25	-	32021165	32021482
331905893	chr6	32020420	32020631	32020438	32020612	TNXB	NM_019105	1	44	26	-	32020447	32020770
331906760	chr6	32020592	32020796	32020613	32020775	TNXB	NM_019105	1	44	26	-	32020447	32020770
331741590	chr6	32017653	32017802	32017673	32017784	TNXB	NM_019105	1	44	27	-	32017775	32018098
331742136	chr6	32017777	32017950	32017796	32017929	TNXB	NM_019105	1	44	27	-	32017775	32018098
331742469	chr6	32017929	32018111	32017950	32018092	TNXB	NM_019105	1	44	27	-	32017775	32018098
331743322	chr6	32018074	32018203	32018094	32018186	TNXB	NM_019105	1	44	27	-	32017775	32018098
331946855	chr6	32016883	32017104	32016905	32017086	TNXB	NM_019105	1	44	28	-	32017047	32017364
331947764	chr6	32017037	32017224	32017055	32017204	TNXB	NM_019105	1	44	28	-	32017047	32017364
331947955	chr6	32017189	32017391	32017206	32017370	TNXB	NM_019105	1	44	28	-	32017047	32017364
331719583	chr6	32016012	32016215	32016038	32016194	TNXB	NM_019105	1	44	29	-	32016140	32016427
331720661	chr6	32016172	32016369	32016195	32016350	TNXB	NM_019105	1	44	29	-	32016140	32016427
331721880	chr6	32016300	32016524	32016323	32016503	TNXB	NM_019105	1	44	29	-	32016140	32016427
332026111	chr6	32015482	32015697	32015502	32015677	TNXB	NM_019105	1	44	30	-	32015511	32015789
332028111	chr6	32015649	32015820	32015670	32015799	TNXB	NM_019105	1	44	30	-	32015511	32015789
332005487	chr6	32013873	32014054	32013897	32014034	TNXB	NM_019105	1	44	31	-	32013952	32014233
332007848	chr6	32014000	32014183	32014025	32014163	TNXB	NM_019105	1	44	31	-	32013952	32014233
332008894	chr6	32014143	32014285	32014161	32014265	TNXB	NM_019105	1	44	31	-	32013952	32014233
331569084	chr6	32011606	32011824	32011624	32011805	TNXB	NM_019105	1	44	34	-	32011784	32011906
331569015	chr6	32011597	32011766	32011614	32011747	TNXB	NM_019105	1	44	35	-	32011526	32011669
331569084	chr6	32011606	32011824	32011624	32011805	TNXB	NM_019105	1	44	35	-	32011526	32011669
331819595	chr6	32011310	32011533	32011328	32011515	TNXB	NM_019105	1	44	36	-	32011214	32011333
331701712	chr6	32009977	32010200	32009995	32010183	TNXB	NM_019105	1	44	41	-	32010043	32010139
267353701	chr6	32009352	32009575	32009376	32009557	TNXB	NM_019105	1	44	43	-	32009548	32009711
332005487	chr6	32013873	32014054	32013897	32014034	TNXB	NM_032470	2	13	1	-	32012783	32013905
331569084	chr6	32011606	32011824	32011624	32011805	TNXB	NM_032470	2	13	3	-	32011784	32011906
331698561	chr6	31978751	31978970	31978773	31978951	TNXB	NM_032470	2	13	3	-	31978930	31979052
331569015	chr6	32011597	32011766	32011614	32011747	TNXB	NM_032470	2	13	4	-	32011526	32011669
331569084	chr6	32011606	32011824	32011624	32011805	TNXB	NM_032470	2	13	4	-	32011526	32011669
331698405	chr6	31978736	31978908	31978756	31978888	TNXB	NM_032470	2	13	4	-	31978762	31978815
331698561	chr6	31978751	31978970	31978773	31978951	TNXB	NM_032470	2	13	4	-	31978762	31978815
331698191	chr6	31978565	31978775	31978584	31978756	TNXB	NM_032470	2	13	5	-	31978480	31978600
331819595	chr6	32011310	32011533	32011328	32011515	TNXB	NM_032470	2	13	5	-	32011214	32011333
331701712	chr6	32009977	32010200	32009995	32010183	TNXB	NM_032470	2	13	10	-	32010043	32010139
267353701	chr6	32009352	32009575	32009376	32009557	TNXB	NM_032470	2	13	12	-	32009548	32009711
267530692	chr6	31976630	31976853	31976651	31976834	TNXB	NM_032470	2	13	12	-	31976813	31976976

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
267524436	chr6	31976453	31976675	31976472	31976649	TNXB	NM_032470	2	13	13	-	31976197	31976492
327014053	chr9	32552365	32552489	32552385	32552464	TOPORS	NM_001195622	1	2	1	-	32552432	32552626
326648858	chr9	32541445	32541662	32541467	32541636	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326659382	chr9	32543586	32543809	32543612	32543788	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326663638	chr9	32541612	32541832	32541637	32541809	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326667095	chr9	32543762	32543948	32543789	32543924	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326670255	chr9	32541781	32542004	32541809	32541980	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326679579	chr9	32543902	32544122	32543925	32544098	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326721486	chr9	32542948	32543161	32542972	32543135	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326728944	chr9	32541953	32542175	32541981	32542155	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326735576	chr9	32543108	32543316	32543136	32543290	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326744122	chr9	32542135	32542356	32542156	32542334	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326754230	chr9	32542309	32542507	32542335	32542480	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326763089	chr9	32543270	32543461	32543291	32543435	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
326780372	chr9	32543414	32543634	32543436	32543611	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327889062	chr9	32542457	32542681	32542481	32542652	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327891942	chr9	32541269	32541490	32541295	32541466	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327902384	chr9	32544070	32544250	32544099	32544228	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327902573	chr9	32542627	32542832	32542653	32542804	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327907908	chr9	32542779	32542998	32542805	32542971	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327909152	chr9	32544201	32544326	32544229	32544302	TOPORS	NM_001195622	1	2	2	-	32540542	32544324
327014053	chr9	32552365	32552489	32552385	32552464	TOPORS	NM_005802	2	3	1	-	32552432	32552626
328103731	chr9	32550745	32550871	32550766	32550854	TOPORS	NM_005802	2	3	2	-	32550772	32550966
328104188	chr9	32550828	32550995	32550848	32550974	TOPORS	NM_005802	2	3	2	-	32550772	32550966
326648858	chr9	32541445	32541662	32541467	32541636	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326659382	chr9	32543586	32543809	32543612	32543788	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326663638	chr9	32541612	32541832	32541637	32541809	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326667095	chr9	32543762	32543948	32543789	32543924	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326670255	chr9	32541781	32542004	32541809	32541980	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326679579	chr9	32543902	32544122	32543925	32544098	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326721486	chr9	32542948	32543161	32542972	32543135	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326728944	chr9	32541953	32542175	32541981	32542155	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326735576	chr9	32543108	32543316	32543136	32543290	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326744122	chr9	32542135	32542356	32542156	32542334	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326754230	chr9	32542309	32542507	32542335	32542480	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326763089	chr9	32543270	32543461	32543291	32543435	TOPORS	NM_005802	2	3	3	-	32540542	32544324
326780372	chr9	32543414	32543634	32543436	32543611	TOPORS	NM_005802	2	3	3	-	32540542	32544324
327889062	chr9	32542457	32542681	32542481	32542652	TOPORS	NM_005802	2	3	3	-	32540542	32544324
327891942	chr9	32541269	32541490	32541295	32541466	TOPORS	NM_005802	2	3	3	-	32540542	32544324
327902384	chr9	32544070	32544250	32544099	32544228	TOPORS	NM_005802	2	3	3	-	32540542	32544324
327902573	chr9	32542627	32542832	32542653	32542804	TOPORS	NM_005802	2	3	3	-	32540542	32544324

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327907908	chr9	32542779	32542998	32542805	32542971	TOPORS	NM_005802	2	3	3	-	32540542	32544324
327909152	chr9	32544201	32544326	32544229	32544302	TOPORS	NM_005802	2	3	3	-	32540542	32544324
261742834	chr17	7579743	7579966	7579766	7579943	TP53	NM_000546	1	11	2	-	7579839	7579940
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_000546	1	11	3	-	7579700	7579721
263746824	chr17	7579214	7579396	7579237	7579374	TP53	NM_000546	1	11	4	-	7579312	7579590
263767242	chr17	7579353	7579549	7579373	7579525	TP53	NM_000546	1	11	4	-	7579312	7579590
263780413	chr17	7579504	7579722	7579525	7579698	TP53	NM_000546	1	11	4	-	7579312	7579590
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_000546	1	11	5	-	7578371	7578554
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_000546	1	11	5	-	7578371	7578554
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_000546	1	11	6	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_000546	1	11	6	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_000546	1	11	7	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_000546	1	11	7	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_000546	1	11	8	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_000546	1	11	9	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_000546	1	11	10	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_000546	1	11	11	-	7571720	7573008
261742834	chr17	7579743	7579966	7579766	7579943	TP53	NM_001126112	2	11	2	-	7579839	7579937
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126112	2	11	3	-	7579700	7579721
263746824	chr17	7579214	7579396	7579237	7579374	TP53	NM_001126112	2	11	4	-	7579312	7579590
263767242	chr17	7579353	7579549	7579373	7579525	TP53	NM_001126112	2	11	4	-	7579312	7579590
263780413	chr17	7579504	7579722	7579525	7579698	TP53	NM_001126112	2	11	4	-	7579312	7579590
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126112	2	11	5	-	7578371	7578554
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126112	2	11	5	-	7578371	7578554
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126112	2	11	6	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126112	2	11	6	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126112	2	11	7	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126112	2	11	7	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126112	2	11	8	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126112	2	11	9	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126112	2	11	10	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126112	2	11	11	-	7571720	7573008
261742834	chr17	7579743	7579966	7579766	7579943	TP53	NM_001126113	3	12	2	-	7579839	7579940
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126113	3	12	3	-	7579700	7579721
263746824	chr17	7579214	7579396	7579237	7579374	TP53	NM_001126113	3	12	4	-	7579312	7579590
263767242	chr17	7579353	7579549	7579373	7579525	TP53	NM_001126113	3	12	4	-	7579312	7579590
263780413	chr17	7579504	7579722	7579525	7579698	TP53	NM_001126113	3	12	4	-	7579312	7579590
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126113	3	12	5	-	7578371	7578554
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126113	3	12	5	-	7578371	7578554
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126113	3	12	6	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126113	3	12	6	-	7578177	7578289

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126113	3	12	7	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126113	3	12	7	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126113	3	12	8	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126113	3	12	9	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126113	3	12	11	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126113	3	12	12	-	7571720	7573008
261742834	chr17	7579743	7579966	7579766	7579943	TP53	NM_001126114	4	12	2	-	7579839	7579940
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126114	4	12	3	-	7579700	7579721
263746824	chr17	7579214	7579396	7579237	7579374	TP53	NM_001126114	4	12	4	-	7579312	7579590
263767242	chr17	7579353	7579549	7579373	7579525	TP53	NM_001126114	4	12	4	-	7579312	7579590
263780413	chr17	7579504	7579722	7579525	7579698	TP53	NM_001126114	4	12	4	-	7579312	7579590
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126114	4	12	5	-	7578371	7578554
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126114	4	12	5	-	7578371	7578554
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126114	4	12	6	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126114	4	12	6	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126114	4	12	7	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126114	4	12	7	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126114	4	12	8	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126114	4	12	9	-	7576853	7576926
239556324	chr17	7576581	7576709	7576607	7576680	TP53	NM_001126114	4	12	10	-	7576525	7576657
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126114	4	12	11	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126114	4	12	12	-	7571720	7573008
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126115	5	7	1	-	7578371	7578811
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126115	5	7	1	-	7578371	7578811
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126115	5	7	2	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126115	5	7	2	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126115	5	7	3	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126115	5	7	3	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126115	5	7	4	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126115	5	7	5	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126115	5	7	6	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126115	5	7	7	-	7571720	7573008
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126116	6	8	1	-	7578371	7578811
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126116	6	8	1	-	7578371	7578811
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126116	6	8	2	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126116	6	8	2	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126116	6	8	3	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126116	6	8	3	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126116	6	8	4	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126116	6	8	5	-	7576853	7576926
239556324	chr17	7576581	7576709	7576607	7576680	TP53	NM_001126116	6	8	6	-	7576525	7576657

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126116	6	8	7	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126116	6	8	8	-	7571720	7573008
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126117	7	8	1	-	7578371	7578811
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126117	7	8	1	-	7578371	7578811
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126117	7	8	2	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126117	7	8	2	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126117	7	8	3	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126117	7	8	3	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126117	7	8	4	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126117	7	8	5	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126117	7	8	7	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126117	7	8	8	-	7571720	7573008
261742834	chr17	7579743	7579966	7579766	7579943	TP53	NM_001126118	8	10	2	-	7579700	7579940
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126118	8	10	2	-	7579700	7579940
263746824	chr17	7579214	7579396	7579237	7579374	TP53	NM_001126118	8	10	3	-	7579312	7579590
263767242	chr17	7579353	7579549	7579373	7579525	TP53	NM_001126118	8	10	3	-	7579312	7579590
263780413	chr17	7579504	7579722	7579525	7579698	TP53	NM_001126118	8	10	3	-	7579312	7579590
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126118	8	10	4	-	7578371	7578554
262610073	chr17	7578408	7578587	7578429	7578561	TP53	NM_001126118	8	10	4	-	7578371	7578554
262328803	chr17	7578121	7578317	7578142	7578294	TP53	NM_001126118	8	10	5	-	7578177	7578289
262570290	chr17	7578244	7578450	7578268	7578428	TP53	NM_001126118	8	10	5	-	7578177	7578289
242506164	chr17	7577512	7577637	7577534	7577616	TP53	NM_001126118	8	10	6	-	7577499	7577608
261728171	chr17	7577372	7577571	7577393	7577549	TP53	NM_001126118	8	10	6	-	7577499	7577608
242286013	chr17	7576967	7577186	7576987	7577161	TP53	NM_001126118	8	10	7	-	7577019	7577155
241053357	chr17	7576753	7576958	7576774	7576931	TP53	NM_001126118	8	10	8	-	7576853	7576926
240338133	chr17	7573839	7574063	7573864	7574040	TP53	NM_001126118	8	10	9	-	7573927	7574033
239777409	chr17	7572817	7573040	7572838	7573018	TP53	NM_001126118	8	10	10	-	7571720	7573008
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_000366	1	10	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_000366	1	10	1	+	63334838	63335142
327871372	chr15	63336057	63336269	63336078	63336246	TPM1	NM_000366	1	10	2	+	63336226	63336351
327874343	chr15	63336226	63336449	63336247	63336421	TPM1	NM_000366	1	10	2	+	63336226	63336351
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_000366	1	10	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_000366	1	10	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_000366	1	10	5	+	63353068	63353138
327391814	chr15	63353303	63353519	63353326	63353494	TPM1	NM_000366	1	10	6	+	63353397	63353472
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_000366	1	10	7	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_000366	1	10	8	+	63354775	63354844
326553941	chr15	63356152	63356372	63356174	63356351	TPM1	NM_000366	1	10	9	+	63356263	63356389
327457033	chr15	63357922	63358127	63357943	63358103	TPM1	NM_000366	1	10	10	+	63358095	63358292
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_001018004	2	9	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_001018004	2	9	1	+	63334838	63335142

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327871372	chr15	63336057	63336269	63336078	63336246	TPM1	NM_001018004	2	9	2	+	63336226	63336351
327874343	chr15	63336226	63336449	63336247	63336421	TPM1	NM_001018004	2	9	2	+	63336226	63336351
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018004	2	9	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018004	2	9	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018004	2	9	5	+	63353068	63353138
327225237	chr15	63353837	63354046	63353861	63354022	TPM1	NM_001018004	2	9	6	+	63353912	63353987
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018004	2	9	7	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018004	2	9	8	+	63354775	63354844
328245228	chr15	63363181	63363401	63363209	63363378	TPM1	NM_001018004	2	9	9	+	63363289	63364113
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_001018005	3	10	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_001018005	3	10	1	+	63334838	63335142
327871372	chr15	63336057	63336269	63336078	63336246	TPM1	NM_001018005	3	10	2	+	63336226	63336351
327874343	chr15	63336226	63336449	63336247	63336421	TPM1	NM_001018005	3	10	2	+	63336226	63336351
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018005	3	10	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018005	3	10	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018005	3	10	5	+	63353068	63353138
327225237	chr15	63353837	63354046	63353861	63354022	TPM1	NM_001018005	3	10	6	+	63353912	63353987
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018005	3	10	7	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018005	3	10	8	+	63354775	63354844
326553941	chr15	63356152	63356372	63356174	63356351	TPM1	NM_001018005	3	10	9	+	63356263	63356341
327457033	chr15	63357922	63358127	63357943	63358103	TPM1	NM_001018005	3	10	10	+	63358095	63358292
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_001018006	4	9	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_001018006	4	9	1	+	63334838	63335142
327871372	chr15	63336057	63336269	63336078	63336246	TPM1	NM_001018006	4	9	2	+	63336226	63336351
327874343	chr15	63336226	63336449	63336247	63336421	TPM1	NM_001018006	4	9	2	+	63336226	63336351
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018006	4	9	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018006	4	9	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018006	4	9	5	+	63353068	63353138
327391814	chr15	63353303	63353519	63353326	63353494	TPM1	NM_001018006	4	9	6	+	63353397	63353472
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018006	4	9	7	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018006	4	9	8	+	63354775	63354844
328245228	chr15	63363181	63363401	63363209	63363378	TPM1	NM_001018006	4	9	9	+	63363289	63364113
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_001018007	5	9	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_001018007	5	9	1	+	63334838	63335142
326789697	chr15	63335836	63336000	63335857	63335982	TPM1	NM_001018007	5	9	2	+	63335905	63336030
326789867	chr15	63335931	63336154	63335949	63336134	TPM1	NM_001018007	5	9	2	+	63335905	63336030
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018007	5	9	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018007	5	9	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018007	5	9	5	+	63353068	63353138
327225237	chr15	63353837	63354046	63353861	63354022	TPM1	NM_001018007	5	9	6	+	63353912	63353987
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018007	5	9	7	+	63354414	63354476

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018007	5	9	8	+	63354775	63354844
328245228	chr15	63363181	63363401	63363209	63363378	TPM1	NM_001018007	5	9	9	+	63363289	63364113
327092437	chr15	63340605	63340827	63340622	63340809	TPM1	NM_001018008	6	8	1	+	63340636	63340906
327092471	chr15	63340781	63340928	63340798	63340907	TPM1	NM_001018008	6	8	1	+	63340636	63340906
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018008	6	8	2	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018008	6	8	3	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018008	6	8	4	+	63353068	63353138
327225237	chr15	63353837	63354046	63353861	63354022	TPM1	NM_001018008	6	8	5	+	63353912	63353987
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018008	6	8	6	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018008	6	8	7	+	63354775	63354844
326811682	chr15	63361959	63362178	63361980	63362154	TPM1	NM_001018008	6	8	8	+	63362069	63362831
326949898	chr15	63334901	63335065	63334922	63335041	TPM1	NM_001018020	7	9	1	+	63334838	63335142
326951786	chr15	63335024	63335200	63335042	63335183	TPM1	NM_001018020	7	9	1	+	63334838	63335142
326789697	chr15	63335836	63336000	63335857	63335982	TPM1	NM_001018020	7	9	2	+	63335905	63336030
326789867	chr15	63335931	63336154	63335949	63336134	TPM1	NM_001018020	7	9	2	+	63335905	63336030
326553909	chr15	63349125	63349345	63349146	63349322	TPM1	NM_001018020	7	9	3	+	63349184	63349317
326512150	chr15	63351728	63351950	63351755	63351929	TPM1	NM_001018020	7	9	4	+	63351762	63351879
327655593	chr15	63353001	63353204	63353022	63353180	TPM1	NM_001018020	7	9	5	+	63353068	63353138
327391814	chr15	63353303	63353519	63353326	63353494	TPM1	NM_001018020	7	9	6	+	63353397	63353472
328191331	chr15	63354288	63354504	63354314	63354481	TPM1	NM_001018020	7	9	7	+	63354414	63354476
328451225	chr15	63354685	63354907	63354713	63354882	TPM1	NM_001018020	7	9	8	+	63354775	63354844
328245228	chr15	63363181	63363401	63363209	63363378	TPM1	NM_001018020	7	9	9	+	63363289	63364113
241686109	chr9	135804087	135804309	135804115	135804289	TSC1	NM_000368	1	23	3	-	135804154	135804339
239601827	chr9	135802500	135802723	135802521	135802696	TSC1	NM_000368	1	23	4	-	135802588	135802691
262563269	chr9	135800844	135801010	135800868	135800982	TSC1	NM_000368	1	23	5	-	135800974	135801126
262586949	chr9	135800956	135801156	135800983	135801131	TSC1	NM_000368	1	23	5	-	135800974	135801126
239640371	chr9	135798702	135798913	135798724	135798889	TSC1	NM_000368	1	23	6	-	135798735	135798879
239690455	chr9	135797110	135797239	135797132	135797212	TSC1	NM_000368	1	23	7	-	135797206	135797360
239713728	chr9	135797186	135797387	135797213	135797365	TSC1	NM_000368	1	23	7	-	135797206	135797360
241045502	chr9	135796661	135796872	135796688	135796843	TSC1	NM_000368	1	23	8	-	135796750	135796823
240217793	chr9	135787621	135787782	135787648	135787755	TSC1	NM_000368	1	23	9	-	135787669	135787844
240250121	chr9	135787733	135787954	135787756	135787930	TSC1	NM_000368	1	23	9	-	135787669	135787844
261944952	chr9	135786758	135786982	135786785	135786960	TSC1	NM_000368	1	23	10	-	135786840	135786955
266374592	chr9	135786310	135786534	135786335	135786506	TSC1	NM_000368	1	23	11	-	135786389	135786500
239272325	chr9	135785889	135786113	135785911	135786086	TSC1	NM_000368	1	23	12	-	135785958	135786079
265003575	chr9	135782583	135782806	135782610	135782780	TSC1	NM_000368	1	23	13	-	135782688	135782757
239939495	chr9	135782068	135782288	135782089	135782260	TSC1	NM_000368	1	23	14	-	135782118	135782222
240472077	chr9	135780868	135781091	135780893	135781065	TSC1	NM_000368	1	23	15	-	135780968	135781526
240502685	chr9	135781044	135781252	135781066	135781230	TSC1	NM_000368	1	23	15	-	135780968	135781526
240572887	chr9	135781207	135781428	135781231	135781408	TSC1	NM_000368	1	23	15	-	135780968	135781526
240613793	chr9	135781353	135781567	135781375	135781543	TSC1	NM_000368	1	23	15	-	135780968	135781526

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242274630	chr9	135779717	135779935	135779738	135779907	TSC1	NM_000368	1	23	16	-	135779798	135779841
262406586	chr9	135778955	135779161	135778979	135779136	TSC1	NM_000368	1	23	17	-	135779038	135779204
262455653	chr9	135779114	135779251	135779137	135779227	TSC1	NM_000368	1	23	17	-	135779038	135779204
263223470	chr9	135777861	135778076	135777888	135778052	TSC1	NM_000368	1	23	18	-	135777992	135778174
263267750	chr9	135778013	135778222	135778037	135778195	TSC1	NM_000368	1	23	18	-	135777992	135778174
240418617	chr9	135776908	135777117	135776933	135777092	TSC1	NM_000368	1	23	19	-	135776976	135777086
241494343	chr9	135776046	135776259	135776067	135776231	TSC1	NM_000368	1	23	20	-	135776102	135776224
242563501	chr9	135772873	135773095	135772894	135773069	TSC1	NM_000368	1	23	21	-	135772810	135772997
261800752	chr9	135772719	135772919	135772740	135772893	TSC1	NM_000368	1	23	21	-	135772810	135772997
262317843	chr9	135772455	135772639	135772476	135772615	TSC1	NM_000368	1	23	22	-	135772571	135772732
262375665	chr9	135772590	135772764	135772616	135772737	TSC1	NM_000368	1	23	22	-	135772571	135772732
241849253	chr9	135771575	135771787	135771600	135771762	TSC1	NM_000368	1	23	23	-	135766735	135772141
265403355	chr9	135771741	135771944	135771763	135771925	TSC1	NM_000368	1	23	23	-	135766735	135772141
265431699	chr9	135771904	135772122	135771925	135772101	TSC1	NM_000368	1	23	23	-	135766735	135772141
265465871	chr9	135772076	135772232	135772097	135772207	TSC1	NM_000368	1	23	23	-	135766735	135772141
241686109	chr9	135804087	135804309	135804115	135804289	TSC1	NM_001162426	2	23	3	-	135804154	135804339
239601827	chr9	135802500	135802723	135802521	135802696	TSC1	NM_001162426	2	23	4	-	135802588	135802691
262563269	chr9	135800844	135801010	135800868	135800982	TSC1	NM_001162426	2	23	5	-	135800974	135801126
262586949	chr9	135800956	135801156	135800983	135801131	TSC1	NM_001162426	2	23	5	-	135800974	135801126
239640371	chr9	135798702	135798913	135798724	135798889	TSC1	NM_001162426	2	23	6	-	135798735	135798879
239690455	chr9	135797110	135797239	135797132	135797212	TSC1	NM_001162426	2	23	7	-	135797206	135797360
239713728	chr9	135797186	135797387	135797213	135797365	TSC1	NM_001162426	2	23	7	-	135797206	135797360
241045502	chr9	135796661	135796872	135796688	135796843	TSC1	NM_001162426	2	23	8	-	135796750	135796823
240217793	chr9	135787621	135787782	135787648	135787755	TSC1	NM_001162426	2	23	9	-	135787669	135787844
240250121	chr9	135787733	135787954	135787756	135787930	TSC1	NM_001162426	2	23	9	-	135787669	135787844
261944952	chr9	135786758	135786982	135786785	135786960	TSC1	NM_001162426	2	23	10	-	135786840	135786955
266374592	chr9	135786310	135786534	135786335	135786506	TSC1	NM_001162426	2	23	11	-	135786389	135786500
239272325	chr9	135785889	135786113	135785911	135786086	TSC1	NM_001162426	2	23	12	-	135785958	135786076
265003575	chr9	135782583	135782806	135782610	135782780	TSC1	NM_001162426	2	23	13	-	135782688	135782757
239939495	chr9	135782068	135782288	135782089	135782260	TSC1	NM_001162426	2	23	14	-	135782118	135782222
240472077	chr9	135780868	135781091	135780893	135781065	TSC1	NM_001162426	2	23	15	-	135780968	135781526
240502685	chr9	135781044	135781252	135781066	135781230	TSC1	NM_001162426	2	23	15	-	135780968	135781526
240572887	chr9	135781207	135781428	135781231	135781408	TSC1	NM_001162426	2	23	15	-	135780968	135781526
240613793	chr9	135781353	135781567	135781375	135781543	TSC1	NM_001162426	2	23	15	-	135780968	135781526
242274630	chr9	135779717	135779935	135779738	135779907	TSC1	NM_001162426	2	23	16	-	135779798	135779841
262406586	chr9	135778955	135779161	135778979	135779136	TSC1	NM_001162426	2	23	17	-	135779038	135779204
262455653	chr9	135779114	135779251	135779137	135779227	TSC1	NM_001162426	2	23	17	-	135779038	135779204
263223470	chr9	135777861	135778076	135777888	135778052	TSC1	NM_001162426	2	23	18	-	135777992	135778174
263267750	chr9	135778013	135778222	135778037	135778195	TSC1	NM_001162426	2	23	18	-	135777992	135778174
240418617	chr9	135776908	135777117	135776933	135777092	TSC1	NM_001162426	2	23	19	-	135776976	135777086
241494343	chr9	135776046	135776259	135776067	135776231	TSC1	NM_001162426	2	23	20	-	135776102	135776224

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242563501	chr9	135772873	135773095	135772894	135773069	TSC1	NM_001162426	2	23	21	-	135772810	135772997
261800752	chr9	135772719	135772919	135772740	135772893	TSC1	NM_001162426	2	23	21	-	135772810	135772997
262317843	chr9	135772455	135772639	135772476	135772615	TSC1	NM_001162426	2	23	22	-	135772571	135772732
262375665	chr9	135772590	135772764	135772616	135772737	TSC1	NM_001162426	2	23	22	-	135772571	135772732
241849253	chr9	135771575	135771787	135771600	135771762	TSC1	NM_001162426	2	23	23	-	135766735	135772141
265403355	chr9	135771741	135771944	135771763	135771925	TSC1	NM_001162426	2	23	23	-	135766735	135772141
265431699	chr9	135771904	135772122	135771925	135772101	TSC1	NM_001162426	2	23	23	-	135766735	135772141
265465871	chr9	135772076	135772232	135772097	135772207	TSC1	NM_001162426	2	23	23	-	135766735	135772141
241686109	chr9	135804087	135804309	135804115	135804289	TSC1	NM_001162427	3	22	3	-	135804154	135804339
239601827	chr9	135802500	135802723	135802521	135802696	TSC1	NM_001162427	3	22	4	-	135802588	135802691
239640371	chr9	135798702	135798913	135798724	135798889	TSC1	NM_001162427	3	22	5	-	135798735	135798879
239690455	chr9	135797110	135797239	135797132	135797212	TSC1	NM_001162427	3	22	6	-	135797206	135797360
239713728	chr9	135797186	135797387	135797213	135797365	TSC1	NM_001162427	3	22	6	-	135797206	135797360
241045502	chr9	135796661	135796872	135796688	135796843	TSC1	NM_001162427	3	22	7	-	135796750	135796823
240217793	chr9	135787621	135787782	135787648	135787755	TSC1	NM_001162427	3	22	8	-	135787669	135787844
240250121	chr9	135787733	135787954	135787756	135787930	TSC1	NM_001162427	3	22	8	-	135787669	135787844
261944952	chr9	135786758	135786982	135786785	135786960	TSC1	NM_001162427	3	22	9	-	135786840	135786955
266374592	chr9	135786310	135786534	135786335	135786506	TSC1	NM_001162427	3	22	10	-	135786389	135786500
239272325	chr9	135785889	135786113	135785911	135786086	TSC1	NM_001162427	3	22	11	-	135785958	135786079
265003575	chr9	135782583	135782806	135782610	135782780	TSC1	NM_001162427	3	22	12	-	135782688	135782757
239939495	chr9	135782068	135782288	135782089	135782260	TSC1	NM_001162427	3	22	13	-	135782118	135782222
240472077	chr9	135780868	135781091	135780893	135781065	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240502685	chr9	135781044	135781252	135781066	135781230	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240572887	chr9	135781207	135781428	135781231	135781408	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240613793	chr9	135781353	135781567	135781375	135781543	TSC1	NM_001162427	3	22	14	-	135780968	135781526
242274630	chr9	135779717	135779935	135779738	135779907	TSC1	NM_001162427	3	22	15	-	135779798	135779841
262406586	chr9	135778955	135779161	135778979	135779136	TSC1	NM_001162427	3	22	16	-	135779038	135779204
262455653	chr9	135779114	135779251	135779137	135779227	TSC1	NM_001162427	3	22	16	-	135779038	135779204
263223470	chr9	135777861	135778076	135777888	135778052	TSC1	NM_001162427	3	22	17	-	135777992	135778174
263267750	chr9	135778013	135778222	135778037	135778195	TSC1	NM_001162427	3	22	17	-	135777992	135778174
240418617	chr9	135776908	135777117	135776933	135777092	TSC1	NM_001162427	3	22	18	-	135776976	135777086
241494343	chr9	135776046	135776259	135776067	135776231	TSC1	NM_001162427	3	22	19	-	135776102	135776224
242563501	chr9	135772873	135773095	135772894	135773069	TSC1	NM_001162427	3	22	20	-	135772810	135772997
261800752	chr9	135772719	135772919	135772740	135772893	TSC1	NM_001162427	3	22	20	-	135772810	135772997
262317843	chr9	135772455	135772639	135772476	135772615	TSC1	NM_001162427	3	22	21	-	135772571	135772732
262375665	chr9	135772590	135772764	135772616	135772737	TSC1	NM_001162427	3	22	21	-	135772571	135772732
241849253	chr9	135771575	135771787	135771600	135771762	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265403355	chr9	135771741	135771944	135771763	135771925	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265431699	chr9	135771904	135772122	135771925	135772101	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265465871	chr9	135772076	135772232	135772097	135772207	TSC1	NM_001162427	3	22	22	-	135766735	135772141
262473081	chr16	2098558	2098782	2098580	2098759	TSC2	NM_000548	1	42	2	+	2098588	2098754

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241511459	chr16	2100296	2100520	2100319	2100493	TSC2	NM_000548	1	42	3	+	2100401	2100487
242470420	chr16	2103292	2103490	2103313	2103472	TSC2	NM_000548	1	42	4	+	2103343	2103453
238394789	chr16	2104268	2104486	2104289	2104464	TSC2	NM_000548	1	42	5	+	2104297	2104441
263003709	chr16	2105342	2105558	2105363	2105529	TSC2	NM_000548	1	42	6	+	2105403	2105520
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_000548	1	42	7	+	2106197	2106245
242729062	chr16	2106577	2106800	2106596	2106776	TSC2	NM_000548	1	42	8	+	2106645	2106770
240171476	chr16	2107080	2107278	2107099	2107256	TSC2	NM_000548	1	42	9	+	2107106	2107179
264508710	chr16	2108712	2108903	2108733	2108882	TSC2	NM_000548	1	42	10	+	2108748	2108874
240806165	chr16	2110541	2110721	2110561	2110697	TSC2	NM_000548	1	42	11	+	2110671	2110814
240819712	chr16	2110679	2110895	2110698	2110873	TSC2	NM_000548	1	42	11	+	2110671	2110814
262859053	chr16	2111832	2112018	2111852	2112001	TSC2	NM_000548	1	42	12	+	2111872	2112009
239049443	chr16	2112410	2112632	2112429	2112614	TSC2	NM_000548	1	42	13	+	2112498	2112601
239567295	chr16	2112845	2113057	2112863	2113034	TSC2	NM_000548	1	42	14	+	2112973	2113054
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_000548	1	42	15	+	2114273	2114428
240603774	chr16	2114308	2114529	2114328	2114510	TSC2	NM_000548	1	42	15	+	2114273	2114428
241965729	chr16	2115476	2115693	2115498	2115675	TSC2	NM_000548	1	42	16	+	2115520	2115636
264637151	chr16	2120395	2120610	2120416	2120593	TSC2	NM_000548	1	42	17	+	2120457	2120579
265942670	chr16	2121482	2121706	2121504	2121684	TSC2	NM_000548	1	42	18	+	2121511	2121617
238413407	chr16	2121756	2121973	2121776	2121955	TSC2	NM_000548	1	42	19	+	2121785	2121935
241056300	chr16	2122160	2122305	2122182	2122283	TSC2	NM_000548	1	42	20	+	2122242	2122364
241059673	chr16	2122244	2122434	2122266	2122414	TSC2	NM_000548	1	42	20	+	2122242	2122364
262269489	chr16	2122818	2123020	2122839	2123001	TSC2	NM_000548	1	42	21	+	2122850	2122984
240316907	chr16	2124092	2124307	2124111	2124283	TSC2	NM_000548	1	42	22	+	2124201	2124390
240328351	chr16	2124265	2124487	2124284	2124467	TSC2	NM_000548	1	42	22	+	2124201	2124390
263178907	chr16	2125773	2125957	2125793	2125939	TSC2	NM_000548	1	42	23	+	2125800	2125893
241099729	chr16	2126023	2126214	2126042	2126195	TSC2	NM_000548	1	42	24	+	2126069	2126171
241952764	chr16	2126451	2126671	2126470	2126653	TSC2	NM_000548	1	42	25	+	2126492	2126586
239196326	chr16	2127479	2127676	2127501	2127654	TSC2	NM_000548	1	42	26	+	2127599	2127727
239210463	chr16	2127630	2127826	2127655	2127805	TSC2	NM_000548	1	42	26	+	2127599	2127727
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_000548	1	42	27	+	2129033	2129197
240062671	chr16	2128958	2129157	2128979	2129134	TSC2	NM_000548	1	42	27	+	2129033	2129197
240070744	chr16	2129100	2129276	2129123	2129255	TSC2	NM_000548	1	42	27	+	2129033	2129197
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_000548	1	42	28	+	2129277	2129429
239514320	chr16	2129317	2129528	2129337	2129508	TSC2	NM_000548	1	42	28	+	2129277	2129429
264188845	chr16	2129530	2129750	2129548	2129731	TSC2	NM_000548	1	42	29	+	2129558	2129670
265783146	chr16	2130109	2130280	2130131	2130259	TSC2	NM_000548	1	42	30	+	2130166	2130378
265786298	chr16	2130221	2130426	2130241	2130405	TSC2	NM_000548	1	42	30	+	2130166	2130378
241054930	chr16	2131558	2131723	2131577	2131705	TSC2	NM_000548	1	42	31	+	2131596	2131799
241060031	chr16	2131673	2131875	2131693	2131857	TSC2	NM_000548	1	42	31	+	2131596	2131799
240424518	chr16	2132371	2132565	2132392	2132544	TSC2	NM_000548	1	42	32	+	2132437	2132505
262026071	chr16	2133598	2133822	2133618	2133802	TSC2	NM_000548	1	42	33	+	2133696	2133817

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262033633	chr16	2133756	2133940	2133776	2133918	TSC2	NM_000548	1	42	33	+	2133696	2133817
262600380	chr16	2134183	2134387	2134200	2134367	TSC2	NM_000548	1	42	34	+	2134229	2134716
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_000548	1	42	34	+	2134229	2134716
262616508	chr16	2134460	2134665	2134479	2134642	TSC2	NM_000548	1	42	34	+	2134229	2134716
262623780	chr16	2134595	2134781	2134614	2134762	TSC2	NM_000548	1	42	34	+	2134229	2134716
264924469	chr16	2134864	2135068	2134883	2135050	TSC2	NM_000548	1	42	35	+	2134952	2135027
241388327	chr16	2135107	2135306	2135126	2135287	TSC2	NM_000548	1	42	36	+	2135231	2135323
241393036	chr16	2135262	2135399	2135284	2135379	TSC2	NM_000548	1	42	36	+	2135231	2135323
242589478	chr16	2136074	2136292	2136095	2136272	TSC2	NM_000548	1	42	37	+	2136194	2136380
242600421	chr16	2136231	2136451	2136253	2136431	TSC2	NM_000548	1	42	37	+	2136194	2136380
262161704	chr16	2136637	2136848	2136658	2136826	TSC2	NM_000548	1	42	38	+	2136733	2136872
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_000548	1	42	38	+	2136733	2136872
262388192	chr16	2137794	2138015	2137813	2137998	TSC2	NM_000548	1	42	39	+	2137864	2137942
240855685	chr16	2138022	2138207	2138039	2138186	TSC2	NM_000548	1	42	40	+	2138049	2138140
242281956	chr16	2138128	2138351	2138147	2138331	TSC2	NM_000548	1	42	41	+	2138228	2138326
239348263	chr16	2138410	2138614	2138430	2138593	TSC2	NM_000548	1	42	42	+	2138447	2138713
239351939	chr16	2138538	2138734	2138557	2138708	TSC2	NM_000548	1	42	42	+	2138447	2138713
262473081	chr16	2098558	2098782	2098580	2098759	TSC2	NM_001077183	2	40	2	+	2098588	2098754
241511459	chr16	2100296	2100520	2100319	2100493	TSC2	NM_001077183	2	40	3	+	2100401	2100487
242470420	chr16	2103292	2103490	2103313	2103472	TSC2	NM_001077183	2	40	4	+	2103343	2103453
238394789	chr16	2104268	2104486	2104289	2104464	TSC2	NM_001077183	2	40	5	+	2104297	2104441
263003709	chr16	2105342	2105558	2105363	2105529	TSC2	NM_001077183	2	40	6	+	2105403	2105520
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_001077183	2	40	7	+	2106197	2106245
242729062	chr16	2106577	2106800	2106596	2106776	TSC2	NM_001077183	2	40	8	+	2106645	2106770
240171476	chr16	2107080	2107278	2107099	2107256	TSC2	NM_001077183	2	40	9	+	2107106	2107179
264508710	chr16	2108712	2108903	2108733	2108882	TSC2	NM_001077183	2	40	10	+	2108748	2108874
240806165	chr16	2110541	2110721	2110561	2110697	TSC2	NM_001077183	2	40	11	+	2110671	2110814
240819712	chr16	2110679	2110895	2110698	2110873	TSC2	NM_001077183	2	40	11	+	2110671	2110814
262859053	chr16	2111832	2112018	2111852	2112001	TSC2	NM_001077183	2	40	12	+	2111872	2112009
239049443	chr16	2112410	2112632	2112429	2112614	TSC2	NM_001077183	2	40	13	+	2112498	2112601
239567295	chr16	2112845	2113057	2112863	2113034	TSC2	NM_001077183	2	40	14	+	2112973	2113054
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_001077183	2	40	15	+	2114273	2114428
240603774	chr16	2114308	2114529	2114328	2114510	TSC2	NM_001077183	2	40	15	+	2114273	2114428
241965729	chr16	2115476	2115693	2115498	2115675	TSC2	NM_001077183	2	40	16	+	2115520	2115636
264637151	chr16	2120395	2120610	2120416	2120593	TSC2	NM_001077183	2	40	17	+	2120457	2120579
265942670	chr16	2121482	2121706	2121504	2121684	TSC2	NM_001077183	2	40	18	+	2121511	2121617
238413407	chr16	2121756	2121973	2121776	2121955	TSC2	NM_001077183	2	40	19	+	2121785	2121935
241056300	chr16	2122160	2122305	2122182	2122283	TSC2	NM_001077183	2	40	20	+	2122242	2122364
241059673	chr16	2122244	2122434	2122266	2122414	TSC2	NM_001077183	2	40	20	+	2122242	2122364
262269489	chr16	2122818	2123020	2122839	2123001	TSC2	NM_001077183	2	40	21	+	2122850	2122984
240316907	chr16	2124092	2124307	2124111	2124283	TSC2	NM_001077183	2	40	22	+	2124201	2124390

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240328351	chr16	2124265	2124487	2124284	2124467	TSC2	NM_001077183	2	40	22	+	2124201	2124390
263178907	chr16	2125773	2125957	2125793	2125939	TSC2	NM_001077183	2	40	23	+	2125800	2125893
241099729	chr16	2126023	2126214	2126042	2126195	TSC2	NM_001077183	2	40	24	+	2126069	2126171
241952764	chr16	2126451	2126671	2126470	2126653	TSC2	NM_001077183	2	40	25	+	2126492	2126586
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_001077183	2	40	26	+	2129036	2129197
240062671	chr16	2128958	2129157	2128979	2129134	TSC2	NM_001077183	2	40	26	+	2129036	2129197
240070744	chr16	2129100	2129276	2129123	2129255	TSC2	NM_001077183	2	40	26	+	2129036	2129197
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_001077183	2	40	27	+	2129277	2129429
239514320	chr16	2129317	2129528	2129337	2129508	TSC2	NM_001077183	2	40	27	+	2129277	2129429
264188845	chr16	2129530	2129750	2129548	2129731	TSC2	NM_001077183	2	40	28	+	2129558	2129670
265783146	chr16	2130109	2130280	2130131	2130259	TSC2	NM_001077183	2	40	29	+	2130166	2130378
265786298	chr16	2130221	2130426	2130241	2130405	TSC2	NM_001077183	2	40	29	+	2130166	2130378
241054930	chr16	2131558	2131723	2131577	2131705	TSC2	NM_001077183	2	40	30	+	2131596	2131799
241060031	chr16	2131673	2131875	2131693	2131857	TSC2	NM_001077183	2	40	30	+	2131596	2131799
262026071	chr16	2133598	2133822	2133618	2133802	TSC2	NM_001077183	2	40	31	+	2133696	2133817
262033633	chr16	2133756	2133940	2133776	2133918	TSC2	NM_001077183	2	40	31	+	2133696	2133817
262600380	chr16	2134183	2134387	2134200	2134367	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262616508	chr16	2134460	2134665	2134479	2134642	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262623780	chr16	2134595	2134781	2134614	2134762	TSC2	NM_001077183	2	40	32	+	2134229	2134716
264924469	chr16	2134864	2135068	2134883	2135050	TSC2	NM_001077183	2	40	33	+	2134952	2135027
241388327	chr16	2135107	2135306	2135126	2135287	TSC2	NM_001077183	2	40	34	+	2135231	2135323
241393036	chr16	2135262	2135399	2135284	2135379	TSC2	NM_001077183	2	40	34	+	2135231	2135323
242589478	chr16	2136074	2136292	2136095	2136272	TSC2	NM_001077183	2	40	35	+	2136194	2136380
242600421	chr16	2136231	2136451	2136253	2136431	TSC2	NM_001077183	2	40	35	+	2136194	2136380
262161704	chr16	2136637	2136848	2136658	2136826	TSC2	NM_001077183	2	40	36	+	2136733	2136872
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_001077183	2	40	36	+	2136733	2136872
262388192	chr16	2137794	2138015	2137813	2137998	TSC2	NM_001077183	2	40	37	+	2137864	2137942
240855685	chr16	2138022	2138207	2138039	2138186	TSC2	NM_001077183	2	40	38	+	2138049	2138140
242281956	chr16	2138128	2138351	2138147	2138331	TSC2	NM_001077183	2	40	39	+	2138228	2138326
239348263	chr16	2138410	2138614	2138430	2138593	TSC2	NM_001077183	2	40	40	+	2138447	2138713
239351939	chr16	2138538	2138734	2138557	2138708	TSC2	NM_001077183	2	40	40	+	2138447	2138713
262473081	chr16	2098558	2098782	2098580	2098759	TSC2	NM_001114382	3	41	2	+	2098588	2098754
241511459	chr16	2100296	2100520	2100319	2100493	TSC2	NM_001114382	3	41	3	+	2100401	2100487
242470420	chr16	2103292	2103490	2103313	2103472	TSC2	NM_001114382	3	41	4	+	2103343	2103453
238394789	chr16	2104268	2104486	2104289	2104464	TSC2	NM_001114382	3	41	5	+	2104297	2104441
263003709	chr16	2105342	2105558	2105363	2105529	TSC2	NM_001114382	3	41	6	+	2105403	2105520
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_001114382	3	41	7	+	2106197	2106245
242729062	chr16	2106577	2106800	2106596	2106776	TSC2	NM_001114382	3	41	8	+	2106645	2106770
240171476	chr16	2107080	2107278	2107099	2107256	TSC2	NM_001114382	3	41	9	+	2107106	2107179
264508710	chr16	2108712	2108903	2108733	2108882	TSC2	NM_001114382	3	41	10	+	2108748	2108874

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240806165	chr16	2110541	2110721	2110561	2110697	TSC2	NM_001114382	3	41	11	+	2110671	2110814
240819712	chr16	2110679	2110895	2110698	2110873	TSC2	NM_001114382	3	41	11	+	2110671	2110814
262859053	chr16	2111832	2112018	2111852	2112001	TSC2	NM_001114382	3	41	12	+	2111872	2112009
239049443	chr16	2112410	2112632	2112429	2112614	TSC2	NM_001114382	3	41	13	+	2112498	2112601
239567295	chr16	2112845	2113057	2112863	2113034	TSC2	NM_001114382	3	41	14	+	2112973	2113054
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_001114382	3	41	15	+	2114273	2114428
240603774	chr16	2114308	2114529	2114328	2114510	TSC2	NM_001114382	3	41	15	+	2114273	2114428
241965729	chr16	2115476	2115693	2115498	2115675	TSC2	NM_001114382	3	41	16	+	2115520	2115636
264637151	chr16	2120395	2120610	2120416	2120593	TSC2	NM_001114382	3	41	17	+	2120457	2120579
265942670	chr16	2121482	2121706	2121504	2121684	TSC2	NM_001114382	3	41	18	+	2121511	2121617
238413407	chr16	2121756	2121973	2121776	2121955	TSC2	NM_001114382	3	41	19	+	2121785	2121935
241056300	chr16	2122160	2122305	2122182	2122283	TSC2	NM_001114382	3	41	20	+	2122242	2122364
241059673	chr16	2122244	2122434	2122266	2122414	TSC2	NM_001114382	3	41	20	+	2122242	2122364
262269489	chr16	2122818	2123020	2122839	2123001	TSC2	NM_001114382	3	41	21	+	2122850	2122984
240316907	chr16	2124092	2124307	2124111	2124283	TSC2	NM_001114382	3	41	22	+	2124201	2124390
240328351	chr16	2124265	2124487	2124284	2124467	TSC2	NM_001114382	3	41	22	+	2124201	2124390
263178907	chr16	2125773	2125957	2125793	2125939	TSC2	NM_001114382	3	41	23	+	2125800	2125893
241099729	chr16	2126023	2126214	2126042	2126195	TSC2	NM_001114382	3	41	24	+	2126069	2126171
241952764	chr16	2126451	2126671	2126470	2126653	TSC2	NM_001114382	3	41	25	+	2126492	2126586
239196326	chr16	2127479	2127676	2127501	2127654	TSC2	NM_001114382	3	41	26	+	2127599	2127727
239210463	chr16	2127630	2127826	2127655	2127805	TSC2	NM_001114382	3	41	26	+	2127599	2127727
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_001114382	3	41	27	+	2129033	2129197
240062671	chr16	2128958	2129157	2128979	2129134	TSC2	NM_001114382	3	41	27	+	2129033	2129197
240070744	chr16	2129100	2129276	2129123	2129255	TSC2	NM_001114382	3	41	27	+	2129033	2129197
239505060	chr16	2129148	2129362	2129170	2129342	TSC2	NM_001114382	3	41	28	+	2129277	2129429
239514320	chr16	2129317	2129528	2129337	2129508	TSC2	NM_001114382	3	41	28	+	2129277	2129429
264188845	chr16	2129530	2129750	2129548	2129731	TSC2	NM_001114382	3	41	29	+	2129558	2129670
265783146	chr16	2130109	2130280	2130131	2130259	TSC2	NM_001114382	3	41	30	+	2130166	2130378
265786298	chr16	2130221	2130426	2130241	2130405	TSC2	NM_001114382	3	41	30	+	2130166	2130378
241054930	chr16	2131558	2131723	2131577	2131705	TSC2	NM_001114382	3	41	31	+	2131596	2131799
241060031	chr16	2131673	2131875	2131693	2131857	TSC2	NM_001114382	3	41	31	+	2131596	2131799
262026071	chr16	2133598	2133822	2133618	2133802	TSC2	NM_001114382	3	41	32	+	2133696	2133817
262033633	chr16	2133756	2133940	2133776	2133918	TSC2	NM_001114382	3	41	32	+	2133696	2133817
262600380	chr16	2134183	2134387	2134200	2134367	TSC2	NM_001114382	3	41	33	+	2134229	2134716
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_001114382	3	41	33	+	2134229	2134716
262616508	chr16	2134460	2134665	2134479	2134642	TSC2	NM_001114382	3	41	33	+	2134229	2134716
262623780	chr16	2134595	2134781	2134614	2134762	TSC2	NM_001114382	3	41	33	+	2134229	2134716
264924469	chr16	2134864	2135068	2134883	2135050	TSC2	NM_001114382	3	41	34	+	2134952	2135027
241388327	chr16	2135107	2135306	2135126	2135287	TSC2	NM_001114382	3	41	35	+	2135231	2135323
241393036	chr16	2135262	2135399	2135284	2135379	TSC2	NM_001114382	3	41	35	+	2135231	2135323
242589478	chr16	2136074	2136292	2136095	2136272	TSC2	NM_001114382	3	41	36	+	2136194	2136380

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242600421	chr16	2136231	2136451	2136253	2136431	TSC2	NM_001114382	3	41	36	+	2136194	2136380
262161704	chr16	2136637	2136848	2136658	2136826	TSC2	NM_001114382	3	41	37	+	2136733	2136872
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_001114382	3	41	37	+	2136733	2136872
262388192	chr16	2137794	2138015	2137813	2137998	TSC2	NM_001114382	3	41	38	+	2137864	2137942
240855685	chr16	2138022	2138207	2138039	2138186	TSC2	NM_001114382	3	41	39	+	2138049	2138140
242281956	chr16	2138128	2138351	2138147	2138331	TSC2	NM_001114382	3	41	40	+	2138228	2138326
239348263	chr16	2138410	2138614	2138430	2138593	TSC2	NM_001114382	3	41	41	+	2138447	2138713
239351939	chr16	2138538	2138734	2138557	2138708	TSC2	NM_001114382	3	41	41	+	2138447	2138713
326980928	chr8	63998231	63998434	63998248	63998416	TTPA	NM_000370	1	5	1	-	63998377	63998612
326981222	chr8	63998383	63998545	63998404	63998528	TTPA	NM_000370	1	5	1	-	63998377	63998612
326981277	chr8	63998506	63998699	63998524	63998681	TTPA	NM_000370	1	5	1	-	63998377	63998612
327932377	chr8	63985351	63985526	63985379	63985502	TTPA	NM_000370	1	5	2	-	63985494	63985647
327933093	chr8	63985476	63985695	63985503	63985666	TTPA	NM_000370	1	5	2	-	63985494	63985647
326707214	chr8	63978310	63978501	63978339	63978478	TTPA	NM_000370	1	5	3	-	63978463	63978656
326707450	chr8	63978455	63978645	63978480	63978617	TTPA	NM_000370	1	5	3	-	63978463	63978656
326713731	chr8	63978592	63978809	63978618	63978781	TTPA	NM_000370	1	5	3	-	63978463	63978656
327768532	chr8	63976652	63976833	63976676	63976805	TTPA	NM_000370	1	5	4	-	63976765	63976875
327774331	chr8	63976781	63976970	63976806	63976942	TTPA	NM_000370	1	5	4	-	63976765	63976875
327692981	chr8	63973657	63973856	63973678	63973828	TTPA	NM_000370	1	5	5	-	63972048	63973984
327696773	chr8	63973800	63974016	63973829	63973989	TTPA	NM_000370	1	5	5	-	63972048	63973984
328123565	chr18	29171747	29171971	29171769	29171943	TTR	NM_000371	1	4	1	+	29171730	29171934
327232882	chr18	29172820	29173041	29172849	29173016	TTR	NM_000371	1	4	2	+	29172859	29172989
327476785	chr18	29175028	29175249	29175050	29175223	TTR	NM_000371	1	4	3	+	29175083	29175218
328001167	chr18	29178455	29178668	29178477	29178648	TTR	NM_000371	1	4	4	+	29178531	29178986
326753068	chr6	35480456	35480679	35480477	35480657	TULP1	NM_003322	1	15	1	-	35480589	35480647
327222376	chr6	35480284	35480495	35480306	35480474	TULP1	NM_003322	1	15	2	-	35480416	35480467
327381268	chr6	35479891	35480083	35479909	35480062	TULP1	NM_003322	1	15	3	-	35479957	35480047
326829498	chr6	35479312	35479519	35479338	35479500	TULP1	NM_003322	1	15	4	-	35479425	35479583
326830507	chr6	35479443	35479611	35479464	35479592	TULP1	NM_003322	1	15	4	-	35479425	35479583
326984840	chr6	35478599	35478823	35478619	35478797	TULP1	NM_003322	1	15	5	-	35478638	35478787
327801779	chr6	35477526	35477749	35477547	35477727	TULP1	NM_003322	1	15	6	-	35477604	35477705
327168240	chr6	35477363	35477553	35477384	35477532	TULP1	NM_003322	1	15	7	-	35477411	35477527
328430545	chr6	35476907	35477125	35476927	35477103	TULP1	NM_003322	1	15	8	-	35476986	35477089
327506679	chr6	35473965	35474177	35473984	35474157	TULP1	NM_003322	1	15	9	-	35474051	35474056
327519936	chr6	35473689	35473912	35473710	35473893	TULP1	NM_003322	1	15	10	-	35473780	35473950
327522197	chr6	35473822	35474025	35473843	35474006	TULP1	NM_003322	1	15	10	-	35473780	35473950
327404415	chr6	35473448	35473658	35473469	35473636	TULP1	NM_003322	1	15	11	-	35473518	35473630
326710700	chr6	35471369	35471560	35471390	35471539	TULP1	NM_003322	1	15	12	-	35471514	35471625
326714780	chr6	35471509	35471728	35471531	35471703	TULP1	NM_003322	1	15	12	-	35471514	35471625
326710700	chr6	35471369	35471560	35471390	35471539	TULP1	NM_003322	1	15	13	-	35471336	35471434
327767106	chr6	35471247	35471461	35471268	35471439	TULP1	NM_003322	1	15	13	-	35471336	35471434

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326947881	chr6	35467594	35467798	35467615	35467776	TULP1	NM_003322	1	15	14	-	35467758	35467929
326966956	chr6	35467757	35467966	35467777	35467944	TULP1	NM_003322	1	15	14	-	35467758	35467929
327918863	chr6	35466175	35466397	35466196	35466372	TULP1	NM_003322	1	15	15	-	35465651	35466237
327920869	chr6	35466039	35466234	35466060	35466212	TULP1	NM_003322	1	15	15	-	35465651	35466237
327661528	chr7	19156283	19156488	19156304	19156465	TWIST1	NM_000474	1	2	1	-	19156294	19157295
327665046	chr7	19156419	19156556	19156438	19156537	TWIST1	NM_000474	1	2	1	-	19156294	19157295
327666891	chr7	19156501	19156720	19156524	19156701	TWIST1	NM_000474	1	2	1	-	19156294	19157295
328433017	chr7	19156865	19157079	19156882	19157061	TWIST1	NM_000474	1	2	1	-	19156294	19157295
327925235	chr7	37889937	37890138	37889964	37890115	TXNDC3	NM_016616	1	18	4	+	37889980	37890037
327003158	chr7	37890101	37890325	37890122	37890296	TXNDC3	NM_016616	1	18	5	+	37890231	37890337
327008511	chr7	37890264	37890458	37890288	37890427	TXNDC3	NM_016616	1	18	5	+	37890231	37890337
327987543	chr7	37896693	37896913	37896713	37896887	TXNDC3	NM_016616	1	18	6	+	37896876	37896947
327992376	chr7	37896866	37897004	37896888	37896976	TXNDC3	NM_016616	1	18	6	+	37896876	37896947
327049001	chr7	37901559	37901782	37901587	37901754	TXNDC3	NM_016616	1	18	7	+	37901630	37901746
327217417	chr7	37902961	37903110	37902990	37903088	TXNDC3	NM_016616	1	18	8	+	37902998	37903064
327457508	chr7	37903878	37904096	37903903	37904069	TXNDC3	NM_016616	1	18	9	+	37903950	37904023
327464073	chr7	37905070	37905269	37905095	37905241	TXNDC3	NM_016616	1	18	10	+	37905127	37905219
326441540	chr7	37907200	37907417	37907222	37907394	TXNDC3	NM_016616	1	18	11	+	37907304	37907500
326469389	chr7	37907370	37907532	37907395	37907506	TXNDC3	NM_016616	1	18	11	+	37907304	37907500
326639133	chr7	37916372	37916586	37916397	37916558	TXNDC3	NM_016616	1	18	12	+	37916434	37916609
326640262	chr7	37916513	37916734	37916538	37916705	TXNDC3	NM_016616	1	18	12	+	37916434	37916609
328255836	chr7	37923802	37923989	37923829	37923962	TXNDC3	NM_016616	1	18	13	+	37923905	37924049
328257664	chr7	37923935	37924136	37923963	37924108	TXNDC3	NM_016616	1	18	13	+	37923905	37924049
328268305	chr7	37924696	37924888	37924724	37924860	TXNDC3	NM_016616	1	18	14	+	37924747	37924854
327069070	chr7	37927737	37927960	37927762	37927935	TXNDC3	NM_016616	1	18	15	+	37927879	37928030
327076304	chr7	37927916	37928124	37927936	37928097	TXNDC3	NM_016616	1	18	15	+	37927879	37928030
327996565	chr7	37934018	37934162	37934044	37934131	TXNDC3	NM_016616	1	18	16	+	37934068	37934212
327996834	chr7	37934125	37934348	37934152	37934320	TXNDC3	NM_016616	1	18	16	+	37934068	37934212
326764729	chr7	37936386	37936603	37936409	37936580	TXNDC3	NM_016616	1	18	17	+	37936472	37936709
326783746	chr7	37936556	37936775	37936581	37936753	TXNDC3	NM_016616	1	18	17	+	37936472	37936709
327698456	chr11	88911094	88911317	88911116	88911295	TYR	NM_000372	1	5	1	+	88911040	88911940
327716940	chr11	88911272	88911451	88911296	88911430	TYR	NM_000372	1	5	1	+	88911040	88911940
327733337	chr11	88911404	88911627	88911429	88911603	TYR	NM_000372	1	5	1	+	88911040	88911940
328478416	chr11	88911580	88911801	88911604	88911777	TYR	NM_000372	1	5	1	+	88911040	88911940
328485207	chr11	88911758	88911975	88911778	88911947	TYR	NM_000372	1	5	1	+	88911040	88911940
328294643	chr11	88924262	88924391	88924286	88924370	TYR	NM_000372	1	5	2	+	88924370	88924586
328304872	chr11	88924343	88924567	88924371	88924544	TYR	NM_000372	1	5	2	+	88924370	88924586
328270233	chr11	88960823	88961026	88960849	88961006	TYR	NM_000372	1	5	3	+	88960991	88961138
328270927	chr11	88960979	88961190	88961007	88961162	TYR	NM_000372	1	5	3	+	88960991	88961138
328149343	chr11	89017823	89017999	89017851	89017972	TYR	NM_000372	1	5	4	+	89017941	89018122
328149692	chr11	89017960	89018167	89017977	89018139	TYR	NM_000372	1	5	4	+	89017941	89018122

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328466719	chr11	89028253	89028406	89028278	89028389	TYR	NM_000372	1	5	5	+	89028311	89028927
328158355	chr11	17565699	17565897	17565719	17565879	USH1C	NM_005709	1	21	1	-	17565819	17565963
327117373	chr11	17554706	17554900	17554727	17554874	USH1C	NM_005709	1	21	2	-	17554802	17554869
328003793	chr11	17552894	17553112	17552913	17553094	USH1C	NM_005709	1	21	3	-	17552946	17553089
326630983	chr11	17552676	17552863	17552694	17552844	USH1C	NM_005709	1	21	4	-	17552701	17552839
327822070	chr11	17548750	17548907	17548768	17548889	USH1C	NM_005709	1	21	5	-	17548770	17548878
327057196	chr11	17548419	17548614	17548440	17548593	USH1C	NM_005709	1	21	6	-	17548563	17548587
327986997	chr11	17548201	17548393	17548222	17548368	USH1C	NM_005709	1	21	7	-	17548300	17548357
327787735	chr11	17547794	17548018	17547815	17547993	USH1C	NM_005709	1	21	8	-	17547894	17547988
327393407	chr11	17545894	17546118	17545916	17546096	USH1C	NM_005709	1	21	9	-	17545998	17546082
327331849	chr11	17544922	17545061	17544942	17545033	USH1C	NM_005709	1	21	10	-	17544966	17545025
327601892	chr11	17544678	17544867	17544700	17544847	USH1C	NM_005709	1	21	11	-	17544758	17544814
326776971	chr11	17544187	17544408	17544209	17544387	USH1C	NM_005709	1	21	12	-	17544331	17544473
326778981	chr11	17544355	17544568	17544378	17544547	USH1C	NM_005709	1	21	12	-	17544331	17544473
327982334	chr11	17542784	17542987	17542807	17542963	USH1C	NM_005709	1	21	13	-	17542893	17542958
327040782	chr11	17542364	17542575	17542389	17542554	USH1C	NM_005709	1	21	14	-	17542417	17542541
327329791	chr11	17538830	17539053	17538849	17539030	USH1C	NM_005709	1	21	15	-	17538948	17539021
328164846	chr11	17523396	17523567	17523417	17523546	USH1C	NM_005709	1	21	16	-	17523486	17523527
327758215	chr11	17522931	17523114	17522952	17523091	USH1C	NM_005709	1	21	17	-	17523029	17523082
327561651	chr11	17522507	17522725	17522528	17522702	USH1C	NM_005709	1	21	18	-	17522598	17522697
327024814	chr11	17519624	17519848	17519646	17519828	USH1C	NM_005709	1	21	19	-	17519709	17519818
327951096	chr11	17518201	17518410	17518223	17518389	USH1C	NM_005709	1	21	20	-	17518305	17518360
327180831	chr11	17515746	17515957	17515769	17515936	USH1C	NM_005709	1	21	21	-	17515442	17515923
328158355	chr11	17565699	17565897	17565719	17565879	USH1C	NM_153676	2	27	1	-	17565819	17565963
327117373	chr11	17554706	17554900	17554727	17554874	USH1C	NM_153676	2	27	2	-	17554802	17554869
328003793	chr11	17552894	17553112	17552913	17553094	USH1C	NM_153676	2	27	3	-	17552946	17553089
326630983	chr11	17552676	17552863	17552694	17552844	USH1C	NM_153676	2	27	4	-	17552701	17552839
327822070	chr11	17548750	17548907	17548768	17548889	USH1C	NM_153676	2	27	5	-	17548770	17548878
327057196	chr11	17548419	17548614	17548440	17548593	USH1C	NM_153676	2	27	6	-	17548563	17548587
327986997	chr11	17548201	17548393	17548222	17548368	USH1C	NM_153676	2	27	7	-	17548300	17548357
327787735	chr11	17547794	17548018	17547815	17547993	USH1C	NM_153676	2	27	8	-	17547894	17547988
327393407	chr11	17545894	17546118	17545916	17546096	USH1C	NM_153676	2	27	9	-	17545998	17546082
327331849	chr11	17544922	17545061	17544942	17545033	USH1C	NM_153676	2	27	10	-	17544966	17545025
327601892	chr11	17544678	17544867	17544700	17544847	USH1C	NM_153676	2	27	11	-	17544758	17544814
326776971	chr11	17544187	17544408	17544209	17544387	USH1C	NM_153676	2	27	12	-	17544331	17544473
326778981	chr11	17544355	17544568	17544378	17544547	USH1C	NM_153676	2	27	12	-	17544331	17544473
327982334	chr11	17542784	17542987	17542807	17542963	USH1C	NM_153676	2	27	13	-	17542893	17542958
327040782	chr11	17542364	17542575	17542389	17542554	USH1C	NM_153676	2	27	14	-	17542417	17542541
328210245	chr11	17537655	17537879	17537678	17537851	USH1C	NM_153676	2	27	15	-	17537788	17537837
326625185	chr11	17533330	17533499	17533352	17533475	USH1C	NM_153676	2	27	16	-	17533449	17533601
326628301	chr11	17533456	17533654	17533476	17533626	USH1C	NM_153676	2	27	16	-	17533449	17533601

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326855910	chr11	17531893	17532117	17531916	17532094	USH1C	NM_153676	2	27	17	-	17531952	17532068
327791842	chr11	17530847	17530997	17530869	17530977	USH1C	NM_153676	2	27	18	-	17530903	17531385
327794668	chr11	17530950	17531172	17530971	17531150	USH1C	NM_153676	2	27	18	-	17530903	17531385
327797967	chr11	17531126	17531300	17531146	17531281	USH1C	NM_153676	2	27	18	-	17530903	17531385
327799048	chr11	17531255	17531431	17531282	17531403	USH1C	NM_153676	2	27	18	-	17530903	17531385
326507065	chr11	17527330	17527528	17527353	17527504	USH1C	NM_153676	2	27	19	-	17527377	17527496
326985972	chr11	17526091	17526299	17526112	17526274	USH1C	NM_153676	2	27	20	-	17526194	17526244
328164846	chr11	17523396	17523567	17523417	17523546	USH1C	NM_153676	2	27	21	-	17523486	17523527
327758215	chr11	17522931	17523114	17522952	17523091	USH1C	NM_153676	2	27	22	-	17523029	17523082
327561651	chr11	17522507	17522725	17522528	17522702	USH1C	NM_153676	2	27	23	-	17522598	17522697
327024814	chr11	17519624	17519848	17519646	17519828	USH1C	NM_153676	2	27	24	-	17519709	17519818
327951096	chr11	17518201	17518410	17518223	17518389	USH1C	NM_153676	2	27	25	-	17518305	17518360
327238087	chr11	17517054	17517259	17517072	17517235	USH1C	NM_153676	2	27	26	-	17517116	17517224
327180831	chr11	17515746	17515957	17515769	17515936	USH1C	NM_153676	2	27	27	-	17515442	17515923
327178801	chr1	216595157	216595359	216595183	216595337	USH2A	NM_007123	1	21	2	-	216595194	216595882
327199910	chr1	216595318	216595538	216595338	216595516	USH2A	NM_007123	1	21	2	-	216595194	216595882
327217447	chr1	216595495	216595715	216595517	216595689	USH2A	NM_007123	1	21	2	-	216595194	216595882
326945226	chr1	216591754	216591938	216591779	216591910	USH2A	NM_007123	1	21	3	-	216591856	216592021
326955211	chr1	216591885	216592051	216591911	216592027	USH2A	NM_007123	1	21	3	-	216591856	216592021
328231341	chr1	216538293	216538427	216538321	216538400	USH2A	NM_007123	1	21	4	-	216538295	216538427
328233132	chr1	216538379	216538542	216538401	216538514	USH2A	NM_007123	1	21	4	-	216538295	216538427
327097914	chr1	216500875	216501052	216500902	216501025	USH2A	NM_007123	1	21	5	-	216500933	216500996
326549028	chr1	216498623	216498820	216498651	216498794	USH2A	NM_007123	1	21	6	-	216498647	216498941
326556784	chr1	216498774	216498972	216498795	216498948	USH2A	NM_007123	1	21	6	-	216498647	216498941
328445985	chr1	216497403	216497560	216497425	216497532	USH2A	NM_007123	1	21	7	-	216497510	216497694
328450326	chr1	216497509	216497682	216497533	216497654	USH2A	NM_007123	1	21	7	-	216497510	216497694
328451678	chr1	216497628	216497848	216497656	216497821	USH2A	NM_007123	1	21	7	-	216497510	216497694
326605171	chr1	216496727	216496948	216496749	216496926	USH2A	NM_007123	1	21	8	-	216496816	216497037
326613137	chr1	216496902	216497111	216496927	216497083	USH2A	NM_007123	1	21	8	-	216496816	216497037
327786822	chr1	216495128	216495254	216495161	216495233	USH2A	NM_007123	1	21	9	-	216495225	216495318
327786833	chr1	216495223	216495355	216495247	216495332	USH2A	NM_007123	1	21	9	-	216495225	216495318
327142229	chr1	216465480	216465621	216465505	216465600	USH2A	NM_007123	1	21	10	-	216465517	216465712
327146935	chr1	216465576	216465798	216465601	216465770	USH2A	NM_007123	1	21	10	-	216465517	216465712
327374976	chr1	216462563	216462785	216462589	216462757	USH2A	NM_007123	1	21	11	-	216462622	216462752
327286869	chr1	216424210	216424387	216424238	216424360	USH2A	NM_007123	1	21	12	-	216424245	216424440
327294373	chr1	216424340	216424518	216424361	216424490	USH2A	NM_007123	1	21	12	-	216424245	216424440
327120629	chr1	216420404	216420615	216420427	216420589	USH2A	NM_007123	1	21	13	-	216419927	216420568
328126846	chr1	216419879	216420093	216419905	216420072	USH2A	NM_007123	1	21	13	-	216419927	216420568
328137348	chr1	216420045	216420269	216420073	216420244	USH2A	NM_007123	1	21	13	-	216419927	216420568
328148212	chr1	216420223	216420446	216420245	216420426	USH2A	NM_007123	1	21	13	-	216419927	216420568
327036164	chr1	216405216	216405440	216405241	216405418	USH2A	NM_007123	1	21	14	-	216405295	216405478

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327039688	chr1	216405391	216405592	216405419	216405565	USH2A	NM_007123	1	21	14	-	216405295	216405478
327864450	chr1	216390701	216390837	216390722	216390815	USH2A	NM_007123	1	21	15	-	216390729	216390892
327869260	chr1	216390791	216390990	216390816	216390963	USH2A	NM_007123	1	21	15	-	216390729	216390892
326567401	chr1	216380520	216380661	216380546	216380634	USH2A	NM_007123	1	21	16	-	216380615	216380773
326569443	chr1	216380609	216380829	216380635	216380801	USH2A	NM_007123	1	21	16	-	216380615	216380773
326460882	chr1	216372882	216373093	216372908	216373072	USH2A	NM_007123	1	21	17	-	216372969	216373463
326476254	chr1	216373027	216373238	216373053	216373213	USH2A	NM_007123	1	21	17	-	216372969	216373463
326490267	chr1	216373185	216373385	216373207	216373361	USH2A	NM_007123	1	21	17	-	216372969	216373463
326494470	chr1	216373338	216373541	216373361	216373512	USH2A	NM_007123	1	21	17	-	216372969	216373463
327646398	chr1	216371595	216371811	216371623	216371783	USH2A	NM_007123	1	21	18	-	216371657	216371926
327652758	chr1	216371758	216371982	216371783	216371955	USH2A	NM_007123	1	21	18	-	216371657	216371926
328246168	chr1	216369735	216369942	216369758	216369916	USH2A	NM_007123	1	21	19	-	216369895	216370064
328253266	chr1	216369894	216370113	216369917	216370087	USH2A	NM_007123	1	21	19	-	216369895	216370064
328370853	chr1	216363423	216363616	216363450	216363594	USH2A	NM_007123	1	21	20	-	216363565	216363709
328373974	chr1	216363575	216363783	216363595	216363755	USH2A	NM_007123	1	21	20	-	216363565	216363709
327536863	chr1	216348544	216348707	216348569	216348683	USH2A	NM_007123	1	21	21	-	216347292	216348824
327546811	chr1	216348660	216348882	216348684	216348854	USH2A	NM_007123	1	21	21	-	216347292	216348824
327178801	chr1	216595157	216595359	216595183	216595337	USH2A	NM_206933	2	72	2	-	216595194	216595882
327199910	chr1	216595318	216595538	216595338	216595516	USH2A	NM_206933	2	72	2	-	216595194	216595882
327217447	chr1	216595495	216595715	216595517	216595689	USH2A	NM_206933	2	72	2	-	216595194	216595882
326945226	chr1	216591754	216591938	216591779	216591910	USH2A	NM_206933	2	72	3	-	216591856	216592021
326955211	chr1	216591885	216592051	216591911	216592027	USH2A	NM_206933	2	72	3	-	216591856	216592021
328231341	chr1	216538293	216538427	216538321	216538400	USH2A	NM_206933	2	72	4	-	216538295	216538427
328233132	chr1	216538379	216538542	216538401	216538514	USH2A	NM_206933	2	72	4	-	216538295	216538427
327097914	chr1	216500875	216501052	216500902	216501025	USH2A	NM_206933	2	72	5	-	216500933	216500996
326549028	chr1	216498623	216498820	216498651	216498794	USH2A	NM_206933	2	72	6	-	216498647	216498941
326556784	chr1	216498774	216498972	216498795	216498948	USH2A	NM_206933	2	72	6	-	216498647	216498941
328445985	chr1	216497403	216497560	216497425	216497532	USH2A	NM_206933	2	72	7	-	216497510	216497694
328450326	chr1	216497509	216497682	216497533	216497654	USH2A	NM_206933	2	72	7	-	216497510	216497694
328451678	chr1	216497628	216497848	216497656	216497821	USH2A	NM_206933	2	72	7	-	216497510	216497694
326605171	chr1	216496727	216496948	216496749	216496926	USH2A	NM_206933	2	72	8	-	216496816	216497037
326613137	chr1	216496902	216497111	216496927	216497083	USH2A	NM_206933	2	72	8	-	216496816	216497037
327786822	chr1	216495128	216495254	216495161	216495233	USH2A	NM_206933	2	72	9	-	216495225	216495318
327786833	chr1	216495223	216495355	216495247	216495332	USH2A	NM_206933	2	72	9	-	216495225	216495318
327142229	chr1	216465480	216465621	216465505	216465600	USH2A	NM_206933	2	72	10	-	216465517	216465712
327146935	chr1	216465576	216465798	216465601	216465770	USH2A	NM_206933	2	72	10	-	216465517	216465712
327374976	chr1	216462563	216462785	216462589	216462757	USH2A	NM_206933	2	72	11	-	216462622	216462752
327286869	chr1	216424210	216424387	216424238	216424360	USH2A	NM_206933	2	72	12	-	216424245	216424440
327294373	chr1	216424340	216424518	216424361	216424490	USH2A	NM_206933	2	72	12	-	216424245	216424440
327120629	chr1	216420404	216420615	216420427	216420589	USH2A	NM_206933	2	72	13	-	216419927	216420568
328126846	chr1	216419879	216420093	216419905	216420072	USH2A	NM_206933	2	72	13	-	216419927	216420568

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328137348	chr1	216420045	216420269	216420073	216420244	USH2A	NM_206933	2	72	13	-	216419927	216420568
328148212	chr1	216420223	216420446	216420245	216420426	USH2A	NM_206933	2	72	13	-	216419927	216420568
327036164	chr1	216405216	216405440	216405241	216405418	USH2A	NM_206933	2	72	14	-	216405295	216405478
327039688	chr1	216405391	216405592	216405419	216405565	USH2A	NM_206933	2	72	14	-	216405295	216405478
327864450	chr1	216390701	216390837	216390722	216390815	USH2A	NM_206933	2	72	15	-	216390729	216390892
327869260	chr1	216390791	216390990	216390816	216390963	USH2A	NM_206933	2	72	15	-	216390729	216390892
326567401	chr1	216380520	216380661	216380546	216380634	USH2A	NM_206933	2	72	16	-	216380615	216380773
326569443	chr1	216380609	216380829	216380635	216380801	USH2A	NM_206933	2	72	16	-	216380615	216380773
326460882	chr1	216372882	216373093	216372908	216373072	USH2A	NM_206933	2	72	17	-	216372969	216373463
326476254	chr1	216373027	216373238	216373053	216373213	USH2A	NM_206933	2	72	17	-	216372969	216373463
326490267	chr1	216373185	216373385	216373207	216373361	USH2A	NM_206933	2	72	17	-	216372969	216373463
326494470	chr1	216373338	216373541	216373361	216373512	USH2A	NM_206933	2	72	17	-	216372969	216373463
327646398	chr1	216371595	216371811	216371623	216371783	USH2A	NM_206933	2	72	18	-	216371657	216371926
327652758	chr1	216371758	216371982	216371783	216371955	USH2A	NM_206933	2	72	18	-	216371657	216371926
328246168	chr1	216369735	216369942	216369758	216369916	USH2A	NM_206933	2	72	19	-	216369895	216370064
328253266	chr1	216369894	216370113	216369917	216370087	USH2A	NM_206933	2	72	19	-	216369895	216370064
328370853	chr1	216363423	216363616	216363450	216363594	USH2A	NM_206933	2	72	20	-	216363565	216363709
328373974	chr1	216363575	216363783	216363595	216363755	USH2A	NM_206933	2	72	20	-	216363565	216363709
327536863	chr1	216348544	216348707	216348569	216348683	USH2A	NM_206933	2	72	21	-	216348594	216348824
327546811	chr1	216348660	216348882	216348684	216348854	USH2A	NM_206933	2	72	21	-	216348594	216348824
326592393	chr1	216270439	216270574	216270467	216270550	USH2A	NM_206933	2	72	22	-	216270425	216270555
326597329	chr1	216270529	216270695	216270551	216270669	USH2A	NM_206933	2	72	22	-	216270425	216270555
327664856	chr1	216262292	216262444	216262316	216262416	USH2A	NM_206933	2	72	23	-	216262355	216262481
327666438	chr1	216262389	216262605	216262417	216262578	USH2A	NM_206933	2	72	23	-	216262355	216262481
328301083	chr1	216259917	216260095	216259944	216260074	USH2A	NM_206933	2	72	24	-	216260061	216260162
328302045	chr1	216260050	216260197	216260074	216260171	USH2A	NM_206933	2	72	24	-	216260061	216260162
327299330	chr1	216257929	216258136	216257958	216258113	USH2A	NM_206933	2	72	25	-	216258040	216258219
327302963	chr1	216258089	216258312	216258114	216258284	USH2A	NM_206933	2	72	25	-	216258040	216258219
327994420	chr1	216256705	216256897	216256730	216256869	USH2A	NM_206933	2	72	26	-	216256798	216256928
327996620	chr1	216256839	216257036	216256867	216257012	USH2A	NM_206933	2	72	26	-	216256798	216256928
327070226	chr1	216251364	216251578	216251388	216251553	USH2A	NM_206933	2	72	27	-	216251431	216251704
327079807	chr1	216251531	216251755	216251554	216251727	USH2A	NM_206933	2	72	27	-	216251431	216251704
326887206	chr1	216246288	216246512	216246314	216246490	USH2A	NM_206933	2	72	28	-	216246439	216246642
326893980	chr1	216246469	216246678	216246491	216246651	USH2A	NM_206933	2	72	28	-	216246439	216246642
327796382	chr1	216246193	216246376	216246217	216246350	USH2A	NM_206933	2	72	29	-	216246231	216246311
328423185	chr1	216243274	216243479	216243296	216243453	USH2A	NM_206933	2	72	30	-	216243443	216243634
328426529	chr1	216243430	216243559	216243454	216243531	USH2A	NM_206933	2	72	30	-	216243443	216243634
328437214	chr1	216243505	216243676	216243532	216243648	USH2A	NM_206933	2	72	30	-	216243443	216243634
327325072	chr1	216221797	216222020	216221823	216221999	USH2A	NM_206933	2	72	31	-	216221876	216221989
327470601	chr1	216219743	216219929	216219770	216219908	USH2A	NM_206933	2	72	32	-	216219773	216219934
327476478	chr1	216219883	216220094	216219905	216220067	USH2A	NM_206933	2	72	32	-	216219773	216219934

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327019393	chr1	216173667	216173850	216173687	216173828	USH2A	NM_206933	2	72	33	-	216173745	216173904
327027961	chr1	216173808	216173989	216173829	216173961	USH2A	NM_206933	2	72	33	-	216173745	216173904
328405844	chr1	216172176	216172377	216172199	216172350	USH2A	NM_206933	2	72	34	-	216172229	216172400
328406936	chr1	216172273	216172497	216172301	216172470	USH2A	NM_206933	2	72	34	-	216172229	216172400
327791907	chr1	216166277	216166402	216166300	216166377	USH2A	NM_206933	2	72	35	-	216166362	216166509
327793880	chr1	216166351	216166556	216166378	216166530	USH2A	NM_206933	2	72	35	-	216166362	216166509
327062782	chr1	216143838	216144041	216143864	216144015	USH2A	NM_206933	2	72	36	-	216143967	216144118
327073046	chr1	216143995	216144201	216144016	216144174	USH2A	NM_206933	2	72	36	-	216143967	216144118
327245340	chr1	216138502	216138711	216138521	216138686	USH2A	NM_206933	2	72	37	-	216138659	216138821
327250811	chr1	216138660	216138884	216138687	216138856	USH2A	NM_206933	2	72	37	-	216138659	216138821
326771643	chr1	216107825	216108005	216107853	216107977	USH2A	NM_206933	2	72	38	-	216107958	216108137
326774488	chr1	216107957	216108105	216107978	216108081	USH2A	NM_206933	2	72	38	-	216107958	216108137
326779272	chr1	216108061	216108275	216108082	216108247	USH2A	NM_206933	2	72	38	-	216107958	216108137
328165894	chr1	216074062	216074285	216074086	216074257	USH2A	NM_206933	2	72	39	-	216074097	216074247
326499211	chr1	216073319	216073540	216073344	216073514	USH2A	NM_206933	2	72	40	-	216073417	216073559
326507816	chr1	216073489	216073706	216073515	216073678	USH2A	NM_206933	2	72	40	-	216073417	216073559
327886126	chr1	216062226	216062443	216062250	216062417	USH2A	NM_206933	2	72	41	-	216061768	216062396
327888073	chr1	216061728	216061948	216061754	216061921	USH2A	NM_206933	2	72	41	-	216061768	216062396
327902559	chr1	216061894	216062110	216061922	216062089	USH2A	NM_206933	2	72	41	-	216061768	216062396
327913828	chr1	216062056	216062275	216062084	216062249	USH2A	NM_206933	2	72	41	-	216061768	216062396
328414947	chr1	216052031	216052255	216052055	216052233	USH2A	NM_206933	2	72	42	-	216052106	216052440
328420650	chr1	216052211	216052379	216052234	216052354	USH2A	NM_206933	2	72	42	-	216052106	216052440
328425708	chr1	216052333	216052482	216052355	216052454	USH2A	NM_206933	2	72	42	-	216052106	216052440
326571807	chr1	216051033	216051253	216051060	216051229	USH2A	NM_206933	2	72	43	-	216051100	216051222
328115533	chr1	216040178	216040388	216040204	216040367	USH2A	NM_206933	2	72	44	-	216040349	216040512
328119468	chr1	216040344	216040486	216040367	216040464	USH2A	NM_206933	2	72	44	-	216040349	216040512
328121409	chr1	216040445	216040614	216040465	216040586	USH2A	NM_206933	2	72	44	-	216040349	216040512
327040244	chr1	216019055	216019259	216019081	216019231	USH2A	NM_206933	2	72	45	-	216019166	216019375
327047938	chr1	216019208	216019407	216019232	216019380	USH2A	NM_206933	2	72	45	-	216019166	216019375
326440772	chr1	216017490	216017696	216017517	216017673	USH2A	NM_206933	2	72	46	-	216017636	216017838
326456921	chr1	216017652	216017874	216017674	216017846	USH2A	NM_206933	2	72	46	-	216017636	216017838
326716319	chr1	216011148	216011371	216011172	216011346	USH2A	NM_206933	2	72	47	-	216011333	216011445
326721485	chr1	216011321	216011522	216011347	216011495	USH2A	NM_206933	2	72	47	-	216011333	216011445
327555936	chr1	215990283	215990459	215990309	215990433	USH2A	NM_206933	2	72	48	-	215990339	215990537
327558349	chr1	215990411	215990617	215990434	215990589	USH2A	NM_206933	2	72	48	-	215990339	215990537
327803099	chr1	215986970	215987180	215986996	215987153	USH2A	NM_206933	2	72	49	-	215987078	215987246
327820506	chr1	215987134	215987356	215987154	215987328	USH2A	NM_206933	2	72	49	-	215987078	215987246
327141073	chr1	215972183	215972398	215972210	215972377	USH2A	NM_206933	2	72	50	-	215972249	215972467
327154185	chr1	215972356	215972562	215972378	215972535	USH2A	NM_206933	2	72	50	-	215972249	215972467
327386757	chr1	215963373	215963513	215963395	215963486	USH2A	NM_206933	2	72	51	-	215963401	215963624
327392837	chr1	215963463	215963684	215963487	215963656	USH2A	NM_206933	2	72	51	-	215963401	215963624

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326812376	chr1	215959949	215960125	215959971	215960102	USH2A	NM_206933	2	72	52	-	215960012	215960216
326846604	chr1	215960080	215960295	215960103	215960267	USH2A	NM_206933	2	72	52	-	215960012	215960216
326922409	chr1	215955978	215956202	215956006	215956180	USH2A	NM_206933	2	72	53	-	215956080	215956277
326923627	chr1	215956159	215956283	215956181	215956261	USH2A	NM_206933	2	72	53	-	215956080	215956277
328432427	chr1	215955243	215955463	215955266	215955436	USH2A	NM_206933	2	72	54	-	215955384	215955538
328440982	chr1	215955412	215955630	215955437	215955603	USH2A	NM_206933	2	72	54	-	215955384	215955538
327544264	chr1	215953037	215953246	215953059	215953224	USH2A	NM_206933	2	72	55	-	215953185	215953383
327564140	chr1	215953204	215953428	215953225	215953400	USH2A	NM_206933	2	72	55	-	215953185	215953383
328395149	chr1	215939942	215940161	215939970	215940135	USH2A	NM_206933	2	72	56	-	215940023	215940130
328463489	chr1	215932914	215933109	215932938	215933083	USH2A	NM_206933	2	72	57	-	215933002	215933185
328469448	chr1	215933058	215933255	215933084	215933228	USH2A	NM_206933	2	72	57	-	215933002	215933185
328161654	chr1	215931807	215932017	215931834	215931990	USH2A	NM_206933	2	72	58	-	215931937	215932094
328163685	chr1	215931937	215932145	215931965	215932123	USH2A	NM_206933	2	72	58	-	215931937	215932094
328292438	chr1	215916490	215916695	215916511	215916667	USH2A	NM_206933	2	72	59	-	215916519	215916677
328293814	chr1	215916641	215916850	215916666	215916825	USH2A	NM_206933	2	72	59	-	215916519	215916677
327967650	chr1	215914662	215914886	215914691	215914861	USH2A	NM_206933	2	72	60	-	215914717	215914879
326906096	chr1	215901205	215901427	215901230	215901406	USH2A	NM_206933	2	72	61	-	215901372	215901726
326916172	chr1	215901386	215901608	215901407	215901587	USH2A	NM_206933	2	72	61	-	215901372	215901726
326948126	chr1	215901563	215901775	215901588	215901753	USH2A	NM_206933	2	72	61	-	215901372	215901726
327848302	chr1	215853426	215853650	215853452	215853623	USH2A	NM_206933	2	72	62	-	215853491	215853718
327853848	chr1	215853600	215853795	215853624	215853767	USH2A	NM_206933	2	72	62	-	215853491	215853718
328020912	chr1	215847373	215847593	215847393	215847568	USH2A	NM_206933	2	72	63	-	215847442	215848958
328025938	chr1	215847971	215848194	215847991	215848173	USH2A	NM_206933	2	72	63	-	215847442	215848958
328029631	chr1	215848477	215848694	215848501	215848671	USH2A	NM_206933	2	72	63	-	215847442	215848958
328032968	chr1	215847542	215847753	215847569	215847731	USH2A	NM_206933	2	72	63	-	215847442	215848958
328043179	chr1	215848149	215848363	215848169	215848335	USH2A	NM_206933	2	72	63	-	215847442	215848958
328049808	chr1	215848651	215848820	215848672	215848799	USH2A	NM_206933	2	72	63	-	215847442	215848958
328049885	chr1	215847711	215847845	215847732	215847819	USH2A	NM_206933	2	72	63	-	215847442	215848958
328057086	chr1	215848307	215848523	215848336	215848500	USH2A	NM_206933	2	72	63	-	215847442	215848958
328057130	chr1	215847796	215848017	215847820	215847990	USH2A	NM_206933	2	72	63	-	215847442	215848958
328063312	chr1	215848768	215848990	215848789	215848964	USH2A	NM_206933	2	72	63	-	215847442	215848958
326591178	chr1	215844262	215844465	215844282	215844437	USH2A	NM_206933	2	72	64	-	215844314	215844635
326605692	chr1	215844405	215844608	215844434	215844588	USH2A	NM_206933	2	72	64	-	215844314	215844635
326610820	chr1	215844565	215844712	215844588	215844687	USH2A	NM_206933	2	72	64	-	215844314	215844635
327372344	chr1	215823900	215824055	215823925	215824031	USH2A	NM_206933	2	72	65	-	215823934	215824143
327376580	chr1	215824011	215824179	215824032	215824151	USH2A	NM_206933	2	72	65	-	215823934	215824143
327756169	chr1	215821822	215822025	215821850	215822003	USH2A	NM_206933	2	72	66	-	215821870	215822108
327765902	chr1	215821981	215822199	215822002	215822175	USH2A	NM_206933	2	72	66	-	215821870	215822108
327682308	chr1	215820835	215821026	215820857	215821004	USH2A	NM_206933	2	72	67	-	215820864	215821072
327690105	chr1	215820984	215821108	215821005	215821085	USH2A	NM_206933	2	72	67	-	215820864	215821072
326513356	chr1	215813790	215814001	215813817	215813981	USH2A	NM_206933	2	72	68	-	215813900	215814076

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326525765	chr1	215813960	215814132	215813982	215814109	USH2A	NM_206933	2	72	68	-	215813900	215814076
327787188	chr1	215812439	215812636	215812467	215812608	USH2A	NM_206933	2	72	69	-	215812497	215812580
327350217	chr1	215807710	215807934	215807738	215807912	USH2A	NM_206933	2	72	70	-	215807801	215808045
327359301	chr1	215807886	215808108	215807913	215808083	USH2A	NM_206933	2	72	70	-	215807801	215808045
327936002	chr1	215802014	215802232	215802039	215802205	USH2A	NM_206933	2	72	71	-	215802156	215802377
327953130	chr1	215802185	215802408	215802206	215802382	USH2A	NM_206933	2	72	71	-	215802156	215802377
327155762	chr1	215799029	215799183	215799055	215799159	USH2A	NM_206933	2	72	72	-	215796236	215799212
327157939	chr1	215799138	215799359	215799160	215799337	USH2A	NM_206933	2	72	72	-	215796236	215799212
327644156	chr10	75757911	75758053	75757933	75758031	VCL	NM_003373	1	21	1	+	75757872	75758133
327644620	chr10	75758013	75758138	75758031	75758121	VCL	NM_003373	1	21	1	+	75757872	75758133
327185468	chr10	75802659	75802868	75802692	75802843	VCL	NM_003373	1	21	2	+	75802841	75802911
327185611	chr10	75802833	75802983	75802860	75802952	VCL	NM_003373	1	21	2	+	75802841	75802911
327025644	chr10	75830388	75830611	75830408	75830583	VCL	NM_003373	1	21	3	+	75830428	75830578
326824613	chr10	75830671	75830894	75830695	75830868	VCL	NM_003373	1	21	4	+	75830733	75830841
326701550	chr10	75832432	75832642	75832452	75832615	VCL	NM_003373	1	21	5	+	75832488	75832610
327790105	chr10	75834355	75834562	75834383	75834536	VCL	NM_003373	1	21	6	+	75834501	75834661
327790236	chr10	75834535	75834696	75834559	75834669	VCL	NM_003373	1	21	6	+	75834501	75834661
328416170	chr10	75842137	75842340	75842165	75842312	VCL	NM_003373	1	21	7	+	75842212	75842302
328242879	chr10	75842969	75843181	75842991	75843157	VCL	NM_003373	1	21	8	+	75843124	75843271
328250076	chr10	75843137	75843307	75843158	75843284	VCL	NM_003373	1	21	8	+	75843124	75843271
326454759	chr10	75848913	75849135	75848937	75849113	VCL	NM_003373	1	21	9	+	75848954	75849107
327996487	chr10	75849724	75849932	75849751	75849907	VCL	NM_003373	1	21	10	+	75849781	75849956
327999272	chr10	75849881	75850097	75849908	75850069	VCL	NM_003373	1	21	10	+	75849781	75849956
327959790	chr10	75853990	75854211	75854013	75854189	VCL	NM_003373	1	21	11	+	75854029	75854219
327966625	chr10	75854171	75854297	75854190	75854272	VCL	NM_003373	1	21	11	+	75854029	75854219
328110604	chr10	75855337	75855498	75855357	75855475	VCL	NM_003373	1	21	12	+	75855414	75855613
328117793	chr10	75855450	75855674	75855475	75855648	VCL	NM_003373	1	21	12	+	75855414	75855613
328356800	chr10	75856908	75857123	75856936	75857097	VCL	NM_003373	1	21	13	+	75856962	75857090
326988697	chr10	75860531	75860754	75860552	75860727	VCL	NM_003373	1	21	14	+	75860706	75860855
327006032	chr10	75860704	75860887	75860728	75860860	VCL	NM_003373	1	21	14	+	75860706	75860855
327202891	chr10	75863536	75863750	75863557	75863722	VCL	NM_003373	1	21	15	+	75863578	75863686
326455887	chr10	75864675	75864855	75864701	75864831	VCL	NM_003373	1	21	16	+	75864809	75865111
326473472	chr10	75864812	75865029	75864832	75865008	VCL	NM_003373	1	21	16	+	75864809	75865111
326487839	chr10	75864988	75865140	75865009	75865117	VCL	NM_003373	1	21	16	+	75864809	75865111
326827641	chr10	75866956	75867147	75866978	75867121	VCL	NM_003373	1	21	17	+	75866988	75867112
328338645	chr10	75868598	75868818	75868620	75868795	VCL	NM_003373	1	21	18	+	75868729	75868914
328346744	chr10	75868751	75868966	75868772	75868941	VCL	NM_003373	1	21	18	+	75868729	75868914
327094893	chr10	75873862	75874081	75873886	75874060	VCL	NM_003373	1	21	19	+	75873942	75874145
327110264	chr10	75874036	75874258	75874059	75874231	VCL	NM_003373	1	21	19	+	75873942	75874145
327271585	chr10	75874378	75874595	75874402	75874572	VCL	NM_003373	1	21	20	+	75874553	75874657
327283301	chr10	75874551	75874719	75874573	75874693	VCL	NM_003373	1	21	20	+	75874553	75874657

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
327245809	chr10	75877629	75877829	75877651	75877807	VCL	NM_003373	1	21	21	+	75877781	75879914
327263179	chr10	75877787	75877993	75877808	75877965	VCL	NM_003373	1	21	21	+	75877781	75879914
327644156	chr10	75757911	75758053	75757933	75758031	VCL	NM_014000	2	22	1	+	75757872	75758133
327644620	chr10	75758013	75758138	75758031	75758121	VCL	NM_014000	2	22	1	+	75757872	75758133
327185468	chr10	75802659	75802868	75802692	75802843	VCL	NM_014000	2	22	2	+	75802841	75802911
327185611	chr10	75802833	75802983	75802860	75802952	VCL	NM_014000	2	22	2	+	75802841	75802911
327025644	chr10	75830388	75830611	75830408	75830583	VCL	NM_014000	2	22	3	+	75830428	75830578
326824613	chr10	75830671	75830894	75830695	75830868	VCL	NM_014000	2	22	4	+	75830733	75830841
326701550	chr10	75832432	75832642	75832452	75832615	VCL	NM_014000	2	22	5	+	75832488	75832610
327790105	chr10	75834355	75834562	75834383	75834536	VCL	NM_014000	2	22	6	+	75834501	75834661
327790236	chr10	75834535	75834696	75834559	75834669	VCL	NM_014000	2	22	6	+	75834501	75834661
328416170	chr10	75842137	75842340	75842165	75842312	VCL	NM_014000	2	22	7	+	75842212	75842302
328242879	chr10	75842969	75843181	75842991	75843157	VCL	NM_014000	2	22	8	+	75843124	75843271
328250076	chr10	75843137	75843307	75843158	75843284	VCL	NM_014000	2	22	8	+	75843124	75843271
326454759	chr10	75848913	75849135	75848937	75849113	VCL	NM_014000	2	22	9	+	75848954	75849107
327996487	chr10	75849724	75849932	75849751	75849907	VCL	NM_014000	2	22	10	+	75849781	75849956
327999272	chr10	75849881	75850097	75849908	75850069	VCL	NM_014000	2	22	10	+	75849781	75849956
327959790	chr10	75853990	75854211	75854013	75854189	VCL	NM_014000	2	22	11	+	75854029	75854219
327966625	chr10	75854171	75854297	75854190	75854272	VCL	NM_014000	2	22	11	+	75854029	75854219
328110604	chr10	75855337	75855498	75855357	75855475	VCL	NM_014000	2	22	12	+	75855414	75855613
328117793	chr10	75855450	75855674	75855475	75855648	VCL	NM_014000	2	22	12	+	75855414	75855613
328356800	chr10	75856908	75857123	75856936	75857097	VCL	NM_014000	2	22	13	+	75856962	75857090
326988697	chr10	75860531	75860754	75860552	75860727	VCL	NM_014000	2	22	14	+	75860706	75860855
327006032	chr10	75860704	75860887	75860728	75860860	VCL	NM_014000	2	22	14	+	75860706	75860855
327202891	chr10	75863536	75863750	75863557	75863722	VCL	NM_014000	2	22	15	+	75863578	75863686
326455887	chr10	75864675	75864855	75864701	75864831	VCL	NM_014000	2	22	16	+	75864809	75865111
326473472	chr10	75864812	75865029	75864832	75865008	VCL	NM_014000	2	22	16	+	75864809	75865111
326487839	chr10	75864988	75865140	75865009	75865117	VCL	NM_014000	2	22	16	+	75864809	75865111
326827641	chr10	75866956	75867147	75866978	75867121	VCL	NM_014000	2	22	17	+	75866988	75867112
328338645	chr10	75868598	75868818	75868620	75868795	VCL	NM_014000	2	22	18	+	75868729	75868914
328346744	chr10	75868751	75868966	75868772	75868941	VCL	NM_014000	2	22	18	+	75868729	75868914
327102210	chr10	75871570	75871788	75871595	75871766	VCL	NM_014000	2	22	19	+	75871667	75871870
327116031	chr10	75871746	75871920	75871767	75871900	VCL	NM_014000	2	22	19	+	75871667	75871870
327094893	chr10	75873862	75874081	75873886	75874060	VCL	NM_014000	2	22	20	+	75873942	75874145
327110264	chr10	75874036	75874258	75874059	75874231	VCL	NM_014000	2	22	20	+	75873942	75874145
327271585	chr10	75874378	75874595	75874402	75874572	VCL	NM_014000	2	22	21	+	75874553	75874657
327283301	chr10	75874551	75874719	75874573	75874693	VCL	NM_014000	2	22	21	+	75874553	75874657
327245809	chr10	75877629	75877829	75877651	75877807	VCL	NM_014000	2	22	22	+	75877781	75879914
327263179	chr10	75877787	75877993	75877808	75877965	VCL	NM_014000	2	22	22	+	75877781	75879914
264379746	chr3	10183398	10183622	10183417	10183605	VHL	NM_000551	1	3	1	+	10183319	10183871
264380150	chr3	10183582	10183768	10183600	10183747	VHL	NM_000551	1	3	1	+	10183319	10183871

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
326808049	chr3	10183718	10183928	10183735	10183910	VHL	NM_000551	1	3	1	+	10183319	10183871
261851066	chr3	10188157	10188371	10188177	10188343	VHL	NM_000551	1	3	2	+	10188198	10188320
263306606	chr3	10191498	10191690	10191517	10191662	VHL	NM_000551	1	3	3	+	10191471	10195354
326904257	chr3	10191367	10191541	10191392	10191516	VHL	NM_000551	1	3	3	+	10191471	10195354
264379746	chr3	10183398	10183622	10183417	10183605	VHL	NM_198156	2	2	1	+	10183319	10183871
264380150	chr3	10183582	10183768	10183600	10183747	VHL	NM_198156	2	2	1	+	10183319	10183871
326808049	chr3	10183718	10183928	10183735	10183910	VHL	NM_198156	2	2	1	+	10183319	10183871
263306606	chr3	10191498	10191690	10191517	10191662	VHL	NM_198156	2	2	2	+	10191471	10195354
326904257	chr3	10191367	10191541	10191392	10191516	VHL	NM_198156	2	2	2	+	10191471	10195354
239690565	chrX	48542158	48542374	48542179	48542351	WAS	NM_000377	1	12	1	+	48542186	48542374
239707767	chrX	48542331	48542485	48542352	48542462	WAS	NM_000377	1	12	1	+	48542186	48542374
239105469	chrX	48542632	48542856	48542652	48542835	WAS	NM_000377	1	12	2	+	48542672	48542812
242072470	chrX	48543858	48544080	48543879	48544058	WAS	NM_000377	1	12	3	+	48543936	48544022
242743578	chrX	48544059	48544257	48544081	48544235	WAS	NM_000377	1	12	4	+	48544123	48544225
239500287	chrX	48544204	48544409	48544226	48544383	WAS	NM_000377	1	12	5	+	48544335	48544376
240629784	chrX	48544366	48544540	48544389	48544520	WAS	NM_000377	1	12	6	+	48544470	48544523
263059537	chrX	48545062	48545247	48545085	48545223	WAS	NM_000377	1	12	7	+	48545170	48545344
263098226	chrX	48545203	48545415	48545224	48545393	WAS	NM_000377	1	12	7	+	48545170	48545344
239902735	chrX	48546322	48546526	48546347	48546501	WAS	NM_000377	1	12	8	+	48546443	48546485
242193485	chrX	48546581	48546802	48546602	48546775	WAS	NM_000377	1	12	9	+	48546689	48546842
242231624	chrX	48546757	48546888	48546776	48546867	WAS	NM_000377	1	12	9	+	48546689	48546842
262397860	chrX	48546920	48547092	48546944	48547072	WAS	NM_000377	1	12	10	+	48547049	48547455
262401836	chrX	48547039	48547260	48547057	48547241	WAS	NM_000377	1	12	10	+	48547049	48547455
262403303	chrX	48547224	48547447	48547242	48547427	WAS	NM_000377	1	12	10	+	48547049	48547455
262407971	chrX	48547410	48547548	48547428	48547529	WAS	NM_000377	1	12	10	+	48547049	48547455
242465971	chrX	48547674	48547898	48547694	48547875	WAS	NM_000377	1	12	11	+	48547709	48547823
264807684	chrX	48549372	48549579	48549394	48549558	WAS	NM_000377	1	12	12	+	48549498	48549817
239085638	chr8	30915870	30916042	30915899	30916014	WRN	NM_000553	1	35	2	+	30915888	30916059
239088279	chr8	30915995	30916135	30916015	30916110	WRN	NM_000553	1	35	2	+	30915888	30916059
239999590	chr8	30916620	30916744	30916647	30916716	WRN	NM_000553	1	35	3	+	30916669	30916781
240007153	chr8	30916692	30916882	30916717	30916854	WRN	NM_000553	1	35	3	+	30916669	30916781
241445317	chr8	30921795	30921926	30921823	30921899	WRN	NM_000553	1	35	4	+	30921805	30921950
241452310	chr8	30921875	30922046	30921900	30922019	WRN	NM_000553	1	35	4	+	30921805	30921950
239080303	chr8	30922300	30922500	30922332	30922475	WRN	NM_000553	1	35	5	+	30922431	30922579
239082195	chr8	30922435	30922565	30922459	30922537	WRN	NM_000553	1	35	5	+	30922431	30922579
239084035	chr8	30922505	30922662	30922533	30922629	WRN	NM_000553	1	35	5	+	30922431	30922579
262051564	chr8	30924418	30924642	30924442	30924618	WRN	NM_000553	1	35	6	+	30924549	30924698
262083925	chr8	30924593	30924807	30924619	30924779	WRN	NM_000553	1	35	6	+	30924549	30924698
265753063	chr8	30925654	30925832	30925678	30925808	WRN	NM_000553	1	35	7	+	30925774	30925843
265754052	chr8	30925801	30925969	30925828	30925945	WRN	NM_000553	1	35	7	+	30925774	30925843
239960609	chr8	30933558	30933745	30933586	30933719	WRN	NM_000553	1	35	8	+	30933689	30933803

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239970449	chr8	30933692	30933916	30933720	30933887	WRN	NM_000553	1	35	8	+	30933689	30933803
240004984	chr8	30938307	30938522	30938335	30938494	WRN	NM_000553	1	35	9	+	30938383	30938812
240019202	chr8	30938467	30938686	30938495	30938658	WRN	NM_000553	1	35	9	+	30938383	30938812
240024360	chr8	30938630	30938834	30938659	30938806	WRN	NM_000553	1	35	9	+	30938383	30938812
239174003	chr8	30941240	30941417	30941268	30941384	WRN	NM_000553	1	35	10	+	30941215	30941295
262208262	chr8	30945246	30945470	30945268	30945442	WRN	NM_000553	1	35	12	+	30945292	30945436
262075988	chr8	30946338	30946555	30946363	30946530	WRN	NM_000553	1	35	13	+	30946406	30946481
330151403	chr8	30947843	30948042	30947871	30948013	WRN	NM_000553	1	35	14	+	30947981	30948048
330151527	chr8	30947981	30948193	30948010	30948167	WRN	NM_000553	1	35	14	+	30947981	30948048
262969364	chr8	30948344	30948496	30948371	30948468	WRN	NM_000553	1	35	15	+	30948350	30948458
264507191	chr8	30949301	30949524	30949326	30949496	WRN	NM_000553	1	35	16	+	30949346	30949414
239542949	chr8	30954172	30954329	30954205	30954301	WRN	NM_000553	1	35	17	+	30954284	30954366
239543300	chr8	30954273	30954441	30954302	30954415	WRN	NM_000553	1	35	17	+	30954284	30954366
264146212	chr8	30958358	30958506	30958382	30958481	WRN	NM_000553	1	35	18	+	30958365	30958471
264503242	chr8	30969036	30969173	30969060	30969148	WRN	NM_000553	1	35	19	+	30969131	30969315
264519159	chr8	30969127	30969312	30969149	30969288	WRN	NM_000553	1	35	19	+	30969131	30969315
264527429	chr8	30969280	30969447	30969301	30969418	WRN	NM_000553	1	35	19	+	30969131	30969315
262964168	chr8	30973806	30973943	30973827	30973915	WRN	NM_000553	1	35	20	+	30973870	30974044
262978349	chr8	30973890	30974073	30973916	30974049	WRN	NM_000553	1	35	20	+	30973870	30974044
262290449	chr8	30977653	30977877	30977680	30977848	WRN	NM_000553	1	35	21	+	30977759	30977940
262312212	chr8	30977828	30978030	30977849	30978004	WRN	NM_000553	1	35	21	+	30977759	30977940
238916569	chr8	30982020	30982209	30982045	30982181	WRN	NM_000553	1	35	22	+	30982038	30982139
238374239	chr8	30982300	30982466	30982328	30982440	WRN	NM_000553	1	35	23	+	30982424	30982516
238378845	chr8	30982413	30982568	30982441	30982537	WRN	NM_000553	1	35	23	+	30982424	30982516
264599258	chr8	30989758	30989934	30989780	30989911	WRN	NM_000553	1	35	24	+	30989881	30990022
264611149	chr8	30989885	30990097	30989912	30990069	WRN	NM_000553	1	35	24	+	30989881	30990022
240546347	chr8	30998857	30998992	30998887	30998968	WRN	NM_000553	1	35	25	+	30998946	30999116
240548524	chr8	30998950	30999146	30998969	30999124	WRN	NM_000553	1	35	25	+	30998946	30999116
262566121	chr8	30999091	30999275	30999112	30999246	WRN	NM_000553	1	35	25	+	30998946	30999116
262566121	chr8	30999091	30999275	30999112	30999246	WRN	NM_000553	1	35	26	+	30999197	30999291
262591353	chr8	30999224	30999383	30999247	30999355	WRN	NM_000553	1	35	26	+	30999197	30999291
242598516	chr8	31000055	31000193	31000086	31000163	WRN	NM_000553	1	35	27	+	31000142	31000217
242598542	chr8	31000142	31000349	31000165	31000326	WRN	NM_000553	1	35	27	+	31000142	31000217
242324680	chr8	31000935	31001121	31000963	31001093	WRN	NM_000553	1	35	28	+	31001066	31001139
242324749	chr8	31001053	31001222	31001082	31001194	WRN	NM_000553	1	35	28	+	31001066	31001139
238709446	chr8	31004500	31004646	31004529	31004625	WRN	NM_000553	1	35	29	+	31004569	31004644
238709495	chr8	31004598	31004728	31004623	31004700	WRN	NM_000553	1	35	29	+	31004569	31004644
264777716	chr8	31004782	31004974	31004812	31004949	WRN	NM_000553	1	35	30	+	31004880	31004992
264785472	chr8	31004924	31005090	31004950	31005062	WRN	NM_000553	1	35	30	+	31004880	31004992
264738144	chr8	31007791	31008011	31007817	31007985	WRN	NM_000553	1	35	31	+	31007857	31007971
240509797	chr8	31012133	31012272	31012161	31012244	WRN	NM_000553	1	35	32	+	31012140	31012271

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240518556	chr8	31012220	31012373	31012245	31012347	WRN	NM_000553	1	35	32	+	31012140	31012271
241851549	chr8	31014783	31014928	31014810	31014905	WRN	NM_000553	1	35	33	+	31014884	31015046
241861104	chr8	31014885	31015107	31014906	31015080	WRN	NM_000553	1	35	33	+	31014884	31015046
239400853	chr8	31024427	31024629	31024448	31024603	WRN	NM_000553	1	35	34	+	31024538	31024746
239407043	chr8	31024578	31024802	31024604	31024774	WRN	NM_000553	1	35	34	+	31024538	31024746
239369610	chr8	31030403	31030586	31030424	31030558	WRN	NM_000553	1	35	35	+	31030511	31031277
239377772	chr8	31030536	31030760	31030559	31030732	WRN	NM_000553	1	35	35	+	31030511	31031277
262310331	chr11	32456141	32456265	32456160	32456246	WT1	NM_000378	1	9	1	-	32456246	32457081
262314456	chr11	32456228	32456422	32456246	32456404	WT1	NM_000378	1	9	1	-	32456246	32457081
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_000378	1	9	1	-	32456246	32457081
262327187	chr11	32456458	32456678	32456479	32456661	WT1	NM_000378	1	9	1	-	32456246	32457081
266345890	chr11	32456672	32456881	32456689	32456864	WT1	NM_000378	1	9	1	-	32456246	32457081
266347323	chr11	32456810	32457019	32456827	32457002	WT1	NM_000378	1	9	1	-	32456246	32457081
238600226	chr11	32450009	32450200	32450030	32450179	WT1	NM_000378	1	9	2	-	32450043	32450165
238649441	chr11	32449432	32449631	32449449	32449609	WT1	NM_000378	1	9	3	-	32449502	32449604
242606698	chr11	32439076	32439274	32439102	32439246	WT1	NM_000378	1	9	4	-	32439123	32439200
240947991	chr11	32421398	32421620	32421419	32421596	WT1	NM_000378	1	9	5	-	32421494	32421590
240690866	chr11	32417762	32417983	32417784	32417960	WT1	NM_000378	1	9	6	-	32417803	32417953
240486609	chr11	32414143	32414354	32414169	32414326	WT1	NM_000378	1	9	7	-	32414212	32414301
239708127	chr11	32413425	32413638	32413451	32413616	WT1	NM_000378	1	9	8	-	32413527	32413610
239529153	chr11	32410532	32410755	32410556	32410732	WT1	NM_000378	1	9	9	-	32409322	32410725
241419475	chr11	32452031	32452213	32452058	32452194	WT1	NM_001198551	2	10	1	-	32452076	32452363
238600226	chr11	32450009	32450200	32450030	32450179	WT1	NM_001198551	2	10	2	-	32450043	32450165
238649441	chr11	32449432	32449631	32449449	32449609	WT1	NM_001198551	2	10	3	-	32449502	32449604
242606698	chr11	32439076	32439274	32439102	32439246	WT1	NM_001198551	2	10	4	-	32439123	32439200
241656493	chr11	32437913	32438136	32437936	32438114	WT1	NM_001198551	2	10	5	-	32438036	32438086
240947991	chr11	32421398	32421620	32421419	32421596	WT1	NM_001198551	2	10	6	-	32421494	32421590
240690866	chr11	32417762	32417983	32417784	32417960	WT1	NM_001198551	2	10	7	-	32417803	32417953
240486609	chr11	32414143	32414354	32414169	32414326	WT1	NM_001198551	2	10	8	-	32414212	32414301
239708127	chr11	32413425	32413638	32413451	32413616	WT1	NM_001198551	2	10	9	-	32413527	32413610
239529153	chr11	32410532	32410755	32410556	32410732	WT1	NM_001198551	2	10	10	-	32409322	32410725
241419475	chr11	32452031	32452213	32452058	32452194	WT1	NM_001198552	3	9	1	-	32452076	32452363
238600226	chr11	32450009	32450200	32450030	32450179	WT1	NM_001198552	3	9	2	-	32450043	32450165
238649441	chr11	32449432	32449631	32449449	32449609	WT1	NM_001198552	3	9	3	-	32449502	32449604
242606698	chr11	32439076	32439274	32439102	32439246	WT1	NM_001198552	3	9	4	-	32439123	32439200
240947991	chr11	32421398	32421620	32421419	32421596	WT1	NM_001198552	3	9	5	-	32421494	32421590
240690866	chr11	32417762	32417983	32417784	32417960	WT1	NM_001198552	3	9	6	-	32417803	32417953
240486609	chr11	32414143	32414354	32414169	32414326	WT1	NM_001198552	3	9	7	-	32414212	32414301
239708127	chr11	32413425	32413638	32413451	32413616	WT1	NM_001198552	3	9	8	-	32413518	32413610
239529153	chr11	32410532	32410755	32410556	32410732	WT1	NM_001198552	3	9	9	-	32409322	32410725
262310331	chr11	32456141	32456265	32456160	32456246	WT1	NM_024424	4	10	1	-	32456246	32457081

TABLE 16

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262314456	chr11	32456228	32456422	32456246	32456404	WT1	NM_024424	4	10	1	-	32456246	32457081
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_024424	4	10	1	-	32456246	32457081
262327187	chr11	32456458	32456678	32456479	32456661	WT1	NM_024424	4	10	1	-	32456246	32457081
266345890	chr11	32456672	32456881	32456689	32456864	WT1	NM_024424	4	10	1	-	32456246	32457081
266347323	chr11	32456810	32457019	32456827	32457002	WT1	NM_024424	4	10	1	-	32456246	32457081
238600226	chr11	32450009	32450200	32450030	32450179	WT1	NM_024424	4	10	2	-	32450043	32450165
238649441	chr11	32449432	32449631	32449449	32449609	WT1	NM_024424	4	10	3	-	32449502	32449604
242606698	chr11	32439076	32439274	32439102	32439246	WT1	NM_024424	4	10	4	-	32439123	32439200
241656493	chr11	32437913	32438136	32437936	32438114	WT1	NM_024424	4	10	5	-	32438036	32438086
240947991	chr11	32421398	32421620	32421419	32421596	WT1	NM_024424	4	10	6	-	32421494	32421590
240690866	chr11	32417762	32417983	32417784	32417960	WT1	NM_024424	4	10	7	-	32417803	32417953
240486609	chr11	32414143	32414354	32414169	32414326	WT1	NM_024424	4	10	8	-	32414212	32414301
239708127	chr11	32413425	32413638	32413451	32413616	WT1	NM_024424	4	10	9	-	32413527	32413610
239529153	chr11	32410532	32410755	32410556	32410732	WT1	NM_024424	4	10	10	-	32409322	32410725
262310331	chr11	32456141	32456265	32456160	32456246	WT1	NM_024426	5	10	1	-	32456246	32457081
262314456	chr11	32456228	32456422	32456246	32456404	WT1	NM_024426	5	10	1	-	32456246	32457081
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_024426	5	10	1	-	32456246	32457081
262327187	chr11	32456458	32456678	32456479	32456661	WT1	NM_024426	5	10	1	-	32456246	32457081
266345890	chr11	32456672	32456881	32456689	32456864	WT1	NM_024426	5	10	1	-	32456246	32457081
266347323	chr11	32456810	32457019	32456827	32457002	WT1	NM_024426	5	10	1	-	32456246	32457081
238600226	chr11	32450009	32450200	32450030	32450179	WT1	NM_024426	5	10	2	-	32450043	32450165
238649441	chr11	32449432	32449631	32449449	32449609	WT1	NM_024426	5	10	3	-	32449502	32449604
242606698	chr11	32439076	32439274	32439102	32439246	WT1	NM_024426	5	10	4	-	32439123	32439200
241656493	chr11	32437913	32438136	32437936	32438114	WT1	NM_024426	5	10	5	-	32438036	32438086
240947991	chr11	32421398	32421620	32421419	32421596	WT1	NM_024426	5	10	6	-	32421494	32421590
240690866	chr11	32417762	32417983	32417784	32417960	WT1	NM_024426	5	10	7	-	32417803	32417953
240486609	chr11	32414143	32414354	32414169	32414326	WT1	NM_024426	5	10	8	-	32414212	32414301
239708127	chr11	32413425	32413638	32413451	32413616	WT1	NM_024426	5	10	9	-	32413518	32413610
239529153	chr11	32410532	32410755	32410556	32410732	WT1	NM_024426	5	10	10	-	32409322	32410725

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222164840	71138	GACAGCAAAUGGAAAAAGAUAGGCA	71139	CGCTGTCCTUCAAGGTCTAACTTAUAAA
222164848	71140	GAAAUCTUCCACGAGCAGGGT	71141	CCCGCGGGAAGAUGAAUAAGG
222164895	71142	TAGAGAAATAUGCTCCAGTGGUAAGT	71143	TGTAAGAUAAATTCCCUGACCCCAGT
222164938	71144	TGCTTTATGGGAUAAGGAATAGAATTGCUT	71145	CATCCATGCUTGACACTGAAAUCT
222165273	71146	TCATGATGAGAUTTCAGTGUCAAGCA	71147	TGTCTCTCCAUTTGCCGCAUAT
222165518	71148	GTCGCUCTCCAGCUCCAG	71149	CTGGGCCCGUTGTCUGT
222166455	71150	GAACCAGGGCCUGTUGGT	71151	GCTTCCAGCUCCTCUAAAAGCA
222166546	71152	ACAAAGTATUAAAGGCCATCTGTACCUG	71153	TTCTCCCTGGUCATCTTCTTCTAUGAT
222167249	71154	AGTTCTGTTAAAGUTCATGGCTTTTGUG	71155	AGCGTTTACGAUCCTCTTTCAGUG
222167339	71156	ACCUGGTTUCAGAGAGAGAGAGG	71157	CAAATCCTACTGAAUTGGTGATCCATUG
222167391	71158	GGGTCAGGGAAUTTATCTUACACACA	71159	AACATAGAAACAACACUGGCTGAGTUA
222168421	71160	GCUGGACCCCGCGAAUG	71161	AGCAGCUGCACCAUGCT
222168809	71162	GGAAACGTGUGCCAGTGATUCT	71163	GACTTTGGAAACGCUCATGTTUCA
222171016	71164	GAAAACAACAGCCUTAGCAUGGT	71165	AAAGGAUCAGAGCUGGACGC
222171152	71166	GGAGGTTTCUGAAATGTGTATAGCTUGT	71167	TCATCCAAAGUTTCAGGGTTCUCAG
222173340	71168	GCTCCAGUCCAAAGUGGAAGAT	71169	CTCGTTCTAGUTCTTGCTTCUGGAA
222174650	71170	GTCCCAUAGTGCUGAGAACCC	71171	ACAAGGTGAGGUTCTAATCCATTCUCT
222175536	71172	CGACUACAAGGAATCAUGCAGGA	71173	GGGCTGCAGUGCTTTCCTUAA
222175751	71174	CGGGCAUGAAAGTGGACAUAAAAG	71175	ACUGAAGAAACAGGUGGAGAACAAG
222176282	71176	CAGCGCCCCAAUCCTUACT	71177	AATTATTATTGGAGUGCAAGCGAAUG
222176787	71178	AACTGCTTAGTAACUAGCAGAAGTGTUC	71179	GGAUATATGCCAUACCCCAGCAAA
222177921	71180	CGAGAGCUGGAGTTGGATGAATUAG	71181	ACUCCAGAATTTUCAAGCCAGAGG
222178746	71182	AGTATGGATGCUCCCTTCTCUGT	71183	ATGAGGAGGGCGAGUCAUC
222179109	71184	AACTAGUACCGGAGAACACTUCCT	71185	TGTCTTGUCAACTGGCCTTUGA
222180599	71186	TTTTAGAACTAAUGGACATTGCTTUGCC	71187	TCATATGGCCCCUCCCTTCTUT
222181900	71188	GTCAGCACAAAAUTTAGCAUCCAGAAAT	71189	GATAAAACAGTCUTCACCAAGCAGUG
222183051	71190	AACGGAAUTGTUAAGGCAAGCAC	71191	TCTGGTTCAAGUTGGTGTTUGGAA
222184498	71192	AACATGGTGTUGAAGTCCTGCAUA	71193	AATCTTCTGGTAAUGCCTCTGAAAAUCT
222184552	71194	GGGTGGGCUTCTGTTCTCTTTUAA	71195	TCTGAGCCGCAUGGGUAAAAA
222187255	71196	TGTTTGCCCUGTGTAAATCTGUGAA	71197	TGCCACUCAGAAAATCTAGCTTUAACT
222188987	71198	CAAGATGGGCUGCCCTACAUT	71199	GCCACACGUACACCAUGGG
222191725	71200	TTTATGAUAACACCTTATATUACAAACCACCAT	71201	ACCAAGUAGCATTATCUCCAGAAAGGA
222191878	71202	CTCCTTTCUGGAGATAATGCTACTUGG	71203	ACCTCTTTAAAGUACAGTACCTCACCUT
222192581	71204	GCAGCAGUGCACTAAAUAACGAGT	71205	GGGTTTTAAAUACCAGGAGACAUGCAA
222193202	71206	ACATTCACCUGGGCGCTUA	71207	TGCTGATGUCCGGCTGAUG
222194209	71208	CTCCAGAACUTCCTGGTUGCT	71209	GGTGTGTCTATAUCCATCTCCATGUC
222194340	71210	GAACTAATCAGCUAGAGGCGAUCAAT	71211	GCTTTCATTUAACATCTGCCAAUGGA
222195101	71212	GCACCCCAAAAAGCCUTCUG	71213	CGGAGGCUCCCTTUGGAT
222195404	71214	ATGATATGTGGGUATTCCGACTTTGUT	71215	TGUCTAAGTTTTUCAAGCACAGGGT
222197754	71216	GTCTGTUACCTGACAACUGACACT	71217	TCCTCCCACCCUCACTCAUC
222197871	71218	GGGATTGTAUTTGTAGCAATUCGAGAA	71219	GTGTGGCAGAGAGUCCTGAUG
222199718	71220	GCACGCAGAGGUGAAGUGAT	71221	CCCGACUGACCAGTCTTTTCTAUT
222200981	71222	GATAGATGACTUGCTGCTTCCAGUAAA	71223	GGCTGAATTTUCCAAAAAGCAUCAAAAA
222201713	71224	GCTTTCAUGGACTCTGUGAGGAA	71225	CTAGGAATGGACUTGGCTCTGUAAAG
222202160	71226	TCTTGTGCCCCUTCAATGTTCUC	71227	TTTTATTGGTCCCCUTGTCTTCCUC
222203805	71228	AATTCAGAAACUCTTGTCCGGUGT	71229	CCTACCTTGGCUTTCTGGAATAATUCT
222204488	71230	GATAGAGAAAACACUGTCUGCCAAGAA	71231	CTGCAATGTCAUTCATTAGCTTTGAUGT
222204633	71232	GGTGTAATAGCUGAAGAGGAAGCATAUA	71233	GGTTAACCTGCAUAAAATTTAATGTCTUCCA
222206251	71234	CACGAAGUGAGGTTCCCCAUC	71235	GGGTGGGAAAGAUGATTATCCTGUT
222207180	71236	CATTGTCCTGTATAUTGGTTCTGTCCTUT	71237	CUAAATGGGUACGGCAGCAGAT
222209925	71238	CCUAGGAGGUAGGCAGAGACA	71239	GGAGGCGUTCCACTTTGUCA
222213434	71240	AGGTGTGUAAGCAAGAAUGCCT	71241	TCCTAAACGUAAGAAGCAACACTCAUT
222216268	71242	CGGCCTGUGATAGGCACAUAG	71243	TTTTTGGGCCCUGACTCTGUT
222216727	71244	GGGATAACAGAUGCCGAGUACC	71245	TTCAGAUCCCAAGCACUGCAA
222219643	71246	CACAAGTGUCAGTGGATAUCAGGAA	71247	GTGACTUCCACCAGGACTGUG
222222770	71248	CATAGGCAAGACUCCAGGCUT	71249	AGUGCAACAACGCCUACCA
222229645	71250	CCACGCUCAGGTTGGAGTUC	71251	TGAGTGACUGCCTCTCCTCUT
222232757	71252	ATCTGGCUCTCATCTTCUCCCT	71253	GCAAACTTACCAUGGTTGTGUGT
222233370	71254	ACTCCTGUTTAGGCCTUGCAG	71255	TCCATGCUGCTTGGTAAUGAAGT
222233508	71256	GGGAGCUTCCAGTUGAAACAT	71257	AAATAAGAACATUCTTCAGACACUGCCT
222239028	71258	AAGACTGGUGTCCTGAACUAGAAGA	71259	TUGTTTAGAAUGAGGAGAGAGGCAAAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222243185	71260	AAAATGATACUCCCCCTACUCCCA	71261	CCTTATTTTCUTCCCCGUAGAGCAA
222253399	71262	GCATTGCCAAUCGCATAUCCT	71263	TGTTCCTTCCGAUTCCTGGAAUG
222258987	71264	TCAACTCAGGUAAAATGTCAGTUCCAAA	71265	TGCATGUGGAAGTGTUGGAGAA
222259284	71266	CAAAGTTGUGTGTTGTAAGUGGAACA	71267	CCAAGAAAGGCUTGTGTCTACATTTUT
222262238	71268	TTCTCATGAATTTTUAAACTCTTGTAGTCAGUA	71269	CAAATGCGUTGGGCTUCCAT
222262253	71270	AGAATGATTUAAGGCTACAGAUGGAAGC	71271	TCCTTGATCUTTTCCTCTUGAGCAAA
222265348	71272	CAGCCTGCTCUTCTAATTTGTTTACTUT	71273	GACTCAAAAACTUCCTCCTCTTCTUCT
222266855	71274	TGGATCAGGUTCGTGAATATAUGGAAAAT	71275	ACCTGTTTCTTGUGTTTTCATAGTCUGT
222270072	71276	TCAAGGAACTUCAGAAAATACACCAGUT	71277	CAAATCACCUTCCTCTGUGGGT
222273966	71278	GGAGAATUGAGCCCTGGUGAC	71279	TCAAGGUGAAGGACGACAACUAC
222284310	71280	CAAACTCTGUTGGCACTUGAGAA	71281	AGAGCACCUCCUACACGGA
222288194	71282	TTGTGUGGAGCGCUGGAAT	71283	ACATAAGCAGCAGCAGUGACUC
222289365	71284	AAAGACAGCAAGAGCUCCAAUCA	71285	GCAAACTAGAAGUGTCCACAGGTATAUT
222289513	71286	GCGTAGCGCAUGGCTAAGUT	71287	AGAAGAAGCAGAUGACGCUGAC
222290732	71288	AGTAAGTGTUGCACAGCCTGUAA	71289	GTACCTUGGAGGTGCAGAUGAG
222293302	71290	GAAGAAGAAGCUGUCGGAGCA	71291	AAGTGAAAACGCACUGCCATUAG
222297663	71292	GAAUGCCUAGACCCCAGAGAAG	71293	TGATCCTUCAGCTCCTUCCCAT
222298895	71294	GTACCGCUCCTGGAAGGTUAG	71295	GCCTCACGCACUTCCTGAUG
222301696	71296	GGCTTCAAGTUGTCTTTTTAATGAUCCT	71297	GTACCTGCTGUAAGTCTTCACTTUCA
222302327	71298	CAGAGATGTCUCCAAAGGTTCCUT	71299	TGATTTGATTTCCUTCTCCAGTCTGAUT
222305856	71300	CTGCAGCUTGATGACCUCGT	71301	TGCGTCUGGAACCTCCTTTUT
222306820	71302	CTGAGAAGTTTAAAUGTTGGGTAGTUCCT	71303	GCCTCAACACUTCTGACCATCUG
222308689	71304	AAGCAGAAAGAGACUGTGAUAACAAGAA	71305	CACCGTAGATUAGGTGGTTGCUAA
222309251	71306	TCGAACAGAGGCUGCAAATAGAAUAAT	71307	TCCACTGAGUGGCATCTAAGTTUG
222310655	71308	GTTGAGGCACTUTGTGATGCTTATAUT	71309	TCUCTACAGAGAGUAACACAGCAAGA
222316698	71310	CCUCCTGGGUGCACCAA	71311	ATGACAGCCUGCUGCGT
222319815	71312	AGAATTAGAGATGCUGAACAAAAGGACUT	71313	CAACAAAGGGAGAAGCUACGTAAUGA
222321230	71314	TGTATAACCCTCAUCCATTCTTTTGUGG	71315	TGCACCAAAAGAGAGUTCATATCACUT
222323044	71316	ATTAGGCCTTCTUGTATCATGGATGUG	71317	AGTGTACCAACAAUAACATGAAGAUGGT
222323192	71318	GGTTGTAGCGUATGCAGUCAAC	71319	AGUACAGACACGGCCTCUGA
222325224	71320	CCAGACAGCCGUGACTUACT	71321	ACCATTTTGAAGAUGAGTCAGAAAATUACCT
222332343	71322	GAGTUGAAAGCACUGCCGAT	71323	TCTTGGCUGAGAAGCUCAAAGAG
222334565	71324	GTTTCTTGTGUTTCCGCTGUCA	71325	CTCTTCTTGAAGUTTTTCAGCCTTTUCT
222335589	71326	CCCTCCTCTUAGAGTCCAGAUGT	71327	GAGCCTAGAATTUTATTACCCAGAACUGT
222337017	71328	GTGGCUACCAAAGCAGAACTUG	71329	TCTAGCTTTTAAGTUATGGAGCTCATTTGUT
222340350	71330	CCGGCUCACAGACCCUCT	71331	TTCCACCUCGGAGGAGUCA
222342358	71332	TGAAGAAGTTGTCAUAATTCTGGCTCUT	71333	TGAATAGAATGGUCCTCTCCAUCACT
222347361	71334	CAGGAAGTACUTGCTGTCTUCAGG	71335	CCACCACUAACGCCAGCTUT
222347382	71336	TTAAATTGGTUGTGTTTTCTUGAAGGCA	71337	GAGTATCUGAAAACCGGGCTAAUGA
222347971	71338	GGAATTGAGAGGUCCTTCUGGGA	71339	CGTTCCCTUGCTTCACATCTUCT
222348822	71340	CATGTCAAGCAAGAUGGCTUCA	71341	GAATTTGCUGGATTACCUCCGAGA
222349353	71342	ACAGGGUGCTUGGCAGAC	71343	GTGCTUGGCCCCTGAATUT
222351381	71344	CTCTTTCCCAGUCACCAGTTUGT	71345	CAGAGTGATCUGGTCTTTCCCCUA
222353493	71346	GCTTTCTCTCACUGAGTCTCCCUAT	71347	CATAGTATTCTTUGGTTACCTCGGCUT
222354520	71348	GAGCTAAGAAAUGGAAAAAUGAAGGCAT	71349	AGACCTACTTCCUCTTTGGCTCUT
222358631	71350	TGAAAACAAGCAAGCUCTCCUGAA	71351	TCTTTCTAUGCAAAAACACTCACUCAGT
222359413	71352	TGAGTCTAGCCUATAGTATGATTGGCUT	71353	TGCATACTCATUTTCTCAGGTTTUGACA
222362633	71354	CTGACAGAAAAGAGGAUGTTCTUAGCA	71355	GTCTAAAATATUGCTTGTACCGUCACAG
222363434	71356	GTCACCTCUTCTCGGTUGCAT	71357	CAAAGTGGTTUGGAGTGTTTGAAUGT
222363548	71358	GCACCAATCTTUCTTCTGCCTTTUG	71359	CCAAAUCAAGAAACCTGTTUGAGAGAA
222363725	71360	GCUGAAUCCAGAAACCAGCACA	71361	CCATTTTATAACAUACAGCCACAGGUT
222372092	71362	AGGCCGCGAAGUCCAUC	71363	AGTTCCAGCUCCCCTTCCUT
222373002	71364	TGTACCCTGUGTCACTGAGCUA	71365	ACAAATTGTTACATUTCTGAAGCCTGUG
222373936	71366	TCTATACCATTGCUACCAGTTCTTTUCC	71367	GTGCTGUCTCTGACGUGGT
222375807	71368	GCCATCACAGCUTTTGTTTTTCTUGT	71369	CCTTTCAGAAGGUGCAGAAATACUCA
222378160	71370	GGTTTCAGCUCCTTGTTUGGGT	71371	CCTGAAAUCAACCCTCACCUAACT
222382863	71372	GTUGATTATGGAAGATUCCCACAAGAGT	71373	CTCAGTATTUTGGCCAGUCCCT
222383137	71374	CCTTGAGCGAGGAUGCCATUAT	71375	AGAAGGGAGAUCCTTCAAGGACATUA
222386339	71376	TTTTAGCTGATGGUGCTTTTTGTGATUT	71377	CAGAGACCCUGACATTCATCAATACTUA
222389561	71378	TGGAUAGGATTCTTTCUGAGGGAAGG	71379	CTTCATCCTGTUCCAAATCACGATUG
222391345	71380	GCTGCAGATUCGTTCAGAGUCT	71381	AGCCACGGAAAUATCCACTGTUT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222393516	71382	GCATCUCAAGCAGACGTCGTUA	71383	ACACCATTCATGUCTATAGGAACGTUT
222398760	71384	GGGCCUAGGTTUCACCGA	71385	GCTCCCUCCCAGCTCCUA
222399018	71386	CAGUGAGGGACGGGCAAUAG	71387	ATTCCATAAGGCACUCAATACGCUT
222403638	71388	CGTTTTGTAUCCACTCCTTTTCAUGAGA	71389	GTAGATAGUGCCACAAGCTGTCUG
222403679	71390	CTGTTTCTTACUAGGAATCAACCCUCAA	71391	CCGGUAAGTAAGAGUGCCAACC
222407313	71392	AGTTATTACCUTGTTGCCTCUACCCT	71393	CCAGACTGUGAGCCAAGGAAUT
222410260	71394	ACACTCATUACTTCCGGGUACAGA	71395	CCATGTCUGAAAAGTAAGTAATCUGGCA
222411296	71396	AGATGUAAAGACCTCUGAGGACCAG	71397	AAGCACAUGCAGAATAAGAGAGUAAACA
222414448	71398	CTGTAGATGGUGCACTTGCATTTUT	71399	CCTGTGGTCCUCATTTGTAGCUAT
222414936	71400	ACCUTGTAAGAUGGCAAGAAACACAA	71401	GAATCTCTGTGCUACCTTCCAGAAUAC
222417293	71402	CCAGCGUGGGAGAAAGAAUCT	71403	GCTGUCCCGAGCTAGGUGA
222418050	71404	CTCCCACTUCATCTTGGAACUCAAAT	71405	CTAATTTCCATGCCUTTTTCAGGCAUA
222419902	71406	CUGGCGCGGGAAAAUGT	71407	CGGCUACUCAGCCCAACC
222421427	71408	CGAAGTCAACUGCCAGACTCUT	71409	GCCAUCGGGCTCCTGUG
222421876	71410	CTGGAATAUGCTTTGGAAAGUAGGGT	71411	GCATTTTCAAAAGCUGTTTGCUGAA
222422859	71412	CACAGCUGCCGUGGAAAG	71413	TGGGUACCAAGGACTGTUCAGA
222424733	71414	CCAGGTTACUGAAAGCACTTCCUT	71415	ACCAAACTTGGUGAAGTAATTTAUGGGA
222426227	71416	AGAGCAGAACAGGAGUGAAGUCT	71417	CCAGATGGACUTGCTGGAUGG
222436139	71418	GGGCAUCTCCTUAGAACGCT	71419	TCTGGAGUGCAGCTTTGACTUC
222436285	71420	GTGGGUGGTGGGCAUGAA	71421	GACGCCAGCCCUAGCUC
222438400	71422	TCCGTAGGTTUTGGTCTCGGUA	71423	ACAATACTTTUCACATCGTCAGUCACA
222439364	71424	GGGAATACUCCAGCUCACAGG	71425	CTUGGACAGGGCAAAGGAUGT
222440440	71426	CTACCACUGTGCAATGAAUAACGAAAA	71427	CCTTCGGTUCCCAATTGCUCA
222442079	71428	AAAACAAGAGAUGTGACTGACGAUGT	71429	CAAGAAAATGUCGACCAGCATATUCAT
222443847	71430	AGATGTGACUGACGATGTGAAAAGTAUT	71431	TCAATTGAAGUAACTCAAACATUCAAAACA
222444283	71432	ATTTAAATAGTUGCCATTCCAAGTGUCT	71433	GCTCCGTAAAUAGCACCATTAGAUGAAT
222444647	71434	GGCGTCCGUGCCTTCUT	71435	CCATGAGGCUCTGACTUCCC
222446210	71436	TTGCCTCTUATATTTCAGGTUGAACAGT	71437	TTCTCTTACTCUGAACTCCAGTTTCUCT
222448053	71438	GCACCTAGGCUAAAATGTCAAGAACUC	71439	TGTTGCTGAGATAUTTCACACCAGTAUT
222449983	71440	TCTGGGTTACUCACTAGATTTAATCUGGAT	71441	GGAGTGGAAAUGAAATGCTCTTAACTUT
222450842	71442	AGGGTGTCTCUCTGTGGCTTUA	71443	GACTCTGUAGGCTGCAGTTCUC
222451061	71444	CAGCUTCAAAGGGATAUACAAGAAAGGA	71445	AACACTTATTAAGTUAGCCCAAATAAAAUGCC
222453945	71446	GAGCTGATTGUAGCAACATACTACUCAA	71447	AGACAGAUACAGACAGAGTGCTTUCT
222454752	71448	GCAGTGGTGAUACCCATTTTGUGT	71449	GTGTGTGTAAGGAUGATACTGGTUGA
222456063	71450	GAGGUCCTGCUGACACACA	71451	GCAGGAGCUGGUCAACAGG
222459888	71452	GCTTTGCCUGTGGUGGAAAAT	71453	TGCATGCTCAGAUTAGAAACTGTGUA
222461291	71454	CCTCCTCCUGCAGGTTGUAGAT	71455	CTGACCCTCUGAAACCTCCUC
222472100	71456	TGCTTCGUCAACATAGCTTTAUGGA	71457	CGTCCCAACUTGGCTTTCUCT
222474390	71458	AGAAAATCAGCUTCAAGACACTUCAAGA	71459	ACCCACATAAUAAAAACCCGCACUT
222474653	71460	CTCCAGUGGGCTTUGGAGAA	71461	TTGACATTTTAGAUGGAGGAAAGCCTUA
222475686	71462	TCGGTGCAUGTGAACGTTCUT	71463	CAAAGCGUCCAGCTCCUCAT
222479079	71464	TGCTCAACAGAUGATTATTTCACCCTUT	71465	CCCCTCTTTACUGTCTACTCTGGTUT
222482150	71466	TGTGTGATGTAUTTGCTCTTGGTUGT	71467	AGGACTCAGAGCUCCTTCTGUC
222484306	71468	CCAAGUGAACCCAGAAAATATTCUCCAT	71469	CTTTCCTTAUAAAGCTTACCCGUCACA
222484346	71470	CAGAATTCATCAUAGCAAGCTGUGAC	71471	GTAAGGCGTGUCTCAATATTTGACATUT
222485418	71472	GCTTCCAGAUGGTGGAUGAACT	71473	CCACUCUGACCACACCAAACC
222485734	71474	TGGTTCAAUAGATGACCUCCCCAT	71475	GGGAGGUAUGAGGAGAGAAAGG
222486589	71476	ATGTGGGTAAGAAACUGAATCTGCTAAUT	71477	CAACACCUGAGTCCACCAUCA
222486702	71478	GGTAACAGTGAUGATGTCAAATGCTTUT	71479	AGGTGAACACAUATAAGCAATCTCAUGAT
222488467	71480	AGCAGAGTAAUCCAGCTCAGUCT	71481	CCCUAAAGCCCAGCACTUGA
222488576	71482	ATGTAGTTTTCUGGTGAATTTGGAGUGA	71483	AAGGCUCAAAGGGAATAUAAACCAAGAT
222493828	71484	CTCTAATTTGTGCUGACCAGCTGUA	71485	CCCCCTGUTTACCCTGATUGG
222494797	71486	TCAGAGGACCCUTCAGCCAUAA	71487	GATCTTCGTCTUGTTGTAACACTTTUCA
222505386	71488	CAGACCCUGAGGATACTGTGCUA	71489	ATGAAAAAGGACGCCAUGCAUC
222507899	71490	CCCCAGCUGGATTCCAAATUCT	71491	CCATTUCCAGCCCCATTCTUCA
222507991	71492	CGCACACCCUGCCACUAA	71493	AGCTGTTCUTCCACCTGUCC
222513007	71494	TCATTTGAUGAAGAGCATAGACAUGCAA	71495	GAAGTTGGTGGCCUTATATCCTAATUCA
222513132	71496	TGGTGCGATUTTCCTGTTACUCT	71497	CGTACTUCCCAGTTTGGTGUGG
222516765	71498	CCATACCCCUAAAGCACUCCCT	71499	GGAGTCCCAGGAUCTCTCUGA
222517254	71500	CUCCTCTGUGAAGACACGCT	71501	AGCTGTCACUTGCTGGTUCAT
222517767	71502	AAGACAGGACAUCGTCCCCUA	71503	CACCCAGCCCUGCTTUACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222520150	71504	GGGAAACAGCUCAGATGGCUAA	71505	GGAAGTTGAATTAUTACCCCCTGCUC
222520505	71506	GTATTUCCGCCGACTCCTTUGA	71507	CTGTCGAATGUCAGAGGCCUT
222523072	71508	CCACCUCGTCCTGUAAAGCA	71509	CGCTACUACGCCATGAAGAUCC
222524420	71510	TTTGTGATCUATTCCATCTGUCCAAAC	71511	TCGTGAAUAAGCAGATCCTTTUCCAAAT
222524510	71512	CTTCCGACCUTTGCCCTTUG	71513	CCTGGACUCTCTGTGTCTUCAG
222529352	71514	TCTTGTCCTCUCTTGCCACAGAUA	71515	GAGCUCTGCGGAUAAAGAGAGAC
222530791	71516	GTAAGAGTGCAAAAAUCCAGTCAGGUAT	71517	GGGCTTTATUTCCGAGCAUCACA
222530987	71518	TCTUCGCACAACGGCTTCUT	71519	GTGTGGCAGUTTTCGGAUGG
222533287	71520	AATGACCAGGCGAUCGCTUA	71521	GCTTGGACAAAGACACUATACTUCACAAT
222534318	71522	GGAGGATGGAGUCTGAAAGCUG	71523	AGTGATTGACAGUGTTGACTCTCAUAG
222535192	71524	ACUAAACAACGAAGCCGCTUGA	71525	ACCTCTTAAGUGCAGGCTUGG
222535245	71526	TGAAAGAUGCAGACTTTTACTGUGAAGT	71527	TTTCCATCUCACAGACCTTGCTUAG
222536388	71528	AGTGCAGTTTTAAAAUCCTTTTTCTGTAUGG	71529	CAGAUAGAGCCTGAAGUACACAGAGA
222536443	71530	ACAAACUCTTGGTACTUCAAACACGA	71531	TTCCCAATCTCCUTTTTCATGTTCTCUT
222536518	71532	TGTTCTCTGTGUACTTCAGGCUCT	71533	GCACACUGAATAGCCTUGGAAAAA
222538062	71534	GGCTCTAUCTGAAACCTUCACAAGAT	71535	AAAGAGATTAGATUACCTCGCACACUG
222538939	71536	CCAAGGCUATTCAGTGUGCGA	71537	AGGAATCCACUAGTTCTGTTATGAUGGA
222540515	71538	AACCGUGAGGCCATGCUT	71539	CCCCAGATATTCUAGACAGTTCAGTUT
222543757	71540	GTCAATATGCUAGGACTGTCTGGUT	71541	GCTTTGAAACAAUCCTTTTTCTCTCCUT
222546482	71542	GTGTCAATGAGUATAGCATTTGCUCAAC	71543	AGTCTGAAAACCAAUTTGATCCTGUGAT
222547294	71544	CAGCAAAGAAGUAGAAGGAACCAGUT	71545	CAAGTTTUCAGAAAAGAAGCCAUGACAT
222547983	71546	GAACTTAAGGGCUCTCGAGCUT	71547	GCCAAGUCACACCTGTACTTTUT
222549675	71548	GTGATGUGGAAAAGACCTGUGAC	71549	GGGCCCTUGTGGAATCAGTUC
222551487	71550	CTGTGTGUCAGCAAGAACAACATTATUT	71551	TCCTTTCCATGTUCTCCTAACTCTTUACT
222552803	71552	GCCCCCUCCATCTAACUACCAG	71553	ATTTTCAUCCCAGAGUGCAGGAA
222554659	71554	AGACTTTTGAGACAGUGGATGTGAAAUT	71555	TUTCTTCTGAAATAGUCAGCACACAGT
222554662	71556	GAATTCCCAGGCUTAGCCATGAUA	71557	GCAATGCTUGATTGGTTCAUGGAAG
222555831	71558	AGAATCAAAGGACUGTGTGCUGA	71559	CCAAACATUAAGCAGCACTATTGCUAAT
222559481	71560	TGCATAUAGGGAGCUGAGGGAAT	71561	AGACTCCTUCCCTTTCCTGTCUC
222560115	71562	GACCGAGGUTGGCUCGAT	71563	CCCGAGAACUGAGGGTGGUA
222561786	71564	ACCTCTCCUAGCAAGTCUCCA	71565	GGTGATAUCCCGCCGAAUCAT
222562654	71566	ACAGTCCUCAAAGAAGGAAATGCUC	71567	ATGGAAGAGUCTTTGTGGTUGCT
222563980	71568	CCTTCCAGGCUGACTTCTGTCUA	71569	CAGCTCCCUAAATCCTCCUCAC
222565189	71570	CCCCTTUGCCCGCTUCT	71571	GGGAGGAGACGUCAAUGCC
222566968	71572	AGTCGGACAGCAUCATGCAUC	71573	GGTCAAACAGCUCTCCAAAAGCUA
222571047	71574	ATCCTCCUTGTCCUCGGACT	71575	CCGAGGAGGACCUCACUGAA
222573315	71576	CAGTACCUGCCTCGCACAUAG	71577	GGCAGATUAGGCAACCGAAUGA
222573743	71578	GCGTTACUCACGTCCTTCTUCAC	71579	TCCTCTCCTUCTTCCCCATUACC
222574295	71580	AAGCTGATATGTCUGATTTGGTTCCUT	71581	TGGTACCAGGAGUGTTTCUCCA
222575058	71582	CAAAAGUGCCAGCAGUACCAAG	71583	CAATGCATCCCAUCTTACAGAGUGA
222575486	71584	CATATACTUACCATATCGGCUGCGAT	71585	CAAGCACATGGAUCAGTGTTTTCTTUA
222582307	71586	GGCAGGTGGUCATTGAGAAUGAT	71587	GTGTTTCAGCUTCTTGTGGTGUT
222587210	71588	ACGCTCUACCCACTGCAGUA	71589	GGCCAGTATAAUAAACAAAGTGTGAUGG
222589963	71590	AATTTCAATGGAUCACCCCCAUCA	71591	GAGAGCTTTGTUTAGGCACATTTTUAGT
222590510	71592	GCUGGTACUGAGCAAGAAGACAA	71593	CAGACAAAAAUGGGTTGTTGGTTCUAC
222590775	71594	ATCACCCCCAUCACACTTTGTTTATUAT	71595	GCTGAGAGCUTTGTTUAGGCACA
222592843	71596	CTAAAAATGTGCCUAAACAAAGCTCUCA	71597	CCTTGAACCGATUTTAGATGGCATCTUA
222595304	71598	CAGTTTTCTGTCGUGAACGTTTCTTATUT	71599	CCACTTAATUAGCACTTTCTTTGCAUCT
222595566	71600	CACTCUCAGGCACCTUCCA	71601	CCACAGAGACCGGCUTCAAUA
222596754	71602	ACATCACGCCAGUCAACAGUC	71603	TGGTACACCCUCCCTTCGTAUC
222597478	71604	GGGAGGACUGACCUAAGCAAG	71605	CTCTGCTCUGGTTTGCTACUCA
222598226	71606	CTTGACACCUGCGAUGAGGAA	71607	CCATCACCCCCUCCTCTUGT
222602826	71608	TCTGTTAAGCAGUCACTACCATTGTATUC	71609	GAGCTACCTUGGCAACTTCUAGAT
222602870	71610	CTAGAAGTUGCCAAGGTAGCUCA	71611	ACCCTTATTGAGACAAUGCCAACATUAA
222608818	71612	GAAGTACACAUGCTCCTAGGCTUT	71613	CAGUAGTTCACCUCGCCAGT
222610938	71614	CCAGAGGUCCATCTCGCUGA	71615	CTTCTTGGTUGAGCTTTCTUGCAAT
222611830	71616	CUTCTCAGACUGGCGAGGT	71617	CCTGTTCTUGTATTCTCTGTUCCAAACA
222613119	71618	GGTACTACAGAUGCAGTTGGTTTACUAA	71619	ATATTCATAGTGGCUCCTATTAAAATCTUAACC
222613231	71620	GGGTGAGGCAGUCTTTACUCA	71621	CGTTGTACACUCATCTTCCUAGGGAT
222613250	71622	GGGAUCCCAAGGAAGAGAAGUGA	71623	CACTTCCCTUGTGGGAATGUCAA
222615042	71624	CATACAGACACUTCATTTGGAGUACCT	71625	AGTGTGTGCUACTAGAACUCAAAACAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222616774	71626	AAAGGCAGCACAAAUACACTAAUAGACA	71627	GGAATCAGCAAGUTACAGTGUAACAG
222619143	71628	GAGCAAACCGAAGCUGAACUT	71629	CCTGCTGTUGTTAAATCTATTTUGCCA
222619712	71630	CGAAUGGACCAUGAAACAGCCA	71631	CTTAGCAAAGTAGUCATGGCATTAGUGA
222621410	71632	CATTTCACATTCAUTCTTCTCTGTGUCC	71633	GTTAGAACAAGCAGCUCAGATCUGT
222625425	71634	CCTGTTGCUGGTAGCCGUAA	71635	CTGGAGGGAAGCUGTACTGUC
222629880	71636	GCTACTCTCCUGAACTCTCTCACUC	71637	TGCATCAGAACCCUCCTTGAAUC
222634980	71638	CTCCCAGUTGCAACGTUAGGT	71639	GGUCCACGGAUCCAGAAACAAG
222635553	71640	CCTGCCUGGATGGGTGTTUT	71641	GTAGATTCTCGCCUCTATTGAGCUG
222636793	71642	CGGGCCAGCAGCUCAAUA	71643	GGACUCTTAAAGATTTAUACCACCCAGAT
222638754	71644	GCAAGCGAGACCCUGCUC	71645	GGAGCUGCACGACUACCA
222639818	71646	ACCCACAGCUCCTCUCCAT	71647	ACCCTGCUGCCTTCAUCC
222642629	71648	CCATCGGGUGCTTGATGAUGT	71649	GCAAGAAGGGCAAGCUGUC
222647379	71650	CTGAGGATGCUGTCGCAGUA	71651	CCCGCCGUTGUCAGACC
222647788	71652	CGTACGUTGGGTUCCACAAG	71653	GAGATCTCTGUTCGAGTCCCUAGA
222650366	71654	CACAGACTCUGGAAATGTGUAACCAA	71655	CCCTCUGGAAGGTACATUGCC
222650932	71656	CCACCACTUTGGCCTGCUT	71657	GCGACAUGCGTCTUCGG
222652277	71658	GGTAAAAATGTGAUGATCTCTGCAGGUA	71659	GGGCAGTCTGAUTGCTTTTAATCTCUT
222653756	71660	ACATACTTCACAUTGGTGTTGGUACAG	71661	TCAGGUAGTGAAATUAAAAGGCCAAGT
222654021	71662	CTGTCACAGAGACUGTCTGATCTUT	71663	TGCCCTGTTGUGGTTAATAATGATTUCT
222657782	71664	CCAGGCTTGUCAACTTACCAGTUT	71665	CATCGCCACAUTTCCUAGCC
222658180	71666	TCACGTGUCCCCCTUCCA	71667	GGTTCCTCCUCTCCTGGTCUC
222658484	71668	ATTTTATTTTUGGCCCTCAACTUGGAC	71669	GATGTAGGGCUGGAAGTGGTUT
222658515	71670	GCAAGAGAAAGAACAAGUTTCATUGAGA	71671	CTTGTCATGGUCACAACTCCATCTAAUA
222660555	71672	CAGTCATGTGAUACTCAAGTAAGCTCUT	71673	TTGCTTACTTTCTUCTCCAACAGTCAUAT
222662461	71674	CTGGGAGAAAUGAGCTTGTCUGA	71675	GCCUGGCCACGAAUAGCAG
222662947	71676	TTGGCCUCACACGTTCCUAC	71677	TGGAAAACCUCATGCUGGACAA
222663987	71678	GGTGCTGAAGGAUCAGTTTCTAAAGUAA	71679	AGTTGCTCTAAGUGATGATTCCTTUGT
222664184	71680	AACAAAGGAAUCATCACTUAGAGCAACT	71681	TGAAGGTGAAACCUTAGTGTGAAAUGT
222664325	71682	GATCTCTCTUGCAGCCTCGUT	71683	CTTCTCAACACCUCAGCTGACUC
222665131	71684	GUTCTUAGACCGGAACCGGAA	71685	TGGTGCCUCAAGGACAAUGAC
222665635	71686	GCTGTGCCUTCAGGGTUCT	71687	TCACCTGUGGCTGGCTUC
222665764	71688	CCGCTCCUGAGAGGCUT	71689	GGCCACCCAAGAAGUAAAAAUAAACT
222666532	71690	GGTGACCCCUACAGTCGUG	71691	AGAGGCAGATUGAGCCCACTAUA
222668951	71692	CAGTGATCTUGATGTGGCCAUCT	71693	GCATGGGAGGGUTGATGUCC
222669308	71694	AGACCTTACAAUTTCCATGATTUCCAGT	71695	CCACATGTTAATGUCATTTCTTGGCAUA
222670784	71696	GAATCCATTCCCUCTTATTCTGGAAGUG	71697	AGCATAAGTTCTUCATTTTCAGGGUCT
222672154	71698	CCCCUTTCTCTUCCAGAAGCC	71699	GTTATCTCCACUGGCCACAAAATCAUA
222672272	71700	CCTCAUCCACGGACUCAGGAT	71701	CAGTATCTCTGAUTTTGATGCCATTUGT
222673095	71702	GCUGGACGAAAGCCUGAACAA	71703	CAGAAACUACTCAAACUCCCACCT
222673281	71704	GGCAAAAGCCCAGUCCUC	71705	GTAACGTGTGUGTGTCTGTGUCT
222680486	71706	ACATTTGGCUGTGACTTCUAAGAAGAAA	71707	GCTCACTAACUAACGTGAAAGCCTUAC
222681021	71708	GAGTGGTTTUGCTGGAACUGAAAT	71709	GGTTACCUGACTGCTAGTTUCACT
222681059	71710	TCTGTAACUAATGTGTCAGUAGCAAAAACA	71711	AAGTCCTUGACCCTTTGCTGAUT
222683199	71712	CTCCAGGCAUGATGATGUCCAT	71713	CGGCACAUCCCATCTUAGCAG
222683971	71714	GATACATTATGUGTGTACAAGUGACCCA	71715	AAGCUGAGAACATGCUAAAGAACCA
222684242	71716	GCTGAGGUCCTGGAGATTUCT	71717	CCCCTGATAAAUTAACATACTTGCUCCT
222686000	71718	TGATTCGGGUGTCTCTTCUCAGT	71719	TCTCUCGCGAGCAAGCTUC
222687006	71720	GAACCUCUACCCAACACCACA	71721	TGTGTTTUGGGTAGTGCAUACAACT
222689454	71722	CTCATCATCAGUGCATAGCTTCUCA	71723	GGTGAGGACUTTGCTGGTUGT
222691654	71724	GGAGAGCCUTACCUGAAGGAG	71725	CAGGGCCUGACTGATTGATAAATUCA
222691663	71726	GCAGTTGAAAAACUCCTAGAAGCCAUA	71727	TGCCAAACAGCUATCCATGAAAATAUCA
222694002	71728	ACAGCACCCGCUGCTUT	71729	CCAGCTGUCAGTCATGGTGAUA
222694630	71730	CCCAACCTTUTCGTTGCACUG	71731	TCAAACCGCAAUTCCCAGATTTCUAT
222695036	71732	GATTTCUTGCAGACUCCGAAGGA	71733	CCATATCATCCCAAUCATTGATGGUACT
222700201	71734	ACCUCGCCACGGTCTTUG	71735	CCACCTCUGTCAGGUCAGG
222701931	71736	GCACTCCAGCUGATTTCAAUCC	71737	TGCCAAGAUGTGGTTAAACUCAGA
222702138	71738	CCGGGATACUGCTCTCAAGAAATUAG	71739	ATTTCTGAGCAGUGCTTACTCTUACAA
222706131	71740	GTUACACCACCCCAAAGUCACT	71741	GTCATCCTTCUGTTCCTCAGUCAAAT
222713071	71742	CAACAGGGCCAGACUCCATAUT	71743	CTGGGAGUATGGAGGCUGAGA
222713530	71744	GGGACAGUCGAAGAACTUCAG	71745	GCTGCCCAUACATCTCAUCCA
222716012	71746	GGAAGGAAGTTUGTGAGCAGAGUT	71747	TCCAGGATUGGAATTACACAAGUCAAAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222718976	71748	GTGAGAGGUGAACAACCCCUAA	71749	GAGCCUCACCTGCCGUA
222719457	71750	CGGAAGAATAGAAUGGCACTTTTUCAAC	71751	TTGCTTGUAAAGACGTCTGTGUCT
222719902	71752	GGTCTCUGGCTCGTTGUGA	71753	CATGGGAGAGCUGGGCUAC
222720125	71754	CCACCACAGCUCCAGUCC	71755	GAGGTTGCUGCTGCTGGUA
222723458	71756	GUTAGAACAACUCCGGGCAGA	71757	CATTTCTCCCUTATGCCGTGTTUT
222723538	71758	CAGGACGAGUATGCGCUGAA	71759	AGGGTGTTTGAUCTCTTTCATGACUG
222723909	71760	GCCGGAATTATUAATGAACAAGAACAUGA	71761	TGCTCATAUAACACAGCTTCAGCUT
222724520	71762	GGGACCGACAUAAAAGAACUCACA	71763	AAAAAGCATTTCACUTACGATGACGUT
222725328	71764	CACAUGGCACAGAUGGAGGAAA	71765	TTCCTTTTGAGAGUTAGTATCTUGCAAT
222726251	71766	CAGCCACAGGCUCAGTCUC	71767	GCAGGAGGCAGGGAUATCUT
222727421	71768	CGCTCCUACCTTCCTGUGAC	71769	GGAGTACAUTTGCGCGTUCA
222727607	71770	AAAAACTCACUCAAATTCUCAGCAAGG	71771	TTCCCTTTAGAAUGCAGCAGTCUT
222728323	71772	CAGGTAAGUGCTAGTCATTCUCACT	71773	CCATCTGCCUTGTTGTTCATTTUGG
222728834	71774	CAACGUGAACGCGCAAAUG	71775	CGTGTCGUTGTGGCAGUT
222729852	71776	GCUGACAGCAGCCUCAAG	71777	ACACUCGCCUGCAACCA
222734835	71778	GACCTACCTUCTGGAACCTUGAA	71779	GTGTATAGUGCACCAGGUCCA
222737398	71780	GAAAATTCTTCUTGCCATATGUGAGCA	71781	GCTCCTCCUAAGCCACTTTTTATATCUT
222738097	71782	CATATGUGAGCAAGCAGCUGAAA	71783	ACAAAGGCCCAAGCUCCUC
222740386	71784	GATATAAAAAGTGGCUTAGGAGGAGCUT	71785	GGAAGAACAGGAUAGAAAGACTGCTUAT
222742444	71786	GTGGAAGAGTUCTTGAAAGAAGCUG	71787	CAACGAGGUTTTGTGCAGUGA
222742627	71788	CAGCACAAAUGTGTGCACCUT	71789	AAAATAGTUCCCAAGGCATTGAAUCAAC
222743290	71790	GGGATGUAAAGTTAACUCCAGCCA	71791	TTGTCACTCTCUTTTCTTTTTCCTUCCT
222748274	71792	GCAGATTCTGCUAATACCCTGCAAAUAG	71793	TTTGTGCCUGGCTGATTCUGA
222755331	71794	CATCTAGACCAGCUTCTCCCACUA	71795	GCTTTGCTGGUCTTCCATCAUT
222756079	71796	GCCTACCAATTAUAGTGAACGTTACUCT	71797	TGTTTCTGTGAUGAAGGAATATCTGUGG
222767728	71798	CCGGGAAGCAACAACUCUGAT	71799	GGAUCCAGGAUAACGGAGGCT
222768447	71800	CAGACTGCAGGGUTCTAGTTTAUCT	71801	GTGAACTGACAGAAGUACATCTGCUA
222770598	71802	CGTCATGTGGAUCAGCCTATTGATTAUA	71803	TGTGGACGTAUTCTCACTGCTUG
222771981	71804	GGCCCTGUAAAGCAGCACAUAT	71805	CCCAACUCCTTTTGGUCCACAG
222775082	71806	GGTGGUGACCAGGGAGTCTUA	71807	ACGCAGUGCAGCTGAGTAUC
222777284	71808	CAAAGCAGUAAAACCGAACATATGTCUT	71809	CCTTTTGAGGCUGACCACTUC
222778166	71810	ACATCACCAAGUGCACCUACC	71811	GGATTGTGGCCUTCTTTGAGTUC
222782278	71812	CCATCCAAGTUCTGCACAGAGUA	71813	ACATCCTATTTCAUCTTCAGCTGAUGAC
222785067	71814	GACGCTCUCCACACACAUGA	71815	CGACTUCGCCGAGATGUCC
222786472	71816	TCCCTGTCCUGCCCCAAUAA	71817	CUGCAGACCCACAGUGACAA
222786889	71818	GTTCACCCCGUCCCUGAA	71819	CGGTGCCACCUGTGGUC
222787394	71820	GCGGAGGGUCAGGUGGA	71821	CGCACCGGGCAUCTUCT
222789201	71822	TCAGAGATACTUTAGGGACAAAAUCCGA	71823	CATCTCTGCCCUTTCTTTCTUCCA
222789744	71824	ACATACCAGTTCCUATGGTTCCAGTUA	71825	AGCAUACAGGGCCTUAAACCAG
222791338	71826	AAATTTCACUCCACTTACCUACCAAGG	71827	ACTAAAACGACAAUACAAUGACCACCAT
222793833	71828	AGTGTCAGTAGUAGTGATGGTTAUGGT	71829	TTGCACTATGTATUTTATGGGCTAGGUC
222794331	71830	CAAGGTCTUCAATGATAAGCUCCCA	71831	GGAAAGGUCAACATCATCATCAUCAAAA
222796899	71832	CACCTAATCTCAGUCCCACTATAGAGUAT	71833	TCGAGGAAGGGAUGATGAATGTTUG
222798076	71834	AGTTTTGCAGUTATGGTCAAUACCCA	71835	CTTGCCCAUCTTTCATTCTGUGAAG
222799918	71836	GCAGCGGUCACACTTGUAGG	71837	CCTTCCTCGUGCTGACTTUGG
222801826	71838	CTTTACATGGCTUTTGGTCTTCTAAGUG	71839	CATTCUGGCACGCTTUGGAAAAA
222802772	71840	TCAGGAGACCCCACUCATGUT	71841	GCATGGTTTGUCCAGGGCTAUC
222803668	71842	CTCACTAUGAAAAACTGTAAAGCUGCAA	71843	AGATGCAGCUACTACCCAGCUA
222808332	71844	ACCUGGAAACGUGAGCACAG	71845	TGGTTCCTGAAAUAGAGTTCACATGTUT
222808720	71846	CTGCCATTGAUTAGACTGCUGAG	71847	CTTGGTUACAACCAGAATGGUGAGT
222809429	71848	CGGGCTATTUAAGAGGGATGGUACT	71849	CAAAGAAGGCACUGGAAAAGGATTUG
222811857	71850	GCACAGGAACCUGGTGGAAAUC	71851	ACAATGTGAUAGAAGAAGAAATCCGUGT
222812353	71852	AGTTGAACTCUGGAAGGCAAAGUC	71853	TGTGGTTGGAACUTGAGGTGTUT
222814596	71854	GAACTCCTTACUGTTTTTCACGAAAUGA	71855	GCTGATTGTUGGTTGGAGGTUAGT
222815094	71856	GAAGGGTTCTUCCGGAGATACUG	71857	AGAGCAAGAAGAAAUCATCTGAAGTCUT
222820600	71858	GATCCTGGTAUTCTTAGCAGGTUAAAGG	71859	ACGCACAGAACACUCAUGGAT
222822218	71860	CCATTCTUAGAGCGAACTTCACUCC	71861	TGACAGTACACUGCTTCAGTTGAAAUAA
222822751	71862	TCAGATGAACAGACUAGCCACTTUG	71863	AGTTGCAAAATUGAAAAAGACCAAACUT
222822985	71864	GCUAAAGTUACCAGCCACACAGA	71865	GGGAAAAGTGGAUTGTTTCTGAAGTAUG
222824298	71866	CACTCAUGCACGCTTCTGTUC	71867	AGAACUCTGGTTUGGCCACAAA
222825282	71868	CAGTGAAAAAGCAAAAAGUGAGGAUGAA	71869	AGCACCATTUGTAGCACCUGAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222826428	71870	TCCTGTTTATACUGAGAGCACTGAUGAT	71871	GACACAAAGACUGGCTTACATTTTGAUT
222829506	71872	CCAATAAAUCGAGGTCAGCCUAAACC	71873	GCAAACCGGAGUATTTTCAAUAGCAAAA
222833299	71874	CCACAAATAGTACUTCTCAGACCGTTUC	71875	GGATTGTTAAUGGGACAGTCCUCA
222835503	71876	CCGTGTTCGCTUTCTAAGTAGATTCTUA	71877	CCTCAGTGATUAAACATTGATGTUGGT
222838061	71878	AAATCGAGTGGGUTCTAATCATGGAAUT	71879	TCTCTTCTTCTTCAUGCTGTTCTTCTUC
222840073	71880	GCAGCAACUGATGAAAAGTUACAGAA	71881	GGTTTACTTGGUTCTCCCTGUGA
222840891	71882	TTGTACCAGAAGAUTAGGGCTCUCT	71883	CTCACCCGCAGUCTGUCT
222840927	71884	TGGACTGTAGUTCCAGACACGUAA	71885	AGCACTTGACUGGGACCCUA
222845942	71886	CAATTGAGCAGAUTGTGUGCAGAT	71887	GTGTCTCAAAATCUATTTCTTCCCCUCT
222846020	71888	CAATGTCTUACAGGTATCTTCUCAACCT	71889	GAAGCAGTUTATATATTGGUGCCAAACA
222846722	71890	CATCACTTAATUGGTTTTTGGCTTTUGG	71891	CAAAGTTCGCGACAUATCATCCUT
222846773	71892	TTTCCCCAAUGCCTTCTCCUG	71893	AAGGUCAAAGGCGGUAAGAACAT
222847305	71894	AGCTGTTATCAAUATCAAGATGGCUGT	71895	GCTAAAUGGAGCACAAATCTCTCUACT
222847417	71896	CACCUACTGCUGAAAAGAGAGAGA	71897	AATGGCTCAUCGAGGCUCAG
222851068	71898	GGCAAGCATUTTTGGAGGAAAUCT	71899	CCTCTCGTTTTCUTCTTTCTTACCTTUC
222856433	71900	TGTTGTCAATGCUTGGTACTCAUGAT	71901	GGGAATTTCCCAACAAUACAGAGTCUT
222856780	71902	CCCTCTGUGACCCGTCCUA	71903	CACTCACAUGCATGCTTUCCC
222857638	71904	CTTCCTATGUCACCATCACAUCCC	71905	AATCCAAACACCCCAGUAATUACCA
222862702	71906	TCUGCAGACCTUGACCAGAGT	71907	GCAAACCACUGCAACATGAACAUC
222867868	71908	GCCAGGCCCCUTTATCTCTUA	71909	CCACTGAGAGUGACCCTAATCUCT
222869257	71910	AAAUCATAGGTCAAAUGAAGCGCAAC	71911	TGUCTACTUCAGGCAGGAGGAA
222870001	71912	CTTTCAAGAGAUTCACCCAGATUCCA	71913	CUCGAAAACCAGACAAGCUAACC
222870435	71914	CCCAGGAUAAGGAUGGAGAGCAT	71915	GTGTGUATCTGTCCUCCGGAAG
222876091	71916	CCTTACCAUCACACTUCCAGCAG	71917	CATCCGUCCCCACCUAGAAG
222879003	71918	GACTCCTGCGUGTCCTTTGTUA	71919	TGATACCCAGGGUTTGGAGUCA
222881666	71920	GAGGGAAUGCACGTACCTGUT	71921	AGTGCTGATUGACTTTAGTTTATUCCCA
222881883	71922	CAGCCTTAUCTCCGCGUCA	71923	ACTGTTTTCTCCUCTCACCCGUAT
222884262	71924	CCAGCTTTUACATGGCAAUGACA	71925	AGCGCGUATCTGTUCCAAAAGAT
222885161	71926	CTTGCTACAAAAUCATAAAGUGCAACGA	71927	AATTCCCTTCCCUTCTTATGTCTTUCAG
222886771	71928	GCUCTGAGGUCCACAAGAGGT	71929	CAGAGCUGATUCAGACCCACAA
222892556	71930	CTCTTTGTTUAGCTTGAACAUGCGA	71931	CTCAUGAAGGCGCTCUCGAA
222895407	71932	TCCTGTATGACAUGGATGCCUCT	71933	GTTAGAGUCTTCCUGCCCAACAA
222895587	71934	TGAGAAACUGCCATGCGUAAGAT	71935	GGCTTCTCUTTCTTTCCAUGCAG
222898859	71936	AAAGTCGGAGCAUGCTTCUCAA	71937	CAGCCAUAGAAAUGAGCAAAACCAG
222899148	71938	GCGTGAAAUCCGAGTCCTUC	71939	TTGAAACATGCACUACGATGTACACUAT
222902031	71940	GGCAGCUGTGACTCTUGAGAC	71941	AGGTCCUCAGCCCTTAGCTATTUAA
222903910	71942	TGACTCACCACUGTCCTCUGT	71943	CATCTTCTTCCUCTTCTAGCCTTUCAG
222905503	71944	TCCCUTAAGUGCCAAGAGGAAC	71945	AAACCTGGCUGTGCAUCAAAAAT
222906595	71946	ACATUCCAGAAGCGGAATUCCA	71947	GAGCACAAGUTCAAATAGCAAUCAGAT
222908297	71948	TTTTTGAUGGCAGCATTCGAUGG	71949	ACAGCGGTUGACATCTAATATTUGACA
222913496	71950	GCGGAGAUAACTGGGTGTGUT	71951	CCCTCUCAGGACAGAGGAUACT
222917470	71952	GGGTGUGCGCTCACCUC	71953	AUCCCACAGCGCAUCCA
222922922	71954	TGAAAAACUGAAAGAGATGAAGGUAGCA	71955	GAUGCACUCCAACAAAGAGAACAAC
222924649	71956	TGGTGATGCUGACGTGGUT	71957	CATGTCUCCCAACCCCTCUC
222928100	71958	GGAGAGGCUGCCCUGAGA	71959	GCCACUGCGCTTTGCTUT
222929181	71960	GCTCTATGGUCACGCCCAUC	71961	GGAGGTUGGGAACGGTTTCUC
222930507	71962	GAGATGAGCUCCAAAGGCAGUT	71963	TGCTGAGTAGTTUGGATTTCTTTTAGCUT
222935598	71964	CGTTCCCCAGAGAUTCCAAUAACT	71965	TTAATGTCAGGACAAAGUCCGGAUT
222937217	71966	GCAGAAACAGAUTGAAGAGAUGGAGAA	71967	GGGTUGGGAGGACTTUAACCT
222938761	71968	CCAGAUCAGGCAACUGGAGAAA	71969	CCCCGAUCAGAGGTGCAAUG
222941690	71970	GAGTATAACTACGAUCTGCCAAACTUGA	71971	TCACCATGGACUATTTCTGCTTUGT
222945169	71972	GAGCTTTTAAGUGGTAGCCATAGTAUGAT	71973	GCTTCTGTUGCTTGGGACUGT
222952376	71974	ACCTTTTGACAAUAGTGGAGATGCUAC	71975	TGTTTTAAGAGACAGCUGGCAGAATUAT
222955640	71976	GCAAGCGCAGCAUCCCAUA	71977	GAGCUCAGGAAAGTGUCCGA
222957374	71978	CCGCAAAGAGGUCCTAAGGUT	71979	TGTAACCGGCACAUGCUCAG
222962576	71980	TUGTGATGGAATTUGAAGACCACAGA	71981	GCTTCATCAAUAACAAAACGUGCCA
222963426	71982	CTGGCCUGCTCTGCATTUT	71983	CCTUGTTGAATCTATUCGGCGAGA
222964581	71984	TTTCAGCACTTCAUCTGTAATCTTCUGT	71985	CAAGTAGAAAAAGGGCUGGAAAATUGT
222965497	71986	GGTGACTUGGATCCCGAUCT	71987	GGGACAUCCTGGTTTTTAUAGAGCA
222967155	71988	CCTTTTGGGTTTUCCTGTAAGTAGTCUA	71989	ACCTGTGUGAGAAAATCATAGCUGAG
222969030	71990	TTGCACGTAGAUGATCAAAATGTCUCT	71991	TGCCAACTAATAGUCACGTATGTGATUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
222970328	71992	GGAGAATCTCTAUGAGAGGAAGCUCT	71993	TCGTTCACUCAGTGTGGGTTUT
222972175	71994	CGCCACACUGCTTCCTTTUG	71995	CGAAGAAGACGAGGGUCUGGA
222974856	71996	ACAGGAGAATAUGGAAATCTGGTGACUA	71997	CACTAAAACUCTAAGGGCUAAGCCA
222977422	71998	CATTTUGACCGCCTTGCAUCT	71999	TCTCTTTGTCTUCTGCATTTACTUCACA
222979401	72000	TGAGCTUGGCAGGGTTGATAUAG	72001	CCAGTGAGACUGCTTTATTAAGCTTGUT
222980066	72002	AGGCCACTUGGCTCCTCUAT	72003	CCGCCUAAGCCCATCTCTAUC
222981204	72004	GCTCUGAAGACAGAACCUGACA	72005	ACTTACAUCCAAGGAAGTCAGCTTUT
222984915	72006	CTTATCGTAGAUCAAGTCCAAAAGCUGA	72007	ACTGCAAATTTAACUGCTGTGCTTTAUT
222987957	72008	CACUCACCCTUGCACCGA	72009	GGCGCTGUGACTTACAUGGA
222991746	72010	CAGTTTGTUCCCCCTGTTAUACCC	72011	GCAAAGTGGGAAGAAUTTCATCTCCUAA
222996668	72012	ATAATGCCTATACAUTTTGTTGGTTTTACAUT	72013	CTTCTGAATGGUCTTCTCCAGGUT
222996885	72014	CCAUTTTGAACCUGGAGAAGACCA	72015	GCTAGGATTTTTCUCTGAACTGTCTGUT
222997242	72016	GACTTTGGCTGUCAACTTTCGAAUT	72017	GGGTTTUGGCTCCTTUCGG
222998755	72018	CTGCAAATTUATATCCATCAUCCGAAAGG	72019	ACCAGAGAAAUCCAGAGGAAAGTCAUAT
223000431	72020	TTCTTGTGTAAGAAUCCGTTTTAGTUCCA	72021	GGATCACTCGGUACCATGTTGTAAUAT
223004537	72022	CCGTGGAAAUGGGCTTTAGUAGAA	72023	ACTTGATTCTTTTUCCTCAGTTGCUCT
223005482	72024	CAGTTCTTTCUGTGGGTATUGAGCA	72025	TTCTCAAGGCUGTCAAATACAACUCA
223012141	72026	GATCGUGGAAGAATACCAATUGCC	72027	GTGGCATTUACGAATCACTTCTUCA
223012860	72028	CTACCATGTGACUGGCTTATTTGTAUGA	72029	CCTCTGCTGUAAATACAAAGCTTUCAA
223015469	72030	GCCCTCCTUGAGAAGTGAGTUA	72031	GTCGACACAAGGUACTTCGAUGAT
223017601	72032	CTCTTTGACUGGACCATGAAUCCT	72033	ACAGGACCTUCTTAAAATACTGCUCAC
223020999	72034	TGATGGACUGGGCGGTAAATUC	72035	CACTCGTGGUGACCTTGGUT
223022307	72036	GCUCCACGCAGGCAACTUA	72037	CCGACGAGAUAGAAATTGACTTUGAGAC
223023504	72038	CGGACTUGACCGTCAUGGG	72039	TCUGCGGCAAGACGTUCAA
223026331	72040	CGGTGGAACAGUGATGAAGUGA	72041	CCAGCATTCUGACATTAGCTUCAAAAC
223029675	72042	ACCACCAGGUTGCTCUGAAAT	72043	GCCCTAUGCAAAGGTTACUGCAA
223029959	72044	GCCTGCCACAGUGTTCAGTUA	72045	TGTAGAATTCUGTCATCCUGAAGACCA
223031596	72046	CGCAAAGUGGTGGGTTUCAGA	72047	TGCCCAUGAGCTACGAUGAAAAG
223035091	72048	GCTTGCUACCTGGCUGGAAT	72049	CCTCCCGCCAUGGATTTCUC
223037706	72050	ACTCATTTTTACUCAAACTATTGGGUGGAT	72051	CCCTGAACATGUGTAGAAAGCAGATUT
223038330	72052	CCGGTTGAUGTCCAGGCUAAG	72053	GCAGGUAGACGGAGACUCAACA
223038506	72054	GTCAGACTGTACUTCCATACTTGATUCAT	72055	GGTTGTGGAUCGGCTCGTUT
223039345	72056	CCAGCTGTCUTCGACACTTCUC	72057	ATCCTGTAAAGUGCTTTTAGTGGGAUT
223039877	72058	CTTUAGAGGCGCCCCAGUC	72059	GGGAGUGGCCTTTCTTTUCC
223040709	72060	CTGCCAGCTCUCTAAGTCTCCUA	72061	CCACCACCGAGACAUCACTUG
223041857	72062	CCTTTTGTGGCUAGAGGAGUCT	72063	CATCAGTGACCUGAAGGAGGUG
223043830	72064	GTGTGGTGUAGATTTTGCAUGAACA	72065	GTACCATCAATATUCTTTTTCACACAACTUCC
223047037	72066	AACTCATCAACUGGACAGGTTTCAUAG	72067	AGACCACAGGCAGCUGAAUAAG
223048617	72068	GCGAGGGUTCTCCGGGUA	72069	CGGATCCGCUCGAAGTUG
223048618	72070	CCCCCAGGCGCUCTAUG	72071	CCTCTCCAUGGGATTCATATUGCAG
223049351	72072	GAGGGTUCTCCGGGUAAGG	72073	CCAUGGCCCTUGCGGAT
223050670	72074	CGCTCAGGUCCAACTUCGAG	72075	CACCTCTTTGUCGTTGACCTUCA
223051911	72076	CCTTCTACGUGAACGTCGAGTUT	72077	GAUGCAUCCCCCACGCT
223053703	72078	GTCACGTGCAGUTTCACTTCUG	72079	CUTGCAATGCAUGGAGAAGGT
223054323	72080	CCGAATGAGGGUGATGTTTTUCC	72081	AGAGCCCUGAGTACAAGCUGA
223055961	72082	AATTCTGGTUCTGGCTCUAGGAGA	72083	GGAGCAGGUCAACCTCAUGT
223057680	72084	AUGCAGAUGGAGCGCAAAAAG	72085	CCATUGGCGTCGAUCAGG
223058787	72086	TTCAGCTGCCUGTGGTCUG	72087	CAAAGAACCACUCACCTGTTGAATTUAA
223059174	72088	TGCATGUGAACGGTGCUGAT	72089	CCTGATGAGUCTCCTAAGCUGAAG
223060065	72090	GGTTGTAGUCGGTCATGAUGGT	72091	TGGCCTGUGTAGTGCTUCAA
223060116	72092	ACAGAAAUTTAUGGCACCCAAGGAA	72093	GGCAAAGAACCACUCACCUG
223061250	72094	CCCGCUTCCUGAAGGACAA	72095	AGGTAAGGCGCUTCTCCUG
223061572	72096	ACACTTCGAGAGUTCTTCCAAAGUC	72097	AGGCAAAGUGACATATGTAAGCAUACAA
223061587	72098	CTGGGCCUTGCTGTTAAATUCAA	72099	AACAAGCATAUGCACATTTTTAGAATUCCAT
223067622	72100	ACCTTUCCAGAGAGAACTTCCUGA	72101	GCCACCCCUGGTACTGAUG
223069902	72102	TTTTATTTTCTTTCUAGGACTCTCAGCAUGT	72103	TCAACAUAGGAAGGCCTCATCUCT
223069905	72104	CGCUGGTTUCCGAAGACGA	72105	GCGGACACUGTGTUCAGAACT
223073479	72106	AAGGCAAAGCAUTAGGTACTUGGT	72107	TCCATCTTGUCAAAAGTTGTCUGAAGAA
223074051	72108	AAATGTTCCTUCAAGTCTGTGCCTUA	72109	TGCCAGATUCTTGGTAGUAACCCT
223079261	72110	TCTTGAAGUGAACACCACCAAAAAGAUA	72111	CCTTGAGAUTCTGGUGGACAGAGA
223082092	72112	GCACCAGUCCAGTATUGGCT	72113	TCCTTCCTAACAGUTTACCAAAGTUGAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223082408	72114	CCTGTTCTTTCUGTCTCATTAGTGGUT	72115	GAGAAGGUGGAACAAAATCCGTAUCA
223082955	72116	GCTTCTTCTTCCUCTTCAAAATGCCTUA	72117	TGAGGCTTTCACUTGAATGTAAAATAATUG
223085343	72118	GGCATTCUCAGACACAGACUGA	72119	CCCAGCAGUACTCAGATGAUGAG
223088530	72120	GTTTTGAAGCUAGGGAUGGAGGAA	72121	GCTCTCUCAGGACCTTGCTUG
223092791	72122	CATGCATCTCUCCCTAAATCTGUGG	72123	TCTCTACAAUGGAGCCCAGCTUA
223096061	72124	CAGAGTCAACAAACCAAUTTAACAGCUA	72125	TCUATGATCAGGUGCACCCAGA
223100270	72126	AGTTGGTGUTCTGCACGUCAT	72127	CCGAGCAGCACUTGTTTGUA
223103332	72128	TCCCAAAUCTATTCCTAAUCCCACCT	72129	AGGCCCTAUTGGACAAATTUGGT
223104068	72130	CAGUAGCAAAGCCTATGAUGAGAACT	72131	GGGATAGAGCGAAUACACAGACUC
223104608	72132	TGGATTATGCUCCCCACCAAAUT	72133	GCAGTTACTGTGAUGTAGTTGTCTATGUT
223106451	72134	GCTGTCUGCCAACACCATCUC	72135	ACAAATCTGCUAAAACCCAGAGAACUAT
223107326	72136	CAACATTGGUGTGTAACAAAAUCCGT	72137	GATGAGATACACAGUCTACCTGGUAAGA
223107583	72138	AGATGTGUAAGCGCAGCCUT	72139	ACAGAAAAGCUGCACTTTAGGAUAACA
223115559	72140	GCCTUAGGAAGAACTTUCCCAAAGAG	72141	CCTCCTTCUGCCATGGAACUG
223118898	72142	AGGTTCCTCUGTGCAAAGCUC	72143	GAGAAATGGAGAAUCAGCCCCAUA
223119828	72144	TGCTCACGAAGUTTATCCACAUCA	72145	AUTTGATCTUGGAGGCAGCAGAT
223123591	72146	AATTGTCACGAAACAAUGAGCTTTUCA	72147	TGCTAAGGTTACUCCATTTTCTGACTUT
223129514	72148	GAUGAAATCAGACUCCGACCAGAA	72149	CCTAACTCTUAAGAAGGGCTGCAUAAAA
223133556	72150	GAAGTTACCCGUGAGTTCGTATTUCT	72151	CAGCCTCUTGGAAGAUGCCAA
223134257	72152	ACACCAGTGCCUCTATCCCTUAA	72153	CTUGGCGCCACCCAGAAUA
223138926	72154	AUTCTGGGUGGCGCCAA	72155	AAAGATTUGATGGTAACAUGAGGACAGT
223139147	72156	CUCACATGAGACAAUAAACAGAAAGCC	72157	GCATGTGGCCUGAAGTGTCTUA
223140553	72158	GAGCCCCCUGAACTGTGTUAT	72159	AGTGACTCCUCCACGACUGA
223141663	72160	CAGACUCCCCAGUCAACCAG	72161	CAAGGAGTTCCCAUGCACTTATCUT
223146647	72162	CTATCCCTGGUGAAGCATGTCUC	72163	TTTTAAGTTACTGAUCGGCCATTTCUCA
223148608	72164	GACTACCCCUTTGCCAGTCUT	72165	ACTTTTUCGCCACGCCATTUG
223149212	72166	GCUGACCGCCACTUCCAT	72167	GGACUCACGTGTGUCCCT
223155579	72168	CCACCCCUAGAATCTGCCTAUCT	72169	GATGATACGTCCGUGATTGATGATGAUA
223156542	72170	AGGAGGAGGGUGTTGAGTGUT	72171	CATCTTCAACCUGGAGAAGGAUGAC
223158968	72172	TTCATGGTACAUCACTGACAATGCAUA	72173	GATTTCTCCUGGCTGTCTCUGAA
223159355	72174	ACAGCAGGCACUAGGGACUAA	72175	GGCTAGGCTCUACCTCTTCCTUAC
223161250	72176	CCCAACCAGGAUGUACAGCAT	72177	AACGTTCTUTGTCCCATUGCAG
223169258	72178	GGGCCAAACUGAGCAGAGUC	72179	GGCATTCTCUGCTCTCTCTCTAAUACT
223169999	72180	GGUAAAGGCCGATAUGGAGAAGT	72181	AAATTGACTGAAUCAGTGTGUACCCA
223170095	72182	TGCAGUAAAAGGCCCACATGUT	72183	GTCGAGACAUCTTGACTGATGTUGT
223175118	72184	GGTAAAAUAAACACCAAGACGTGGUAA	72185	CACCAGAAGTCAUCAGAATGCAAGAUA
223177753	72186	GTGGGCAAAGAACAUGTTATUCACAA	72187	CTTCTCCCCUTTGGCTGATCUG
223177865	72188	ACATCTGACUGAAAGCTGTATGGATTUT	72189	GCATTGCTCUAGGAATTATAGTAGGTUGT
223178786	72190	TCCCGTACTUGGTGAGGGTTUA	72191	GGTGTGUGAGAAGAACAUCAAGAGG
223180129	72192	GTGGATAGACGACAUGGAGGUT	72193	ATCATACAGCAGGAUGTTGATGGTAUC
223184524	72194	TCTGGGAGCCCUACCUGAA	72195	CUGACCAAAGCCGCTGUG
223186865	72196	GGGAAGUCGTCCTGGTUCAT	72197	CCGUGCTCTUCACACCCA
223189535	72198	GCACCATGACUGACGTATTUGCT	72199	GCCTTGCTUCATATTCCAATUGCC
223190183	72200	CTCUGCACCAGCGTCTUG	72201	TCUGACCGCCACCCUCT
223191977	72202	CCUTCCTGCTTUCAAACAACACAA	72203	AACTCATCAAAAAUGGAGAAAGGUACACT
223192411	72204	TCACCGACCAUGAAATAATTUCCAGT	72205	GGTGAAGACAGUCATTGUAGAACCA
223193687	72206	CUTACAAACAGATAUGACCAGAAGGCA	72207	GCTCTTCGCUGTTTTATCACTUAGAAAC
223193788	72208	GCAGAGAGCACAUGGGCATUA	72209	AGAAGAUCCCAAACCCTCTCAAUCT
223194452	72210	TTGTATTTGATUGCGTCATAGUACACCT	72211	GAACGTTGGCUCTCTACTGGUT
223198077	72212	GCTCACGGCUCACAACAAUG	72213	GGACTAACAGGAUTTTGGCCTCTTUT
223198887	72214	CUGGGCUGAACAGACAGAAGAT	72215	GGCACGTTTAATUCTAGTTACTCTCTCUT
223199473	72216	CTGUAGATCTGGUGGCAAAGGA	72217	CAUCCAGAAGGAGAAUCCAGCAC
223204617	72218	AGCGCATGCUTTTTCCTGAUG	72219	CTTACCTAGGCUTTGGGATUGGG
223209775	72220	AGAAACAGGAUTGCTGCTTCUCA	72221	CTAGGGACAATUCTGGTTTAGCTUCT
223211645	72222	ACCGAAAACACUTTGGAGCTGUA	72223	TCAAACCACGCUGTGTCATTUAAAAAT
223211663	72224	GGGCCAAUACAGGCCAUGAT	72225	GGTGGUCGGGTCCTAUGGT
223213616	72226	TTCUAGAACAGGCAAATUCAGAGAAG	72227	TUTTCCAGAUGGAGCCACGAA
223216196	72228	TCATCTGAATTTGAUCTGGAGAGGTUG	72229	TTTAACAAGUCACAAGATGGACAGUGA
223221577	72230	CTGTTCCTCAGUTTGTCACTAAAATCUC	72231	GCAAATTACCUTAATTTCCATAGUAGGGACA
223224502	72232	TGTTTAGCUCAGACTTTTCTUCAGAGAC	72233	AGCCTCUGCCCTTTUCAAAGAT
223226597	72234	CATCTACCTTGUAGGGCTCACUG	72235	TTTGTGTGTGUGGTTGTTCTCUCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223234899	72236	AGTCTTTTGAGCAGUTACCTATTTTGUAGAAA	72237	GCCCACCAGAAGAAUGATAAAAUGAGT
223235434	72238	GGTTACTTTAGGUGCAGAAAAGACUG	72239	ATTCCAGGCAGGUTTTCTCATATTCUT
223236603	72240	TTTCCTTTGATAGGUTTGATATGTGACTAAUAA	72241	TCTGAGTCAGUCTTATCACCTGUCA
223240815	72242	AGTGAUGAAGCTGCAGUACACAC	72243	GTTGCACTUAAGCCATAATGACGTTUA
223241048	72244	CCACCTTCTAUGAACTCCCAGUCT	72245	ACCAUCATGTCCUGGAGGGAA
223242236	72246	GGCTCCTAAAUGTCACCACUGA	72247	CTTCGUGCACTCGGUCAAG
223242481	72248	CGGCUTTCUCGGCCAGA	72249	GCCTTCGGUCACCTCUGT
223246682	72250	GCTGUCGCCATUCAGCGT	72251	TGTGTCCCAGUAGGGCTTTUC
223247682	72252	GGAACAGAGAAAAAUTGACTCUCCAGAA	72253	CTGTGATGTTUAGATGGGAGATGUCT
223249048	72254	GTCUCCCACGAUGCACCAA	72255	GAGGUGGACAGGUGAAGCAG
223249581	72256	AACAAGUGGTTGUCCAGCAGT	72257	GGCAGAGAATGUGGCATGTTGAUA
223250648	72258	ACCCCTTATCCUCACCCCAAUA	72259	GTGTGTGACCCAAACUTAATCTTTTUCT
223252821	72260	CCTCAUATCCTCTTUGCAGCAACA	72261	GCAGAUGAATACCTUGGCGGAA
223254000	72262	CTGCTGCUGCTTCCATTAAGUC	72263	GGTGCUTTATGGTTUGGAGGGAT
223254481	72264	GGGTACAGAGCCAUTTTCTGAUG	72265	TTCGGCCCUTCCATTUCAGAG
223255532	72266	GCTTCAAGCUGTTAGTGAGUCCA	72267	GCTACAUCCTATCTCTTUCCAGCAA
223258804	72268	CCTTGGGCUAAGAAAGCCUACA	72269	CTGACCATUACCAGAAGTUGCCA
223259539	72270	GGAAGACUGCAGGAUGAGGAA	72271	CACCAGCUGUCACCAGGAG
223259720	72272	GGCACTGTCCUGATAGATAAAGTCTUT	72273	TGCTCTATTCCCAUTTTTACCGTUCC
223261543	72274	GCTCGATGCUCAAACCCCUA	72275	GCUAGCUCAGGAAAAGAAGAAGGA
223261736	72276	TGTGGTCAUGGGCCAAATCUC	72277	CTGCAGUCACTGTGAGGUAGAC
223261895	72278	GTGATCACCACAUTACCGTCUGT	72279	GCCTCCAGGUCCAACGUG
223262074	72280	TCCGGCUCCTGGUGACA	72281	GTCATAATUGCGGGCCUCCA
223262160	72282	CGGGCACGUTGGACCUG	72283	AGAGGAGGGCUCGGUGAAA
223262376	72284	GGAGACUCACTCGGGAUCCT	72285	GGGTAGAACUCGTCAGUGAAGA
223264297	72286	TGACATCCUGCAGACGCTTUT	72287	CATCGGUCTGCTCUGCAGT
223264351	72288	GTCAAGGAGUGGGAGAAAUCAACA	72289	CTTCTGGAAATAUGCATTCAGGACUAAGA
223265514	72290	AGAGAGTAUGTTCACGAAUCAGAGACA	72291	GAUCAAGTAUGAGGCCAGGCT
223266972	72292	AACCAGGCGGGAGAUAUACCT	72293	CATTCAAAGGCAUAGAGACACUGGAT
223268881	72294	CAGATACTTGUGCCCAGCAAUC	72295	TGTAGTTCGGAUCTGATATGTTUGCAT
223269928	72296	CACTGACCACCAGUATAGTUCCA	72297	CCUGTGAAGAATUGGAGGCACT
223270696	72298	TGACGGUTCACCTUCAGCAC	72299	TGCCAGGAUATCTGCCUCAAC
223271455	72300	CTTTCAGGGUCCATGTGACATUC	72301	CAGTGACCACCUGGAGACATAGUA
223271587	72302	AAACCTCCCCUTCAGAGUCCT	72303	CAGGTCTAGCAGUCTCCAGCUA
223272390	72304	GACTAGCAUAACGAAGTGACACCUT	72305	GATCCTCTCUGTGGTGACCUCT
223273342	72306	GAGGGUGACTTAGAAAAUAGCACAGA	72307	CATCTGGCAUCAAATAAGUGGAGAGA
223275237	72308	TGGUTTTAATUGGGAAAGGAAGAGCAT	72309	CACAAAUACACCAGCGAGGACTUA
223276627	72310	ACAAGTGCACAUATACCCACTCCUA	72311	CAGACTTCTGTAAGUTCTCCAAGACAUT
223281376	72312	ACCAAUCATGAUGCCGGAGAAAG	72313	TGACTUGGGACCAACUCAAAGG
223282603	72314	CCAGCAAUCCCGCCUCA	72315	CUGAGAGCAGCCGUAGCA
223283109	72316	AGGAACAATTCUGCTCATTCACUAGAC	72317	CTTCTGGGCCUGTTTCTCTTTUC
223284405	72318	ACCATCUAGCTGCAUCAGGAGAT	72319	GTCATCTGUCTTAGTTGTCUGAGAGG
223285061	72320	TGATGACATCUCCTGTGACTCUCA	72321	TGTATACAGTTCCAGUTAACATCTGGUT
223285617	72322	TGAGUCCGAAGAGCTCUCCT	72323	CGCAGGACGUGTTTGAGAUG
223288157	72324	TGTCUCAGAGGGAAGAGAUGGT	72325	GGCCTATTAAUCTGTGCCACGUA
223288694	72326	CCCGAAUGCACTTACUAGAAGAGG	72327	CCAGGACTCAUAGCTCCAACUG
223289199	72328	CATCUGGCATCTUGGCAAACC	72329	TCCUAGCCCCACCTTCGUAA
223289373	72330	GCCAGCTCCUTGAAAAAGCAGUAT	72331	CCGCUGACCCCATCCTUAC
223291112	72332	ACAGCTTTCTAAUTGCTGGATTATGUAT	72333	GTCTTCCAAATUGGTCATCTGAGAAUG
223292186	72334	CATTAGGUCGGCUGGAAGAAGT	72335	CTGACTCTGTAACAUTCCATTACCGUAA
223294348	72336	CCATTCTCAGAUGACCAATTUGGAAGA	72337	GGTCACTACGUTAGCTCACATTTUAAAGT
223296249	72338	CAAGACCAUGAATAATCACCTTUCGGA	72339	CCTTGCCTTAAAGGUTGTACATTTTCUT
223299103	72340	TTTCTATGATATGCUCTATTTTTCCCCTAUAAG	72341	TCCTGCATTCCGUTATATTTTCACAGUA
223299251	72342	GGAAACCATCAUACAAGAGAAACUCACT	72343	AGCAATTAUCACAAGAAACATCUGGGT
223304037	72344	CGTGCTTUGAGAGTGATCTGAAUT	72345	GTCCAGAAGAAGCCAUAGCTUCA
223304441	72346	ACAAGGAAGTATUGAAGATGAAGCTAUGG	72347	TCGAGAGAAGCUGTACTTGGAUCT
223305399	72348	GGAGUGACACCTUGAACACGAA	72349	CGGAAAAUCTTUGCAGGAGGGT
223307258	72350	TCCUGATTTTTGUAAGAAACACCCAGAT	72351	GAGACCACCTTUTGCAATCTAATTTGUA
223307757	72352	AGGGAGATGAAUGGGAACTGAGUA	72353	TTGAGACUCAGCCATTCUACACAC
223312913	72354	CCTGGCCTUGCTAGTTCATAAUCA	72355	ATGGUATAAGGTGTACUAGAGGGAAGAC
223322098	72356	TGTCCCGUTTGTGACUGCAA	72357	TCATGGTGUGCCTATGGCAUC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223322625	72358	CCACCCCCACUTCTTCAUGG	72359	CTCACGCAGGUTCCCTAUCT
223332223	72360	CCTGAGTCUCCCATCTGTCTAUGT	72361	CACACUCCTCAAUGGCAGGT
223333005	72362	CAGGGAAAATCUCTCCAGCTGUA	72363	GTCAUCGAGAGGACCTUCCAC
223340972	72364	ACTGACCTCUCGTCTGGAGAAUC	72365	GCAGGCUAGCAGGGCTAUC
223346864	72366	TGCCTCTGUGAATATCCCUGGAA	72367	GCCACAGTCUTGATAGCATCAUGG
223347388	72368	GGGCATCCUTTAGGGTCCUG	72369	TTTTGCCTTUAGTGGTCCUGAAAAT
223356244	72370	CCUGGCAGCGGGTACUAA	72371	CTTCCUTTGCTTCUCCCAGAGG
223358944	72372	CCACCAGUACCATCACTCTUGAC	72373	GTAAATGGATGUACGCCTACCUACT
223372348	72374	CCCAGTUCCACCCCGTTAUA	72375	CACAACCTGCCUTTCTGATTTCTUAC
223374020	72376	ACAGTGCTGACUGTGTAATCTTGAUT	72377	GTCTGCGAUACTGUGAACACCAT
223379060	72378	GGCAGAAAACCCUACTCAGUCA	72379	CCAGAGGACAUGAGTTCAATGGUA
223388896	72380	CAGGCGGUCCCCATGUA	72381	CCCTCCCUCTTCTCCUCCAG
223396098	72382	GAGAAGAGUACCCCTUGCCAAT	72383	AAAGAACACACAUTGCTGTGGUAAAAA
223396471	72384	CTCTTGATCCUTCCTATACCAAAUCACA	72385	ACTGCTCTUCACATCTTCCTUCAG
223399585	72386	CAGAUATCAACUGACCCAGGCA	72387	TTGTGCATGCCAUTCAAAGGATTUT
223400109	72388	GCACCTGUCCCACTCTCTCUT	72389	CTGAACGGCAUCAAGGCATUAC
223416464	72390	GTTCCTTGGTUCATGTCATTGTTUGT	72391	TGGGCTGTAGAGAAUGATTGATGTTTAUT
223420452	72392	AAAGTGTAAGAATTAUGCCAATGTGTTTUGA	72393	GCTGGGTTATAAUGCCATCTCTTUGT
223420515	72394	ACAAGAATTUGAAGCTGCCATUAAACAA	72395	CTCTGTTCTGUCAACTCTAAAAATTCTCUCA
223420540	72396	CCAGCUCACTGCTAATTUACAACAA	72397	GCATTAGTAATACTUACTTGCTGAAATTGAAUC
223423206	72398	CAGTTAGGGCAGUTGGCTCUT	72399	CAAGCTCTTATCUGAGCATCAGGUC
223427396	72400	GGAGCAGCACUTTCCTCTGATUT	72401	CTTCCATGUCCTCAGGGCTUC
223430086	72402	AGCAAGACCAAUTATTAAAGGUGACAGT	72403	ACACUGATTTACCTUGAACACGAGAAA
223432375	72404	GGTCCTTGUCTCCAGAGGAUGT	72405	AACCACAAAGUGCCAGTCCTUA
223432807	72406	CAGATTATTGGGAGCCUATTTGTTCAUCA	72407	ACAGGGAUGAGTUGAAAGAACAGAAG
223433067	72408	TGAATCTCTCUCCCTAAGGAATATUGCT	72409	CCAACTCACTUTCCATCATCTCUAGAT
223433634	72410	AGCACAAGACAGUCCGACUC	72411	GAGUAGCAAAUCAAAAGCCACAGAAAAT
223434462	72412	CAACAGAGTTUAACATAAGCATGAUGACAT	72413	TGGATAAAUGAACTGGAACUGGGAAAA
223435409	72414	GCCTTTATTTTUGGAAGGAGATGGTUT	72415	GCTGAGGATUGCATAGATACAAAGTUGA
223436026	72416	TCATCTTCTGCTUCTGTTTCAAAATCUCT	72417	AATCATTCTGAACAUCCGCTCUGT
223436077	72418	ATTGCTAAGUGAGGTATGTCTTTTUCCA	72419	TTACACAAACATCUGGAGACACATCUT
223437149	72420	TGGAUCCAGGGCTTCTUCAGA	72421	CCCTTCACTGAUAAATGTGAATCCUCAA
223438220	72422	GGACTCUCCAGCTGGGACUAT	72423	GAAACGCTCUCGCCCCUA
223438756	72424	CAGTTCCAGTTCAUTTATCCAAGTTGTUT	72425	AGAAGTAGATUCAGCCAGAGAAGUGA
223438771	72426	AACTTTGTATCTAUGCAATCCTCAGCUT	72427	TGACCTAGCUGAAACTGAUAGAGGAAAT
223438922	72428	AATCCTCAGCUTTCACTTCTCUGG	72429	TGACCTAGCUGAAACTGAUAGAGGAA
223439321	72430	CCTCTATCAGTTUCAGCTAGGTCATTUT	72431	TGGATCCAGACAUTGAATTGTCUCT
223440315	72432	GTGTGTTUCAGAGTGGGUGAGA	72433	CCCAAGGGUAAAGAGAAGAATGGUG
223441179	72434	CTCTAAGCCCAGCUGAGATCTUAC	72435	TGTCCCACUGGAAAACTGGATTTAUT
223442538	72436	CAGTCCUCACTGGCGCUT	72437	CACCTGCUCAAGGGTCTCUAC
223442548	72438	CCTCAGAAAGCAUCACCTCAAAUG	72439	GTGCTTAATUCAAGTCAGTGGTTUCAA
223443770	72440	ACCACCCCAGAGUAAGAAGCTTUA	72441	AACTTGGTGAUCTTCTCATTGGTUGT
223447459	72442	CATTGCCAUCCTATCCTGCUCT	72443	GCTTCTTUACACCACGCTTAAUCA
223448345	72444	AACTCCAGCCAUCCCAAGUC	72445	CACAGCUCTTCCTCUCAGAACAC
223454192	72446	ATCCAAACGAUGTGTTTACTGUCAGA	72447	CCTGAGCUCGGGTCAUCAGA
223455681	72448	GAGGCCAUCAAAGCTCAGGTUAA	72449	GGGTACCCAUGTCCTTGCUG
223459480	72450	GGGAGGACUAGAGGCACTATUC	72451	GAUCCACAAGCCCAACTTUCAAC
223459586	72452	CTCTGTAAUGGCTAGAUCCCCAGA	72453	GGCCAAUGACATGCTUCCAAAA
223460541	72454	CCTTCAATGACUTTCTAGTAACUCAGCA	72455	GAGTGGGUCCCATCAGTTUGA
223462024	72456	TGACCAGCTAACUCTCTTTGTTTGTUT	72457	GCAAUTATGTTAGCUAGGAGCAGAAAGT
223463337	72458	TTACATGAACTCUATGTCGTGGCAUT	72459	CCATGATAGGCUCCTGAAAACTAAAAUC
223465409	72460	GCAGGGAUACCTGGAGGAUGAT	72461	CTAGTTTGGTUTTCCTCTCCTUCCC
223465859	72462	CCACAAAATGGAUCCAGACAACUGT	72463	GCTTGCTCTGAUAGGAAAATGAGATCUA
223467808	72464	CAACAGGGACCUCCGUCAG	72465	AACAAGGGUCAAGGTAATCACAAUCA
223471334	72466	AGATGGGCTGUGAAATTTTATCTUGGA	72467	TGCTATTTTGACUTCACCTTGATUCAGT
223482884	72468	ACCTTCCAGAAAUCCAGTTCTTCUACT	72469	AGAGGUCCAGAGGTTTCCUACC
223483293	72470	TCCCAGCUTCUCAAGGACAGT	72471	TTCTGGCCAGUATAGAGAGTTCUACAA
223483934	72472	ATCATCTCTTUGAGGTACTGCCCUA	72473	TTGGGTTTCAAGAUCCCTTATCAGTUC
223484216	72474	GCUTGAGAUGGGAGCAAACAGT	72475	TGAAGAGCCACCUGCGAAUC
223484756	72476	GAACTGAUAAGGGATCTUGAAACCCA	72477	AGCATTCATUGATGTCTTCTGUCCAAT
223491540	72478	TGAAAAACTUCAACAGGAATUGGCAAAT	72479	TTCTTCATUAGCGGTTTCTACTUGCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223495661	72480	TGUATTAAGGACATTCUCACCAAACACC	72481	TCTTTTTCCCUCAGGCTTTCTGUT
223498101	72482	TCCTGGCACUGTCTTCCCUAA	72483	CCCTACTGCTUTCCTTTCCTCAUC
223498571	72484	ACTCTGCCTCUCCCAACTGAUA	72485	CAATCAGGCAUCGTCGGAAATATUC
223500187	72486	CATGGTAAGGUTTCTCTCCTGUGT	72487	CCAGAAGACCUCTCATGCCUT
223500523	72488	CTGAAAAGCUGGCCTUGGAAC	72489	TTCCACACTTUCACGTTCTCTCTUT
223504149	72490	CATCUGAGCAAAGACAAACCUGAAC	72491	AAGTTGTAGCAACCUTGTTTCCAAAUT
223505437	72492	TTCTTGAACTTCUGAAACCACTATCGUAA	72493	CAAACATCTTGGUCACGACGAUAC
223505887	72494	TTTACCACAGCAAUGTGTGTTCTTUG	72495	CTGTCCTUGAGCATCCCTUGT
223507169	72496	CATGACAAATCUGCCTGCTGUG	72497	CATGAAGCCAGUGAGTACCUAGAAAG
223510004	72498	TTTTGAAGAAAAUGGCAAAGGTUCCAT	72499	GCCTTGTTCTUGCATGTCTTTTATTUGT
223512051	72500	ATCAGCTAACACAGGAAUTATTCAGCUT	72501	GAGCATCCTCTGUAAGGACTACTTCUA
223513338	72502	CAAAGGACTTAGAACUTACCCAGTGTUA	72503	CTCAAGTUGGATTTGACUGACAAGAG
223514492	72504	GAAAATAGTUGAAGAAAAAGTGGCUGCT	72505	TGACCCCAACUCATCTTCTCTUAGT
223516717	72506	GGTCAAAGCAAUATGGACTCUGAGAAC	72507	GCATTCGUATCCACAGAUAGCAAAAGAA
223518210	72508	AGGGTTGCUAGAGCTCCTTGUA	72509	GGAGCTGGACUAGACACCTUG
223518218	72510	CACUGAGCATAUCCAGACCCA	72511	TGGTCTGTTGUCCCTGGTGUA
223519358	72512	CTGTTCTTTTGGAUAGCATGAAGCTUT	72513	CAGAUAATTTTTATGGUGGGACGAGGAT
223522631	72514	TGTTCATAGAACGUAGGTAACATGUGG	72515	AACTGTCTCAGGAGUAGGAAGGAUT
223523988	72516	TCCCAGGUGCCAGTGACUAA	72517	GGAGAATAACUCCTCGGTTCUAGGG
223524609	72518	CAGTTCAGGAAUATGCAAAATTCTGUCA	72519	GCATTTCAACAACCUGGCTTTCTAATUC
223524897	72520	GGGTCAGATATAUCAGCATTAACCTUGA	72521	TCTGTAGTTCUAGCAGCTTCTTTTCTTUT
223526436	72522	TTTTAGGCUACAGATUGCAACCCA	72523	CTTCCGTAAGGCAUCGTAACACAUAT
223526953	72524	GGAAGCAUGUGACAACAGCAGA	72525	TCTCCTTGAUGGCCTCUGAACT
223529483	72526	CAGGTTGTTGAAAUGCATACTAGTTUGA	72527	AACTTCAACAUCTTGAGGGCTUCT
223532289	72528	GCTCCGGAAUTGCCGTTUAG	72529	TGTCTGAAUGTCTCCCCUGGT
223532950	72530	CTACTGGAUCCTGGGAGGTUCA	72531	CACTATTCTCUGAAGCTGGCTUGT
223533762	72532	ACTAUCTCAGCTTCUACCCCAACA	72533	AATCTGACTTTTGUGAGCTTTCTAGGUT
223536280	72534	GUGTTGCTTTUGAACAGGGCAA	72535	CCCAGCCCAUGTAATTTUGACA
223539842	72536	AGGAGAUAGCCTTTUCAGGCAAG	72537	CUTATCTGAGCAGUCCACCACAAAT
223540041	72538	TGTCCCTTCUCTGTCCTCCAUT	72539	CAUGGCGATGUCAGCAGAAAG
223543451	72540	GCATTGTGUCAAGACAAGAGGUCA	72541	CTAAACTACCCUGAATTATGGCUCCAA
223543832	72542	CTTGACCGAGGAUGGAGCUAA	72543	GTCCAGAAGGGUACACAGUGG
223545729	72544	GCCCCAGCAGAACUCUCA	72545	CCGGAGUGCCACCTCUC
223546357	72546	CGCCTCCUCGTCGTCUT	72547	GGGUAGCCCTGGUAGCC
223547092	72548	AGAAGAAUGACATGCTGTTUCCAAGT	72549	ACATCTTCAGGTTUTCTGTCTAATTCCUT
223547417	72550	CTCAACCAACUGCTCACGUC	72551	AACACUGCGAGGCCAUGT
223547457	72552	GGGCUACCAGGGCUACC	72553	GCGTGGUGGCTCCTTTGUT
223547643	72554	ACATGGCCUCGCAGTGUT	72555	CCCTCCCCACUCAGCUGT
223551163	72556	GCTTCCAGUAAAGATCGUACAGAAGAAT	72557	AGCTCTGUCTTGCTCUCGAAG
223556064	72558	CCAAGGAGAAGUTGAAGAACAAACATUT	72559	AGGACAAAGUCTATTACATUGAAACAACCA
223556325	72560	CATGATGUGCCCCAUGGAAC	72561	GTGTTAUGGACGGCTGGTCUT
223556481	72562	AGCACTTTAGGUAGAGAAGTTUGCAAT	72563	AGCGTAATACCAGUCTTTTTCCTTTUCT
223557787	72564	CCATATGTCATUTTCATTTCAGCUCCCT	72565	TGAGAATACUCAGGGCAAGACUCT
223558525	72566	CAAATACAAGCUGAAAACTTTGGCTUAC	72567	GTCAGACATAAUGCATGCTGAACTUAC
223558752	72568	ATTGCTTCTUGCTGATCTUGACAAAG	72569	TGTACTGCCAAGUTACTTACATTTUCAGT
223559776	72570	CUCGCGAGCGCAATUCC	72571	CAGACCATGAAUGACTTCGACTAUCT
223559778	72572	TGTAAUTTGGCTCUGGGCAGAA	72573	GCAGGTTCAUACAATGGTGTTTATUCAAA
223561270	72574	GAAGCACAAGUATTCUGGGCAAAA	72575	TTAAATAACAGTAAAACACUAATCCAGCCAAUA
223561744	72576	CGAACCCCACAGUAAGGAUGAGA	72577	AAGTCATTGCCUGGCACAAAUG
223571185	72578	GCCCACCCUAATCCTGTGUT	72579	CCAGTCCAUTCCCAGCUACC
223574253	72580	GTTCCCTUGCCAAGGAGTTUG	72581	ACAGTGTCTTTUGGTTTTCCTCTTTCUT
223578223	72582	CCAGCACCCUGAAGCTAUAGT	72583	AGGAGAATACAUCCCCGAGTCUG
223579249	72584	GTCCAATACCAUTCGAAGCCUGT	72585	CTCACCCCUTGGTCCTGTUC
223580432	72586	AGCAGTGGUGGATTTGUGAAGT	72587	GCATGGGCUGTGTAGGTGUC
223582489	72588	CCTTTCAGUGAGTTTTCTGAGUGCT	72589	ACCTCAAGCAAAGUTTTAAGGCAATUT
223583369	72590	TGATTTATTCTGTTUTGTTTGCCACCUT	72591	GCTAGAAATAGTUGTATTCTGGCTUCCT
223586299	72592	TCUTGCATTUGAAGAAGGAAGCCA	72593	ACATGGCATCUGTACAGTGTCTAUAAC
223588249	72594	AGGCAAGUATAAAGGAAAUAAGCAGCA	72595	CTACTCTCTGAUTATATGCTTGCTUGGA
223590454	72596	GCTGTTGUCACTATTGCATAUGCT	72597	AAACATGGCCAUAAGGACTTATCTGUT
223591089	72598	AACGTGGTTTGUTAAATGGTAGTTTUCC	72599	AGGCGATGAGUGTGAGACTUAGT
223591659	72600	CGAATCUCATGCCTUCCAACC	72601	GTGGCGAAGCCUGATCCAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223592024	72602	AAATCTGGCUCCGCAGGUT	72603	TGGTAATAGGUGAGAAACCCTATCGUT
223599813	72604	GTGTAGCCUGTAGCTGGGAUG	72605	TTCUACAACCAGGACCAUGAGAAG
223601257	72606	AATTCGAGUGTGGGTTTUCAGGT	72607	GAGGAGCAGGCUGCTUAGAAAT
223601702	72608	CAGGCACCACUAACTTAUGAAAAGGA	72609	AGATGTUGGCGAGTGUAACCAAG
223603221	72610	GCAACAAGAGUGGAAATGUGGGT	72611	TGGACACTUGCCGGAAGTTUAT
223604539	72612	GATTAATTTGCAGGUTATTGCGAGTGUT	72613	AGGTACCUTTTTAACTTCUAAAGCACAT
223604918	72614	CCTCCAUGAGGATGAGCUCAAAA	72615	CCCTTGAUGCCGAGTCCUG
223605033	72616	GGAAGTGUGAAAGCATTGAUGGAAT	72617	ACTGAATAAUACACAGGTAAGAAATUAGGAAA
223605569	72618	GCCUGAGCAGGTTGAUGACAG	72619	CCTGTAGUCAGGAAGGACCACUT
223613512	72620	CGAAGAAGUGAAGGAGTTCCTUAGT	72621	GCAGGAGUGTGAATGGACUGG
223613698	72622	TGACCACGGAAAAUTACUGAAGAACA	72623	TTTTATTTTGATUTTCCAGGACUGCAACT
223613821	72624	GTAGCAACUCACCTGGCCTUA	72625	GAGATCAACCCUGAGGGATTCUG
223619994	72626	TTTCTCCAGTUGGTTACATACTUGGAC	72627	GCAAACAACAUTCCATGAUGACCAAAT
223620023	72628	CCTGTAAACATCUGCATTTTCCATTUGT	72629	GCATCTTTTTCCUCTTCCTTTCATTUCT
223621703	72630	CAGTACTGAUGGCTGCUGGAT	72631	CAGTGGTGUCTCTGTGCTCUG
223625037	72632	ACCCTTTCTCUCCCAGCTTCUAAT	72633	CCTCATCATCGUTCAAGTTCTAGUGAG
223625846	72634	GCATTAATACAUACTTTCTGUGGCGAA	72635	CACCTTAAACTUCATTTTGGTTCTGUGT
223629856	72636	AGGACCUCCAGGAGAGCUG	72637	AGCTTCCCGUTGGCCTAUG
223631289	72638	CUGAAUCCCGAGAGGCCAA	72639	CGCTACTTCCUCCTCAAGAATGAUG
223632022	72640	GTGTACATGAAGUCCAGGAGGAUG	72641	AAGGGATCACAGAUTCGATATGTCUACT
223632140	72642	TGGCGGTUGTTGAACATGTUG	72643	TGGAGTTGTTTATUCTTCCTTGCTGUAT
223633960	72644	CTTCCCACUACTTTGCAAGUAAAACC	72645	TCCTTTCTTCCCUTGTTCCCTATATUGA
223635300	72646	CCTTGTCGUCCCCCUGGA	72647	TGGTGACCCUATGCTCTGUGT
223636632	72648	GCTCCTUGTAGCCAAUGAAGGT	72649	GGGTCUGACGGGTAGAGUGT
223637505	72650	CATCCAGCUCCTTCCACACUA	72651	CAGCTTTTGGCAUGGAGACTUG
223642669	72652	ACCTCCGGGUGTGCAGAUAT	72653	AGAUGCCCACCTCCUCCA
223646417	72654	CGCACUCCGCAGACACUT	72655	CCCATCAGUGCAGCTCUCC
223648833	72656	TGTGCTTAAGUGACCTTACACCATUT	72657	TTCCAGCTTCAUAACCATGTTCCUT
223649026	72658	GGCTGTTGUGCCCTTCTCTUA	72659	TGCCCUAAAGGACACAGTATUGG
223649266	72660	GCAGCCAAGAACUGAACCAAUG	72661	GTCAGCTCTUCGGTCACCTUT
223650918	72662	GCAGCAACGCGUAUGCAC	72663	GAACCUCATGCUGGACAAGGA
223656075	72664	CAGCCCGAAGUCTGTGATCTUA	72665	ACTCGGAGAAGAACGUGGUG
223656371	72666	GGTTCGGCUCTAGTCAUCACAAG	72667	GGAAGAGTTTGCUGGTTGGAATGUA
223656496	72668	CCCCUAGAGAGCAGGGUGAAT	72669	CCAGUAACAGCAGCAGGTATTUCT
223659859	72670	GTGTTTGTGUGTAACTACTGCUCAGA	72671	AGCAACATCAGAUAAAATCCAAGAGCUT
223663943	72672	GCATAGTAAGTUGTATTTGTGTCUGCCT	72673	GACAAAGGAAAAUACGCACCAUAAAACA
223664384	72674	GTCAACTGACUGAAGAGAAGAATGACUT	72675	CAGCAGAAATGAUAAGCATGCACTAAUT
223664421	72676	TTTTCGAAAGGCUCTCATTUACCAGA	72677	CCGACCGAAACCUGGUGAAG
223664505	72678	GCCAACACAAGAGAAAAUATTTGCUG	72679	CTTTTGACCAAAGUACTGACTTGCTTUT
223666210	72680	CTAGCAGTTAATTUGATTTTCCGAAGTUGA	72681	CAACAGAAAUGAGAAGTGCATGGAAUT
223666239	72682	TTTACTCACGUTTTTCCCATCUAGCA	72683	CGGAGGACGGCAUATUCAGG
223672105	72684	GTACAUGAAGGGCAGTTGGGUA	72685	GCUAACCAGTUGCCACAAACC
223672356	72686	GUGATCACCAAUCGCCCAAAG	72687	ACCAGCAGAGAAUAGAGGGAGAAUT
223676910	72688	CCAGCCTAAAACUTACATACACAGAAUG	72689	AAGGGTTGCUCCAAAAATCTUACCT
223680961	72690	TGCTGGAAAGAAUAGTCATUGGAACC	72691	AAACAGTCAAGAGUCATCGAATACCAUT
223689434	72692	CTTGGATTTCCCUGTATGATCCTTCUT	72693	GATTCCATGTGAGGUTTGATAACGTTUT
223690725	72694	CGGCCTTAAGGUTAATTCTTGAAGUACA	72695	TCTAUAGGACCCACTTCUCCCAAG
223690762	72696	CTATATGTAGAGGCUGTTGGAAGCUG	72697	AGCATTATGAAGGUCCACTGAAGUT
223695388	72698	GAACTGCTAGCUTATGCCTTCAAAAUT	72699	CCTGTCTCAGGUCTATGACCUACT
223696232	72700	CTGTTGTAGUGGAAATACTGTCCTUGA	72701	AGGAAATGGATTUTGGAGTCCTCUG
223696816	72702	GGCTGTTCCAUTCGATATCCTTTTUC	72703	ATCGGAGAAGAAACACUAAGTGCTUT
223696973	72704	ATGATCTGCUTATCTGCUGCC	72705	GCGCTTAAATTUCTCAACTTCTTTCUGA
223700378	72706	GAUCCAAAAGAAAGCGGTUCAAGT	72707	GAAGAGGCGUCCTUAGCAGAG
223701627	72708	ACTAGAACAUGATAGAGCUACAGAACGA	72709	GCCGATCTAGAUGTTTAATTGTTUCAGG
223702035	72710	GCCTTACCCUCTGCCAGGATUA	72711	CCAGUGGAGAAGGAGGUCGT
223702142	72712	CUCCTAGCUCCAAGCCAGAA	72713	GTAGGCTUAGACAACTCTGCUGT
223706191	72714	AACTGGTGTACUTGATAGGCATTUGAA	72715	CCAGCATTGGAUCTGTTGTCATCTTAUA
223707208	72716	CACCATCCCCGUCTTCTCUC	72717	AAAGTGTCCUGCACTCTGATGAUT
223708886	72718	GATGAUCCAGATGTUAGGGCAGT	72719	GGTTTTGCACAAGUTAGGTTTGTTTUG
223709468	72720	AGACTGGACAUAGTTTCTGGGAGAUT	72721	CCACAGCAAACAGAACUGTTTUAGA
223709781	72722	AGCAGAGTUAGCTTGTCACCUG	72723	CCTCCUCCCCAAACCAGTACTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223710778	72724	TGATGAAAATGCUGATGAGGCTUCT	72725	CAAAGCACTGGAUCTAAGAGTCCTUAC
223715643	72726	CACAAGAGCUCCCUCCCT	72727	GGCGGCAGCCACUAGUC
223719430	72728	GCACTTCACAACUCCTTACTGCUT	72729	TCAACGTCAUCTAGAGGAATTUGCC
223719489	72730	AAGACAAAAUGCAGAAGAAAAAGUCAGG	72731	AGTCCTTTAGCCCUACTCAGGTUAA
223720140	72732	ACTTTGCTCUTGTTCCCCUGAC	72733	AGCAGCTUGGTGTCTCUCAAA
223721909	72734	ACCCCAGCCUTCCCUGT	72735	GGGCCACAUCGTCACUCA
223722248	72736	CCGCAAAGACAGACUCCCAUT	72737	GCTGTTTATCTUCTGCTTTCCTCUGG
223723826	72738	GCGAGTGUGTGGGAAATCUGG	72739	AGATCATGCAGCAUCGCTTCUT
223726849	72740	CCTTCUGAGGTCTGCUGCAAA	72741	GGGACAUGCCATAGGUAGCAAT
223729103	72742	CGTGCUGCCACACGAUAC	72743	GGCCCUACAUCACAGGAGGAA
223734461	72744	CGAGCGUGCGTCCTCUG	72745	CCAGGCCCUCTCCUGACT
223734469	72746	CCTAGACCUGCTCTCTCGGAUAC	72747	AGTCTCCCCACACUCACCTUT
223738516	72748	ACCTGCTATGUGTTCCTGTTUGG	72749	AATGGCAGCCUCTGCTUAGAAA
223738570	72750	CUCAAGCAAGTUGGCCAAAAAGA	72751	AGGCUACAGCGAAUCAAAGCA
223739184	72752	GTTCTAGCAATGCUGGATACTTACAUCA	72753	CCTTCAAAAUCCATTCCAATUCCACAG
223741192	72754	GCCCGGACUTGCTAUCCT	72755	CAGCTCCUCCAGCGACUC
223741661	72756	GCCCAAATTGAUTTCGATGATCTUCA	72757	ACCTTTATATCGTUACTCTGAATCTTATCTUCC
223743505	72758	GTGGGTTTGUGTTGTGATGCUAT	72759	GGGCTGUAGCATTTGAUGGG
223744517	72760	TTTTGCCAGUAAGCAAGTGGUT	72761	GCATTTTCATCUCCTGGGCUGT
223745545	72762	CCTCTCCAUCCCTCCAAGCUAT	72763	CUGAGCTGTCUACACCCACAG
223745817	72764	AGATCCGGAGCUGCTCUCT	72765	GTTTGCTCACUTGGCTTTCCTUC
223746080	72766	CGACACACUGCGACCCUAC	72767	GCTTGCUGGGCTGCTUAAGAA
223747275	72768	GAAGGTGGCUTATCCACAGCUT	72769	GGATCATGACCUCCTCACCUGT
223747788	72770	CUGTGGAUCAGGAACCCAAGG	72771	CGGTGTGAACACUTTCAATTGUGT
223748019	72772	CAGCCCUCACCTCTGCUT	72773	GACCACGAGCGCCUCUT
223751049	72774	CGGATCTCTUCCATGAGGAUGA	72775	CCTCATTTCUCCTCCATCCUCAG
223751577	72776	GCATTTGGAGUATTGCTTUGGGAA	72777	AACAGGCUGAGGAAGGCTUAC
223752673	72778	GCACACACCACACUCGAUGA	72779	AGCAAGACACAGCCAUCAACTUA
223753735	72780	TGGAGGATCAGUCATCCATGAATCUA	72781	CAATGAGGCCUCTTATACUGCCAAA
223756615	72782	CTTGAAGATCGUCAGTCCTTTCGUA	72783	ACCCUCAAAGAAAACCUGGCT
223763257	72784	TGGGAAGTUCATCTGGCACUG	72785	TTTCTGTCCTCUCTGGCACTCUA
223774806	72786	GCCCAGGGAAGUGGTATTGUA	72787	GTGAGGCUGAACTGGAUCCAA
223777089	72788	CCTTAAAACTUTGCTTGAGGUGAGT	72789	CCCATTACATUAAGAATGGCCCATTTUG
223777262	72790	GGTAATATATGCCUTTTGAGCTGTCTUGA	72791	GCACTAGAATTUGCTGGCTCAUGT
223778582	72792	ATGTTCCATGAUCATCAGTCCTTUGT	72793	TGGAATACATCTCUCTCATGTTCTCUGT
223781850	72794	CTTTTCCCGUAGGCTGATCCTTAUT	72795	GCAGCCAACAUGCGAACTUG
223782434	72796	GTCATTAAACTTUAGGAGCAAGCCATUG	72797	AGTTGGGCAATAUCAGTGAAGTTCUT
223782500	72798	TTGTGGTGGAGUTATTGATGACGUT	72799	AGACATTGAAGGUGTCAACCAAUAAACT
223784312	72800	ACACAATTTCTUGCTGACAATCAUCAC	72801	GCAACTGTGAGCUGTTACTATGUAAGAC
223784672	72802	AGCCATGGTCUATATATGCTGTCUGA	72803	CCACATAUGGAGTGAAACUGGGAAG
223785700	72804	GGGCATATUCTGCACTCAUCC	72805	GTTGTTTGTAGCUGTAGTGCTTGATTUT
223786588	72806	CAAAACGAAAUCCTCCAGCAUCA	72807	GGGTCTATGTACAUTGAGATTCGGUT
223787473	72808	CTGAACATCGUAAGAGAAGCTCUAAAGA	72809	TCATGCUGGAGCCAAATTTCCUAT
223789639	72810	CTTAATACATUGAGCAGTGTTGGCTUT	72811	CTTCTGGCGAAGCAUATTCATTCTUT
223790319	72812	GGGAGUGAGGATGGCUACAG	72813	ACTGTCAUCGAACGCACCUT
223791861	72814	CCCACGUACCGCTCCUC	72815	GCAGAGUGCCAGCTGAUGAA
223793368	72816	CTGATAGCTGUACCCGCTGUG	72817	CTGCCTTUGGGAAGTAGAAUAGGT
223793663	72818	CGGUGGAGGGAGGTCUCA	72819	CGCTGTCUCTGCTCUCCAG
223793811	72820	CAGCGGAUGATGAAGGTGTUG	72821	CCTGGUGGGTGGTAUGCAAG
223795289	72822	GCTCAAGAGUGAGCCACTUCT	72823	TGACTCTGTCUCCTCTTGTCTTCUC
223799394	72824	GGTAGUAAACACCCCCAATUGAGAA	72825	TTCACCUTGCUGGCCAGT
223800280	72826	TGAAGTCTUCATGGATGTTUGCCA	72827	AAGTAGCTACACUGCGCGTAUAAG
223801498	72828	GGGACATGATUTTCGTCAAGATUACA	72829	AAATACGTGACGUGCAACAACTUAC
223803795	72830	ACTCTCTGGUGCTGTCCACTUA	72831	GAATCACATUAGGGTTCTCTTUCCCA
223804202	72832	CAAGAGAATCAAGUAGAGAATCCUGCAA	72833	ACAAACCCAAGCUAGTGGUGAAG
223808104	72834	GCTATTTGGTTUGAGAAGCGATUGG	72835	CCTGCAACUCAGAATGTAGAAAAAGUG
223808364	72836	GAACCCCAUTGAGGCUGCT	72837	GTGAGCTTTTCUTGGAGATCCUACT
223817361	72838	TTAGGTTUAGCATGAGCTTUAACAGACA	72839	AGCTAATCACAUGGCTGTACUCAC
223818723	72840	CCCACTAGAAAUGCCTGCAUGA	72841	CAATATTGTTTGTTUTTATCCCGTCCUT
223820599	72842	TGCAAAGTACCUAACTCCACTGATTUC	72843	ACAGCAAACCAGUCAAAACACTUAC
223827065	72844	TTCTTTCTATTCCUTCCTCTCCCTUACA	72845	TCTGGATGUGGAAAGAGACGAUAGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223833499	72846	TCACCAACAGUAAATCCAACAGATUCT	72847	ACTGGATATTGAAUTTCTGCAAGGAGUT
223834985	72848	TCTTTAAAUCACAGCCGTCAUCAC	72849	AAGCAGGTTTCUGTCGTCATTGUA
223838981	72850	CACCTTGAGGUCCCGGUA	72851	CGGCTGUGCCTCAGGUT
223843295	72852	TGTTTUGAAGGGCCAGGTUGAA	72853	TGCAGTCACUGTAGAATCATUAAACCAT
223845412	72854	CGACTCTGTCUCAATGAACTCCUT	72855	ACCAAAACCAGGCCCUGUG
223845660	72856	CCCGGCUGAGGTCCUCT	72857	AGUAAAGGCGUGAAGCAGAAGT
223846069	72858	GCCTGGUGGGCTTCTUG	72859	ACAAGGCCCCUGGGAGUA
223846085	72860	GGACTTCTGCUTCACGCCUT	72861	GGAAAGUCCCCGACGTTUG
223858394	72862	CCTTTCTTUAAAAACAAGCAGCCACUA	72863	TCTAGCTCTTGUCGAAGATTTGAGTUC
223861114	72864	CAAGTUGAGGCACTGAAGAUGGA	72865	CCTCAAGTTUACAAGAGGGAATACUGAA
223862141	72866	GCTCTTGATCUCCTTCTCTCUCAGG	72867	AGTTAAUCCCCACAAGCCTCCUAT
223862626	72868	TCTTTTGTGGCAUCTGAAACAGTTUG	72869	CAGGACTTCAAUGTCTAGTGTTCAGUAAA
223866047	72870	TGCGCGCUCTCGTGATUAT	72871	GUGAACCGAGCCGUCGT
223867689	72872	GCAGCAGAACGUGGCTCUT	72873	CAAGACCAACCAGCUGCAGUA
223872198	72874	TCTUCACCACCACATTCUGCAT	72875	TGTGACAGAAAGUGAGTGAGCUG
223873840	72876	GAGGCCUCAACCAAGGUCA	72877	GCGAUGCCAAGGAGGUCAT
223880353	72878	GCTGAGGAAGAACCUGTGCUC	72879	TGGTTTGTGGUCAAGACAGAAUCA
223883139	72880	CAGGTATGCACUCCAGAAAGCUA	72881	GGCAGATGACUGGCTTTTACUAGAT
223888229	72882	CCCTGGCAGGUTCATCGUT	72883	ACTGGAGCGGGAGAAUGAAAUG
223889694	72884	GCCATGTCCTUGGGATTCTAGAUAG	72885	TUGAAATGATTGTTUCCACAACACAGAA
223894851	72886	ACTGAUAAAAGCAAAGCCAUGCAC	72887	GGTACAGTTCACAUGACAAGTCGUAT
223897475	72888	AGCTCCTGGUTTTTGGTCTUCAG	72889	CGGUTGAATAAGAUGGAGGAGGAA
223910120	72890	AGAGACTGATTUCTCTCCAGCTUACA	72891	CGTTGCCTTTUCTGAGTGTTTCUT
223911986	72892	GTTGATTTCAGGGUGAGAGATGAUT	72893	GACAATATCUCCATCAGCCUGGAC
223913735	72894	CAGGTCAGCAUTCTCTCGGUT	72895	CUACAGCACCCUGGAGAAACA
223915026	72896	CGCCAACACGUTTGAACUGAA	72897	CATTTGACCUTGTCATUCACACCAG
223916103	72898	TTTAAAGACCAGCUATGCAGCTUCT	72899	ACCCTAAGGUCAACACTGUAGGAAA
223916149	72900	GGCAACTAAUAGGCATTCAATACGUGA	72901	GCTTCATATTCTUCTGCCCATGAGAUAT
223918824	72902	CTCGCCGUGCCACTTTTUC	72903	AGTGCGAGCUGTGCAACUA
223919754	72904	TGAACTCACUGGTGAGGUAGCA	72905	CCTCACACACAUTCCTCTTGAUGT
223926967	72906	AAACTTAAGGTUTTGATGGCCUACCT	72907	AGTTTGTCGUGGTAAAGTGAGUGA
223927302	72908	GGACUGAGGAGCAGAGUCAGAA	72909	CGTAGGTCAUGAACTCAGTGAUGA
223927319	72910	CCAGCCACUGCGAGUACAC	72911	CCTUCCCCGGGCTCTUC
223927896	72912	GCCUAGGCCCACGTUCT	72913	GGCCCGAGUCGAGCTUC
223929301	72914	CAGCUCCGAGTCCAUGCT	72915	CGGCCGACGGUGACTUC
223929840	72916	TGGTGTTTCACUTGCTCAGTUCT	72917	AGAGTTAAGACAAGCUCCAAAGAAAGTUT
223930973	72918	CCTGTAGAUCTTTCACATTUGGAAAAGG	72919	TGTTGTTTAAGAUGGAGCTCTCCUG
223932892	72920	CGGTATTTGCCAUCTTTAAGACTGTTUC	72921	AGATACCGGAUAATGACTCAGUGCT
223935120	72922	AACAATCAAGCUTTGAAGATAGUGGACT	72923	CATATTTGCTCAGGCUTGTTTTACACUT
223936450	72924	TGTCTUCAGGCTGATGTUGCC	72925	AGTTCGCACCCUCAACGTATUC
223936703	72926	TTACAUCTCCATGAGUAGGAAGAAGGT	72927	CCATATUACACAGCCCGAGAACUAAT
223939058	72928	GGCAAACAACCAGAUTTGAAAUGGA	72929	AACTGGCUTGAACTUGACGGAT
223939737	72930	CGGGAGCCCCCGUTCTAUA	72931	CCCCTACCUGTGGATGAAGTTUT
223940369	72932	TTGCTCGTGCUGGTTTCTATUACA	72933	GTAGCTTCCAAGUTGTTAACGGAATUT
223940638	72934	GAATUAAAGGACAGGAGTTCAUCCGT	72935	TTGTCTTTTCACUCAAATAGCACTCUCT
223941064	72936	GTAGGGACAAAAUATGATGTCAGCAUCT	72937	GTGATCAGCACACAUTACAGACTTUC
223944056	72938	CGTAUGGAAGAAAAACCCUCACAGA	72939	TGGTTATAAATTUCACCAGCGTTGUAGT
223946770	72940	GAAGAUCTGCTCTAATUGAACGGGAA	72941	GGAGGTCCCCGUTAAACCTTTUA
223948400	72942	TCCCTTGGAAAGUCTGTAATGTGUG	72943	CTTGTGGCTTUAATGATGTTCCUCAAA
223948714	72944	GCCAUGGAGTACCUGGAGAAGA	72945	CCAGCACUGAGGTTAGAAGCUG
223950351	72946	ATTAACACACAUCAGTGGAACTTCUGT	72947	AAACGTTTTUCACCTTAGCATTTUGT
223960162	72948	GCAAUCCAAAAGAAUAGCAGCCAAA	72949	CACCATCUCCATATCATUGAGACCAAAT
223962614	72950	CAGCCCACUCTAGACTTTTCTUCAT	72951	CAGTGGACUTCTTTGCCCUGAA
223967627	72952	GCAGTCTGTCGUGCAATATCTATAAGTUT	72953	CAGGAAAACACGACAUGTGAATAUCC
223971374	72954	CTTTGTGGAAUAGCCCATGAAGAGUA	72955	CGACAGACTACUTTGGTTCTCTTTUGT
223973563	72956	CCAGTGCUCCTCTGTGTCUAA	72957	TGATCTCCUCATTGATGCUGGAC
223979161	72958	GGCCCCUTTCACTCACUGAAAT	72959	GGTTACATAAATUGGTCCGACAACATUC
223980312	72960	CCAGCUACGCCGGACAAUA	72961	AAGATATTUGAGAAGCATGCUCCGA
223982077	72962	CTGTATGCCAUGACCCTTAAGCUA	72963	AGTGGGCUGACCTTUAACCAC
223982445	72964	TCACCTGAGUTGTACCTTGCUG	72965	TCACCCATCCAUTAAAGGGTCCTUA
223982831	72966	CCTCCGCAUCTCACAGAACUT	72967	CTCAGCAGGAUGGGUGGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
223985495	72968	TCACTCTTGGUCTTATCTTGCCCUA	72969	TCTACCAAAGAGAUAAAGGGCCAAUACT
223987009	72970	AGATTCAGATACCUTCACTGCAGTUC	72971	TTTTCTCCTCUGTTTTCCAAUGCAAC
223989334	72972	CAGATTCAACUTTCACGTAUCAAACCA	72973	CCCCUCGGACCUGCAGA
223993863	72974	AGGACCCUCGCAGACATUAAAG	72975	ACCACCAUCACCACTGCUG
223998169	72976	CGAUGAGGGAGGUGGCAGA	72977	CCTGGGTAUGCTCCCCAUT
224007475	72978	GGCATATTUAAGAACAGGCATCTCUGAT	72979	TCTTAAAGACTGUAAGACTCATATGUCGGT
224007686	72980	TTTATGAAGGAGUTATGTGTGTGUAAAACC	72981	ATTGCTGTTUCGAGGTCATATGTUACT
224011664	72982	AACTACTGCCGCCUTATCCTCUA	72983	TCCTAGCCCAUCTGTGAGUCC
224016278	72984	GAGCCGCAGGUTTCCTTTCUA	72985	GGTCATCAATCTAUTCCATCAGGCTUAA
224021488	72986	ACTGCAGCAAAGACUGGTTCUC	72987	GCTCUGCAGCAAATUCAACCAC
224029111	72988	CTCAGCAGGGCAUTCCAGTUA	72989	GCTCTCAGTCUTCTTCTCTCCUACAG
224029287	72990	ATCCUGAGCAGCTUGCAAGT	72991	AGCATTTGACAUCATCACTGTTACCUAA
224031566	72992	CCAAUGCAGCGAACAATGTTCUG	72993	AGCTGCTGAAAAUGTAACTTTGTAUCCT
224033491	72994	TGGATTACAGGUGCTTATGAAUCAACA	72995	ACGGCAATAUTACGAAATCCUGAAGAAT
224035069	72996	GGATTTCGUAATATTGCCGUCAAAGAAA	72997	GGCTTTTTGUGAGAACACAGGTTTUA
224036656	72998	GAATTACATTCCUCCCACACCCTUT	72999	CAATTTCTCUTTTGCCTCUGCGA
224037245	73000	GGATACTCUCTGTCCCUCCCAAA	73001	GATTCCTTGUCTTGGTCUCCACT
224038045	73002	GTCCCACCUCCGUCCAA	73003	GTTGCCUCGGGCTCUCC
224043938	73004	GATTGTCTTTTUCCTCTTGCCCTTUT	73005	CCATTCCAGCAUATCGTCTTAGTGUAAT
224044664	73006	CCCAATTATUGAAGACAGTCGUGAAG	73007	TTCACTAGGCAUGGATATAGTGGTAUGT
224044937	73008	GCCTTCCUTCTCCCUGACAA	73009	GTCCTGCGGCUCTCAGUC
224046182	73010	GACTTAAGCCAAGUTAGGGAUCACC	73011	GGGATGCAATGCUCTTACTCAGTTTUA
224046808	73012	TTTTCACUGAAGAAGCAAACUGCC	73013	ACACTTCTTTGUCCATACACACTTUACA
224047523	73014	CAGAATTATUGCAAGTGGACTGUGAAAT	73015	AACATACCTTGUTGGCTACATCUCC
224049755	73016	GTGGAGGCACAUCTCUGCAT	73017	CCAGGTGCUGAGGCTGTTTTUA
224050788	73018	AAUTGCGGAGACUACAAGAAGAAAGAA	73019	CTGTACCCTUGATTGTACTCCUACAAAT
224051474	73020	GTAGTATGCAAAGAUTGTGCTCCTUCT	73021	AATTAATTCTAAAGTTUAGACGATGTTTTGGUT
224052491	73022	TGCATGTTUGAGCCACTTCCUA	73023	CTTCTTCTGAGGAACAUTCACTCTGUAA
224054474	73024	TGAATTCAGUGGGTTTTCTAUGGG	73025	TTTCCAGTTUGTCTTCAGUAACACCAT
224057205	73026	ATTTTGCTGUGTAGTGAATUAAGGCT	73027	TCGGCCACCGUTGAAUGAT
224061751	73028	TGATCCTGAGGUTTTGCTTCAAATUG	73029	CGCGUCGCTTCACATUAAACAG
224066656	73030	GCAATCAGACUCCACAAATTCTTGTUAA	73031	CTGAAATATGTCUGGATTCCATGUCCAA
224071437	73032	GCAAGAACTACAUGCTGCTGAAAUT	73033	CAGACACTGUATCACTGCCTUCA
224072838	73034	CACCTGTGCUACCTCACTUGT	73035	CCATCATAGAACUCCTTGTGGATCUC
224076188	73036	CCTGGCCGAGUTGGTTCAUC	73037	TGATGTCCGUGCGTTCCAUC
224076414	73038	AGTTACUGAAAGAGGAATGTGGUACCT	73039	TGAGTTGCATUTTGGTTTGTCAUCT
224083543	73040	CTTCTTCAAAGUGCCTGAGCTCUA	73041	CGGCCCUGGGTTACUCAC
224085470	73042	GGGAGAAAGAAGAAAUCCACCTUGT	73043	TCTGAGTCUGAGGAACTGTCUGAG
224090423	73044	CUCCCCTCAUCCAGCAAGAAAA	73045	GGCTTUGAACTATGCUGAAGCAG
224090430	73046	AGAGACUCCCAAAGCTGCTTUT	73047	CTCTGCCCAUCCGACUGAG
224091517	73048	GTGUCCCCCAACUACGACAAG	73049	CAGCCTACCUTCAAGGTCTUCA
224092577	73050	CUTGCCCAGTTUCGACAAAGAA	73051	TTGATCAATATUCAAATCATGGTGUGCT
224095560	73052	ACGTCAAGCAGUAAACATGATGUGT	73053	CTCATGACTGGUTATTTCTCCACTAUGT
224096113	73054	GGAAGAAAUACAGCCUGACGGT	73055	GGAGGUAGACTUCCAGGCAGAT
224098398	73056	CATTTCCACACUCGATAAACGACAAUG	73057	CAGAGTTGGGTTUCTCAAATAAGGTGUA
224098602	73058	AGTTCTCAGAGAGUAGAATCAACTGUGA	73059	GTTATGACUACTTTCCAUCGAGAACCA
224099404	73060	GGCUCCGCCAAATGGUGA	73061	ACGAACGCGUTTGAAAAGTTUCT
224101720	73062	CAGAGUCAGAAAGCACCAGUGA	73063	CTGCCAUCTAAGGUGGCCAT
224104146	73064	GATCATCAAATGCUCTTTAATGGCCTUT	73065	CCTGTATCTTTTAUGAGCACCATCTUCA
224106159	73066	CAGCCCUCCACAGUCCAAG	73067	CUGACGGCCUCAAGAAGCA
224109544	73068	GGAAGTCCAUCTCCTCCTCCUC	73069	GGTGGAGCUCCTGATCTGGUA
224111881	73070	TGTCCCCATUGGTGAATTTCTTGTUAA	73071	ACAGCTGUCAGCTTTAAUAAGCC
224112676	73072	TGGAAAAACACUGGAAGATTACUGACT	73073	CCAGGATAGAGAUCCAAGATTTUCAGAA
224114012	73074	AGUGTTCCAAAGTUAAAGAAGGGCAT	73075	GCGGTCAGUATGGAGAGGUT
224114318	73076	TCATTTTGGAAGUTCACTGGTCTAUGAA	73077	GTTGCTTTAAUCACATGCGAUGGA
224114665	73078	CCTGCTCCUAATCCACCTCATUT	73079	TCATCATGTATACUTACAGGGCTTTUGG
224116042	73080	TGTATTATAGGCGUCATTGATGGCTAUG	73081	CTCCAATTCTUGCAACCTGTTACTUG
224117115	73082	CATACCCGCAUTGATGTTGTGAUAGA	73083	TGGTUCAGCCTGUGACAACC
224119138	73084	CGCCGCCUCTTTCCAAAAUAAA	73085	CCAGGCUCTGTUCAACGG
224119999	73086	CACTCACCUCCTCCGGAAUG	73087	GCCCCGGCUCTCGGTTAUA
224120101	73088	CTTGCTGTGUTCTGGTCCUGT	73089	AGTGTTCTCCGGUACTAGTTAGAAUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
224122610	73090	GTCTTGAGCAGGAGUTGTTATGUG	73091	CAGAGGACTGUTTCATACAAATTCUGA
224125467	73092	GGTCCUCCATAGACUCAGGGAAA	73093	GTGACGATGUTGTGCACGUC
224127854	73094	TGCAGAACATAATUATTGATGGCCCUT	73095	GTGCTTAGGATGUGGTTTATACTAGGUT
224129299	73096	AGTAATTTTGCTTCUTTAGGACACCAUGT	73097	CTTCTCCUCAGACGCTUGCT
224131270	73098	GAAATTGCACACUGAAATTAGGACGUT	73099	CTATGAAACCCUCATGTUAAGCAACAAG
224133794	73100	GGAGATCCUCTACAAAGGGTUCAGA	73101	AGCCCGAATTUCTTCAAAGGAGAAUT
224134424	73102	CTGTCCTGGUACATGGTGUCA	73103	GAGGACGGCCUGATCACAUC
224142869	73104	GGAGAAGATTUATGCAGGAGUAGGG	73105	TCAGCUCAACCTUCACACAACT
224145182	73106	GTATTTCTUCCAGACGCCAACGUA	73107	TGAUGGGCTGGUGACAACAT
224147413	73108	GCCGGATGUAGAACGAGUCC	73109	GTGGUGAGGAAAGCTGCTGUA
224171465	73110	ACTTGGGTGCUGGGTAGTGUA	73111	AGCTTTTCTCCUTTTCTTACCAGGUG
224190541	73112	GCTGAAGAAACCUGTAGCUCCT	73113	GACACCAGCUGCTTGACUACT
224203064	73114	GATGCAGUCCACATAGCCUGA	73115	CUCAGCAGACAAAAUCAGCAAAGAG
224218883	73116	TTGATTTTCTCGUACCAGGATCUGAAG	73117	CTGGGCATCAUATAGCATTCTCUGT
224218928	73118	GACAGTAGGUCAGCACATUCCA	73119	CAGTGAUGCCTCCACCUCAAG
224232526	73120	ACUACTGAACGAAUCCCAGCAAAAA	73121	CCGCTCCCUATCTAGGGUACT
224233178	73122	CTCCCCUCAGAAATGTGUGCAT	73123	GAGCAAACUGGAACUCAGCCT
224239366	73124	GAGAUGGAAGATGUGGGCAGAG	73125	TCCATCTGCUCAGACCCUACAG
224246137	73126	GCTCGUAAGCCCAGTGTCTTUT	73127	GAAUCTGGUGCCACCCAAGT
224248945	73128	AGAAAGTTCGAAUTCGGGAAAUGAGT	73129	CGACTGTGTTUTTCCTCTAGCUGT
224263135	73130	GACCTACUGAAAGAGCUGCAGAA	73131	CTGCAGUGTTTTCCTGUGAACC
224300627	73132	CGATGAAGCAGAGCUGAGGUT	73133	GCAATUCGCGCCUCCCA
224308442	73134	CCAGUCCCGAAGATCUGGAAGA	73135	AGTTCAATCUCAGCGAGCUGT
224312077	73136	TTGGCGAAUCCACCAACUGA	73137	GCTGUCCAGGGTGCUGAAG
224312925	73138	GCUCCAGCACCAACTGCUT	73139	GGCTCGCUAGCTCUGGAC
224313145	73140	CCTUCAGCACCCUGGACA	73141	CTACTGCUGCCACCAUCCT
224313424	73142	GCAGUCCAGAGCUAGCGA	73143	CGGGAGCCACUCAGCUACT
224318535	73144	GAUTTGATTGATUACAGCACGGGAAA	73145	CTTACCACTGGAGCAUATTTCTCTAGUC
224321448	73146	CATTCTGATGCUTACCAGACUAGAGAAA	73147	ACCCCAGTCTGAUCCAGAATCTAAAAUA
224323988	73148	CATCCATCTGUCCTGTTCTGUCC	73149	GCATCTCCCUGCCCATGUC
224334698	73150	CACCACATTUAAAAGCGTCTGAACTUA	73151	TGTGTGTUGTTTGTTGTTUAGAAAGCAG
224335792	73152	CTGAGCCACUCTTCTCTTCCCUA	73153	AGATGGACUGGGACCTTUAGACT
224341469	73154	GCAAGAGACAGAGCAUCCTGUT	73155	CAAGGACACCUCAGGAAGGUT
224342451	73156	GGGAATGTTTUCAGAATTGTTGUGAG	73157	ACAAAGAUGTTCTGUAGAGCCAAAGAT
224357617	73158	AATGCTGATGGUATTAAAACAGTTTTUAAGAA	73159	GCAATGGACTUCACCTCATCAAAAUG
224358740	73160	GAGACTGUCAAGAGGUGCACA	73161	TCTGGAAGACCUGTTGCAUGAC
224359488	73162	GGTTTTGATUCCACATCTGGTGATUAGA	73163	GTACCCTCAUAGGCAAAAUAAGGAAGAAT
224367525	73164	ACAGACTGCTTUCCAAAGATTCTTGUAA	73165	ATTGAAGCCAUACCTGTTTUCCCA
224371825	73166	GCCGAGGAGUCCAGAGUGA	73167	GGGCTTTCCUCCAGCCUT
224372544	73168	CCTCCUGCGTUCCCCAT	73169	GCCGGCTUCTCACTTTTGUG
224373216	73170	GTGATGACCUGAGACAAGAUGCT	73171	CCCAACCAAAUGGCATCTTTTATATGUT
224374140	73172	GGGAAATTGUCCAGGCUCAAAC	73173	CTTGGCAGCGUCACTGTUC
224374237	73174	GTTATCAAGCCUCCCTGAAACTAUCA	73175	CUTTTGTGCTTCUGGGCAGAG
224374299	73176	TGCCUCGCCATCTCUAGGAA	73177	TCCAGTTTGTUGATGGCCTCUC
224375399	73178	GAGTTGTCAGCUCTTCCCCUT	73179	GCGCUGAACAAGTTGGTCUT
224375522	73180	AAAAGCCACGAGUCTGGTUGAT	73181	GGATGCTGAUGGCAACGUG
224376366	73182	AGACAGTTTGACUCGTCCACATUT	73183	AAGACCTCAUCAGCAGCTUCC
224378547	73184	CCCAGGCUGGTGAAAAAGAAUGA	73185	CTTTCCAGCUTCTTCCTTGUGG
224378730	73186	CCACUCCAAAGCCACAGUCC	73187	AGAGACACUCGGGTTGATAUGAGA
224380515	73188	CGTCTUCCACCGCCTUCA	73189	CTGGCCAUCTGCUCGGA
224380899	73190	CGCCCAACCUGACUCCAAAA	73191	TGAGCCUGCTTTGCUGGT
224381820	73192	TGGAAAGGGCAGUGCCTUAG	73193	CGACTCAGAGGAGUGCTTGUG
224383150	73194	AGTTGACTUGGGCTCTCTTTUGT	73195	AGCATCACAACCAUGAGTTUACACAT
224383411	73196	CGCCUTCUCCCCAAAGACAAA	73197	CTGATGTCUCGGCCCTCTUC
224384454	73198	CAAACGCAGCAGCUCCTUC	73199	GCCCCATUGCTGGGCTUT
224384637	73200	CAAATGAGGAACAAGUTTGCCTUCC	73201	GCTGCTACCUCTGCACTATGUC
224384992	73202	CTTUCACCCCCTUGGACACA	73203	CTGGUCAGCGTGCUGGA
224385829	73204	TCUCCCCACCTGUGGAAGAA	73205	TGACTGACCUCCACUCCGT
224395033	73206	CCACCATUCAGCTTGGTUAACA	73207	TCTTTGTACCTCUTTGTTCCTTCTTUCA
224395176	73208	CTCAGTTCGGUGAAGGAAAUCAGT	73209	TCACTAGUCCCTTGUCAGCCA
224404303	73210	GCCACGAUGACTTCCTTCTUGA	73211	GCCCAUAGACCAUGAACGAGT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
224404546	73212	AACAAAATTUCACGTCACAUACAAACCA	73213	CCTGCAAGGUGTGGAGTUACAG
224408636	73214	CATGGCUGAACCAGTCUGGAT	73215	AACATTGTTUGTTGGAGAGUCCCA
224409287	73216	CCAGCAGCUTCAGGTACUCAA	73217	GTGAAGUGGACGCCTCUCC
224410546	73218	GTGCTTTCTUTAGACTGTCUCGGA	73219	GTTGTATCTGACCUAGTAACCCATTUGA
224411115	73220	CCTCCCGUTTTGCCTGTUGA	73221	GTTTTAAUAATTTCCCCUACGGCAGGA
224412167	73222	TGTCTGTTCCCUAATACAGTCACTUCA	73223	CTTGTTCTUCAAGCTGCTGTUGAT
224414266	73224	AGCCAAACAACAGAUCCTCACUC	73225	GCTTCTACAAGTUAGCTGACTTCCTUA
224415366	73226	GGCTAAGCTTUTTCCACTTCCUG	73227	CAATCTCACTTTUCCTTGCTGTTCTAUT
224417294	73228	CCAAGAUCAAAGTACACTGUAAAAAGCAA	73229	CUGCATCATATTTCUCAAGGAACCAAT
224418822	73230	AGCAGAAGCAGUCTCAAAUGCT	73231	AGTTTGTGCAAGCUCACTCTUCA
224419132	73232	GTGCAGGAGAAAGUATCACTCTGTTUA	73233	AAGAAAATCTTACCUTGGTACAGTUGCT
224423966	73234	GAAAGCUGAAATTGTUGCCAAAGG	73235	GAGACCUCAGCAUGCAGAACT
224425364	73236	TTGTACGTTATAGGCUCTGATTTCTTTUGT	73237	GCATCAGATTCCUTTATGGCAAGUC
224425371	73238	TGTTCCUAGGATGACAUGGAGAAACT	73239	TTGGTCAATTTCUACCTCTTTTTCCUGT
224429561	73240	GGAGGCACAAAAUGTGAAATTCTUCAAT	73241	GGTGATATTATGUGAAGATGATGUGCAG
224431601	73242	GCCAUGTCTACUCAAGACCAACAT	73243	TGTTGTAATTTUAAGTTGCTGCUGGAG
224431844	73244	GTGGGTCUGATACAGGUAGCAA	73245	GCACAAAAGAACCAUTGATTUACAAAAGG
224432485	73246	CCTGCUCCCCAGATGAAACUC	73247	GGTTCTGAAUGACCAGTTTTAAACAUGAT
224432586	73248	CTGAGAAAAUGGTGGTTGCUGAAC	73249	GTTTTTAAUAAGGAAGCCUGGCACAC
224438950	73250	CCCACCCAUCCGGACUCA	73251	CACCCCTGUACCAACCAUCA
224443588	73252	CCGACGUGACGTTUGCAG	73253	TGTTGAACATCCCUTCCTTGTCTUG
224448993	73254	ACAGATAAGTTUACAGCAGCAGCUT	73255	GATACCTTATGUTCCGCTGCUGA
224453627	73256	GGATTGUGGGAACGAACUGCT	73257	GGCCAGAAAGCCUGAACATTUT
224454757	73258	CAATCCCAGCACUGCTGCUA	73259	CAGAAGAAGGCUCCUGCCA
224456272	73260	CTTGGCAGGAGCCUTCTUCT	73261	TCUCAGGCCCCAGUAAACAAAC
224456610	73262	TCTTCTGCUGAGCCTGCTUG	73263	CTGTCUCAGGCCCCAGUAAA
224460601	73264	CCCTAGGAAUAAAAGACATACACGUGAA	73265	AATTTGTAGGCTUTCCTGTTCTCAUCA
224460718	73266	ACAGGTAAATGGUTGCAGTTTTGUG	73267	CAGAAAGAAGTACAUGCAGGAAAAAGUT
224465893	73268	GTTCACCTCACUGAAACCTTTGUG	73269	CTATGGCCUGCTGTAUGAGCAA
224468057	73270	GGAGAAATGGAGAAUGCTTTAAGGUCAT	73271	GTCCTAGTTCUTCCTTGAGTTTTUCCT
224468823	73272	ACTCUCAAAAGGAAAAACUCAAGGAAGA	73273	TCTAGCTCTCUGAATCTGTTCCCUT
224469873	73274	AGCTTTCCAAACUGAAGGAAGATTUAGA	73275	TCAAATTGTCCUTTTCAAACTGCAUGG
224470258	73276	AGCTAAAAGATTUACAGCAGTCTCTUGT	73277	GAACTTCTTGTUCAAGTGTACCCTTTUC
224470869	73278	AGAAAAGGGUACACTUGAACAAGAAGT	73279	CAACATGTCTUCAAGGGTTTTCTTTUCA
224472290	73280	GCACAACTUGAAGCAGAGAAUAGCA	73281	GTCTTTGGATTUGGACTTAATGGAGUCT
224473632	73282	GAAGACCTTGTUGAAGAATTGAGCTTUT	73283	GCAGAAACAATCUCAGCTTTCAAATCUT
224476901	73284	TGAAGCACAUAAGTCCCTTAGUACAGT	73285	CATTCTGTCUAACACAGCATTCTTTUCT
224477574	73286	CTCCTGTUAGCCAAGAAGAAAGATUGAT	73287	GTGTTCCTTTGCUTTTCAATCTCTTCAUT
224478109	73288	TCAGTGTTGGUGGACAAGUGAAT	73289	GTATGTUGGCAGGTTAAAAAUAAAGGCT
224481857	73290	GGACCTCAAACAACAAUGTATTCAGCUA	73291	TCAUCTTTTACTTUGAGAAGGCAAGCA
224484489	73292	CTATGCACATTGGAUGCACAATAGTTUT	73293	TGAGGGUTGGCAUCGGAAC
224486101	73294	CCUTCGGTGTTUACAGACCCA	73295	GCTGTTUACGGCCTGGAACUT
224486223	73296	AGAAACATUGGAAATGGGUGAGGT	73297	TCACCATGTTUCTGTTTCAATTGTUCAG
224487753	73298	GCATCTGAAUCCAGAAAGGAACUAGAAT	73299	TTCTTCGTGACUAAATAGAAGCTGTGUT
224487846	73300	GCTGAATUAGAGAGGCUGAGAACAC	73301	TTTCATTCTGTAAACCAUCTATCTGCTGUT
224488249	73302	AGAATCCUCGAATTTCAGGUCCAAA	73303	CATUGGGACCCCAUGAGGAG
224492689	73304	GCCTTTCAUGAACGTAAAATTUGGACAT	73305	ATCACGTACTTTUTCAGCTTGACATUG
224492841	73306	CAATGTCAAGCUGAAAAAGTACGUGA	73307	ATGCTTGGTTTUGCTGTCTTAAAUCC
224493871	73308	GCCGUGGGACCCAACAUA	73309	GAGGGAAUGGAACCTGCUGT
224494459	73310	CAGTAGGUTTATAGAGCUGGAACAAGAAA	73311	AGTATACUAGCAAAGAACATTCCACUGA
224495045	73312	CAGCCAGACGCUGCAATATUT	73313	GATGTCCGGAGUTCCCACUG
224497142	73314	ACAGGGAACACACAGAUGATAAGTUT	73315	CCCTCCUGTAACCATTGUCCAG
224499364	73316	GGCTTCCCUCCAGTACAGUCT	73317	GCTTGCAAAGUGCTGCAUCT
224503004	73318	ACAGGAAGAGCACAGUCACTTUG	73319	CTCACUGACAAGCTCCUCGT
224503527	73320	ATCTGTCCUGCAGAAGCTGAUG	73321	TTAACCUGCAGGAAGUCAAGGG
224504696	73322	GGACTAGCAUTACCTGGCAUGG	73323	AGGTCCCAUCATGCCTTGTUG
224506289	73324	GCAACCUGCCCCAAAGTUCA	73325	TCGGAUGACCTCCUGCAGAT
224508908	73326	CCTCCTCUGAAAGCGAGCAAAUAG	73327	GAGTCACTTTCCUGAGCATCTTCATTUA
224510214	73328	CAUGAGACCACCAGCCTTUCT	73329	CCGATCCTUGCCAGGAAUCAT
224512937	73330	GCCCACCCUGAUGAGCAAT	73331	GGGATCAUGATGTTCTGTUGGG
224514773	73332	GCCCCATUGCTGAAGTGCAUA	73333	CATGACTATTCCCAAUGGCTAGCTUT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
224515944	73334	CGGGAUGCGGCTGGAUG	73335	CGATAACCGGGAGAUAGTGAUGAAGT
224518902	73336	TTGTTACTGCAUACACATTGTGACCTUA	73337	GATTTCTTGCUGAGAGATUCCACAAAG
224520324	73338	CTCTGCGACAGCUTATAATGGAUGT	73339	AGCTGGATTATAACUCCTCTTCTTTCUCT
224523510	73340	TTGACAATAGUCAGTAATGCATGUGGAA	73341	CCCATAGCAAUCATTTTGTGCTTUGAA
224528031	73342	GCAACATGACUGTCCTTTCACCAUAT	73343	CTGGATTTTCUGTTGCTGGAUGG
224529387	73344	AAGCTTCGUCTGATTCAGATUCCAT	73345	CCAATGTACTTTUCTCCCCTGGTTUT
224532793	73346	ACAAGTAAUAAAGGCCCACGAATUCT	73347	GGCTGTTUCATTTGGCCUGA
224532942	73348	GTGGGTCAAGUAAAGCACCTTCUA	73349	TGATGTCCTUGGAAGTTGAGATAATTUGT
224533629	73350	GCCAAAUGAAACAGCCCCUT	73351	GGTGGCTGTUTGACCTTCACUA
224533747	73352	AAGAGACUGAGCCCCCUGA	73353	CAACAGGTCAUCTTCAGAGTCAAUACT
224537542	73354	GGCCAUCTCAGAUCCCAACT	73355	TCCTCTCTTUTAAACAGATGUCACAAGG
224539101	73356	AGCATGCUCAAGAACCTCATUCA	73357	GCTTCTAGGGCUTTTTGTTTCCUAACAT
224540558	73358	CGCCATUCTGGGTCTUACCT	73359	CCAGAACAAAAACCCUCTAACAAGAAUC
224544591	73360	GACACCTATAAACUTTTCCACAGCUACA	73361	CTCCTTGAGCCUCATCTGTACTUC
224545285	73362	GCGGAATTGGUCTAGGCAACUA	73363	CCCAGAACTUCTGTCTTCCUGAG
224547648	73364	CTCAAGAAACAGTUCTCTCAGTTCTCUT	73365	CCACCCATATTUCTGGGACTATGUT
224549064	73366	AAAACAGAGGAUGTTTGGGUGAGAAT	73367	CCCACATTTTGTUTTGCCTGATTATCUT
224551347	73368	TTTTCTTGTUCATCCAGCCUGAGT	73369	TTCTGCCTCTUTCTCTTGGTTTUCA
224553937	73370	CCTGGTAGAAAUGGAATAAGTCCTCCUA	73371	TGGATAAACCUGTTTGTTTGGUAAGGT
224555286	73372	CCTTCAAGACUCAAGGGTGATAAUGAAA	73373	ACCTTCCTGAAUAGCTTTCCAAUCAAAA
224556289	73374	CCTTAAGACUCCAGCCUCCAAAAG	73375	GGGTCGAAUCTCTAGATCCUGAT
224561892	73376	CATGGTCTAUCCCCTGATUCAGAAAA	73377	GAGAGAUTCCTGATTUCAGGGAAAGG
224562476	73378	GCTCAAGCTUGCCATCTCTUC	73379	GCTTGTGTCUCTGCTTACUACGAT
224563669	73380	GAGAUACCATTCCUACAGAAGGCA	73381	ACACGGAAAGGCUTGTGACTUT
224564510	73382	CAGTGTTUCAGAAAAGGCAAAUCCAA	73383	GTTTTATCTCAGUTCCTTTTTGGUCAGG
224564759	73384	AGGUAGACAGAUGAGCCAACAGA	73385	TTCTACCTTTTUATTGGCTCCATUACCA
224566238	73386	GAAGAAGTGUCAGCCATTCAUACCT	73387	GAACATGTCCTATUTGAATTTTCCGACUT
224571597	73388	AGAATCAGAGCAGCCUAAAGAAUCAAA	73389	TTTGCTTTACGUGATGACTTTGTUGG
224578555	73390	AGAAGAATGTAUTATTTCTGCCAUGCCA	73391	ACCTGTTTTGUGATGGTAGAAGTTUGT
224579200	73392	AGACAATTTAAGUCCCAAGGCATCUC	73393	GAGCTGGGUAACACTGTAGTATUCAA
224579341	73394	AUTAATTCTGCTAUGCCCAAAGGGA	73395	TGTGGTATAGGTUTTACTGGTGAAGTUG
224582559	73396	AGAAACCAACUTCACCAGUAAAACCT	73397	GGAGCTTATCAUTGAAGACCTUGGA
224582579	73398	GCCCATACACAUTCAAACACTTACAAUT	73399	AATCGAGGGTTUCATTTGACCTCUT
224584522	73400	AACTCCTTTAUTCAGGTGGAUGCC	73401	GTCCCACUAGGTGAACTGTGUT
224584997	73402	GCCTCCAAAGGACUAAATCAGATGAAUAA	73403	GGCTTGGAGCUTCTTTGAUGAAA
224587028	73404	GACCTGTATUAGTACGCCAGUCAAC	73405	GGACTTAAAACUGGAGTTTGUGCCT
224587150	73406	CTCTTTACTUTTCAGTGTCUACGAGCA	73407	TCTAGAGTTTCUCCTCCGATGGTTUAA
224587792	73408	CTACTCUGGGCACAGGCAUAG	73409	GACACTTGUGAGTACTGUGGGAAA
224591330	73410	GGCCATUAACAGTGCCAUCGT	73411	GGCATGGUGCTCAGCUC
224591923	73412	AGTGAGATUGCTACAGTTCTUGAAGAC	73413	AGCUGGACGGAGGGAUCT
224592690	73414	GGAAGGCCUCGCTGAAGUG	73415	CTACGGCUTCGGGCUGA
224593002	73416	CCCCGCGAGCUGTTCUC	73417	AACGACCCCAACCUGAUCC
224593724	73418	CTCGCTCUCCGTCAGCUC	73419	GUCCGTGGUGGCCAAGT
224598520	73420	AAACCAAGUCAGCTGCCUGT	73421	GGGATTCGATUGTTAGATCACTUAGAGA
224599382	73422	GGCCCGGACCACUAATAUGG	73423	CCCUTCCTTAGCTUCGGAGACT
224601222	73424	GGGTCGTUCTCGCTCTUGA	73425	GACGCACAUGCACAAAUCGT
224602906	73426	GAGGCAAAAGGCGAUTGTCUG	73427	CCCCTTCUCTAAGCGCAUCAAG
224607366	73428	GGCAGGUCGAACTCCTTCUC	73429	GCGAGUCGGACCGCAUA
224608239	73430	CGAGAGAGACAGAGUGACAGAUG	73431	TTTGATTTGTGTCUTGTGTCTTGTTTCUT
224608621	73432	ATTCAGTTCUAGCAGCUCAAGCA	73433	CGCTTCTTTGUGTTGTTATTCACUGG
224612376	73434	AGACTTCTGUTGCCTTGAAAUGAGT	73435	CTATTACCUGAAACATCTTCTGUGGGAA
224614189	73436	CTCCCTTAGUGCAACAGGACATAAAAUAT	73437	TCCACUGGTAGATCUAGAAAGAGGAAAG
224614765	73438	TCTTTTCCCACCUGCATTGTUCA	73439	GGGCTTCAUACAAGAGAGTACUCAC
224629092	73440	CCCTCTGUCTCTCTTCCTUCCT	73441	GGAAGGCGGGUGGAGAUG
224631730	73442	CTCCTCCCAAUTTCTTCCTTCCUT	73443	CCCCTCCUCATGAGUCCAAGAT
224642519	73444	AGTGGTATTTTATGUGACTTTTCTATCATAUGT	73445	CAGTCATCTGCUGTGGTTGAAAUT
224642543	73446	GAAATTUCAACCACAGCAGAUGAC	73447	GTGACAAGAAAUCAAGTAGCAACAAUCA
224645888	73448	GTGCTAAUAGAGGAGCACTGTCUT	73449	GUCCCCATTCUAGCAGCCAAT
224663398	73450	GGGTGUCAGGTGGGAGUGA	73451	GGGAAGGACGUTTACAAATGUGAA
224665546	73452	CGUGGAAGGCGCAGTUC	73453	CGGAAGCGCUCCTGGUT
224666269	73454	CCTTGGTCGCUTCTGTAGCUC	73455	AGCAGCTTTCUCCCGTACCUA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
224667524	73456	CAGCCAGAGCACCUCUGA	73457	CTCGCUGGAGGTGAGGUT
224667734	73458	CAUCGAGCAGGAGCUGGAG	73459	CCATCGCUGCCGGUCAT
224668442	73460	GCUAUGACCGGCAGCGA	73461	CUGGCCTUACCCGGAGAA
224670152	73462	CGGACUGCAGCTCCAAUGAG	73463	TGCTGCTGUCGAAGGACUG
224672554	73464	CCCUCGCAGAACUCGCAA	73465	CACCTGCGUCTCCAUGGAA
224676149	73466	GTACACGCUAAAAGGCATCTUACAAAT	73467	CCTTATAAAUGCGAGCTGUGCAA
224678216	73468	GCAGATCUGGCCCAACGAUG	73469	ACAAGTGCACCUGATACACUCAA
224695921	73470	TGTATTGCCTUTACATTGCTCTUCACT	73471	TGCCTGAATTUCAGATAACAAACTCCUT
224704840	73472	TGCTAGTGAGUGACTAACCAAGUCT	73473	GCTGTCCAUGCATTTGACCUC
224704972	73474	TGCTAGCAUCCAAATTAGGCTATUT	73475	CCAAUTTATGGUAAAGAGGAGGCAAGA
224705829	73476	TGAGTTGATGCACUAATAACAGGTACTUC	73477	AATTCCCUCCCAACCCCTCTAUA
224709057	73478	GGAATGCCUCCAGAAAGCAGAUAG	73479	TGTAACCATAUGAGCTTGTCAUACAACA
224709902	73480	CAATTGGUGCACCTCTTTUCCA	73481	GCCCUGUACACGGAAACGG
224713333	73482	CATGGCUGGAGGCAUAAACC	73483	GGACACAUCCCUGACCCAAC
224716824	73484	GAGTTGGGAGTUACATATTGGTAATGAUACA	73485	GGCTCCCCTAUACTTCTGTAGATTUCT
224718117	73486	CCAGATAGTTUGTATGGCTGUGGT	73487	TTGGGTTTUACACACACATAACTCCUT
224726605	73488	ATGGCCAAUATGCCACCUCA	73489	CTCTGCTUCCCAGGCCTUAC
224727001	73490	CTTGCCUGCCCTGCATTTTAUC	73491	GAGGAAAACCAUGAGCAGAAATTTUGAA
224735920	73492	TCACAGGCTUAACCAATACGTGUT	73493	CTTCGAAGATCCUTTAGTCCTTCAAGUC
224737023	73494	GTGTTTATGAUGCACTTCCATUGACAA	73495	GAAACAGGTAGAAAUAGCCCATGUCAT
224737416	73496	AGACGAAAGCAUCAACACUCCAT	73497	TGCAGTGUGAGAAGTGTAACCUG
224738509	73498	GATACTTGACUACCATGTTCAGCUGT	73499	CTCTGGCUGCAAAGTTATCTGCUA
224739952	73500	CTTACATTGCATTUTAAAAGACATGCAUCA	73501	TTCCCTTAAGAUCACGTACTGTTUCAC
224740447	73502	GCAATAAAGUGTCATTGTCGUGAAACA	73503	TCUTCAACTACACTUCCCAGACCT
224744628	73504	CATCTCTGTATAUGGATGCCTGTTUCT	73505	CCTTACATCCUGGTTCCAGTTTTCTUC
224749788	73506	GGAGACGGAGAAAAUTCTGGAGUT	73507	CTACAGAAAAGUCAGGTTTTGTGTGTUT
224752671	73508	GCTCTTTTAATUGCCCTTCTGTUCA	73509	GAGTTGGCUGCAGTCTGGUAT
224752921	73510	GCTGGCTTTUGTGACGGAAAUG	73511	CTCGTAGGGAGAAUCTTCCTCUCT
224754133	73512	CCCTGGUCGGGAACTUGA	73513	AGCAGGCAGCAUGTCUGAG
224756301	73514	CAGGACCAGAAUTCTUCCCAGA	73515	GGAGCUGGCAGGACTTCCUA
224758268	73516	GGGTAGAAAACAAACUGATTCCTTCUG	73517	TTGGGATCTGCUGAAGAGCTATUG
224758836	73518	CCTGGATTUGCAGGCATGAUAAA	73519	CCAGGAGGAAAAUTTCGACCAUCT
224764638	73520	CAACUCCCAACAAUAGGGCAGT	73521	CTCCAGCUGCTCCTGAGAUAG
224767278	73522	CCAGATGAUGTGCCAAAAAUCCC	73523	GCTGCTGCUGAAACATCTCTUC
224769124	73524	GGGCTTTTUGCCACTCCTTUG	73525	AGTACTGCCUGAATTTGTCATGGTUA
224769868	73526	CCCCACACUGGGAGAGAAUC	73527	ACTTTGTGCUCCTGTGAATTCTTUCT
224771570	73528	CCAAACCCCCAAGGAUTGUCT	73529	GGTTATUCCCAGGCTCCAUGT
224777109	73530	TGCUGAAATUACGCCCAGGT	73531	GATUCCGCAAGCCACTGTUG
224778157	73532	GCTGACCGTUCTGGAAGATCTUG	73533	GATTCCTTCTUCCCTGCTCCTUT
224778196	73534	CATTCAUGGCCGCCUCCT	73535	GCAATGCCTUACGCTTTTCACUAA
224783365	73536	GATGAACAGGAUGATUCCAGGCT	73537	CCCACUAGGAACCAUCCCAAAC
224786698	73538	TGGAGUACAGGGACTUCAGACAT	73539	ACAGTGTUAGGAGACTTTCTGUAGACA
224789312	73540	GACCATTCCUTCCCATGTCUCAG	73541	CTGAACUGGAGGAGCTGTGUT
224801535	73542	ACTACCTCUCAACCCTTCCAGUAA	73543	CCCAGCAUTGGTGACUGGAC
224843784	73544	TTGTACTGTUAGTGGATGTCUAGGGAA	73545	GCAATTTGCAGTUTAGTTGTCTCCTTUG
224859727	73546	CAGCAAGAAGAGACGAUGCCUA	73547	TGTCCCTTCCACCUATGTAGTCTUAC
224956096	73548	TGGTGCATAAAUGTACCACTGAGUT	73549	GCATTCAGAAUCCGCACAAAGAATUT
224958832	73550	AGGCTAAAAGAUGGTGAATTGUGGAAT	73551	TTCCATAAGGCUTTGTTCAGGUGA
224973534	73552	GTGCCAUTGCAGUGCAGAAG	73553	CGCCGCAUCATGUCCACA
224974483	73554	GGGTTTTUGACACTACATUCCAAAG	73555	CTGAGGCAGCAAUCTGUGAGA
224979763	73556	CUTGGAGATGCUCCGGGAAAA	73557	CAAACTGCCCAGUGTAGGAGUC
224984253	73558	CCCACCCTUTGAGCCAACUA	73559	TGACTTGUGAAACCAATGAGTTCAUCA
224985943	73560	TCCAUACCCCGAGAGCATTUG	73561	ACATTGTTGUCCTGGATGCUGAG
224995126	73562	TGGACAUCTCGGTAUCACCGT	73563	CAGTCAGTUTCTAAGTTCUCCACACA
224997894	73564	GGTCTUGGAAACCCUCAGCAAA	73565	CGGGTTCTUTCGGTCACUGA
225009187	73566	TTGTATAGCACUATGGTGCGCUT	73567	CCAGGAGGUTGCCGATACUG
225015307	73568	CGCCCUCGGAGCUGAAG	73569	CCGTCCUGCAGCTCCTUT
225015835	73570	GAGCCGGACCUGAAGAACUC	73571	GGTUGCCCGAAGCCGUA
225016197	73572	GGCCCGCCCUGAACAAUAA	73573	CTCCGGCCGUAGGGTUG
225016684	73574	GGCTUCGGGCAACCCUA	73575	CCGTGGTCGUGAGAGTTCUG
225017167	73576	GCCGUCTUCCACCAACAACAT	73577	GTAGTAGGAGTUGTACTGGTGGTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225027382	73578	GCCTCUCTGAGTGUGGAGAGAAA	73579	TCGGAGACUGACACCAGGUAT
225033011	73580	CAGTTCCCCCUTTGTCACCUA	73581	GGGTCTCTTUATCATGGACTTUCAC
225033329	73582	GGCCGUGAACTCCTCAUCAAA	73583	CTTGAGCACACUTGAGGGUGT
225042649	73584	GCTTUTGTGGCCUACCAGAGT	73585	CCCTCCAUAGGGCCAUCAAG
225045615	73586	GATGAUGATGATGACUGGGAAGACAT	73587	TTTGAGCAGUAGATGACACUGGAAG
225048191	73588	CAAATCUCCCAAGGACCUAGCA	73589	ATCCAUGGGCCGGACAUAAG
225050967	73590	CTGGAGUAAAACTGCGGUCAAAA	73591	TCCATTUACAAACCCTCTTCTUGGAA
225052638	73592	ACAGACTGTCUTCCAGTGTCAUCT	73593	GGCAATGATGAUTTGCTATGGTTTTUCT
225058042	73594	TGTGGAGAUACAGGCCTGATUCA	73595	CTTCCTGGUGGCAGAGAAUCC
225058119	73596	CAGTCCTGTUCCTATGGGTUCAT	73597	AACTGGAGUACACAAGGCAATGTTUA
225062040	73598	GATCTCATGGAUGATCTGACTUGGG	73599	CTTTCACCCCACUGCAGGUA
225066898	73600	CATGCATUGTCTGGCTUACGG	73601	TGGCACTCACUGTCAGTGTTUT
225069792	73602	AGCTGAUAGAGGAGAAGGGTATUGG	73603	CGTGTCCTUGGTGCTAGUGG
225073259	73604	AGCAGATUTGTGCAAAUCAAGCAA	73605	AGCCCTCGUCTATCTGUAGCA
225075308	73606	AAGUGTTGCAAUGCAGCAGAAG	73607	CATCTTCAGTUTGGTGAGCTUGG
225080165	73608	CTGACUACCACCCUAGGAAAGACA	73609	AGAACATTTCCUGGGAAATAAGAGCUT
225085532	73610	TGACCCACUCAUCCCAAGACA	73611	CTCCCTTCCUGCCTCATTUCAG
225086310	73612	GCTCCTUCCCGGTTTTGTUCT	73613	TTCAGCAATCAUACCTTGTCCTCUG
225090146	73614	GCTGCTGGUGTGGAAGTTGUA	73615	GAGTCATCUCGTTGGAGTUCCC
225090238	73616	GGCUGAAACACCAAGACUAGGAAAAA	73617	GAAGGTTGGGUTTCTCTTTCTAAGUCAT
225099443	73618	CACTGCTGUGAAAGATCAGAAUAAACAT	73619	ATTTGCTGGCUGCTAAATTATGCAUT
225101720	73620	GACTUGAAAGTGCCUGCCAAAG	73621	CGGACATTUTCATCTCAAAUCCGT
225102835	73622	AGTCUGAGGAACCCCAGGTUT	73623	CAATAGCGTGGAUGTGTTTTTCTTTCUC
225103085	73624	TCTTGTTTCTCAGUACTCTTGGTTTCTUG	73625	ATCCACTTCUGCTGCACTUCAT
225105839	73626	CTGCAGGUGGTGCCUGT	73627	GCATATTGATTUCTCTGTGTGGTUCA
225109757	73628	TAGGATGAAGTACUCTCCTTAGACCUAA	73629	CTCAGGCTGGAUTTTGATGATGAUG
225109766	73630	ACCTCAAAAATTUACTGTTCCCTTCUCC	73631	TTCCGGUAGCTTGTGTUGAGAAAT
225111789	73632	GCCTCAGUGATTCUGCCAGAG	73633	TGCATTCTACAUGTGCATGTTUGG
225121006	73634	GTTTTGGCTGUCTTAGGAACTACAUGA	73635	GAGUTCATCUCCCGACACAACA
225122006	73636	CTGGCACTUCAGGTATCTTCUAACT	73637	TCACCAATGAAAUCCTTTTCGUCAGA
225122942	73638	TGAAGATACCAGAUCCTTGGAGATTUCT	73639	ATTCTGTGACTTCUGAAGGTGATCTTUT
225123165	73640	CATGTCCACUCTGGCCUGAAA	73641	ACUGATTCTCCUGGGACACACA
225124762	73642	GAGGUGGGAGGAGAAATUAGAGAAC	73643	GCTTGTGATTCTUTTCCTCTCTCCUA
225125930	73644	GAAGAAAATAGAACUAGGCTGGGAAGUAA	73645	GTTCTGGTUGAGATGAAAGGATUCCA
225127853	73646	AGTTGCTCTTUGTGATGGCAUGA	73647	GGCTTGTGTUGAGGCTGATACAUT
225132422	73648	GATCCACAAAAGUGAAGATACCCUCAA	73649	ACCATGAGGAGAUAGGAAATACATCUGT
225134000	73650	ACAGAAUGTCTGAGAAUAGCAAAACCA	73651	GCGACAGTAATCUGTTAAGCCATTTAUT
225137489	73652	GAGGCUGAAATCAAAAGUGGCT	73653	CCTGCTTGTTCUGACTCCTGTTUT
225137867	73654	GGCGUGAACCGAACAGAUGA	73655	AATGTGATTCUGCATGCTTGGUG
225140519	73656	CCTCUGCAGGACAGTGTUGT	73657	CTGACTTTGGUCAGCCAGTUG
225141771	73658	GGGTATGTCAUTGAGGACCUCAAA	73659	CCTTCCCACCUTGAGGATAGTUC
225143641	73660	AGGUATATCAGCUGGACAGAGCA	73661	TCAGATGGCACUTGAGAAAGACTUAC
225144662	73662	CTTTATGTCCCUGAGTGCAGAGUAT	73663	CAACTGCUGCTGCUGAGG
225144702	73664	GCACCTGGUTTGCCAATGAUG	73665	CCTCCUCCCCGCTTTTTCUAAG
225146179	73666	CCGAGGAGGGUCTCTCTTCTUC	73667	GCAATATCTATUCACCCAAGGAAACAAUC
225147999	73668	CAATAATTGTGTTCCCUTAAGATAGACTGUGA	73669	GCGTAGTTTGATUCTTTTGTTTCTCCUT
225149469	73670	CAACAAACAAAUGGCAGCUGGA	73671	GGGAGGATCUTTGGATTCAGAAUG
225150085	73672	CAGACCCAGACAGUCTCUGA	73673	CTTUCCCCACGAGCCUACAC
225150291	73674	CAGAGCCAGAAGGAAUCTGUACAA	73675	CCCTGCUGGGTCAGTCTUAG
225152679	73676	CGACAGUGCCACGAGUCAG	73677	TTCCAACGGUTTGCCTTTGUG
225154888	73678	GGAGATGUACAGCGTGCCAUA	73679	GATAGGCATUGCCATACTGGTUG
225156035	73680	AGCCTAUGGGTGCTCTAUCCAA	73681	CACACCUCGGACACACCUG
225156157	73682	TGGAGCTUAACCAGTGATAGAACUAGAA	73683	AGCTACACATUGAAGCTTTTGTCUGA
225157523	73684	GCATATCACTUCGTGCCTCTUCT	73685	CACTCCCAUGTGATAGUGCCA
225157619	73686	GATGTTCCCCUCTACAAGGAUGG	73687	CTCAGCCUGGAUCCGAGAAG
225160732	73688	GTCAAGGTUCTCAGGCUCCAT	73689	CAAAGCCUGCAACTGGAAGAAAUAC
225160828	73690	CCTTCCCCUCAGCAAGATGTAUA	73691	ATGTTTTGCUGGGCATTGGUG
225161815	73692	AAGUCUCCGGCACAGCAG	73693	CCTTGGGCUTGTCTTUGGAAGT
225163228	73694	ACCGGCTGTAAUCATGAATTAGAAAUGA	73695	CTACUTTCCCAAAGAUCAGGCAGAA
225164669	73696	CUATGGCUCCCGAGACCAG	73697	TGGGCCUGAGAGAGCCTUAG
225164710	73698	ACAGCACTATUTGGCTCCAGUT	73699	CAGCCATACTATUAATCCCTTGTCCAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225166839	73700	CGAATTCCCAGUTGAGTCTGUGG	73701	CTGCTCAAAGGAUTTCCTCTTCUGAT
225169206	73702	GCTGTUGAGCACGATGAACUT	73703	GAGCCCCCAGAAAUCTGACUG
225170056	73704	GGCUGTACUCACCAGGGACT	73705	ACACCGCCAGCCUCTTATUC
225170060	73706	CTTGGATTTUGGCAAAGCCTTTUCT	73707	GAGATCAGGUCTCTCTGGGUCA
225170797	73708	CCAUTCCAGTTUGGCCGAGA	73709	CCTGTTGGCAUAATTATAGGTCATGUCA
225173327	73710	CATACAGGCAUCAGCTGAGGUT	73711	CCTCTGATCUGTGTGCAGCAUT
225175818	73712	CTTACTGCUGCAGGACTCUGT	73713	CUTGUGACAAGGCCAGCAAA
225176601	73714	ACAGGAGGGUCAGGTCGATUT	73715	CCAGGACCACCAGUGACAUC
225177314	73716	ACAGGGAGGUGGCTGUACAT	73717	CCCCAAGACAUCATGGCCTAUC
225177733	73718	CAAGTTGAAGUGAGATGGTCAGGAAUA	73719	GAATTCAAGGUGGAGGAGCCAUT
225178542	73720	CGTGGCTUTCATTTTGGAUCAGA	73721	AAGATGTTTTGTTUGTCACCGGTTUT
225180821	73722	TGATGGGAACUGGACCUCCT	73723	TGACTCTUGAAGAAATCCCTAGUGAGAA
225181971	73724	GTAGAACTGCUCCTCCAGCUC	73725	GAGUACCCTCTGUCCAAAGCA
225184395	73726	TGAGGAUCAUCACGGAGGGT	73727	GAUGAGTTCCUCAGAAGGCAGAAG
225185505	73728	CCGCTTAAUAGCCCTCUGGAC	73729	GATACTGATGAUAAGCAAGGACTGTCUT
225185808	73730	GTTCUCCACCACCUCACGAC	73731	GGCCGGTGUCTTTCCTCTTTUT
225188467	73732	CACACTTCUCCCTGGCCAUAAT	73733	CAAGACGGCUTCCAGGTACTUA
225189402	73734	GGGAGTAGAUGATGGTCUCCGT	73735	GATCGGACAUCGAGTTCTGUAGAG
225190901	73736	CUCTGATCATUCCCGGAGGAG	73737	CTAAGCAGGAUCGUCCCCAAAT
225191021	73738	CTGGCTUCAGGTGUGGGT	73739	CAUCGTCAACCUGGAGAGCAA
225191933	73740	TGGTCCAGGUTGTTGCTGUC	73741	GACACAGTACUCGCAGTGCUT
225198494	73742	GCTTCCTGTACUTGTCCTTTTCGAUT	73743	GGGTTGGGAUGATGCCTGUC
225207010	73744	GGGTCGCUCTCGTGGUG	73745	AGCUCAAGCGCCACAUGAA
225207431	73746	CCGGCCUTGTGCATGUG	73747	GCAAGTCGUGCGAGTTCUG
225209736	73748	CGAGTCGAUGGCCAUGGG	73749	ACGCCGCCUCTCTUCAG
225211125	73750	CCATCTCCUCGGCACUGA	73751	TUTCCUGGGCGACAGCAA
225211487	73752	TCAUGCGCAGCAGGTUGA	73753	GCTTCCGCAUCTACCUGGA
225213060	73754	ATTGCTCTGGAACUTGAAGGTCUT	73755	GCGGCAACCCUAUGCAC
225213992	73756	GCCCGUGCGTCTTCAUGT	73757	CAGCGACACGUGCGAGUA
225214480	73758	GCTGUCGCCCAGGAAATUCAT	73759	CTTCAACAGCGCGUGGTUC
225214534	73760	GTUCAGGAGCCGGUGCAT	73761	GTGCCTUCGACCGAGUCA
225214807	73762	CAGGGTGCCUGCCTCAUAG	73763	CGGTGGAACCUGACATGUGG
225215312	73764	TGAACACCTUGCCGCAGUA	73765	CAGCCUGCGCTTCUCCA
225215608	73766	ACGAGUGCUCGGACGAC	73767	GCUCATCCCGUCCGAGAAC
225217519	73768	GAAGCCGUGCGTGTTCUG	73769	CCGCTTCUCACGCTGUCT
225218200	73770	GCGGAGCAGCUCCTCUA	73771	CTGCGUGTCTCCUCCCA
225219362	73772	GGACAGGGUTGGAAAGGCTUT	73773	GCACAATGACUCGGCACTUAC
225221131	73774	GATGAAGGCACUGCAGCCUA	73775	TGTGTATGGGUGACTATTCTTGGTTUC
225222024	73776	CTGGAAAAGAGUAATTCACACAAGCUC	73777	TGACACTTGGAGUAACAATTGCCTTTUA
225249715	73778	GAGGGAAAGUGATACUAGACAAGAAAACT	73779	GCTTTCUCCCACTCCTCUCCAA
225258408	73780	GCCTACUACAGAGGGCTACAGUT	73781	GGCTGCUCCACTAATCTCUCAG
225265247	73782	CCATCCAGUGACAAATCCCATUACAT	73783	TGTTCTCGAGGUAGTAAGATCTCCUG
225268126	73784	TCCGCCAAAAGAUCCCAGAUT	73785	TGGTGGAAGAACCUTCTCUAGGG
225273458	73786	CCUTCTGGAAATUACCCCGAGAG	73787	AAAGGUGGGAGAGCUAGAGGAAT
225274954	73788	GAATCCAGAGAACACAUACCATCUGT	73789	CTCCTCGAGAUGGCACAGUC
225279217	73790	CTGTCCUCCCAAACCTCAGUAG	73791	CCAUTGTCUGCAGGAACGGT
225280024	73792	AGTTGCUGCAGGGTAGCTUG	73793	CCATCAACCAUGCCACTGTTTUT
225287268	73794	AGTAATTCAAAUGCTGCUCCAGGAA	73795	GAGCCAAAAAGCUTCTTCCCTUG
225291009	73796	CTCTTGACAGCCUTACTTCACUCT	73797	GAGGTGACCUTCAAAGUCAGAGG
225291080	73798	GAAAGUGATGAUGAGGAGCAAGGA	73799	GTGAGGAUTCAGGTGUGGAACT
225295366	73800	CCAACTGAGTUCCACCAGCTTTAAUT	73801	TGCTGTCAGUGAACATTUGCAAG
225297063	73802	CGCTACGCAUGGGATCTTUACAT	73803	TCAATCCUGGCAAGACCAGUG
225298935	73804	GGAAATGTUCACCGCAGTCUGA	73805	GGUCCAGTACUCCCAACAGG
225300064	73806	CTGGGTGAUCAGAGCAATGTUACA	73807	GTTTGTGCTUGGTCCCAACTUC
225305180	73808	GAGCCACAGUGCATCACTTUC	73809	ACAAGGCACAAUACACAGAGCUT
225307988	73810	TCCCACTAUGAAGGATCCTGTAAAUGT	73811	AGAAACGAGAGCCUTGGTTTUCA
225309080	73812	CAGGGUGAGGTCCCTAUGACA	73813	GCATGTGUGGCATTCTUAACAACT
225310638	73814	GATCCCUCCAGTTTTUCCCAGT	73815	TGTTCTCGGCAUTTGCCTUAAGA
225311157	73816	ACGATGACTGUATTGGACCCUCA	73817	AGAGTGCTCCUGCCTAAAGAGTAUT
225312048	73818	CGGTGAGUCCACGGAUACAG	73819	GTCACCAUTCACCTUGGACAGT
225312335	73820	TTCTGCCAGAUAGCTGUGAAACA	73821	GGAATCCATTTCUTCCAGTTTCCUAGAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225318475	73822	AGCGTCAAGAAUGAGAAGACTTTUGT	73823	TCACUGAGCCCCTUCCCT
225324192	73824	GGAUGAGAAACCCAATUGGAACCAA	73825	CTCAGTACUGGCCAGCAGUAG
225326057	73826	CAAAACCAUGAGGAGAATACTUACGGA	73827	GTATTCCATCGAUCGTCACACUGA
225326238	73828	CTGTCCUAAGCACTAGCAGCUT	73829	TCTTCTTCAAUCCTTGGCACUCC
225326289	73830	AAACCAACGUGTTATGAAACCAUCA	73831	TGACTGTCUGGTCATTTGCAUGT
225329345	73832	AAGTTTAGTGAUACGACACAAGAUCGG	73833	TAATTATTTTCTGCCUACCCGAGACUA
225329957	73834	AGTCTGTCCCAACUACATAGATUCCA	73835	GGAAAACCTGGUAGCCTATGCUAAG
225330478	73836	CCCGUGAAAGGAAACAUGCAA	73837	TGATGTGGTAUCTATCTTGGUGGACT
225331053	73838	CTTGCATAGAAGACUTGAAAGCATTUGT	73839	TCAGTCTTACCUAGAAGCACTGTTUACT
225332276	73840	TCATCCCAGUCTTCCCUCCAA	73841	CTACAGAGGGAUCACCAUGACC
225332696	73842	ATGAACGUGCCTTGCCCUAA	73843	TTGCAGUATGAGTTTUCCCCACA
225336186	73844	TTTGAATGACUTATCTTCTGAUGCACCA	73845	ACTCACTATACTGUCCACTGCTAGTUT
225336880	73846	AAGGCCTTTTAGAUAATCCCATAAGUGA	73847	AAGAAGTGTTTTGAUCCACGGAAAAAUT
225339560	73848	CGTACATGUCCCCTTCCACTUT	73849	CTGGACGAAACCCCAUGTCTTUA
225340594	73850	TCCTCTCTAUCCAGAGGTTTTGTAGTUT	73851	GCTGCTCTGAAUGTCTTGGTCUA
225341116	73852	GTCCCATACUGTTTTCATTGACUACCA	73853	CCTGGAAAGAAAACACUCTCCUCAG
225341622	73854	CACACCGAGGACUCAAGAAUGA	73855	GCACAUCAGGAAAAGCACTACATUT
225343210	73856	CGGTGCCAACUCCAATTUACC	73857	GGCACTTGUATTGGTTTCTCUGAAGA
225344247	73858	CGTGGAUCAAAACACTTCTUCAGAAAAT	73859	TCGGTTCCTUGGAATAAATAGGTATCUCA
225345574	73860	TGCTTTTCCUGATGTGCCTGAUAAA	73861	GGTGAAATTCAUCCCATCATCTTTTUCT
225345681	73862	GAACACCAACAGUGATATGTACTCCUA	73863	CCTCUACAGGGCCCCTATTATUAGA
225346010	73864	GTCCCAAAGUGCAGCTTGTCUA	73865	CATATTTTTGUCAGGGAGCUCAGGAT
225351033	73866	GCCTCTTCTACACAUCAAATGCATGUAT	73867	CCTTTAGATUCCCGTGAGTUGGT
225352137	73868	CTAACCCCUCTGGAGGAAUGG	73869	CTCTGACTTTUGCTTGATAGAGGTUCAT
225359204	73870	AAAGATGTACAAAGUCCTGGATTTCUGA	73871	CTCCAGGGCACUTTCGTTATCUAT
225360840	73872	GCTUACACCATCCUCAGCCAAG	73873	CACGGGATUGAGCTAATACACATTUG
225364666	73874	GATATTACCCAGAGUTGTATGGUGGAA	73875	TCCTAGTGATCUCCATGTCATCCUG
225366909	73876	CTGGAGGAUAAAGAGGACTTCCATTUG	73877	CGGTTTTGTCCAUGGGCCTAAUA
225375365	73878	CACACAACTGCCUTAGAATGTAAAACUC	73879	GTGGCTUGACAGTCAAUGAAAACA
225377843	73880	TCTGGAAGUCACCGATTCCCAUA	73881	TTTCCUACAGCCAGTGCTUGT
225379651	73882	AAGATGCTTTTGUCCCTTCTTCTUT	73883	TGGTCTTTGUCTGACTCUGAGGA
225382577	73884	CGATTGTTAATTUTAGGGCCCATUGT	73885	ACCAACAACGCUACCTUCCA
225383787	73886	GCTGTGTUCAAGAAATCGCUGAAAA	73887	GCCTGGTCUACAACTTTCCCUAT
225388114	73888	GCTAGTCUGAGCTCCCUGAAC	73889	GAUTTCTGCATTUCCCAGCACAT
225389268	73890	GCGATAGGUCCCCGTGTUT	73891	CGGTGACCUTGCGATGUGT
225390503	73892	AGTGCTGCTAUGGATGAAAAGGUC	73893	AGCAGTTGCAUGACTACTTGUAAAGT
225391089	73894	GCGGCUGGUAAGGGAAGAG	73895	AGGCUGGAGCCCCTGUA
225391692	73896	CGGCCGGGUCGATGUAG	73897	CCGAUGAGCAGCCACCUG
225394704	73898	CGCAAGTTGAAAGCUGTCAGTTAAAUAA	73899	ACTACCCUCCAAATTATCAGUACAGGAAA
225394792	73900	AAGGAAGGGCCAUTAGAACACAUC	73901	TGATGGTCTTTUCTCTCCCTCUCA
225397029	73902	CCATTCCACGCUGCCATUG	73903	CGCATCCUAGACCTCACTTCUG
225398125	73904	TGAAATGTGTGUGATGCCTCTUGT	73905	GAGGATGCUGTCCTGAAGGUG
225398831	73906	CTCACTCACACUTCAGCATCTUCA	73907	CCAGGGACUTAAGGGACCUGT
225399199	73908	TTCCAAAGATCAUTATGGCACTTUCCT	73909	ACTTACCAAAGGUGCTGCTCUC
225399677	73910	CCCAGGCGCCAUCTAUCAC	73911	GCTTAGAUCAAGCTATCTCAATUGCCA
225399757	73912	AGGATGGAAAAAUAAAAACGCAUAAAACT	73913	AGCCGTTTACCAUGAGATCCTTATUG
225399885	73914	CCAAACTCACCCUAATTTCTTCACAUACT	73915	CCTGAGTTAAACAUGTGCCTCCUT
225401088	73916	CTGTTGGTACUGTTTGGGTGGUA	73917	AGCTTGATCAUCACTCCACUCAAC
225402179	73918	CAGGCUAAGGGATGGCAGUAG	73919	AAACGGAGGUCGCGTTTACAUA
225403221	73920	GGGAGAACAGCCAACUCAUCC	73921	TGATGCCTCUGTGCTCTCCUA
225403465	73922	GGTTCCCCAAGAUGCCTTGUT	73923	CACAGATCATUCAGTTGCTTTTUACAGT
225405071	73924	AGCTTGTCUGAGTGGGATGUC	73925	AGTGAGTGUAGCCATTCATTTTTCUGT
225408463	73926	GGTCTCAAGTUTGTGGCTCTTUG	73927	TTCACUGGCCTCCTCUCCT
225408912	73928	GTGGGTUGGAAAGCTCAGGAUT	73929	CCTTCCAUGGGCACCAUGAG
225409436	73930	AAAATCCATTGGCUTTTAGTTGCCAUT	73931	TCAGTGGTCUGTGCATACTGUAGA
225410451	73932	GGAGCGCUGUAGCACCT	73933	TGTGCCUACCACGUAACCAAA
225411455	73934	CCTGCAAACAUTAACCAUGACCAAT	73935	ACCACACCTGUGAATTCTGAATUCC
225411627	73936	GACACCACGUTGCUGAAAACAT	73937	AGTAGGGTGAAGUGACTTTTTCTUGG
225415004	73938	CACAGAGTUACTTTTGGCAATUACCAAT	73939	CCCAGATCUCAGCTGTACTTUCAC
225417180	73940	ACAGGGAGACAUGAACCCCUT	73941	CGCTGACAUCTCCATTTCATUCACA
225418705	73942	CAAATAGACGUGGGCTGUCCT	73943	CAACUCCAAAGAATATUCCGGAGACT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225419196	73944	TCACAATGAGUTCAGGCTTAUGGAG	73945	CGGTACTTUAAGGAGCTTTTGTGTTUG
225421529	73946	AGGACCCCUGTUAGCAGAGAG	73947	TGCATACAAAUACACAGACACACAUGA
225426052	73948	CAAGAAUGCAGCGTUACAGACAAA	73949	ACTGCATGAGGUTGCTCTAGAATTTTUA
225427967	73950	GAAATCACATUGAATGGTCAUGCAAAC	73951	ACATTTTGCCAAGAAACUGCACTUAC
225430388	73952	GCAAAAGGCAAGAAAAAUCAGATUGGAT	73953	TTTTAAACAGGCUGAACCTCTCCUC
225435205	73954	GGAUGAGAAAGGCAAGCCUACA	73955	TTTCTCCCCCUCTTCTUAGCCT
225436497	73956	CAGTTGUGGCCCTGUAGGAC	73957	AGGTTTCUAACGCCTGTTTTCTTUCT
225436956	73958	ACGTGTTAATAAAAGGUGATCAGCCUT	73959	TGGTGCCUGTGGAGAGGUA
225439251	73960	GACTCTGUGGACAAGUGAGCAT	73961	CCGAAACUCAGGCAACUCAG
225439546	73962	CTCACCCATGUGGCTTAACCUT	73963	AAAAATACCTUAGAAAGCCGGAAGUCA
225439977	73964	GATAAAATATTGGTUGACTTCCGGCTUT	73965	GCAAGTAACCUATTTACAAAUGCCACAT
225440403	73966	TGGACTUCGAAGAGCGCTUT	73967	TGCCCAAUGCTCGCCUAC
225460613	73968	CCACGCAUCCCGCCTUT	73969	GGGCUCATTUACCAGAGAGACAG
225460620	73970	TTUCAGCCCAGCGGATTUCT	73971	GGAGCUCAGGGAUCCCCA
225461361	73972	AGAAATAGGTCTUCAGCGATCTACUCA	73973	GGTTTCTTTGCUTCTGCTAAAACTUCA
225462845	73974	GUCCAAGAACAUGAAAGGGAAAAGG	73975	CCCGAACAGAGUGCAAUGCT
225467306	73976	TTCTTTTATAGUCAAACGAGCUGCAGA	73977	GGTTACTGCAAUCAAAGAATCCTTGUT
225467996	73978	GGGACAGUTCGCUGGACA	73979	GTCUCACCCCAGACTGGUT
225471220	73980	CCATGGUGACTGCGAGUCC	73981	ATCGCCACGUCCCTTAGUAAC
225471531	73982	CACTTGGGTCUTTTTGTGCCTUT	73983	GUTCACGTUGGGCAGGGA
225474364	73984	CAGCCGAGGCCAGUACTAUG	73985	GATAACCCCAGCUGTCCUCAAT
225489391	73986	GCUGGAGACCGCACCUG	73987	CAGCGGAUTCUGCAGCAA
225490780	73988	GGGACCCAAUCTGCTGCUT	73989	AGATGGCGGCUCAGAUGG
225491190	73990	CCCATCUGGCCAAGCUGT	73991	CCAGTUCCAGCAGCCUCAA
225491370	73992	GGTAGCCUCCGGGUCCT	73993	GTATGAATCCACAGUACCGAGAAATGUT
225491507	73994	GGGTCTUCTGTTGACUCACAACC	73995	AGCGGTCUACTTATTCTGTTUCCAAAA
225492496	73996	CATGCCGGCACUCCCUT	73997	CCAGGCCUTGAACATCAUGAAC
225493995	73998	AGAGCCAGGACAAGAUCTAGACUT	73999	CAGAAGTGUCCCTGTUCCAGT
225494740	74000	CTGTGGATTCAUACTCGCCAUGT	74001	CCAGCCUGCAGAACCUGA
225495517	74002	CTGGCTCTUCATGGATCCUCA	74003	CTTTCGTGCCUCCCATCCTUAG
225499340	74004	GTATTTTCTCTUAGGTTCTCCAGTUGCT	74005	TCTGCATCAAUGATGTTTATGACCUGA
225499915	74006	CCUACAGGGCTTUCCCAGAAC	74007	GCCCCAAGUTACAUCCACGA
225507439	74008	TTCTGUGAGAGGAAUCCAAAGCC	74009	GCAAAGTTGCCAAAAUAAAACTCAGGUA
225507865	74010	GCAGCUGCATTTTCTUGGACT	74011	GAAGTTTATCAGCAAUGGCCCTTUC
225513496	74012	CTTGACGGUCACAGTGTCCUT	74013	TGTCAATCTUCTCTTCATTCTUGCCA
225520367	74014	CTTAGATAUGGATATGTGTGUGCCACAA	74015	ACTTTGACATGUGAATATGCTCTUCAGT
225521189	74016	CTCCCUCTCACCUGCAGAGA	74017	ACAAGGUGACGGUGCAGAG
225525002	74018	CTCTAAGGUCTCAACAGUCAGCAG	74019	CCTGAAGCUCTGAGCCACAUT
225525028	74020	ACCAAACAGCUTTGUCCACCA	74021	CCCAGAGAGCAUCTTTGACUGT
225525840	74022	GTCGCTCUGAACCGTGUAGAC	74023	TGTCAAGGGCAAUGTAAGUGCT
225526048	74024	GAACCGTGUAGACACAGUCAAAGA	74025	ATGACTCCAACUACATTGUCAAGGG
225526158	74026	CCATCTCCUAACACTGGCTCUGA	74027	GCAACAUGGAGACTGGUGAGAC
225528190	74028	CCCCTUCAGATCTTCUCAGCA	74029	GCUTCGATTCUCCGGAAAAAGG
225529821	74030	TCTTGCTGATGUACCAGTTCTTCUG	74031	TCCCTTTCCCUGACTCCATCUT
225529900	74032	CCUTCTGAAAACUCCCCAGGAA	74033	CACCGAAUAGTTACGGUCGGA
225530287	74034	AGCTUGCGGAAGTCAGTUCA	74035	GCGTCCCUCGCAAGUCAG
225530996	74036	CCGCUGCAGACCCTCUAC	74037	GGAGCAGCAUGGAGCCUT
225531129	74038	CACAGCAGGCCUCTCTTCUG	74039	GGUCCCAGCAAGCATCUGT
225531462	74040	GCATCCAGGAGGGUCTGAAAGAUA	74041	CATCCCCACCCUTCACUCAC
225531955	74042	ACTGTAAGCAUGAGAACTTGTGUGT	74043	CTGGCTGAGAACUGGAGTACTUC
225532195	74044	CAGAGAGAAGGAGAGAUGCUGAG	74045	CTTCAGGGAAUGCCTGGUGAA
225532534	74046	CTTTCTGTCTUAATGCCTCAGUGAAGA	74047	CAAAAGCATATGAUCAGGACATGUGG
225533394	74048	GCCCCTCAUACATTGATAAATTGGUACA	74049	AAAAATTAAATUCCCTCACCTGUGAGGA
225533947	74050	GGTTGAACTTACUCTGTCACCCTUAG	74051	AGGCCTCACUCCAGTCTTCUT
225550183	74052	ATCTAGCCCCCUCCCCAUAC	74053	GAUGGGACAGCACCGUGA
225551071	74054	GGTCTATCCUAACACGGCUCACT	74055	CCCATAUCGAACCAAAGCTCTGUT
225558520	74056	GCCGUCAATTTCCUCAAAAGCA	74057	GTCAGCAACAGCCUTTGTAAATGUC
225558661	74058	AGGGUCCCCGAGGUGAG	74059	TGGGCCUGAACTGCCTTTUT
225563387	74060	GCTCTCTGUCCCCACTCTUCA	74061	CCAUCCACAGGGCCAAGTUC
225566072	74062	GTTGCAATGUTTCTGTCTUACACCAT	74063	GGAGGAUGCCATAACAACUCCAG
225568061	74064	GCATTGATAGUCCTGGCTCUGAAT	74065	CTACTGCCCUGTCTGCUCAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225571638	74066	CTUCCAGCACCGGGUCT	74067	GTAACCCTGUGCCCTCCTCUA
225571993	74068	GCACCCACUAGCACTATUGCC	74069	ATCCAGCAGAAUGUGAAGACACA
225596011	74070	CTCTGTAGCATAUGCACTTGAAGGAUT	74071	GCGAAACCAGUTCGGTCTTUCA
225596379	74072	CCCCTGGTUTCGCAAATTCUCA	74073	GGAAUCGTTTGAAAUCACAACGGA
225601657	74074	CTACTTAGAGGUGCTAATCCCGAUT	74075	CCTTCTTUGGCAGCCAAGUG
225602292	74076	AACAAGAACCACAGGAUTCUCAAGT	74077	AGATGAACAGCAUGGGCUCAG
225608075	74078	CACCCCCUCCTGTGTTTCAUAG	74079	CCAGAUGTCTGTGUCAGAAGCA
225609948	74080	AGAGAACACUTACCCCUGGCA	74081	TGAACCGTTGUGGGTACATTUACAG
225612611	74082	TCTTTAGCTTUCACTCTTCCTACTUCCT	74083	CAATGAAATCTAUAGTCTTACAGCUGCCA
225613002	74084	GCCUGGTUAGGAGCAAAGGAA	74085	GCATTGACGUTTACATTATTTUGCAACA
225614092	74086	ACAUCGAGGATAAUGAAGGGAACCT	74087	GCTAACAACCUCATTCCUCCCA
225614923	74088	ACAGGAACUGACGCAGGTCUA	74089	CATACTGGGUAGAAGGCTTUGGG
225615366	74090	GGGACCUAGAGCAACTTACTAGUT	74091	CGTAGGCAACAUTATTGACTTGTTTUCC
225617579	74092	CTGTGATTUGGCCAGGCTCUA	74093	AGTCAGGAGAGCUACTCAGTTAATUGAT
225618062	74094	GGCCCTGCAUCGTACTCUG	74095	TCATCACTCGUCATGTCCUCACT
225620375	74096	GAGCTUCTCGTTCUCAGCGT	74097	CTGGGTCCUGGGCAAGAUT
225622350	74098	TTTATCTTCCCAUTTTCATCACGUGGA	74099	GTTGCATCTGGUCTTTTCTTCTTTGUAT
225625657	74100	AAGGTTGUCAACGAGAAAATGAAACUC	74101	AGACTATCTTACCAGUCTTGAGGCAUAA
225627040	74102	CTTATAGAGTAGUAGACCAGCCCCTUAA	74103	GCAACGUCAUCAACGGCAAT
225627705	74104	GCCCUCCCAGCACTTACATUG	74105	AAGACTAACCCUGCAGTGCTUT
225631412	74106	GGCAGAAGGGAGAGUTTGGUA	74107	TTTCCCUCTGCTCCUAGGCT
225633463	74108	CTGATGTTCGCUGCCTCATUT	74109	TGGACATCUCCTATGTUGAGGCT
225634648	74110	CTGCTCCATGUATGAGGACATCUC	74111	AGGGAAGUGAGCUGAGACACT
225636022	74112	GGGTAGAGCUGTGGATTCATTUT	74113	GACGGACATTTUTCCTCCCTCTUT
225643957	74114	TCCAGGCUGUCCAGGGAT	74115	AAGGGUAAGCGTTGCACUCT
225644652	74116	GCCCAGAGUGCAACGCUT	74117	GTAATCTCCUGCCCTCGAATTTUG
225655358	74118	TGTGAAGGCUGCTCTGGAGAUA	74119	TTTGCTCACTGUCTGTTCCTCUC
225660664	74120	AGACCCUACACGGGAUGGT	74121	CGCTGGUGAACGTGGTUCT
225661337	74122	AGCTUCACCAGGAGATCCTTUG	74123	CCTGGGCAUCTTCTTCCTCTTUT
225662516	74124	GCAGGCGAGGCUACUGA	74125	GGGAACAUAGAGGGCAUGCAG
225666630	74126	CGCACCAAACAGCCUAUCC	74127	CTGCCUCTCAAGTUCAACACAAC
225668416	74128	GTGCTAAGAGAAAGUGATGACCAGUT	74129	TTTCTTACTGAAGAAUGCCGTCTUCT
225671791	74130	GAGACCUGTUAGAAGACGGCAT	74131	CCAGTAAGGGUAGGATGGUGAAG
225678370	74132	CAGGCCUGGGAGTTCTTCUAT	74133	ACTTGTCTTCUAACCCATCTTTTTCCUT
225685124	74134	CTGTTCUCAAATACTGCUGGGACA	74135	GGGAACGCCAACUTTCTCATTTUT
225687463	74136	GCAGGTCAAAAGGUACAAGATTGTUACT	74137	TCCCACAGACUTTCACATAAAAUACCAC
225691124	74138	TGTGATAGGAAGCUGTGGAGUGA	74139	CTGGAAGATCAUCGAGAGCTAUGAG
225692591	74140	TCAGAATGTCUACCCAATACCAGTACUT	74141	GTACAAUAGCAGACACCATCUGAGG
225692713	74142	GGTCGAUGAAAGTATAACTGTUGCC	74143	GUCAGAAACAAGGUCCAGGAACT
225697496	74144	AGACACGCUATCATGCGTUCT	74145	GCAGGAAUGCCTCCAGACTUAAA
225699618	74146	CGGAGCCUTAUGAACCAGAGA	74147	CGCATTGUCGAACCAUGAAAAAC
225701836	74148	ACAAGAAUTTTATTTCCUAGGGAGCCA	74149	CCCGCUCAGAGCCAGTTUC
225704086	74150	GTGAGGGCUTACTGGCCAUC	74151	AACACAGAAUCCACTGGUGAACT
225704141	74152	CCTTCTCTGAGUGGTAAAGGCAAUC	74153	GTTCTCAAAACUGCATTCTGACTTUCA
225705662	74154	GATGACGGGAACUGGTTCUGT	74155	CTTCCGAACUACAGCTCTGGUG
225708536	74156	CCAAGCCUCACCCCACUC	74157	TGGGCATCCUCTGTCCTATCUC
225708863	74158	TGACAATGCGUCATGTGATUCAAAAC	74159	GCAGAUCCUGAAAAACGCAAACT
225710619	74160	AGAACCAGCUGCTGCTGTAUC	74161	TGAATATGACTUGGAACTCTGAGAGGUT
225722132	74162	AAGTTCUACAAACCTTAAGUAACACCAG	74163	CGAAAUACTGTUGCCAAGCCAAA
225722148	74164	AATCTCAGACUTTGGCTUGGCA	74165	ACTGGTTCTGCAUGAAATTCTCTTCUC
225727031	74166	TTGAACAAGAUGTGTGGTACTTUACCAT	74167	CTCTTACCUCCAGCGAGCAUT
225727055	74168	ACAGUGAGACAGAGAGUGACCAT	74169	ACTGGGUCCGACGTTTUCC
225730148	74170	AGAGACAUGGCCCTCACUGT	74171	CTGCGUCCATCCTTCUCAGA
225732730	74172	CCAAGGAACGGGACUCAUCT	74173	TCTCCCGCUGCATUAAACACA
225735429	74174	GTTCTCCAGACTUTACTTATTTTCCTCTUCT	74175	GTAACACAGTGUCCAGAACAGAACUAAA
225735454	74176	TCCTTTTTCTTUTGCAGCTTATTUGCT	74177	ACAATTTCTGTCCUCAGTAGCTCTUG
225736284	74178	ACACUGTGTTACTUAGACCCAAAGAAAA	74179	CAGAAAACAGCAAAUAGAACACCAUGT
225744031	74180	CTTGGAAGGAUGACCTCAAACUCAA	74181	GAGGTTTTTGUCCGAGTGGUG
225749631	74182	CTTGACCUCCACCGTCTUGT	74183	CCTGCTCCTUCTGGACTTCCUA
225763808	74184	GGTCCTATTCUAAAAGCCAGAGCUT	74185	GATTAGGGCUGTGTACGUGCT
225766972	74186	GGCTCCTCTUCCTTTCTGGAUT	74187	ACTCTCAGCUCATCCTCTTCUCC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225769994	74188	GCCATGACUCCGTGTGUCAG	74189	TCTCTTCCATUCCTGGGACTGUT
225771654	74190	GAGGATTTUGAGCACGUGAAGAAC	74191	AAAGAATGAACUCTTCCCUCCAAAAGAA
225776907	74192	GAGGCUATGTGTUAGGGCAGAA	74193	TTATCCATGTCTUTAGGGTGATGCUG
225777077	74194	CCACCUCCCCAGTCTTACUGT	74195	CCAGGUGATGCTUGAGAAGAGAA
225779016	74196	CAUCTTUGCCAGGAGAGCCAT	74197	CAGAGGGCCUCUCAGGAAAC
225792353	74198	AAUTGGGAATGTTUGCACCACAG	74199	AATAGCTTCUGCAGCTTCCTUGT
225797753	74200	CCUGAAGCCACGGGUGT	74201	CCTGTTAATTCUGGCATACTCTTACUGA
225798259	74202	GTCCTCTGUGAACTTGCUCAGG	74203	ACACATCTGCUAAAGGCTTTGGUT
225803356	74204	CTTTUATTCTCTAGCUCCGCAGCA	74205	CTTACCCTGTUGGCCCTTTACUC
225810007	74206	TTTCCCGTCCUCTTTTGCTTGUA	74207	CTTTTAGCTCCUCAATCAATGTCTTGTUT
225813804	74208	AGAGTGGCAGUGCTTGAAAAUCA	74209	CCAGTCCAUTTTCCACCTUAACAGG
225815096	74210	CTCCGCAGGAUCAGCTUAAGG	74211	CCAGCCAAAAGAAUATCTGCCUACA
225817173	74212	CTGGAAGUATGGGUGAGACAGG	74213	AGATGCGCTUAACATATGACAGUGAA
225819257	74214	CACAGACCUGGGTGGCUA	74215	TGCCCUGACGCCTCTUC
225822526	74216	CAGCUGCGAGTCTTUCCCT	74217	CATGCCCAACGUGTCCAAUG
225823750	74218	CAUACAGCTTCUGGGACAGGT	74219	CACAGCCTUGCGTGTTGUT
225824727	74220	TCAAAACCCUTCTGCUCACACT	74221	TGACCCTCAACCUCGATCAAGUA
225830363	74222	TTGCCGGCAUGTTGGAAAUC	74223	ACCTTGGTATAACAUCTCCATTCCTUCT
225836854	74224	GTGAGCCACUAAGCATTGAAATGUT	74225	TGGTCCCCATCUCTTTAAATACTCAAUCT
225840369	74226	CUAAGGAUGGGAGGCACGAAA	74227	CTCATACCTCUCTGCCTCCCUA
225841991	74228	AATGTGTCACCAUCCCCAGUC	74229	GTTGGCGTUGTTGCTGCTAUT
225844212	74230	GAAGACGCCCACUTCCAAUG	74231	CCATGGCTCUTGTTCACATTCUG
225845932	74232	CCCCAATGGUACGCTGAUCAT	74233	GCGGGACAGUGGGAGUAG
225852873	74234	TTAACTTCATTGUTTCTGCTCTCUAGGG	74235	TTCATTCACAUCCAGCACAUCCA
225855433	74236	GGACTAUCGCATTGTCUGCCT	74237	CCCGAGUCCCCTGTCCAUA
225856876	74238	TGGTACCTTTUGAGGTCTCTCUCA	74239	GCCAAAGTCCUCGGACACUT
225858736	74240	GTGCCTCCUGAAAAGAGAGUGG	74241	AGTTGCUGCAAGTCAGTUGAAAAAT
225861948	74242	GACTGAAGCCUGGCAGGAUAC	74243	CCACTTTCTAACCUCAGAGTCCUT
225864443	74244	AGGTGUCGGAGTGTCCUGA	74245	GGAACCAUAGCCTTUGCCAAA
225866345	74246	CCCCCGGAUCCTCCTGUAG	74247	TGGGCCTUGAAGGTTCCUG
225867560	74248	GUGCUGCCCCCAAACAAG	74249	TUAGAGGCGAUGGGCACAG
225867637	74250	CAGCCACCUCCTTCUCACT	74251	GCAGGAUCCATUGGGAGGAAC
225867746	74252	CTCTGTTATTTCACUTTATGCCTCCUCT	74253	ACCGAAATATAAUCATTGCAGGUCAGAT
225869103	74254	GUCCAGCGACACCTUCCAA	74255	GTCTGCAGGAUGTTTCCTCCUC
225869286	74256	GGCCTGUCAGCAGCACUC	74257	GCCGACTUCTTGTCCGAAUACAC
225869334	74258	GGGAAUCACCCAGGUACAGT	74259	ACTTUGCCGTTGGUGGAAGT
225870293	74260	GAGACCCGAAAGUGUGGGT	74261	GCCCCAUAGGCCAGTGAUG
225871061	74262	CATCCGUTTCACCCUCCCA	74263	CTATGGCCCCUCCCCUAGT
225873270	74264	GCCCTGTTUGTTAACCATGTTUCT	74265	GAACACTTCACUTAAAACATACCUGCAC
225873536	74266	CCATGGCTCUGAAATCCACTATUG	74267	CCGAAGTAGCAGUAACCAGTTUAGT
225873579	74268	CCGCTGGGUGTCAGCTUA	74269	GGUGCCCACCAGUAGGT
225874019	74270	AGGACACCAAUATUAAGGCAGAAC	74271	AAGTCTTTTCCAAAUCGAGGCAUCT
225875386	74272	CGCCUGCCACTGTCACUA	74273	CACUCCCAGCACCTGCUC
225875907	74274	CTGATTATTCAGAUGCCTCGATTUGGA	74275	TCUGACAATTUCCACAAAACCAACAAAA
225876733	74276	CCCCTGCUGTCCAGTTCATUG	74277	CAGCGUGGGCAGGAUGT
225877579	74278	TCCCAAUGGGTAGCTUCAGGAT	74279	CTCAAGCTCTCUTCACAAATAGTATCUCT
225879368	74280	CAGTAGTCAAAUGGAATCACAGTTTCUC	74281	ACGTGTATTAGAAAUGAGACGTTUAAACCT
225884344	74282	ATTCTTTGCTGUGTACTAGTGGGTUT	74283	CAGAATAUGGCCGGTCUGGAG
225884701	74284	CCCTGGGAUCCCTTCGCTUA	74285	CCTCTTACCUGATCTTGGCCTTUG
225886045	74286	GAGGGAGTGGUGAGAAAGGGTAUA	74287	GGTGAAAUACCGAGTGCCTCUG
225887934	74288	CACCAUCAGGUACAGACACCAA	74289	TTUGTCTACACCUGCAACGAGT
225890191	74290	CGTCTCCACGUGGTGCUT	74291	TCCUCACCCUCGCCAGA
225893938	74292	CUTCGAGATCTUCCACCACCAC	74293	AGTCUCCAAGGCGGCUAGA
225895126	74294	GGAGAACUCCCAGTGCTTGUC	74295	GACTAAAGCCCCUCCTCUCCT
225897075	74296	GGCTGTACGGAUGGAACCUT	74297	ATTGGAAACCGGCUGCAAUG
225899532	74298	GGCCTGACUCTAGGTTUGCAT	74299	CACTGTCACCAUCACCTAATATAACAUGA
225902236	74300	CTGTCCCUCCAGAGACAAACUG	74301	AAGTGAGUGCCGGTTGGTUAA
225905543	74302	TGATACCTCAGUAAAGCAGGAAUAGGT	74303	CGGACUCUCAGGGACAACCA
225907585	74304	TGAUCCCUGGACAGGAAGAGAA	74305	GCCCACACATAUTTCTTAACAGGTUAGA
225909414	74306	AATATATTTATGAUACACTCCAGGAAUGCC	74307	GCAGTTATGTCAUCATCTAGATCAGUCT
225912626	74308	GCCAAUGGGCAACACAGGAAUA	74309	CACTAUACCAACAGCAGCTCCUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
225914479	74310	CGGTCAGTGUGATCGTCACUT	74311	TGATGTTGCCUGCTTACCTGUC
225916488	74312	TGCAATCAAAGCCAAAAUTATGGCUAA	74313	GTAAGATAGTUGTTCGTGTCCUCCAT
225919091	74314	TTTCCTUACACCGGTGCUAGAAG	74315	GTTTGAGTCACUTCAGTAGATGGAUGA
225919823	74316	CGAGAUATTGUCAGCAGAGAGAGAGT	74317	CTTCCACCUAAAAGCAAAGTTUAACCAA
225921729	74318	GGTCCAGGUGGCCUAGGA	74319	CGGGTCCUGGGCTCUCA
225923404	74320	CCCUGGAGCCACAUGCC	74321	TCAGGGAACUCACGCATCAUC
225928617	74322	CTTTGGTCTUCCCTCAGAAAGUAAC	74323	AGCCUCUGAAGACACCCCAT
225929764	74324	GGGTGTCTUCAGAGGCTAAUGA	74325	TGGAACACAAUGGAAAAAGATCUCAGAA
225937169	74326	ATCTTTTCAGCAUTTGGAGGCUACT	74327	GAATTGTAAUGACCCTGGAUGCCT
225939326	74328	GCTUGGAGATAATGATUGGGAAGAAGAA	74329	TGCCTCATGGCACUATCTATACCUAT
225941304	74330	CTGGAAAATGAAUGCTCTGAGCUT	74331	CTGAGGAGCUGGGCCAUC
225942695	74332	GCAGGUACCGUGCGACAT	74333	GACCCCGCCACUCUCAC
225943133	74334	CACGGGUCGGGUGAGAG	74335	ACACAAGCTUCCTTTCCGUCAT
225946458	74336	AGAAGGGAGGGAAGGUTTAGAAUCT	74337	CCGTGACTGUAGTGTTCTCTCUG
225947047	74338	GGGUGCTGTGUGAAGGGA	74339	CCTGACCCUGAGCCTCTUG
225964544	74340	TCAGGCTCUCCTGTCTTCTCTUT	74341	CAACCUCAAGAGAGUGGACAGAAT
225964824	74342	CACUGGCTCTGUGCAGAACT	74343	GCTTTAACAGUGCGCCTTCTTUG
225982197	74344	TGUGCAGUCCAGGAAACAGAAA	74345	CTGCATTTTGTUGGTTTGACAATTUACA
225984505	74346	GTCAGGCCUGGGACTTCTUAT	74347	CAGATGCAGAUGACCCCACTUA
225984800	74348	AGATTAAAGCUTTCTGCAUCGAACCA	74349	TCGTTCAGAATGUCTTCACTGATTCUC
225988226	74350	TACACTAACTUGGCGCTATTUCCA	74351	GGTGCCTTCTUCAGGGTTAATTTUAGA
225991712	74352	CUGGGTUCAGCAGAAAGAGGA	74353	TGCTACCTTATAUCCCTTCTCACCTUAG
225996869	74354	CCGCGGTUAGGTAGGAAGTAUT	74355	GAATGCCGUACCCTACUCCAG
226002581	74356	AAACCTGCGUTAGGGTCUCAG	74357	CTCAATAGTAACUCTGGCCATAGCUT
226006007	74358	CTCCGAAGCAGUCACUGAGG	74359	AGACAGCCACCUATGAGGACAUA
226007401	74360	TGCCCTTGUGAAGCCTGATTAAUT	74361	CCAAGCACUGAAUCCGCAAG
226007838	74362	CTAGTGTTCCUGGTCCTGACUT	74363	GGATTGAAGAUCGGAGGATTATCGUT
226010029	74364	AGAACAAAACUATGGCTCUGAAACCT	74365	GUGAGAGTGAUCAGACCAAGCC
226010327	74366	GTGAUCACAGTCACUGACACC	74367	AGTTTTCAAAGACUTCGCCCAUGA
226010800	74368	CAGCCCCACUTGCTTTTGUG	74369	TCAGUGCCAUGGGCAAGAG
226012585	74370	TGAAGAATCUCCCTGGCUCAGA	74371	AGGCAGCGGCUCTAGTAUCA
226021347	74372	GACTCTGAGGUTAGAAAGUGGCAAA	74373	GATATGTCCUTTCTTCTGATUCAGGGT
226021474	74374	GCAGGATUACCTGGTUGGAAAGT	74375	CTGTCTGCAUTCTGTCTUCCCA
226022266	74376	GCTGCAACUAAACAGGTAAATTCUGAGT	74377	CTGCACAGGUGACCACATTTATAUC
226034552	74378	CTTGTTCAGCUTCTGGGTUCAGAT	74379	CTCAGTGATGUCTTCCCTGUCA
226040990	74380	TGCCTTCCTTCUTGCCTATTTTGUT	74381	GATCUGGCAGCCCAUCAACT
226043318	74382	GCCUTTAAAGUCACGAAAGCACAA	74383	GTCATTTGTTGGUTTTCAGCTTCUGT
226047692	74384	CCACCCTGGUGCTGACTAUC	74385	GGATGATTUACAGGTCAGTAUCAAACCA
226048161	74386	CACTCCAAGUCCTGTGAUGGT	74387	CAAAGGGTGCUCCTGGTACUC
226048551	74388	TGTGCGUACTGTCCTUCGG	74389	CTTAACCACAACUGGTAGTCCATAGUG
226048694	74390	CAGAGTGGAGAUGCAGCTGUA	74391	CTCUAGGAAGAGACACAAACUGGAAT
226051720	74392	CGCTGUCCAGCAATACCTUGA	74393	GGTGCTGAUGGTCCTGCTGUA
226052050	74394	CCTCCAGGUGACAGCAAUCAG	74395	TGGCAGATTUACAAATAGCCUAAACCA
226053197	74396	GCTACGGGCAAUCACTCTCCUA	74397	CGAGAUCUGAAGCCAGAGAACAT
226054400	74398	CCCAGAAUGCAGTTCGCCUT	74399	CAACAGCTAGAGAUGCTTCATTTUCAAT
226056969	74400	GTGGCATGUGATGCCTAUAGCA	74401	CCAACCAATUGAGAAGTTTGUAACAGA
226064057	74402	CCUCGCCTGCUGAGCAT	74403	CCGCCUGGGUGAAGAAGG
226064324	74404	CGCCAGCCUGACTCGUG	74405	ACCCCACCCUGGGCTUA
226066464	74406	AGTAGGTCTTUGCCTAGTTCATCGAUA	74407	CTTATGTCCATGUGTGGTTCTTTTGUAG
226066486	74408	GTUCCACCACTTGUCACCAGA	74409	CATCTGTACCUCCCCTTTGAAACUA
226073334	74410	TCAAGGAAAGCAGAGUGAAACAAAAUG	74411	CTTGGAUCCGCTTGCCATUG
226082697	74412	TCTCCCCUCCCCTUCCAAAA	74413	TCGTCUCGGAGCAGGTUG
226083642	74414	CUGCTGUGCCACGAGGT	74415	CGCATGUAGGGTTGGATGUC
226083770	74416	GATATAGAGTAUCCTTGCACUCCCAAA	74417	CACAAAGAGTCUACATGTCTAGGGTCUA
226084686	74418	CCTACTUCAAGTGCGUGCAGAA	74419	GATTGCCCUCTCCCAGGTTUAG
226085386	74420	ATTTCTGACAAUGAACTGAGAGTUGGT	74421	GGCTGTUCCAATTCCUGAGCA
226091160	74422	CCCCTTCTCCUTTTCCCTTGUT	74423	CCCCAACCCUCTCTCCTATGUA
226092825	74424	GTTTCTTTAGCCCUGGTCCTCUT	74425	GAATAAATCTCTTUGCGTCATTGAACUGA
226098551	74426	CTCTCTCTGUTTCCATCTCCUCCT	74427	GGATATCUGCCGTCCGTGUT
226099940	74428	GCCCCUGTCAGUGGACA	74429	AGATGGTGCUGCCCTGATUC
226101558	74430	GCCUGGCUCAGCAAACAAT	74431	AGAGGCACCUGCCUCAAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226103103	74432	GCCAUCGCCAGCATUCC	74433	GCCCCUCAAGCTCAGACUCT
226103170	74434	CCAGUCCGAGAGCCAACUG	74435	CGCTCACCAUGGTCUCAGG
226103783	74436	CCCCCACCUGCUGAGGA	74437	ACACAGGCAUGGAAAGAAGAGUAG
226105400	74438	ACCTGGCCTUTTTCTTGTCCTUT	74439	GCTAUGGCGACCTGCUCAAC
226109098	74440	TCAGCCUTCCTUCGCAGAAA	74441	GTCTCATGCUCCTGTTCAUGGA
226109796	74442	GGTTTTGTCUGCAAGATACCAGTUC	74443	ACGAGCCTCACAAUCTTCTCTATAAAUCT
226111293	74444	GGACCCACTTCCUAAAATAGAGAACAUT	74445	CATACAGCAAGAAACACUTTCGGAUT
226112184	74446	GCTTCTGTTUGCCTAAGCACAUT	74447	GCCATGAGTUGATGGAAGAATCUCT
226113858	74448	AAGTCAATATGTTUACCGACCCAAGAUAC	74449	AACTATTAACTGAUCCCTCCCCUCAA
226114572	74450	ACATGGGTATUCATTACCTACCCUGAA	74451	GCCCTCTGAUGCATGCTTTTATATUACA
226115158	74452	CATGCCUGAACCAGATGCUC	74453	GCAGAGAGAAACACACUAGAATTTGGUA
226122844	74454	CTGTATCTUGCCTTGCCTUCCA	74455	ATCAGCAGUAACATACCCAAUAGCC
226124728	74456	TTTGCTTTCTATTCUTCCTTGCTTTGUG	74457	AACCGGCTCTUCTGATAAAAGTTTUAGA
226129361	74458	CTGTACTCGUCTGGGTCAGUG	74459	ACTCTAACAGAUGGTATGCAGUAGGT
226131374	74460	CCCTCCCTCCUACTTCCTCTCUA	74461	CCCTCGCACCUGAGTGAUG
226131433	74462	CTGTCAUAGCGCCACTCUCT	74463	CCGCTGUGGGAGAAAGCUC
226132778	74464	CCTGUCCCCGCTGUCAC	74465	AACTAAAAGTGTUGGGAGCATTCUCA
226133769	74466	AGAACGGCUACACACAGTUGG	74467	CCTAGACCUGCGTCAGTUCCT
226134213	74468	AGAAGTAGACAGUCAGGCGCUA	74469	AGACACCAUCTGCAGGAUAGGT
226135563	74470	CCACCUCCTCTGGAUACCCAT	74471	CTCACTCTGACTUCTCTTGTTTGTTCUA
226135820	74472	GGGCTGAUCAGGCUGCT	74473	CGAGGUGGGAGACTGGUT
226136019	74474	CTGCAGCAGUACCGCACUA	74475	CAUGAACAAGACAAGCGUGGA
226137688	74476	AATTCTGCTTAUCAGCAAAAAGGAAUGG	74477	CCTGTCCCUGCCAGUGAA
226138905	74478	CAGAATGAATTUGAGGAGTTTCAGAGUT	74479	CCACCTCUGAGGTCCUGAAGA
226139089	74480	CTAGATATUGAAACCCCCAAGGAGUC	74481	GAAACTCATGGGAUGCTTACACATUT
226139930	74482	ACCTUGAGAAACTTGCAUGCGA	74483	GGACCTATTGGCUGTTTTCCCTTTUAA
226147485	74484	ACUGACCCCGAGGACUCA	74485	GACACTAACACUCTGATCTCCAUCC
226152178	74486	AAAGGGTCUTACCAAGATUGGCA	74487	ACAGTGTCCACUCAGGAACTCUA
226159122	74488	GGGTGGTAGGUATAGTTGTCTATTUCC	74489	ACCCCTTTCAUCCAACAGAAGATTUT
226159954	74490	CATGGTAUTGGAATAACUCACAGGGA	74491	AGACTTGATTTUGCCTTGTATGGCUAT
226160708	74492	CAAACUGTACACUGCCCACAGA	74493	CAGGAGAGGAGUTGGGAAATGUG
226162760	74494	TGCACTGAGUCTGCTTCTGTUT	74495	ACGGTCAAAGGUGAAGATGUCC
226163432	74496	AGGTTCTTGGUCCTCAGGAAUAGAA	74497	CAGGGCATAUCCAGCTCCUC
226164949	74498	CUGCGCCGGACCATGUA	74499	CTUAGCACCCCGACACCUT
226165080	74500	ACGAAGTTGAGAGUTCCTTCACCUA	74501	CCAGCUCCAUGCAGCGA
226165378	74502	CCAAGAGUGCCAAGUGCGA	74503	CCACCCTACCUCTCTCACTCTCUA
226169376	74504	GGGAGUCCGAGAGCAGCAUA	74505	TTTGTCTGTCUGTCTGTTTGUCGT
226174495	74506	TCTGGAAUCCAAGCAGAATUGCT	74507	AAUCCCUCCCAGAGAAACAGAGA
226175883	74508	AGTTTGGCAUCGTGCTGGUA	74509	TGGACACTTUCTTTTTGAGGUCGT
226176170	74510	GGCATGGCAUTGAGAGTTAGGUT	74511	GTGGTCACACUCTGGACCTACUA
226184349	74512	TCCAGAGUATGAAUAGCAGCCCAT	74513	AGCTTTTTACAAGUAACAACTCCACUGT
226187758	74514	CTTTTTCTCTTTUGCTGATGCTAUGCT	74515	GCCAAGAAACGGUCCAGGUA
226187887	74516	CCCACAGCCAUCTCCAGUA	74517	TCCCCCACAGCCUGATUG
226188436	74518	CCCCAAGAGCAGAUACUGAGAC	74519	GCCAGTGCUCAGTGGACTUAAC
226189682	74520	GATACATCUCGAGGCCAGTCAUC	74521	CTATTCTGAGUCCTCTTTCTGCUGAAC
226191167	74522	GTCTTCCCUCTGGCCAUGAAT	74523	GGTGTAAAUGCACAGCTTCUCC
226195659	74524	GCCUCCAAACUCAAAGAGACCA	74525	GCTCTGGCAGUGGTGAUAGAA
226196214	74526	AAATGAATGGCUGCCCCGUA	74527	GGACATCAUACCCATCATCCUCAT
226200498	74528	GCTTTTAATCCUCCACATGGAATCCUA	74529	GAGAGUAGCAGUAACGGCACAG
226204935	74530	CGAAGGAGAUGTTGACUGAGAGG	74531	AGCUTCCCAAGTUAAAGAAGAAACAGA
226205360	74532	CTCTGGAACUGGGCACACUC	74533	TGAACATCATGGUCCTCCACAUC
226205447	74534	TGGUCCCGAGGAGUCAGAAA	74535	CCCAAAGTAGUCTGGAGACUCAC
226206526	74536	GUCTTCTCCAUCACACCCCAA	74537	AGCTAGTAGCUGAGAGCTCUGT
226208233	74538	TTTCCAAGTUGGGATTCTTAGTGUGA	74539	GTCACUGGGTTGGUCCCAT
226209376	74540	ACTGGGACTTGCUTTGTTTTTAGAATUG	74541	CCAAGAAATCGGUACTCTTTCACUCAAG
226209611	74542	CAGGTUAGAGAAGGGAGGACUGT	74543	CAGCATUAGCAAACCTUGGCT
226215024	74544	AGCTAATGACUAGGGCCTTATATCCTUT	74545	CATGGCACCAGUTTACTCAGAATTUAC
226215586	74546	TGGTTCTGATTUCTGCTCTGCTAUG	74547	AGGTTGCGGUAACATAAAGGTGUT
226220622	74548	AGGGACAGACUGTCATTCAAAAUAGG	74549	TCGCGATCUAAAACCACAGAACAUT
226224197	74550	TGCTAGCAGUCTTGGTACTTTGUAA	74551	TGUATACAGCCUCCCACGCT
226229404	74552	GTTTTATTTGUCCGCTGCUGGT	74553	CATAGCAAATGCUCAACTTCCGTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226232414	74554	GATGCATCTGTUACTATCTTTTGCTUCT	74555	GCTGCCACUCCCTCUAGGAT
226235931	74556	TCAGAAAUGAGAAACCACCAAUCACA	74557	GATGATCAGTCAGUTTATCCTAAGGCAUT
226236166	74558	ACCTTCCAAGAGUTTTTGACATGATGUA	74559	ATTTTAGAATCAGUGATCGCCTCTUGT
226237097	74560	TGATGCTGAUGCCCCCAAUAC	74561	GCTGTGAGGAUGCCAGTTUCT
226242022	74562	CCCATCGTGGUAGATCCGTTUG	74563	CCAGTCTCCUAAACTGCCATCTUA
226244636	74564	GTAATTCAACUAAAAGAAAGGCAGCUGT	74565	TTGCCTUGCCTTTGTGTTUCAG
226251204	74566	AGGAGUATATGGCAUAGCAAAGAGGAA	74567	CACTATTTTCATAUGAGACTCCGTCUGG
226252274	74568	TCCAAGAACATTTUTGCAATTCTTCAAUCT	74569	ATGTCTTCAACGUTACTACACTGCAAUA
226253923	74570	CCTATGGGUGCCCTTCUCCA	74571	AGTATGGGCUCAGCTGCAATUAC
226255605	74572	GAACUGGAGCCCAGCTACTUA	74573	CTGACCCATAUTCCCCTGCUC
226256825	74574	GCCCCTTCUCCCATGTTTTCUT	74575	TCGGTTACCGUGATCAAAATCUCC
226259787	74576	GGGAATGCAGUTGAGGAUCCAAT	74577	GGGTCCAAAGAACCUAAGAGUCT
226262330	74578	GUGGCGGCGAGAAGAUG	74579	CGTCAGGCUCAGGTCCUT
226263553	74580	AAAAGATAACCUCACACCAGAAATUCCA	74581	GAAGAAAAAUGATACCTUAGACCCCGAA
226268593	74582	CTAGCCTTCCUAGACCATTTACCUC	74583	GCTTGCCAUACAGAGCCACTUT
226269921	74584	CCTGGTGUGCCTCCCTUC	74585	GGCTGGCGUATCCCAGUT
226272414	74586	GGGCTCCACACUCAACTACUC	74587	TGGCCUCACCTGUGAGGAT
226273120	74588	ACAGTGGCAUCCCCAACAUC	74589	CCATCAAGCUTGGGUCACAAC
226275264	74590	TGACTAAAGUCTTCACUCACCAAGGA	74591	GCCCAAGTCTTAUTCACATGTCTTCUAA
226279815	74592	CAGACAGGCUTGCAGGCTUA	74593	CGACGTUGCAGGGUACCT
226280984	74594	GGGAACCUGGCGUCAGT	74595	CTTCCUGGACACGCUGGT
226281085	74596	CGCTCCUCGGCCAAGUC	74597	CAGACCCUGCCACTCUCA
226281541	74598	GGCAGCTAGUGGCTGTCUAA	74599	CUCTCCUCCGAAGAAACAGCA
226281759	74600	CCUTCAGCUAAGACAGCCAGT	74601	ATGTTAACTTUGATGTCTTCCUCCAACA
226281763	74602	CGGGCAGCAUCAUGCAC	74603	GCCGGCAUCTCCCAUACC
226282930	74604	GGAGGUAGGGAUGGAAAGGAGAT	74605	AGUAAAUGAGAGGCCCCAGGA
226286447	74606	GGACTGACCUTGGTGTTGTUG	74607	TCTCUCCCCCGGTCUCAG
226292480	74608	CCAGTTCTGAUTCTGCTGCUCT	74609	CCACTGAGCUACCAAGGTTTUCAAA
226293222	74610	CGTGCCUCCGTAGGTCUG	74611	CUTCATCTUAGAGGCCACGAACAT
226296151	74612	CUGGAGCCCGUGAAAAAGAG	74613	CCGGAUGGAGTTGUCGGT
226296830	74614	GCCGAGAAGCUGTGCATCUAC	74615	TCGGAGGAGCAGAUATGUCAGA
226300413	74616	GTGTGGTUGTCTCCCAUAAGAACT	74617	TCCTGTGAAUCTTCACTTTCUGCAA
226301845	74618	TTGCAGAAAGUGAAGATUCACAGGA	74619	TCTGACATCTCUTTATCTGCAACUACCT
226304836	74620	TGTTCTGUCACCAGATTATGGTTUGT	74621	CCTTTGUCGACCGGUGCAA
226305670	74622	CCTGCCUCTGGCCTTTUC	74623	GGGAAGGUGGGCTCCUC
226306973	74624	CGACCUGACCAACATCCACTUC	74625	CGGAGTGUCCCTGCCTUA
226308315	74626	TGGCCAGAAAGAAUATTUGAAGAGGT	74627	GAAGAUGAGGGACAGTTTGGTUAGG
226310120	74628	GCATTCUGATCATTTGUAGGCGAAA	74629	CTUTTCTCCAAAATUCCGCAGCA
226313178	74630	TGCUGCGGAATTTUGGAGAAAAG	74631	ACCAAAGCCAGGAAAUACAUACACAT
226327144	74632	GCCCUGCAGTGAATTTUGAAGA	74633	GGATCUGTGGGTTAUGAAACCGT
226339152	74634	GTGTGATTACAGUCAAAAGGCCUCT	74635	CGAACTTCUCAGAAAAATGCCAACAUAC
226349499	74636	TGTTGTTAAAUGAGGATTUCCCCAGAT	74637	AGGACCACUACCTTGCUGACA
226355988	74638	GAATCAACTCUGAACGGAAAGCUG	74639	CTCGATGTTGUTCTGGGCAAUG
226365721	74640	AGGACAUCCAGAAAGCTTUGGT	74641	CUAAACCUGCAGCAGGGAGAT
226376853	74642	CTGAGGGCCAAGGGUAACUT	74643	CTGGAGUGAACCCCCAGTUAG
226385016	74644	CCCTTCCCCUTCTCACATTUCA	74645	TTATCCATTAAGUGAAGGGAAGCUCAC
226385797	74646	GGAAGCCCTUCTGTTCTGAGUT	74647	TGACCTTTGAAGCUCCTCTTCTUC
226388747	74648	CCAAAGAATUGGAACAGCUGAAAACT	74649	TCCCCAAAUCCTGTCAGTCUCT
226389671	74650	GTTGACCAUGCTCTGTTTGCUG	74651	CACCACAGCUGATGTTACCTCUT
226402406	74652	GGTAACGCUGTTGCCTCTUG	74653	CTGAGCUGGACTTCTTUCGGT
226403604	74654	CAGATUGGAAGTGGUGCAACAA	74655	GCAGCAGUGCCCGTCUC
226403739	74656	CGGGAGCGGAGCAUGUC	74657	AGGGUCGCCAAATUAAAGCGAT
226418226	74658	CTGTTAGTGTTTGUCGTAAGTATACAGUGT	74659	AGAGAGCTGCUGCAACTAGAUG
226418238	74660	CAGATTTTTGAUCACCATACUGAAGAGGA	74661	AGAGGTCCCAUCAGCCTUGA
226418538	74662	GCAGCAGCUCTCTGGATUCAA	74663	CCCCAAAAAGGCAUATACAACATUCAAA
226420836	74664	AGGGAACCCUCCGAGUCA	74665	GCGGCCUCTCUCCAGGT
226424468	74666	GGCACTGUCTGCATCTGUAGAG	74667	GCCAAGAGCUCATGCTTTCCUT
226424948	74668	GAGAGCUACACGTUCACGGT	74669	AATTTCUCGGCCCCTTUCCAA
226426452	74670	GGAAACAAGTCUTCACTTTTTCTGTUAACAT	74671	TTGGAATGUGGAGCCCATCUC
226426486	74672	GAATTATACTGUGAGATGGGCUCCAC	74673	AGAUCCGTACCUGCCAGGAT
226429377	74674	CCTACCAGUCTGUGCAGCAA	74675	CCTTATGUGGAACCCCCACCUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226429415	74676	GTAAAGATUGAGCCCTGUGGACA	74677	AGGCCACCCCUTGTATCAGUA
226431181	74678	AAGAACTUCAGGCGCCAAGUA	74679	GGCAAGTTCAACAUTATTCCCTTTUGT
226435281	74680	GCCGCUCACCCTGTGTUC	74681	CCTCCGCCUCTGGCATTUT
226437988	74682	GAATCCAGCCUGAAGAGTTGAATUAGA	74683	CTTACAGCUGCACGUCGGA
226438348	74684	CACGATTTCATUGAACACTTCCUCT	74685	CCGGCCAGGGUCACCUA
226440605	74686	CCAGGCAAUGAGGGUGGA	74687	GCCCTGUTGGTGTUCAAGGA
226440780	74688	CCTCGAGCUCCTCGCTUT	74689	AGGAACCCCUGACACUGGA
226445640	74690	GAACAAGAAUCTACAGGAAUAGCCACA	74691	GTCATGCCUGCCTTTCTGTGUA
226450228	74692	GGTAATTAACAAGUATGCGAAUGCAAGA	74693	CAAAACGACUGCAGGAGTGGUA
226454444	74694	GTGGCATTATTATUTCCGGTTTCTTCUT	74695	CATTCACAAUCCAAATTTCACAGUCAGA
226456974	74696	ACGCCTTGUCCAGCATCTTUT	74697	GCACGTTCAUCTGACGTGUGT
226458465	74698	CCACTTCCTUGGTTTCTCCTTUGT	74699	GCGACTGCTUCTTCAGTTACTCUAT
226460535	74700	TCCTTTTTAGAGUTCAACTTGCTGUGA	74701	CCTTCTCTCCTGUGACCATAGAATTTUA
226461443	74702	CGGACGCUCTCTTTCAGGUG	74703	AGCAGGUGAAAATGGCUGAGA
226463941	74704	AACCTTAGUACAAACCTCGGTTGUC	74705	AGCATGATTTATTUATGGGCCACCUT
226465757	74706	GCCGTAGACUGTCCAGAAAATATUAAGA	74707	CTATTCTGUCAAAAAGCTCTCCUCCA
226465840	74708	TTCTGGAGUACTGTAGUGGAGGAG	74709	CAUGAGCAATTTUGAAAGGACAACGA
226469509	74710	GGGAGCTGUCCTTAAAATTCUCCAA	74711	TCTGGTAGCAGGUCTAAGATATAAGGUG
226472872	74712	AGCTGGCGCUAAAGAAUAGCC	74713	GGCTTATGGTTUGCTTAGTTTTCTUCAT
226475571	74714	GCTTACCTCACUCCTCCCCAUT	74715	CAGCGAGGUGAAGCCUAGAG
226477007	74716	GGCCCACGAGCUCTGUAG	74717	CAAGTUAGGGCCCGGACUG
226478350	74718	GATGGAGACACTUGGAGAAAATGAGTAUT	74719	CAGTCACAGACCUGCATAATTATTUGT
226481749	74720	GGCTCTTCUCAGACATGTGAUCAA	74721	CAGATAGCACCUTCAGCACUCT
226481864	74722	GCACATATGCACUCCCAGTAUACA	74723	TTGACCCUGTCATGCAGUCC
226484528	74724	CGAAAAACUACTGUGGACCACAAG	74725	CTAATTAGAACUGCAGATGCTAUACACA
226491965	74726	AACATGCTTACUGTTTCAGAGAGUGT	74727	GGCAAGTUAGGCATTATGCAAATUACT
226492928	74728	TGCGUCCACAGCAATAUCCAA	74729	AGTACGUGGACGACGTCUG
226498107	74730	TGAGGGTGUCTCCCCTTTUCT	74731	CCTAACCCUGAGTTCCCCTTUG
226500750	74732	GCCAGGCAUTGTTGAACAUGAG	74733	GGGATUCCCTATACUGAGACCAT
226504887	74734	GCCCCGUTAAGTCCACUGAG	74735	TGACTTCTCTUGGTTTGGTTGUCA
226506912	74736	CCTCTCTGACUCCCCTGUGAAA	74737	CAUACTCTAGCUCCCCAAGCAC
226509452	74738	GCCCUGCACAGGUACAGAA	74739	CGAGUGACCCCAAGACUCC
226511546	74740	AAGAACCUAAGAAAAGGAAAAUCAGGCT	74741	TCCTTCTGTUGCATCTGGGTAUG
226512583	74742	CACATTGCTTUCTGCTCCCAUT	74743	GCCTTTCCAGTUTATGCTGATTCATTUT
226513775	74744	CAATTTAAGGUCACCCTCCCUCA	74745	AAGTATGGCCUTCTTGCUGACA
226520194	74746	CGTGAATCUTTTTATGTCTUCAGCAACA	74747	TGGAATGGGCUTCTGAAAGTTCAAUAT
226524117	74748	TTTCTCCTAGAUCCTGAGGAATTCTUGA	74749	GGAAATCATGUCTGTTGAATAAUGGCA
226525022	74750	GTCCTGTTUGGCTCCCTTGUAA	74751	CCCGCACUGACATGCUAGG
226528688	74752	GGGAAGGUCCTAGTGCCUCT	74753	CAACAUCCAGCAGGUAGAGAGAA
226531309	74754	GGTCATGGAGUGTTGCCATCTUA	74755	GTACCCUCAGCATGGCCAUT
226532029	74756	AATGCTTGGGUAAGAAAACATGUCA	74757	GGTTGTGGAGAGUTGTAATGGCAUA
226532812	74758	CTTGCTGAAGCAUACCCCAUCT	74759	GCCTGCAAGGUTTTAACUGGAC
226533895	74760	GCTCTGAGCCAUACTACCTCCUT	74761	GGCTGACUCAGAGGUCCGA
226534663	74762	TCTGCCACACAUTTAGAAAGAAUCAGT	74763	AGCCCCCAAACUTGATTUCAGA
226535422	74764	TCACCAGTGGAUTCTGTGTTGTUT	74765	AGTCTGTCGTAAUAGCCAAGAATTUAACA
226537231	74766	AGGGAAGUCGGAAGAGCUGAT	74767	GCATGTTGGUTATCTGTCAUCAAAACT
226537898	74768	ATACTGTCTACTTUAGAAACTAAGAATTUGGAG	74769	CCCACACCCAUTTATCTCCTTAACUAAT
226541936	74770	ACCACAGCACAUACACATTTUAGCA	74771	GGTATCCACCUTTCTCUGAGCAT
226547084	74772	GGUTGCCTTGCUCAACAAAACAAA	74773	CAATGCTCCAUGAAAACCACAUAAAGAA
226547181	74774	GTCAGAAAAGGGUCCCAGGUAG	74775	CAGATGCTTGUGTGTTCTGCTUT
226550378	74776	AGAATATGGTTTTTAUGACACAGAGTTGUGA	74777	GGCCTGGTTTUGCAATCATTTACTTUT
226559633	74778	GTTGTATGCCAGUTCTTCCTTCUGT	74779	GAUGUGCACGAACAAGCAACT
226562213	74780	GCAGAAGACCCUGCAAAATCUC	74781	ACTGAATGGUAAAGAGTGGAATCTGTUC
226563461	74782	GGTGCCATUCCACGACTAGTUC	74783	GCATTCCTTTUAGATAGCCAGGTAUCAC
226565267	74784	GCAGAAATCUCTTAGAACUGGAGGT	74785	ACACAAACAAAUGATGCCTGCAUT
226567767	74786	GUGAACTCACUGACCACCGA	74787	GTGCAGTGTTUAGCTCTTCCATUAC
226568220	74788	GGCCUGACACACAATTTTTAUGGG	74789	AGCCUCAAACCCCAGTUCAG
226568959	74790	GCTGTTGCUGCGATGACUGA	74791	CAGUGCUACCCAAACCCAGAG
226569257	74792	GCTGCTGCCUGGACTGUA	74793	TGCCAUCTCUCCAGCACAC
226570291	74794	GAGTCAUCCCAGGTGGTGUC	74795	TGCTCTTCCUAACCCTCUCAACAT
226570881	74796	GGTGCAGUGGTGACTGUGT	74797	ACCATACTCTGUCCATTTCTGGUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226571694	74798	GAAAATGTGUTTCTTACCUCAAGCCAT	74799	GGTAATTCTTGCUGATGGATTCUCAACT
226572534	74800	GTAATGTTTGTTUTTAGCTCTGCUGCAT	74801	CTTTGCAATUACCTTTTCTUCCACAGA
226573464	74802	CAGCCTGTATUTGAGAAGCATGUG	74803	TCUCCUGCAACGCAGAGG
226574550	74804	CCAGCCAGCUTGCGAUAAC	74805	GAGCACATGAAUAAATGAGCATCCAUT
226576061	74806	GCCGGCGUTCAGAATGUAG	74807	GCAGAAGCAGGACUTGTACCUT
226576715	74808	GAACGTUCATTCAAGUAGGCCAT	74809	CTCCAAATCUAGGACCTAGGACUCA
226578267	74810	ACTTTCTCTGUCAGCCCAGUCT	74811	GGGTTCUCCTTAACTUCAGCCAA
226578332	74812	CCTGGCAUGGCAGGAGUAG	74813	ACCACCCUCAAGAGCCUGA
226581053	74814	CCGCCAUCGCTGATCACUAT	74815	CGCTGTGATUCCAATGGTCTUG
226582103	74816	CTCAGGGUCCCCACTTCTCUA	74817	CATCAGCACAGUTCGUGAGGT
226582784	74818	GCTCCGGAUGTTCTCGATCUG	74819	CAAGAGAAGGCUCACGAUGGT
226586445	74820	TTCCTCCCCUGGTCTCAUCAT	74821	GTCACACACGCUGACCTCUAA
226587281	74822	GCATCAUCAGCCCGGTAGUAG	74823	GCCGGTAAUCCCCACTCTCUT
226587590	74824	CTGACGCCUTTGTCCTCATUC	74825	ATCTCTCCAATCUGACTCCTTTTCTTCUA
226588389	74826	GAACCCCTUTTCCTATGGAUCGT	74827	AGTTCTAGCUTGTCCAAUGCAACA
226588885	74828	ACATGGTCUAGAAGTGGGCUCA	74829	CUGCACAAAACCUCACAGAGAAAAA
226591604	74830	CUGGGCCACTUGCCAGA	74831	TGCCCTGUCCTTCCCTTCUA
226594583	74832	GCCCCAGCUACCUGGAT	74833	GGCAGCGAUGAGGGTCUG
226596194	74834	GTCGCACCUTCTCCACTAGUC	74835	TTTACGGCCAACGGUGGATUAT
226597228	74836	GTGATGAAGAUTGTGGCGTGUT	74837	TCTCCAACCTUCAAAGAAACTCUGG
226599064	74838	CCTCCAGUCGCCTCAGUAAAG	74839	TGGCTGAAAUTGGTGUCGGT
226604741	74840	GATAACCAGAAUAAAGACCAAGUGACCA	74841	TCACTTGCCAGCUGGACTUAC
226605363	74842	GGAGCUCAGAGAAGGGTCTGUA	74843	GTGATTTCUGGCCCAATGTGUT
226605487	74844	CTGCTGCUGTTGGTUCGT	74845	GGATGUTGTACTGUCGCAGGA
226606215	74846	AAGAUGGCGGACGTGCTUA	74847	ACAGCCAUGCCGGACTUAC
226607155	74848	TCGAACTTCCUCCTTTGGAAAUAAACT	74849	CCAAAATTTUCTTACCATGUCCACACC
226608394	74850	AGAGGCAUCAAGCCUGGAC	74851	GCUAAAGGCGAACCTGGUGAT
226609731	74852	CCAGCAUCGCCTTUAGCAC	74853	GGAUTGTTUCCCACCCAAGCA
226610226	74854	GGCCTTGUACACTGTCCCAUAG	74855	CTGCAGGCUCATACCATCCUAA
226614803	74856	CTTGTTCTAGTUCCTTAATGCTCTCTUCT	74857	CCTCATCTCACUGTTGTGCTTUG
226618259	74858	GGATCUAACAAAGAGCCACACUGT	74859	TTACAGCTATCUGTCTGTTCATTGTUGT
226619980	74860	ACATTGATUCCCACATCCAGUGAG	74861	TCCATGGCATTCUGAGTTTGATTTTCUA
226620190	74862	CATGGAAAUGACCAAATGTCTCUCAAAT	74863	CCTCTCCGGAAUAAATAGTTTTCTCUGT
226620608	74864	CTCAGCCUCATTTCUCAACCGA	74865	CCTCACTATTGAGUATTTTGGGCTTGUT
226621758	74866	GCAATCCAGAUGCTATGTCTTCUCT	74867	TGCTATTTGCACAUTTGATTGATCTTGUT
226622376	74868	TCGTAATGAACCAUTTCAGCGAUCA	74869	GGCTTGTTGCUATCTCCTGATUACA
226622394	74870	GAACACACTACUGGCCAGCUA	74871	TTTAGGTTTCTGUACACTTTCGTCCUC
226623971	74872	TTTAACCACACUTTGCAGATCTUACCT	74873	GGAAAGGTCTUGAAAAGCAGTATTTUGT
226624450	74874	AAATTCCTCUGCACCCATATGUGAA	74875	TGAGTTACTGUGGAAATCTAGAGCTGUAT
226625343	74876	ATGGACATUACCAAGAGTCATACAGTUG	74877	ATTTTCCCATCTUCTGATGTGGTCAUAA
226625742	74878	TGATAAAGATTCUCCTCAGTCAGCUGAT	74879	CCTGATGAAAATAAUGGCTTTGTGGUAG
226626071	74880	CCCGAAAAAGAAAUGATGCUCCAA	74881	AAAGGATTUGACAGGCTCUGCT
226626951	74882	TGCTGTTTGTGGAUCCAGTGATAAUT	74883	TGGCAAAAUCATTTGCAUAAGCAAGA
226627956	74884	ACTGTGGUGGAGTTCTTGAUAAACAAAT	74885	CTGGCCTAGUACAGATTTCACTGTAUG
226628010	74886	AGGTTAUGGAACTAAAGCTUCAGGAAAT	74887	CTGGCATCCUGATTACAAGTCUGT
226628425	74888	CUAAGGAAAGAAUACAGCAGAGCCT	74889	TGGTACTCUCCGGTGCTAGAUT
226629130	74890	GGGAAGGAAAAGUGTTGGUGGA	74891	TCCUGCCAAUGGCACCAAA
226629282	74892	GGTTTGCUGCAGCCTGUAAAAA	74893	CAGCATTGACAUGAGTTTGAAUGACT
226629446	74894	GGGCAGAAACUCACATAGTCUC	74895	GGTCATTTCCAUGGCATCATTACAACUA
226630001	74896	GCCATTATTTTCAUCAGGACAGTTCUCT	74897	TCATCTTGTCAUGGCAATAGUCAGG
226630568	74898	CGTGATTGUCATTTGGUGCCAT	74899	GGCCTAGTAGUTATTTCATCTGGUGAGA
226630701	74900	CACAGTAACUCAGACGTAACUAAGCA	74901	TGGTAGATGAACAGUTTGAAAGGCUAAA
226630807	74902	CCAATTATUGCCCAGTGCAAAAUGA	74903	TGTCCTTTGGTACUGGTTTGAATAACUT
226631415	74904	AGAATATTAGCCAUGACCCCAGAATCUA	74905	TGCTTTAGCAAAUTTTTCTCCTCTCUCA
226632595	74906	GGAGAAGCACCAGAUCCTGTAAUT	74907	CATTGTGTGCCUTATTTCCTAATUCAAGT
226633046	74908	GTCAGGTTCCUCTTGCAGCTUAT	74909	CGGTTAAGCTGUTTTTGGCTATTATGUC
226633134	74910	CTCTGCTCCUTGTCCTTTGTUAGA	74911	CATCTCCCCCAGAUCTTGACTATAUACT
226633253	74912	CCACCCCTUCCAGAGCAAUT	74913	TGGTTTCAGCUCCATTATGAGACTTTUT
226635312	74914	TGAGGAAAAGUTTAAGCAAUCCCACA	74915	AGTTCAGAAGGACCAAAUCCAAUGAC
226635566	74916	CCACGAAATCTATUGGCTAATCAAACTUT	74917	AATGGAGGUTGGTCGGTUGAG
226635582	74918	TCTCCAGCAAUGCTAAAGATAGUAGAGA	74919	TGUTGGGCAATCUAGGCAAAAAGA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226638502	74920	CTCTCUACCGCCAAAGACAGTTUT	74921	AGTTGTGTCUGCTGGAATCTGTUC
226638922	74922	CACACAACTGCCUTAGAATGTAAAACUG	74923	GTTAGGTCTGTCUGTTCTTTCCTTTUCT
226639252	74924	TGTAGTGTCACUGGTATTGAUGACCT	74925	TTCAGTTTACCUGCAACAGAUCCAA
226640199	74926	GGTCTCUAGCAAAGATUCAGGCA	74927	AAGGCCTTTTCCUCAGTTTCTATGTUAA
226642008	74928	TCCTGATGAGAUCAATTCTTCAGACUCT	74929	TTCTTCTTCTTGUACCCACGTTCTUT
226642480	74930	CGGACTTTUCGAGGGCCUT	74931	GCCGCGAGUGAGGGTUT
226643258	74932	AATGGGAAAAACUTGCAAUAGCCAAA	74933	GGTUCAAGACAGAGCUCACCT
226643556	74934	GCGGGAUGUGAACCACGA	74935	GCTCACCUCTGGUGCCAAA
226646276	74936	CCCAGGGTUGGTTACTCTTUACA	74937	CTAAAGCTTGTGUCCAGTGATATGGTUAT
226647836	74938	CACCUGGCTCCTTUCCACA	74939	CTCACCTTUGCTCTGGTUGGA
226649437	74940	CGAGGACACCUGGGTAAAGTUG	74941	CTGACGUACCTGTGCUGGAA
226649626	74942	GTTCCCTUGGCACTCCTUAGT	74943	CUGGACCCCACACCCUT
226656623	74944	GCTTGGGUCTCCGTCTUCAT	74945	CTGAAGTCAGUGCTTTCGGTTTUT
226669094	74946	CCAGGTCAGCCUGTGGAATUT	74947	TTGCGCAAGAUGTGCTCAAUG
226677039	74948	CAGCTGTCACUCCTCATGACUT	74949	CCGGCUCAAGCCTCATCTUAC
226678230	74950	CCTCCTTCCCUCTCTCCTTCUG	74951	ACACUTGATCACTCUGGAGAGGAA
226687535	74952	CCCAACAACTUCCTGTCCTACUAC	74953	TTTCCGUGGCACTAGGTGUC
226688060	74954	CCATCCAUGGAGGAGTTGAAGUT	74955	CTCTAGUGAGCACCTGACCUG
226691978	74956	GTTGCCCAUGGCCTUGAC	74957	AGAAGGUGCTGGAGCUGAC
226692613	74958	CGCAGGCGGUCATTGUCA	74959	GGCCAAGAAGUCGGUGGA
226693517	74960	GGCUGCAGGTGCAUGGT	74961	CGGCCUCTTCCCTUACCAG
226693890	74962	AGTGCGCGAUCTGGAACUG	74963	CGCUGGTGAUCAAGCAGGAG
226694375	74964	GCTGGGCGAUATCCCCTUG	74965	CTGATGGATCUGGACTGACAGUT
226697631	74966	CTGTTTCTGAGUCTCTGCAGUCT	74967	CCCACACUTCCAGTUGCGAT
226699202	74968	GCATTACCACGUGGGAGUGA	74969	GCTCCAACGAGAUCGAGAUCC
226701748	74970	GGAGGCACCGGAAUCTCCUA	74971	GCUGCCAGAGAGCTCCUT
226704161	74972	ACAGTGACGCUGTAGGUGAAG	74973	CCTCCCAGAACAUCACCUACCA
226707678	74974	CCATGUACCCACCGUCGAT	74975	GACAUCTGGACTUAGCCAAGAAGG
226708043	74976	GCCACGCUGTTCTUGCAG	74977	CGCATAGCGGCUCACTCUT
226717821	74978	GCCAGCCUGCAUGGCAT	74979	CAAAUCAAACCCGCAGCTAAUGG
226717930	74980	CCGCUCACCTGGTUGGG	74981	CTCCUGCAGCGGUGGAA
226718354	74982	GGCCUCACGCTCGATCUG	74983	CCCUCACCCGUGAGCAT
226718611	74984	GGGAAGCCAGCUGGUGA	74985	CGGAUGGCCACCAUGAACA
226719562	74986	GCATTTGTTTTCUTGGCAGTGCUT	74987	CGCAACGCCAACUGCUC
226719808	74988	GCTGTGCGCUGTTTGAUGAAA	74989	AGCGCTCUGCAAGACCUG
226719940	74990	GACTCTGCUGAGGCACGUT	74991	GCCCTCUGCTGCUACCAC
226720781	74992	GCACCACCCGCUTCATCUT	74993	CTGGGCCUGGAUGACGAG
226721283	74994	CUGGGCGACTUCAGGGT	74995	CTUGCCCAGGCCTGUGA
226721641	74996	CCTGGGCCUGCATGGAUA	74997	CCCCGUGAGCCTGAATGUG
226721978	74998	GGGCTCUTTGACTGUGGCT	74999	CCTGTCCCCUTTCCTTGCUT
226723901	75000	TCACTGGCAAAAGGGUTTAGAACUT	75001	GCCTTGGATUCTCCTGGAGUC
226733872	75002	TCTGGAAGACCUGCATTCCTUG	75003	CGTTAGGACUCTGCCTTCAGUT
226762818	75004	AAGGCTTTGTAUATTATTGAACCAUCACA	75005	GGTAGGTTCCCAUAGTGTCAATTTUGAA
226762848	75006	TTTCGUAGAAACGGAAGGCTUCA	75007	ACTCACAUAAAATCCCUGGAACAAAAGA
226781087	75008	CCAGAAGGGAAAUGGCAGCTUT	75009	GTTTTCTGACCUTTGCCTCUCC
226783603	75010	TGGAGACCCUGCATAUGCCT	75011	CACGCTGAAGGAUGGTATCAUCAT
226788499	75012	GATGAUCAGCAGCGTCUGGAT	75013	GCTGCCCUTGTAGGCCUAAAA
226794852	75014	CTTAGGTAAATGCUGAACTGTGGAUAGT	75015	GCCCTCAUCTAATGTCUCAGGGA
226799646	75016	CATGTTTTCTCCGUAGGATGCTCUA	75017	CTCCGACUTGGATCCGUCAC
226801798	75018	AGAGGGUACGAGCTGCTAUGT	75019	CAAGTTTACAACUGCATGTTUCAGCA
226808644	75020	AATGTCAACTTGTTUTTACATGCATTATTCUAA	75021	GGAGCCAAATAAUTCAGAATCTCAAGUG
226808649	75022	CAGGTACAUGGTAAAGCATAAAUCGC	75023	GAAGCACAAAGCAUCAAATAAGGTCTUA
226813041	75024	GCAGUACCGUCAGGACCAAC	75025	ATTATGGACGCGUCTCTCTCTTUC
226818035	75026	CGTTTGGCUGAACCAUCACAGA	75027	GCAGACTAAAAAGCUAGCTATGTCATUG
226835964	75028	TGGTAAGGAAAAGUTACATGTAGCGUT	75029	TGTTCAGTCTGUACAATCCCTTCTTUG
226836402	75030	CGCCTTGAUAAAGAGAGATUGGCT	75031	AAGAGGUAAATGTAAATGUGGAGAGCAT
226963440	75032	CUAGATTCTUGAGAACGCCAGACA	75033	CCACAGATTCAGACUTGGACTATGAUT
226965718	75034	CCCTGCCUTCATAACCGUAGA	75035	CCCGCAAAGACAUCAAACCUGA
226967918	75036	CGAGGUCCCCAGTTCTGUAGAT	75037	GCTCCTCCUTATGACTCCATUCAAA
226971562	75038	CTCTTATAAAGGCUTCCGGGUCAT	75039	GCAGGCUTGACUCCAGCAG
226972570	75040	CCAGGTCUAGGCATGTACTGAUAC	75041	GGAAGAAGAUGTCCGUGAGAACAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
226973363	75042	CUGCCAGGAGCAGAUCGAA	75043	GCCCTCAGAUGTCCACGUC
226973939	75044	TGGACCUGGCTUGCACAC	75045	GAATGAAGCTTUCCCTTCTGGTAUCA
226984041	75046	CCACCCCCTUCATCATCATAAGTAAUG	75047	CTGGACTTAACGAAUGCTTACCTUCT
226985742	75048	ATATTGAACAUGAGTACUGCCAAAGAGT	75049	CCATUGGGCAGCTGTACUAGAG
226986838	75050	GGGATUACCGGCATCCAAGUG	75051	CTCCUGGCAAAGATGGACUCAA
226987709	75052	ACAUACAACAGGACCAGCAUCAC	75053	CTTCUGGCAGCCTTTCUCAAAC
226988760	75054	CATCATCTGCUCCCACCGUAA	75055	ACACATACCUGAACTGTTTGGACTUG
227017797	75056	CCCTGACACUTGGAGCAGUA	75057	GAACATCGUCAACCTTCUGGGA
227018072	75058	AAACAATGGACACUCAGAAGUCACA	75059	CTAGAAGCACUGTAUCGACAGGAC
227019787	75060	CCAACGGAGACUCCTGUACAA	75061	CCAACGGAGUCAACCGTTUC
227025256	75062	GCCCTTACCUCCATGGGUACA	75063	TGTCTTTGGGACUGTGGTTCTUC
227030577	75064	CTCACCUACAGACCACTTCACUT	75065	CCACTATCTGCUGGTGTGGTUG
227031257	75066	GCCGGAAAGGUAATGACTCUGG	75067	AGGGATCUGAGCACCTTTUACAAAG
227035892	75068	GTTATAATACGGCUTCAGTTGGUGGA	75069	TTCTGAACAUTTGGAUCCAGACGAA
227036993	75070	GGACTTGATCTCUGTCTATAGTACTCUGG	75071	AAAGCTGACUCGACGAGAGTUT
227037134	75072	CCCTTAGGAAUCCAATGCTTUGAGAAAT	75073	TTGGTTTGAUACACAAAATACCAGUACCT
227037238	75074	GGCCTAAUGACATTCTTTTCAUGGT	75075	TGCAGAGAACAGCAAAUAACUCCA
227038387	75076	CCTTTCUGGGCCTGAGGAUT	75077	CAUGCCGCTCUCCACCAT
227040507	75078	GGTCUCCAGGTGCCUCAG	75079	CGAAUGCGUGGCGGAGAT
227040672	75080	CCATCTCCCUGCCCAUCT	75081	CCACUGCTGCTCUCGCT
227041516	75082	GGCCTUGAACACCTTCCCAUA	75083	GGCCGCCAGCUAGTUGA
227042352	75084	GGGAGCUTAAATGACUCAAAGGT	75085	TGTTCTAAUGGCCCTTCCTTGUC
227045676	75086	GGAAAAGACCCAGUGTUGGGAT	75087	TTCAGCCATCCUGTTTCTCTTTCAAUAA
227045723	75088	CCGCTCUGGGCTGTGTTUAAT	75089	CCAGGAUCTTGCUGACGGT
227045837	75090	CAGCTGUAGCCCCUGGT	75091	CAGCCCAUGCTCACTTGUC
227046797	75092	GCTCACATUTCCTATTCCUGGGT	75093	CCAATGGAGGAGAAUTAGGCCTTTUAA
227047681	75094	CCTGAAGAAGACCUTTGACTCUGT	75095	ACTTCUGACAGGACCCUGCT
227048776	75096	CGUCAUCCCAACCAGGACAAC	75097	GCAGGGCAACCCUTCACUC
227050525	75098	AAGCCTTCCAUCTGAAGTATGAUGAAG	75099	CACACACAAGCAUATTTTAGAAUCGGAA
227056752	75100	CACCCCCUGTTGGTGTCTTUA	75101	TGTUACCCCGGTGUCAACAAG
227057161	75102	GCTGCATCCCUTGCCAGAAUA	75103	ATGCAGAAGAAAGGCGUTTUCAG
227061426	75104	CTGGAACAAGGUTCCCACUGT	75105	GCTGTAAAGGTUGCTTAGTTTCTCATUT
227068030	75106	CCAGGUGAGGGAGGUGAGT	75107	GCCTCCUCCTTTCTTCCUCAG
227070807	75108	GCCAUGACCAUCACCACAAGA	75109	CAATGGCAUCTACTTCTGUCAGCA
227071677	75110	GTAGACCUCCGAGGTGTTGUT	75111	CAGGAGAUGGACGAGAAUCCC
227075151	75112	GATTCGTTCUGGGACTCTUCCAT	75113	CCCACGUTTCAUAGCCAGGAAA
227076499	75114	AGACCGAAAAGAAAAUGGTAGCUAGAC	75115	TCAGGAAGTGUCTCTTGAACUCCA
227077992	75116	GGGTGAUGGATTGGAGTUCAAGA	75117	ACTATATUCACCAGGATUCCCCAGAG
227080104	75118	AGGTGACATGUATTTTGCTCTGTUCA	75119	CCTCTTCACCCUCACATTGCUC
227081124	75120	TGTAGCAGUGCATTTUCACCGT	75121	GGAAGAUGCCAAGCGGAAUG
227086461	75122	TGATGGCTGUCTGATTAGCUAGGA	75123	TCCCCCAUTTCCCACCUACA
227086677	75124	ACCTCTTCCUGTGCCAAAACUG	75125	AGGGTGTCAAUTACCCACAUAAAGG
227114580	75126	GGAATUCAAGGTAGUCCAGGGT	75127	CCCATCCATTCUTCCTATTCCCTTUAG
227116259	75128	CATACAACUGTTTTGAAAAUCCAGCGT	75129	CCUGACAAGUAAGCAGGGAGAGA
227127621	75130	AGTGGCTGGGUATTCATTTTCTTATGUT	75131	CAUAGGCATCATTUCCAGCAGAGA
227127662	75132	TTTCAGCTGATGAGUAAAGAATCTCCUG	75133	ACATCTGATGCTUATCCTTTTCAACCUT
227127718	75134	GTAAAGTGACTCAUGAATACAGCCUACT	75135	CCAGACCGUGAGATCTACGAUGA
227129353	75136	GGTCCUGGTGTCTCUGAGGA	75137	GUGGAAGAGGCGGCCAUT
227132288	75138	GCAACUGCTCGTCTUCCGA	75139	GGGAATTCAGUCCCTTACTGGUT
227132856	75140	GAAATCTTACCUGACATCATCAGAGCUT	75141	AATCAATGCCAUACTGACAGGAAAUAGT
227133842	75142	GCCACCCCCGUCATCUT	75143	ACCCAACAUCCTGTGUCAGT
227134030	75144	TGCATTCATTTCCAUTTTAAAGTGCTACUAC	75145	TTTTAATAGCAUGCCTGGTUCAAGAGA
227137262	75146	CCTTCCUGCAGTCCTTGCUAA	75147	GCCAUCCATGTTCUGGAAAAAGG
227139038	75148	CCCACAGAGCCUACAAGATTGUAA	75149	GCTTTCAGAGCUGTTAAGGTACUACAC
227140502	75150	GTTCTGTCACACCUCCAATCTUAAAGT	75151	CTGGGTTTCTTTUCAACTTGTAATAGUGT
227145522	75152	GGCAGGAGUTGAGTATGUAAACCC	75153	AAATTGTTGAAGUCAGAATTGGUGCAA
227150064	75154	TGTTGATTAGUTCAAGCTCTUGCCT	75155	GGTTGGGUGGCGGTTACTUAC
227153276	75156	CAUCTCAUCACCAGAGGCAGAT	75157	CATTAGTTTTCCAAUTGGCCTCTTUAGT
227157666	75158	CAGCTUGATGGAGAUCGACACAT	75159	GGTACTUGGGCGGCACTUAC
227170428	75160	TTAAAACGUGAAGCTAACCCUCCA	75161	AAATCATCUGGTTTGTACUCGCAAAAC
227180775	75162	GCACCTTGUCCTGTCTGTGUC	75163	GGGTGACCUCTTGCCAUCAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227188630	75164	GGCGCCUGGGTTCTCAUC	75165	AGCTGCUGCCUCCAGAC
227188884	75166	TGCGCGGGUTCCATGUA	75167	TCUGCACCCAGACCCUGA
227190154	75168	GGTGCAAGGAGUTTGGTTTGUG	75169	CTGCAGCUGGCTCAGTTUAGA
227190318	75170	GCAGCCGAGCCAUGGUT	75171	GCAGGACUCCCCCTTGUC
227192043	75172	CTACCUCCTGGCUGGAGAAG	75173	CGTGAAGUCTTCCCCAUCGT
227192295	75174	GGCTGAGCUGCCCAAUG	75175	TCTCCACCACGGCUTTCUG
227192489	75176	TCCUCAAAGAGCUGGAGAACCT	75177	GGGCTCGUTAGGAGCUGA
227197215	75178	GCTTGACAAUGCCTGTTTTCUCT	75179	CATATTGGCUGTCCAGCCGUA
227204054	75180	CAATAGACTTGUGTCTTCACCTUGCT	75181	CCGCAGCGUCUCCACAAT
227207264	75182	CTGGAGAUCAACCCUGACCAC	75183	ATGCGAUAGATGCGGTUGGA
227207279	75184	AACCGGGUCAATGTGUGGAAT	75185	GGAGAGAGGCCACGUCTUC
227207963	75186	CGCCTUGAGAGCGAGTACTUT	75187	GUAGGGAGGCGGGAUAAAGG
227207996	75188	GGGAAGAUGTTCAGCGUAGAGT	75189	GGAGGGUCCCGGUAGGT
227209435	75190	CAGAGATCAUGGTTTCTTGACATUCAC	75191	GUTCTTUACGAACAGCCAAGCC
227211972	75192	CCAAUGGAAAAGAAATGCUGCAGAA	75193	GCCAGCUACAGATGGUACAGG
227215247	75194	CTTCTGGCUTTTCCCTUGAGGAT	75195	AATTAAGCCAUGTGAGACTUGACCA
227217160	75196	TTTGTAAGAGTGCUTAGCTGGATTUGA	75197	TCCGAACCTUCTTGGTTAAGCTUT
227220326	75198	TCATTATCUGAGGAGCCGGUCA	75199	ACCCTGCTAAUTTGTCACAAGUACAA
227223206	75200	TTCGTCTTCAGCAUGAGAATAAGATGUT	75201	GATGCGGCCACCUATAATACTCUAC
227223245	75202	GTGAUGGGTCAGTUGAAAGCC	75203	AACAAACCAGTGUCTTCTCTTCATUACA
227224920	75204	CCAACAUGACTTACTTGAUCCCCAT	75205	AAGTTGAAACAAAUGTGGAAAUCACCAA
227229303	75206	CGUGCCACCCAGAATATTUCGT	75207	ACGACCAAGUCACCAAGGAUG
227229650	75208	CGGGUGTCUAGGAGGCACA	75209	CCTGAACCCAGACAGUGACAAAATUAT
227230833	75210	CCAGCCCCUGGGUACAC	75211	GTTTGCCCUGGCUGGAC
227232177	75212	GCAGAGAGGGCUGCTTUG	75213	CCCTAGCUCTGCCUACCCT
227232251	75214	CAGCACCAGAAAUACAAGCTCTUAAAA	75215	GAACACAATTGUAAAATATAACAAGGCUCCC
227232971	75216	CGCACGUGAAGTGGGAGUAG	75217	AAAGTGTCCCUCTTGTCTCTUGG
227234030	75218	GCCAACATTAUGCTTCTTTATAGCTUCT	75219	GCTCTATATGCCAUCACTGCAGUT
227234918	75220	TGGAGGUGGCCGAGTUG	75221	TTCTCCCCCUCTTGGCUCT
227236164	75222	CTTGCAGTGGUGTTTGTTCTACATTUA	75223	CATGGAGUTCCTGTCTUCCAGAA
227236675	75224	AAACAGUAAACAGCAAGACUGACCT	75225	ACAGTTACGGUTCTAATGCTTUCCA
227236969	75226	CGAACCCACAACUCCCUGAAG	75227	CAATCGCCTCUTTCAGGTTGTTTUT
227239284	75228	CCCCAAGAAGUTCACACUGAAAC	75229	GGTTGAGACGUTCGCCTTUC
227240187	75230	GCAGGAAGUCAAGTCCCUGAGA	75231	CTGCACTGUGCTGATGATGTUG
227241414	75232	TCUGCAGGGACCUGAGGAA	75233	GUGGGCAUGGAGCAGGA
227241495	75234	GCAACCAAAGUGCAGGACAUC	75235	CCACAATGGUCTGAAAATGATTUAGCAA
227242104	75236	TCAACUGGGCAATTTCUGCCT	75237	TGTAGACGUCCTGCAAGGTTUT
227242979	75238	GACCGCUCCCCCTGAAUC	75239	GGAGCGUCGTCCCTUCC
227244596	75240	TGCTCACGCUCTTGGCUT	75241	GGCGGUCACUCCACAAAC
227247139	75242	TTTGATCTGUCTTGCCTTTUACCCA	75243	CCGATAGTAACACUTCTAAGCAGAAUGA
227248023	75244	GAAGTATGAGCCUTGATTCCCTUGA	75245	ACTATAAGCAUGAAGCTCCAACAUACC
227249221	75246	CTTATTTGCAGUGAAAGTATGCUGAGA	75247	TCCCCGAAATUATACACATGACUGAAG
227250651	75248	GGGAAUGACGAGCTCCCTUC	75249	TGTCTAGATGCUTGCATGTCAAUCA
227252159	75250	GCTGTTCUCAAACACTGATCCACUT	75251	GCTGATGAATGAGUCTCTAATGTTGGUG
227255223	75252	ACTTACCTATAUGAGGATTGAGAGCUGT	75253	GGGATGCTUCAGTTTCCTTUACAGA
227256116	75254	CTCAGCCCAGUGGGCTTUA	75255	CCCTGAUGGGAAGACGATUGAG
227257676	75256	CTTCTGGUGCTCCCGAUAGT	75257	GCCCUGAGAGAAAGGCTTTCUA
227257853	75258	GAGAUGAGTGACAUGGCCAACT	75259	GCCACCCAGAAGUACAGUGT
227260538	75260	GGATUCCCACCACGCAGTUT	75261	AACATGTTGCCTUAGTAATGTCTCTCUC
227262516	75262	TGATGGUGGCACACTUGACAG	75263	CGTGGACAUCCAGCTAAAGTATTTUGA
227267157	75264	ATCAGTCTGGUCACGGTTUGG	75265	CCATGGCCUGCAGACTTCTUAT
227269096	75266	CAAGTTTGGAUAACTGAAAGTUCACCAT	75267	TGAAACTGCGCUCCTGTCTUC
227272362	75268	GGATCUTCCAGACUGAAGCCA	75269	ACAAUGGGTTACAUGGCAGCAA
227280469	75270	GGAAUCTCUCCCGCCAAGT	75271	CCGTGCCCUCGTTTUGG
227280908	75272	ACCATUCGAGCCGCGUT	75273	ACAGCCGCCCAGAAAUTCUAC
227282151	75274	CAGGGTTTATCUCCAGGTGTTUCT	75275	ACTTTTTGATUACAGGTGGTTGTGUCA
227285149	75276	TCTTAGGGCTUGAGCTTTCATGATUC	75277	AGTCATCACTTTTUGATTACAGGTGGUT
227285226	75278	TGTGGTACAAUCATTCCTTGTGCUT	75279	CCTGCAAGATUCAGGCACCTAUG
227285334	75280	GGAGATGUCACCAATCGGTTUGA	75281	AAGTTGTATTTGACAGUAGATAGTATTTUGGA
227287895	75282	GTGTATTCCAAGCUGAAACAAAGTAUGT	75283	GAACUGGCGGAAGAUAAAGAGAACT
227288562	75284	GTAGUTCTCTTTATCTUCCGCCAGT	75285	CTCGGAGGATCUCCCTCTAAACAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227292504	75286	GCCAGTTCAGUAAAGAGTTCTAAGCAUT	75287	TGGAATGACUCAGTGCATTUGGT
227293926	75288	CCTGTGTATACAUTCCTGGCTCUG	75289	TTACTTGGATTTUACTGCGGACAGTUA
227297552	75290	TGCTAATACTGTAGUGCATTGTTCTGUT	75291	CCAAATGGGUTTCATGTTAACTUGGA
227297776	75292	AGCACAAUCCAAGCTAGGCUAAG	75293	TCACAAGTGTUTTGTGCGAGUAGA
227298253	75294	TCTCCTTCCGUCGGCATTTUT	75295	GTGCACGAACAAUTCTTAAGATCTTUGA
227301377	75296	CCGGCACCUCATCTCTGAAUT	75297	CTGGTACAGCAUCATCACCAUCAT
227301777	75298	TCCATACUGCCCCTTTAACGTUT	75299	CTGAATTTACTGCUGTTTTTGGAGTCUT
227302248	75300	ACAAGCTUGAAGCACCCAUCA	75301	GAAAAGTACATCGAUCAAGAAGAGCUCA
227304677	75302	TTGATGAGGUAGATCCGGUCCAT	75303	TCUTCGGAGAUGAGCAGCAC
227308615	75304	GAAGGUGTGGCUGAACACAAAG	75305	TTTGTGCCAGCUGACTCUGAA
227310356	75306	GGGCTTTGUTTTGTTGAGCUCT	75307	AAAGAGUCGGAAGACAAACCUGAAAT
227311817	75308	TTGAGCTCTTCTUGATCGATGTACTTUT	75309	AGAAAGAGUCGGAAGACAAACCUG
227312943	75310	CCTGGCTCUTGTAGGCACTUA	75311	GAGATCTCTCUGATCCTATCTUGCAC
227317667	75312	CTCATCAGAACCAACAUCTTCAATTUCA	75313	GCAGTGATGTGAUTTCGTGTTTTCTTUT
227319244	75314	ACAGUGAAAUGGCAGAAGACCT	75315	ACTTGCATCUAAAACACCCACATAGTUT
227323489	75316	TCAACCAAATUACAGTCTGACTUGAA	75317	GCTGCAATTGUCTAATGTTTTCCUCA
227331767	75318	TGTGUGAGCAGCCTGCATUA	75319	GGCAACTACTTUGAGATGAGTACCTAUT
227333543	75320	TGTAGATTCAGATUATATTTTTAGGCAGUCACA	75321	CGGAACCCAAAAGGUGACAUACC
227333601	75322	GCTTATGCTACAGUCATACATACCTUCA	75323	CCTTTTTCCCCUCTACACAGUACAG
227335193	75324	CCAGGAACAACAAAAUCAGTUGCT	75325	CCCTATTTGTCUAGGTGTCTTCUAGGT
227335232	75326	CCACUGATGAUACAAAAGCAAACAGA	75327	CAAGTTTGUATTCTGAAAAUGCAGGAACA
227339237	75328	GTTTTGGGAGCCUTGTTATATTTUACAAT	75329	TTTCTCTTCCATCUCTCTCTGACTCTUT
227339244	75330	GAGAAAACAAAGAGUCAGAGAGAGAUGG	75331	CTTTCAGATTCATTUGGTAGAGTGACTUCT
227341007	75332	GGACCCCCAAUCCCTCATUC	75333	AAGGCATCTGGUGTTAGGTAGGUA
227344561	75334	CCTGTGCCUCTGCTGCATAUT	75335	AGTCGACTGTGUTTAACTTTGAGTTTUT
227344833	75336	CCTGCGGGAUTTCACTUGCT	75337	GGCCATACTCUTGTCCTCAATTGUA
227347287	75338	GCAATGAGUCCTGCTCCACUA	75339	TGTGGGCCUGCAAGAACTAUG
227350132	75340	GGAGAAAAGGCAGACUTTAAGGGAUA	75341	CATATCAAGTUGCCAAAGGAATGGAAUT
227351007	75342	GGAGCAUACCGACTTAAATUCCAGA	75343	GCAAAAGTGAAGACUGGCTCTATUT
227351614	75344	GTGTUCAAGGGAGTGGUAGCAG	75345	CCGAAGTGCTCUGTATTTTTATCTGUGT
227353866	75346	GTCTGACUGCACATCUCCGT	75347	CTCTCCCCAUAACAGACCTTTTTACUC
227367167	75348	AAAGGCAGTUTTGGACCCAUCT	75349	GCAACAAUCACAGCAGTTUGGAT
227369383	75350	GTTTCGGTUGGCTTTGGUGAG	75351	TGAATGTCAAGAAACCAUGATCTCTGUT
227371495	75352	ACCAATGGAGUTTGAAGTGCUGA	75353	GGGTGUAGACACTGTCACUAAGG
227372478	75354	TTTTTAAGTCCAGCUTTCCCTTCTUCT	75355	GUATCTCCGTCAUAGGGAAGGGT
227374060	75356	GUGGGCUCCCACAGAGAC	75357	AGGGCACCCGGGAUATAUCA
227377050	75358	TGCAGAAGUACCCUCAAGCAG	75359	AATCTCCCUGCCAAGGAAAGAUG
227379339	75360	GGGCCUACCTTAUGGGACAAA	75361	GCTGTGGUCATGCTGAGAUGG
227380079	75362	GCTGACGTATTTAAUGGAGGTCTCTTUA	75363	AAATAGCTTGAGUTTTCCGAGCUCA
227381998	75364	AGGAGTTTTTGUCAGAAAATGGCATUC	75365	GCTCUGCATACAGTUCGGAGAT
227382601	75366	GGAGACACAUGTCGTGGUCAG	75367	TTTGAAGAGGACGGAAUTAGCTGTUAAT
227382888	75368	CCCTCGGUCATGGACCUCA	75369	CTCTACCTUGCCTGTCCCATUC
227387562	75370	TGUCAAGGGAGAGGGUCAGT	75371	GAAGCUACGGCATCCCCUA
227387971	75372	TCTUGGCCGAGGTCUCGAT	75373	CTCTCGCTUTCCACCTCUCA
227389291	75374	CUACCTTTTTACTCUGCCAGGGAAT	75375	AAGATCCUGAACTGAGTTUAAAAGGCA
227389424	75376	TGCCTTTTAAACUCAGTTCAGGAUCT	75377	TGAAAAACTCACCUTCATGGAAAGAUAACT
227391271	75378	CCTCACGCCUGGTGUCT	75379	GGTTGTGGUACCAGCGGAUG
227391405	75380	CCTATCGCTCUGCTCTCTCTTTGUA	75381	ACGCAGAGUGAUGAGAAAACCC
227392160	75382	TGAACTCACTGUCTAAGGTCCUAACAA	75383	GGGCAAUTTCTGCCUGAAAGG
227392369	75384	GCCUGGCGGGCAATTCTAUT	75385	CGGCCGUAAGTCACAGGATUC
227392596	75386	GCUACCUGGGCAACGACAC	75387	GTCCCCUAACCCCAUGCT
227394142	75388	GAGAAGCCCAUTTAGCCATGGUA	75389	GCCTGTGAUCAAGTGTGTTTTAAUCAAT
227394252	75390	GAGGAGGAGGUGGAGACTTTUG	75391	AAATGUGGAAACCAGAGCACCUA
227394335	75392	TTGTAAAAATATCUCAGCGCGUAGGA	75393	AGACUAGATAGCGUCACCAGCA
227396590	75394	TTCCCCACTGAUGAATCATTGTTCTUAT	75395	GCATGTTTTCTTUTTAAGGTGTGCAUGT
227398087	75396	CCGCACACCUAAGGAAAAGAUG	75397	TGAAAGCACUGCACTCTCTTGUT
227399931	75398	CTCAACATCACUCAGACTTTTATCTUCCT	75399	GGGTCCTTUTCGGTCTCTUCAA
227403991	75400	AGAGAGTGACAUTGTTTTAGCTTTCUGT	75401	AGGGCAACACCUCUACAAGGA
227404319	75402	CACCGAAAGCAAAUCATUCAACGA	75403	GGUGGTGGCUCACCCAG
227404538	75404	GGGCCUCAGCCACTCCUA	75405	AGGGUACCTCUGCACCGT
227409291	75406	GCCTAAGCAAUATAAATGGCUGCAGA	75407	GTGTTTCTCUGGCATCTGAUGGT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227410308	75408	AAUGAGAAAGAAUCAAGGGCAAGGT	75409	CCCCTTCTUGGTTGGTAGCUC
227410698	75410	GTCATTCAAAACAAUGGCTGGUGT	75411	TCCCCGUGCTTCAUGAGAAAG
227412507	75412	CCTAGAATUGGGAGCTGAGAGTGUA	75413	GGGAAACAGAAUTGAGAGCAUCAC
227414633	75414	GACTACAAAACUCCCCTUCCCAA	75415	CATGGUGGCCCAAGCTAUGAA
227415199	75416	TTTCATACTCACUAGGAAAGCAACCTUT	75417	GCTGCAAATATCUAGCTGTACCTACTUC
227417568	75418	GATUGAAGAGCCCACAGGUGAT	75419	CCGTTGTACCUATTGCACTCCUC
227418506	75420	CCTTCTATTATUGCCATGCGCUGA	75421	CTGTAAAGCCACAUTGTGACAACTTUT
227418661	75422	AGCAGTAGTAGGUGATGTTTACCUGT	75423	GCAGTAUACAGCAAGCCCACTUAAAA
227420097	75424	AGATTGCAGATTCUGTTTCCTTCTTCTUT	75425	CCUGTGGAAGAAAUGGCAAACAAT
227421031	75426	CCATGAGCUGTCGCUGCAT	75427	TTTCCCATCCUTCAAGGCUCAG
227421567	75428	AGAGTAGAGUGGTGGAUCCAGAC	75429	TGTTTGGTTUGGAAGTCCAGAAGAUT
227422404	75430	GGAGCGAGAGACGCUAGUG	75431	ACAGCCTTTUACAGGACCUAGAGT
227425169	75432	TGTGTTCAAGGUTAAAGTACUGCAGA	75433	GGCCCAGCCAUAAATATGTTTTGUT
227425846	75434	CCAGATGAAGCCUCCCTCUGAT	75435	GGACAAGCAGAUGATATCCCUAACAAAA
227427736	75436	CTCGTTCUGGGCTGATUCAGA	75437	GGATACCTUGGTCCAGAUGGAGA
227429471	75438	AGGAGAGCAGACAGCUGGUA	75439	GTGTTCUCCAGGCTCCUGAA
227432455	75440	ACCCTCCACUGTACGTCTCUT	75441	CCTGGCUCAGCTCTGTGAUG
227439869	75442	CCCTGUGGGACAGAACAAUCC	75443	ACAAAAGGAUCAAGGUGGCGAA
227441502	75444	CCACCCAUGTGTTCCUCACAAG	75445	CCACTTCUCACCCCATCACTUA
227441552	75446	GGTCATCTCAUCACCATCCAUCT	75447	GCTTTCTGCCACUGTCTCCUG
227442256	75448	GCCCCUGAGCGTCAUCT	75449	TGTGCGTCACUGTACACCTUG
227442524	75450	GCGACGUGGAGTTCCACUG	75451	CACCTUGAGCACGGTAACGUA
227443116	75452	TGGAGGUGAAUGGCAGCAAG	75453	CUCCAACCCCUAGACCCAAAT
227443439	75454	CCACGTCUGCCCCTCUCT	75455	CAGCAGGCCUGGACCTUAC
227444016	75456	AAGCCTATCTUGTTTTGAAGCCUACA	75457	GATCATCGAAUACCCCTTTGACTUACAA
227444926	75458	AGCCCTAUCCTGGCTGUGT	75459	TGACCAUCCAGCTGAUCCAGA
227445718	75460	GGTCGTATUCGTCCACAAAAUGGT	75461	GGCAGGAGACCCUGUAGGAG
227451834	75462	CCCTUCAGAGAATGTCUGCACAA	75463	GCCAGAACCCAUCUACAGCAAG
227452153	75464	GACTCAGTUACTACCTGAAAAUGACACT	75465	ATTCTCATTGTGUCTTCCCTCCTCUA
227452948	75466	TGGAGGUGGAGGAAGGACAAUT	75467	TTCCCGTGUCAGTGGCTAUG
227455083	75468	CAAAGCGUCTGCATTUGAAGGA	75469	ACTACCTGUGCAATGCCTGUG
227458238	75470	TCTGCCTTUGGATTTCCGTCUT	75471	CCTGAGGUTGCCUACAAAGGG
227460306	75472	TGCCCATUCATCTTGTGGUAGAG	75473	CCCGAGAACUTGCCGGTUAA
227460346	75474	GGGAGTGAUAACTTGAGGTGUCAT	75475	TTTAAGCAGGCUGAUGGCAGT
227462486	75476	TGTATTGCAUGCATTCCCCTUACA	75477	TGCTTUCCAAGTAGTTGUGGCA
227463777	75478	TGGTAATTCACAAGUGATTGAGCUGAT	75479	CCATTAATACCUGATTCTCUGCCAACAA
227465156	75480	CAUCCAGGACAUGCGCAGA	75481	GCCAUCAACAACACCAAGTCTUT
227465584	75482	CCTGTACTGGUGGATGTCCUCA	75483	CGGAAGCAGGUGGTCATUGAT
227467698	75484	AAGGTCCTCTTTUGAAATGTACCACUT	75485	GCGGACATAGAGUTTGATGTTGTTCUT
227468833	75486	CCAGCCUCGATCTGTACCUT	75487	TCCCGCUCCGACACATUG
227469012	75488	CAGCGAAGCUCTTUAGAGGAACA	75489	CTCTGCUCCTAAGGCUGCAT
227470067	75490	CGGTAUCCAGGATGUCCAACA	75491	GCAUGAGAGGUACCAGGGAGAG
227471428	75492	AGTCCTGGAUCAGTGAGAGUGT	75493	GGCAUGGGACAGAGTCGTUA
227471681	75494	AGCATUGCAGGAAGAGAAAAGUAGT	75495	TGTCTTTTACCUGAATGTTTCTTCTUGGA
227476693	75496	CCUTTGACCTTTTUGAGAACAAGAAGAA	75497	GCCTAAAACCUCCCAAGACTUCA
227481668	75498	TTTCTACAGAGGUAACCACAGAATCUCT	75499	GAAGAACCUGGGCCAUCACAA
227482950	75500	CAGCTGATUCCCTCCCCUT	75501	TCTGCACAGGUGGCAUGAG
227483565	75502	ACCGTGGAAGAUTTAACGAAUGGG	75503	TGCCGCCUACAACTCTTACTCUA
227485480	75504	CACCCCUCCUACCAGCAG	75505	CACCCCUTTCCCCUGCAT
227487033	75506	CCUAACAGATAUGCCAAAAGCAGAGA	75507	CGTGCUCAGAGGAUGAACACAG
227490842	75508	GGCAACCCAGAAAAACUGCAAUG	75509	TTTAGGATGUCAGCTGGCAGAUG
227491082	75510	TGGTGUAGGAATGGCGUGAAG	75511	GGAGTTGGCUGTGAACGAGUA
227492323	75512	CCCAGGGUCTGCCUACCA	75513	CATTCTGCCCCAUCCCCAUAG
227495405	75514	GCTGCTACAUACCGCTTCTTCUG	75515	TCTTCATCTTGTUCCTTGTTCTATTGCUT
227497817	75516	CACGGCCUCCCTTCTTGUA	75517	CAAGAGUGGAAGCCAUACACAC
227505112	75518	CCTCATCACUGCTTCTGTGUCT	75519	GGGUTCTGUGCCAGAGGA
227507280	75520	CGCCGGGCUACGCTUAC	75521	GCUCCCAGUAGCAAGAAGGGA
227507796	75522	GCCCCCUCCTGAGUGACT	75523	GCCCACAUGGCCAAGUACA
227508650	75524	GCTGGUGACCACGCACUT	75525	CGAGGCUCTCACGUCCCT
227508959	75526	CTTCGTCTUCACTCACCACUGT	75527	GGGAACCGUCCTCUGCG
227514370	75528	GCCGCCGCGUGTACUAC	75529	GAAGGCTUGCACGAGAAAGUT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227515284	75530	CCCCAGCGCAACUTACUCC	75531	GCTTCTTUGCGCATCTGUCT
227519289	75532	CCTCCCUGCCCAAAGTGTUA	75533	CCCTGCACAGAUTTGACACTUAC
227519822	75534	GUACCCCUGGCGGAGAAG	75535	GCAGAGUCCGCCGCAUT
227524795	75536	TTTCAGGGACUACAGCUGAGGA	75537	AACGTGGUGAAGATTTGTGATTTUGG
227527976	75538	GGUTCTTATAAATAUCCCGGGCAAGG	75539	AGTTGGTTAGGUTAAGGAAATGCATUGA
227529268	75540	CACGGCUGACTGATAUGGCA	75541	TGGTGGTAUACGGGAAGCUAGAG
227530063	75542	CCAUCTUACGGAGCCCCAAA	75543	GGGCTGTUCCCCGATTUCAG
227532890	75544	AATGAUGGGCTGACUGAAAACCT	75545	GTCCGAACACCGUGCUG
227533739	75546	GCAATAATATGUCAGGACAACGCGAUAT	75547	GCCTCGCCAUCATTCUCGAC
227536267	75548	CTGAGCAGAUCCCGTCCTUG	75549	CTTCATGGGAGUGCCCTTGUT
227538470	75550	TCGATACCACUGGCCUCAAC	75551	GGGTAGGGUCATTACTUACGCT
227540496	75552	CACCUGGTACGUCCGCAA	75553	CCCACTGACUTCCTTTCCATCUA
227540757	75554	CTCACTUAGCCACAGCGAUGT	75555	TGGAGCAAGUTCTGATUGACCAA
227541265	75556	CCCACCAAGCAGGUAAGGUC	75557	AGAUGCCGGCGTGUGAA
227542030	75558	ACTGAGGCCUCCAGUGAGT	75559	GGAGCCAGGGCCUCUCA
227543844	75560	CCTGTGGAAAAGCUGGGAACUT	75561	CTGGGAUCCCCTCCAUACAGT
227547667	75562	CCAGCCUAACCAGGGAAGUT	75563	GACTGGCUGACAGGAGACUG
227550127	75564	CTTTCAGGTGUACCCATTGCUCA	75565	GAAGCTGGUGCTGCCTTTUC
227553840	75566	GGCCGUGGAAGATCTGGAUG	75567	CGGUGGGAGAAAAGAAGGUACT
227554000	75568	AACTCATGGAUGCTGATGGGUT	75569	CGGCACUGACCTGCTTUG
227560037	75570	CAGCUACCUGGGCAGCA	75571	GCCGCCCUTGAGACUGT
227560128	75572	CAGCCGCGACAGUCUCA	75573	TCAGGGUGACGTCGTCGUA
227560610	75574	CCCTGTCCCCAAUAGTGCTTAUG	75575	CACCTCAACTUCCCTGTCCTTTUT
227560900	75576	CGCTCGUACCCGCUCAAC	75577	GACGGTAGUTTCGCTCTUCCA
227561996	75578	GCTGCAUGAAGACCGGACUC	75579	TGCTGACUACGGAGACACCUT
227563986	75580	ACTCTAGACAUCAGATCGGGCUT	75581	GACAAGTCTAAUCTGGAGCTGAUCAC
227567194	75582	GCCACACAGGUGCATGTUAGA	75583	CCATTTAGGGAAACUGAGCCTCUT
227583556	75584	GCCCCGGACGGUACUCA	75585	GAGTCCAUCATGGCGUGCT
227583662	75586	GACGGUACUCACCGAGCAG	75587	CGGAGGCACUTTGGAAGAAUG
227587050	75588	GGCAGGUTGGGCATUGGT	75589	GCCUGAACCCUGGACCCT
227607747	75590	TCATGAAAGAGUCAATAGGUCAGAGAGT	75591	TCTCGGAUGGATACCCATUACCAT
227608571	75592	GACAGCCUGACCTCACCUT	75593	GGTCGTGUGTGCAGTUGG
227609865	75594	GGAGCTCTUCAAGCTGCUGAA	75595	CCCGCCUTATUCGGGAACA
227611083	75596	TGAACACTUCTTCCAGGUCCAAG	75597	CCAGTGAGCUTATTTCACACGUT
227613086	75598	TTCTCAGAACCCUCCCCTUCAT	75599	CAAACCAGUTGUAGACACGCA
227614048	75600	GCUATTTCUGCAGGGCGGAAT	75601	GGCCCGCUGTACGTGUC
227614542	75602	GCACAAGCUGGCCAUGGA	75603	CCTTGTCCCCACAUACCACTUAC
227617379	75604	GGCTGTCTCUGGTTATAGGATGUG	75605	CTGTTGCTAGCUAAAGTTTCCTTTTCUT
227622284	75606	AACCCTTATGGUTTTCTTATGGTUGGT	75607	TTGCAGGCCAAGGUAAACUCA
227624023	75608	CGCTTCAAUCTTATTCAGGAUGGT	75609	AAGTACGAGUTTGTGGUGACCAG
227624711	75610	CCTCGGUCTGCAGCUACA	75611	CCACGGGCCUTGTGTTGTUA
227627830	75612	GACGUGCACAACCTCGACUA	75613	CTCGGUCAAACAAGGCCUCA
227629274	75614	CCTUCCCACACCCUCCCA	75615	CGCCUCCACCCCUGAAG
227629815	75616	CAGCUGCGGGATAACTTUAAACAA	75617	GTTCTGGUCCTCGGUCAGG
227631354	75618	CACCCTUCCCTCTUCAGGAAA	75619	GCTGACAAAGCUTCATTTAGTTCCUC
227631818	75620	TGTTTCTAACCAGCUGAAGAAAACUACA	75621	GAGGTGGUGCACAGAACAAAUC
227635538	75622	TCCACUGCAGCCAUGGG	75623	TGATGTGAGUGGTGCTCTCUCT
227635602	75624	CUTGCCUGGCAGCACAAA	75625	CACCTGTUGTGCAAATTGUCAGA
227636588	75626	CGCCATAAGGUGGTGGTUGT	75627	CCTCCTTGACUGAGCTGGUG
227638719	75628	ATTCUCCCAGACCUGACCGA	75629	TCTTTAGGCUTGCCTTTTGUCACT
227639267	75630	GAGCAGCCAGAGCUTCAAATTTAUT	75631	CGTATATTGGAACUTTCTGTTTCACTUGC
227640499	75632	GGCCUCAACGCCCAUGT	75633	GGAGCCCAGGCCUTTCTUG
227641799	75634	GCTTCTTCCUGTTCATCCTGGUG	75635	CAGCTCAGAACCUGGTATCTACUT
227643534	75636	AGCACCCAAAAAUTATCTTACCCUGA	75637	CTTGCGGTTUCGAGTCTGAAUAC
227646644	75638	AAGTTGAATGAUCACCTACGCAGUT	75639	TCATGAATTATTUGGGACGGACAUAAGG
227646672	75640	CACUGACCAUGCGGAAGGAT	75641	TCCCCACAAUTCCCGCUAC
227650148	75642	CTGGTGGCUTTATGGTGGUG	75643	AAGGCAUGAGGTGGCUAACAG
227650454	75644	CAGAGTAUGGCATGGGTCUGA	75645	ACCCCAGTUATTAAAGCTTTUGGCA
227651008	75646	GCCCTGUGGTGCTGUCA	75647	TCCTCUGGAGGCCAUGCT
227652440	75648	GGCCGCUCGCTUCAAGA	75649	GTTTTATGTAUAGCTTTTGCATCUGCCA
227654708	75650	CAGUTCATTTCUGGCACAGCA	75651	TGTTCTCCTCTUGAGCATTCATTTGUAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227660438	75652	CCTCGGAGCUGAGCCAAAUG	75653	CCAAGAACACCAUACUGAAAGCCT
227668336	75654	TCCTUGAAACGCCCAUCGT	75655	CGGCAAUCGCCAGGCUA
227668395	75656	TCACCGUTCTAAAGUCGGGAGA	75657	GCACTGAGGUGAAGGGATACUG
227671500	75658	GGCATCACAGCCUACCAGUC	75659	GCACCCUGGTGATGTCGUT
227671727	75660	CTGUGTCTCATCUGCAGCCT	75661	GGTAGAGTGAGAUGCCTACAAAATUCAT
227673321	75662	ACTACTCCCACUGTCTCUACACC	75663	GCCCGTUAGGTTGGCTTCUC
227673797	75664	GGCTCCUTGACTGUGCGA	75665	GTGCGCCCCAACUCTTUG
227676098	75666	ACACTGAGUGGCCTCCTGUA	75667	CCGAGGCAUCAAGCATTCGUAA
227681814	75668	GGGAAGAAUGUGCGGAGGAT	75669	CCACAGATAUCACACTTTAGTTTUCCGT
227684640	75670	CTGCAGTTUACCTGTTTCUCCCA	75671	GAAAAGUGCCAATGTUAAGAAAGCAGAT
227685062	75672	TCTGTTACTTACGUGGACATTTCTUGAC	75673	TGACAGTGGAGCAUGTGTTACUC
227685184	75674	AATCAGCAAACAAAUCAAAGCTCAUGAT	75675	CCATCCTTACCUCTATTTCTCTTUCAGG
227685428	75676	TGAACTAGAATGAUTAGCATAGGCCUCA	75677	CTGGCCUGGAGCTTGAATTTUT
227687344	75678	AGATGGACACCCUGAGGUCAAT	75679	AGGATACAGCCUGTGCACAUC
227687912	75680	ATTCTTCTUGGTGGTGCUGCT	75681	GGGATGGGAUAGCATTGAATCUCAT
227689332	75682	AGGACUTGTGGTUGGACGAAA	75683	TTCGAAAGTUGCTCAACTTCTAUGAGAA
227689572	75684	GAUGTTATTAACUGGAGGAGGGAAAGAC	75685	GTGGGACAAAAUACCTGAGTTTAGAGUA
227697858	75686	GCAACTCTTAGGUTGTGTACTAACUGT	75687	CTGGTCTAGAGAGUGAAGCAAACUC
227699352	75688	GCCCACCCAGAAAGUACTUCT	75689	GACGTGCTCCUTTTGATCTGTUT
227700387	75690	CATCUCACCACCCACACGUA	75691	ATCTGTGTGCUGGTGCTCUC
227701314	75692	ACCTCAGGGUGAATACACAAGTTTUT	75693	GUGCCTCCAAUGAGCACAAG
227701875	75694	GCAATGAGCUCACAGAAGUCAG	75695	AATGAACAATTTCUCCTTTCCTCTCCUT
227703162	75696	GTTGGATTGUAGACAAAGGTTUGGG	75697	CCTGTTTUGGCAGCGTTUCAT
227704017	75698	CAGUGAGUGAAGCAAGGGAAGA	75699	GGACATTCTCAUGAACTTCCTGGUG
227705522	75700	CAUCCCCAGGGCACUGAT	75701	GGGCGUCACCTGGTGUA
227709923	75702	TGUTTTCAAACAGAUCAAAAGGAGCAC	75703	ATCTTTCUCCACCACCCCAAATAUC
227711614	75704	CCATTCTGUCGCTGGCUCA	75705	GTTCCCTCCTUGCCAAAATAAATGUT
227712152	75706	GTTGGAGGCAUTCGACTTCCUA	75707	GAAAAACUGAGCCAGGCCTUAC
227712800	75708	GCAGAAATATTUAACTCTCCCCAUGGAA	75709	CAAATGTCCUGAAATTCTGTCAGAUGAA
227713919	75710	CTTCATCATCUGAAGACTCTTCCTUGT	75711	GCAGCCATUGCCGAAATCUAAAA
227714278	75712	TTCCTTGCCAUTCCAGAACUGT	75713	AAGAAATTGAGUTGATAAGTTTUCAAGAAGAG
227716821	75714	CCAUGGAATCTGUCAGCAACCT	75715	GTGCGCTUCCGAACGAUG
227718952	75716	TGATCGTUGGGCAAACACAAATUC	75717	AGTACGCTUGGGAGTCCUCA
227719938	75718	GAGGCAAUTTTGUCACAGCAGA	75719	TGATAAUGGCCCCCTGUGAAAC
227721433	75720	CATTTACAAUGCAAGGGTAGCTGAUT	75721	CCCTCCTUCAGTTTAGTUGAGGAT
227722022	75722	GATCGGCCUCTTCAUGCGA	75723	AACTGCTAAUGGCCCGTUCT
227722141	75724	ACTTCAGGAGCUACAGAGAUGCT	75725	GAAACUAAAGACAGGCTCGACUCA
227732000	75726	CTTACCTTCUGGCTCTAATGUGGT	75727	GGGATTAACGUCCACATGGAGATAUG
227732313	75728	GTGCCTACCUGTGTCTGUCC	75729	TTTGCAGGCUGGTGCAGAUAT
227734483	75730	CGGATCCGCCCAUTCTGTTTAUAAAA	75731	AAAAGCUGAGTACCUGAAGAACAACA
227735291	75732	CCTCCCATCUCCCTGCAAUAAC	75733	CTGACTGUCACCTGCAACTUCA
227736447	75734	GAGGAGCUGGCAGUGGAA	75735	TGGCUACCACGCCUGAG
227737199	75736	ACACTGUAAAACTGAATGGUGAGAAGT	75737	GCATCAGGCUCTTTCTCTGTCTUC
227739551	75738	TCCAGGCUGGAATACTAGUAGCA	75739	GGAGTTGTTUCCATGGTCATTTUGAAAA
227742364	75740	CATCAUAAGGGAGCCGCUCA	75741	ACAGTGGATGUTAACGGAATATCUAGGA
227742373	75742	GCCAAGCAGAGGAACUGAGAUT	75743	AGGAGCTUGATTTGCATGAUGAAGA
227743000	75744	AAGCTGAGUCAATCAGAAGUGCAT	75745	TCGCATTTUGGGACTAACTGCUT
227747129	75746	GCATTCTTGUCCCCAGCAUC	75747	AGCCAAGGUCATUGCAGGAAT
227748141	75748	CCCTCACCACUGTCCCTUCT	75749	CCCUCCACCCAGCTCUGA
227749241	75750	CTCCAGCTUGGGTTTCTGUCA	75751	ACCAAACTGCCUTTTTAGTCACTAUGAA
227752479	75752	GTGCAAGGTUTACACATTTTAAUCCCAT	75753	TGTTTTGAGCTUGTTTGCTGAATGUT
227756646	75754	CCTGGTTTTCUTCCACAGCATUC	75755	AAACATGGUCCCCTTGAGTGUC
227756753	75756	GGGATGAGUCAACCAUGCAAAG	75757	CTTTTGGACAGTUGATGATGAAGAGTUT
227758327	75758	CCAAGCTUGCCCTCAGGAUAA	75759	GGATTTTATTUGGAGGATCTTCCAUGGG
227759354	75760	AATTCCTCTGGAUCACATTTCCCATTUAA	75761	TGTTTTAATATGGCGAUGTCTCTCTUGT
227759808	75762	TGACTGGUTTCCCAUGAAAGCA	75763	CCTCTTCCACAUTTGACTTCAGAUGA
227761566	75764	CGTGAAGUCATCTCCATGUGAAAAACT	75765	GATTTTCACTCUCCAGCTCCUCT
227762777	75766	CTGGCAGGGCUTGTGTTCTUA	75767	CCAGGGUCTTTTUGAGCAGAGG
227764265	75768	TGGAGAGTTTUGTAAGGCTTTAUCAACA	75769	AGAAAGGTAATTCTCUTTCTCTCTCTCTCUT
227764512	75770	TCTTCCUGGAACACTGGTCUCT	75771	GCAAAATCTGGAUTGTGTTAATTCTCUCT
227767006	75772	GCCTTCTCUGGCATTGACAGUA	75773	CACAATGCAUCCAATGGUCCAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227768245	75774	GGTTATTGAUCAAGTCAGCCTUGGT	75775	TTGTTAACAGGCAUTGGACAAAAUCC
227769296	75776	AGGACTUCCTCCCAUCACCAA	75777	GTAGAAGGCAGGGUCTTCGTAAUC
227771785	75778	ACGAGACUCACCCAACATGUG	75779	TCACTAGCAGGAUCCAAGGCTUA
227775974	75780	TGAATAUGGCGGCCACGTUT	75781	CCTTTGCUGCTGCTCCTAUCC
227776768	75782	CCTGCUGGGAAGTAGCUCAGA	75783	ACACACTTTUACATCTTCGTCAUCGT
227777011	75784	AAAGACCUGTTGGGUGGACAA	75785	CTATACACUACCGCTTCCAUGGG
227778156	75786	TGGGATCTGUCAAGCTTTCAUACC	75787	GTAAGTCACTUATTAACCCAGAAUCGGA
227780579	75788	GTCTCATTGCTGUGTAAGTAATTGTTUCC	75789	GGTGAGTTGCAAUGTCCGTAATTUT
227781072	75790	TGCTUACAGCTATAAAUGCAGGCT	75791	TTCCTTCTGCUACAGCTCTGATUG
227784576	75792	TCTAGGTTCCUGATCAGTAUGGCA	75793	TCAGTTAACGGTUAATATCACACAGCUT
227784587	75794	GGTGCCTUGCAGATTAGGUGA	75795	CTCAGTTTCCCAGUATGATCTTCATGUT
227784624	75796	CACATACTCAUCCTCGGCCTUG	75797	ACCUGAATCCAGUGGAGGAGAA
227784698	75798	CCTAATCCTCAUGACACCAAAGUGAAAA	75799	AUCAGGTTUCCCCCACAGAAAG
227785418	75800	CTCTGCATGUCTAGTGATGTCUGG	75801	CCCCTGAGTAUGAAACTTTTGCAGAAUA
227785555	75802	CCGTGGUGGATGACUCGAA	75803	CCAAGTTTCTCUTCCATAAGTTTUAAACCAA
227794227	75804	CCCTGACGUACATTCAAAGGCAUT	75805	GUTGCTGTTTUCCCCACCAG
227799111	75806	CTAAGTUGCCCAGAGTGGGATUT	75807	CCTTGTCTTACAUACCCTGTGTCTUC
227799714	75808	ACAGTATAATATCUCCTGGCGCUCA	75809	GCTGCACUGATCCCCACAUT
227801665	75810	CATGCATCCUTCATGGGAATTUAAAGG	75811	TTGCTGAGAAAGUCACTGCUGA
227802474	75812	TGGTTAGGTCAAGGUTGTACTTTGTTUT	75813	AGATATCGCAAUTTTGATCAGCCUCA
227804434	75814	CACAUGCCACAAAAGGAACTTUCT	75815	GAAGGTTGCUTTGGGCAAGUG
227805115	75816	TCTTTCAGCCAUTAAGAGAGCTCTUG	75817	CGGTATTCCTTTUCCATCTCTCACTTUA
227810152	75818	ACTAATTGCUGGTCTCAACUGCAT	75819	CTCTTCTAGGTACUCTGTCTGATCTTCUT
227815112	75820	GAAAGGCAGAAAACUGATACAATUGCT	75821	TGCAGGTAUCACACAAATTACAGAAGAUT
227816152	75822	TGTCTTTGTCAAUTCCCACTGCUT	75823	GTTCTGGAAUTTCCCTCACUACACC
227816834	75824	CATCCAGUGGCGGGACAUAG	75825	CTGTAGAGCUGTCCCCCAUAG
227818293	75826	GGGTACCAAAGUGATCCTCCATCTUA	75827	ACATCCUGCACGTTAAGTGUAAAAGA
227819221	75828	CCGAGAACAGUGAUGAAGGACT	75829	CCCCACGUGAACAAGTGACAUT
227820775	75830	CCTGACCAACUTTTCCCAGTTUCT	75831	ACTTTCTTCTTCUGCCAAAATTGTTGUT
227821568	75832	CCTCAAAACUCAAAGCUCCACCA	75833	GATGACCCACCUGCATGUGA
227826863	75834	CGGCTTUGGGTTCTGUAGACT	75835	AGAGCCAUGCATCTTTATUCAGAGAAAT
227828085	75836	CTCGTAGCAUCGTCCTCAUGT	75837	TGGCATTUGAAGGGCTTCUCC
227829164	75838	GTAGCTTCCUTATAGCACAACUGCAT	75839	CTGGTUCACACGAATGTTUGCT
227830783	75840	ACGTCTTCCUTCTCTCTCTGUCA	75841	CTGAGGTUCAGAGCCAUGGAC
227832178	75842	AAGGAAAGAAGAACCUTGGCATCUT	75843	GGATGAGAGCUCCTGAGTACTCUA
227833011	75844	CGGCACAUCAAGCTGCATUC	75845	CGGGCAGAGUGGAGGAAUC
227835801	75846	AAGGAACAGGGUCTACCUCCAT	75847	CGAGTGTTGCUGTCATCAACTUT
227835840	75848	GCAGCTGUCAATTCTCATGUCC	75849	TGTGAGTTUGCCTGTTTTCTCUCT
227836292	75850	CGCGTTGCGUCGGAAGUA	75851	ACGACTCTGCUGATTTGGTCATAAAUT
227840780	75852	CCAAGGGCUCACATTUCAGGAG	75853	TTGGTCTTTTGUACCCTTAAGCCAUAA
227844936	75854	GGTGCCUGCCTCATGGUT	75855	ACCAGCCCUGTGCCAUC
227846111	75856	GCCCACUGTCTGGGUCAA	75857	GCACACTGAAGUGGCACAGUA
227847409	75858	GCUGAATGCCUCCCACGA	75859	GCACTCGGCUCCTTTCTGUAG
227848493	75860	ACTTCTTGTCAAAAAGUGAATGCTTGUT	75861	TGTGCATCCCAACGAUCATGTTAAUA
227849931	75862	GCTCACATACUGACCTGGCTUT	75863	CCTCUCGTGGTAUGGCAGAC
227850556	75864	CCTGGTCACAGAUCCAATGCUT	75865	TTCTTATATCAUGACCATTCTGCACCUC
227858404	75866	GAGAAGACGCGACUGUGGAA	75867	GTGCACCUGGGTGAGUCC
227858973	75868	GCATGTTCUTTTTCTAAATUGCCCACA	75869	GGACATCTCCUTCCTGTTGTTUCAG
227864954	75870	GAGAAGGAAAACUATGGTAGGAAACUGG	75871	AGAGUTATGCUGGCACAAGCAA
227865704	75872	CATTCATATTTGUCTGAGTTCCTGAUCCA	75873	TCAAACTCTGUGGCATAATCAGCAUT
227865869	75874	CCCACAUCCACCTCUGGGA	75875	CGTCTUCAGTGCCCUGGAA
227866508	75876	AGAGACTGTCUGTTTTTCAGGTCTUC	75877	AAGAGAACUCCAGGTGCTTGUC
227869979	75878	GGTACTCATCUCAAAGTAGTTGCCCUA	75879	GGGCTCACCUGGGAATUAGAAAA
227874069	75880	GGGCGAGUTTGCACACUCA	75881	CCCTCCUCACCTTTCAGCAUC
227874155	75882	CCTATTACCTCCUCGAGTGCTTUG	75883	CTCACTTGGGAUGTTTTCATCTCCUA
227875346	75884	CCAACUAAGGGCCTGATCCUACT	75885	GTAGGAGAGGUCAGGTTUCACAC
227877076	75886	CTGTCACCGUAGCCGUGAA	75887	CCTTGTCAGUGGCATCGTCUG
227877337	75888	TGTCACCGUAGCCGUGAAG	75889	ATCUCAGACACCAGGUCCGA
227880055	75890	CCACTAUAAGGACCCTCCCTUCT	75891	TGCAGAAAAGACCGUTGGACUC
227881193	75892	GCCGUCCCGGGAGACTUA	75893	CACTGACCCUCTCCCTUGAC
227882867	75894	CCAAGCCAGCCUCACCUC	75895	GCAGUACAAGGCCACAGACTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
227883715	75896	GATCTGAUGGATGGUCGGGAT	75897	TCTCCACAUGGTGCTTGCAUT
227884778	75898	GTTGTACACTUCCCACTCCTUGA	75899	GCCTAGCCAUCCTCTTGTCUCT
227888727	75900	CAGGCCCAUTGAGAGAGAUGT	75901	CCTCCCUCCCTCCTCUGG
227892781	75902	CCTGACCUGCACAGCCUT	75903	CCCACCUTGATGUGGAAGGA
227894304	75904	GGAGGCCCAAUGTTTCTCUGT	75905	CCCCCUAGAGCACTGATGUCT
227898228	75906	CGCTTTGTCUACACCTGCAAUG	75907	CTCTATAAAAUACGTGGCTGCAUGG
227901591	75908	TAGATGCATUCTGCTCCUCGAA	75909	TCCAAGTCCTTUAGGAAAATGTCAUAGG
227907248	75910	CCAAGAGCCAAGUGGTCUCA	75911	TCCTATGTGTUCACCTTGTGTUACAG
227908584	75912	TTGCAUGAGAAAGGGTGTUCAGA	75913	GGCTGGTCTUCCTCCTCTTTTAUT
227912457	75914	TCATTCAATGCUGGTGGAAGUCA	75915	GGTGTGTUGGAGCTCAUGGAC
227915089	75916	AAGAGAGAAGCACUGAGTTAAAAACUGA	75917	CCAGAACGAAUGGCTUCAGAGA
227915472	75918	GGTGUCCCTGGAGUCCAAC	75919	GCCCUCAGCACCACUGA
227918651	75920	GCCAATTGTTCUTTGTTCCCTGUT	75921	AAGCCTTTGAGUTGGTACTGUGA
227918663	75922	AAUGGGAGGUCAGGGAGAGAAA	75923	TCCUCCAGCGACTAUGGACA
227920004	75924	TTTTGCCTTTAGGAGUCTGATGACTUT	75925	GATGTGTCCUGAATGTTGCTGATUC
227930926	75926	TGAACCAGCAUATAGAACATGUCCAAAA	75927	TCTTCAGAGACCACUCTCCTUGA
227932117	75928	GGGCTTTCUGAAGGAGGUAGAG	75929	GGGTGCTAGTTUATAGAATTCAGAGUCA
227932896	75930	AGGCATACGUAACTCACCACTUG	75931	CTGATGGACCAUCGTTGGTACATATUAA
227934283	75932	AGGTGCTGGAUGGAAATAGUAACC	75933	GCTTCCTGGGCUAGTGACCUA
227935487	75934	GCGTCTTATTCUCTGGGATGAAUGA	75935	GTTCTGATCUGACTTTGCATTGTUCAG
227937469	75936	ACACCTACUGCAGGGAUCACA	75937	AAGAAGAGGAAGGUGGCATUCAG
227941325	75938	GCACGCAUCCGACTGTUCAT	75939	CTCTCUGCCACTTCUGCGA
227941446	75940	CGTGGGCUCATCTTGGAAGUC	75941	GTTGGAGTGTCTUGAATTATGTGTTTCUT
227941641	75942	CTAACCTCTUCAGGCTCAAUCAGT	75943	GAAUGTAUCGGGAAGGACCCA
227945219	75944	TGATCCUCGCCGTTGGTAUG	75945	CCCATAAAGTGGUTGATTGTGGTTUAA
227947597	75946	ACCUCCGUGCAGAAGAGAGT	75947	GGGAGGTTUCATGGAGTCAAUAGG
227948164	75948	CCCACUCCTTGCTTCUCAGAT	75949	TGGTGACAGAGGACAAUGTGAUG
227948598	75950	CGUCGCUGCAAGCCAAA	75951	GTTTAGCGGUGGGCAACUAAC
227948622	75952	CCCTCUGGTGATGUCAGGGT	75953	CTCCGAGGAGCUCAUCACA
227953864	75954	GTTGAACAGAACAACCUCTGUCACT	75955	CATACTCAGGAUGCTGTTCCACTUAC
227956383	75956	TGCCTGCAGUGTCTATCTATGTUG	75957	GCTCTGTGACUGTGCCTCTUG
227956808	75958	TTCCCUGACCGCTTTGCUAAA	75959	CAAAGUCAGGCACGTTCAUCAC
227958806	75960	CGAGGCCAAAGUCTGCTATCUT	75961	ACAAGTCGGCUAGTTGCAUGG
227959097	75962	ACTCCTCCCUTGATCCUAACACT	75963	CCACCAGCCACACUTGUAAC
227961502	75964	ACTGCTGGAUCATATGCATTUGAGT	75965	ATCTGCTTTCTTUGATTCTTCGGAUAA
227963366	75966	ATCCGAAGAAUCAAAGAAAGCAGAUAA	75967	CAGTGCUCAAAACCAAAATGCCTAAUAT
227964014	75968	CAGCGGACUGGTGTGGUT	75969	AGCUTGAGTCCUGGGCAAG
227968922	75970	TTCAGAGUGGACTACATCCUGAGT	75971	TGCCTGAAGUGTGGTTUGGAT
227969917	75972	CCCAATAGCAUGCCACCCUA	75973	TCTCCGCUGCTCTCTGAAUCT
227973101	75974	AGGAGGTUCACCTTCCTCUGAAA	75975	GCCTCTAUGCTTGCGUAACCAG
227973420	75976	GCTGCCUCCGCTCACUC	75977	GCCGGAUGCUGCCAAACT
227974277	75978	CCGGACACAGCUTGGCUT	75979	CCAGGCCCGAUGGUCAT
227974391	75980	CCUGCGTCGUGGAGAACA	75981	GGGCAGAUGACGCUCAGG
227977149	75982	CGGAGAAGUAGGTGGTGUCACT	75983	ACGATGUGCAGAGCAUCAACT
227977990	75984	TCAAACUCCTATACCUGCCCAAGA	75985	AGTACTGTUACCAGGACTACAGAAGUT
227978570	75986	GCAGCAGUGGAAAUGGCAAT	75987	AAATGCCCACUGGGACCUC
227979101	75988	CCACCTCCUCCCCTGUGAT	75989	GGGAGCCCCUGUGGAAG
227979609	75990	GAACCTCATCAUGGCCTCACUT	75991	GCTCCTGGAUTCTGCGGTUG
227980669	75992	TGTTCACTAAUTTGTTGCCUACCAGAA	75993	TGAAGAGGAUGCAGGGAATTATACAAUC
227982321	75994	CCAGCUCAAAGCAAGAGTGUCA	75995	GCTCCGUACGCTGAGUCAAAG
227982794	75996	TCCAGGTTTTAUTGGCTTGCACUA	75997	CCTCUCGGAACCAGTUGAGAGT
227983074	75998	GGACCAGGAAGGACUCCACUT	75999	GTGUGGCCAGCGTAATUCC
227986788	76000	GAGAAGCUCAGCCUGGGA	76001	CACAGAUGCCAACCUCAACCT
227989373	76002	GGAGACUGGGAGGTGGAAAGTUA	76003	AGTCACAGAAGAGGAUGAAGGUGT
227989378	76004	CAGGAAGTACUTGGCCACCUG	76005	CTCCCCGAAUGACCTTCUGT
227991413	76006	GGATTTTGCAUCAAGAGCATCAUGT	76007	AGAAGTTTGTTTTUGTTGCCTCTGATUT
227991950	76008	GUGAGCGACGACCAGUCC	76009	GCTTGACGUTGACCCUCACT
227994902	76010	GGAGAGGUGGAGAGGCTUCA	76011	CTCACGTTGGUCGTCTTCTTGUA
227995723	76012	GTATGAACCCACCUCCCAUGAC	76013	GGCCACUGACATCAUGGCT
227998881	76014	CATATTTCTTACUCTCAACTGGTUCCGA	76015	GGTTAGTGCTUGGTGAAGACTTCUA
228000054	76016	ACAGCAGGAGUGGATCAAUCAG	76017	CCCATCTGCUGCAAAAACCTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228001452	76018	CCTCUTAAACCCAAUGCCCAGA	76019	GTGCCCCTUCTTCTTCCCAUAG
228001553	76020	CACATTTGACUGTTTTATGCUCAGCAA	76021	CCGTGTGAAAUGACTTACTGATCAUGT
228001706	76022	GCCTCAGCAGCGUGTTTCTUA	76023	TTGGTCTCCUGCGGTTUACAG
228004057	76024	AAGGCCTTTAGUTCTGTATGACAUCT	76025	ACATCCUGGAGGATTGTTCGUACT
228004159	76026	GAATGGCAATUACCTACCTGTTCUGT	76027	ACGUTTGTTTTTCUGGCGAAAGAG
228008295	76028	GGGCAUCAAATTCCUGGGACAA	76029	GCAGUACCAGCAUGACACCAG
228009583	76030	AGTGAATGCACGUAAGTATTTAGCTUCA	76031	CTGGCCAGUGCTAACTUGG
228009593	76032	TGCAAATCTGTTUCATTGTGACTTCTUC	76033	AAGTGAGTCUGAGGATAGTTCAGAUGAT
228009831	76034	TCTCCCAGAUAAGATGAATACTGUGGT	76035	TCATCCTCACTGUGTGCTATGTTTTAUT
228012459	76036	ACCTAGCCAGAAUTTTTCTCATCTTUT	76037	GAGCUGACAGGCGATCTUGA
228013043	76038	TTTCTGCTGCAAGUACTTCTGAUGT	76039	TTCACUGAGGCCACATGATCTUC
228015527	76040	TTTGAGGCGUCTTGCAATCUCT	76041	AACTAGTTTTATATTUCCAGCTTCAACTTUCA
228016994	76042	GTAACCTCAUAGAATCGGCAGUGG	76043	ACCCTGTCUGGGTGCUAAGAT
228017886	76044	CGAGTCTTGUCAAGAAGCATTCATCUT	76045	AGATTTCTCAUCACTCTTTCCACAUGAC
228018196	76046	TTGGTCAAGTCUCACATGGCTUAAT	76047	GCACAAGTTTUCCAACTATGAACTCCUA
228020040	76048	GCTGTTGCCTUTGATACTGGTTTUT	76049	GTGCAACTAAGUTACAGTAGATCUCACA
228023540	76050	GTTGGTGGCUTTGCAGTGAUAG	76051	CATCCAGGCCCACUAATCUAAACAT
228024756	76052	GTTTTTCCTCUTCCCACCCTUCA	76053	CGAGAAACATACUCTGACAGAGATGUC
228024922	76054	TGCTGTTTGTAUTTCCAGGCCUT	76055	CCAAAGUCAGGGTACGTUCCT
228026211	76056	CAACTACAGUCTGGGAUGCCAA	76057	ACCUGAGAGUCCGCAAAAGG
228030652	76058	GTGTGGCGCUGAGTGTACTUA	76059	CACATCCAUCTGGTACGUGGT
228034759	76060	ACCCCAGTTGUGGGTACCTTUA	76061	GGTCGGAGGAGACGUAGAGUT
228035285	76062	CCCACUCATGCTCUACAACCC	76063	GACAAGGAUGCCTGACCAGTUA
228040530	76064	CUCCCAGCAGGGACACUC	76065	AGUGTAAGCCUCGGCAAACAA
228043678	76066	CCTCCCAGUCTGGAGAUGAGAT	76067	CCACTCCUCCAAAAAGGCTUCAA
228043861	76068	AAAAUTGACATCAUCCCCAACCCT	76069	ATAAGTATGAAUGCCTACAGAACUGCAA
228046539	76070	ACTGTGTCUCAACAAGCCTUACAAAA	76071	GGATTAGAGUTGGCATACTUGGCA
228049669	76072	CACAAGCUGGCTGGGUCAT	76073	CATCCTGUGCCGAAUGAAGAAC
228055766	76074	GCATCACUGTAAACCTUGCAGACA	76075	CTTTCTUCCCTCTCUCCACCAG
228055971	76076	GAAGTCUGGCTTCTTGGUCGT	76077	CCTCCTCCTGUGATCTGCAATCUA
228057279	76078	GTTGGCUGCATTCAUCAAGCA	76079	CGCCTGCAUTGGATTCATGTUC
228063208	76080	AGAGATTAACCGUGCCGAAUGAAA	76081	CCAGAGGCAGUCTGAGUCAC
228064692	76082	CTAAGGCAATCCUGACATTTGCAUC	76083	AGTGTGACCCUGACCTCUGT
228066078	76084	GTCCACUCCAAUCCAGCCAT	76085	AATTGTGAAGGCAUGGTGTTGUG
228070439	76086	AGCTGTGTTAAUTTTATAGCAGUCAACCA	76087	CGTGCTUGGCGGGTAATTCTAUT
228070591	76088	CCTCGUACCCCTCCAUCAAC	76089	GTATAACCTTTCUCCTTCTCCCCCUA
228071498	76090	TGAUCAGGAAGAACUAAACAAGACCAAG	76091	CAACAUGCAAAGGCTTCUCACA
228074384	76092	CAGGCUCAGCAGATGAACAUGA	76093	TGCTGGAACUGGTTATGGTUGG
228074500	76094	TGGCAGGUCCUAGCAGAAGAT	76095	CCCUTGAGGACTUGAGGCAAAAA
228077410	76096	CCATGCAGAGUGAAAGGATAUCCC	76097	GCCTTTTCTTTUGCTTCCCTTGUT
228088143	76098	TCAGCGGCUCCACAAGUAAG	76099	AGAACCUCCAAACCTCTCTCUGAA
228093614	76100	CCTTTGGTUAGAACAGCAGUCAGA	76101	CCAAAGCGUACTGACTATUCAAGGG
228094922	76102	TCTGGCUCTCCTGCUCCAT	76103	GCCTCCUCGTGCTCGUG
228097582	76104	CCCCCGAAUCGGAATCUGAC	76105	TCTCAGGCUCGGTCUCGAA
228097614	76106	ATCAGCAAGUGAATAGCTCUACAAAA	76107	TTGTAGCTCUCATTTGCTGUGAGAA
228098565	76108	CAAACATCCUTACCAATTTTGUGCAGT	76109	AGCGATGTGCAUATATAATGGAAAGGUT
228098947	76110	TCAGAAGTCAUGGGAAATATUGCAAGT	76111	ACAACGUTAAGACTUACCCAGCAG
228099466	76112	CCGAAAUCGAGUCCGAGACC	76113	GGGCTUCGCAACTUGAGA
228099766	76114	CUCCACCTUCGGCCAGT	76115	GATCTTTGUCCTCGGGCTUGA
228100342	76116	CGACGCCUCCCCAAGUC	76117	GGCGGGUGGGCTTCTUT
228102396	76118	GGTGTCCACAUTCCTCACGUC	76119	GTTGAGGATGUAGGTGATGAUGGT
228103822	76120	GCTGCTGCUCTGCCTCUT	76121	AGCAUAGGACGGGAAGUGGA
228106314	76122	ACGGGTATTTCCUGCTTGTAGTAATTUAG	76123	TGGTAAGCUCCACGTTGAAGUT
228107297	76124	ACAAAGACTGUGAGGAAAGTTTCATUACAA	76125	ACAGTGTCACGAACUCCAGTAGUAT
228107362	76126	GGAGGAGAGUTGGUGAACGG	76127	AGAACATGCUGGTGAACAAGAUGA
228110050	76128	AACAAGCTGCUCTCTTGTGATUCT	76129	CCAAACTCACCUCTGACTTCTCUCT
228110560	76130	TCAATGATCAGGAAAUGCTGTATUCACA	76131	GGGAAGACUTTAGTGTCAGUCACC
228112207	76132	CAACACUGCAAACCACTTUCAGG	76133	TGAAATGCTUGGCGACTCCTUT
228116434	76134	CCTTCTGTCCUCGCAGGTUA	76135	GCTGCAUCCAAGCCCUCAG
228118059	76136	CCAGCAGCUGCCCAACTUA	76137	TCTTATCTCCUCTGGGTTTUCCACA
228122368	76138	GTGTCCUCCACACCAGAAUCA	76139	AAGACAGCCACUCAATGGAGTUAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228122834	76140	CCAGGCCUTCTTTGGUGACT	76141	CAGCCTTTGUGGAACGTCTUC
228123523	76142	GGCCCAAGGGUGACUCA	76143	GGCAGAGGUCUCCAGCAC
228124408	76144	ACCATTAATTGCUGTAAGATCTGCUGA	76145	TGCTGCACAUCAAGGTGCUAAT
228125907	76146	GTCACTCTCCUGGTCCATCUC	76147	ACCUGGAGGCCAAAATGATUCC
228130219	76148	CAGCAAGAAGGUGGAGAUCGT	76149	GAAACTCUGGCCACCTGUGAT
228132817	76150	CAGGAAUAGGCCCTGGAAUGG	76151	TGTCCCATATTUCCTTGTTGCAUCT
228132843	76152	GGTCATGATTTTCUAGAGAGGAGGTUCT	76153	CCTAACTUAGACTTCGGGUGGAAAAA
228133392	76154	CAGAAUATGCAGUACCCAAACCCA	76155	CTCACATGCAUGCCGATUGT
228137447	76156	CCATCTGTAGCUGGCTTTCAUACC	76157	TGTTTGTCTCCUCTTCATTGTCGTTTUA
228140361	76158	CAGTACTCATCAAUGGGCTCAATCATAUA	76159	GCAAGAAAAGUCAGAGCTAGAUGAAAC
228141845	76160	GCTGAAGAGGAGUTAGAAATTGAGAUGA	76161	AATTGCTGTUGCTCTCAGCCUA
228141972	76162	GGATGCAGCAUCACAUGCAA	76163	CTGTTGCUGAAGGAGUCGCT
228144654	76164	AGATATGTGGUGATGGCATGCTTUAA	76165	GCAGGAUGGATTCUGAGCAGAG
228147507	76166	AGGATTTTGGGTTAUCTTACTATTTGCAGUT	76167	GCATATGCUCATTGGAGTCAUCA
228148641	76168	GCATATGCTTACUGTATGGGACUG	76169	TCTGCTTTUGCGACTTACGAAUAGAT
228152251	76170	ACTCTGTCCUTGGCAATGAGUT	76171	TGCTCCCCAAUAAGGTTCACAUC
228152766	76172	TGCCAGTCUACAGGCCTAUCA	76173	GAGAGCGCACUTGATUGGAG
228153452	76174	CGGTCCCUTCCTCCUCACT	76175	TCTCCUCCGCCCCTCAUAC
228155185	76176	GTTTTCTTCCAACUGTCCTTGCUG	76177	CAAGCCAGGUAGAUGAAGAACAGAT
228157467	76178	TGCTTGACTUCCAACTGCTACTTAUG	76179	GCAGCAAUGGACATTTTGAGTUGAA
228161862	76180	TUCAAGGAAAUGAGGAAAGGGAACAT	76181	CAAGAGGTCCUGTCTTCAGAUGAAA
228162393	76182	GCCAGCAGAUCCCTAATTCUCT	76183	CAGCTACCAGUCCAGGATGUG
228162598	76184	ACAGCAAATTAAUGACTTTACCCTUCCT	76185	GAAACAAATTACCUTGCTTCTGTUCACA
228162941	76186	TTGTACUTGTGACAAATUAGCAGGGT	76187	ATTCTGTTTCAUCGCTGAGUGACA
228163085	76188	CCCACCAACAAAUTAAUAAGCCAAACC	76189	GTTCTCAGAGCUAAGTATCAAGGATTUCA
228165872	76190	CTCATCTUAGGCTGTGCTGUGAA	76191	GGGTGACCTUAAACAGATGTTACUG
228166776	76192	TCTTGAGATGCUTTTAGAGCTUCAGG	76193	CGGTAAAGUGCCTCCAAAGTUG
228171474	76194	AGAAGAACUACGACAGGCACUG	76195	ACCACCAAATACUTACAGGGATTCCUA
228171934	76196	GAGTCCTUGAGGAGTACCCAAUAGAA	76197	AGCGATGAATGUACTCTCCTGAGTAAUA
228175276	76198	GTTUCCCCACAGACAAGTUCC	76199	TTGCCATGCCUGGATTGCUA
228176804	76200	AGGUGAAACATAGGUACCCCCAT	76201	AGAGATGGCAGCUGAGTCATUG
228177075	76202	GCTTACCAUCATTGGCTUGAAAACA	76203	TCTTTACTCTGTCAUTGGTGGTTTTCUT
228195374	76204	CAGUGUCCCGAAGGAGAAAGG	76205	AACTTGTGGCAUAGACTGTTTGCUA
228201032	76206	GGTAGATTTGUTAGCATTTCCAUCAAGG	76207	CAGAGACTTTUGCCAAGGAAAUCAG
228206539	76208	GTTCCTCCTCUACCACACGATUC	76209	CAAGAAGUAGCAAGCTGGCTTUT
228212085	76210	CTGCCTGGUACTGCCCTATUG	76211	GGCATGGACUCAAACGTGUCT
228214219	76212	GAGATGCTTAAGUTCAATAGCAGTTUCC	76213	TCUCACAGCAGAGCAGTTUGAC
228214393	76214	CGAGAGCCUGTGCATTUCAGA	76215	CCTCCAGTGAGUCATGCACTTUT
228220296	76216	ACCCTCTGAAGCUCAGGTCAUA	76217	AGGAACUGTGCAAGAUGACCAAG
228224582	76218	AGCATGTCCTUAGGTTTTACCCATUC	76219	ACTGCTAACCCAUATGTCGTCTTTTUAT
228225481	76220	AAATGTCTAGCAAAUCCAAAAAGUGCAA	76221	GGCUGAAGGGCGAGATGUG
228226906	76222	GCCCUGGTCACCUACAACAC	76223	CCUCCCCACCAAAAUGAGAAAACT
228229141	76224	TCAGATTTCTCUCTCCTTTTCCUCCT	76225	CCATTGGUGGCACTCTCGUT
228232085	76226	CCAGACACAUGTCCTCCCUGA	76227	GCAUCGAGCAGGGCTCUAAC
228237968	76228	CCUGTCCTTUGGACCACACC	76229	ATCGCGTTUAGGCTTCATGAUACT
228243184	76230	ACTGGTATAAAGUTGAGTGGGCUAGA	76231	CCTGAAACTGTCUTCATCCTCAATGUAA
228247801	76232	AGAATTTGTTAGUGGCCTGGAGUC	76233	ATGAAGTUGGCAAAACAGACTGAATUT
228250309	76234	GTGAGCCTCUGGAAGTCGUC	76235	AATGTGTUCCCACCCCTTUCA
228252798	76236	TGTGGCCCGGCUATGACUA	76237	GCCTCCUTAAAGAAGTUCCACCAC
228261037	76238	CTGTTCCCACCCUGGCATUA	76239	GGCTGGAAUACTGCUACAACCC
228266244	76240	GGGCGAUGGGTTGAUGG	76241	TGCAGCUGCGGATGGAUAG
228266355	76242	GGGCGAUGGGTTGAUGGG	76243	CACUTGCAGCUGCGGAT
228267757	76244	GCTGCTCCUCTGGGTTGUG	76245	CCCATGGCCUCTTCTCCUG
228268495	76246	CCCGCTCAGUACGGAGTUG	76247	GCCTAUCCCCGGGACUAAGA
228274503	76248	ACTCACTGUCGCCTGCTTUC	76249	GATGGCGTUGTTGATGGCUT
228275541	76250	CGAAATGAUGAAGTCCCACGUGA	76251	GGCTTGUGCAGCTGGUACAT
228277925	76252	AGGTGGUCCCGGTCAUCA	76253	AGTCTUGGCAGCTGTUGCT
228278153	76254	CCTCCCCTGUTCCCATTACTCUA	76255	GAAGTTCAAAUGCCCTTCCAGUG
228280083	76256	GAGGAAAAGCUGCTGTTTCATUGT	76257	GATCGAATCTTATUTCTTAGCACCCUGT
228281272	76258	CTCUCCAAGGCCAAGTUGGT	76259	TUGAGCGACAGCCCGUT
228282140	76260	GGTGTTTGACCUGGTGATGCUT	76261	GAATGTACTCUGGAGCAGCUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228284244	76262	TTCCTTTTCCUAAGCAAGACGTTTTUG	76263	CAACTTUAGAAGGCGGAAGCTCUA
228285053	76264	CTCATCTACCUGACCAACCACAUC	76265	GCACTTGTACACCUTCATCTGCUC
228295080	76266	CATTTTUCAACCAGCGCAGUGT	76267	TGCCTGTCUCTCTTGGCTTUC
228295996	76268	CATCTUGTGGTATCTUCAGGAGGA	76269	TGACGCTTAATTTUCCTTTCCAACTCUA
228298283	76270	GCUGATGTGTUGAAGGCCACA	76271	TCACATTCACGAAGUCCCCTTUT
228301321	76272	TGGTCTCCCUGCTCAGTGUA	76273	TCTTGTTCTUCAGGAGATGATTCTGTTUT
228307739	76274	TTGGGCGAAUGCAGTTTTUCC	76275	ACTGATTTGTGAAUATGCCTACTGTUCA
228309377	76276	GTGAAAUGCAGCAGCCACUAAA	76277	CAGTCAAGUGGATGGCUCCAG
228314166	76278	TGAGTGTATACTCUATCAAACAGGGCUT	76279	AGCCCTATUGAGCCTGCTAAGAUA
228316772	76280	CGCCCGAGACUCACACTUC	76281	CCGCTGGUGACCCACTUAC
228319748	76282	CATGGTUCGTAAGGCAUGGG	76283	TGACCCAAGAUGAAATAAAACGTCUCT
228321124	76284	CCATTCTTACUGTTCTAGCTTGUCCT	76285	CACACCUGGCCAAGCTUAC
228329940	76286	CCCTAAGTGGCUTATCTGTGCTUT	76287	CTTCGCTUGGGCTTAAUGAGG
228332530	76288	GCCTTGGTGUGCATTCTTCUC	76289	CAGAGAGGGUCATCAGTGAUACAC
228333610	76290	TTACCATAGCUCCAAACGTCACUC	76291	GCCAGCCCAAAGACUCACATTUA
228336517	76292	AGTTTCTGCUGGGACAGGUG	76293	CTGCGCUCTGCTATCTAUCCT
228340627	76294	ACAGACGAUGCCACUGACAA	76295	GCCGCUACCGCACCUAC
228345756	76296	CUATCACAAAAUGAACGGACAGAACC	76297	GCTGACACGAUTGGAGGCUAT
228351347	76298	GCATTGUCAGAAGAAACCUGGAAG	76299	TGTGACCAGUTGTGUAGAAAGCAA
228355903	76300	GGCUGCCCGCTAUCCAT	76301	GGGTACUCACAGGGUAACGGT
228356960	76302	GAAGCAGGGAUTCAACCUACCT	76303	TCAGAGACATUCTCCTCCTACUCAC
228357335	76304	CGGCCUTCTGCCUAACGG	76305	AGGCCTGUCCAGAAATCTCUGA
228358167	76306	CCCAAACATCAUCCATCTATTAGCUGT	76307	GAGAAGGAAGACCUGGCTTGTTUA
228358514	76308	ATTGATTCCUTTCCCCACUAAAGCA	76309	CCTGACGCUGACCTGUCC
228359079	76310	CCATATGGCCUCTGGTAGAGTUG	76311	CUCCAGAAGGCAGGAAUGAAGA
228363818	76312	AGAAGTGTUGACAATGTTTTCUCCCA	76313	AATGGAGGUGCCUGACAAAGT
228369840	76314	GCTTCTCCUCCTGCTTGTCAUAG	76315	TGTTTTCCAACCCUGCATGTATCAUA
228377063	76316	GGTGTGTAGGAUGTGACACUCA	76317	GGATCCACCUCTGGCCUCA
228388569	76318	GTGCCCACCUTTCTCCCAUA	76319	GGGTUCCGAAAGAGCTGGUC
228389587	76320	ACAGTAAGGGAAGUATTTGGCTGUG	76321	TCTGCAGTTATUTGGTGAGATGUGT
228394031	76322	TGTTTGGACAACGAGUACAGTTTTAUCT	76323	GTTTAGAGTCCTCAUTGGCACTTACTAUG
228394314	76324	CCATAACACCCACCUCTGCUT	76325	CACTGGGCUCCCTGTCTUAC
228394464	76326	GAAACUCTTCAGCTUCCAGAGGAA	76327	AACTGTACCAAGAUCAATGGGAATTUGA
228396900	76328	CCGACCUAGTGCATCTTTUAAAACAA	76329	CATAGGCATUCCCAGTACAAAGTAUACAA
228397738	76330	ACCCATGAAUACCAGTGACUAGAAAGA	76331	CCCTAACTCUGAGTCTTGTTTCUACAG
228398999	76332	AATGATAACGGCAUCTTGGTAATCTUCT	76333	ACTCCAGCACTUTGGATATTGACTTUAA
228399064	76334	GCTTCAGACTTCUCAATATCTTCCAUGA	76335	ACTCTAGACACATAUACAAACATACAGCTTUG
228399362	76336	ACCTAGCAAUGGCACAGAAATUGT	76337	GACCAGTGCTUACATTTGGTTTTGUAG
228399992	76338	TCTTCCTTTGTAUTGCCTGTAAACUCAA	76339	CTCACTCUCATCTGCTGUGCT
228401508	76340	CAATACAGGTTTCUCTTGCTTTATGTUGT	76341	CTGATGGTGAUTGTTGAATACUGCAAAT
228405476	76342	GCCTCTCCCUCCATGCUCA	76343	GGCTCTUGATCTCCCUGCAA
228406832	76344	AGTGATGUCCACCCTGTUCCT	76345	ACCTGTGATCUCTTCCAGAGUCT
228407857	76346	TGAGTUGGCAACGCTGAACUA	76347	CCATGCCAACAUATTCTACAGTGTTCUT
228410883	76348	CAGAGCAGCUCCAAGTGTTUG	76349	CCATGCTGAGAUGTATAGGTAACCUG
228410885	76350	TCTTGAGGTAGUTGGAGAGATTUCCAT	76351	GGTTTCUCAGGCAGGCUGAAG
228412673	76352	CACAGAGCAUTCACACCCUCA	76353	GGGTAATCUCACCCCTCCUT
228414528	76354	ACTTCTTAACAGGUGGTTTGTTCUGG	76355	AATTGCAGTGAAGUGCTGTGAAUG
228416250	76356	AGATTAAGUCCCAAAATUCCCAGGAG	76357	TGCTCCACCAACUTAGAACAATUAACAA
228418200	76358	CCTTTGTCTTTGUTCTGCATTTTGUCAAT	76359	ACTTTAAGCAUGAACACTCACTCCUT
228428556	76360	CCACCCCAUAUGCCACACAAA	76361	TGGTCTAACACAGCUTCATTCTTCTCUA
228434291	76362	GCTAACCCCUCTTACCTTGACTUC	76363	GGGACAACAATCUTGGCTATGTAGTUAT
228442590	76364	GTAGAAGAGAUGAGTCAGGTUGCT	76365	TGGAGCCUCTAAGGATCUGCT
228448200	76366	TCCAATATCCCCAUTTATAGCTGAGUCT	76367	CGCTGGUGAGGAUAACAACAC
228449482	76368	GCATGCTTGCAUACTAAACGGTTTUT	76369	GCAGAACCAAGAAUTTTAUAAGAACGCA
228450133	76370	GTAAATGGUGGTCTAACTTCUGCGT	76371	TTGCCTCACGUAGAGTTGTAATCUG
228462338	76372	GAGGCAUCAGAAGUGGGAAGAG	76373	CCGCAGTTUCTCATTGAGGUAGAAT
228468412	76374	GGGACTCCAAGUTTTCAGAAGUAAC	76375	TCTAGCCAGGAUAGATGGAGAUAGGA
228470998	76376	ACGGACACCAGCUTCCTCTUA	76377	CGAACCGACUTCTCTCCGUAG
228471147	76378	TTGAGATCATCTCCUAACTCCCTATGUC	76379	GTACATCAGGGUACTTTGAACATUCCAT
228471264	76380	GTCTTTAGGCAGGUGTGTGUGA	76381	GUCCGAGGAGGACAATGUCAAG
228474926	76382	TGUCTGCCGTUGAAGAGAGG	76383	CCTTCTCAGAUGGAGCCAGGATUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228475831	76384	GGTCAGGTGGUGGCAGTAGUA	76385	AGGAAGTATGGCUCCCAAAGATTAUAGA
228481137	76386	TCTTGTTTTGGTAAUCTACAGCCTGUT	76387	CGTGTTUCGGAATGTCCUCAC
228486714	76388	CACCACCUTGTCCCUAGACC	76389	GTAGCATCTCUACCCCAAAACTGTUT
228487585	76390	CCAGTCAUCCAGAACTUCAGCAG	76391	TGTCTGAGTGTTUTGTTTTGGTTTTCUT
228491214	76392	CCAGCCAGAUTATCCTTTCUGAGT	76393	TCAGUGGCGGTTCTGUGG
228492247	76394	TCTCCUTGCATCTCUACCACAGA	76395	TGAATTGTTCTTTUAGTAGTCACTACGTUGT
228493439	76396	GGTCGCCUGTTTTGGUAGGT	76397	AATTTGTAATAUGGGCGCATAACATGUG
228494382	76398	TTCTAGAAAACUGGTATCUGCAGGT	76399	ATCATGCATCUCCAAACTCAACUCA
228494752	76400	CGGUCCGAAAGCTGCGUA	76401	AGCAATTTCTTACUCTCTCTGCAAGTUT
228498071	76402	CCGGTCAGGUTTCGGTGUA	76403	CTCTTCTTTTGUCCCCTGGGUAG
228500518	76404	ACAAAGTAUCTCGTGACUGGGAAGA	76405	CAGTTCGGAAUGCACTAAATTCAGTTUT
228511354	76406	CCTGAUGGTGGAATAUCACAAGAACA	76407	GTGTCGAGCAGUACTCTAAACAUGAG
228515237	76408	CAAACTAGCCCUCAATCCCUGA	76409	CAGCAGUCTCCGCAUCGT
228520120	76410	AATGAGUGAGAAAGCACATCTGUCA	76411	AGAGAUTACATATCCUGGGCAGGT
228521634	76412	GCAGCAGAAGAUCCGGAAGUA	76413	CATCGCUCCGCTAGGUGT
228528732	76414	TTTGTTGCTGUGACTTCCCCAUA	76415	TCGTCACAAGUCCACAATGTAGAAUAG
228532997	76416	CCAGGAACCCUTTTATGGCTUCA	76417	ATGACAGCTCACCUGTCTAAATTCTUT
228533196	76418	ACGTGGAGTAAUACACCTATGAAGUGT	76419	GACTTCAUCCCATACCTAGUAGACCA
228534174	76420	AGAGCTGGACAUTGAGGTCTUCT	76421	TCAGTGTCACAGUGTTCTTTGUGAA
228537413	76422	TCCCCCAUCCUGGGACAA	76423	ACCTGTTGUGCTCACTGCTUAG
228538049	76424	CCGTATTTCCGGUTACTGAGACTTUG	76425	TCCTCCCCACAUACACCATGTAUT
228543907	76426	CTATTACATCACUGGTGCGTUGACT	76427	GCTCCACAAAAGCUGAGTUGG
228553361	76428	GCGAAGCACCAGAAAUCAUGGA	76429	TCUCCACACAGGCCUCCT
228562186	76430	CCTCTCTUAACCCCCTTCCCUA	76431	TGATGAAGATGAUCGGGAAGCAUAAG
228565229	76432	CCCACAUGCAGATTCCCAUCT	76433	CGCATATGGTAUCCCTCAACCUAC
228566289	76434	CATTTAATUACCCTACAGGUGAGAGCAA	76435	CCCTCCUTGGTAACUGAGACC
228568810	76436	GTCUGAGGAGCCCGTGUC	76437	TGCAGGTGUCGAAGGAGUAGT
228570701	76438	GGGTAACCUGCGGGAGTUT	76439	CTTCUGGGAGGCCAAGTACUC
228571915	76440	CCCCCAGCAGGUTGATGATAUT	76441	CAAGTAAATGAGUCTCAACGTGTTCTUT
228573792	76442	CCTGGGAGUCCCCCUCA	76443	CTGATCCCAUCCCTCCTTUCC
228574154	76444	TGGTGTCCUGTGCCUACCA	76445	GCAGGGCUGAAGCCTCUC
228586085	76446	CAAGGAAUTTGAUGGGAAGAGCCT	76447	CAGAATGGCTUACCTTCTCAACCUT
228587413	76448	GGGUGCCAGAACCACTTGAUT	76449	CCCGTTCTUCATCTCCTTUCCAG
228602982	76450	TCTGCAAGCUCATGAAAGAAATCTUAGA	76451	AGGCAAGAAGGCAUGAAACAGUA
228609358	76452	AGCATUAAAACAAGGAAAGCAAAGUGG	76453	ACCTCTUCCATCAAATGTUCACAGAAA
228630698	76454	GAGAAAAGAAAGAGACAUGCATGAACAUT	76455	GTACTUCCAGACCAGGGTGUT
228631538	76456	CCUGCCCTTUGCCCAAC	76457	GGUAGAGCACATUGGGCACAAA
228636601	76458	GGCAGGAGUCAUGGGAGAAAAC	76459	AAATGTTCTGTUCTCCTTCACTTUCCA
228637488	76460	CCACCCGUGTCCTTCTTCUA	76461	CCTTTGTUCTTCCCTCUCCACAG
228644290	76462	ACAGTCACCCCAAUCACCUACA	76463	TGAAAGAAGACCAAACUGAGTACTUGG
228652178	76464	GCACAGCAGAUACTGCCAATUT	76465	AATCCCTTGGAGUTGATGTCAGUC
228652940	76466	GGAGCCGGGCAGUTACTUA	76467	CACATCCAUGGAATATGTTCTTTUGCAT
228655984	76468	CTTCACAATCUCCTTTATTCTTCGTUCCT	76469	GGCGTTGAGCACUAAATTGAATGTATUA
228666460	76470	GGAGAGGAGAAGUGTAGGGCTUA	76471	CTCCAATTCCACUATTTACCCCUCAG
228669968	76472	CGTAGTGAAAAUCCTCCAGACUGT	76473	GACCATGACAGAGAUTACGAAGAUGAA
228671793	76474	TCUGCCTTGAUAAAGGAAACCAAAGAA	76475	CATCAAAACUACTTTCTGGUCAGAGAGA
228677473	76476	TCCAGCATTTTCAUCTTTCTTCATCAUCT	76477	ACAGAAGTCAGAAUCTCCACGTGUA
228683242	76478	GTCCAAAAGUGTTAAUGCCCAAGT	76479	TTCACTGTAATCUCTGGATGTTTTGUGT
228687797	76480	CACTCCATGUCCTCGTTTACUGG	76481	CCCTCACTGAACCUCTGCATATTTUT
228691940	76482	CGTGATCCUGCTGAACAUGGA	76483	CACATGCGUCACTTTCTTTTTGUG
228698614	76484	CCAAGACUCCAAAGCCCAGUA	76485	GTTCAGCCAUCCAGAAUGGGT
228701017	76486	CTTTTGGAAACAGCUCCAGGTTUT	76487	CTGAATAAGATUGAAGCGGCTCUG
228702319	76488	TGATGTGTAATUACGAAACCCUGACC	76489	GAATACTGTTGCUATGGTGATCTTCUCA
228704890	76490	CCTACCCUTCACCAGGUCCA	76491	CCCCCACAGUAGCTTUCCA
228705004	76492	CCACCUGAACCGAGCTCUT	76493	GCGCAGGUCCCAAATTTUCAC
228706599	76494	GGAGGGAGGUCAGGGACUA	76495	ACTGCCCUCATCTCTCUCCAG
228707482	76496	GCCGCACUCTAGTAAGTGGUT	76497	AACAACTGCTTUAACAGCTGCTTUT
228708504	76498	CTCCTTCTTGAUCCTGGTGGUG	76499	ACCCAGCUGGTCCUCAAAG
228708699	76500	CCCGUGTCCTGTUCAAACACT	76501	TCATCACACAATCUACATCTTCTGCAUT
228709018	76502	GGCTGACGGGUTTCCTCTUC	76503	AATGGACGUGGAUAGCAGCAA
228709192	76504	GTCCAAGTCCUGTGAAATTTTTCTCTUT	76505	TGAAATAACAGTUTGCTTTGTGTAUGCC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228710582	76506	TTGCAGTTAAGUGATTATATGGGAUGAG	76507	ACCTTTAGCCUCCAATTATCTCCTACUT
228710892	76508	GCAGAGATCCUGCATATTTTGAUGAAAA	76509	CTTCTAAAGCUCACTGGACACAUC
228714017	76510	CACAGACAGGUTCTGGTUGGT	76511	CAGAGTGTCCUTTTTGTGAGAAGAUG
228714798	76512	GTTCTAATCUAAAGGCTGTCUAACCAA	76513	GACGTGTGGUCTTACGGAGUAT
228720538	76514	CAGACAAAGCCCAUTTTTCTUCCA	76515	ACCACAGUAGGCCCCAATTUC
228721900	76516	CCUGCUGGAGAGCCAAGT	76517	AGCTGAGACCCUGCCUGA
228725988	76518	CACAGCCUCCGTAGAUCAAACA	76519	GGAGAGATGAGGUCTGGGATAUCA
228726104	76520	ATTTTCCACUGCTCTUGAGGCT	76521	GGCGCCUCAGAGCTATUACC
228727185	76522	GGAGUCACCAGGAACCGTTUA	76523	CCTCTCCCTUTCCTCTGTTCUCT
228732352	76524	CGCTTCUCCAAGTCCCCATUG	76525	ACCCTCCTCTUGTGTATCTTTCTUACAT
228732632	76526	ACCACCUGCATUCAGGAAAAGT	76527	GCTGTAAATTCUGGCTTATAAGGTGTUC
228733500	76528	CUAAGGAGAAGATTUCCCACAGCA	76529	GTTTTCAUGCCCTTCTGCUCAAG
228736616	76530	ACTCAAACAAATACUAAGTTATGCTAGUACAA	76531	TGACACCUCGACATTTGAAUCAGAAG
228739614	76532	GTTTTGATTUCACCCTCTCCTCUCT	76533	GTAGUAGAGCCCACAGGCATUG
228741312	76534	CACTGCTUAAAGGAAGCGCTUT	76535	GCCCAAGAGGCUGTAGTUGAAAT
228741519	76536	CTGACTGCUGTGACCCACUC	76537	TTGCACTTGUCCACGCATUC
228742456	76538	ATGATCCUCTCTCTUCCCCCAAT	76539	CTGAGCCACAUAGACTACATCCAUC
228744254	76540	CGTCTCTUGCCGGAATGUCAG	76541	ACAGAATGCCUGTAAAGCTAUAACAACA
228746318	76542	CTCTGGAGGAGGAAUGCCAAUG	76543	TTTGCTGGUCACCAUCAGGAA
228747837	76544	GGCCGCUAGCTTTUCAGACAT	76545	GAGGCTUGAGCAAAUGAGGGA
228751448	76546	TCCATTTCUGAAACAGGCATGUCA	76547	TGATGCUCATGTCTTTUCCACCAG
228752557	76548	CGAAAGTTGUGTAACTGTGTTTUCCA	76549	AGTGTAAGTGUGAACACCACAAUCT
228755568	76550	CAGAAAGCACCGAUGCTCUGA	76551	CAAATGCTTUGGAAGAAGTCTCTATUGA
228758323	76552	AAGGTTCCAATUGCTCTTTTGTTTACAUC	76553	AATTGTCTGAGAAGGAUCGAATGCTTUA
228759659	76554	TUTAGAATTCTCUGCAGCACCCAA	76555	ACAGGGCCCAGUAAATCTCUCA
228759872	76556	CAGGTAAGCTGUGTGATATTAACCGTUA	76557	TGAGCACATGUCAAGAGCAAATCUT
228760046	76558	GGGTTCTTTATCUCTCTCTCTTTCUCA	76559	CCACACAGCTAUCTCATAAGGTCUCA
228764124	76560	TTTGGAGACAAAACCUATTCACAGCUA	76561	GTTCCAGAACUCCTCGGTTATUCT
228765454	76562	CATGAAGCCAGCCUCAATTGUC	76563	ACTAGGATGATUGGAGTGTTGTGTTTUT
228765905	76564	TCCACACCCCCUCUAGGAC	76565	GCTGUGGGAAGAUGCCAGAAAA
228766607	76566	GCCACCUGAATACAGGTTAUCAGT	76567	CATCTATTGCUGGCACCATCUGA
228766717	76568	CAGTACGUACCAGCGATGAATCTTTUA	76569	AGGAAGAAGATUTCTCTCCCCAUGT
228767305	76570	CTCACAATGACAGUCACCTGATAUCAA	76571	CGGTGTGGGAGUATTAGATTGGAUG
228767432	76572	GTCTTGCCACACAUCCCTUCA	76573	GTTAATAATCACAUCCTGCTTCACUCAC
228768728	76574	AGTCGACTAGAUGGGAATACAUGAT	76575	TTTTUCCAGAACCGAAUGGAGGAA
228770787	76576	CCAGAGGCAGACUACAGCUGA	76577	GTGACCATGAUGAGAAGTCUCACAAAT
228773031	76578	ACATGAACAGAAACUTGAAACAAAATUCCA	76579	GTCTTUAAGCACAGCTCCCUGAAT
228773918	76580	GAGACACAAATAGUTGGCAAATTGAUGT	76581	TTTGGAAAGAGGGCUCAGAGUC
228774349	76582	GGTATTCCTCCACUTACCTGTTTTGUAA	76583	CAGGGACAGUGTACGAAGCUG
228775790	76584	TGAATTCATTTTTCUGCACAGGATCTUT	76585	TTCTGTAGUCTACTTTGUCCCCAGT
228783762	76586	GCAGTATGGCAGUTCCTTGGUT	76587	CCTGAGGUGTTTTUGGAGGCA
228784339	76588	ATAATCCAUTGCCTGTCUAAAGAACACT	76589	TTGCAGAAUGGTCGATGUAGGG
228785921	76590	GGTGGCCCAAAGUAAAGCUG	76591	TTCTGCCCAUTCATCTTGTGAUAGAG
228786007	76592	AAGCAGAUACATCCACTUCCACAG	76593	CCTTAGACCUGCAGTTTTCATGAAUT
228790709	76594	CAGGTATUGCAGTTCTGUAGGCA	76595	CCACUTTCTCUGCCACCAAGT
228793209	76596	ACAGGCCACUACCTAUGCAAC	76597	TCCTATATAAUGGGAAGATGTGGCTUCT
228796687	76598	GGCCCUCCCCTTCTCCATUA	76599	ACTCTTCCUTGCTTCUCACACAG
228796869	76600	CCGTCTCTUCCACTGAAAGUGT	76601	AGTTTGTUCCAGGCTGTTCUCC
228798297	76602	CCTGCCUGGATCAGTGCUAC	76603	GGTGGCUCATGCCTTUCAAGA
228799359	76604	TTCATATTTGTTTTUGATGTCCCCCTUG	76605	ACGTCGATCGUCCTCAATTCAUAAG
228801263	76606	GTGCTGGAGUCATTAACTUAGAAGAGAA	76607	AGACGCTGATUCAGCATACTGUG
228801564	76608	CATTAAGAGGUAGAACACAGTATGCUGA	76609	AAGTCTGGTTUCATGTTGTCTCUACAAA
228805660	76610	GCTACTGUCCCCAUAGGGAGA	76611	CACCACTTCAGAUTACTCAGTTCACTUA
228806351	76612	CTTTTAGCAGGGUGGAGAGUGT	76613	CTTTCCCUTTGTAGAGUCAGCGT
228811161	76614	TGGTGTUGGCTTTTATTCUGCCT	76615	CCAACTACCTUGTAACAGAAAAGCUAAC
228812034	76616	GGTGAAGTCUTGTAATCAACUCAAGCA	76617	CCTTTTGCTAAGAUTCCACACTTUCCT
228812840	76618	GAGAGUACCCCUGCAGGAGA	76619	TCCCACUGGGAAGCAGAGUA
228816570	76620	ACCTCUCCAGAGCGTGTGUA	76621	AGATCGAGGUGCCTCTTCTATTUCT
228818307	76622	GAATAAGCAGTUCTCCCACACTUCT	76623	TTATCTCGTUGCATGGCTCTUCA
228820941	76624	GAGCGCUCTAGGTTGCUGAT	76625	CTCAGTTGAACCUCCGTATAUAAGAAAGT
228823341	76626	CAGAAGAGCGAGAUCCGAGUT	76627	CCTCATGAUCACAGCCTCCTUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228827336	76628	AGCCCCGACUCCTTACTTTUACT	76629	CAAATGACCCACUCAGAAAGAGTAGAUT
228829961	76630	GACTTUGCACACAAAACACUGAG	76631	CUACCGCATGUACCAGAAAGGA
228831085	76632	CCAGATCCTAAUTTCAAAAGTTGUACCC	76633	TCCCTGCTUCCTCCCATCATUAT
228833383	76634	GCTTTCAUGTTTCTTGUCAGCCAT	76635	GGCCAGAAAUCACCCUCGAAA
228834071	76636	GAGACCTTGGUGAGCCTCTTUA	76637	CATGCAGCUGAAGGAAAAGAGTUG
228834105	76638	AGTTCTGTCTUAACATGCAGGGTUT	76639	CCAGAGGTTUCCAATGTAGTUGGG
228835894	76640	GATTAACAAGUGCAAAGGAATTGCCTUA	76641	TCAAAGGAAACUCAATGCCCTUACA
228837269	76642	CGGCCATTAAUTCGAGACTGTTUC	76643	GAGCCCCUTCTCCTGCTUAC
228844690	76644	GGATTGGUGGACGTCTCCUG	76645	CAACGCTTCAUGCTCCACTACTUA
228850312	76646	CATGACCGGCUGCTTTGUC	76647	GAAAATGTCGUCGGCCAUGAA
228850403	76648	TGGCTCCCAUGGAAAGAUAAAGG	76649	ACAACTCGGUGGTCCTGUACT
228856206	76650	AGGCTTCGTGUCAAACTCTAGAUG	76651	AGCTGUGGGCACGUCAG
228857053	76652	CAGCGTGGUCGTAGGUGAA	76653	TCCTTTCTTTCTUTAGCTTGAGAGUAACC
228857751	76654	TTCTCTTTCACUTCCTACAGAUGCAC	76655	TCAGAAAUGCAGGAAAGCATCTUCA
228865671	76656	CTACACCUGCCACATGGATGUAT	76657	ATTGAGUGCCACCCUAAGCC
228866715	76658	CAAGCCCAGAGAAAUAGCACUGA	76659	ACAAGUCAGGGAAGAAAACAUCAGG
228871697	76660	GGTCTCUGCAGTGUCGAGAG	76661	CTACTAUCACAAACATGCCTUCAACAA
228877049	76662	AACAGUGAAGGGTATGTTUGAAAAAGT	76663	TGGACAAUCAAAACTTAACTCCUGGAT
228878666	76664	CCTTCAAAAAGTUGGGAGTCAAAGUAT	76665	TCCAGTGCAUCCATGAACTCUG
228880608	76666	GCCCCACAGCAUGGACAUA	76667	TCCTGGTGCUGAAGGACTUG
228887501	76668	CAATGTAGCGGUCCACCUGAAT	76669	GGGAAAAGAUAGGACTTGGGCCUA
228888648	76670	AGTCCAGCTUCTTTAGCTGCUT	76671	GGTTGUAAGGCCCTGCAAUG
228890575	76672	GGCUGCTCTUGCGAGGT	76673	CTCGTTCGCUCTCCAGCUT
228890947	76674	CGUGAUGGCCGAACCAGAA	76675	CATCAGAUACACAGACATGUGCCT
228892223	76676	GGCCTTGGUAGAATCGACTATGGUA	76677	GGGAAGGCAAGUGUGAAGAGAA
228897936	76678	AAATACAGAGCACUTCGGCTTAUGT	76679	AAAGAAATAGGGCUTCTGACCTGUG
228900893	76680	GGGTGCACUAGGTACCTUAACT	76681	GCCTTTTCCTGUCTTGATAATTCTTTCUG
228905439	76682	AACATTCAGCUGACTGCUCCA	76683	ATGGGTCAGGAUACTCTGAUGAAGA
228905712	76684	CATTTTTGTGCAUCTTTGTTGCUGT	76685	GCACGTACUCACCATTTGTCTTUG
228907146	76686	TGTCCUACGCGGACCUGA	76687	GTGGGUACGCACCTUCCA
228909210	76688	GCGTGCCCUACTTCAAGGAUAA	76689	AGCGCACUCCGACGAAUC
228909796	76690	GCCACTAGAUAGTCCTCUGGGAT	76691	CTTACCGTCCUCTCTTTCCTTTGUAG
228913018	76692	CCAGAGAGCUTCAGCCATTCUT	76693	CACAGAAUGGAUAAGCCAGCCA
228914987	76694	GGTGUAGCACAACAGACACUCA	76695	ATTGTUTTCCTGTGAUCCAGAGCA
228923437	76696	GATCTTCATCAUTGTGGAACUCAGGA	76697	GCAGCTCUGACTCTGACUCAT
228928112	76698	CAAATGCCCAUTGACTGTTGCUT	76699	GTTAATGCAUGCCTCTTCCTTTUCAG
228928425	76700	CCTTACAGUTCGTTGGUGCAGT	76701	GCCGTGCTUTCTCCTTTTGTUG
228935464	76702	AGCTTGGUGAAGCCCCTTTUA	76703	GGTCTGAUGAGCTGCTATTGTUCAT
228938894	76704	GGACCTTCCAUTCAATAATGAGUACAC	76705	GAAGTACAGCCCAAUGTAGAGUACAA
228941477	76706	GCTCAGGGAGGUTTTGAGUGAAAG	76707	ACCCTACTTAUTCACCCCCUGAAG
228941652	76708	AGTAATGATGACUAAAGCAAGGGATUGT	76709	GGGATTCCGUCATATGGCTUGG
228944033	76710	CTCTAACTGCUGTACAACCUGCAT	76711	GCCTAGTTTATGCUTAAACATCCTGGUA
228953917	76712	GGGAAGGAACGGUCACCUAC	76713	TCUCTCUGGACACACAGAACCT
228955869	76714	GAAGCCTCCUGGACAGACUAAA	76715	CAAAGCCACUGTCAAACGTGUC
228956773	76716	ACCTTACCCUCATCCTGTGCUA	76717	GGTGGCAGCUGTACACCUC
228956984	76718	TTTGGGAGTUGATGACCTTUGGAT	76719	GACAGACCCACCAGUCACUC
228957137	76720	CTGGCCGGCCUGGAUAT	76721	GGTCCAGGGCUCGAAAGUG
228960740	76722	GAGCUGGGACCCUGGAG	76723	CTUGGGCACACCGUCAGA
228961855	76724	CUCACGGAGCUACAAGAACCA	76725	GCATCUAGCACAGTCACTGUGT
228964552	76726	CATACGGCCUGGTGTCCAUT	76727	GCATCCAAGAGUGGGTCCTCUA
228966197	76728	CCCTGGACCUGGATGCUG	76729	CAGTCCUCCCCATCUGCAA
228966707	76730	CTCAACCUCCTCTTCCTCUGGAT	76731	GTTAUGAAGGAACCTGCUCCAAGA
228967394	76732	CCAGTGGGUGGTCATTCCUC	76733	GCTGCAGGUGTCTTCACAUCA
228970654	76734	AGGUGGCTGUGCGAAGAG	76735	CGGAGUCGTCCCCUGAG
228971278	76736	CGCCTTUCGAGCAGTACUCC	76737	GCTAGGGACCCCUCACATUGT
228971628	76738	TCCTCTTUCAACACCTCUCGGA	76739	TGTTTCAGTTUCAGTTCCTCATGTUCA
228973959	76740	ACAUCCTTAATCCUCACAACACGAAC	76741	GGGAGAGAACAAUGAUAAAGAAGAAGAA
228985079	76742	GAGGAGCTCGAAGUTTCATCTTTCUT	76743	CGGCTUCCCAATAACAGUAGCAG
228987188	76744	TCGGGCCUCTGAGAACAAUC	76745	GCTGTTGAUGGTCTGTTUCCAC
228993618	76746	ACACCCUAAGACCCCATCUCAG	76747	TGGGTCCUTGAGCUAGGAAGA
228993942	76748	TTTGCAGCAATUAAGTGAGGCATUT	76749	GGACCUCAGAGCAGCCAAUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
228995216	76750	TCCTTTGATUCCAGCACATTAAUGGT	76751	CCCTGATGTUGACATTTTTCATTUCGT
228995302	76752	TCACCTGAAACAUTTTTAGCCATUCCT	76753	GTACCACUGGGCTTGUACCAT
228995997	76754	CAAAAGTTGTUGGTGTTGCUGAAC	76755	TGAAATATGCCAGAUCATCATTCTTTGUACT
229005560	76756	GTGGCUAGCAGCCTTGTTUG	76757	CGUGGTTACUGGGAGGAAGAG
229011428	76758	AGACCUTCATCUCCACCCAGAT	76759	GGCACAGCUGUCCAGGAAG
229017893	76760	GGGAGGGUCCAGTCGUAGT	76761	CCCTCCAGGUGAGCTCCTUAT
229021753	76762	CTGCACTACUCCTCCCTAUCCA	76763	AGTCCCUCCCCAATUGCAAAG
229022653	76764	CGGGTCAUGGCCTUCACAC	76765	GAACTCCCUGCCGTTCTUCA
229023268	76766	AACCCCACUCCCTCCAUCT	76767	GUGAGUGAGCGGAGGCA
229038654	76768	GCAUGAAAGCAGUGGGAACCAT	76769	GAGACTAATTUCAAGCCCTUGGGA
229040206	76770	CGGAACAGTUCACCCCAGUA	76771	CTGGACAACAAACUAATTAGCACTTTUCA
229042522	76772	GGGAAGGAGAGAUGAGTCCAGUA	76773	CCCATGUCATCGTCCUCCAG
229045339	76774	TCUCCGGGCUACAGCCT	76775	GCGCTGCUCAGCTGUCT
229045535	76776	ACCCCGGUGTCCCAGUA	76777	GAAGTGGUTGTCTCCUGGCT
229046897	76778	GCACCTUCTACCGCUCACT	76779	GUGUGACCGAGGGCACT
229050467	76780	AATAGCAAAGGUCAATTUCAGCAAACAT	76781	TCTTCTTUCCACCTTGTUCACAACA
229051666	76782	AGCATTAGAUACACACCTAACGTTCUG	76783	AGAGCAGCGCAUATCATTATTUGGT
229052979	76784	TCUTCAGCUCACAGGGAACCT	76785	CATCTUACCAGGCAGUCGCT
229055506	76786	CCAGUGACTGCUGCCACAA	76787	CUAATTGACAGCUCCCCCACA
229057986	76788	GGACCUGCAGGACTUCCAAC	76789	GCGATCUCGCGATCAGTGTUT
229059179	76790	GUGGACACAGUCAGCCAGA	76791	CATCCCCUCCCTCTGCTUT
229063412	76792	TGTAGUCCCCGCCTTGTTUC	76793	GGGACTCCUGCTCCTCTUGT
229068919	76794	CGGCTCCTUCCGCTAAACUC	76795	GCTTGGAGACCAUGATGTCCATAAAUAA
229069206	76796	CUCCCCTCTUCCACGAAGT	76797	CCCACCUACCCCTCCTATGUG
229070337	76798	GAGAUTGTATUACGCCCCAGGA	76799	CCUAAAAGGCGGAAATATUCAAGCA
229072319	76800	TCCUTCUCAAGGGCGACAAG	76801	CTGTCAGGUTTAAAGCCUACCCA
229075496	76802	GAAGAGTCCGCUGCTGTAGUC	76803	GUGTCACUGACGGAGAGCAT
229076909	76804	GGGACTGCCACUTTCCATCTUC	76805	GCCACCCAAAGAAGUGTCUCC
229077372	76806	GGAACUCAGGAGCUCGGAAA	76807	CTCGUCCACCAGCAUCAGG
229079003	76808	CCTCCCUGACACCCTGUGT	76809	CAGGTUCGGCTCCCUCAG
229081028	76810	GTTTCGCUGCGGCACUG	76811	CAUGAGCACGGCCACAUT
229081504	76812	CCGTGGUGCTAGGGUCA	76813	CCUGGAGGCCCACTCUCT
229081669	76814	CUCCAGCCAGCCCAAUGT	76815	CTTTCTGTATUTCTCCATGGUCCCAA
229082232	76816	GGUGGACAUGGCCAGCAA	76817	CCTCTGCUGACCCCCATUAC
229089321	76818	CCCCTCCTUCCAAATGGACTUA	76819	TTCCATTGGTUATACAGGACAUGGG
229090101	76820	GGTGTTCTGTUCTCTCCCGTUT	76821	CATTTTGAACUCCCCGTTGGUC
229093790	76822	CCAAGCCCUCGAGCAGTTAUT	76823	TGCAATGTTAGTTUTTCCCCCTTTCAUA
229095982	76824	CAACGCCAGCUGTAUCACCT	76825	CCGTGCACTUTGGTCATAATGTUT
229106647	76826	CGGGCCCUCCGTTATTACTATGAUAA	76827	TGTAGGAGATGUCAGAAGGGTACTUG
229108204	76828	CCTGCUCCGCACCTUCAG	76829	GCGUGCCCTACTUCAAGGA
229109703	76830	GAGCTGTTGCUGTCACCCTUA	76831	CGCAAGAGCAGCUCGUC
229111222	76832	CUGGAAGUCCCCGCACA	76833	TCAGCGCCGACUTCAUGAG
229111677	76834	CCTCCAGCAAGCUCAGGUT	76835	GGCCGGAGUTTAGCCAGUC
229114711	76836	TCTCACTGCCUGTCTCTGGUT	76837	CCTGTAUGACACCTGCATUCCAC
229121332	76838	GCCCTGGGAUCAAGAACCTUC	76839	GCATTGTGUCTTGGTGGAUGAC
229122311	76840	CGACCGAGUCGTCCATGUA	76841	AGTATTGTGAUGCGGCUCCA
229127456	76842	CCAGCGGGUGCCTUCAG	76843	GGCCTCGUGACCACUGT
229134027	76844	GCCCCAGGCAGAUTCCTTTAUA	76845	CAGATCAGGGAGUTCATTTGGUGAT
229143130	76846	CTGTCACTTCCUCCAGCTTCUT	76847	AGCTAGAAGGCCACUGATGAGUA
229159917	76848	TCGCTTCAGCAAUGCAATGATAUG	76849	AAAAACAGGCCAGCUATGAACTATGAUA
229160551	76850	AGAGAGAACUGGTCAGCTGCUA	76851	GCCTTCUCAGCAAAGAGACUAGAGAT
229169527	76852	GCGGAGUGAACGGCTAAGUT	76853	GGACATTTTTGUGGGTTTGGAAGTAAUT
229180702	76854	CCAAGAACCCGCAUCTTGUCA	76855	CTTACGTCUGCCTCTGTGUGT
229184746	76856	AGUAGACUGGCCCACGAAGA	76857	GTAGCAACGUGGAGTTCATGUG
229198434	76858	ACTCTGCGUGTGTCTCACCUA	76859	CATTTTGGCCUCCATCTTCACTUC
229208392	76860	GCGGGTCACUGTACACCTUA	76861	CCTCTTTAGCCAUGGCAAGGUC
229219217	76862	TTCCTTTCTCUCGGCTGCAUT	76863	CTCTTCGAACUTGGGTAAGACUGG
229222079	76864	CCATTGCUGAGAAGCAGCCUT	76865	TGGGTTCCTAUACTGAGGTCCUAAC
229225984	76866	GTGTACTTUCCAGAGATGAAGCACUAC	76867	GGTTTAAATGTGUCTGAATGTAGCAAUGA
229226368	76868	AGTGTCAGCTUGAATTAAATGAGGTCUT	76869	TTTCCGAATUCCAGTAGTGGAUGG
229233334	76870	CCTAUGCCAACAGCAGCUCAA	76871	ATGAGACGTGUCCACAATCTTACTUAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
229235447	76872	AAAAGGCATTTTAUGAGCAAAGCAUGA	76873	CCCCCAUAGCCATCCTCTCUAT
229246162	76874	ACUTTTCUGAGAAGCAGGCGAT	76875	AGAAACATGCTTUCCTCCAAAGAACUA
229247294	76876	GGGAGATATUCTGTGCTATUCCCAAA	76877	GCTGCTCTTATTUTTGCTGGTTTTCTUA
229249824	76878	CGGAGACUGCUGCAGGAAAC	76879	GTCTCTTUCAGGATCCGCAUCT
229251007	76880	TGGAGCCGCUGACACCUA	76881	CAGGACCUGGCCCUGAC
229251688	76882	GCCACTTGCAUACACCATGUC	76883	CCTCGTCUGGTGGAATGGUT
229252734	76884	AGTAATTCCUGTTCCTCUCCACAGT	76885	GCTGACAUCGTAGCCTUGCC
229256427	76886	GGAGACAGCAAAAAUGCUAAAAAGAAGA	76887	CTCTGGGUGGCTGCATCTUA
229260883	76888	CCCGTGUCCCTACUCCAGAAT	76889	CTCAGCCCACUCACTAUGGG
229265400	76890	AATAGCAGCUACCATGGATGTGUC	76891	TGATGCTTTAGAUACCCTGCTTUACAC
229271159	76892	CGGCTTTTCUACGTGGACTUACC	76893	GCCCACCACACUAAACCTCAUC
229275479	76894	TTGACAGGUCAAGGCUGGAAG	76895	CCTGTTGAUGAGCCCAGTUG
229276928	76896	ACTGTUCCCAGGACGTTUGT	76897	GACATCTTATGGUGCACTGAAAUGG
229288067	76898	GCCTCCCAGCUCTGAAACAUA	76899	AGGCTTGAUCACCTTTAUCCAAAAGAAT
229288760	76900	GCACAACCCGGGUACCTUT	76901	GCTTATTCCTCTUTTCTCCTCTTCAUCT
229294358	76902	GGUGACGGGACTGTUAAGGG	76903	CATCAGCAGUTCCACCACTTUAGA
229299501	76904	CUCUGGCGGGAAGGGAT	76905	ACUCGTGGGUCCCGAACT
229300131	76906	CTAAAAGAGGCCAAGGUACTUCACT	76907	CCTCTACCACAUCAAACTGTGAUGA
229306028	76908	GGGACACCAUTAGCAUGACAG	76909	CGAGTAATCACAGCUCCCTTTCTUT
229308196	76910	TGGGCAATGAUGCTAATGCTAAATAUCT	76911	GAGTATTCGUCAACCAAGAGGAGTTTUA
229308600	76912	CCAGAATCAUAGGGATAGGGAGAUACAT	76913	CCUTTGTATCUGAGCACCAAAAACA
229309471	76914	CCGCCCUACTACGGAAACUC	76915	GGGCTTTCGCUTGACCTCUC
229309639	76916	ACGCCCATCATAUTTCTTCAGAATAGUG	76917	TCTCACTGGCUTCTCCTCUACAG
229313295	76918	GGTGTAAGGGUTCAGGAGGCUAT	76919	GCATTTCUCGGGAGATGTUCAGG
229317323	76920	CCCCGACGGAGUCAAGTUT	76921	ACTGAGCUGAGATTUGCGAAGAG
229322587	76922	GCAGATTTTAUCCGTGGTGTGGUT	76923	CTTGTAATTCUCCTTGTCTTCUGCCA
229322652	76924	CCTTCAGGCUGTTCCCGAAUAAG	76925	CGGTGGACGUCACGGUAAG
229332805	76926	TCTCCTCCUGAGCTCCTGAUG	76927	TGTGTUGCCAGAGAGUACAGAAG
229337946	76928	CCUGAGAGAGAGGAGGACUCT	76929	GAGACTGTTTGTAUCTGTAACTGTCCUT
229339090	76930	CCAAAGTCTUCACAGAGCTAUGCC	76931	GGCTTTUCAGCAGCAGCTTTUAC
229348225	76932	AGATTCTTUCACATGGCGGUCAA	76933	AAUCGCUGAGGGAGGGAAAC
229352887	76934	GCTGCTGUAACTGCTGCAUCT	76935	CCATACTTTTAACCUTCCTTGGGAAGUG
229353274	76936	GTAAGUGCTGGGTUAAAGACACCT	76937	GACCCCGUGATCCGAGAAUG
229356259	76938	GCCATTTCCUTGTAATTGTTGUACCC	76939	TGACGATCUCTCCTGTCTUCCA
229361991	76940	TCCATCAUCACAGGACUGAAAAGG	76941	TTCACTGGGCUGTGCTTACTUT
229365652	76942	TGAAGGAACUCACAGGAAGCUG	76943	CTTTTCTTACCUGCCTTGAACTCTTTUG
229373236	76944	TCACAAGAATUCAAGACAGGAACACUC	76945	ACTGCTGTTGGUACAGGTTTAAAUACT
229375186	76946	ACCACAGTGAGUGCAGTTGTUT	76947	GCTCGAGATAUCATGAGTGATUCCAAC
229377639	76948	CCACTTTUGCAGCAACCTTTUCT	76949	TCAGGAATTUAGTGGTTATGTUCAACAAGT
229377657	76950	GGCAGCTTTTATUCTTGTCATTGCAUAT	76951	TGCAGTTAGAGUAACTTGTAAGCTATUAGGA
229380425	76952	GGCTCATGAUTCAGAGGCUGA	76953	CTCGTCCATAUAGCTGTTGTAGTUCAT
229381883	76954	GCCTCCCCUTCAGAGTTTCTUAA	76955	CCATCTAATTGAAUGAGCAGTGGAAUCT
229385729	76956	TGGTTCUGCGCAATATCUGCT	76957	GCAGGCGGUACUCAGACAAAT
229389465	76958	CAGCGUTAGCAAAUGCAGCAA	76959	GGCAGCCUGGTTCTCGAATUA
229395272	76960	GCCTCTCUCCCCACUGAC	76961	GTGAGGCCCGGCUACTUAC
229400517	76962	GACGAAAUGGGCACGTUGT	76963	CAUCGGAGGCTTCUCCACAG
229404451	76964	GGTGTTCATGAAUTAAAACTCCTGUGT	76965	GCGAGGGUCAAACATTTCCUG
229404678	76966	AATGAAGCAGTTUGGTGATTTGTGTUT	76967	GTTACATTCAUTCCCTGTGAUGGGA
229405671	76968	CGAAGCTCCCAAUACAACAACUGT	76969	CTGGAGAUGACTGCCTTTAUGACC
229409963	76970	GAACACCTAUGCTGTACCACATUCT	76971	CGCCCAGAGUGCTGAAUACC
229410421	76972	CCAGTTCCUTCCTCAGACUCAGT	76973	GCCACTCTCTCCUATAAAAACCTACAUC
229413961	76974	GGGTCGTUGGAGTATGAGGUAAG	76975	CGCATCCTCUGTGTTACTCCUG
229414721	76976	AGTCCCTUGGTACCTTCUCAGAAA	76977	CGGAUGCCCCCGTGTUC
229414927	76978	CCTGACCUGGTGCATCCTUT	76979	GCACCUGCAGCTCATAGCUC
229418580	76980	CCUCACAACGAGCCCAUCC	76981	TTCAGCCUCGAAGGGCAUT
229419673	76982	ATCACATAGCAUAGGAAGAAAACAGCUT	76983	CTGTGACATACCUACCTGAAAAAGGTUT
229420008	76984	CTTTCTGUGAAGGGCTGTGTGUA	76985	CATGTCACCUCCCCAAGACUT
229424289	76986	CTGGCUCCAGAGGAGGCUA	76987	CTGCTGCCGUCGACTUG
229424328	76988	CAGGAAAUGCCCAGCAAGAGUA	76989	GCACTGACATCUAGGGCAAAATCUT
229426746	76990	GCUACAGCCCACCTCCUGA	76991	CTGGTCUGGCACCACUGAA
229428303	76992	AGATCTTGCCCUTTCCAGCAUC	76993	TTGCCCAAAGACUGATTACCAGUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
229429002	76994	TCTCAGAGCUTCGACCAUGGA	76995	CTGGATTTGAGGAUGATTCAGGUGA
229429083	76996	CCCCTTCCTUTGTCTGCCTTUA	76997	GGTTCTGAGACCCUGTGTGTUG
229429984	76998	GGCTTUCCCGAGTTAUCGCA	76999	CTGCUGCCCGTGAAGTUAGA
229430071	77000	CTGCTTGGCAGUCTCTGACAAUAT	77001	CGGTTTGATACUGAGCTGCATTUG
229431636	77002	CAUCCCAAGAGGCTGUCAGA	77003	CCGUCAAGCGCGATUGG
229433623	77004	CCCUGGAGTUCCGCAAAGAC	77005	TCCATCCCAGCUTCACACCUA
229438828	77006	CACTCCCGUCAACAUGGACA	77007	CCCCGGAGAGGGUACTTTUC
229439280	77008	CTUCGGCCCAGCACUCAT	77009	AGCAAGGTCUGGGACCTGUAA
229439652	77010	TGGAAGGAGCCGCUGAUG	77011	TCCCGGAGUCGGGATCUT
229439813	77012	GGCAGCCUCAGCGGAUAC	77013	CGGGAUCGGCUGCGAAT
229440665	77014	GCCAGACGCAAGAUCCAUC	77015	GCUGGCCACCCCTUCAT
229442557	77016	TGGAGGGAAUGGAAAAATUCAAAGACA	77017	AGGAGTATTCCUGGTCCTAAAGAUGAAA
229445359	77018	AGAGGCUGCAGTCAACTTCUC	77019	GCTCAAATGGCAUAGTCTCCUCA
229449892	77020	AGACAAUCCCUGCGGACAAG	77021	CCAGTTAGGTCUTATCCTGGCCUA
229451556	77022	GGCAACAAAACUCCACAGUAAAGG	77023	CCAATAATCTTCUCCGTTCTCTCTCAUT
229459160	77024	TCAGCTCTGCAUTTCACACGUA	77025	CAGGTTCTCUGGAGCAATACUGA
229466346	77026	GGTCACUCTGAGGAGUCAAAAGT	77027	CCAAAUGTAUCCACGGCCCAA
229467224	77028	CCCATCATCACUCACTGGCTUT	77029	AGCCTAGTTGUTCCCTCCATUG
229475225	77030	GGGATGGUAGCCCAGGTTCAUA	77031	CCTTGCCAGAUGATGAUGACGAG
229483363	77032	CCACCAAGAUCATGCAGCUGA	77033	ACTTAGATGAUGACAGAGGGTTTAUCCA
229484537	77034	GCAGTTTCCCACAGAUATTCTAAGUCAT	77035	GTTCCTGCCUGGTGACCUAC
229494595	77036	CCAACCAGUTTTACGCCUCCT	77037	TGCTCTUGCCGGAACUACAC
229497753	77038	TCTGTTGTTUTAAAAGCCTTUGGAAGAC	77039	TCACTCTCCTTAUTTTCTGCCTCAATUT
229502504	77040	GGGAGGCACUGACTGAAGTATUAAAAG	77041	AGGACTCAUTTGATAGATTTUGGAAGCA
229506673	77042	GGACCCAGAGGUGCUGAGAT	77043	GCCACTUCTTGGTGTUGCAG
229514242	77044	CACTCTTACACUTACGCCCAAGUA	77045	GTCGTGGACUGGAATGGGUAG
229530828	77046	GGTGCUCGGTTTUGGACCAT	77047	GGGCTTTUCCGCTCTUCC
229533655	77048	TCACCCTCCUTCTCTCTCCUG	77049	CGTGGTGGAUGGACGTCTUG
229535241	77050	CTGGAATCUCAGCCCCTTCUC	77051	GGUGGACAGCGAUGGGT
229535277	77052	GTCCTGTAAGGCUTTGGTATCCUG	77053	AGGCUGGGAAGACACTTCTUG
229538700	77054	CCGCCGAAGGACGUCUC	77055	TGGGACGACUCCAGCTUCA
229540304	77056	GAGAAAGAGUGCCTCAAGUACCA	77057	CTGTACUCGGGCACGUAGG
229540899	77058	CCACCCCAUCACCACCUAC	77059	AGGGAAGAGCUGGCTCCUA
229547905	77060	CCCAUCAUGGCAAGCACAGA	77061	CAGTCAGCCCAUCATTCAGATUCAT
229552513	77062	CAATGCTGTUAACAAGATTTGGCCTUA	77063	ACAUCAAAGUGGACGAACGACT
229556175	77064	CATGACACAUGAGGTGGCTCUT	77065	ATCTAAGTCAAUTACAGGAAACAUGGCT
229568209	77066	CTCCTGUCAACACCAUGGAGT	77067	TGCTTGTTUGGCTTGTGTTCUG
229572416	77068	CCCCGTCTTTGUAATATTCTCTCTCUCT	77069	CTTGGAAUGAGGGACGGTUCT
229574891	77070	GACGGTUCCCCGGTGUT	77071	GCTCCGGCUCTCCTUCC
229575668	77072	CCAGAGUCAGGTGUGCGA	77073	CTUGGCCCGGCTCTUGT
229583064	77074	TTTGTCTTCTCUAGCAATTTTGACUGGA	77075	CTTTCTATGGAGCUGGGATCAATCUG
229584337	77076	ACCUGTAGACCTAGTUACCAAAAGACAA	77077	TGCAACGTTCUGACTACTTGAAUACAT
229588098	77078	CCTGAGCTAGTUTGATCTTCAAGTTTUC	77079	ATTTCTAGGACTTUACCACTACCTGCUA
229589418	77080	AGCTGCUGGAGAAGAGAUACGA	77081	GGTCTTGUAGGGAGGACCUGAG
229589663	77082	CCCCAACCUAAGCACTGTUAGT	77083	CTGATTCTGCUGGTTCTTTGCTUG
229591568	77084	TGAACTTCGAAUGGCGAUCGT	77085	CATGUCCAAGAGGACAGUAGCA
229592211	77086	TCAAGUAAATCAGAUGCCGACACAA	77087	TCATTTACUGACACAACCAATACCAUGT
229603945	77088	GGTCAGCACUGTACCTCUGG	77089	AGGAGTGUCTGTGCCCUACA
229606520	77090	TCTTCAGCUAATTTTTCTGCAUCCCT	77091	TCGGCAACAGCUATCACCTTUC
229608278	77092	AGTTCCUCAAAAGAGAAAUCACGCA	77093	GCTAAGGCAUAGGAATTTTCGTAGUACA
229613949	77094	CACTGGTGCGAUCCCACAAUA	77095	TGGACAGAAGGCCUTATAACATTAGTTUC
229615654	77096	CTTCTGGAAUTGTGCTAGTUGGG	77097	CTAACAACGCCUTCTCUCCACAT
229616947	77098	CAACCUTATGATTCAUCAGGAGAGCAT	77099	AGGGTTGTTAGUGGAGCATATGATTUT
229617041	77100	GGGCCTTUCAGTGAGAUACCT	77101	CATATCTTTGTTCUCTGCTCTTAGCUCT
229620102	77102	CTTGCATTAUTGGTTGGUGGCA	77103	GCTGGTCTTCUAGCATATAGCTGAGUAA
229630617	77104	GAAAACCTGCAGAUCATCAGAGGAAAUA	77105	CTGCTGUCTGCATTTAUGAACCC
229630761	77106	TCTGGAUCCCACACCTTUACCAT	77107	TCTGCAGAGUTGTTAGCGGUT
229638019	77108	CATCTCCUCCGAGCCUGAAA	77109	GCTGTTTTCTCUCGGATCTCCAAATTUAA
229652260	77110	TGGTTTCCCCAAUCCACCCUA	77111	GGTCUCCAGGAGCTGAUCACA
229652521	77112	CAGGGACGUCTCCUGGAGAT	77113	GAACTTTUCAAGCTGCUGAAGGA
229661236	77114	GCAGTTACUGGGCTTGUCCAT	77115	GAGGCGGAGAAGCUCUAACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
229661294	77116	GAGCTCUGGCTCUGGCA	77117	AGACGUCCCTGACCTUACAGT
229663297	77118	GCTTAGUGCCTTGTCUGGGT	77119	CCAGACTCAUGCCCTCTCTCUT
229673061	77120	CAGCAUGAGCTCCCAUCCAT	77121	ATCTGGTTTCUTCCTTCTTCUCACAG
229675987	77122	AGCACACTGUCACTATTTCAGTAACUC	77123	AGAGACTGGAGAAUGTATACACACCTUA
229686118	77124	GCTTAATTCUACCTTGTAGCCUCCAAT	77125	CGGCCAACACUGTCAAGTTUC
229691846	77126	GCATGGTUGGCATTGGGTUC	77127	GGGAAGCTGUCCATCAGTAUACA
229694068	77128	GCACAGTGGAAGUATGCCCAUA	77129	CTTAAGTGTTTUTCCAGTGTCUGAGAAC
229697855	77130	ACTCCACCTGUATGTCCCACUAAT	77131	GGAUGTAATATTTTCUGAAGAGCCAAACA
229700862	77132	GAGTGTGCAAAUCCCCCATCUA	77133	GGGTCGGUCATCGTCUACAAG
229701879	77134	CGTCAAUGGAACAAACCCAUCAC	77135	TCAGCCUGGACCGGUCA
229711434	77136	AGCATGGGUGCAGACAACATUA	77137	GCTCUAGACAACAAACCTTGUGGA
229715479	77138	CTATTTCAGCCCCACUCTGCUT	77139	CGGGTCUCCATTGTCUAGCAC
229718864	77140	TCACTCTTCTUGGTACCACTCTUCAT	77141	CTAACACCCUGTTCGCACUGA
229721082	77142	CCCTATGCUCTGACAAGGGUACT	77143	GTGCAACTGAAAGCUGTGATTCTTTAUA
229726822	77144	CCAAATGCUGGTAACACTGUGG	77145	AGTGGAACUGGAAGAGTGAAAAAGUAAG
229727395	77146	AGCTCTTUGAGGACAACTAUGCC	77147	TGGTCAGCUCTGAAUAACCAAGAGA
229732310	77148	GTCCCUGCATCCUCGCAT	77149	GCCTGCAGUTCGCTUGT
229736596	77150	GGTCGCGGUTTGTCTCTCUT	77151	AGACUAAGCGCCUCAGGGT
229736609	77152	GGAAAATCTUAGGAGATACAGGGAAUGG	77153	TCGUTCTGTUCCAGCCGAAA
229742508	77154	GCATGCATATTUTGTCAGCGGUA	77155	ACCCTTCAUCCTGAACTUAGGAGAA
229746037	77156	GCTCUGCACGCGTGTGUA	77157	TCCCTCACCCAUGCCCUAT
229746342	77158	CTUGCCGGGCUGGAAGT	77159	CGCAAGGGCAACUACUGGA
229746471	77160	GCGGCCACGAGUTGTUGA	77161	CGCAUGAAGAGGCCCTUCC
229746968	77162	ACAGAGACTCCUAGTTAGACCACTTTUT	77163	GCTGTAAAGUACGACUACCACAAGT
229747025	77164	AAAAGAAACTCCUACGTGGTGUGT	77165	GGCTTTGGCUGTGGTCAACTUA
229749627	77166	GCTATCCTGACUCTGCCCCUAA	77167	CAGCAUCAACCACACAUACCAG
229750319	77168	CCTTCUCGAACATGTCTUCGCA	77169	TCGCGAAGUTCCCGTTCUAC
229754105	77170	TTGCCAGCCCUTCTTATTCTTCUC	77171	GCAGAAGCCCCCGUACUC
229754607	77172	CAGGTCAGUGGATCCCCUCT	77173	CAATGGAACUATCCGGAACAUCCT
229754964	77174	TTGGGATGUCTGATTATTCUGAACGG	77175	CTCCAGACTCTUTTTGACCAATATTGUT
229756001	77176	GCGAUGAGCGCCACGUA	77177	CUGCUGGCCCCAGAGAC
229758507	77178	TTAAATGCCTUAGAGTGTTCCTCAAUGT	77179	CAGAAAAGAUGGAAACTTTGGACTUCAA
229759257	77180	GTGGGTGGGUTGGATGTAUGA	77181	GGUGGTGAUCAAACAGGAACAG
229760520	77182	CCTTACCTGUCAAGTTCTTTAAUCCAAGT	77183	TCGTTACCUGCCTCUGGAGAAT
229764158	77184	GTTTTGTAGTAGCCCUTCTAAGCCATUA	77185	CATGCAGAAAAUGATGAUGCCCAA
229765066	77186	TCAGCGTGAACAUTTTGGTAAATUGG	77187	TGTAGCAATTGGGCUAAATCTGTCTTUA
229766197	77188	CGTGGGATGUTTTTGCAGATGAUG	77189	CTGCAGUGGGACCACTATTAUCT
229767104	77190	CUCAGGAGAGACAGCTTUGAAGT	77191	GCGATTTUGGACTACCTCAUAACCA
229768853	77192	GTTTTGTCCCACGAAUAATGCGUAA	77193	TCGTTTTAUAACACAGGCAACTGTTUG
229771207	77194	CCTCTUACCCACGACAUCCAG	77195	CCCTCAATGTAUCCCTTTGGCAUT
229771536	77196	GTCGUAGGCGAAGUCCGT	77197	GCCCUGCCCACCCTAUC
229776726	77198	AAGCCUATGUGCGGAAGCA	77199	CCCATCACGUTGCCTTTATCCUC
229776979	77200	CTCTGCTCUGCTCCGUGAC	77201	GTAAGCACAGAGCGUGTGTUC
229778181	77202	GCCCAGAAUCGCUCCCT	77203	AGGGTCCCUGGGAGATGUG
229778349	77204	GGTGATGGGUTTGGGTTGATUG	77205	CAGCTTCATUCCCACTGCAGAUA
229779601	77206	GGTATTCTTGCUTAAAGCTCTGCUG	77207	CUTCCTTCTCCAUCCAACCACAT
229780257	77208	GCGGGTCUTCATAAAGGUGCT	77209	TGTAAATGCTTCUGCACAAGCTUAC
229781040	77210	GGGTGTGACACUGCTTCCUC	77211	GGGACCAGUCAAGGTGUGT
229787891	77212	ACCUTGACTGGUCCCCAGA	77213	GCCCCUGACAGACACATCTUA
229788422	77214	CAGAGATCUGGTTCCACTTUGGG	77215	CCAUACAGCAGCCAGUACGA
229788545	77216	GGTTGTCTAAAGUAATAACTCCATUGGCT	77217	GAGCTGAAGAGGGUAAAAGTCCUT
229788733	77218	AGGAGTCCUCTGTCCCTCTUC	77219	GAGGUTGTATTAUAGGCCAGCAGT
229788737	77220	ACCGTUCCAAAAGCACCUGA	77221	AGAGGACUGACTATCGGACUGAAA
229789564	77222	CCAGGAAGUTGCACCGAUAGG	77223	GGTTTGGGUAGTAGAGCAUGGA
229791820	77224	CACTGAAACAACUTTACAAGTGUGGAT	77225	CTAAGAGTTTAACCUGCCGCCTUA
229794068	77226	AAAAAGAAGCUAGAAGACCTTGGTGAUT	77227	TGTCTCTTGTAGGUTTCAAGTTGACTUC
229798736	77228	GCAGAAUACTGTCAGTCUAGAGGAAGAG	77229	TTTTGGTAAGCUACATGTCATAACUGAGAG
229804987	77230	GAAGGUCAAAGAGGUGGAAGGA	77231	GCAAACATGUACACCCGCUCT
229806631	77232	CTGTTTATGTTTUGCCTCTCAGGTUC	77233	GCCTGTGUCATGTCTGGUACA
229811892	77234	AGAGTUCCCAGGCAACAAACUT	77235	AAGAGGTAGTUGGCCTGCTUC
229812654	77236	GAGACCCTAUGGGCACTTTGUC	77237	GAAGAAUCAGCCUCGCAACAAAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
229817109	77238	AGAGGAATTGTAGAGUACTGAACAGGUA	77239	TGGAAACAGGUATTGATGAAGAUGACC
229822631	77240	GCAGCACUGGTATCAUCAGCA	77241	GTCCTGUAATACTGTCTUGAAAGCAGAT
229824845	77242	CCTGTTTTCTGAAUTCTGCTTCCAUCT	77243	CAGCAACGTTUAACTTCCAAATGTGUAT
229824988	77244	GCATCATTTCCUAAAGCGCTUGA	77245	GGAGACTAACAUGGGCTGGUT
229832790	77246	GGCCAGGGUAGCTCTTTUCAA	77247	GGATTGTGTGTUCTGTCCTCATTGUAT
229835374	77248	AATGCTGACAUGATATTACAGTGGUAGG	77249	TTTCCGAGCAUATGCAACTAGGUT
229842797	77250	GGGCCACCUGGAAAGATACUC	77251	TGCACAATTAGTUCGAGAAGTTGAUGT
229847418	77252	GGATTCUCAAAAGCAGACACCTUCT	77253	CCAGTATAUGAAGGAAGGTGTTACCUGA
229847973	77254	TGCTTUAAAAGACAGACGGAUGGAA	77255	CCACAACAGGTUCAATCTTGGCTATUAA
229854786	77256	TGTTTTCUTCTCTTTAGUGGCACACT	77257	TTCATCACTUACGCTGTTGATTTCUCT
229858420	77258	GTCCTCGACGUCCATCUGT	77259	CTGGACACAUGGCACCUGT
229865373	77260	CAGGATGUGTCCGGAGUGG	77261	AGAUGTCCAACAAGUCCAAGAAGAG
229865486	77262	GATCAAAGUCCACAAATUCGAGCAT	77263	TCATTACAACCATUCCCTAGCTCTGUA
229870056	77264	CCCCCTCAAAAAUGCTGGTGAUA	77265	ACAGGTCCCUCACATAATCAAGUAGT
229879088	77266	GCACTTUGACAGCTCCUCGAA	77267	GGAAUGTTGCUGGAGGAAGGAA
229879988	77268	TCTGGCACUGATGGTTGCAUT	77269	TGGGUCCCAAAAATTATAUAAGCACAGA
229903863	77270	AACTAGTTTGTAAUCTCTTGCCTCTTUG	77271	AGTCAAGAACTUCAGAGAAAGGCAAAAUA
229909299	77272	CGGTTGTCATUGCAGACTCCUA	77273	GGTATACATTACAAUGACCTGAGGAGAUT
229910389	77274	CCTGGACCTUGAGGGATTGTUT	77275	CCACCTCACAGUTATTGAACATCCUC
229913773	77276	TCCTTCCUTTCCTCCUGCGA	77277	TCGUCCCACGGCTTCUG
229914948	77278	GGATGTCCUGCGCCUCA	77279	CCCCCGGCCAUCTAGUT
229917685	77280	GATACACCUCCCCTCTUGGAAC	77281	GCTTATCGUGACCTCTGTUGCT
229919273	77282	TTTGAAGATCAUTTTCTCAGCCUCCA	77283	GCCTTTCUCCACTTAGATTTTCUCCAAT
229932120	77284	GCCAGAAAUCAAACCCGTCUGA	77285	CTTTGTTGCUTGAAGCGGUGT
229937482	77286	CACAATGCCTUGTACGTGAAGAUG	77287	TTTCAATACGGCAUGGTTAAGAACCUAA
229944271	77288	TTCTAAGGAGAAUGAGGAGGCAGUA	77289	CAAAGTGGTCAGUTCATCATTCTGTUG
229947003	77290	CCACGGCAAGACAGUTATUCA	77291	AGACACAUCCAGGCUACAAAACC
229948530	77292	TGTCUGAGGAACGTCTCTUGGT	77293	CGGTCTUACCGGCTCTCTAUG
229950067	77294	TCTGTTCTGAATUGCTGTCTTGTTAUGT	77295	GGUACAGGCGAGGGTGAAUT
229952504	77296	AGCCAATGGAGUGACTGAATTUCAA	77297	TGCTGAAAUAGCAGTAACAGTAUGAGG
229956014	77298	GTTAGAAAAGGAGAUCTCTGAACTUCGG	77299	TTTCUAACACCAGAGCCAAACUGT
229957439	77300	TTCCTCAACCAGCUCTTCAUCAG	77301	GGATGTAGAGCCUGGGACUGT
229958107	77302	GTCTGTCUCCTGGCAUCACAT	77303	AAAGUCATCAGCUCCCACACAG
229961932	77304	CAGTCGUGGCUGAGCGT	77305	CCGGATUGAGCCGGAAGUC
229964583	77306	TGTTCCUACACCTCCUGCCAT	77307	AGGUGCAGCAGGAAGUGAAG
229965034	77308	GCGAGGGAAAUGCCTTCACTUT	77309	GAGGCCCUAAGGTTTTGTTTAUGGA
229965806	77310	CAACACAACTUCCCCAACAAGUG	77311	TCTACTUACTGGAGTUGCAGGCT
229966463	77312	CAGTCTCUCCCTCCAGCAUCT	77313	GAGAACGCACCUCTTUGCC
229967121	77314	TGUTCCUACCCCAACAGCAC	77315	AAAGAGAAUGGAAAUGGCCCAGAA
229968094	77316	CCTGTCTCUGCCTTAGGTGUGA	77317	CCACGCACAUTTGACCAUGA
229972415	77318	GCTCCACAAUGCAGAUGAGACA	77319	GATGAUCGCCCCTTCTTCUGG
229974672	77320	CATCTGCACCAUTGATGTCTACAUGA	77321	TCTACATACATCCUGGTCCCCTUT
229975242	77322	CATTTACTCUTTTTGCTGAUGGCACAT	77323	GCACTCAGATTUGATAAAGAAGTTGCUC
229976759	77324	GCATACCCAAGACCUTGAGUGAAAA	77325	GCATTGTACAUAAAAGGCACTUGCAT
229976976	77326	GCTCTTCTCACUCATATCCTCCTCUT	77327	TCCTTCCUGTCCTCCUAGCAG
229979714	77328	CAGGAUGACAGCCAGTTACGUAT	77329	ATCTGGAAGATGAUAAACCCTTGCUC
229983662	77330	CCGGCTUCTCGGTGUGT	77331	CGUTGGAGGUGGCAAGGG
229984849	77332	CCAGCACCUCGATGTTTATAAAUGCT	77333	ACACAUTTAAAGACTUAACCCCACAAGA
229989043	77334	TGGCCACCACAUTCUCAAAGAG	77335	CCACACCACUGTCCTAUGCAG
229991948	77336	CTCGGCUCTCTTCGGTUGA	77337	CCATGGCAAUCCGUCGAG
229993934	77338	CGGAAGAGCUTCCATGGAGUC	77339	GCAGUGCAGCUGGAGAAAGT
229995515	77340	CGGACCGGCUCCTCUAC	77341	TGTCAGAGGCCUCGCAUC
229996143	77342	CTGCCTTCAAUTCATTCCACUCAC	77343	TCCGAAGCCUCAAAGCTAAUCAA
229999963	77344	GGTTTCAGCUATTGGGAACCUGA	77345	AGAGTCACUGTGGAAGTAGUAGGAA
230002244	77346	GCCCAGCUCTGTUCAAACCAT	77347	TGTTTCTGGAAAGCUGAGTCTTTTCUAC
230002338	77348	TCCCTTTCTCUTAAGTCTCCUGGT	77349	CCCTGTTCUGTGTCCTACTUCAG
230005614	77350	TGATTATCAGCAUAGGCTGGAAACUG	77351	CCTTGTGUCCAACTGGAAGGUT
230008216	77352	TGTCCTCUGACCCATCUGCT	77353	GGACAGGCUGGCATUGGT
230014990	77354	GAAACCTGGAACUCACCTACCUG	77355	TCTTCUGCCACCCACCTGUA
230019503	77356	CTGTAACTUCGACCAACACCTTTAAAUT	77357	GCCTGAGAGUGCACACTAAAUG
230020038	77358	TCCAATTTCCCCUGCACAACUT	77359	CAGTACTACTCACUAAAGAGCTGTCCUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230021341	77360	AGGAAGATGTUCTGAGCTTACUGGA	77361	GCAACUGCAGATUAAGCCAACAG
230023992	77362	GTGGATAGGAUTCATTCATTAATUGCCAAAT	77363	CCUACAGCCAGGAAGGUACCA
230026174	77364	CACAAATTUAGGCACTTUCACCACAA	77365	TTCTAGAAAAGAGUCTCATCGUGGA
230027566	77366	GCTGAAGTCUCCCCTGATCUGA	77367	ACCATGTTTCUAGGTTGAACUGCT
230028966	77368	GGTATTATGAUCCAGAGCTGCTUCAA	77369	GGAGGACGATTTUAGAGAATAGTGAAATTUCC
230030492	77370	TTTCTTTTCCCUCTTGCCTUCCA	77371	TCCAAAACCATGCUCAGAAGAAGAAUAA
230036634	77372	CUCCGAGAACUCGCAGGAC	77373	GCUGTGGUAGCCGCACAT
230045709	77374	CCGTGAUCCTTTTGAGUGCAAC	77375	GGCAGTCCUTGTGCTTTUCCT
230066712	77376	AAATGTGATUGCCTGGGTGUCT	77377	AGGGTATTUGGGTACCUGAAGGA
230069833	77378	AAACAGAAATUGAGAGAAGGCUCCA	77379	GACAGCAGCGUTGAGATAUCAAAG
230070772	77380	CAGCCAGAGACUACCACAACAUT	77381	ACATTCTCATGGUCTTCTCCTTTUACAG
230075336	77382	TCATTTCTUCCAGTGTTCTAATUGCACT	77383	TGGAAGCACAGACUGCAATTTGUA
230095797	77384	GGCAGAAAGAGGACUCCUCAGT	77385	CGACTGCCUGTGAAGTGGAUG
230108947	77386	CGTGTTGAUGCTGAGCUGAAT	77387	CCCTAACUAGTTTCTTCCTUCGCA
230112426	77388	CCAGGAGTUTGCTTTGCAUACC	77389	ACATGTTGAACAACAGGUGATTCGUA
230113015	77390	TGGGTGTAGAUCCGGTCAAATAAUG	77391	TTTCATCUGAGAAGCAAGGAGUGG
230118761	77392	AATTTCTUGACAGGTGGGAUCGAG	77393	CCAUCAUAAGGACAGCCCCAAA
230119681	77394	CTCCTCAGGCAUGGGTTCTUA	77395	CTGCCTACUTCTACTTCCUCCCA
230122619	77396	ACTCACTTGGCUGTGTTTCCUT	77397	AGTGGCCAATTUCCCATTCTAATAAAGUT
230129759	77398	GCCCAGGUGGTAGTAGGTGUT	77399	CCAGGAGCACUTCCTCTTUGA
230132147	77400	CATGTTTGGGUTTGCTGACGAUA	77401	ACTCGGUCGTAGGUGAGGAC
230132659	77402	TCTGTTCAGTUGAAGGAATTTCUCACC	77403	GATCCUTATCAGATTCTUGGACCAACAA
230134061	77404	GGATTUGCAAGGCGGCUAC	77405	GGAGGACAUTTTCGGCTCUGAAAT
230136099	77406	GAGCCGTCUGCGGAAAAUC	77407	TGTGCCAGCAUACTGCTCTTUT
230138524	77408	TGCTTGCCUGTGAACCAGUAA	77409	GCAGAAACUCCTTCAGGTCAUCAG
230140959	77410	TGGTAAACCAAAAAUGCACTTUCC	77411	AAATCUCCCAAGAGGAAUGACAAACA
230144073	77412	GAGAGAGCAAACAUCCTCTTTGUCA	77413	AAAGAGAGGCACUCATGUCAGAAC
230145713	77414	CTCAAGGGTUCACCGCCAUA	77415	GAGAGAGGCACUAAGGCTTCTUAC
230146744	77416	CTTTCTCCTUGCTCTTCTCTUCCA	77417	GGAAAGAUGCGATCGTAAGUCGAG
230146842	77418	ACAATGTTTAAAGGUGGTAGCTGTUGA	77419	ACUCATTGATAGTTGUGAACCAACACA
230148893	77420	CCAGCTGGGUCATCATCTUGA	77421	GCAGATTGACTCUGAGCTGAGAAAAAUT
230151224	77422	GGGTTCTATCACUTGCATCATATGTTUT	77423	CCTTTATAAGCCUGTAATTTGGGACAUCT
230151333	77424	GCCCUGAGATTCCAGUGGAAC	77425	GTGCCAUCCCGACTGTAATUGA
230156850	77426	AAAGAATTGTUACCTGAAGAGCUGGT	77427	CTGTGTAGUAACGCAAAGGATTTTCTUG
230160328	77428	CTCACTCACAUGACAGAGAAUCAGG	77429	CCCTCTGCGUTCCTGTCAUAT
230165208	77430	GAGTTUGCCCCCATGUACAAGA	77431	CCTTCTTCUCCTAGCCTAAGUCAAAAT
230167957	77432	ATGUGACAAGGGAGGUGAAAAAGT	77433	GAGUACCACGACCCAGUGT
230168113	77434	AGGTCACTUACCTTGAACCAGUCT	77435	TGCTGTGACTAUGTCATGGTTCTUAAC
230168148	77436	TTCCTTTGAAACUGTCTTTGTGAACTUG	77437	GCTGTCCAGGAUTCTGAGTATAUGG
230169366	77438	CACCTAGUGAACAAGGGUCCAA	77439	TTGCTGAGGUTTCTCCCTUGAC
230173300	77440	AACAACCCCAAUCCTTATGGTUCA	77441	AGTACTCACCAUGTTGGGCATUC
230173849	77442	CAGCATGACCUACCATCATUGGAA	77443	CCCAAGGAUGTTATGTUCAGGCT
230175199	77444	CACCCTGTUGTTTGTTTCAGUGAC	77445	GGAACAGGAAATAUGTCGAAAAGTTCUC
230180169	77446	AAAAAGGCAGUTCCTGGUGGA	77447	TCAATTTAGGCUCCTAGTGGGUACAA
230183882	77448	GTCACTGACAAGUCCCCTTGUT	77449	ATGTCACGGCAGUCGTUGA
230184933	77450	CCAACCAUGGTGTTGTGTUCAT	77451	CTGAACCCTGUAACTCCTTTCCUC
230185926	77452	GTGAGUTACATACCAUACAGGGCAAG	77453	CCGCCCACCUCGGAAAUT
230187475	77454	GGTCAGTTTUCTCTTGCAGUCGT	77455	CCGGAGGUCCCAAACAGTTTUT
230189710	77456	TGAGAACAUCCGCCGTGUG	77457	CTATGGTGGGUGATTAACTGCTUGT
230191972	77458	CUTGGCATCGUCGGCAAAG	77459	CACTAAGAAAUGGAAAACCGTATCCGUA
230192237	77460	ATAGCACTCUCCAAGCTGCTUT	77461	GCTTACACTCCUTTCATACGCTTTUC
230192486	77462	CCATCCCAGAUCCGTGAGUG	77463	CCATTCCCAGGUCACCAUCAA
230192636	77464	CACAGGAAACCUGTCACCAUCA	77465	ATGGCATCGUGGCCTTCUT
230195609	77466	TCAGGAAACAAAAAUTTGTGCTAUGCAA	77467	GGACCCATUAGAACCAACUCCAT
230196134	77468	GGGCTGGCUCCGATGUAT	77469	CAACGUAGCCATCAGTCUCAGA
230196615	77470	GCCTGGAGCAGAAAUGAGTACUA	77471	ACACAGACCUCAGAGCUCCT
230199961	77472	AGCAGTCATATTUAAAACATCGCCUACA	77473	ATGTCAGAUATAAAGAACUCACCGAACAG
230200993	77474	GCCTGGGAGCUGCTGUT	77475	AGCCATUCCTTTATGTTTUAGGCAAGAT
230202484	77476	TCTCCATGUACTGGTAGCUGGT	77477	CCAGAAACUCCTAGTTCUAAGACAGAGA
230202649	77478	GTGCCTGAUCAGCTGTTGUG	77479	TTCCTAACCUCTCCCCTGUGAA
230202748	77480	TCTACAGCGGUACAGUGAGGA	77481	TGCCCATCAGUCTCTCTGCTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230209475	77482	CTGGCACCUCTGCACAAUC	77483	TTGGCTGCCAUGTTGTTCTTUC
230217499	77484	CATAGCGCAACAGUTGCAGUT	77485	TCTCTTCTTGATTUTCTAGGGACCCUT
230219976	77486	CTGTAACTAAUGAGCAGGATGACAAGUA	77487	CTTCCTCAAGUCAGCCACCUC
230220494	77488	GGTCTATGGCUTCAATTGCATUGT	77489	GCATTGATAACACCCCUACTGCTAAUT
230225633	77490	TCGUTCCUGGAGAAGGAGAACT	77491	ACAGGAAACAAACUGTCCATCTATUCC
230232136	77492	CCCAACAUGGAGGGCTUGG	77493	CACTTCTCACAUCACCCCTUCT
230233743	77494	CCAGTTGCUACTTGCAATGATAUACAC	77495	TGATCACATGCTUACAGTTTTGTGGUAA
230235757	77496	TTGTCAUCAGAACCACTAACTATUCGG	77497	TGCCTTCATTTTUCTCTTCACCAGTAUT
230247996	77498	GGGTGAACUTACCTGCUCACT	77499	GACCTCATGGAUGGAGATACATUGG
230250500	77500	CCCTTCTCCAAGAUCATCCTGTUC	77501	GGCTCTCACAGCAAUGATGACTUT
230250609	77502	GCCAUAGGTTGACAUGACCGAAT	77503	AGTATAACUGTGCGCCUGGAC
230263596	77504	AGGGCGAAAUGTACTCCAGTTAUC	77505	GUAAATTTGCUAAGAGCCGAAGCC
230273779	77506	TGGGCAACACAUTGTCAAAGTUAAAAT	77507	AGGAGAAGCUCCCAAGUGACT
230274674	77508	CAGAAGUCAGCAACTCCTUCAAGA	77509	TGAATUCACCCAGCCCAAACUAC
230282076	77510	ACTGGAGAGAUGCTTTCTTCTUGG	77511	TCGUGTGCAGAAUGAAGGAACT
230284630	77512	GCTCAAUGAACATGCCAUCCA	77513	GTAUGAACCGCCUGACCCAA
230291651	77514	CUCTGCCCAUCCCACCAG	77515	CTGACCCCUGGCACTCUT
230294694	77516	GAGCAUCCACCAAGAACTTTTUCC	77517	GAAGTTTUGCAAGCAGAGAAGTATUGT
230295723	77518	TCATGCTGGATUGGCCATATGTATATTUT	77519	TCAACCTTCTCUCATCACCAACAUC
230298214	77520	GGCACTTGUACAGGTGTCTUCA	77521	CCAGGCATCUCATAACAAAATGAUGAAT
230300946	77522	CUTTCCTTTGGUGGGAGGACT	77523	GCAGCCTTTUGTAATATCCGGUAAGA
230304086	77524	GAAAGCUGGGTGCCCUCAT	77525	GAAGCTGTUCCCGGTGUG
230307348	77526	GCCCGTUAACTGCAGATGUCT	77527	GAACGTCAUGATGGGCCCUA
230311806	77528	CCTTGGCAGUGTCACTCUCAT	77529	ACCCTCACUACTCAGAGTCUGG
230314694	77530	GAGGACTGGGUCGAAACAGTUAAT	77531	CGCAAAGAUGGCCTCTACTTUACC
230314844	77532	AGTCCTTTTUGCACACTCUGGAT	77533	GCATGATATCUCCCCCTTUGGAA
230318142	77534	CACTGGCCAUTACAGCAGATUC	77535	GTCTTGUGACAGGGCTGCUAAT
230323883	77536	AAGCAUCAAGTTGTCAUGGCAAAAA	77537	CATATAAGCAUGACTCCACCUGAGT
230324108	77538	TGACAGGAGGGCUACATCCUT	77539	CCAACAAACACUTCTTUAGCACGA
230325182	77540	GAACAUGGCAGAGCAGCUAGT	77541	GGGTAACCUTCCCGGTAUGAA
230325967	77542	GGTATTCTGTTGUTTCATGTTTCCTGUG	77543	TCTCTAGGUACAGAAGGCAUAACACT
230330912	77544	GGGAUTGCTTATCUCAGACAGACT	77545	GGAGACTCUCACCCATTAUGACC
230331325	77546	GGGAATGGAGAUGTTCTTACUGGAG	77547	TGGGACUGAAAGAGTACTATGUGAGAAT
230331827	77548	CCAGGAGCUTTCACCAACCUG	77549	CTCATCTUCAAACCGTCTCCTGUT
230334334	77550	CAGGTACUCTGTTGCCUCCAT	77551	CTTCCCTGTTAGAGUTTGCTCAGTATUT
230343071	77552	CACCACGUTAAGAACAUCGCA	77553	GGGAUAAGAAAACAGCCATCACUGT
230343224	77554	GGGAGAACAUACTGTGUGCCAAT	77555	GGTTGGGAAAAUAGGACATAGCTTTAGUA
230352458	77556	GATACACTGUAACAAATTCTGCATGAUGAA	77557	TGTGCTUGCCAGTCTATCTUCAG
230353202	77558	GAATGACCCUGCAUAAAAAGGCA	77559	GTGATUGAGCGGCACAACTUC
230354183	77560	ATGTTAGCTGCUAGCCTCATTGUT	77561	GCTGCTGGCUTCATTCTGTTUG
230385903	77562	CCCAAGCUAAGGGCATGCTUA	77563	GGGAAGCAGGUGGATGAGUC
230392156	77564	CCACCGTCAUCACCTTCCTUT	77565	CCCTTCGCACUTCTTACACTUG
230392972	77566	ACAGCUGACGGTGGAGUCT	77567	CCGGAGCUCTACGUGCT
230396934	77568	GGCUCAUGAGAGAAGACGGAAT	77569	CTTCCTCUCGCCCAUCACAG
230397849	77570	CCATATTCAUCCACTTTGGUGCCT	77571	GGGCTTACTTCUGTGTTGGTATCTUG
230397881	77572	GACAGCUATGAGAUGGAGGAAGAC	77573	GTTCCTTUGGAGGTGGCAUGA
230398944	77574	CGGAGACGAGCUCATGAGUC	77575	ACCTCCTGCUGACGTCTTUC
230399983	77576	GCAGCCAUCAGGTTCUGACA	77577	GGAGGUCTTTTUGCAAAGCAGAAT
230403910	77578	CAAGGCUCCTGCTCAUGAAAGT	77579	ACTCTTTATCUGCCAATTAACTCACCUC
230404087	77580	TGAGGUGAAGGCAACCCUAGAA	77581	AAGGAATGGUGTGCAACCAUCT
230408003	77582	AACTTACAACAAUGGAGGCUCGAA	77583	TCAGCCTCAGAAUTTCTTTTTCTUCACA
230412616	77584	CAACAGCCAUCACUGGAACAC	77585	GCCACCAAAGUCATTTGCCATATAUCT
230413627	77586	GGTGTCUAGCCCAUGGGAGAA	77587	CCCAUCACACACCATAACUCCAC
230418951	77588	CTTACCCTATUCGAGTCAATTCTUGCT	77589	GCAAGTTCTTUCAGAATCTCTTGGAUGA
230419342	77590	GTUCACCCACCAGAGTGAUGT	77591	TCCCTCCCUTCACATGCUGA
230422213	77592	GAGGTUGAACCTTAAGACUAACAACAGT	77593	CCTCAGAAAGTCAUTCACACGATTCUC
230423770	77594	CCTGTTTGGAUAACTCAGCACUGAA	77595	CGTCCACUCAGACTCATACTUCC
230430455	77596	GCATCCATCATAUCTTCCAAATCCUCT	77597	CATATTTGTGTCUGATGGGCAATCTTUC
230431041	77598	TCTACCAGACTUGGCACCTTTCUA	77599	CGAGGAGAAGAAAAGUGAAATGACUAGAT
230438047	77600	TCTCTGGGACCAUGAGATGAAUAAGT	77601	TCTCTCAGTUTTGTCACCTUGCC
230441605	77602	CCAGAGGCAUGAAAUGGACCAAT	77603	GTCCTTTTTCCCUTTTCGTGTTCUG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230441803	77604	GCUCACCCUGCAGCACT	77605	CAGCCCCAGCUCATCUCT
230445320	77606	CAGGGAUCTTGAGGCUGCAAA	77607	CTAAGTCCGCUTCTGGTCUCC
230451474	77608	ACUGTTTUCAGAAGAAGCGAAGGT	77609	ATGUATTCCTTTTTCAUCCACAGGCT
230456073	77610	ACTGTGCAACAUTCCCAGGUT	77611	ATGATGAUGACGTTTUCCCACCA
230457371	77612	ACGCGGCTUAAATGAAGTGAAUG	77613	GGCGATACUGAGGAGGATTTTATTGUA
230461276	77614	CUTAACUCAGGCCCGGGAAA	77615	GTCTGAGGCUGTTCACTGACTUAC
230468120	77616	CATCGTCAGGCCUCAACACAUA	77617	GCAGAGAGGAUGTGTTTTCATCAUAAGT
230471658	77618	ACCTUAGCAGGGCCAACCUA	77619	TUGACGTCAUCCAGGACAAGG
230472820	77620	TGGGAAGAUGGAGTAAGAGAAGUGA	77621	CCTCCAATCTAAUAGACGACAACTTAUCC
230474380	77622	TTTAGGTUCGCCAGTTGGUGAT	77623	TCTAGGTGTGAUGGGATATAAGAGCAUAC
230479056	77624	CAGAAGGTCUACATGGGTGCUT	77625	AGTCTGTAATUTTGACATGGTUGGGA
230481328	77626	GAACCTAAUGCCATTTCCTUCCC	77627	TGAACATCAUCCAGGTATCUGCAAAA
230481741	77628	GGCAATAGACCCCUGCTCCUA	77629	CGTCGTCCAUGTCTTCTTCAUCC
230482015	77630	AATACAGTGTGUGCTGCTAACCUT	77631	CTGTTCUAGGCAGGACTUCCAC
230482361	77632	CTGGCCCGAAUGTGATTUAACAT	77633	CCTCATUAAAGAAGAATGTGGGUCAGT
230482671	77634	TCAAAUGGAAAGCCACTGAACUGA	77635	AAGATGTTGACUTTGAATTGGCTTUGAAT
230483103	77636	CGGAACGUGCTGGUCAAGAG	77637	TGCTCCTTGGUCCTTCACCUAA
230494492	77638	AGTGCCAUCAAGTGTCAAUACCA	77639	CATTCCTCCUTCATCACCTUGCT
230494883	77640	CAGGGAGAAAGUGCTCAUGGAT	77641	CAGTCUCAACCCAGCTCUCAC
230495367	77642	CAACTTCUACCGTGCCCUGAT	77643	AGUAGACACAGCTUGAGAGAGAGAG
230495533	77644	GGACUCCTTCCTTUCACACAGA	77645	GAGCAAAUGGACAAGGAUGAAGAAG
230496898	77646	CAAGCAAGATUGCTCTCAAAAAGAUACC	77647	TCTTAGTGAAATCUCCAAACCATGUGAA
230503742	77648	TGGCTAGCCCAAAAUCTGTGAUT	77649	GGAAAACCUGGGCATTAACTGAATAUC
230504735	77650	CAAGGCUACAGATCATCTUACAAACCA	77651	AACTCATTCAGAUCTCAAGGTUGGG
230505350	77652	TGGATGATACUCCATCTCCCGUAAA	77653	GCCAGGGCUCCTGATACUGT
230507676	77654	TCCAAGATGCAUTTACTTCTAGGTTUGA	77655	TGUTAATCATTAGTAGUCCAGAGAGCCA
230508708	77656	GACACTGTCTGUGTCTCTTCTTCUT	77657	TTCAGCACCUACCTCTCUCACA
230508812	77658	CTACCATUAAGAGGAAGTTAGACACUGG	77659	CATCACTGGGUCAATTTCTTGTUCAA
230510878	77660	AGGAAATGTTAAUTGCTGCTTTTGUGT	77661	GGCTATCATCUGAATTTTCCCAAGAAUT
230511947	77662	ACAGTTTGCCAAGUGAAATAGUACACT	77663	GCATACAUCAGACAGCACAGAATUGAT
230512699	77664	CCATCACCAGCUGAAAAGUCACAT	77665	ACTTACTTGTCUGCAGTTTTGGTAACUT
230513775	77666	GTCGAAAATACCUTCAACACCCAAAUT	77667	CAAACCAGACAUACATAACTGTACAUGC
230513883	77668	GCTCCAAGCUCTCTGAGGUCT	77669	AAAGCCAGAAGCAGGAUATTCTCTTAUC
230514653	77670	TTCTCCUCGCCTCCAGTUAGT	77671	GGTGAAGGCAATUTACTCTTGAACTGUA
230519467	77672	GGACCAAUAGGGCCUAGGGAA	77673	GGGACTGAGUCCGCTTGTTAUC
230524172	77674	GAGUGACCTCCUGCAACAGAA	77675	GTAGGTAGGUGACACTTCGTTUGA
230528253	77676	GGACAUTTGCTUCCGGCAGA	77677	CCCTGGTAUAAAGAGGAGAAAAGAGUGA
230530162	77678	GGTTTGTGTGUGCAGTGAGTTUT	77679	CAGATTGUGGAGTTATUCGAGGCAT
230531168	77680	CGTCACTGUGTACCCCUCACT	77681	CCAAACAGCCAGAUATCACTGUCAT
230533775	77682	TGAAAGAAAGCUGTAATGGCUACACA	77683	GGTGAATGCCCUTGGTCAATATAAUGAT
230534130	77684	AGACTUCCGGAACCATCACUG	77685	CCCAATTGATTGUGAAAGTCCACATAUT
230535354	77686	TCAAGTGTCATTUGCCATCCTAAAUACT	77687	GGGTGATATAGUAGATTCGGTGCTUG
230538184	77688	CGCGGCATGUCTATAGAAACTTTUT	77689	ATGCATCAAACUAGTTCCTUGGAAAGA
230538832	77690	GCAGTGUGCCAAACCAGAUG	77691	GCATAAAGCGGGUGTTCAGGUA
230541989	77692	TCTTGGCUCTTTAATTUGGCAGACA	77693	TGCTGACAUCTGTTTTCTGTUCCT
230544561	77694	CTTTCTTCAGGAUCGTCTCCATCAUC	77695	ACTTTTGACATTAUTGCTTCTCCTGUGT
230546735	77696	GCCCTCAUCCCAAGAAUGAAGAC	77697	GCCUAACAACCGGCACAUC
230549511	77698	GTTCTTTUGCAAACAGGATCTCAUGAT	77699	ACTTTATCGCCUTCACTGCCTUT
230553670	77700	GAAUGCACGCTGAUGGGAAAAG	77701	CCCCGTGACAUCTTCCAGTTTUT
230557479	77702	CGGATGTTUCTCTGGCTAUGGA	77703	TGACAACCCCUCCCTCAUGT
230558335	77704	GGAAUGUAGAGAAGCGCAGCAT	77705	ACACCTTGATTTUGTTCTTTGGGTUG
230558801	77706	AGTTGGTGAATUCCAGTATGGGTUT	77707	TGTACAAGUACCCCTCAGACCUC
230561874	77708	CTCTTAGCUCCTCTGCAGUCA	77709	CTGTCCATTTUTCCCCTTACTUGAAGA
230562535	77710	TTTGATGTCTAUCGCTGTGGCUT	77711	GGTTGATGTCAUCAGTGTAGTAGUCA
230564142	77712	TGGCTAGTTTGAAUCAAGATGCACUT	77713	CCTTACAAUCCGATCGATTCCUGA
230565239	77714	GGACGUCACAGUGACCGA	77715	CTACCUGCGCCACAUCCAT
230565305	77716	GACATTCCAAAUGGCTGCAAACUAA	77717	CACTTCTTTACAUCAGGTGTCATTUCCT
230567627	77718	CUCCAGAGCCGUGCGAAT	77719	GATCGCTTTUCCGAGCTTCUG
230571820	77720	AATCACAGCAATGUTTCTAGTGGTCUAA	77721	GAAGCTTCTCUGTCGTTTTCCUG
230572700	77722	GCTCAUGGCCATCUCAGACAG	77723	CTGGGCTGTAUGAGTGTGAGAUA
230573040	77724	GGACTTAGCGUCCAGTGACUC	77725	AAGAGAAUCGCAGGAAAUCAAGACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230573582	77726	GACGTAGGUAGTGCTUGAGACC	77727	AATAGCATUGCAGAGAGGCGUAT
230576288	77728	TTTTGACTTAAUGCACACACAAUGCT	77729	ACCAAACATGACUGACTTCAGUGT
230576805	77730	GCTGUGCCGGAACATTCTTUG	77731	CTTGAAGCUGGTCCAGCTCUT
230582892	77732	ACCAATGGUCACCAGGTUAGAAAAA	77733	CCCAACTTUCAACACATTTTCACCAUAT
230583042	77734	GGAGTCGAUGCAGACGTUGT	77735	CCTGGTGUCCAAGGAACUGG
230584347	77736	GTGGGCCUCGUCGAAGAC	77737	GCCCTGGUAACCCTGCUC
230584366	77738	AGGTGAAACUGTGCTTGTAUCCC	77739	TTTCCAGCAGUCTGTAGCCATUT
230585581	77740	CCCUACACACACTCTUGACCA	77741	TTGGUTGGCCATTUGCAAGAAG
230591099	77742	GAACCUCCTGCGTTUCCAGAA	77743	GTCATCTGUCGCACATTGGTTUG
230600404	77744	GCCAGGCTTTUGAATTTCTCCTGUA	77745	GTGATTGGTTTUTCTTCACATCTTUCCA
230601886	77746	GCAGAUGAGGATCUAGGGAAACC	77747	GCCCTCUGACGTATCTCTCUCC
230602394	77748	AGCTCTTGATGAUTGCAGGATCAUT	77749	CAGTTCCTCUTCGCCTTGTUC
230610618	77750	CTGAAACTUCCAAACCTCCCUCA	77751	TGCCATTCAUGGAGCGAATCUT
230614465	77752	GCTGCUGAGCCTGAATCTUCT	77753	TGACCAAATCUGTTATAGCTAATUGCCT
230614938	77754	ACCATGTCCUCTCTTTTCTCTTUGG	77755	ACATGGGCUTTCTTGATGUAACCAT
230620724	77756	GCCACAGGAAGCUGAGAAAGAUG	77757	CTCATCCACCAACUCCTTAAAACUCAA
230628101	77758	CCCAAATUAAGAAGAGCAGTGUAGAGAAC	77759	GGCAGAAUAACATGGCTTUGAGACT
230632980	77760	CTTTCUCCAGGCCAGGAAAUGA	77761	GCUGAAACTCUGACGGCAGAA
230635054	77762	AGTCATGCTUAGGATGGATCCCUT	77763	ACAGACACGUGAAGGCAUGAG
230642947	77764	TGAAGGTCAUAGTGCAAACGTUGA	77765	CAAGTGCUAGTCCACUGGCT
230647094	77766	CAAAGACUTCCGAATUCCCCAGA	77767	GGAGCGCUTGCCUCAGAA
230648785	77768	GGACACATCAGUTTTCCTCTCAUGAT	77769	GCTGTCATTTUCTTCAACTTCATUAGCA
230649010	77770	GCTAATGAAGUTGAAGAAAAUGACAGCA	77771	GAAAACCCATGAUTCAGTCCTGAACUA
230651672	77772	ATCAGGTCCUTCCCATAUCCCT	77773	GCACATTTACCUGTTGGATGTTATCUG
230651948	77774	CCGCTATCACCUTCAGGAAGUT	77775	GCTAUAGAGAGAACCCAAATCUCCAG
230653886	77776	CTGGGTCTUCATCAGAGAGUCCT	77777	ACCTGGUGCAGCAACTCTUT
230653984	77778	GTGTCTCTCAATUCTTTAGCCCCTUT	77779	GGGAGATGAAGUTTTAGATCAGGAUGG
230654547	77780	CATCCTGATCUAAAACTTCATCUCCCA	77781	GAGAACTGGGUAAAGACATGUACACA
230657001	77782	GCTCTCTUGGAGTGTCTCCUCAT	77783	CCGGGATUAGCGAACTUCCAG
230658591	77784	GCTCAGTGUGCAAGTCGUAAGA	77785	GCTCTTGGGAUGCAATGTGCUA
230663064	77786	CACCGAUGACCCCATCTUCAA	77787	CCGGCCUCTCGCTGAAUAT
230663761	77788	CAACAGCTUTGCTAGGAUCCAGA	77789	CTCTCTTTCTCCUTTTTCAACCACUGA
230665165	77790	GGGCATTTUCCATTCATAUGCAGAA	77791	TCCGAAGGAAGAGGCUGACUAT
230665536	77792	GCCTAAGGGUGAAAGATUGGCA	77793	GCUGGAGGCCCAAACUAAGG
230668181	77794	CCTGATCATACUCCAGGAAATCATCTUC	77795	GCTATGTTUCCCCTCCTUCCC
230669015	77796	CCUCACCACAGAGCATCTUCAT	77797	TGTCAAGTTCUAAGACTCTGTACTCUGG
230670910	77798	GGGTCCUCGGGTGACUCA	77799	CCGGAUACTUGGACCAGCAA
230671200	77800	CTATGTCCTATTTUCCCAACCAGCUT	77801	GGTATTCTCUCAGCCGGGAUG
230671277	77802	CTCACGCUGCTGAAGGTGUA	77803	CCUGGACGGTGUGCGAA
230674767	77804	CAGATCTGUCCCACGCUAGA	77805	AGGCATTTUAAACAGCAAGTCTTUGG
230676205	77806	TCAACGGTTTAUCTAAGTTGTGUAAGCA	77807	TCTAGGCTUCAGATAAGTTTUGCCAAA
230679219	77808	CACGGATCUCAGCAGGACAUC	77809	CTTCACATGTTUGTCTTTCCTTTTGUCT
230679559	77810	AGAGGACACCUTGGCTGGUAA	77811	GCCTTATTTAGAAUGACAGCACAGGUAAT
230679876	77812	TGCCTGTGGAUCCCTAGCUAT	77813	CGTAGCATTTAUGGAGAGTGAGTCTTUAA
230680850	77814	CTGGAAAGGUGGTUCCCAAGA	77815	GTGAAGGGCAAUGAAGGGUACAT
230683371	77816	GTGTGTAACGGAAUAGGTATTGGUGAAT	77817	AAGCAACUGAACCTGTGACUCA
230683680	77818	ACCTCCAUCAGTGGCGAUCT	77819	CAGAGGAGGAGUATGTGUGAAGGA
230685005	77820	CUCTGCAUAACCGGGACCT	77821	GCTGCTGGAGUACGTGAAGUG
230685164	77822	CTCTCCUGCACCACAUGCT	77823	CGCCGCUGATAGCGUCT
230685688	77824	CTCCCUGAGGCTCAGCCUA	77825	CCAGACACCGUTGGGAUGAA
230687200	77826	CUAGAGAACGAGCGGGUCAG	77827	AAAGTUCCTACCCTUCGCAGAAG
230690925	77828	ACGAATACUGACAGCAATGCTGUT	77829	TGGAGAGAUCAGGTGTAAATAGUGAACT
230691015	77830	CCTCCATGUAGCTGCCGUAG	77831	CGATGGAGACAUGCTCTTTGATUG
230693004	77832	CACGAGCUCAGAAGCAGGUA	77833	CTGACTTGAAGUTTTTGTCTGTTTCUCC
230693331	77834	GGCTTTGGAUGCATTAAGAAATUCAAGAT	77835	ACACCTTGGTUTCTTCCATTTTCUGT
230696791	77836	CCTTGACUAACATACCAGCUGCAA	77837	ACACTGACUCTCCATGTTUGACC
230698106	77838	CCAATCUGCCGGCACATGTUA	77839	CCCACAGAATAUCGATCCTATGTUCAAT
230699580	77840	CCAGGGTATGUGGCTACATGUT	77841	ACTTCUCACACCGCTGTGTUC
230700935	77842	GGTGCCCTUGCTCTTCCTTUAG	77843	ACCTGCTTATUGCAACAAGTATTGUAGA
230702380	77844	CAAGAGGUGACAGCAGAGGAUG	77845	AAGAGGGTCUGAGGAAGGAUAGG
230702871	77846	TCTAGGCAUAAAGATGTCATCAUCAACC	77847	TGAACTGATAAAGUGCACTGGAUGAAAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230703444	77848	GGCATTTTCUCAAAATCTTGCCCUAT	77849	TGGTATTTGCAUCTGTTGGGUGAAA
230703626	77850	TTGCATTTTGGUATATCAACACCCUCT	77851	TTCTTAGAAGUGCTTTTCTTGGUGGAT
230704422	77852	AAATGAAGTTGUTTTGGCTGUGGAG	77853	TGATTCTTACCCCAAAAAUTCCCTGUT
230706296	77854	GAGCGGCAAUTCACUAACAAGAA	77855	TGCCATGACAACUTGATGCTTATUAAAC
230706997	77856	GGCAGGAACUCCGATCTUGT	77857	AGGCTTCTGAAAUGGTTTTCTCATAUCT
230707368	77858	GAGGACCUAGAAGCCCUCCA	77859	TTTGCGAGAGGUAATGAAUGACACT
230709646	77860	TCAGCTAAAGGGAACUGCTATTTTUGAA	77861	TUGGCCACCAGGAAGTUCAT
230709960	77862	GGTCAGAGCTGUATTATTCTCCTCTTUG	77863	ACATCTGTCACUAATTGCCACTCAUT
230712171	77864	CCCCAUGAAGGAGAGCCUCA	77865	TGAATGGCTAGUACTGATGGTTUCAC
230715519	77866	CAGGTCUGCCTGTATGCAUCAT	77867	GCAAGTACTAUGAAAACTGTGAGGTUG
230715631	77868	TCTGTTACCUGGTGGTAGTUCCT	77869	TGGTCCTTCGTUTTTCTTCTAGTTCTUT
230718430	77870	ACTACCACCTUCTAGCTGAGAAAAUCT	77871	TTCCTGGUTGCGGCUGT
230719694	77872	GTTATCTCCAGGUTGCCCAUGA	77873	CACGTGTAUCTTCTTGTCTTUGCAG
230720233	77874	CCAGCUAAGGAGACCACUGGA	77875	CTTTCTGGAGUGTGCGUACCA
230722952	77876	CTGGGAGAGUGAGAGGGTGTUA	77877	ACTGCAGUCCTCAAGCATTUAG
230723358	77878	GTAGCCGUCGTCGTCGUA	77879	GGGTCATGUCTTCAGGGCTUAG
230724079	77880	CCTCGATAGUGTTCATTTCTUCCGT	77881	CTATATCUCACCAGAATGCCAUGCT
230724801	77882	AGGCATTCAGAUCTAACATTTTGCUCAT	77883	CGTCAAACUAACCGGGTUGAGAG
230725276	77884	CATGGACAGUTGGCUCAACCT	77885	CAGAAGAACTAGGAGUTATGGTCTGTUT
230725745	77886	AGGAGGGCAGAGCAUTTTTCTUA	77887	CUCAGGACCUAAGGACACAGAC
230729295	77888	TTGACAAUGCTCTUCCCAGGAAAT	77889	TTGGATTTUCCATCCTGUGGCA
230729795	77890	ACTTCTGTTUCCCGATTTTGCUCT	77891	GCCTCACACAUTGCTACAGGAAAUAAA
230732661	77892	GCACCUTACCTTGTUCAGGCAA	77893	AGGAGGAUCGAGCTCACUGT
230732778	77894	GAGCATGUCCAAATTGCCTGUT	77895	TTCCUGAGGAGCAGAUGACCT
230738160	77896	TGAGGTGACCCUTGTCTCUGT	77897	CCAGCACTTUGATCTTTTTGAATUCAGT
230742871	77898	AGCTCTCTUGAGGATCTUGAAGGAA	77899	GGAAATATACAGCUTGCAAGGACUCT
230745406	77900	GGGTAUCAAGAAGGCCTTGGUC	77901	AGGACACACAGGAAAUGGCTUAC
230745595	77902	GACCCAGCUCAAGCTCTUCAA	77903	GGCATCAUCCTTCTTTCTCUCCAG
230745822	77904	AGTGGGTTUCCCTGTCTCCTUA	77905	CTTGGACAGUCGCCCCUAC
230746948	77906	TGCAUGACACCAAGTCCTUGA	77907	GGAGCTTCUCTTCTTCCUCAACAG
230749210	77908	GGATCUCAGGAAATTCCGTUGCT	77909	GGTTCAAAGAUGCTTTCCAGCUT
230751341	77910	AATCTCUGCCGCTTGGTUGA	77911	TTGTCTTCTTTATUGCCGTTTCTCATTUT
230760312	77912	CATATTTTCAATAUGAAAACTGTTCCAGGTUAG	77913	ACATTGGAUCACAACTGCTGCTUAA
230761339	77914	CACTTACCUTAGCTATCUGGACACA	77915	CACACCUAGTCCGGTUGCT
230765484	77916	GGATGGUTGGGCUCAGACAC	77917	AAATCATCAGCACCAUTAGTACAAUCCA
230774505	77918	CCTTTACTTCAUCAGCTCGTCUGA	77919	GCUTTTAGAATAATCAUGGGCCAGACT
230779586	77920	GGTCCCTUCTCAGATTTCTUCCC	77921	GTTAGTTTGCUGCGGATUAAAACACA
230781525	77922	AGAACGCACGUCCACCUT	77923	TGAAAACUTGTAATCTUCCCCAGGAG
230789109	77924	TTTCTACTTGTTTUCAGAATCACTCUGCT	77925	GGAGAAUTTTGGCUGAAGACAACCT
230790029	77926	CTTACCCTCTUCTTTGCATTTCTCUCT	77927	TTTTCTTAGTUGGCACTCTATGUGCT
230790215	77928	GGTTCCAGGAAUGAAAGCACAUAG	77929	TATCAAGTATCTCAUCCTGTGGAGAATAATUAA
230790587	77930	GGAAACAGCCUGGTTCTUGGA	77931	AATGACTTTCUTACCTTCGAUGCCAT
230792239	77932	AGTAAGTTCUAAGGGTTAGCCUGAA	77933	GGACCCCUACTACAUCAGCAAG
230794363	77934	CTCTGTCAACUTCCCGCUCA	77935	GCTTCATTAGGCUCTACTCTCCTTTTUA
230794779	77936	GAGGCCGUAGTCCGTCTUG	77937	CCCAGCTTCUCATCCTCCGUA
230794960	77938	GAATGAGGTCAAGUTCCCATATGUAAGA	77939	GGCUCATUGGAAGAAACCAAACAT
230795000	77940	GCCACTCGUCCCGCTUG	77941	CGTCAGUGCCCACCCTAAUG
230797643	77942	GTGGTTCUGGGAAGCGUACT	77943	TGGCTAGCACUGGAATTCACTUAC
230799413	77944	TGAGAGACUGACAAGGAAAGUCCT	77945	GATGCACTGUCTGCTTCTCUGT
230803047	77946	AGGAAATTGAAGUTGTGAGGAUGAAGAG	77947	GCCGATGAAACAAAGUGAGAAGAUG
230803994	77948	GGCAACAGCAAUCCCCAAAAUG	77949	ACACACGCUTGGCAGTGUAAT
230805461	77950	GCCATGGGAACUCAATAGAAAAUCCT	77951	AAAACTATACGACACUTACCAAAGTCTGUT
230808576	77952	GGTGACACAGGUTTGACTUGACT	77953	GGGCAGATCUCTGTTGGAGAUG
230809211	77954	ACCTCTUCAGAGGATCTGUGGAA	77955	CACAGTTTGUGCTGGGATUGG
230813536	77956	GCCAGGCUCCUAGACCCA	77957	CTCCAGATGUTCTTCGCTAAUAACCA
230813954	77958	TCTTTCUAAAGGGAGCCAACAAUACC	77959	AGGAUATTGAAGTUCCAAAGGCCAT
230814901	77960	CAGCACUCACAAATTCCTGGUC	77961	AGACCCCUGGAACTGCUACAT
230817110	77962	GGAAGCCGGAAUATTGGATTCUCA	77963	AGCAGCTTCUAAGTCTAGGCTUCT
230818739	77964	AGCCCGUAGGTACCCTUGT	77965	CTGAGAGTCUCCTCTGCUCACT
230818999	77966	GATCTTGCTTTUCATAGACATCTCUCA	77967	TTTAACCGAGUGAGCACCTUCC
230820839	77968	TGCCUTCUGCCAGGAAACAT	77969	AGTGCTTTATUGCCTCACTACUGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
230821754	77970	CCAGCAAGCGACUCAAAAATAUCC	77971	GAAACTACAUCTGTGGACUGCCT
230824453	77972	AGTTCTATGTTGUCCTTGTAGGTTTUCC	77973	GCTCTCATTUCCAAGGAGAACTCUAGT
230825291	77974	TCCAGAGAGCUCUGGGAAGAC	77975	GTGGCTCUGAGGAGTGACCUA
230825726	77976	AAGAAGGTUGGTGTGGCATUACA	77977	GGCTCUGAAAGAAGGCCUGA
230829554	77978	TGTTATCTCUCAACCTCTTGAACAUACT	77979	GUCCCGAAGACUGAAGCAAACT
230831118	77980	CCCCCACUCCAGAAGAATUAAGG	77981	CTGCAAGTAGUGGAACAAATGTAGTTUT
230836387	77982	AACCAGATTUCAGGCCTTCTTUCA	77983	GGCCCAAAUGACATCAAGAAAATGUT
230837406	77984	GGGACTTTGGAUTTCGGAGGAATAAUA	77985	AACAAAACCUATTTUCCAAGCACACC
230840345	77986	CTCATTUCCCAGGGCCTCTUA	77987	CTCCCTCAUCCTCTCCCCAUAG
230840712	77988	CCCCCTGUGCCTCATGTTATAUT	77989	TCCGAGGTUGGAGATAGAGATGTUT
230841011	77990	AACGGTTCCAAAUATGTTATCTUCGGT	77991	CAAACTGCCCCUTGATCCAUCT
230842631	77992	TGUTCCACTACTUGCAGAAACAGAAAT	77993	TGTAGGCTCAGACAUAACATTTTGTUGT
230843385	77994	TTTGTATGGCCAAUCAGTGCTGAUA	77995	CTTTCTAGGGAUACCTGATTCUCAGACT
230845062	77996	CCUGCCAACAACCCTCUAGAC	77997	AGATCACCGACCUTGCUGAC
230851330	77998	GCTTCTUGGATGGAGGUGACAA	77999	AGGCATTTAAUGAAATCAGTGTTTUGCT
230851855	78000	CACAGGUCAGAGTGCAUCAACA	78001	GACCTCCACCAAUGACACGUT
230855348	78002	GGGUGGCAAAGTUAGCAAGGA	78003	CCTGCTCAUGCTTCCGTCUG
230868083	78004	CTCTTCCUGTTTCAGUCCCCAT	78005	GGGACATGTCUGTCAGAGGAUA
230871208	78006	GGCTGUGAAGAACATCUCCCT	78007	CCAGATGGAACAACUGCTCTTTTUAC
230878131	78008	GTCAGTCCATAUGTCCAGTTGCAUA	78009	TGCAUCCCAGCAAGTCTUCAT
230878857	78010	GAAGTCATCAUAAAGACCACTCAGAUAG	78011	TCCTCCTCCUCCCAGAACTUAAAAA
230879724	78012	AAGGCATGTTTCUAATACTGTGTCTCTUT	78013	GCACAGGAUAACTCTTTGCAUCAGT
230881645	78014	GTTCAUGCCGACAAGUGCAG	78015	CCTGGACCAGCUCTGGATTUAG
230894755	78016	GTCCACATUGACCTCAGUGCT	78017	GGCCAAAGAUAAAATGCTTACUGGAAAA
230898405	78018	CCACCCUAGCAGUAGACCGA	78019	TCTCTGACUCCTCCCCATUCC
230908059	78020	GATATGTTTGCUGCAGGGCCTAUA	78021	CTCTTGATTCAGCUTACCTCTTTCAUAGT
230911493	78022	CTGTTGGUGCACAAAAAGACACTUAT	78023	TGGCCAATUTCTCCACAUGGT
230915896	78024	CCCTTGTCTUGCAGGTATGACAUA	78025	CACACCUGGAACUGGGAGAAG
230924464	78026	ACCTGGAGGUCAGACTATTTTAGUAA	78027	GGAGATCTUCAGTTTTCCTGAUGACT
230926262	78028	AGAGACUGAGAACACACAGCATUG	78029	CTTGGTTTGUGGACCATTTTGTUGA
230937396	78030	GGACGAGGAGCUTATGGTTCUG	78031	ACAGTGGTATTACUGCACCATGAAAUT
230940261	78032	GGAACTGGAUACAGTGCCGUAA	78033	CATTGTTAGCTUCCACCAAAGTTTUAGT
230941721	78034	TCTCTCTCCTUCCTTCCCCCUA	78035	CACCTCTAAGGGUTGCCAAAATCAUAT
230942108	78036	AGAGCAUGAGAATTTTCUGGAAACCAT	78037	CCAGAUTTCUACAAAAGCACAGACAC
230946397	78038	GTATTCATGAAGACCUGGGACTTTUCT	78039	CCAGATTTTCUTTGTTCCAGUGGGAT
230949266	78040	GGAACUAACAGACCAGGAGAACUT	78041	CCGGCATACUCAATCACCATCUC
230950419	78042	CAGCTTCAGGUCACTTTCCCUAT	78043	TGTGGGACUCTGTCCTUCGT
230952414	78044	GTTGTUGCAGCCAGCAGAUG	78045	CTTACTCTCAAUGATTCCTGGAAUGAGG
230953583	78046	ACCAGGCCUCCTCATUCCA	78047	TGAGATGCATAUAAAAGTAATGTGTCCTTUCA
230956099	78048	GGAACGGUGGTTTGGCUGAT	78049	AAGTGAGUGAAAGAGACACAGGAAAUT
230956728	78050	GCATCTCTGUATCTTCCACUGGGA	78051	CACCTUACAGACACCGGAATACUG
230958611	78052	CGGUCAGCACUCAACCAGAG	78053	ACUCTACAGTGCUGGAGACACA
230959346	78054	CCUGAGCCCCTGTUCCAA	78055	AGAGGAAAGCCAGAGUGTGUG
230962597	78056	CCACAGACUCAGTUCCAAAAGAACA	78057	CCCAGGUGCGTCACTATGUC
230963303	78058	AAACCACAACUGAGCTUACACCA	78059	CCTGCAGGAGUACAGCACAAAAUAT
230965802	78060	GGCTGAGACCUGAGTTGATAAAATTUCT	78061	GGAAAGCTGAUACCTATTTCAATACCUACA
230969521	78062	TTCTGUAAGAGAAACATTGAUGCAGGT	78063	AAAAGAACTGTGUGAGTGCAAGUG
230975468	78064	CCTCTGGAGAGUGCAGTGGTUA	78065	CAAAGTTCGUTCTGCTGCUCAAG
230976955	78066	GGGATTGGUAAGGATGACAGUGT	78067	CGTGTGAGAGCAAAUCCTTTGACTAUA
230977265	78068	GAGCATTTGTTACUGCAACCACTAUC	78069	GTAATGCTTUCCTTCCGCTTTUGT
230985927	78070	AGCCATTTUGAGAGGACACGUT	78071	TTGCATAATGCCUTTACTGACCAAAAUT
230990667	78072	TGATGCUTTGGCTUCAGCAAGA	78073	GGGTCAACCUGATTTAATCCACUCAC
230993793	78074	GTTTGTCTGUTCAGCAAGUGGAC	78075	GTTGCCATUAGCACCTACUCCAT
230995822	78076	TCAAAGAATGAAACACAUGCTGAAGUG	78077	AAACUGACAGGGCCAAUGACT
230996229	78078	GGTGGCTGTTGUATTTATTTCTGTCUC	78079	ACCCAGGGUATAAATCACGTUAAGACT
231004130	78080	CCCTGAUGCCCCTTGTCTTUA	78081	CAAGGUGGAGAGGGACUCAC
231006814	78082	CAAAATGTAAACCGAAUTCTGCTTCUGA	78083	TCAGTGGTCUGCTGTTCTUGG
231010473	78084	CCTCCTCUCAGAGTTCCTUCCT	78085	CTGTCACUCCTTGGAGGTUCAC
231011331	78086	AGGACCTTUTGGTGGTGUGG	78087	AGTGGAAAGCCCAGUTCAAGAUG
231030592	78088	GAAATGGTTTUCAGAGCACACUGT	78089	TCACCCGAAUGAAGAAGGACTUG
231033272	78090	AGCATGGTCAAGUCCTTCTTCAUT	78091	CAAAGAUGTTTTAUACACACCACAAAGCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231036093	78092	GATCTGGCUGTCGTCAAUGGT	78093	GGGTGGGATUGCACTCTTGTUT
231036528	78094	CCACTAUGCAGAGGCTGACAUA	78095	TCCTTCUCCCAGCTTCTCTTUGA
231053496	78096	TTCCCCTAAUGGGTCACCTUCT	78097	ACGTCTTUGACGACCCCATUC
231054642	78098	AGGAATTAGCCUAACCTGGAGTUGA	78099	GGCAATGGCUTTAATTGACUGGA
231054993	78100	AGTTCCCCAGGAAACUCCTAACUT	78101	GAAGGGACTCTTUGTTCTACTGATCAUT
231061093	78102	CAAGACUCTCUCCCCAGGGAA	78103	GTGGGTCCUGGTCCCAGUA
231068532	78104	CCAGCCTUCGACAACCTCUAT	78105	GAGGACACAUCAGGGCTTCUG
231102396	78106	CCCTGCGUATGTGGGATUGAG	78107	GCTCTGATUGACCGAATGGUGAA
231105420	78108	CCAGGGAGCUCTGACUGGA	78109	CTATGTTCCCTUTCCTCATTTCCTUGAA
231106070	78110	CAAGGAGCCAGGCAUTTTTCUT	78111	GUATACGCTUCCAGAGAACAAGGAG
231111493	78112	GATGTGCUAAATGCATACAUGGCA	78113	TGATGCAGATUAACACGCGATTGUA
231113397	78114	CAATTGTTCAUGCTTGGUGCAGA	78115	CUGGAAAGCAGCGCAUGAAG
231113718	78116	TTTGAGTTAAGATAGGUTACTTAGTATACCUGA	78117	TGCTTTCTCUTCCTTGTTCAUCACA
231113815	78118	ACCCCAAGACUTGCTACATTUGT	78119	TCTGTGCAACAAUGGAAACATCCTUA
231115990	78120	TTCCGACAACUCCUGGGAAG	78121	CGCTCUGGGAAATCTGCUACAAT
231118245	78122	TCCTGGATTAAAUCAAGAAAATGGGAATUCA	78123	CCATAGGTAGAAAUACTGGCTAAAUCCT
231118321	78124	TTCACTACTAGUAAACTGCAGTCCTTUG	78125	ACAGACAATGTCAUCACAGGAGGAUA
231121598	78126	CCAGGGACCUCGGACTTCUA	78127	ACATCUACCCCGAGCAGTUCT
231122767	78128	ACTTTCCTTTCAUTCTCCTGTTCTTUCT	78129	CAGAGCCCUCACTCUCCAGAT
231126210	78130	AGCCACGGGUAATAATTTTTGTCCUT	78131	TCCAAAGCCAUCCACTTCACUG
231127428	78132	ACCCCATGAUCTCATTCTCTUCCA	78133	GACCTUCAGAGACACUGCCA
231127677	78134	CGTTTGAGCUCCCGCATGUA	78135	CTTCUCTGGGCUCGACGAC
231127821	78136	GACTATATCTTUCATCCCTTCCUCCCT	78137	CACCAUAGAAGCCCACGAUGT
231128360	78138	GTTCAGTCTTCUTCATTGTACCTUCCT	78139	CCGGUCGGAAGAAGGUAAACAT
231128405	78140	TTATACTGTCTTGAUTCACCTTGACAAUAAA	78141	ATGCAGTTGCUTCAGTACCCAUAA
231128421	78142	GGGAGACCAAGAAUACATTAUGGGT	78143	TGATGGCUACAGCTTAAGGTTGUC
231128649	78144	TCAGCGUCTTGTCTTUCAAGGG	78145	CTCCATCAGUGTGTCTGTTGUCT
231129322	78146	CTGCCCAUGAGGAATCGAUCT	78147	AATTTTCTGATUGGGCCTAAGCUCT
231130507	78148	TTATCGAGGAAAGGACUGTAGAGCUA	78149	AATGATACCAACCAUTTCACACAGUCT
231130641	78150	TTTCTCAGAGCAUGAATGATUGGAAGT	78151	AGCCACAGUATTGGACATTAUCGG
231132733	78152	AAAGAATGGUCCTGCACCAGUAA	78153	AGGCCTGCUGAAAATGACTGAATAUAA
231133990	78154	CCAGCUCCAACUACCACAAGT	78155	AGGTACTGGUGGAGTATTTGATAGUGT
231135341	78156	GTGUACACAACAAAACAGGUGCAAA	78157	AGAGGAGAAACUCAGAGATAACCAAUACA
231136341	78158	GGTAATGGUGCCGATAATGUCCAAT	78159	CCAAAAACUCAAGGAAAAAGGAACTGUT
231137078	78160	CGACACTACCUGGGCCAUAC	78161	GAGCTTUCCACAAGAAATCACTTUCAAT
231140516	78162	CAGCACCAUCACCACTTACCUT	78163	GCATGCAGUACCATACAGGAACTUAC
231147136	78164	CTCCAUCCAGTTGGCTUCGT	78165	TGAATGCUCCCATTGTTTCCUCAG
231148393	78166	GAGGCAAACGTUCTCCTTTCTCTAAUAA	78167	TGGTATAGTGCUGGTTTGTTCAACAUAT
231150679	78168	GCATGAGUGCAACTCUCCGT	78169	CCCAACTCUTAAGGCCATUGCT
231153938	78170	GGTGCTUGACAAAAACCTGTUCT	78171	GCCTCTTUGAGCCATTTCTTCTUCA
231158942	78172	GGGUTGGGAUAACAGAGCAACA	78173	TTCAGCACAAUCAACCAGAGAAUAGT
231161228	78174	CCCCAGCUCCAGCTTCTAUCT	78175	CCUCTTTTCATCCUAGACCCCAAC
231167100	78176	AGCTTTTCTGUTGTCCCGGAUT	78177	GAAAUCAGCGCAGGAAACAUCT
231171217	78178	GTCCTTTCTGACAUTTTGACCTCUCA	78179	GACACGTCUCCTCCATGUAAGT
231173790	78180	TGCATTTGTTTGTUTTTCTTGTCTCCUT	78181	GCAGAAGCTGTUGATTTCTCCAAAAUA
231174510	78182	AACCAUGGAGGGTTTUGAAGAAGT	78183	CTGGUGAAGAAGGTCUCCGAT
231179114	78184	ATTGCATAAGGGUTTGTGTTAGACUGA	78185	CCTTTTGATCACUCCCACCTUCAAG
231179417	78186	AGGACTACAUGGGTCACTAUGGT	78187	CCCCTACCTAUTCTTGCTCTCCUC
231180683	78188	TCAGGTACAUCTGTGAGUGAGAACA	78189	AACCAGTAAGCUAACTTGTTGTAAAUAACCT
231187713	78190	TGTGCTCTTTAUCTCATCAGACTTTUGA	78191	AAAAUGTCCUGGGAAGCCCAA
231188508	78192	ATTCTGTAAGTGAUGCTGCTGATGTUAT	78193	TGATAATGCATUTTAAAGTTCTACUCACCCA
231188521	78194	GCAAACAACUGACCAGCCTUT	78195	CATTTGGTCCCAAUGTTATTCACATTUCT
231188807	78196	GTGTCACAAGCAUGATTTTATTGUCCT	78197	ACTTTTGGTUGGAGGCTCACTUAC
231189965	78198	CAUGGGTCAGGUCACAGAGAAG	78199	AAAATAGTTUCCACCAGCUCCAAGT
231190470	78200	TGTAGAAGTCTGGUTAGATCCAGCUT	78201	TCCATGATGCUCAAAATTAACTUACCCT
231191963	78202	GGCTGAGGCUGTTCCATAUGAC	78203	GTGGCCGACCUGTCTATCAUC
231192551	78204	ACACAGGTTGCUGTTGTCAGTAAUAT	78205	GTTTTCTCACTUCCCCCTCCTUAG
231198336	78206	GAGGACATUCACAGGGTUCAGAA	78207	GTTCAGAGGCUGATTGTGAUAGACA
231204216	78208	CGGUGAAGCGGGCAUAGAG	78209	GGCTTCGUGGAGCATTTTCUG
231206820	78210	TGTCCTGUCCCCACTCCTTUAA	78211	CCCCTCTTUCTCAGTGCUCA
231206913	78212	AGACCTTTAGGACUTAGCTATATTCUGAA	78213	GACTTAGUGTCATGACUCCAGCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231206950	78214	CCACTATTGCUGGAGTCAUGACA	78215	ACGAAGCAGTUGAACTTTCTGTUCT
231207881	78216	AGGGAUGACGCGGTUGAC	78217	GCCCAGAAGACGCUGTUCC
231208212	78218	CACCACGUCGTCGAUGGA	78219	GGGCGGGUGGAACCTUAG
231212482	78220	GCTGGCTCUGTGCAGAAUCC	78221	TGTCGAAUGTGCTGTUGACACA
231215052	78222	TCAAGAAUGACAATGUCCAAGACACA	78223	CTGCAAGAGUACAAAGATTGGCTTUT
231218729	78224	GAAAGAAAGAAGCGUATGACACATUGAT	78225	CCAAGCTTTGGAUTTCATTTCTGAAGUT
231220326	78226	CTCAAGGACAUTACTAGTGACUCAGAAA	78227	CCAAGCAGTATUTACAGCCAGCUA
231221292	78228	CCAGTGACTTCUACACATTTGTTCTAUCT	78229	GGGTGAUAAGGAAGAGGTACTGUGA
231222418	78230	ACCCCGAGUATCTCAACACUGT	78231	CCATTTGGCUTGGCTTCCTUG
231226755	78232	GGTTGGATATAGAUATAGATATACACACGUACA	78233	CCTTCGGUATAATCACTUCCAAGCAAAT
231227168	78234	CCUGCCCACACACACAGAUAG	78235	ACTTTGCTCCUGTCCTGGGUA
231227779	78236	CTCTTTAGGATUGGACCGGAATAAGUT	78237	CATGCCCAGGGAAUTCATUGAG
231228936	78238	ACAATACAGTACAUTCTCCTATGUGGT	78239	CACCAGCCAUAGGACCGTATTUC
231229243	78240	GTTGTGUAACCGCCATGGAAAUT	78241	TCACATGTUACAGCATGACAGTUCAT
231229586	78242	GTTTTGTTTTUATCTCCCCUCCAGGAT	78243	CCACCAATTGAAAUGTGTCTAGAATUCC
231232247	78244	CCTAAACAGUGGGAATTCUAGACACA	78245	ACACACACACAAAACAAUCTGCTTAAUT
231232550	78246	ACTTCGAAGCAUTGGCUCCAG	78247	ACTACTTTGGCACUTGATTCAAGAUCA
231232885	78248	GAAGAAAACAGCAAGAGUAAAUGCAGAA	78249	GTGGGATTAATTAUTGCCATTCTCAUCC
231234433	78250	GATACTTGUCACCACTCCAACAAUGA	78251	TCTGTACTTCACACUAAAAATGGCGAUT
231237397	78252	GTCTCGUAACGGTTTTTCTCUACCA	78253	CCGCATTACUACATCCAAATCCAUAAGA
231239581	78254	GACUACCAGCAGGACTTCTTUCC	78255	TTTTAGGGCUCATACTATCCUCCGT
231246379	78256	AGAGGCUAGTTTTTGTTCUACGAAAGG	78257	TTTCTCCATTTTGUGGTCATGGTTTUT
231246891	78258	GGUCAACAGTGGAUGAAAAAGAACAAAA	78259	TGCCATCTTCAUTTGTCCCAATUAGA
231247801	78260	GCUCCTCTCTTCUCCCACAGAA	78261	GATGTGGUCGGCTTCATAGUAGAT
231256663	78262	TGACCTTCTATUATGAAAAATGCCUCCA	78263	CGTTTTCTTCCUCTGTTAGGCATTGUA
231258378	78264	AATAATGTTUCCTCAGTCUCCACCAC	78265	GTAACCACTGUCCTTTGCAAATTUGAA
231258570	78266	CCACATCTUCACCTGGCAGUT	78267	GGAAAUCCACAGAGAGCACTGUT
231259522	78268	GACTTGTGTAUCACCTGCTAUAACACT	78269	AGCAUGGACCAGAGACUGGAT
231261405	78270	GTTCCGGTUCCCATCCTUCAA	78271	AGAACAAGAUGAAGGGCAGCATTTAUAT
231263944	78272	CCAGAATTCAAUGCTTTCTCAGCUT	78273	TGCTCCCAAAAUACTACAAGGTGUC
231275066	78274	TGTGCUCATCGCUGGAAGAAC	78275	GGGATGAGGAAAAAUCAATCCAUGCT
231275853	78276	CUTCCCTATAGATUACACAACCAGCAT	78277	CCAGAGACUGAGTTTGUAGGCA
231281127	78278	GATTCUCGCCGCCTGAGUAT	78279	CATTGGTUTTCCGTTUGCAACC
231284497	78280	TTUAGGGCAAAACACTUCCACCT	78281	GCACTTTGGUCTTCTCTCCCTUT
231292723	78282	TGGTTTTGTCAUACTTTGACCTTTGUCT	78283	GCCAAGACTTGUCTGAAGCTGATUAA
231297238	78284	GCCAACAGCUGACTCAUCAC	78285	GUTCTTGATGTGCUACAGGGAACAT
231306028	78286	AGCGGGTUGTGCAGCAUA	78287	TGCCGGAGCUTCTGCTUG
231306411	78288	GGTGTCCAAGAGCUCCTCTUT	78289	AAAGGAGCCGAUTTTACTAACATUCAGT
231311108	78290	GGAAACGCACAGUCAAAGUGA	78291	CACTGGACCAUCTCCTGGATUT
231314233	78292	CCCUGACCGGAGTAACCUT	78293	TGTTUCCAGACAAGCCACUCAC
231316189	78294	TGGGACTAACCAAUGGTGGTGAUA	78295	GGGCCACCAACUCCCATATUG
231316630	78296	CTTTGGCCAAUGGACCCTTTUC	78297	GTAGAGUGAGTGCGTTUCGCT
231317737	78298	GGTGCCGUTCTGCCUAAACAT	78299	CCAGTUGGTGTCGTUGGAGT
231326176	78300	GGGATGACAGAUTTCATGCTTUCCT	78301	GAGGTCUCCAGGAGTGGGUA
231334380	78302	CGATCTGGUAGTTCCCCUAACCT	78303	CATGTUGGGAGAAGUCAAGCCT
231335168	78304	ACAGAACCAAUTTCAGCCTCUGA	78305	GGCCATCUGGAAGCATTAGGUT
231336583	78306	TGGAAGTAAUGGAAACGTGCCTUA	78307	AAAACAUTTATGUGAAAAGCCAACAAGGA
231341760	78308	GTCCCGUCAGAAGAGAUGAGG	78309	CTGTGGTCUGAGGCCTAGUG
231343720	78310	ATCAGAAUCTTCCAGUACAGGACAGA	78311	ACCATAGGATCUTACTCCATAGAGUGG
231347581	78312	AAGGCUGACUCCCAAAGACAC	78313	GATCAGACACCAGGAAUGCCTUA
231355550	78314	TGGUCAAAAGCCCAAUGACACA	78315	CCAGGAUTCAUGCCCGCAT
231358520	78316	CACTTTGGAUCTCAAATTGUGCACAT	78317	AGAAAAUCGCCGAAAGTUACCAAAAC
231360276	78318	CCGTGCACGUTCTAACATGTTTUT	78319	CTTAAGTCAUCGGCCCCAUCC
231360905	78320	CCACAGGTATTUGTAGCAGAGTTUCA	78321	CCAATATGGTAUGACCAACATGGCTUA
231369649	78322	CCTCCCCGUTATGGACGTGAUA	78323	CUAAGGATCAUCCCAGGACAGGA
231374061	78324	GTGTCGTAUCAGCAGGAAATCTUC	78325	GGCTGTCTTUGCATGTTTCATATTTUGAT
231379709	78326	GCAGTATCUAACCAGAACTCTCTCTUC	78327	GCAGGGCUGUCAACCAGAC
231381127	78328	CCTCGAUGGCCGCUAGAAT	78329	CAGCATCUACAAAGGCAAGAAGUG
231389553	78330	TGAACTUCAAAAACCCCCTCUCC	78331	GGCACTUGGCCTGACUACAC
231390045	78332	CATGGGAAUGAACACAGGGAUGA	78333	TCAGTAAGTUGCCAGCACTUCC
231394623	78334	AGGTGTGTTTUTGATGAGTCAUCCA	78335	CTGGCTGAATUCAAAGGTGAAATTGTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231395819	78336	GTATGAAATGTAAAUTTCATGGTGCTGUGA	78337	TCTGCGCTUGGTGAACTCTUT
231397117	78338	GCAGGCTTTTAUGTCTGTCGAGUT	78339	GGGAATCCCCAUCCCAACATUC
231397839	78340	AGATATTGAGUCTGAGGACTUCAGCA	78341	GTTGCATATTUCACCTCTGGCAUT
231402468	78342	ATGUCAAACCCCACGTCCUC	78343	AGAGACCAGUTGTCACCUCAGT
231403266	78344	GTGAAAUCGAAGCAGGACUCCAT	78345	CCCTTCGTUCCTTGGGATCAAUT
231404672	78346	GGTACCAGGGAUAAAGATACATGUGGAT	78347	GAAAAATGUCCAGATGGCTUACAGG
231405687	78348	GATAACUAGGAAAGGATTUGAGCGACA	78349	TCACTGTGGAUGGAGAATGATGTTUT
231407802	78350	CCCCCTATTCTAUTCCTTTCCTCCUT	78351	TTGCCTAGUACATGTCCAUCCAAC
231409323	78352	TGAUGCTAATTTCUCCAACCAACA	78353	CUGAAAACTTUGGAAGACAGAACCAAAT
231410283	78354	CACGCTGGAAUCCTCGTTTUC	78355	GTTTTATTUCGGAGGCTUGCAGT
231411694	78356	GGGACACCAACCCGUCUAC	78357	GGCTTATGGGCUTTTACTCCUCA
231416259	78358	GCATACTTGAAAAUGAAACTGTTUGCC	78359	ATTCCAGAGGAAAUGACACCACTUT
231418373	78360	CTGAGTCTUACCCAAAAGATGGAGAUA	78361	CTGTGCCATCUCATTGTCTCTUAAAAAG
231419236	78362	GCACCGACUTGCTTGTAGCUT	78363	GTTACAGCACCAUCAGTAGGUACA
231420020	78364	TGGCTCCUCGATGCCCUAA	78365	GGAAACTTGGGUGATTCTTGTGTTUAT
231426392	78366	GCAAATGTGCAAUACCAACATGUC	78367	GCCATGCUACAATTGAGGTAUACGAAAT
231434090	78368	CAUAGAGAGCAAAGGUCAGCCAA	78369	CCATCTCACACUATGCCATGAUGA
231439803	78370	GGAGUCTGGAUGGAAGGACAAA	78371	TGAATCCTTGTCUTCTACCCCTGUAG
231440621	78372	TGGCGGUGAAGGCTUGAG	78373	CGCTCUCCCGGAUGAGGA
231441371	78374	GGAACACUCACGGCUCCT	78375	CGACUCACCCCGTGUCT
231442945	78376	CCCATCTGUTGGTGCTTTTUCT	78377	GGTCCCGUCTGTGTCCCTUA
231448837	78378	CCTCGCUTGTATCUCCGAAAGAAT	78379	CGAGTAGAAAAGAUTAAAGGGAACGUG
231455123	78380	AAGCTTCTGTAUGTTTGGGAAAUGAGA	78381	GCTCTTGCTUCAGACTCTGUGG
231456023	78382	CACTGCUCCAGAAACCTTCTUCT	78383	CCCAGAGCUTGTTGTCUCCAC
231457109	78384	ACGTGCACAGCGUGTATTTTUC	78385	AACTCTCCTCUACAGAATTTCUGGAAAC
231457422	78386	AGTTCTGGCAACUGCATCTUCT	78387	GGTTTCTCCCCCUTGCTCCUA
231457477	78388	GATCAAGGTUGAGCTTGTTGATTUGG	78389	AGCTCTGTTTAGUCTCTGGCTCTUAA
231462672	78390	CCAGGTGTUCATCTCTCCTCUCT	78391	ACCACTTCUTCCTTCGTUCGG
231467912	78392	CAACAGGAGAAAGAAGAUGCTAAACGUA	78393	CTGGGTTTTUCCTTTTGCCTTAUCAAG
231469575	78394	GTGACCGCCAGAUCTGTGUT	78395	CGACAAATTCATUACAAATGGCTGUCA
231473939	78396	CTGAGATGGUAACACCCGUGA	78397	TCGACTTCAUACTGGCCAAGUG
231478046	78398	GTAGTGUGACGACATTGAGTTTUGG	78399	CTAACTGCTCUGATACTGACTCATUCAAA
231480141	78400	CCACCGTGGUCCAGATATAUAGCA	78401	CTGUGCAACCTTTTUCACCCAT
231481010	78402	AGCACACCACAGUGTAAATATTTTUCAG	78403	TGTGCGAGAAUTGCTTGAAAUGG
231481274	78404	TGAGTGGUCCCTGGGAGATUT	78405	CTAAGCCTUCATTGCTCUAGCCT
231481279	78406	TGCCATGGAGAAAGAAUTTGAGCUA	78407	AGATGATTCUGAGAGGCAGGUCT
231482571	78408	CTTACCTAAATTUGGCAGTTTCTGGUT	78409	GGTATTGTUGGCTCCCTTUAGAAAGA
231484970	78410	ACCAGAGCAGAGGUCAAAATUAAGG	78411	TCTACTAGTUGTGGGTCCUCACAAA
231485590	78412	GTTCCATTUCAAGCAATTCUCGCA	78413	CCCATGAUGCGGCCACTAAUA
231487299	78414	GCCCTTCTACAUGTCCCACTUG	78415	TCTTGGTTGCUTGATAGGTAGGUACT
231493149	78416	CCCCTGACUCCGTCCAGTAUT	78417	CGAGACACGCCCUTACCUT
231493565	78418	GAATACAUGCGGTGGATTTTUGGG	78419	TTCCTTCACUGAGTTCUGCGAAT
231493730	78420	GCAATTGCAUCAAAGCAACAAAUAC	78421	GGCTCCTCUAACCATGTTTACAACUAT
231494240	78422	GTTTCAGATACUACAGATGACTTGTGGUT	78423	GCACACAAACAGAAUCAACATGGAATUT
231495698	78424	TGTCTCTCTTCUCTTACCCTTTTUCCT	78425	CCCTGGAAACACCUCAAGATTTTCUAC
231498739	78426	GAGCCAAAAACCAGUGCTUCAG	78427	CGTCTTAGTTUCCTTCTTTTCTUCCCA
231499556	78428	CAGCCTGTGUCTGCTGAAGTUA	78429	CCATGAACTCCUGGAGAATAATCCUAAG
231499823	78430	CCGTGGATGAUCACAGGGTUG	78431	CCACAGGTAGUAGGGAAGAATGUACT
231506139	78432	ACACTTTCCTTGUGCTATCAATTTACUCA	78433	GTTGAGGATACTUCTGCAGATTCGAUAT
231508584	78434	ACCCACUATGAAUGAGCAGAAAACC	78435	CCTGTGTGAGGAUGAGCTCTTUAC
231510929	78436	CCACAGGAATGUCTTCCCATTTTACUA	78437	CTGTATTCAUACACTCCCCTTUAGCAAT
231522019	78438	CTACAGTTACCUTCCCTTTTCTCUGG	78439	ACACGTCCTGUTTCCTTGTTCUG
231532480	78440	TGGACTTGUGCAAATGCCUAGT	78441	GGACATTTAUCCAACAAAATGCTACUGT
231536721	78442	TTTCCAGGAATCUAGGTAAAAATGGCUT	78443	ACGTAAATACTAGGUGTAGGTGGATUCA
231537627	78444	GGTGCAAUTTAGGAUACCCCCAA	78445	CGTAGCAAGAUGCGTGATGUCA
231542054	78446	CUCCCTUGCCAAAGGACAAGT	78447	AATGTTTCCUAAAGGGCATCCATGUAA
231547396	78448	GATGGAACAACUGATGTCTTACTTGUG	78449	AAATATGTGCACCUTCCCTCCTUT
231551351	78450	GGGTCAGCTUAAGGTAAGAAACTGUA	78451	CTGGAGGCAGAUTTTCCAAACUG
231555966	78452	TCATAGCUCAGCTGTAAGAAAUGCAA	78453	CTACCAGUACGGCACCACUC
231556993	78454	CCTCCGAUAAGCTCCTCCAGUA	78455	TTTATGGCUGGTGTCTGACUCAC
231560176	78456	GTCTGGATUCACATTAACTCTAUGACCA	78457	ACTTCGCUGAATTGACCCAUGAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231561702	78458	GCUATGAUCAACCAGGCAACAG	78459	TGCCCATCTGUCTTGATTCACATAUAAG
231573509	78460	CCAGTTCAUGCAACAGAGAGUG	78461	ACAAAACACCUAGCAAATGGAAAAUGG
231576131	78462	CATAGACCGUACATGTCAGCGTUT	78463	AGCTGACTGACAAUTCAAAAGTTGTTUT
231577696	78464	CTTTGCAGCGCGUTGACTUA	78465	ACAGCTACTCUCAGAAAGCACTUAC
231588069	78466	ATGACTGAAACTTTUTAAGATTAGAGGGTUGA	78467	GGACCAACCCAAGUATTAAGAGTGTUAT
231591385	78468	AGGCATCTTTGGUCCTATATTGAATGUT	78469	AAGCCCAAUCCGCCACAUA
231591859	78470	GCTGTAUGCCTGGCAUCCAAT	78471	CTTGTACTGCCAGUAGGACTGUAG
231595865	78472	ACCATGAAGUACCAAGTTTCACUGT	78473	TGAAAGAUGCCGCCGUGAT
231600663	78474	ATGCTCCAGTAUTAGTGTTCGCAUT	78475	CATGACCCCUGCTTCCUCAC
231601697	78476	ACTGGTGGTTUGTCTTGAAAAGAUACA	78477	AGGTGGACAAAACUGAGAGCTUAG
231603173	78478	GCAGUCCAAAGAAAGGACCCAUT	78479	TTTTCCCTTTTGUAGTAAGCTGTGCUA
231603895	78480	AAGTGCTTCUTCTAATTCCAUCAGCA	78481	ACTGCAGTATTGAUACCTTTTGTTTCUT
231607889	78482	TGGATACAAGCUGATTCTCCCAUCT	78483	GGTTACTTAACTUGTTTTCAGCAGUCC
231610074	78484	GGAACACCTCCACUTACAAAAGAAGAUA	78485	TTTTGCCCUCTGTAAGAGTUGCT
231611127	78486	GGACCTCATCAUGGTAGGTTTTUGT	78487	GCTGUCAGAACTTGCTUCAGAGAAA
231611576	78488	GAATTGCTGGUCTCAGCTGUC	78489	ACCCATGUGCATGAGUACAAACT
231612233	78490	CACCCCATCCUTAGTCCAACUG	78491	CCATCTGTCUCCGTCTTCTCUCT
231614756	78492	GCCCTUGAAAAAGAGCUGCAGA	78493	AAGACTACCUAAGAACAAGCTCUCAGA
231615718	78494	TCCGGGTUCCATTAAAAGTTGUGA	78495	ACACACTGTGUAAAACCTCCTUACC
231616816	78496	CCAACAGAGGGAAACUAATAGTTGUCT	78497	GCCTCAGUACAAACTCATTAGCAUCA
231617288	78498	TTTCAGGUCAGAAGCCTAGACTUAGA	78499	CTTTCACTCCUGGTCCATCAACUAC
231617896	78500	AAGGACAGAUGCAACCATTGCUA	78501	AACAGGCATGAUGAACTGTCGAAUAT
231619460	78502	GCCCGCUGCTCACCTUT	78503	ACGAUAATTCCTUCCCCAAAGCC
231619521	78504	TGACGAGCUGCAATTTGGTTAUGA	78505	ACTCTACTGGAAGAUTTTAGAAACTCUGA
231625177	78506	TTTAGCUGCTGAGAAUCACGGT	78507	TCTCTCCACACUTCCCACATACTUA
231625192	78508	AGAAAGGUGAAGACACAGGUCAAAA	78509	GGGCAATTTTAATUGGAGGGTCATAAUC
231631651	78510	GGCTCTGACAUCTAGTGTGUGT	78511	CCATCCCCCAUAAACCAAGAACTUA
231635036	78512	CTGCATACAAGGAGUAGGCAGUT	78513	GTCTGTTTTGUCCATTTGGTATCTCUCA
231636552	78514	GCTTTCTTGAGGUTATCTTCACUGGA	78515	GCUGACCACAAAGCACAATTUACA
231637702	78516	GTGGCTTTTUAACCCATAGCTGTUT	78517	CAGTTGCCATAUCACTCTCACACTAAUT
231639116	78518	TTAGACTTCTAAAAAUGCATTAGAGGTGUGT	78519	GCTGAAACUGCTGTTGATGAAUAAGT
231639161	78520	CTCGGCGGUTTATAGAGGAUGAG	78521	GCTACTAGAUCGAGAGGAGTCUGAAG
231642163	78522	ACUTTCUGACCAGCAACGACAAA	78523	CACAAAGGAGAAAUCTGUACCCACA
231649909	78524	TGGCCAAAAUGAGUGGACACA	78525	GGAAACTGAGAGGGAAUCTCTTTCAUAA
231654221	78526	GCTGAAGTTGUAGCAGGAACTACUA	78527	CAAGTAGAAAGAUTTGAAACAGTUGGCA
231656746	78528	CTACATACAUACACCTGGUGGCT	78529	AAAGAACCCCACAGUCCATGUT
231661039	78530	TTTGTTAATGTCCUTGTTGTGCATTUAT	78531	TCUGGAATAUACAGGGCACAAACC
231661458	78532	TGCAGGCAGAGCUGATTUCT	78533	AACACATTAATCUCCATAATTCCUACAGCAT
231661973	78534	GGGCCCAUGTGGTTTGUG	78535	ACAAAAACTUCCTTTCTACTUCCCAGT
231662993	78536	GGAGCGAUACCCCTGAAGUT	78537	GAGACGAGGAGGUCTGCUG
231663922	78538	CAGTCTGTGGUAAGTAACTTTUAGGCAT	78539	GTGGATCUGGGCAAATGAAAATGUT
231664256	78540	CTTCTCAGCACUCCTCTCAAAUGT	78541	GGAAATGGGCAGUGGAGGAUG
231672364	78542	TGGATTTGGAAUATCAGGGUAGAAGGT	78543	ATTTTAATCTCAGAUGTGCATTAAAGGATUC
231674502	78544	AAGGCCTGAUATGTTTTAAGUGGGAA	78545	GGATCTGAAACAACAUTCATGTGUGAA
231675990	78546	CCAAAAGCAUCTGCUGCAGAAAC	78547	GCATGAATCCAGUCCAGATATTUCACAT
231679108	78548	CCTCAGTATTCUCTCTCTTCCTCUCA	78549	GAGCUGGGACCCCUCAC
231679449	78550	AATGGTTGCTGUCTCATCAGCAUA	78551	CAGGCCTAUAAGACTTCAATUGGGAAT
231679983	78552	AAAAGAAUAAACAAGACCACAGACUCCA	78553	GAAGACTTGGAUCGAATTCTCACUCT
231683604	78554	CAUGATACTAAAUAAGCCAACACACCAC	78555	TCCTCATGUGGCTGATGTTTUCA
231684200	78556	AGAAGUTTTGGATCUAGAACGACGAAAA	78557	GUTGGAGGCAUAAGCCAAGGT
231684536	78558	AGGAAGTTCTUACCTCATTGGTTGUG	78559	CCACGTACCCAGUGCATATGAAATUAA
231688652	78560	CTCATTGACTGAUGAAACTTGCTTUGA	78561	CATGTAGAUGGCGGTGATGGUA
231696523	78562	CTGTTGACCUGTCCCGGUA	78563	AGAUCTTCTUGCAGCCAGCAAA
231697556	78564	CCTCCAGUATCTCUGACCACAC	78565	GTGGCTCUGACCTAGAATGCTUT
231701903	78566	AGTACUGTTGCCUGGGCAAA	78567	TCCAGTATTCUACCGTGGUACACA
231706832	78568	GACACTGTCAUCTTCCCACAUACC	78569	GGAAGTTAAACAUGTCAAATGCUGACT
231712764	78570	CTGACTGCAUGTGTGGCTAGUA	78571	TTTGGAATUGACAAGACAGCAACTUG
231722566	78572	GTTACCAGUGCCAATAUCCAGGAG	78573	CATCTGGATCCUCAGGACTCUGT
231726202	78574	TGUTTTAATCTTTUGGCCCCAGGA	78575	CTGCTCCCCACUCAAGACTUAC
231728889	78576	AACCGACATTUAGGTGGACTTCTUT	78577	CCAACGTCCUCGGGAGTUAG
231737830	78578	CAACATTTTGACUGCTACTGTCCUG	78579	CTTGTTGCTGUTGTTGTTGACUCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231738028	78580	ACTTGGACUGACGGAACTUGG	78581	AAGGACACAGCAGUGGTATUGG
231746486	78582	TTTTGTGCAGTAUTAATGCTTGCTGUT	78583	AAAGTCCAUAAGCCTACCTUGCC
231748789	78584	TGATAATTUCCGACCCCCUCCA	78585	TGTGCATAUCAAACCTTGTUCCAGAA
231752447	78586	AATGGCTUGACAGAGTTGUGGAT	78587	GGAAAAAGCUAATGGATGGAUGGAAAAG
231755461	78588	GGCTTCAUGCCCTATTUGCAAG	78589	CTAAGAACATTCUCTGACAGGTUGGAAA
231761358	78590	GTTAAACAGUCAACCGTACTAGUAACA	78591	GAGGTCCGCUCTTTTTCTTUGG
231761491	78592	CTGAGACTTUGCATGGTTTCTTUCC	78593	AACCATGCTGACUCAAGATTTGATAGUT
231761545	78594	GGAGGAGTUCAGAGGAAGACACUT	78595	GGACCCTGAUGGATTACAAGGAUG
231766843	78596	CTTCTTCTCTUCAGAAGTTCCTUCGT	78597	CCAGACGGUCCATCACTUCAG
231769447	78598	CCCAGAGCAGUAACCTAAAATGCUT	78599	ATGAUCACAGGCUGGCAGAG
231772711	78600	CTGTTUGCTTGGAAUGGGACA	78601	GTGGTGTUGGCAGAGGCUAT
231782048	78602	CTAGAACACUACGCAUGCAGGAT	78603	GAGAATTGCUGATCTTCAAGGUAAAACAA
231786701	78604	GGGAAAGGGUCCTCTGAUCAT	78605	GGTTGTTCTUGTGGAAGATGUCCT
231796159	78606	GGTTGGGUTTGTCCTTGUCCA	78607	GGTGCCUCTCAAGGTTUGAACT
231796369	78608	TCGCAAGACCAGGUGGUAAC	78609	ATTTGAAACGGGUTAGAGATTAGUGCT
231796481	78610	CTACCAGGACACGAUTTTGUGGA	78611	GGTCAGGCUGTCUGAGAGAAGA
231796494	78612	GGGAUAGCGGGACTGATGUC	78613	GCUCTATGCCUGCCAAGACC
231802329	78614	TGCGTATUCCTGAGCUGCAA	78615	CGGCAGGAGGUTTAUGGCAAT
231803662	78616	TTGAGGTGUCTCTCCUCGAAGAT	78617	GGAUGAGAGGCGCTGCTUAC
231804623	78618	TCAACTCAAGAGUCAAAAGAAACUGGA	78619	GTTCTCATTCUGTGTCTTCCCUGAA
231805129	78620	GCCCUAGCCTCUCCCACT	78621	TGCCCAGUCCTGCUGAGA
231810854	78622	GGCCCGGAGAGUGGAAUG	78623	CCAAAAGUGACCGCUCGCT
231811541	78624	GCACCACUGAGAACAAGGGATUT	78625	GCTGGTGCUGGACTTTGAUGT
231814171	78626	ACTGGAAGAAUACGACACUCAGGAT	78627	GTGGAATUCCCCATGAACATUCAAA
231818832	78628	CATCTTTTCTGCUCTTCACTTCATGUC	78629	CGAAACCUAGTCACATUGGAGAGT
231822479	78630	CTGGCAGGAGGGUAAGAATGUG	78631	GGGACTTUCAGCGGGAGAUT
231822894	78632	AATGTCTAAATTGAAUGTGTCCTCCUGT	78633	CCATCCAAGACAAUGACAACAUCCAT
231824265	78634	TGTTCAGTGTGUCAAACAGTATTCTUGA	78635	CATAGACAATGGGAUCTTCACGGUAA
231825123	78636	GTGTUGGCCAGCGTTCATUC	78637	ACTCCUGTGTTGUGGCAACC
231825456	78638	AACCGAGAGACAAGCAUCTUCAG	78639	CCAGAGATAAAACUGCAATTCCTCTUGA
231826108	78640	TTTCTTCCAGTCUTACTAGGAGCTUCT	78641	CCAAATCTCCAGGUCGCTGAAUA
231830822	78642	TGAAGCAAATGTUCCAGTGTATAGGUT	78643	CCTGTAAGUGGACCAACATUCCAAG
231832002	78644	CTATTGGCTGGUGCAACAACAUT	78645	ATTCTATGCAAGGAGUCATTCTTCTUAC
231833624	78646	CUCTGAUCCGCCACACAACT	78647	TGTGACCUGTTTACAGTUCAACAAGA
231834658	78648	TGTGCAGUGCTTTGAGGAUCT	78649	GACATCAGUCCCGCTAUCCC
231839234	78650	CCATCATCUGAGCTGGTAATUACAAAGT	78651	AACTAACTCATAGCCAUTATTTCTAACCAGUAA
231840684	78652	CCTTCTAGGCUGCCCAACAUAC	78653	CCCAGCTCAUATTGCCTTCTCTUAC
231843011	78654	CTCACGATTATTTUGGTCAACTTGAAUGT	78655	GGUCTUCAAAGGCACCAGAAAA
231844568	78656	AAGGTCACAAATUTTGCTTATATTCTUAGGT	78657	CATATGAGAUGGTGCCTGACUGA
231844881	78658	TCUTCTCTCAGUCAGGCACCAT	78659	GTAGGTGAGAGUAGGGTTTTAGAGTUAGT
231846244	78660	TTGCCAGTTGUGCTTTTTGCUAAA	78661	CAGCTUGGACACGGCTTUAC
231857517	78662	CACAGCCAGUGCCAGAACUAA	78663	TGGTCCCGGGAUTATTTCCAGAAUA
231859493	78664	AGGTCAGTCAGUACTAAAGTAGUCGT	78665	CCTGAGAAAUGGCAGAGAAACAAAUCT
231864044	78666	TGCCATCCCUAATCCCGUACA	78667	TCAUCCCCAACCTGCUGAAG
231867504	78668	GCCCACCATTUTCATAGTCTGCUT	78669	GGTGCAAGGGUCACAGUGT
231870761	78670	CCTTTCACCUGGCTTUGCT	78671	ACCCUACAGAGACCCCACUG
231872431	78672	TGCTCCAGUACTTGTGGACUGA	78673	CTAATGCCAGGAUCACTAAGTTTGAUGA
231874283	78674	CTGTGACCTATUAAAAACTGCCCTGUAT	78675	ACTGTTGCTTGUGATTTCATTTGTUACA
231875454	78676	CAGCTGAAGAUAGAAGGAGTUGAACA	78677	TTCTATCAGUCAAGAAGUCAACCACAAG
231876115	78678	ACAGGAAGACAGGAAAUCCTCCUT	78679	ACTGCCCAAGUAAAGCTTAGTAACATUA
231880586	78680	GTAGGATACTTGUGGTTGACTTCTUGA	78681	ACTGAAGACAGACUATTCTCUGGAGAAA
231890033	78682	CTAGATCACTGGUGTGGAATAGCUT	78683	CAGTACCTCTTGCUTGGAGAGTTAAAUT
231895395	78684	CUCACTGTUGGCAAAGGCAAA	78685	AAATUGGACACAGCCCTCCUC
231905807	78686	ATTGTGAAATACUTACTCCTGACAUGGG	78687	CCATGTGGCUTTTCTTTTTCGTTUCT
231926584	78688	TGGCAGUGTACTGAAUGCAAGA	78689	GGACATCATTTCCUTCATTTTCCTTTUCA
231929356	78690	TGGAACCTCCUCACCCATTUACT	78691	TCACGAAACUCGCUGGCAT
231938524	78692	GGATGCATGUAGAAAACTACTCTTCUGT	78693	CTCCCCACUAAAGCAGTGCTUA
231939681	78694	TCGAAAACGCCAAGUCTUCCT	78695	GGAAGUGACCAAAGCAGGUG
231945161	78696	TCTCCCACUTCTTCCTATUCCCA	78697	AUGCCCTCCUAGACCAGACT
231957633	78698	CCCGTTGCUGGACTGGAUT	78699	CAGUAACCCCAAGATCCUGAAACA
231964182	78700	CTGCTCTCACAUTTTCAGTAGTTTUGAC	78701	GAAATCUCTGCACTUACCCCCAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
231964591	78702	CACGTCTGAUATCACTGCCAUACC	78703	CTGTGAGCCAAAUCCAAGAATUCC
231965079	78704	GAAGCCUCCAGAACUGGAAGAG	78705	CTAGCTCGUCCCTCACACCUA
231967051	78706	CCAGGTUCAGGGTCATGCUC	78707	ACGTGAAGUGACGGACTGTUC
231974862	78708	GAGGUTAUAGCAAGGGCCCAT	78709	CCTTCCAGCCAGUCTCCATAUAG
231983618	78710	GCATCAGGCAGGUACTTTGATCUT	78711	GGGTAUCAGGGACCTCUCAGA
231986513	78712	GTGAGAGTCACUTTATCAGCTCUGAA	78713	TCCTTTGCCTAUACTTTGCAGTGUAAAT
231990223	78714	GTCATAGGAGGUATGCAACAGGUT	78715	CAGTCCCCTUTCCCTCTATACUGA
231992790	78716	TCTTGTTCCTACUTCGTTCTCCAUCT	78717	GCAGTTGACCGUAGTCTCCUACT
231995197	78718	GGTAATUCCCCGGUGGGAAA	78719	CCCGAGAGGUTCGTTGUAGAG
231996349	78720	CCCAAGCAGGCCAAUCAUAGG	78721	CTACCTCGAGUCTGATGAGCUG
231998053	78722	CAAAGATTUTTAAAGGCGUACGAAGAGA	78723	CATAUGAGAGCACATCTTUAAACAGCAT
232000164	78724	ACTTTTTGAUCCCTGCAACUCAGT	78725	TTTCTCACAUAAGCTACATGGCTUCAA
232002826	78726	GGGTACCUAGGAAAGGATCATAATUCA	78727	GGCTCATAACUCTCTCCTUCGG
232003118	78728	GGGTCTCUCGGACTTGAGUCT	78729	GCCTATACUCGAGAGGCTTAUGG
232003803	78730	CTTGGAAGGUCTCCUCAAAGCA	78731	TTAGCAGTAUCCGCCGUCAC
232009723	78732	CGTCCTCCUCATCTGAATCTUCCT	78733	CUATGGCCCUCAACAGGAGAA
232010741	78734	CCTGGCAUAGGCTUCCCT	78735	ACGGCUAGTGACCAUCCAGAA
232011782	78736	CCCAGUGACCTTGCTCTUCC	78737	AGACAGGCUCCAGATGUAAGACAT
232012340	78738	CCCCUCCAAAGAAACUAGGCA	78739	GGGAGUACCCGUGAACAAACAG
232020668	78740	CATCATCUGGCAAGGCCAUCT	78741	GCTTTGATTCAUTGACAGGTTGUGG
232024822	78742	AAACTTCUCAGCCACAGCTTUCT	78743	CATGGCCCUGAAGATGTTGUC
232033913	78744	GGCTTCTTTGCUTACTTGGTGUCT	78745	CACGAAGGAGUGGTTAUGCAAC
232034043	78746	CCATGTCCTGUTCTGCTATTATGUCA	78747	CCUAGAGGAGCCCCAUAGCC
232036327	78748	CCTTGTTCTUGGCTCCTTTTUCT	78749	GCTGGACGUACCTCAGTTGUC
232037661	78750	ACATGGAGGAUTGCCAGAATCUC	78751	ACCAGCTGAAUCTCTTTCTUGCAAA
232038781	78752	TGCAGAACGGAACUCAGCAAUT	78753	TCCGGGAAGAGUGGAACAATTTUT
232040857	78754	TCTTTGGAGCAAUTCATACTTTCAGUGT	78755	TTCTGATTTTGUGAAACACCATTTGGUT
232041027	78756	CAGAGGCCUACTCATAUGAACCAAAT	78757	TGTCACATGAATGUAAATCAAGAAAACAGAUG
232041911	78758	GGAGAAGCCAGUTCCTUCACT	78759	GTGGCAAGAAGGGUATCTGTACUC
232047089	78760	TCCCTUCATTTTATAACAUGGCCAGAG	78761	AAACCCATUTTCCTTCCUGGACAT
232050300	78762	GUTTTGCAGTTCUCCGGGAGAT	78763	CTTGTTCACACACUCAGCTGATTUAC
232055656	78764	CTACTACCTTCUCCCCTGTTTCUG	78765	AGAACCTTCUCCACCAGCUACT
232056349	78766	CAACTCAAGCUGCGAAAACATAAUAGA	78767	TTGTTCCUGAAAATGAUAGGCCCAA
232057111	78768	ACAATGTGAGTGAUTTCAGGGAAGUAAG	78769	GCAACTTAACCCUGTCCCTTTTATGUAT
232058500	78770	GCCATGGGUTGGGCCUAT	78771	GGAGAAAAGCCUTTTTATTGCTACTUAAA
232061773	78772	CTCTCCUGCACTCCTTUAGCA	78773	GGTCCAAACGUCATGGGACAUT
232065940	78774	TTTCTGGATCTTUACAGGCCATTTUCT	78775	GCTCAGCCCCUCAGGUG
232068160	78776	CACCCGGAAAUCCCGUACC	78777	GGCCACATTAGCAAUTAGCTCTTCTAUT
232072297	78778	CCTCCTTCAACUCCTGGTCUCT	78779	GCTCGTATTGUAAGCATTTTCCTTTCUG
232080424	78780	CACCUGAGCAGGTGATAAUGGT	78781	ACACTTTGCAATUTGTTCCATTCGUA
232083633	78782	CAGTATAAAUTGGCAGUGGAACGG	78783	AGAGGGACUACAGCAGTTTUAGAAAAG
232083975	78784	TGCTGGTAUCTACAACTCUGGAGAA	78785	CTGAGGCCAAUACCCCAAUCT
232095994	78786	ACATTTTGAAACCUGAGAAGAAGGAUGT	78787	TGAGTTAACCUGCAACTGATTTTGTTUT
232096992	78788	TTGTCTTTCCUCATCCTTUGCAGT	78789	CGCCCAGAACUCCATTAAATTATCTGUA
232105498	78790	GATGGTACTCAAGUTATCACTCCACAUT	78791	CATCCACTUCACAGGTAGUCGAG
232113009	78792	TTGACTCTGTUGTGCTTCTATUACAGG	78793	TGAAGTTGTCUTTGGCAAGGAUCAT
232115560	78794	CTTACTGGCTUCTGTTGTTAAATGTUGT	78795	CTTGTTGCTCUGGACAAGTTAAAUCC
232116379	78796	CUTCCUCCAGAAAGGCCCAT	78797	GCCAGUGTATCAAGUGCAAGAC
232120095	78798	CAGAAAGTTTCAGUAGAACAACGAAUCC	78799	TTTGTTTTCCAAUAGCGGAATGUCAC
232122553	78800	CTGCTGTCGUACAGTCTTUCCA	78801	GGAGGCTCUCCTCATCTGUCA
232125747	78802	CTCACCCCUCAGGACAGTTUT	78803	GTTGAGGAGTUTGGTGCTACATUAC
232131275	78804	GGGCUGACAGGAAACACGUA	78805	GGATTTTGCTACCUGGTTCTGGTTAUAT
232136271	78806	AGATGTCTUCCCTTCGGGUGA	78807	GCCTCCGCUCCAAGAGTGATAUA
232139723	78808	GATTTCCUGAGGTTCACGUCCA	78809	TGCATGGCTCUTAGATTTGAGTGAUT
232140954	78810	AACATGTUCCCAGCUGAGAGAC	78811	GGGTCTTTAGGUCTTTTGTGAGAUT
232145904	78812	GCTGTGTUGACTGACCCCUA	78813	GTAGATGGGCUGGCTTACUGAAG
232147392	78814	GCAACCCAGUCCAACTTGGAUA	78815	GCUAACGCAGCAGTUGCAAAC
232152124	78816	GCTGTCCCTUGGGACTGTCUA	78817	CAUGCGGGAGAATUCAGACAC
232152723	78818	ACCCAAACCUCCAGAGAAGAGUA	78819	GTTGTTTATGGCCUGGGATTTGUT
232153993	78820	GAAGGAAGACAGUTCAAAGAGAATUAGGA	78821	CTTCCTCTTCCAGUTCTTCAGGTUT
232157483	78822	TTGCAACAAUGAAACGTGATGUGA	78823	ACCCCCAAUTTCCUCCACAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
232158699	78824	GGCCAAGATUCCGGGAGTUG	78825	GGCATACTGGACUCATCTCTCCUT
232160081	78826	GAAGTTGACCUTAACTCAAATGGUAGGA	78827	CAGCATCCGAUGACAAATTTACAUCAAA
232163531	78828	CCCGACGGUCTCTCTUCAAAAT	78829	GCUGGAGGAAAAAGUGAAAACCT
232169834	78830	GCTCCGAGUTCTGAGCTTUCA	78831	AGUCCCAGGAGCGGAUCAA
232171580	78832	CGAAGGACAAGGUTGCCCTUT	78833	CCAACAGUGAAACCACTTTGAAGUC
232173336	78834	CCCGGAAGAAAUTAAGCAUGAAGAA	78835	CGTATCTTGGCUCCACTTCAUGT
232173602	78836	CCUCCUGCGAGGGACAAG	78837	TGGUCACTGTUACCAGGACAGA
232174467	78838	AAAGCTCCTTUGGTGGATGTGUA	78839	AAGGAGUAAAAACTCAUCCACAGCAT
232175072	78840	AGATGCGTAAUGCTGTGGAUGA	78841	ACTCTTCCATUCAACAACATGTTUACCT
232176106	78842	ATCCTAGAGTAGGAUATAGGTTTTATCUGAAAA	78843	GGCAGACCUTGGTTTCCAUAAAGAT
232178011	78844	CTGCACCCACUAAAATCTGGTUG	78845	CTTCGGTACUCCCCCTCCUT
232178384	78846	CCTGTCUCGGGAAACTTGATUG	78847	AGAAATCTGCAGUAAGAGGCACATUT
232185712	78848	GTGTTTGACCAGAUAGTGGTTCUGA	78849	GCATCAGTTTCUGTGCTGGATTTAAAUT
232185765	78850	GGTTCCUCATGCGCTUCCT	78851	ACCUGCCCCAGCAGAUG
232187510	78852	GCUGGGCAGCGTGTUCT	78853	GAGCUGGAGCGCCUGAT
232190402	78854	ATGAGGTTGACUCTTTTTGTGATGCUA	78855	CTCTGGGAAUGCAGATTCTACAGTUAA
232190910	78856	GAGGTTCTCTUGTTCCATAGTTUCAGAA	78857	TTTGATGGCTUACCTCTTTAACAGUGAA
232193218	78858	TCTTCTTCTAGCAUTTGGAACAGCUC	78859	AGGGAAAAATAUGCTATACACACTUGGT
232193379	78860	GGAAAGTCAGUTTGTCTTAAUGCAACA	78861	TCTGTCAAATACCAGUAGAAAGTAAAAAUGAAC
232195697	78862	ACCCACTUAGAGTCAAATUACAAACCAAT	78863	CTTCGGGAAGCCUTAAGGAATATCUT
232197002	78864	CGAGGGCACUTACUCCACAAA	78865	GAUCAGAAAAACUGGCCCGAGA
232198762	78866	GAGAAACUGGCCUGGAGGAAG	78867	TGTACACCAUGAACCCCAACAAATTUA
232201046	78868	CACTGTCCTGTUTTGATATCCCAGAUT	78869	CTTGATACAUCAATCCGTGTTUGGG
232203142	78870	AGAGAATCTTACCUGCTCTTGTACUGA	78871	CAGTTTATCCCCAUACTCCTACTTCAUT
232204972	78872	GCTCCACAGUGGTTCCACAUAT	78873	CTAATGAGCCCCAUCCCTTUCAG
232205193	78874	GGTTCTACCACUCCTGCCTCUA	78875	GATGCAGGGAGUTGGGTTTTUC
232206013	78876	ACAGCTGTTGAAUTAATATCCTTCACUT	78877	TCAGCACTAAUGATGCCTCGUT
232207325	78878	GAACCTTACCTGUAGATTCAGTGGUG	78879	ACAGCATGGAAACAAGAUTGTGTCTUA
232207751	78880	GCTGCTGTTUGAGGTTTATTTTGTTCTUA	78881	CTCTCCCAUGGTTCCCTCAUT
232210669	78882	AATGCAATUCCCTGTCUCCACAT	78883	CCCTTTCCTACUAGGATTAAGGTCAGUA
232214717	78884	TCAATGTUCCGGCACTTCUG	78885	CCCAAGGUCAAGGAGATTATTGAUGAG
232214841	78886	TTGAGTUCGCAGCTCTTUAAGGA	78887	TTTTAATTTGCCTUCTCTTCTGTCCUGA
232215157	78888	TCTTTTCACAUTTCAGGTCAUCAGGAA	78889	TTGGAAACCTACUTTTCACAGAAGUCAT
232218348	78890	GAGAAGGGAAACUGCTCTTUCCA	78891	ACCCCAACCACUAAACAAATCCTUAC
232219152	78892	CTTGATCAGAAACUGGCAAGCUC	78893	AAACTTGTAAAAUGACCCCTGGTTCTUA
232220542	78894	GCAGGCCAACUACCTCTUGT	78895	CTCCUCCAGAAGAGAAGAAUCCC
232223103	78896	GTTTGTTGTTCCUGAAGGTTACUGG	78897	TTCTTCGCUGAATGGTAAGUGAAT
232225997	78898	GGAGTAGTAAAUGATGCCTGGUGT	78899	GAAUTACTCAGCUGCGGAGGAT
232227053	78900	GGTTGTTATTGTUTTTGGATTGCCUCA	78901	GTGGGCAUGTCAUCAGGAAAC
232229960	78902	CACATGTCCGUGTACACTTCTTTGUA	78903	GAGGUGGGAACAAGTUGGAGA
232231008	78904	GGCCTTTCTUCCTGGAACATUCT	78905	CAGCCAGAAAUGTTTTGGUAACAGAAAA
232233181	78906	CCCCAUCAGGAGGGTCTTUCA	78907	GGACACCCCUTTGTGACTCAUAC
232234090	78908	AAAAUGACTCTCUAAAAGGAGACCAACC	78909	GGCCCATUCATCAAGCUCAGT
232236793	78910	AGGTCAGTTCCUGTTTTTACGTUGT	78911	CGAAGGGUAAGGCGTTGUCAT
232237229	78912	TGAATTCGGAUGCAGAGCTTCUT	78913	CCAAAATCTGTGAUCTTGACATGCUG
232242025	78914	GGCTCTGACUCACCCTTGTTUT	78915	TCCCCCAGUAAGTCCCTTCAAATUA
232242412	78916	CTUGGCCGAAAACGAGCUG	78917	AATCAAAAGTCUGTTCCGACUCCAA
232242923	78918	GTCCAAAGTCTGCUATTTTCATCACATUG	78919	TTTGTTCUGGCGGTGTTTUGAAAT
232244328	78920	GACCCGCAGAUGTCCAUGA	78921	CATAGCAAAUGGCAAGTTCUGCT
232244408	78922	ACGTATTTTGGCUTTGAAATGGAACUG	78923	CTCUCCACCCAAACCCTTGUAG
232244465	78924	CCUAGACAGCACCGTAAUGGG	78925	AAGGAGCAGCUTGGCTAAACUT
232245242	78926	AGTGGTTTTGAUACGGGCTUCA	78927	AGCTGTTTCCUATATGAGGGCUCT
232252230	78928	TCAACUAACACAAGTCGUGAAAGGAG	78929	CGTGTTCGACCAUTCATAAATCAGGUA
232253993	78930	TGCCAGGCAACAGCUCTUAC	78931	AGATGACUGACAGAGAAGAACAAAUGAAT
232255049	78932	CCACTCCUCAGCCTUCACC	78933	TGCTUGCGCGACTUCCT
232256745	78934	AGATCUGCGAGGAAUAGAGAAGGA	78935	TGACAGAUCCTGCCTTCUCCA
232258477	78936	CACTGGGCCCAAUATGACAUCA	78937	GCCTAUGAGCCGGUCCAGA
232259796	78938	ACACCAAAGGCAACUGAUAAGGT	78939	TCCCTGGUAGATGGCTACTUCC
232260099	78940	CAGGAACGUACTGGUGAAAACAC	78941	CAGGAAAATGCUGGCTGACCUA
232263042	78942	GAAUGACGGCUCGGAAGGA	78943	GGATTACCGACUGCTCCTCUCA
232263203	78944	CGCGCUGCCAGATTTGTUC	78945	TGUAGCGGGUCCCCCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
232263253	78946	GAGGGCCAUGTCGCUGT	78947	TGATCCAGGAGCUCGCUGA
232263267	78948	AGGGCCAUGTCGCTGUT	78949	GGCGCCUGAUCCAGGAG
232264321	78950	AGAATCCAACATCUGAATACACCACAUT	78951	GAACATTGUGAACGACTGCCTTAUG
232266636	78952	CAGAUCCCUGGACCAACACAA	78953	GCTACTTTCUGACTTGCATTATCUCCAT
232266922	78954	CACAAAGUTAGTTTAUGGGAAGGAACCT	78955	ACCATTCATTTUGAAGGCTAGGGTTTUA
232268177	78956	GAGAACTGAUAGAAATTGGATGUGAGGA	78957	TGGATTTCCCAUGTGGTTCTTTTUAACT
232271814	78958	ACCAACCCAUTTCTCACCAUCC	78959	GGCTGGAAAAUGATCATCTCCGATUAA
232275139	78960	GAACACTTACCAGAAUACTGAGCAGUT	78961	GGGAATGAUGCAACATAATATGCTTUCA
232275914	78962	GGAATUCCCATTTGCUGGCAT	78963	GTTTATGACUGGAAGGATTGATGCTTUC
232279141	78964	TAGATCTAGAAUGAATCCTTACCUGCAA	78965	GGTCTAACUCAGTGGCAACUACAT
232279369	78966	GTAATGATGGGCAUCTGCTGUGA	78967	TCTCACTGUGCACCTCCCUA
232284595	78968	TGCAGTTCAAUAGTCATGACAAAGUCT	78969	AGAACAGCAUCCAGTGUCACC
232287439	78970	CTGTGTGCTAUTGGTGTTTATTUGCAT	78971	CAATAATCTGCAGUGTGGATAGAGUAACA
232287458	78972	ACCUGATGAAAAUCCCCAAACACA	78973	CTGGTCATUGTGGGTCUGACAT
232289819	78974	GCCTCTTATCAUCAGAAAACCUACCA	78975	CTCCGGTGGTTUGTAAACTATACTTGUAT
232290485	78976	CTCUCAAGGCCCAGCCATUAT	78977	CAUGAGCTATTUCCACCACCCT
232292902	78978	TCCTTTGCCAUTGTTAGCATUCCT	78979	CATAAAACGGCTUCAGAATGTAAGTGUA
232296708	78980	CAGCTGAGTUTTCCAATGTCAUGAT	78981	TCACTGTATTTTAAAUAAAAGAAGAGACUCACA
232297927	78982	GCAAAAACGCCCUGCTUGAC	78983	TGAAGACAGACAUGGAACGUCAC
232300074	78984	CCACGTCAGAGUGTGGGATUC	78985	ACTGAGCTTAACUTCTTTCCTGCTTUT
232302945	78986	TGCTCTUCCTTCTAACAUAAACAGCAA	78987	CTTCCTCTGTCUTCTCTCTCTTCAUACT
232303005	78988	TGAAGGTGGAUCCTGCCCUA	78989	GACTGTCTUGACCCTCAAATUCCA
232303549	78990	CTGAAGCAGTUAAAGGTGAAGTGTUAAA	78991	ACATCATGAGAGGAAUGCAGGAAUC
232309174	78992	GGTACCAGGUCAGTACTUCCCA	78993	CTCTTUGCCCTGTAUGACGAGAA
232311534	78994	AGCAUAACTCATTCAUCGCCACAT	78995	TGGCAAGAUATTGTUCGGAACCC
232313481	78996	GTAGTTTACTTGAAUAGTGACAGGUGGA	78997	GGTCCAGTGGGUACTTGAACAAUG
232318587	78998	TCCAACTTGUGGTTTAAAATGUAGCCT	78999	CAGGAGGATGGCAAUGGAAGATATAAUC
232318991	79000	AAGAGUCAAGTUGGAAGGCCAT	79001	CCTTTTCAUCAACAAGCAGTTUGACAA
232320233	79002	CATTTCATTTTUCAACAGCTTGCTAUGG	79003	ACAACAGGAGUGCAGTTCCTAAUT
232322908	79004	CACTGTGUCCTCCTCGTUGAT	79005	GAGGATGGGTTUTTCTCTTCCATGTUA
232325641	79006	GGAGCAUACCAGAGCTTGGUG	79007	TCTTTGTGGAUGAGAGAGTTCCTTAUCT
232327091	79008	TGUCCACCAAGUGAGGGAGAT	79009	GCCCCTAUGTCCCAACUGAC
232335912	79010	AUTCATTTATATGUACACAGGGCAGCA	79011	TGUCAGUGAGGAGGACACAGT
232336130	79012	GTGCAGUCCGTCGUAGAAGAA	79013	CAACGCGGCGUTAAGGAUAC
232338668	79014	TCAUCCAAGUGGGACAAAGGG	79015	CCAGACCTTCUCTCTCCCCAUA
232340060	79016	CTTTCGGTGAUGAGGAAAAGAAAAUGG	79017	CGGGAGAGCGGCUACUG
232341031	79018	CTAGATACCCCUCTGGAAGCTCUT	79019	CGATCGCACACAUTTGTCGUG
232351167	79020	AAAGTAAGCUGTACACATTUGAGGAGAA	79021	AGAUAGCTTGCTTUGGACACAGAC
232354611	79022	CCTTTGTUCAGTGTGGCUGGT	79023	AAAACATGTAUGCCAGCTGTUAGAGA
232356272	79024	CTTCAAAGCUGTGCCTGTUGT	79025	ATGAGAAGAAUGAAGCGATTCACUCA
232358265	79026	GTGTATGGGCUTCAGCAAGTTUC	79027	CTCACCCUGAACAGCACAATUC
232384922	79028	CCCAGGCUCTGAGAGATUGGT	79029	GGCCCACACCUTCTTTAGUGT
232397272	79030	GCTGCTCGUCTGTCTCTTUG	79031	ACCUGGAGACCCUGCAGAA
232399346	79032	CCACCUGAGCACCGUCT	79033	GCCAGCCCCUCTGAGUGA
232406547	79034	TCCTGGAACUAATCCTTTCCUCCAT	79035	GTCCTATGCTUCTGCCTACACUAAC
232409801	79036	CAAGCCUGGAAATGCATGCUC	79037	GTAACTCTAUCGGACTCTCCCAUCA
232410644	79038	GCTCCTCCUCGCCCTCUT	79039	TCGGGAUAGGAGAGCTCGUC
232413753	79040	CCTGGAAGGUGAGGACACUGA	79041	GCACUTCTTCUGCAAGGAGGT
232415337	79042	TGUTTATTGTTUCAGCGGAGGGT	79043	CCTGATTCTTTUGGGCAATCTTTTGUC
232419290	79044	ACCATTCTUCCTCTTTGCUCCAG	79045	CAATTGGCTTUACCAGGGCTTUT
232420265	79046	GGCCACUTCCUCCAGCAG	79047	CTGGGCUCTGACGCTUGT
232425795	79048	AGAACGGUCAACCAUGCAGAG	79049	CCATTTTGCTUCCGTTGTCTCTTCUA
232429859	79050	CAACCTGAUCCAACATGAAAAGCUG	79051	CTATTTTCACACUGCAACAGAAAGACUT
232432173	79052	GCAGATAUGGCAGCTGAGCAAUA	79053	GTGATCUCCAGCCTTGUGGT
232433557	79054	GTCCAGAGTUCACAATCCAGUAGAA	79055	ACACCAGUGTGTCTCTTUGCAG
232438424	79056	CCAACCCCAUGGAAAGATGUGA	79057	GUGGAATUGGCAAAAGAAGAAGACA
232442361	79058	GTCTTCGTTTUGCAGGAGAAUGG	79059	CTTGGCTUCCATGACACCUGA
232442521	79060	CAGUTCTCCGCUGGAAAAAGG	79061	TCTCTCAACTTTUGGGCCATTATTUCT
232445812	79062	CTACAGGAUCCAGATCTAACTUGGG	79063	AGAATGAGGCAAAUCTTTGTGAACUACT
232445874	79064	AATUTTTGGTTTTAGUGGCGGCAT	79065	GTTTGATCGTTTUCTTTGGCTATTCUCA
232451247	79066	CTTGGGAUGGCAGTGTTAGATAUGA	79067	TCAAAAGGCAUGGGUAAACACAGAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
232454985	79068	GAGCACTTAUCAGGGTGGCUA	79069	GTACAAGGAGAAAUACGAGAAGTUGGT
232458215	79070	CUGCAGAAGCUCCAGCGA	79071	GGTGGGCCAUCATGAGACAUAAT
232460433	79072	CTCGAGCCGUTTTCUCGGAA	79073	GUCCTGGAGUCGGAGAAGAAC
232461347	79074	TCTTCAGGAGAGAAUACCAUGGGT	79075	GAGAATCCAGAGCACUTAGAGGTUT
232463787	79076	TGCTTGAGGUGGTCGACTUG	79077	GTGAUCCGGCUGAAGCAGAA
232463812	79078	GGAAAUCTGCAGUGGAGGAGAT	79079	ATGCCACACCAACCUTCTTTTTAAAAUT
232465884	79080	GATCTTTCTCUTGGTGGCCUGAA	79081	GACTTTTUGACACTGAACCAUGGAAA
232466547	79082	GGCAUAGCCGCGGTTTUT	79083	GCCUGCACTUCGACGAC
232468843	79084	CCGACCUCATCCUCACAGGAA	79085	TGTCTGCCAAATUAAAGAGCCAAGAUAT
232469173	79086	CTGAAACTTAUGGGAGAAACAGGACUT	79087	CCATCAAUCACACGTACCACCUG
232469591	79088	TGTTTTCTTTTAGCAAAUGGAACGTGUT	79089	TCAGATTTCUAGCCGAUGAGGAGA
232472076	79090	AGGUAAAATGATCCTUGCCAAAGACA	79091	GCCTTCCTTGAUCATCTTGTAGAACUT
232474892	79092	TCCCCGAACUTCCACCAGAAUA	79093	CTTATCUGCAAGATGGCUGCCT
232481141	79094	TGAGAGTTCUTCCCCAGUGACA	79095	CGATGGAUCAGAGATGGAAGCUC
232481594	79096	GAGTTGTACAGUTCTGTAGCCTUGA	79097	GGAGGGCAAGAGUATTAAGAACAAAGUA
232481890	79098	GGCAAACUCACCCACAACAUC	79099	CCGCCTTUGCTTTGATCTTTUCA
232483118	79100	TUAACCAAGCAGAGGGAUGGAC	79101	GGTCTTTUGGAGTCACTCUGCAT
232483524	79102	TCATTTTGCAGUGAGTTTGCCAUT	79103	ACTGTGTAAATTUCCAGGTTGGAUGAT
232489617	79104	CTCCCTGUTCTCATGUGAAAGGA	79105	TCTGAGGAUGATGATGAGGAUGAAGAA
232490403	79106	CCTTAAATTTAGGUCTACTGTCAGCAUCA	79107	GCTTGCTTTCUTTCTCAGATCATUACGA
232490486	79108	AGTTCUTCTTATTAATGUGGCACCCAT	79109	CAGTAGTATCTUCCAAGCGCTUCAA
232493218	79110	CAGGTTCAGGUCTAGCTTCTCUG	79111	TTGGCCACACUCAACCTUGA
232494379	79112	GGGTGACTGUTGGATCTGTAUGG	79113	AGACCAGGTACUTACTGCTAAAGUGA
232496838	79114	CTGGAAUGCCGGTCGATUCT	79115	TCAACATCTGGGUTTCTGTCTCUAAAAA
232497035	79116	GGGAAUGCTTATUGAAGGGACAA	79117	GCCUAAGACCTTCCUGGAGAG
232500629	79118	GAACTCATGTCUACCTCGTTTGAUAAGT	79119	GCATTCAAAACUCCAGCAGCAUC
232503885	79120	TGAATCACAGUAAGTCAGCAGCUC	79121	GAAGTTTTGTGUTCTGCTTCCTTUCAA
232505733	79122	TGTGGATAUGCGTGAATTUCGAAGT	79123	CGGCCGTTATUTAAAGAGCCGATUA
232506811	79124	CACTAGCAACAACUCTATATCTGGAUCA	79125	AGCTGTGAGCUGAAGATTTCTUCC
232508541	79126	TGTCTCTGGCUTCTCTTTTTCTUCAAT	79127	CAAACTGCTCGAAAUCTTACGCAAAUA
232516804	79128	AACTGCTGUCGCTCATATGGTTUA	79129	GGAGCUGCACAGGAAATTTTTATUGT
232517022	79130	CTGTGACUCAGCTCCTCCTUG	79131	CCCTAAGTGTCCUAGACCTGTGTTUA
232525942	79132	GGAGCGCAAGAGUATCAGTGAUT	79133	GAGAAAGGCUTGCTAGGGUCA
232526302	79134	GTTCTTCTCCCUTCTTCTGCAUGT	79135	ACAATGTGCTUCTGCCCATCAAUAT
232526958	79136	CUAGAGGGUCAGAGGGCAAAG	79137	AACAUCACTAATACCTUGAGGAAAAGGG
232526973	79138	GGAACAACTGUGTCAGCAGCUA	79139	ACATCCAUTAGTTATAAGTUCAAAAACAAACCA
232528324	79140	CCCGGGAUGGGUGAAGAG	79141	CTGGGUGAGCCTTCTCGUG
232530475	79142	CCACCUGACTGAGAAUCGCT	79143	GGGATATGCCAUTTGGACATGUA
232532142	79144	GCTCTTCACAUAGTGCATGTATTTUCCT	79145	AGACTGTCGUGCCGTATUGG
232539411	79146	GTCCCGTGCUTCTGATTGAGUT	79147	GGGCACCAGAGAAUCCGUAG
232542114	79148	AATGACGCTCAUAATCTTCTCTAAUCGG	79149	CTGCTCTCTTCUCTTTATAGTGCTACUT
232542263	79150	ACACCAGGGUCCCAGAACUA	79151	GAGCCATTUGAGAACAACTGAAAUCC
232550196	79152	GACTTTCCCACUCCTTCCCUT	79153	GGGUGACCACAGCGUAGAG
232551113	79154	TAGGAATCCGCAAAGUATTCTAAGCUA	79155	GTCACCATCUCAATGTGGUCAAC
232554547	79156	GTGGTCUCCCATACCCTCUCA	79157	GTCUAAGAGGCAGCCAUAGGG
232556238	79158	CTAACTGCTATUCTCGGGTCAUCA	79159	GTTGCTGGCAUCCTCAAUGG
232559259	79160	GAGGCCAACCUCAUGAAGCA	79161	GGAGAGCAGUATCCCCTGGUA
232563459	79162	ATTCTGTCTTGGUGAAATCTGGUAGAG	79163	TGGGATCAGGCUTCCACTTUG
232564406	79164	TCTTCTUACACTTCACTUCCCCAGA	79165	TCTCTGACUCGGGAAGGGTUT
232565747	79166	CCCTGUCCATACCUAACCACCAT	79167	CAAATGATCGCUATCTAGCAACCCUA
232572207	79168	CAGCTGGUGACACAGCTTAUG	79169	CCTAGCCCCUTGTGGACAUAG
232575060	79170	GCTTGGUACAGGCACCUAGAAG	79171	TGTCCATACCTAUGATTTCCCTCTTTGUA
232575092	79172	CTACCTTCTGUCTTCTTGTCTATTUCCT	79173	TTCCAAAGTCAGCUATCTTGATTGUGT
232575825	79174	AGGAGAGGAACUCACTTACGACTAUAAG	79175	CCTTCAGCGUTGCTTUGGAT
232577674	79176	TTGUACAAGAGCTUCAGGAAGAGA	79177	AAAGCTGTGUGAATGCGTCAAAUAAAT
232579292	79178	CTGATTTGCCAACAAGAUTTCTTACUGT	79179	GACATUGCCTCCTTTUGAAGCC
232580732	79180	ACAGGTGTCUTGCTGGGTTUC	79181	GACATCACCUTTTCGCTTTTUCCAA
232581378	79182	TCTCAGGUCGACGGCUGA	79183	CGACGGGUCCCCACTUAC
232589275	79184	AAAUTATCTCACTTGUCAAGGCACAGA	79185	ACTATAGATGGUGTAACCCGGAGUG
232595919	79186	CCTCTTCUGGGTCTCCACUCAA	79187	CCTAGCCCUGCTGTGGAUAAAG
232596737	79188	ACGAAACTGUTTAGTGGGUAAGAACT	79189	ACAGGGCTTTAAAAUGCTGAGAACTUA

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232601250	79190	GCAACAAAATUGCTTCGTCAUCAAAAT	79191	TGGACAATAAAAGAAUGAGGACTGCUT
232601951	79192	GCACAGGUGTACAATCCTUGGT	79193	GCTTTGGAAGTUCAGTCAACTCTTTUT
232602474	79194	GTTCAGCAAUGGTCAGCAGTUC	79195	GGAUGAGGUGAAACGCACACT
232604202	79196	CGCAUGACAGCCAAGGUG	79197	CCTCCAGUCCAGGGCUACT
232606438	79198	ACCTCGAAAUGCAAGGAGAUGAT	79199	GTACCACTCCCUCTTTGCTCUG
232606809	79200	CCCCUCUCCAACAGGGACT	79201	GCCCAGCUGAGGAGTTUGT
232609526	79202	AATGTTGAUAACAGCCACTGGAAATTUG	79203	CCTAACCTAGGACUGACTGCATUG
232610766	79204	CATCCUCCACGGAGAAGAUGT	79205	TGATGCUGGCACTCCUGAAG
232611153	79206	TCCTAGAGUAAGCCAGGGCTTUT	79207	CCATTGTGCTTGAAUGCACTAGAATCUA
232614404	79208	TGTTTTCTTTUCCCTCCATGGCUAT	79209	GTTTGGACAUGGCAAGCUCAG
232616920	79210	CUGCCCTCAAUAAGGCCAGAT	79211	GTGTGAUGGCTGTGAUGACAAC
232618121	79212	CTCAUCAGCACUCCAAGCGT	79213	GAGTTTGGACCUGAAACCUCACAT
232620064	79214	AGCAAATAAACAUGCCAACCAAGUC	79215	AGAGGAGAGGAGACAUGAATTACCUC
232621917	79216	TGGAAAGCTAGUGGTTCAGAGTTCUA	79217	AGCCTAAACAUCCCCTTAAATTGGAUT
232624440	79218	CTTACGCTUAACTCCAACTGUGAAAAA	79219	GGACAAACTAGAGUCCACAGTTAAGUG
232627176	79220	CAGCAGGCAGAAGAUGTGGUA	79221	GATTTCCAAUGGAGAACTTTTGCTCUT
232629157	79222	CATAGTCATTUGGCCTCCTCUAACC	79223	GTGTCAAACACCAUGAATGAGCUT
232634104	79224	GTCGAGCCUCATCTGAGAGUG	79225	CTCACCTUGCACTTCTCTCAUCAT
232635876	79226	CGTTGTTACUTTGGATCUGAAGGA	79227	ACTCACCAGAAGCUCTTTATACTTUGG
232637182	79228	CCTUACGAAGGATGAAUCCAAAAGG	79229	CCACTGCUTGCTTAGUGAACCA
232640301	79230	CCTATAAGCUGCCTGCAGUCT	79231	TCCAAUTATAUAGGGCAGGCCAAC
232641302	79232	GGCTATGTATTUCTTTTGTGTGTTUGAGA	79233	AACCTTTGTGAUAAACGAACCACUAGA
232641935	79234	CCACAGCTGTAUAGAAAATTCTGGGUT	79235	CTAACCTTTUACCCACCCACAUACC
232642702	79236	GCCATCTGACAUCTTTTCCCAGTUAT	79237	TTTCTGTTAGAUCCACCAGATACUCCT
232644790	79238	CTGTTTUGGCAGGACAGUGAG	79239	CCGTTATATTGTUCTCCTGTGTCTGUT
232648306	79240	CTTGACCCCCAUCCCTTCUT	79241	TTGGCTACAUGCCGCUGAT
232649231	79242	CCCCAAACACAUGCAGUGG	79243	TCGGAGGAUGGGCUGAGAT
232649356	79244	GGGTUCCCCACCAGAAAAUG	79245	ACAUCCTCGUGGAGAGCGA
232652544	79246	GCCGAAGUCAGCGATCTUGA	79247	GGGTACCUGCCGGATTAUCCT
232657919	79248	TCUCUGGGACCGGGCAT	79249	CGAGACGUCCGGCTTTCTUC
232658748	79250	CCTCAGCCACUGTTAGGGUCT	79251	GCAGCCTGAATUATGATCCTTTCCUA
232659486	79252	TCTTAAGATGCTUTTGTGTGACTCUAAA	79253	CCATGAAGTGAUCGGAATACATGUAGAA
232660462	79254	AGGGCUGCGGAGAUCCT	79255	GCAGCTACUTCCAGAGCTUCA
232661279	79256	GGGCTCCUGTTCCTCTGUAGT	79257	TCTGGAAGAAAGUTCCCTTCATTCUC
232665698	79258	CGACATCAGUAATTGCTCUGCCA	79259	ACCCAAAGGAAGAAGAAUTTAGGTUGT
232670808	79260	GTCTGGUCCACATTGCTCUCA	79261	GCTGTCCCCUCACCATUCAG
232675728	79262	GGGTAGGUGGTTCTCCAUGACT	79263	CATTTUGGAAGCCCCAGCAUC
232681357	79264	TCATTTTGUGAACACACTGGTAAGUACA	79265	CCCTTUACGCTGCGTTUGAT
232687558	79266	AGAGGCCAGAGGACUTCUCAT	79267	GUATCTTCCAUCCCCACCAGAAAC
232696641	79268	GTTACCGGCACUGCGUAAAAT	79269	CGTTCCTTTTUGGCAGTCAAGTTTTUAA
232697762	79270	CCGGGUCUGAACCCCAAA	79271	GGACGTGCUCCCCATGUG
232700194	79272	GATCTGGAGCUCCTGGAAGAUG	79273	CGAGCCUGGAGTTTGCAUGAA
232708234	79274	GTGAUAGGAGCCCATGUACGG	79275	CGCCCUCCGTTACTACTAUGACA
232708524	79276	TTACUAGGAAATCATCUCAGCAGAGAA	79277	GAUCCACAGCTCTUACAGCGA
232708871	79278	AGTUGAAAACCGAAGATUAGAGGAACAA	79279	CACACTTACCAGUCTGTGCUGAA
232709227	79280	CTTCTTTTCTAGAUCTGTACCAAGTGUGT	79281	CTCCGAAAGCUGGCAAAACUG
232709749	79282	CTAGTCCGTCUCATCAAATACACACAUT	79283	AAACAACCTATAGTUCCTTTTCTACATCTUC
232712495	79284	CATGGACCTUGGTCATGATGTUCT	79285	TCCAACUCCAGCTGCAUCAC
232714540	79286	CAGGAGCUGAGGTCUGAACAAT	79287	TGACCAUCAAGCCTGCTTCUT
232715112	79288	GGGTGTGTAUGTGTGAATATTTUCAGA	79289	CCCAACATUCACTTCCTGCTUGT
232717900	79290	ACTCAGGATUGGAAGATACTGUAGAGG	79291	TCTGGUAAGGACCATTAGACAUAAGACA
232718674	79292	CGGCGACGCUTGGUGAT	79293	CAGCCGCUGCAAAGCTUC
232719190	79294	GCAGGCUTGATGGUCAGAAAGA	79295	CCCTTTCUCCACTCTGACUCC
232721303	79296	CCACTGUCACAACTGTUGCT	79297	CACCCAUCCCCACCACUG
232721538	79298	CCGCGAAAGCUGUCGAA	79299	CTCGAGGAUCTGTACTGGAUGG
232721961	79300	CGGTTCCAAGCCAUTCTGGUT	79301	GGAGCUAGAGCCAAAGAGGGUA
232722614	79302	GGTTCATCUGCTGGTAGTUGCT	79303	GGCTCGGUGTCCUCCAC
232724478	79304	TGGCCCUGAGCTCCGUA	79305	TGTCTTTCUGCCTGTCTGTAAUCAC
232728927	79306	CCAGAATUCACGAGAGGATAGTAUCAGT	79307	GATACCAAGUAGCTGCCAGTTUCT
232729013	79308	ATTTCACTTTTCUTCTCCTCGUGGAT	79309	GGCTTTGGUTCGGTAUGGAAAG
232729199	79310	GAGCUACACGGAGTGCUGAG	79311	CCGCUGGCCATGGAGUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
232729313	79312	TGCAAAUAAAGGCACACCUGAAGA	79313	GTCTATGCCAAAAUAAGTTTCCAGTTUCA
232730231	79314	CCATAGCAUGCAGGAAGCACUA	79315	AATCCCUGTGGATCUGAAACGG
232731627	79316	CAGGTCGAAGUCGTTGACAUACT	79317	GCTCTTCUCCGCTCTUCCC
232731867	79318	GTCGAAGUCGTTGACATACUCCAT	79319	CCAGCTCUTCTCCGCUCT
232732307	79320	TCATCTTGAACUCCCCGTUGG	79321	AACCTGTGCUCACTGGAGTTUT
232732580	79322	CGAGACGCAAGUTAGGUCACT	79323	AGAACAUCCAGAGGAACAAGCUG
232739288	79324	CACGAGTACUATAACGTTGCAUCCT	79325	GGAGGAAAGTTUCCAGAGATAGAUGG
232741167	79326	GGGAAGGAAGACUTGCTTUCAAACT	79327	GACAGCTATCUGCTGGTGTAACAUT
232741236	79328	TTGTTGCAGACAAAAUGAACACTUGT	79329	GGGAAGACCUTTTTAACAACACUACCT
232741936	79330	TGGCUCACCGAAAAGTAAAUCCC	79331	GCTTCCTCCUGGTTATGTAGTAAAUCA
232743041	79332	CACCATCCUGGGTCTCAAUAAAGAG	79333	CCCAGAAGAGUTGGATGUAACCAG
232743949	79334	CTCTAGATGATUCCAGTGCCCUT	79335	TCCCTAGGAUGGCTTATAAACAUGACT
232744466	79336	CCTACCUGCAGAAGCAAGCUAA	79337	AATCTACTCCCUGAGAAAGAGTTGUACT
232748454	79338	ACTGTGATGUCCATTGTGACTAUCC	79339	AGACTGCTGAAGUTCTTCTTTGUCC
232750814	79340	TCCCATTTATCUGTGTTGCTTTTGUCT	79341	ACTGTAATCUGTATCGCCTUGGAAAAA
232751710	79342	GGGAUCAAATATUGACACCACCAT	79343	GCCTTGAATGAAUTCCAGCAGUGA
232752186	79344	CCATTCACAUCCTGGTAAUCCAAGT	79345	TGTCTCTACUGGCACATTACTTCTACUAA
232754257	79346	GGACAAAGAAGAACUTCAGCAGUC	79347	GCCACATAAACAAUCCATGACCAGUAAT
232758223	79348	GCTCACCAUGCTTCATGTCAUT	79349	GTGCAGTACTATUTCACAGGCATCUA
232760371	79350	GACAGTGGAGAGAUGGCAGAAUC	79351	GCTAGCCACUGTGAGCTAGTCAUA
232762629	79352	GCTTCGGUCCTCAGCCCUAT	79353	ATTTGCTGTTTACUCCTCTTCTCTTUCT
232770623	79354	AAGCACCACAAUACTAACAAGUGACA	79355	AATTCCAGCUCTTTCACATGGUGA
232773131	79356	GGATTTATCCTGUTGGTCTAGTTCTUGT	79357	CTGTCCGUCGTGACACUGAG
232774700	79358	CCTGATCTGTCUCTCTCTGTCTCTUC	79359	GGGAGTACUAGAAAAGGAAAGGCTUAC
232778613	79360	CCTCTGGTTCUGTTTTATACTGTUAGCT	79361	TCTATGGCCTUCAGAATGCTCUCT
232779422	79362	GCAGUATCTACCUGGAGCACAC	79363	AGGGAAAAACUGGAGGAAAGAACUC
232781991	79364	GGGCTUCACAAAGGUCAGAG	79365	CCCCCTGTGUTACTGAATTGCUA
232783578	79366	TGGACAACAGUCAAACAACAATTCTTUG	79367	AGGCATTAGAAAGCCUGTAGTTTTACUT
232792481	79368	GGTGUCAAGGAGCAGAAGCTUT	79369	TGCTCTCCTTTTUCTGAGTACTTTTCUC
232792596	79370	GCAGCTGCUAGAGGCCTTUT	79371	TTCCTTTCCUCCCTGTAUGGGA
232799444	79372	CGCATGCTTTUCCCGTCTTCUA	79373	GTAATCCAAAGUCCACTTCTTGAAGUGA
232802474	79374	CGGGCUCCATCAACAUCACAG	79375	CCACTAGCCCACUCCAGCUA
232815250	79376	CAGAAUCAGAACGGACAUCCCA	79377	GCACCGUCAATATGTTTCCUGAAG
232816140	79378	TCTCCUAGAGGACAGTAATCTTUGCAT	79379	CUTGCUCAAGACAGGAAGACCA
232832391	79380	TCAAAGGAUTTGCTCUCACACGAA	79381	AGAAAAACCTUTTGTTGCTTTUGGAAGT
232833435	79382	CTGACCACGCAAUGTCTTTUCT	79383	GAAATTGAAUGCCACCATGTTCTCUAA
232837566	79384	TTCCACCAGAGAUTCCAUGCC	79385	TGCAGCTACUCAGACCCUCAA
232838090	79386	CATGCAGAGGUCCUCGGT	79387	GGATCAGUACTCCAGUGAGAAGACA
232839964	79388	TGTTTGTTGTTTUGCTTTTCGTGTUG	79389	CAGGTTTGTGCUGTTCTAAAAATGAGUT
232840039	79390	GGCAUTACCTUAACCAAAGAGAGCAA	79391	ACTTAGAATCUCCATGGCUAGGACT
232843682	79392	TCCAGGCUGTAAACTTUGGAAAGG	79393	CAGCTGUGGCAATTTCTGGUG
232845472	79394	CCCAGTCTUACGTGTTGCCTUT	79395	ACCATGCCUTATGGACUGGAGA
232849191	79396	TCAGTGCTGTUTGAGGGAACTUT	79397	CTCAAAATAGAACAAGUTGTTGGGAUGG
232850013	79398	CATTTGUTGGGTCAUCCAGCAAG	79399	CACAAACCCCACACCUCCTATUT
232851661	79400	CTCCATGATCAAAAUGTCATTTGTGCUA	79401	GCAGACAGAUCTACGTTUGAGAACC
232852689	79402	TGTCTCTTTAGGUTCCATGTAGCAGUA	79403	GGCATTTTAGTUCCTTTAGACATGCAUT
232856074	79404	ATGCTTGCTAUACAGACTGCTATACUG	79405	CCTTGTCAAAAGGUTTTCCAATAGCAUT
232862973	79406	TTCAAAGAAGUGAGTTTGGACTUACGA	79407	AGGGAACTUAGCAGAGAGCAAAUG
232863869	79408	ACGAGCTTGTTUAAGGTATGCCTTUAT	79409	TGCTTAATCTGCUATTCTTGCTTUAGGG
232864769	79410	TCACTGTCCACAAUTTCATTCAAGUAGAA	79411	GCAATGTACTAUGTAGGTCTTTCGUGAA
232865451	79412	GGCCAAGCUTGTACCATGUGA	79413	ACCATTCAATAACUATGGCCTCTTCAUT
232868391	79414	GATGACGGCAGAUGCTGTTUG	79415	ACAGGTTCCAGUACCCACATUG
232869692	79416	TGATCTGCTUTTTGTCACTAAUGAGAGT	79417	CAGGTCCTCCAUTTTGTACTGTUCT
232874671	79418	GAAACTTGGAAAACUTTGTGGUGCT	79419	GCAAACACUGCTGCTTCAUAACC
232880320	79420	AAGCAGCACGGGUGTAACTUA	79421	CCTTTCACTCTGUTTTCTTTTCTCTTCUG
232880655	79422	TGGGTCAACAGGUTTGTTCAGUAG	79423	CAGCAATCACUGTTGAATCAGCAAUT
232880737	79424	TGTCGCUACCTCAGTTUGCC	79425	GGTATTTGGTTUCCCAGTCCACUA
232890656	79426	CCAGAAGGAUAAACAGCATACGCUAT	79427	GGTGGAAACGUTCTCTACUACGAAG
232891795	79428	AGAGGTTGGGUCTGCCAGATUA	79429	CACAUCAGCAAAACCATCTUGGT
232891998	79430	GCAACTGGACAUCCTTTTGTUCA	79431	ACCTAGCAATGUCTATCAGACTCTTTUA
232898223	79432	GCTCATGTUGGAGACGTCAGUA	79433	GGTCCTGCUGTGTGGTUAGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
232901363	79434	TGGTGAGCCAGAAUGGAACUG	79435	AATGTATGCATTUATGCTCTGAGGUAGG
232901991	79436	GGACACACGAAGGCAUATATTUGGT	79437	GCTCTTCGUAGTGGTGCATTUAGG
232904479	79438	ACUGACAGAUCGGACGGACA	79439	CCAAUACAGCCCCTTCTTUCCA
232905933	79440	CTGTAGAGTCUGCTTCTTTCCCAUC	79441	GCTTTTCCTUCCCCCTTTCTCTUC
232907682	79442	CCTTGTTGAUGGGAAAAGCCAAUAA	79443	GTGGTTGUCTGCTCAGUGGAT
232908308	79444	CAGAAGACGAUATCCCCACACUG	79445	AGAAATTGTGACAUATCCCTCTCCUACT
232908591	79446	ATTGCAUGACAGGAAAUGGAGGT	79447	CCAGAUGAGAGTCGATUAGGGAAAG
232913830	79448	CCCCAGCAGAGGUTCUAGAC	79449	GTTACAGTCTCUCTTCTGCCTCCUA
232915385	79450	ATGGGAGCUCTTCCTGATCUGA	79451	CCTGCTTTATTUGGGTACTCCUGAC
232921230	79452	CCAAGATUCCCAGTCACCAUCA	79453	GGTGAAATACUTGGCTACCTUGGA
232921730	79454	GCTGAGACCCAAAACUTGTCTTUT	79455	GCCCCTCCACCUCTGAAAGAUA
232921900	79456	GGGAATTCAGGCUTCATTTGGAUG	79457	ACTCAACAATGTAUTCAGCAAGTCCUT
232930759	79458	GGTCGCUGGGATCACCAAUT	79459	CCAGCAGUCCATTCAUCCAGT
232932404	79460	CAGCACCGTAAUGTTTTGTCAAAGUT	79461	GTCCAUCAGACAGAGGAACCTUC
232933928	79462	CAGGGTCAUCTGTCAGCAUCT	79463	TGGCTCAAAGCUGAAAGCAAUAGT
232939739	79464	AACATTATTTAUCCGCATCCTGGUGA	79465	ACATGTGGATTCAUGGACTTAGATTUGT
232947863	79466	GCTAATAAUGAGAGGAATGGAAAGAUGCT	79467	GGAUTTGTAGCTUCCCGCAGAAA
232948025	79468	AGCTGCAGAUTATGAAATTUAACAGGGT	79469	GGGAAUAGGGCTGTTCTUGACAAAA
232951195	79470	GTCTCCAGGGCAGUTAGAACUT	79471	TCTATCUGGGTCTGCUAACAGACT
232951523	79472	GACAGAGGAAGAUGGUCCCAAAG	79473	CAACAGAAGTAUAAGAATGGCTGUCACA
232952206	79474	AGACATGAGGUTCACCGCAUC	79475	GCAGTTACUGCCCTCTCCTUAC
232956961	79476	TGGATTTCCTCUGCCTGGAATUG	79477	CTGTTAGGCAAGAAAUTCCTGGTTTUT
232964706	79478	CATAATCAGUACCACGGCCUGT	79479	TGCAGTTGACTUATTCAGCATATTCUGT
232965197	79480	GGTTACTTTGUGGGAGACTTUCACC	79481	ATCCATTCAUCCCCAACAGTTCTUAC
232971250	79482	TTCTGACTTTTCUTCTCAGGACTGUG	79483	AAGTGCGGTUCATTAGGGCTUA
232972592	79484	TGCAUAGATCACTTTUACAAGGCCAA	79485	CTTACCTTCUCCAGGCTTTUACACA
232974821	79486	CTTCCUAAGGAGAAAGAGCTTATUGGT	79487	AGTGAATTCUGCTGTGCUAAGAGG
232978203	79488	GAGUTGGAAACTCUGGAGAGCAA	79489	TCTGAAGAAGGUGGUAAAGGAAACC
232978808	79490	CCACACUGACGTGCCTCUC	79491	GTCTTTGTGTUCCCGGACAUAGT
232979344	79492	AGATAGCUGATTTCCCCUCAACCT	79493	GGAAATACTGAUCTCCATCCTCCUG
232982311	79494	GAACAUCACTCCUCAACCCAAGT	79495	ACTUACCAACACACGGCCAUC
232982509	79496	TGATAGTAUTGTAGTGGUAGGAGGCA	79497	TGTTTGAAGATUCCACCAAGATGTAUGT
232984355	79498	AGCTCAUCACGCAGCUCAT	79499	ATGTGAGGAUCCTGGCTCCTUA
232985420	79500	CAACAGCCUGACCACCTTCTUA	79501	CGGAATGATUCTGTCAACCCUGAT
232987331	79502	CCGCGAUGATGAGTGGAUGG	79503	CAGCCTTCCUAACAGATCATTCATUCT
232991263	79504	GAGCCCUCAACATTATGCCUCT	79505	CCACCGUCAGGGACTUGAAC
232993028	79506	AGTGTTTTATCUGCATCTGGATGAUCAA	79507	CCCTACUCGGGAGAATTUCAACAG
232993252	79508	ACTGCAGCCAAACUCCCAAUA	79509	TTGATGAGTGUCATCTTGCAAUCCT
232996915	79510	TGTGGGCTTUAGGTCAATGTUGAT	79511	GCACAGTAACAAGAUTTTAAAACCCCUT
232997278	79512	GGGTGGUCTAGGATUGCAAGA	79513	GCAGTGAATGCUATGTTTGTTTACUGAT
232999948	79514	CTATCCACUTGTTCCAUAGGCCAA	79515	CCCATCATCATUATTTTCACAGCTCUCA
233001226	79516	TTTGCAGGTAAAAUCAAGAGTCCACAUA	79517	CUCCAAACATCUGAGGCCACA
233003442	79518	GTATGCUCCAGAATCACUGACAGA	79519	CACUGACCGCTGGUGGA
233003616	79520	AGCAATACCAAAUTTTATTCTTGTTTUAGACA	79521	CTGCAGCAAAGUTCGTAATATCTUCAAA
233007649	79522	CAGCTCACUGAAAGGTTCTTTTGUT	79523	TCAGCTTTTCCUCTGTTCACUGG
233008945	79524	CTTGGAGCCAAGACUAAATCCTTAGUT	79525	TCCCACCUGAATTCUGACCAAAAG
233012558	79526	GGAAUCTCUGAGAGCAACGGAAAAA	79527	GCACTTTUCACACCTGATUCCC
233015782	79528	GTAAGAGCTTAUTGAGATGGCUGACT	79529	TCATTTGGAAGUCCATGCTCCAUT
233019725	79530	AGGTGCUGGTACAATGUAAGACAAG	79531	ACCTGACAAUGATGAGCAGTTUGT
233020548	79532	CACTACCUCAGCCCTCCAUC	79533	TGACATGTTCUCCTTTGGGTTUCA
233021250	79534	TCUCTCAGGGUCAACAGCCA	79535	GUGAGCAUGCAAAAGGAGAACAAG
233021779	79536	TTTAATUACCGGGAGCACCTUCAG	79537	ACACGGGAAAGCAGUCCAUT
233023862	79538	CAACTTTCAGCCUGATAGTCUGGT	79539	AGGUTTGATCUCAGCCCAAGAAG
233025245	79540	AATGAGACTAAAACTUTGAAGTAGTCATTTTUG	79541	CCGACCGCGCAUAAACATTUT
233026000	79542	TCTTCTACCUCTAGGCAGTTUCCAA	79543	CTGAAAGTGTGUCAGAGGAGGAUG
233026044	79544	TGUCTTGTGTTUCAACAGAAGGAGAAT	79545	TGAATTTGCUGTCATGGUAGAGAAGG
233030995	79546	CAGAGAAGCGCAAGCUCAUC	79547	AGTGTGTCATGUGGTTTAGGACATUC
233034073	79548	GCATTTAGGAAGAUTTAGTGGACTUGCT	79549	CGGGAATUGGTAGGCUCCA
233035864	79550	GGAGGAATCAAAAAUTGTCGGGAAUT	79551	AAGATATAGCUGCAGAAGAGGACTUAGA
233037623	79552	CAGAUGGCAGCAAGACAUCCT	79553	AGCTGGGTTTCUGTTAATCTCACUG
233038392	79554	CCTAGTATUGAGGAGGCGUGGA	79555	GCTTGACCACUAGAGAATUGAAAAGAAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233040781	79556	ACGACTACAGUGTCAAATAAACTCUCAAA	79557	CCCACCUCATGCACTGTUG
233042373	79558	TCTCTGGGAACUCTGTATTTGGAGUA	79559	TGCCCAAUCTCUACCAAGCC
233043561	79560	CAGTAGAATAAUCAACAGTGCAUGAGGT	79561	CTAGGTCTCAUCAAACTCTTTGCAAGUA
233044505	79562	CCCCACUGTCGCACAAUGAA	79563	CTTCTTCTCCCUGGCTGTAAAAATUG
233048323	79564	GCAAGUCGAGGGCCGUAAAA	79565	CACATTGCATCAUCTTACTCTCATAGUCA
233052193	79566	GAGGTCTGUAACCCGCAGTTTUA	79567	GUATCAGCCUCAAGCAAAACCAG
233052589	79568	CGTGTTTUGGTCGATCUGGGT	79569	CCAGCTUGGGAGACCUCAT
233055760	79570	GGGTGGTUGGAAACTGAUGGA	79571	GGGATGAACACAUCTACCCCUACA
233058491	79572	TGGUAGCCAGCCAGGUACA	79573	GATCTTCCTGUGGCCCCTUC
233059855	79574	CCCTCTCTGUGACAAATGTTATGAUGAT	79575	ACTGAAATAAAAAGACUCCAACCTTCUGT
233062564	79576	GATCTGCUTCTTGAGGUGGCT	79577	ACATGTAATTUCTGGTCATTUCCCGAAT
233063076	79578	TGTTACGCAGUGCTAACCAAGUT	79579	GCAAACCACAAAAGUATACTCCAUGGT
233066561	79580	TTACTTGGGAAGUCTCATTTGCTUCT	79581	AGCTGTGTTTUGACTCTCTTTTGAUGA
233067705	79582	TTGCTGTUGGGTGTAGTGUAGG	79583	CCTCAGGATCUCAGTCGAAGTUT
233068008	79584	AGAGUTTTTATTTCCUGCCACAGAAAGT	79585	CATGATAAUAACAGGAGCCAGAGGUT
233068526	79586	TTTCCATTTTCUCCTCCATCCTGTUT	79587	CCATCATTGUCCAGATCGUCCAG
233068998	79588	AACAGAGUGAAAGGCAGTCGAUT	79589	CCGCUGCATGAACTAUGACC
233069137	79590	AGGGAGGGUACGTGUGAGAT	79591	GTGAATGUCCCGTAGTTAAUGGCT
233069961	79592	GCGCACTTUGGAGAGAGCAUT	79593	CAGGAGCAUGCCACUAGAGAT
233070959	79594	AGACCGACCUCCTCATUCACA	79595	GGCTGATCTUCTTAGGTCAAGUAGGT
233073674	79596	GGGUCAGAGUACAGAAGAAAGGG	79597	CTTCCTGCCAUGCTGCAUAAG
233074228	79598	CATTTCCCUTGTCACCUGGCT	79599	CGGGAAAATUGAGCTCCTCUGT
233075863	79600	CCAGGUGACCCCATGCUAAA	79601	CGTCCTGUACGAGCTCTUCAC
233076894	79602	CAUTAAGUGGACAGCGCCAGA	79603	CCTTCCCAUCACCCTTTCAGUT
233078915	79604	ACAGACUGGGAAACTGAGGCUA	79605	CCACATGCGCUCCTCCUT
233079030	79606	CTCAGTUCCGGAGAAGAUGGAG	79607	CAACAGCCUGAACTCAGATGUCA
233079040	79608	CTGCAGCTUTTGTCGCAGUAG	79609	TCTACACCCUCGCATCUCAAGA
233080283	79610	GACUCAGCCCGAACCTUCAG	79611	CATGGGCCUTTCUGGAGGAA
233082523	79612	CGGAAGAAAGGCCUCTGATUGG	79613	GTTTCTTCCAUGTGCCCCTCUT
233082598	79614	AAGTCTCTTGGCAUTATTTCTAGTUGGT	79615	CAATGAGAGCUTCCCTCAATGUCT
233083448	79616	TGTCTTCTAAGAACUCTGAAGCAATGUC	79617	AGGGAAGAGGCUTTATAAAACAACUGT
233084770	79618	CUTCTAGGUCAGCAGCAACAA	79619	CACCTTCCAAAAUAGCGAGTAUGGA
233087040	79620	GCACTCGTUCAGTTTGGCATUAA	79621	GGCATTGGCAGAUCCATGCUA
233087051	79622	GAGCTGUCAGAGGATUCGCT	79623	CCAGGAAGAUCTGUGGACCAA
233090072	79624	GUATGTCTTATCTCTUAGGAGGGCAAC	79625	AGCATTTGGUCTGCTTTGATTTUGAA
233093129	79626	CACATTAATAUAGCCAGAAAGGGCCUA	79627	GACTTCGGTTUAACCAAAGCAATUGA
233098213	79628	TGACGGTGTAAUACTCCTTATCGGUT	79629	GTGCTTGACTTUTACTTCTCTCTCUCA
233098930	79630	TCTCAAGCACUCACCATTTGGAAUT	79631	GAGGAAACACAGUCCCTTTCUGA
233099997	79632	TTTTTCUCCCGAGCCAGAATGAUT	79633	CGTGCCTTCUCTGGTTCATTTUG
233102862	79634	GGACCATGCUGTTTCCTGTUGA	79635	GGCTTGUGGAAACGGAATTTGUA
233104626	79636	GAAGCACUAATCGGCTUGCAT	79637	CAGCCTCCAAUCATCTCCTTCAUAC
233105508	79638	CTTTGTGCUGAGGATCAGGGAUT	79639	TCACGTTTUGCAGGGTTTTATAACAAUT
233105956	79640	GATGAAACATCUAGGCTGGACCUT	79641	TGTCTGTAAATCAGUTGAGCCATTACUT
233107004	79642	CTTGGTGGTUTTTAGGAAACTUGAGAA	79643	GTGTGGTCAAGAGUAACCAAGAAUGT
233107506	79644	GCCCCACAUCCCCUACCA	79645	CCCUTGGUGGCCACGAC
233107958	79646	CCTCCTGUTCTCCCUGGGT	79647	GACCGGCACUCGCUCAT
233108744	79648	GCTCCAGGUCCATGATGUACT	79649	CAGCUACAAGGCCTGCCUAC
233109699	79650	GAATACGCCUCCGCGUCA	79651	GGCTAAAGCCUGGGTTTGUGT
233110243	79652	GGAGGACGAGGUCTCCCAUA	79653	GGCGGTUGGGTGTTUACCT
233114794	79654	GUGCCAAGCACTGUCGAAAT	79655	AACUGCUGACAGAAAAGAAGGGAA
233118315	79656	CTCACTATAGACAGAUGATGTTGTTGUGT	79657	GCAGGATCCUCTCTTGCTGAUG
233120383	79658	TGTTTCCAAAGAACAGUTACCCAUGA	79659	ACCACUGGCAAAGCAAAAUAGAAAAC
233122255	79660	ACTGGATCUCAAGGTATTGAUGGGA	79661	GGCCCTGTGUTGCAAAGTACTUA
233123150	79662	AGTTTGCTGGUGGAGATAAGGTTAUG	79663	AGCAUTTCCAAAGAUGGAGCGA
233124610	79664	GTGGTGGACTCUAGTCAGAAACCUA	79665	TGGTGGCCUGTTTGGATUCAG
233127617	79666	AATGCCUCAACCGTGGACAAUAT	79667	TCTTGAAAGGTUCCAAAATAATGTGAUGGA
233131985	79668	GGAAAAGAGUGAAGAAGGGAATGUCT	79669	GAGTGGTTTUGGGAACTTCTTTTCTUG
233132382	79670	TGGAAAGAACCUCTCAACATTGUCA	79671	GAGTAGAACCATUGCTCAAAGGACTUA
233135290	79672	CTCAGCCACCUACUACAGGAC	79673	TGCTGTTUGAGACATCAGTGCUT
233140601	79674	ACCAUCCTTCCATUAAAGAGAGAGAGAT	79675	GCTGTCTCAGUGACAAACCCAUA
233141604	79676	ACACTUCTCCATTCTUCACAAGGG	79677	AGGCTGCGTUGGAAGTTATTTCUAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233141675	79678	ACCCCTTUGAAAGAGAACACACUT	79679	GCTGGCCUGAGACATTCCTAUG
233143073	79680	CACAGAAGAUGGAACTCAGTATUGGA	79681	CCACGCGGACUATTAAGTCUGA
233145116	79682	ACAAAAGCCAGUCTGGGAAGUT	79683	GGGCCUGATACTUGGAGAGA
233146204	79684	TCCATCAGAACUCCACTCTCUCC	79685	AACTGCTTCACGUTTTATTGAGAATUCC
233149050	79686	CACCAUCCATCCAUCCAGGAAAA	79687	CGTGATCCATUCATTCTGCTTATTCUCAT
233149581	79688	ACTGAGAATATAACCUGATAATGTAGGAUAGT	79689	CTACTTCGAATCUCTAGAGCCTGTTUG
233149583	79690	AAGUGTCACCTUACCAAAGGCAA	79691	TGTAGATUCCGCACAAGAGATUCAG
233150560	79692	ACAGGCTCTAGAGAUTCGAAGTAGTTUA	79693	AAAATGGGCTUTACCGTACCAUGA
233151787	79694	TCTTTTTCCCTUCCTTTACAGAAUGCT	79695	ACAAGCAAACAAGCCAUTTACUGAAAAT
233153276	79696	TGAGGCACTATUGTTTGTATTTGGAGUT	79697	CCTCCCTCTTUAACAATCACTTGAAUACT
233155382	79698	GACTTTTGAGAUCCTGGAUGAAACGA	79699	CACUGCAGAAAGCCAAGCATUT
233155477	79700	AAAGTTCUGCAACCCAAGAGUGA	79701	TGGAGAAUCAGACGACAAGTATUGG
233155726	79702	GCCAGTTUAGATGCAAAAUCCACA	79703	AACATCCTGCTACUTTGAGGTTTTACUT
233156332	79704	AATCCAUTCTGAACAUCAACAGGAAGT	79705	TCAGTTAGCAAAUGTGTTCACTCTGTUA
233157068	79706	TGGAGUGTATTCUCACAGAAAAGAGA	79707	ACACCCCGAAAAGAAUGTCAUCA
233158008	79708	GCATGAGACUTCGATGCTTUCC	79709	GCTGATACCAGAACCAUTTCAAAAGUT
233160766	79710	GACAAAUAGGAGCCAGCCUGAA	79711	GCTGGAGACAUCTCACATTGTTTTUG
233164486	79712	GGCCCATGAUAGCCGTCTUT	79713	CTTCGGGCACUTACAAGCCUAT
233164695	79714	ACGACTTCTUCAACAAGATCGUCAA	79715	GCCCTGGATATUCTTTTTGAGACTGAUA
233167176	79716	GCAAGAGUACACACTCCTCATTUGG	79717	TCACAACCCACUGAGGTATATGTAUAGG
233168222	79718	CCTTCTTCACUCTATGTTGTTATCUCCAA	79719	CTATGCTGGCAUGGTCTTCUGT
233168924	79720	TCCTCCACCUCCAGGAACUT	79721	CTGTGTCUGGCCCCCTUAG
233169266	79722	GAGTTAGGAAACAGAUACAGAGGUCAAG	79723	CTTCTGAGUCGAGAGATTCAACTUCAAA
233169270	79724	TCCTCTTACCUACAACGACAACTATGUA	79725	ACCCAGAAAAGAGAUTTGTTCCTGAUG
233171607	79726	TGCTGUCCCAGGAAATTCTGTUAC	79727	AGTGATCATTGUACATGGCTCTCATTUT
233172919	79728	ATTGGTTGGAUCAGGATTCAGTTUCA	79729	ACTACCTCATCAUCTTCATCTGAGAGTUC
233175893	79730	TCCCCTTGGGAUTAGTATCTATCTCUCT	79731	AAGCTTCAACAATUTACTCTCCCATGUA
233175955	79732	GTCTGTGUTATGGCTGUGACCAT	79733	CCACAUTCTCCTCAUGCCAAGAC
233177631	79734	AGACCAGUGACGTGAAGACAUC	79735	GCAATCUTGCAGCUCAGGGT
233179522	79736	ACGTAACCAUGAATCATCCACUCAC	79737	GGTAAATAGCAUTGAGGAAGATGUGACT
233181164	79738	GCAAACUCTACCCUCACAAAAGGT	79739	GCACCUGCTGAACAGUAGCA
233182078	79740	CATGGAGTTGACUTTCTAAAAGGTGCUA	79741	GGTAATGATGUGCATCTGCAGTTAAUCT
233184086	79742	AATGGATGUCAGCTCCATACUCAAC	79743	GCCATAGTCAUCTGCTACCTGUCT
233184441	79744	CTTTGTCTTTCGUGTCATTAATTGAUGGA	79745	CGAAATTGGGCCAUGACAGTUG
233184457	79746	CCTCCAGCCGUGCTTGAAAATAUA	79747	TACATGTATCACUCTGTTAAATCTTCTTUGT
233184959	79748	GCTGCCAACAUTCTGGTGUCT	79749	GCCCAGACCACCCUTAAATCUC
233185762	79750	TTGGTGTGTUTGCCAGCTTUC	79751	ACCTGAGCTGUGAAGGACGAUAT
233186400	79752	GCTGCAAGGUGCTTTCTCTTUC	79753	GCUCAGUCACCCCGAGAGT
233187793	79754	GCGCUCCACGATAGCACUG	79755	CAUCCCAGAGGCAGCAAUCAT
233190057	79756	CTGCCATAUGCTGTGGTTCUC	79757	GCTTGTTCCUGCAACCTCCUA
233195000	79758	TCAAAUCTTCUGGCCACCACA	79759	TCGTGCAGGAAGUGAACTUCAT
233197502	79760	AAAATTAAAGGCAAUAGCACCAAUAGCC	79761	GGAGAACACUGGACAGCTGAAUAA
233202774	79762	GAUGTTAATGUGCACCCCACAAA	79763	GCCCCAGAGAAGUAGCUGGAT
233204277	79764	GTGTGTCTGCAUACATCTGATCUCA	79765	CCATCAUGGGACTCTCCAUCAGT
233209387	79766	CCAGGCTACUGGTGGTTGUC	79767	ACTCTTCCAGAUCCAGGGTGAAUT
233211325	79768	GACTCCCAGGAGAGUGCTGAUA	79769	CTCACCTTTTUACCTGATGCTUGAAA
233213451	79770	GACCGAAGAUCAGGCACCTTAAUT	79771	GACAGCACUGCCATAUAAACACA
233218055	79772	CAGGGTCUGACCCAATCTTCUG	79773	CTTGTCTTUCAGGCCCUGCT
233218407	79774	CTAGCTTCTTUCTTAGTACTGCUCCAT	79775	GTGGAUTTAACCATCUCCCCAGAG
233218621	79776	TTAATACAGACTTUGCTACCAGGACTUG	79777	CCGGGAAUCTGUACGAACCAT
233219374	79778	GUGATAAGGTCTAUGCCCACCAG	79779	CCCTGCCACUAGAAATATCTGTCUT
233220494	79780	CGUTGCTCACUCCCAAGCA	79781	CGTGGGCCUCAGTCUCAAG
233220649	79782	TGAAAGTTAATAUGGAGAAGTTAATTGCUGCT	79783	CACCGTGAUGCCAGCTATTATATTUCT
233220907	79784	TCAATACGAGGCCUGCCCUAT	79785	CUCCACCAGCTUCAGCGT
233221153	79786	CCTTTTCUGAAACCAGCAGACUAAACT	79787	GTTGTGACATTUGCTGATCCAAAAGUAT
233222267	79788	CTGAGACACUCACCCTGCUC	79789	AGGTTAACAACAGGGCUTGAAGUT
233223429	79790	GGGTGTGGUGGGAATCTTGTUA	79791	CATGAAATCAGCAUGCAAATGUACACT
233223748	79792	TGGAGTGTTCAUGTGTTATGCCAAUA	79793	ACTGTCTAATAATTUCTTCTTTCACTACUGCC
233224191	79794	GAGGACGAGUGGGAGGTUC	79795	AGCTGTCCUGGGACTCUCAT
233225221	79796	CAGGCCAUTGUCACAGAGGAT	79797	GTTGTATCCCCCUCCAAGCUC
233230073	79798	CTGAAGTGGCUGCCAAAAAUCA	79799	GAGGTAGGCUGTACTTTUCCCAAAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233249726	79800	CCTCTCCCCUCTGACCCUAC	79801	GGGTATGAGUCTGAGGUCAGAACT
233255121	79802	CTTTCCTAAGUGACCTTTCTCTCUCC	79803	GTACAAAGAAGCAGGAUGCCTUAC
233255448	79804	TGGTGAGTTUGGGATTCTTGTAATUCT	79805	ACACAGCUACAACTGGAGCATUT
233255824	79806	CATCTGTAAAUCCAGCAGTAAATGCUC	79807	GCCACAAUGTACAGGAUGCAACT
233257256	79808	GACUTAGTGCAAUGCAAGACAGG	79809	TTGACACCCCCAUAATATTTTUCCAGAA
233261722	79810	GGGAAACTGUCTTCCCCUGAT	79811	GAGTCAGAGAAUGGGAGAAGTAAUGAAG
233261881	79812	GGGAACTTGACACAUCTCTTTAATTAUAGG	79813	ACACAGATTUGCAACTTGGATUCAGA
233261900	79814	TTTAAGGAAGUGTTGATGGCGUCT	79815	GGTAGTGAGGAAUAGGGCTUCCA
233264683	79816	CATTGGTTTUACAGTGTGTTGCUGT	79817	CCAAAAGACCCCAAAAUCAACTTCCUA
233265462	79818	CTTACAGGUCTCGCTTATUAAAGCAGAA	79819	TGTCAACAUTATTTCCCAUCACACCT
233266616	79820	TTGTTCTTATATUCTGTGAATGGCUCCT	79821	TGGAAGCACUGCGTTTGGUA
233267819	79822	GAATCAATTATTTUCAGCAGTGGGAUGT	79823	TGGGAGCUGGAATGATTTTCTUCAT
233269954	79824	GACTTTTCGTUCTCTTCATTCTTUCCC	79825	GCTCAACCAGUTCCTCAAAGUCA
233273746	79826	CACACUGAGCAGCCTCCTTUA	79827	CGACTCTCCUTTTGGTGGCTUAC
233274780	79828	CCATAGGGTAUGGAGTATCTTGGUACA	79829	GGGACTTUCACCAGGTTCTTTTACUT
233275023	79830	CTGTTTTCCUCCATTTTCAUCGCA	79831	GTTTCTTCTGUCGGTTTTCAAGTTCTUT
233275646	79832	CGAGAAAUATATTGGUGGAGAACGAGAA	79833	CTCACCAGAAUATGGGACTTUCACC
233276468	79834	GUGCGCTTUGAACAAGAGCAA	79835	GTTAGGUGACCCAAATUCAGGAGAG
233279805	79836	CUATATCCGAAAGTUGCAACGAGAAC	79837	TGTCTTGAAGUCGGTAAAAAGCAGUA
233282033	79838	ATGGTCTCTTUCTTGTGGGCUT	79839	GCCACTATGGUAGGAGTGTAACUGA
233282771	79840	GCAAGTTCUCTTGCCTTTUGGT	79841	CTTGCTGTAGATUTGAAAGGTGGATTUG
233288663	79842	CCCAAAGTGCUACAACCTGUGT	79843	CCTGTGAAATTCUGATCTGGTTGAACUAT
233289315	79844	CGCAAAGCACUGAAGTTGAATTTUG	79845	TCTTTGCTTGAGUTGAGCCTTTGATUA
233289389	79846	TTTCTTCAACCGUCCTTGGAAAAGUA	79847	CUTTCTCTTTTUCAGCCACAGGAA
233290267	79848	AACAGCACTGTTAUTACTACTTGGGTUT	79849	CACAAGAAUCGACGACAATCTTAAACUG
233292212	79850	CGTTAAGAGACGCUGTAGGUCAA	79851	GGAGGAGCUGAGACAGCUAGAG
233292906	79852	GGTTGCCTTUGTGTGAATGCUAA	79853	CAGGAGAGAUCCUGCAAGCA
233295506	79854	GTGCGCTGUCAGTACCTGUAG	79855	TGGCAAGTUGAACTGAGCUGT
233299248	79856	TGTTTGCCCUGTGCTTACTUACA	79857	AGAAGGGUCAGGCATCTTCUCA
233301990	79858	GGGCCAGGGAACCUAGGAUAA	79859	GGCACTCCACUATCTTGCATGTAUA
233301996	79860	GCCTTCUAATGAGGCUCCAAAACT	79861	GCCTGTGAGUGTAAAAACATTUGAAGAT
233303345	79862	CTTTTACTTCUGGTTCTTCUAACGGGAT	79863	GGTAGCCGAUCTGCAGTCAAATAUAC
233305581	79864	AATGGTTTTCTTTUCTCCTCCAACCUAA	79865	GGTACTCACGTUTCCTTTAACCACAUAA
233308287	79866	GCTCGCAAGCGCUGTGUA	79867	TCAAGTCCCAUCTTGATTCAAGACUAAC
233308692	79868	AGTGCTAGAGAUGGGAGAAGAAUGT	79869	ACTTAGAGTCCUCCAGGTCATCAUT
233309998	79870	TTCACAGGUGATTGAAGUGGGAAA	79871	CAGCACTCUTCAACACAAGUGAAC
233312721	79872	GTTCCTGAAGUAGAGGACCCUCAT	79873	ACTCATGCCUTCACTGCUCAC
233314485	79874	TGTATGGTCACAUCTCTCACCUCA	79875	TCTCCCTUGCAACAAGTAAACAGTUAT
233318723	79876	CCTTATCCUGACGTAAACACCTTUGAT	79877	GGCAGGCAUTTCTGTAAAAGUAAAGAAC
233325728	79878	CCGGGCTCUGTTCTCACTUT	79879	CCCAGCUGTCACCACUCAC
233326344	79880	AAGAACCCCAGUCAGTTTTCATTAAUCA	79881	CAGGAAAAGACGAACUTGGAAAUCAT
233328658	79882	ACCGCCGUGCCTACTAGAAUA	79883	GCTTGGGATTUTGCTTTAGTGCUAA
233330634	79884	CGTCCGCUGGTGTGCUT	79885	CCUCGCCAGGGAAGGUG
233334549	79886	CCTTTCACCCAUCAACCCGUA	79887	CTGCGCAGGUAGUCAAAGGT
233334974	79888	GCAGAACAUGGGCTCAGAGUT	79889	GAAAGTGUCCACCCCTAGUGAC
233337251	79890	TCCUGGGCCCAAACTTCCUA	79891	GTTCTATTUCACCAATTGGCAUGGAA
233337573	79892	CGCTUGAGGAAAGACAGAGTGUA	79893	CCAGUGCTCACTTUCCAGAGT
233340159	79894	CCAACTCAUGAGGCTGUGCT	79895	CAAGUCAGGCUGGAGAGAAAGG
233344731	79896	ACACTGACUGCTCATTGTCGUT	79897	GGTTGTCUGCCTGCTTCUCAG
233347932	79898	GGAGAAGGACTUGATAATCTGTGGAAUT	79899	ACAGGTTTATCAACUTATGAGGAAAUGCT
233350209	79900	AAAATCATCATGAAUCCAAAGATGTACTTTUT	79901	CACAGAUGAAGGUGGGAAGGAT
233350281	79902	GGGTAGUAAAAGTGAATTCUGGACCAT	79903	GCAUTGAATAGTTGAAUGAAGCACAGT
233350556	79904	AACTGTGCTGUTGGTAAATATAATUGGA	79905	TTTCTCCTCGUGGCTATGTTGUAAAA
233353634	79906	TCTGTTCAGGUGGAGGACCUT	79907	CCACTCCCAGAUTTTGGACTGUA
233356106	79908	CTGTTGCTUCCATTTGCCTATUCC	79909	GGCAAGGTTGAAUCAGCATAAACAUAC
233356818	79910	AGTGGTUGCCACCTTGTUACC	79911	GGGAGAUCCGACAATACAGATUGAAAAA
233359364	79912	CGGAGTUGGAAGCGCGTUA	79913	CGCCCGCCCCAUACTUAC
233361228	79914	CCAGGAGTCTTUTCTTCTTTGCTGAUT	79915	CCAATGCAACAGACUTTAAAGAAGTUGT
233364459	79916	GCUGAAGGGCAGCTCTUCT	79917	GCCACUGGCGGAGCTUC
233364559	79918	GCGGAGAGUTCGGCAUGA	79919	GGAAGATGCUCTTCTCCTCGUT
233364698	79920	CAGUGGCTGAUCGACCAGAT	79921	CGTCCTCCUCGCGGTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233365243	79922	GTCTGTGTGGAAUGCTGATCCUT	79923	CCAAAGUCACAGAGCTTGATCUCC
233365503	79924	AGACTCACUGCGTTCTTUCGT	79925	GCCGGGAAAAGUGATUCGAG
233368471	79926	CCCACAAGCCCUGCTAATCUG	79927	AGTCCAGGAGAAAAUTCACAUGAGG
233369777	79928	AACGGTGGCUTCTACATCUCC	79929	GGGAATGGAGUAGGGCATUGAAA
233372842	79930	TTTCTCGAUCAGGACCAUCAACC	79931	TGGGAAAAACCACGUCTATGGAAAUT
233374474	79932	CCTCCAACAUCCTAGTCAACUCC	79933	ACCGUACAAGAAGCUCAAGCA
233377865	79934	GCCAATTTAATTTCUTTACCTATAATGGUCACA	79935	CCAAATTTUACAAACTCCUGAACCAGAA
233378243	79936	TCTGGTTCAGGAGUTTGTAAAATTUGGA	79937	ACTTACUAGAAAATGCAUGGCCCAT
233378246	79938	CTTGAAGTUGCTAAACAGTUGGCAT	79939	CAGACTATTTUACATGAATTGGCAUCCA
233378654	79940	GATCCACUAGGGATGCACUCA	79941	TCCCUCAGCGTTCAUGCAG
233380037	79942	GGGTCCAAGUTAGGTTAGGUGAT	79943	ATCTGGAGGAGGGAUGGGAUAC
233380365	79944	AAATGTTCTUCACAGGGCUCCA	79945	ACAACTCTGAAUGGCAAAGATACACUT
233382101	79946	CAGCCUCCGUGGACAAGAG	79947	CTCCCUGCTCAGAAGUCCAAT
233383554	79948	GGCAUATCUGAGGCCCAACT	79949	GGAAAGCAAAACAUATTGCTACTUGGA
233384285	79950	GCATGGGACUGTCTCTGGUAGA	79951	GGACACACCAGGCUACUCAC
233388008	79952	TGTTAACATGUCTGTGTTGCTUCCA	79953	AGATGATTGUGGGCTGCACUAA
233389980	79954	GCCAGGACACCAGUGTAUGT	79955	GCAAGGCTTTAUAGACAATGTGTUCCA
233393079	79956	CCAAACTCCUGGAAGTGGACUG	79957	ACATCCCACAGUGCATAAATAACCAUAT
233393848	79958	CATAATTGTGUGCTGTACTTACTUGCC	79959	GCACTCAGGGUGATAGCTGTTUC
233394191	79960	CAGCCUCAGGAAGGTTGUAGG	79961	CTGTCGTAAGUCAGGATTTCTGGUT
233394266	79962	GACAGGUTGUGGGCCAGT	79963	GCTCGAGGUGACCCUGGAT
233396032	79964	GCAGCTGCUGGAGTGTAATAAGUG	79965	CATAAGTCCAAUAGTCACATGGUGGT
233397501	79966	ACGGCAAACCACUGATATCTUCAT	79967	TCAAAGCTGUGATACAGACUGAAGAAA
233399223	79968	GGAUGAGTCTAUAGAGGAGACGGT	79969	GGCUCGGGAACACAUGAAGT
233401480	79970	AAAACTTAAGAGACGAUTGGAGGAGAUG	79971	GGAGTCGUGTACATTACUGAGAACAAA
233402114	79972	ACATCCUGCACCAGCAACUAT	79973	CTAAAGCTCTCUCACTTCGCCUT
233402386	79974	GCCATTTCUGTTTTCCTGUAGCAA	79975	CTCTGCATTAUAAGCAGTGCCAAAAAUA
233404700	79976	GACATGGAAUCACCACAGTTTTGUT	79977	AGTTTAGGAACCUGAAAAAUGACCAACT
233405873	79978	TCTTAGGTGAUCGAATGGAGGCUAT	79979	AAAGAAATCAGACUCCACTTTTCCTUCA
233407041	79980	GTGGAGTCTGAUTTCTTTTGTCAATUAGG	79981	TTTGCTCATGCACUTACAATTTCTUAGG
233407222	79982	CTTGACGGCUGCCCTTCTUA	79983	GCATGCAGGAGAUTTGGTTUCAAA
233415381	79984	ATGCAGAGGACUACACGGGAUA	79985	ACCCACCTCTGUGAATAATTTTCAAGUT
233416676	79986	AGACTGTGAAAGCACUAAACCACTUAAA	79987	ACAGTGACACUGTAATTTTCAAUAACCGT
233424149	79988	GTGACTGTGGUCTTTTCCTGUGA	79989	CTCATGTGCCTUTAAAGAAAAACAGCUT
233429649	79990	GGGAGAGTGAUACAGATTCATTUGAAGA	79991	ATAAAAATCAGTTCAUTTCAGAAAGAAGCUAG
233441081	79992	TGGCAGAGTAAAACAUTATTTCCACCUT	79993	GTTACCTTGCAUATCTGAGATGTGUACT
233441306	79994	ACATAAAACTTCUGCAGTACACATCUCA	79995	TGGTCTTAACCCUATATATTCCCTTTATTAUCT
233441895	79996	TTTTGGTTTGTTTUCTGCTTCGTATTCUT	79997	AGCTTTCCTUGGTGGCTTTATCUC
233442258	79998	TCATTTACTGUAGGTTGGATGCAUCAC	79999	CAGGACUGGCCAGAATUAGGAT
233443884	80000	GGAAAGCTAUGCTATTCAGTATCUCCAA	80001	ATCTCTTAGCUGGAATAGACAAAAUCAAACA
233444902	80002	TGTCATUGCCACTGTCTTTUCCT	80003	ACCTGGUAAGAAAAGCUCAGCAA
233452214	80004	GAGTTGGCCCUAGACTUAGAAGAC	80005	GGCTCTAAAAUGCTCTGTTCUCAAAAA
233452486	80006	GCTGAGGUCCTTTTTGTGUGGAA	80007	CAACAAAAGAAGUCACCGTGUGG
233452984	80008	TGAATUCCGTGCTUGGGAACT	80009	CCTGCAAGAAGGUTGTTTATGGGUAT
233462484	80010	ATTCTTCAGCACUTCTAACTCAGCUT	80011	ATCAGGTCAUGTGACTGGTGUG
233465569	80012	CAGAAGCATTTUCTCTTACCCTUGGA	80013	GTGTGGTTTTACAUAGGCCATTTTTCUT
233466735	80014	CAGATCTGTATTUATTTCAGTGTTACTUACCT	80015	GACTCTGAAGATGUACCTATGGTCCUA
233467509	80016	AGCTCAGACACUCTATCAUCACCAA	80017	CAGCCGGUGGAUGGAGAAG
233467720	80018	GTCTACTGTTCUAGAAGGCAAAUCACAT	80019	GTGGACAGGTUTTGAAAGATATTTGUGT
233470646	80020	TCAGATTTGUACAACCCCAGCUC	80021	GATGUAAGGGAAGCCCAGUCAT
233477072	80022	GCCAGUGGACTACUAAAACCCA	80023	GCGCTCGUTCTCCTCUAAACAAAA
233478904	80024	GGAGGCCTUGAATAGAAAGCUCA	80025	GUTGCAGGTCTUGCAGAGGAT
233480155	80026	TGTTGUGAGCCCTUCCACAAG	80027	CCAGCTGTAGTUCTATTACCAAGTTTUG
233483284	80028	GAGAUAACCAAGGCTGCUACCC	80029	TCTTTTTCTTGUGTTCGTTCTTCUCAGT
233503974	80030	CAAAAUGGAAGCAGCAGTUCAGA	80031	TCCATCAGCUGTTTTCGTTGTAAUAGT
233510195	80032	TGGATGTCAGUCTGCCCTUCT	80033	ACTTAGCTUGGAAGCTGACAAGUG
233511006	80034	CATAAGCCAUGTGGCTCATGUT	80035	TGGTGTUGAGACAGGATTACTCUGA
233513228	80036	TGGTGACGCCACUAAACACTUC	80037	AGTGGATCCCUGATCCCACUT
233518656	80038	GGAGTACTTCUTTGGGTTGACTUCT	80039	TCAGTTCUCCCACCTTCUGCT
233520677	80040	GAGTTATTUCCCCTAACTUCACAAGCA	80041	TTCCTGAAUAGCAGAAAAGGTCTCATUT
233522057	80042	GCTGCTGUCACCACCTGUAG	80043	CACCTGCUGCGATTCUACGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233524283	80044	TCCTCCCAUTTGCAGAUGCC	80045	GGGTGAGUAAGAGACTGATCUGT
233524764	80046	CTTGAGGCCUTTCTUACCCAGA	80047	CAATTACCTGTUAATCAAGGCAAACUCA
233526725	80048	CCTGTTTUGCACTGGCCTTUA	80049	GAGGTAACCACAUAGCTGATCUGAAAA
233529416	80050	GTTCACTGAUACCACCTUAAGGCT	80051	ACCGCTCAAATGUTATCTGGGAAATUAA
233529536	80052	AGGGCAAGGCCCCAUTATAUC	80053	GATAATGGCAGUTCTCACACACAUC
233530458	80054	AGCTCCATACUCTCTTTACGUAGAACT	80055	AATTTGTCTGCTGAUTTCTCAACCTCUA
233530736	80056	GATAACATTUGAGCGGTGUGGAAAA	80057	GTTTCCTCTTTUTAAAGCCTTAATUCCAGAT
233536088	80058	AGAGGTTCCTUAAGATCTCGATTUCCT	80059	ACAGCACAUGCATCTTUCCCT
233536297	80060	GGAAGATGACUGGATGGAAAACAUC	80061	GCATTCTCUACCCAACTCCCUCA
233545013	80062	CCACTGTGUTGTAAGGCCUACT	80063	GATAGTCTTGGAUCTTTGCTCGAAUACA
233545312	80064	CCAAAGTTTGTGAUTCCACATTTCTCUT	80065	CACTCUGGAGAGAGAACAAATAAAUGGT
233547824	80066	CCCTAGCUACAAGACATTCTUACCAAAA	80067	CTTAAGTTTCAAGUTTCTGGCAGUGG
233549608	80068	GACTTGACCACUTATGTTGTCUAAGGT	80069	AAGTCACAGAGCUTAATATTTCCACTUC
233550165	80070	AAAGGAATUGGCCACTGTGUACT	80071	GCTCUGAAGGAAACACCGACAUAC
233550986	80072	TGTCTTGCAGAUATCAAACCTUCCAAT	80073	CTAUCAAGCAAGAAGGCCUGGA
233551762	80074	GCAGATTTATUCAGCAATTCAGCCAAUG	80075	ACCACTTCCAGGUTCTTTTACTUCAA
233554755	80076	CAGUCTGCCTTCUACACAGAGAAAT	80077	CTGTTCTGTCAGUGTCTCACTTTCTTUA
233555182	80078	GAAUTCAGTGGUCAAGAGGGAAACA	80079	TCAAAUGGGAGAAGTGCAAUACCAT
233556313	80080	CTTGCACTTCUCAGAGGGCTUA	80081	CAGTCAGACAGACUGCCTCTUG
233558101	80082	CACTGACUTGATTCCCUGGCT	80083	CAGTCTGTACUGTGCCACAUCAAT
233559313	80084	ACACAGGTCCUGAAGCTCTCUA	80085	CTCTTAUCGGAGAAGAACGUGGT
233561101	80086	GTGTGGTUCAGAGGGACTGUAG	80087	GTCTAGUGAGGAAGGCAUGCAA
233561851	80088	GGCACCTTCAUGCCAGAGAUAT	80089	TCTCAGTTCCUTAGCATAACCCUCA
233564417	80090	GCCAAGCCAAAGUCACAGATTTUA	80091	GGTCACAACAGAUGTGAAAGAGAUCAG
233565032	80092	AGATTTGUTTGGCGUGCCAAG	80093	TCTCTGACAAAAGUGAATGAGGGUAGA
233571847	80094	GGAGGAAGGCAAAUTTGTGATGATGAUA	80095	GATCTTGTGCTUCTCCCTCAGATAUG
233572030	80096	CTTTCCTCTAGGUAATAAAAGGCCUGA	80097	GGAAGCAACAGCCUTTGGATTATATCUA
233576614	80098	GGCAGGCAGACUGAGATUAAGA	80099	GAATAGGCGUGGGTGATGTUCA
233579446	80100	CTGGTAAAGAGACGUGGGAAAUGA	80101	GCCTCTTCUGTAAGACACUCACAAT
233581662	80102	GGTTTGAATUCAGTACTCCCTUGGA	80103	GCCTCGAUCGACGTCCTUT
233583480	80104	TGCTCCCCCUTTAACCUGGA	80105	CCTCCCCTTUGTTAGCACTACUG
233584658	80106	GGAGTAACTAUTTCCCCCAUCCC	80107	GAACCAAGUACTCAGCCTUCCT
233588863	80108	AGTGTCATTUCCGATCACTTTUGGA	80109	GGCACTTCATAUTAATACCTCCCUGAAA
233594021	80110	CCCCAGGAACCUCCAGUAAAG	80111	CATCTCAGAGUGAAACACCCACTUA
233620582	80112	TGATTCTTCCUCTCACTCUCAGGAT	80113	CCAAAATGTTTCTAUATTTCAATGTCTCCAUT
233621867	80114	GTTCCCUGAGCGTTAACGAGUAAA	80115	CGACUCGCAGCTGCCTUAC
233625577	80116	AGGAAGTGATTTUTGACAGAAGTATTUGT	80117	TCTGGCTGCUTCTTGTGTTUCT
233625669	80118	GCCAGAACCAUCACCUGCAT	80119	GGTTGAAAAGCUGGGAAAAGTUAGG
233626392	80120	GTTGGCAGTAATUTTTGCTTTCTTTCUT	80121	AGGCTGTGGTUTCAATGTAGACTUC
233629447	80122	CCCCCUCUAACAGCAACCAA	80123	CTGACTUCACCTGCACATUAAAGG
233630001	80124	CCAACCAGGGACGCUATTAUGAA	80125	GGATACAUCCCAGGAGGGTUCT
233634153	80126	ACCAGGGUACACTCCTCCUG	80127	ACCCCTGTATUCTCCTCCTTAUGT
233636429	80128	TTTTCTCTTTATUCCCCACTGTCTTCUC	80129	CGTCTUCCAGTGCCATUCGT
233636458	80130	CCTCCACTUCTTCAAGGCCUA	80131	GTGTUGAAGGAGGUGGACACT
233639192	80132	CTGUGACCAGCCATUCCAACT	80133	CACCCCTUGAGGGAATAATUGGT
233640920	80134	TCTGTGCUATGGCTUGAAGGAG	80135	CGCCCCCACUAGGGATGTAUT
233644441	80136	CTATAACACUCAGCCAGTTCCUGT	80137	CTGGCCCUGCTGCATAGUAG
233647608	80138	CCTCUCACAGACCCAGAAGUG	80139	CCTCCTGGUCCACAGAACAAUG
233650883	80140	GCCTACCAUCGGCTCTGUCT	80141	ACUAAGGTGGAUCAACGAGAAGAGAA
233651269	80142	AGATTUCCCCAAACACAGCCUT	80143	GCTGAGTTUCGATCGGAUCCT
233652131	80144	ACCAGAGCUCGGAUCCCAT	80145	CAGGCTUCGCCGAGTAGUC
233653515	80146	CACCTGCACCAGAUCCTTCUT	80147	GTCTGAGAGCUCGGATCTUGG
233653618	80148	TGATATATAGUCCATCCTTUCAGCCGAT	80149	AGGCATCCUGAACTTTCCCAAUAC
233654655	80150	CCTTCCCTTCUCAGGTGCTATUC	80151	ACAAAGGCUTACCCTATUGAACACC
233654913	80152	AGGCAGUCTATTGATAAAUCAGAAGCAA	80153	CTATGAAGTACTATAUGTGATGCAACCAUCT
233655744	80154	TGTGTCTGUGACAAATTTGACTGCUA	80155	GGTAAGUGAGAGCUGGAGACAG
233656538	80156	TTCTCTTUGCCAGTCCATCTUCAA	80157	TGAGTCAGAATAAAUCTCACCTGATAGUGA
233656552	80158	GTGCCACCUAAAACATTGTTAUGCT	80159	AAACAGTATGTCTAUTACAATAACAAAAAGUGG
233656845	80160	ATCTGGCUCGGGATCTAGTACUC	80161	ACCCACCTATUACCTGTCACATGAUA
233658427	80162	CTGGCCCUCTCCAAGUGAAAT	80163	CACACCTCTTCUATTTTTGCTTTTCCUT
233658487	80164	GCTTTTCTAACUCTCTTTGACUGCAGA	80165	GGATTGUGGCACAGAGATTCTGAUAC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233659281	80166	ACAACCUAACCAGAAAATTCCTUGGAT	80167	CTTCCTTACCACAUAGGAGAATGTACUG
233660564	80168	GTGGCTUGGGCTACTACAGUA	80169	TCATGCCUGGGTAGTGTTUGG
233661958	80170	AGCTGTCUGCTCCCCATUG	80171	ACAGAGGACCCUCTTTCATUACCT
233663118	80172	CTCAGCAGCCUCCUCGT	80173	GCCGCUCUCCCCAAACA
233663665	80174	TCATCGTCCUCAGCCTCTUCA	80175	GGGTTCCUCGCCCCCTUA
233664155	80176	TGTGAGGAATTUCTCCTTTGTTGUGA	80177	GTTCAGCACUTTGATGGTUCCAG
233667219	80178	AGCCACAGCCGAAAGUTAUCA	80179	GTTCAGGAATTCUTCCAGCTTTCTUC
233671009	80180	CAAGCCAGUGTCCTGACUGA	80181	CCCTTTGCCUACTTCTCCCTCUA
233671933	80182	GGAGGTTCUCTGGATCAAGUCCT	80183	CATCTTCCTCUCTTGTCCATTTCTUACC
233677585	80184	CCCAGCCUGTTAGGCCTUA	80185	TCTTGATTCATTUCCTTCTTTCCTUCCA
233681968	80186	TGCTCCAGGGUCATTTTATUGGG	80187	TTTCTTACCTGUTCTCTCCCUGAGT
233684563	80188	TCTTTCTTTAGCAAACUAACTTACCTTACCUC	80189	GTTGCTTCACCAUTATGTACTGACCUA
233685948	80190	TTCTCATTATTTAUACCCTTTTAAGAATGCUCT	80191	GGTGACTTTTAGUGCATCCAAGATUG
233689870	80192	AGCATTTTTCATUAAAGCATTTCACCACUT	80193	CACAAUCCGCTGGGUCGAT
233689904	80194	ACTAAAATTGUTGATTGTGAUCGACCCA	80195	GTTAGACTTAAAAGAGCUGAAGCACCUA
233690140	80196	TTCCATGCAGGUCATGCACTAUT	80197	CGCAAGCCCUCACTGTTTTUAC
233690946	80198	GGTGCTTCAGCUCTTTTAAGTCUAACAT	80199	TTATACAAATTAAGTATUACGAATTTGCCCGUT
233691452	80200	AAATTGGAAGUCGTTUCAACGGA	80201	CCTGUATCACAGACUGGCAACAAG
233693014	80202	GCGATGCACGGUACCATCUT	80203	ACCCTGTAAUGGATCTTAAAGCATUCC
233693508	80204	CATTCCACCCAAAGCAUGTTATCUT	80205	CACATGTTTTGGAAAUGACTGTAAAATAUGGA
233695721	80206	AACTUGGGCCAGCAACTCUT	80207	TTCACGTCACUGGTCTGTUCC
233699527	80208	CCACCACCAGCUCCTAGTCUT	80209	TTTCCCCTCUCTACCCTCUCAG
233700554	80210	CCCATTGACUGGAGGAAATUGAGAAA	80211	GAACACGATCAUCTGTCCTTGTTUG
233701248	80212	GGAATTTATGCGUATGATTGGCAAUGA	80213	AGAAAATGCATGACUACCCTGGATUAAA
233709944	80214	GACTCTGTTTUCCTTCAGGATACAUCA	80215	GCAGUGTUGGGAGCAAGGG
233713304	80216	GAAAGUCTUCCAGGCAAGGAGAA	80217	GATTGATGAAGAAUTTTGTAGGCGATUGA
233713851	80218	ATCACAAACUAAGAAGCAATGAGGCUAT	80219	AGGAAGATGGUAAGGGATACUGGAG
233714380	80220	CCACCAUCCCACCACATTCUA	80221	CCATGGCCUTTTGTGTTCTUCAG
233714392	80222	GGGCCCTCAUTCTAGTTCCTUCT	80223	GATACATAGGUGATGAGGATGUGCAA
233715676	80224	CTGGTTTCTGGUGGGACCATUA	80225	CAUGCACCGGAAAAGCGAUG
233716567	80226	CACTTGCTTCUTCACTCCAGUCA	80227	AGGTTTTCTGTUGTTTGGTTTGCUT
233718102	80228	TGCGTCGGACUCTCTGTCUA	80229	CAAACCCUGCACTCACCUGA
233720488	80230	CATAAGGTCUGCCGAAGCCUT	80231	GGGAGCAAAGCAAGUGTCUAAAGT
233720804	80232	TTTGAATTTCCAUGGTGTGGUAAGGA	80233	CAGGTTCCAGACAUGGCTATTTTTAUG
233722694	80234	TTGTAAAGATGCCUGTCATGCAGUA	80235	TCACGCAGGUGAAACAGUGAG
233727562	80236	CACCGGGAAGGCCUATCAUC	80237	GTGACGAGAGAGUAGGTUGCC
233729576	80238	CCTACTCUGGACCCCATCTUCT	80239	ACAGCCCCAUCTTTCTTAAGCUG
233737295	80240	TCGAGGAAAAGUCATCGCCTUC	80241	GGCCTCTCUCTTACCCACTUCA
233746178	80242	CCTCCAGAGUGGGCTCCTUA	80243	TCCCGAGTUCTGGGCATTUC
233753022	80244	GAATGCCUGCTGAUGCCAAAT	80245	CTGGTCCCAUAAATCTCTCATCTTUGAA
233757513	80246	GATCTTCTGAACUAGTGTGTTGGUGAA	80247	GAUCTTCTATCTGUCGGACAGGGA
233761441	80248	CCTCTGCUGTGTACTCUCCACT	80249	GCCATGGCTUTCTGTGCTAAAAUG
233764635	80250	CCTCAGTCUTCTTGGAGCUCCT	80251	ACACTCCCTTTUGCCATAAGAACTTTUA
233774929	80252	CCAAGTTATAGACUGTTTTTGCTTGUGT	80253	CAGGCTGCCAAGUCATTCAGUA
233784977	80254	TGTTTTCTCTUACAGGCAAATGTTCUGA	80255	GTAAAGATACACCUGAAGAACTGGAUCT
233788764	80256	TCCAGGAGAGCAAAUAAAGTAAUGCC	80257	GGCCACAGAACUGAAACATCTUC
233789450	80258	AGAGGTTTGAGUTCTTCTTCUAGACACT	80259	AGTGACATUGAGAACAGAGAGAAUGGT
233789894	80260	CTGGAAAUGCCAATTCTAUGAAGCAAAT	80261	CCACAAGCTTUAGAAGCAGCAAUAC
233790238	80262	GGGAGTATGUTGCAGAAGAAAUCT	80263	ACGCCAGCCAUACAAGCATUAA
233796702	80264	CGCGCGUAGCCAUCGAA	80265	GCGCACCUGGAAGACTACUAC
233797725	80266	GGGUAGCCGGTCAUCCA	80267	CUCCACCCCCAUGAGCAC
233799225	80268	TCCAGGUGCGCCTTCUG	80269	AGUGAAAAAGGAACCGGUGGAG
233799616	80270	GCTGAUGATGCGGUCGGT	80271	TCAGAACUGGCAAUGAGCAACT
233802271	80272	GGTTCCTTTTUCACTTCAAACTTCAUCA	80273	CTCTCCUGCAGCCCAUCT
233834986	80274	AACTTTGGGCUTTACGTTACTGUCT	80275	AATGTCCACUGTTTTGTUGAGCAAAAT
233847028	80276	ACCTCTGCUAGCCAGACAACTATAUT	80277	ATTCTTGAAUAGAGGAATGGCGGAUAG
233852334	80278	CCAAGCCAUTAAAAUAGAAGAGGAAGCA	80279	CTTGCTATCTTGACUGTCTCGATCATUA
233852564	80280	CCAAGGAACCUACTGGTGTCATGTAUA	80281	TCCTTTGCTTAATUAAACGTTGCAGTUT
233864390	80282	GCAAGAGAUCAGCUGAAGGACA	80283	GAAATAAATTATGGGAUGCCAGTCGUT
233868115	80284	CAAGUACCCCCUCCGACAAAAAT	80285	CTGCATGGAUGGAGTATTCTTTAGUACA
233868975	80286	CAGTGATUTCTTCAGGUGGAGAGG	80287	CTAGTATCACTCUCTGTCCCATCAUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
233870196	80288	CACAGGTTCAUAACACAACATCUAGAGA	80289	TGTGTGTTGGUCTCGATCATUCC
233872925	80290	CAAAAATCTCACAGUTGGATGGUGT	80291	CCAGCATCTUCAGGTCTATCAATCTTUA
233873154	80292	CCTGCCTUCAGACATTATGGACUT	80293	CCCATGTCTTTUTCACGATTACTGUC
233875108	80294	CACCUCCATTUGAGAGGGCAAA	80295	TCTCCTATCTCUGGAACTAGATCCCAUA
233878468	80296	GCCAGATUCCAAAAAGAAATGGUAAAGA	80297	TTGTCCCTGUGTTTTAACTCUGCT
233880502	80298	CCAAAGATGGAUAACTGCCATTCTGUA	80299	GGAGCTCAGTATUATAGGTGTCCAGUAA
233880699	80300	GAATCTTGGUGAAGGATTGGGTCUT	80301	GATCAGAUGGTAGCTCUAGAGGCA
233882371	80302	CAACAGAUCATCCATTAUCAACGAACA	80303	GCTTCAAGUTTCCTTCCUCACCAG
233884426	80304	CATGGAUGCAGACCACATCTCUA	80305	CGGGCCAGGACUATCAGUAGAA
233884531	80306	GGAACCUGGTCAGGUGACAA	80307	GGCCTTTAUCACCAATCTTAUCAGAAGA
233888141	80308	CUCAGCAGAGGAACAGTTUGAGT	80309	TCACTTUCAGAGGAGGCUACAGAT
233890515	80310	GCCAACGACCAUGTAACAATGUT	80311	CTCATTTTCCAUTTTTAGAGGTGUCAGT
233892308	80312	CAGAACCAGAAGUATGUGCCCAA	80313	GGGTCACUCCATTUGGAAGAGT
233893517	80314	GGAGAAGAGAGUAACCAUCACAGAAAA	80315	TUGCTCTACUGAACCACAAGGAG
233897537	80316	GCACAUCAACAAUAAGCCAGGAT	80317	GTCCTGGAACUGACGCACUA
233898710	80318	ATGCAGCCACUTTATGTTCUCCA	80319	GAGAAGTUGGCAAGCTTGGATUT
233899352	80320	GGCCCCAGGUATCCAACTTUAC	80321	AGAAGAUGGAGAGGAUGGAGAACC
233903660	80322	GCAAACUACCACAACCCCUACAAG	80323	CTGCTGGCTAGCUTTGATTAAAAGATUG
233903822	80324	CCTTCCCUGCAGCTACUCAAA	80325	TTCTTGAGUCCAGAGGAUGGAGT
233904598	80326	GGCTTTAUCCTCAGCTGUGCAA	80327	AACTTTGTGCUTCTTGCCATUCC
233908520	80328	GGTACCCCAGAUATTGGCTCAAUAAG	80329	TCTGTGATGUCCCCAGTTGUG
233910575	80330	TCUCACCCTUACCACAGGACT	80331	GCTGATGTTUGGTGGGAAACUAC
233911429	80332	AGACCTCAGUACCACAGUAGCC	80333	GGAGGGTGUGAAGTTAATCAATGUCAT
233912684	80334	GGGCUAGGAGACAAGAATCUGA	80335	ACGGCUACAGGCTGAACCUA
233913755	80336	CCGCCAAGUTCAGGAATGTTUC	80337	TGATAGTGTUCGTCTGCTUCCC
233915836	80338	GGTTTCAGCUGCCTCUAGACAAAG	80339	AGCCTAGCTAGUATTTGGATCTCUCA
233916305	80340	GTAGTUAGGAGGCTCCUCAGGT	80341	CUCACAGAGAGGGCCAUCAG
233918757	80342	CCAAAAGAGCAGUCACATCTUCAGA	80343	CATCCTGGCACUGCTGGUAG
233920566	80344	CCGCACAGGCAGUCUCT	80345	GCCTCCUCAGCTCUCCGA
233923261	80346	GCCCCTTCUGATGTGGTTTCUAAT	80347	CCGGTTCAAAAUACATGATGCTAGATUT
233924128	80348	GGGATGAGGUGGGATUGGG	80349	AGCACGGCCUCCTCUACA
233924929	80350	GCATAACAGCCGCUTCACCUT	80351	CTATTAGGAGCGUCTACCGTCUG
233930469	80352	CGAACTGUCCCCAACATCAUAAAAAGAT	80353	CCCTGATGUGAGGTGGCUAGT
233934055	80354	AAATGCAGGCUCGAGCUCA	80355	CCGTGAGAUCGAGAGTTGTUGT
233941387	80356	GCATCAUGCAGACCTAACCUGT	80357	GAGAAAGGGUGTCGTCCAUCAG
233949246	80358	CTTAGACAAGGUCTTCCTTCCACUT	80359	CTACCTCACCUGTTTCCTGTAUGG
233950580	80360	ATGGGATCCAAACUGGAAGACAUC	80361	AATGCAGUGCAGGGAGGAUT
233950770	80362	TGTTGCAAATGUGAAGGCAAAUAGG	80363	TGCTTAGAACUATTGCCATUGGAGAG
233954563	80364	GCACTTUGAACATCCUCAGCACT	80365	CAACACCTTTGGUAGTAGCATTTTCTUT
233956100	80366	GGGTCACAUACTTCCTCCUCCT	80367	AACTGAAGCCAUAACAACAGTCTUCT
233956237	80368	GCAGTCTGTAUGTTCAGAGTGCAUT	80369	TCAGACCTATAUGGATTTGGAGCAUCA
233957514	80370	CGTTGATGCUCCAAATCCATAUAGGT	80371	TGTCATGGUCGATATTTAACUCCAACAA
233959039	80372	GATTGTTGAAUATGAAGCATUCCCCAAA	80373	CCAGGGCAAGGUCCATTTCTUAC
233961810	80374	TTTCCATCAGTUAGTTGTGATCTUGACA	80375	GCTGCAGTTUGCTAAGTTGGAGUAA
233965041	80376	GACTATGGGCUTGTTTTCUCCAGAT	80377	GGTGACCCAAACACUGATTCUG
233988415	80378	GCATTGTCCUCAGGCACGUA	80379	TGCTTGTCCUGTGCTCTCUC
233998454	80380	CCCAACCCCUTGCCTCATAUT	80381	AGUAAATTCCAAGGUGAAGGAAACCAG
234012656	80382	TCAGTACAAAAUGGCCAGTGCUA	80383	TCAGAGCCACUTCTAGGTCUCC
234013494	80384	CACAGTUAAAACTAGTCCUCGAAAACCT	80385	TGATCTTATCUCCAGATTTGGTCTCUGA
234017106	80386	CCAAGGAAGCAGACUAGUGCT	80387	CGCTCTTGUCAGCATCUCGAT
234018335	80388	GATCCATCTGTGUTTTCCCCTCTAAAUA	80389	ACTCTGAAATGUCCTTTCCATGTGUT
234019867	80390	CGATTGTTUTCGCCACUCCA	80391	CCUGAAGAAGATGTUCCAGCAGAAG
234020203	80392	CCACCTTCCCUGGAGTAAAAAUCAAAAT	80393	TTGAGAGGAGAGAGUTTACCUGCT
234021275	80394	TUGGACCUCGGCCCAAC	80395	GCTGGCAACCCUCTTGUCA
234023680	80396	CGTTUCAGCAAGCCACAAAGAUT	80397	GGGTCTTTAUCCTTTCTGTTGAUGGAG
234025894	80398	ACAAAUTGUACGACGGAGAGGAAG	80399	CCTTCGAGGGCUTTGTCUGA
234027022	80400	GTCTGTAACCUTGCCTAGTAAUCGAA	80401	CCTTCCACTUCTTGTCCTCAUGG
234027183	80402	CCCGAGGAGCUGUCCAAAG	80403	CAGGAUACAAAGCAGAACTACTCUGAAT
234030483	80404	CGAGAUGCUGACAAGAGCGT	80405	TTCACCAACAACCUTCTCTTUGGA
234034521	80406	TCTGAACCAAGAUCTCCTTCUCACT	80407	GCACTAGUGGCAAGAGGACUA
234035121	80408	AGGCAGACAAGCUTCCAAUGA	80409	ACTGTTAGTTTUAATAGGCAAGGUGGAAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
234036728	80410	CTTTGTATCCUGTGGGTAGGGUT	80411	TGTATCCCCAAGAGUCACAGAAGTAAUA
234044328	80412	GTCTCTTCCUCGTTAAGCATTTCUGT	80413	AGGACTACTTGAUGAAAATGGCTCUG
234045781	80414	CTTCATCACAUGATTCTGGGACUGA	80415	GGTTTTCTCCUTCTCCAGGGAUG
234055713	80416	GGCCTAGAAGAUGACATGCAUGA	80417	ATGGCAATTTCACUGATGTAAGTGTUG
234057208	80418	GGCTTTTTGTCAUTTGCTTCTATTUCCA	80419	CTCTGTGGCUTTAACTAATACTUGCC
234102457	80420	TTTTAACACCACGUCCTCTCGUT	80421	GCUCTTTGTTGCTUCCCAAACAC
234105891	80422	CCCGTGGTUGGGTGAATACUT	80423	CCCAGGAGACUTCACUGAAGG
234115582	80424	CACCAAAGGCAGAUTCCAAAUACAG	80425	AAGAAGAGCAAGGUATAAGGGUACAGA
234156180	80426	ACTTTGGCTUTAGCAGGACUGAA	80427	CAGATGAUGCAGGTAAAACAAUCCAC
234160390	80428	GCCATGGAUCAGGTCTUCCAC	80429	GCTTGAGGAACAAAUCTGGAACTUAC
234166650	80430	GCTGGCTAUCCTACTGCTUCAT	80431	GAGTUCCGAGACCCTCTUGG
234167778	80432	GGGCCTGAUTTTCGCGATGUA	80433	AGTCCTUAAGGGCGGUCCA
234179932	80434	CTTGGCTCUGTGGAGTCGUT	80435	GCTCCTUCACGAGGATTUCCC
234180940	80436	GCTGCACAUCTGCCTGTACUA	80437	CAGCTTCTCAAUGTTTTTCCTCUGG
234182429	80438	TUCCCCUACCCAGAGGACAAT	80439	AGTAGAUCCTGCTCUGGCACA
234182548	80440	GAAGTTAATGTCUCCACCACTGGATUT	80441	CTTCACTUCGCAGGCAGATUC
234185337	80442	ACGGGCUCTAUGCGAAAAGAC	80443	ATTCTAACAGAUAACGAGGTGCCTUAC
234187817	80444	CCAATGTCCUCTCGCTCCUG	80445	ATGGCTGGCUTACAGCTAGTUT
234191801	80446	TGTCTCCTCUGGGCATTTCTTUG	80447	ACCATGCACUTAATTGGCCGUA
234203278	80448	GCACCTTAUGTGTGCCCUAACT	80449	GAGGTTTCCTAAUAGTGAGCTGCUG
234204966	80450	TTGCATGCCAGUCCTCAUGT	80451	AATTGGUTTGGGCUGGAGAAGT
234206466	80452	ACTCAGGCAGUTCTTTAGTTGCUG	80453	CTCTATTCAATACUGCCTACTCTTUGCT
234208648	80454	AAAUCCTTGCGUAGCCCGAA	80455	GCCCCCACCAUAATGUCACT
234212609	80456	GGAAGAACAGCCUAGACTUGGG	80457	ATCTTCTCTCCCUTCCCACCUT
234214972	80458	TCATTAAGAGCAAGUGTGGAAATCUGT	80459	CCUCAACTAUCCACCAGGCAAAAA
234219370	80460	GAGCGUAGCAAGGAGCCAAUA	80461	CACATCCATGTCUTTTCCTACTTGTTUT
234220525	80462	GCTACGCAGUTCTGGAGCATUT	80463	GACATTTAAAUCGCCCCCUCG
234222125	80464	CACCTCAAAGCUCTAAGTUCGAAGA	80465	GTGTAACACACGUCCATTTGATAAUGAG
234223086	80466	GGGAGCCUGGAGTTCTATGTUCT	80467	CAGGATTTUACAAACATAGCAUGCGA
234227975	80468	GAAGAACGUGCCGTUGAGG	80469	ACACTGTGAUACGGGATGAAAATTCTUT
234229363	80470	GGGTTTGTATUCCTTGTCCTTCUC	80471	GAGGGTAGAGGGAAGUTATTGCTTUT
234236334	80472	GGTGUCGGCGTUGGAGT	80473	CTCGCCGCUCGCTTTUC
234237766	80474	GAATTCAGACCUATTCCGCUCCAT	80475	CCTGTAAACUGAGGTACTTTGGTTAUCA
234247138	80476	AGAAGTTGCUTGCTCCUCCAA	80477	GGTACAAGCUGCAGTCATTUCCT
234247736	80478	CCCTUCCCTTCTTTTUCAACCGT	80479	CCCAGCTATUCCACAGATGTTTCUC
234255953	80480	AAATGGUGGAAGATGATUCCCGAA	80481	CTTGGCAGUTGAGGCCCUAT
234281990	80482	CAGTGTTTCTTUTTCATTGCAGATUCCA	80483	CTTTTTGGGUGGCTGTTGTGUAG
234286026	80484	GGAACCCCAGCAUTTCAGUGT	80485	CCAAGUAACCAACTCTGAAAUCCCA
234301468	80486	ACTCTTTACCUCAGATGAGCTGCUA	80487	AGAATTACAAGAAUCCCAAACUCACCAG
234304351	80488	TGTAAAACTTAAAUGTGAGCATCCUGGT	80489	GCTGGATTUACAGATGATTTTGAAUGGA
234331446	80490	AGATAAGTCUGAGAGCTACUGGCA	80491	GGGAGGACTTTCUAGACCCTTATTCUA
234331842	80492	AGGCATAGATTUCCAGGTAGAAACUG	80493	ATTGACGTCAGAAUTGGACACUAGG
234335248	80494	CCGAAGGAGGCACUTACACAUT	80495	CUTGCAGCTGTUACAAACACGAG
234336499	80496	ACTATTTCTGTCUCATCCATGTTUCAGG	80497	TGAGAACACCAAAAUTGGCAAAAUCAT
234338579	80498	AGTGAAGAACTGUTCTACCAGATACUCA	80499	GTGGAGAGCUACTATTTUCAGAAACGA
234355242	80500	GAAAGCCCUCCCCAGUCC	80501	TGCACTGTAATAAUCCAGACTGTGTUT
234381385	80502	AAGTGAAGTTTGUCTCCAAGTGUGT	80503	CTAATTAATCCCUTTTAGTGCCUCCAGA
234382120	80504	CACCAGCCCAUCCATCTATCUG	80505	CTTGACTTTUGTATTCTGACUCCAAGGT
234382961	80506	AGTGAAACAGAAGGAUGCTTTUGAGAT	80507	GAAAACTUCAAATCCATTCUCAGGAACC
234383721	80508	CGTTCACAAUGCAACTCAAATTTTUAGG	80509	TTTAGATCGCAAAUGCCTTGGGUA
234384237	80510	GCCAAAGAGGCCCCUATCUCT	80511	GCUTGTCTTAAATTGUACAGCAAGAACT
234387582	80512	GTTGAAGTCAAUCCCCACATTTAGTUC	80513	GCTTATTTGCTCUCTCATGTTCTGTTUT
234388695	80514	AACAGCTACCAUGGGTTTTATTUAAGGT	80515	CCCAATAACCAAGGCUAGGTCAUA
234395922	80516	GCCACGACUCACAGAAAGAACUC	80517	GCAGCTUAAGCAGGAGGTGUC
234397052	80518	CTTGACCTTGUAGGCGTCTCUC	80519	GGUATAAACGCGUCCAGCAGAA
234397948	80520	GTCTTCTCAUTCTCCAGGUGGT	80521	ACCAGCTCGUGTCCATGUC
234398985	80522	GCGGAUCACCTCGTCCUT	80523	CAGCUGCCCACUAGCCA
234399160	80524	GAGCUGGTCGUCGGAGAA	80525	ACCCGCACCAUCACCAUC
234399762	80526	TCGCTCAAGUCAAACAGGUCAA	80527	CCCCUCCTCUCCCGAGT
234400110	80528	AGACAGTCTGCUAATTCCAGCUACT	80529	AGAGGGUCAUACCGGCACA
234401133	80530	GGGTAATTTUGGGAGTGUGGAGA	80531	TGCTGTAGGGAUTTCAGGATTTCAAUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
234405587	80532	GCACCUAAGAGACTTUGAAAGGGA	80533	ACAGGAUGCCAAACACATACCUT
234406497	80534	ACCACATTTTATCUCAGTCACAGTTUCA	80535	AGCAGGATAGGCAAUTTCTAGATGTTUC
234416067	80536	TGTATTTGAACUATTTGGAAGCUGACCA	80537	GCAAAGAGGUAAGACATGACAAAGUCA
234417516	80538	GTGCTGAAGCUCCTCTTCTUGA	80539	AGACAGAACTGCAAUTTTCCCATATGUA
234421514	80540	GACTTTTGATTGUTTTAGATGACACTUGGT	80541	CCAGTCTGATUACCTGCTTTCTUCA
234421554	80542	TCTTTACCTTUAGGATGGATTTUGCCAT	80543	GTGACAUACTAACCUCGACAGCAA
234422584	80544	ACCACCAUCACAAAGGACAUCA	80545	GATGAAGAAGCUGACACCUGAACT
234424339	80546	ACAGAAGTUTCAATGTACUACCAAGCA	80547	AAAAGCUGGGATCAACAUAAAGCAC
234425985	80548	ACACTGAATGCUTTGTTGCAACUC	80549	ATTTCCTCTGTUGATGTAGACAGUGAC
234426021	80550	CAGGGCAAUTAAAGCATTUCAGGAG	80551	CCAACAACCUACCTTTAAACTAGACUCA
234426180	80552	CATTTACGACTUGGGCTTATGTUCAAAG	80553	TTCTTTTAAAGTGCCAAUATAAATTCCAACAUT
234427537	80554	TCAACAGCAACACCUTCUCCAAA	80555	GATCTGTGGACUAGGTTTGTGGTUA
234428678	80556	ACCCAGCACAUCCCAGTGTAUAT	80557	GCGGAAAACAUCCCTGTUCAC
234431668	80558	TGAGAUCAGGGAUGAGGGACAG	80559	ATATTTTCATCTCCUCTGGGTAACATUG
234433011	80560	AGACTUCAGCCACAGCATGUT	80561	TCTGGATCACUGGCAATAGTTCTAATTUC
234434211	80562	GAGGTCAGGCUGGCTAUCAAAT	80563	GTCCCTTUTCCACTTGUGCAG
234435089	80564	CCTTGAGAGCCUGGATGTUGG	80565	CCACATCAGACUGAGCGTTCUT
234436793	80566	GGGTGGTAAAUTATAAAGTTGCTAUGGA	80567	CAGGGAAGGAGUGGUACAACAG
234437533	80568	CCATGAAAACAGAUCTGCTTCUGGT	80569	TCACTUTGATGAACTTUCCCACACT
234440329	80570	CATGTCAACAUCGCTCTAATUCAGAGAT	80571	GCTTTTCAAAAGGCUTAAACACAGGAUT
234441712	80572	TTTTCATGTTAGAUGGGATCCTTUCCAA	80573	AGTTTGAGCTGAUGATTTAAGACAGUGT
234441992	80574	AGATCCCAGCUCTTTCCUGAGA	80575	GTCCATTTCUCCAGAGTAATCCUCAC
234444604	80576	GCCGCUCGGCTCTUCAC	80577	GGCCGCGUTCCTUACCC
234446488	80578	GACTGCCTUGGTTGATGGTCUA	80579	CAGGTGGATUTTCCATGTCAUACAG
234450346	80580	CTTGAGCACCUGACCAAAAAGAUG	80581	CCAGTGGAGCUGATAATAGTUCCAA
234462822	80582	TGTACAAATAGGUACTCAAAACAGCUCAA	80583	ACAGAGCCAGGCUTTCAUCAAA
234463139	80584	AGAUGAATTATCTGGUGAACGACAAAGA	80585	TGAGAACATUACCGGATTCGAUGG
234463603	80586	CCTACAGGGTCAUTTTCTTGTTCTTCUT	80587	CCTGAAAACCAUGTGGTTGUGT
234467767	80588	GCAGUAGCAGTGAATCUACAGGGA	80589	GCACTGTGTTTUCTATCAATCTCGUAAG
234473379	80590	CCTCAATGAUGGGTGGACAAUAGG	80591	TGGAAATGAATCCUTGTACCCCAAAUAAT
234474926	80592	TGATCGAGTUTCCAGAACCUCAAC	80593	ATTGCAATGGCAUTTAGTGCTATTTUT
234476864	80594	CCCGTCCUCGACTGATUCAAC	80595	TGCAAAUGAGACCCAUGAACCAA
234477984	80596	GTTATCTTCAUGTAGTCCACCUGAACA	80597	CTGGTAATGAUGACTGGAUGAAAGACA
234482705	80598	TGTTCCCCAAGAUTTCATCAAGATUGA	80599	ACCACAGCAGUGACTTAGCTUT
234484139	80600	TGCCCATTUAGTGTTTGGCUCAT	80601	GTACACCUGCAGCCTAUACCC
234484925	80602	TTGCTAACAATUGCTTTGGGTTTCUC	80603	CCAATTCCAGCCUCCTGTCUAC
234489065	80604	TCATTTTGTUGGCTGAGGAAGUCA	80605	GCCUAATTTGAATCAGUCAGGAACAGG
234490968	80606	GCCTGTTGCAGUGACTGATTUG	80607	CACCACAGAGAACAUCAAACGTAAUG
234496587	80608	GGCATTCUTGTCCCGUGAGAA	80609	GGAGATAACATGCUGCTACGAACTAAUA
234498876	80610	GTGCAGTTGUGTTGGATGUGAT	80611	GGGCCAAGUAATAATAACAATGUAGCCA
234503186	80612	ACCAACAGAUCCAGCUCCAAAAG	80613	TCAGGAAUGAATCAATUGACCCAACA
234504857	80614	CCTGGCTCUGAGGGACUGAA	80615	CCTCCTTACCCAUGGAGAAAATAGUGA
234506989	80616	TTTACATGGACACCUTGGTTTTAGUGT	80617	CATCCTGTTUGCTGACCTCAGUAA
234508902	80618	GCTGGGUGCGGGTTGTTAAUA	80619	GGCCAGUCGAAAGTAAUGGCT
234511001	80620	GAGAGATTCUCCCCAACACGAAUT	80621	CTCCAGGGUTCCTUGAAAAGAAAAC
234511691	80622	CTGTTGGCAGGAGAUAGGTTAACUA	80623	CACATCACTTTTTAUGAGAAGCATCATUGG
234513051	80624	GAAGGACCUGATCCACCAGTUC	80625	ATTCTGATGGCUCACTGTAGAAACAUAC
234513998	80626	GCCCGGUGAGTATTCACTTTUGA	80627	CCAACATAUCTGTGCCUCCCAT
234514466	80628	GCCGGCCUTGTACATGTAGUT	80629	CCTCTTCUGCTGGACCAUCAC
234516140	80630	AACCAAGCAGUTCTTCTGAGTUGA	80631	CATGGTCCAATUGTACAGCACAAAUA
234516291	80632	GATTTTCTCCUGCCCAAAUGGAC	80633	GCCCAGCAGCUCAAACAGAUA
234518962	80634	CCATGGATGCUTTACAGGCCUA	80635	GCAAGUGCAGAGGTATTACUACAACT
234519125	80636	GGGCATGCUGCTGACGATUA	80637	CTCTCCACTUCGTCTCCAAUCC
234522816	80638	CAAUTCCTCTUCCACCCAGAGAA	80639	CATAGACATGTAUCTGCGAAAACGUG
234523872	80640	CCTCAGGATGCCAUTAAATGCTACTUAA	80641	CCTCCTTCUGCCTGAGTGTUC
234524686	80642	CATGTTCUCCAGTTCAAGGUCACT	80643	TCTGTCTUGCAGTAAGCACAUGG
234525335	80644	TGTTTGACCACCUGCAGCUT	80645	TGTUGGCAGAACCTCCUCAAC
234529427	80646	GATTATATCATGUCTGCTGCTTAUGGGA	80647	TGCACTGAACUTCCAGAAGAUGAC
234532251	80648	CAGGAACUCCAGGCAGTGUAAA	80649	TCCTTTATGTACAUCTTTGGTTGCUGA
234532728	80650	ATTCTCTUGGGTCATTUGGCCAT	80651	GCACCCCUGCGAAAGACUAAC
234532976	80652	GCTTCACCAACAUCATCTGUAGCA	80653	GTGGTGGGAGUGAAGGAGAAAAATAAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
234538490	80654	CCTUGAACCTGTTTUGGCAGAT	80655	AGTTGGGAAGCUGATACTTCATATUCAC
234538724	80656	GAATGUGTATGGGAUGGCAGAGT	80657	GCTTTGTGGACAACUCATTTCTTGAUAT
234539199	80658	AGTTACTCTCACUCCCAACAGUCA	80659	CTCCAGGTGAAUTTTCAAAGCTTTUAGG
234539541	80660	CGACATGTCUTTCCCCACAAUCA	80661	GTTGAUGAACCGGTCCTTUACAGAT
234543880	80662	AGTAGTCTTTCTGUACCTCTTACGTUCT	80663	TGATAUCCGGGACACCAGTUCA
234545644	80664	CTTCAACCUCAGCTGTTACTUCACA	80665	CAGGCCCAUGCTTACTTTGTTTAUT
234546229	80666	GCACTAGCAAAGUCCGAGAUGAAT	80667	CAACCTTCTGAAGGUCTTCCTCATUT
234549355	80668	CCTGGGAGCCAAAGUCCTTUC	80669	CGTTTCCTTUAGCCTTCTCACUGAT
234553950	80670	CGAAAUGCGCCCATCCTTTUC	80671	AGGAUACGGAGCGACACATTTUAC
234556338	80672	CTTGGTGCCACUAACTACATTTATGTTUT	80673	GAGCCATGTUGATGTTATCTTUCCAAAC
234557749	80674	CTGGCAUAGAAGAAGAAACTGUAAAGGA	80675	TTGTTATGCTUCCTGCAGCUGA
234557893	80676	CCCAGATCAUCCATTGCATUCGAT	80677	TGCTTTCAAAGGCAUGGACATACUT
234562684	80678	AGCAAAGCCAAUTTAUCAGGAGGT	80679	CCTCCGACTGUATGTCAGCAGUA
234563384	80680	CCATGTGAACGCUACTTATGUGAAC	80681	GACTGTTGCTUTGACATAGTACUAGCA
234567815	80682	CTGAGTTCAGAGAUTCTTACCCCAUT	80683	GGAACAGAACCUGATTATTCTTGTGUGA
234573363	80684	AGGGAAACTCUAGATGCTCAGACTUT	80685	ACACTTCCTTCTUTGTGGATCTCTTTUT
234591297	80686	TGCACATCATTGGUATTAAGAAGGGUT	80687	TGGAATAACACCUCCAGCCATUAC
234596971	80688	TCCTTTCTCTGCUTCTTTTCTAGGTAUCA	80689	GCCTGGTUGACTCATCTATAUGGAAGA
234597125	80690	AGAAAGGAUCTGGTAUCCACCCAA	80691	CCATTTTGCCUTTTAGCATTAAGUGAGT
234602209	80692	TGACAGCATTATUTCTTGTTCCCTUGT	80693	AAATGCTTAGTAUCTGCTTGATCACUGA
234650497	80694	GAAAAGGACAGGGAGUGGTGUT	80695	TTCACGAGCUCATGAAGCUGT
234654725	80696	GAATGAUGGCCGGTCCUGT	80697	CAAATACGCUGAATGGGAGTTGUG
234668502	80698	GGACTTAATGUCCAGTGGACTTAGUT	80699	GCCATTGACCUGCTGAACUCC
234674208	80700	CCCCACAGAAACCCAUGTAUGAAG	80701	TGGAAAGCCCCUGTTTCATACUG
234676688	80702	CAACAAGGCUCAGGAGUGAGT	80703	CAATGCCATTAAUTGCCAGTTGGUT
234678034	80704	AGAGGAAAUATCATTCUGCAAAAGAAGCT	80705	TGCCACACUCGACAUGGAAAA
234679711	80706	AACACTATAACAUGATTCACTGGCUCAA	80707	GTTTGTATTACUCACCAGGAUGACCA
234680170	80708	GGAATAAUTGGAGCTTUGCCAGGT	80709	CTGGCATUGGATGTGTUGCAT
234682987	80710	CTCCTTCAUGCCCTTCATCTTCUC	80711	GGCCAGGGUGCAGTGUC
234683375	80712	CCCAGGCCCUTGUCCAG	80713	CGGCAGAAGGUGCGCAUA
234684097	80714	CCTUCCCGGGCTTCCUC	80715	GAGCAGGGUCCTGGAGTUC
234684624	80716	CCACACAACCGUACCACCUA	80717	CCCCAAUCTAAGGCAUAGACAACA
234690261	80718	TGCACCCCAUCATAATATCTTCAGTUT	80719	AACCATGCUGGAGTTTGGUACAT
234693025	80720	CTCTGTTTUCCTGAGATCUAACCACAT	80721	CAGCAAGGCCACGUATTACTGUA
234693458	80722	CATCTAGACGTUTCCTTGGCTCUT	80723	GGCTCGACUCCCTCCGUA
234693612	80724	TGTACAAAUCCGAACAACCCUGT	80725	TCTGCCAGUGCTGGAAAAGTUAA
234711171	80726	GCCAATTTATAATTUCTCATGTTGCCTUGA	80727	ATCCTATAGATGAGUTTCGACCAGGUAT
234711282	80728	CCTTGATTUCTGCATCCAUACAGGAA	80729	TTAGCTTTGGAAAUTTTAGAGTATGTTAUGAAC
234712047	80730	AATGGCTCTGUAAATTCTACCCGTUT	80731	GCTTATGGATAGUTACAACTCGGCUT
234722058	80732	CTCTCATGTGAUGTCCAGGAGUT	80733	GACACCACCGUGTACUCCAG
234724389	80734	GTCCCAGAUCAGCCACTCAUT	80735	CCCACAGCAGUCTUCGAGAG
234725896	80736	CAUCCCAGCAGGTUGCCA	80737	TGTCGCUCAGTCCCACUCA
234729836	80738	TGGCTTTATGCCAUTTATCTCAGTUGT	80739	CAGGATAGACUGAAGACTAGTACTUGGT
234730332	80740	TCAGCTTTAAAAGUTCTGCTTCCUCA	80741	CCAACTCCTTUGTTTGCCATTTCTUC
234733194	80742	GTTTTCACUGTTGCGTUGCCT	80743	GACCTGCAAUCACCAGACUCA
234736983	80744	GGCCCACCCUGGTCAUT	80745	TGCAGAAGATTCUTATAAAGTGCAGCUT
234737858	80746	GTUCAAAGCAGGAAGATCAUGCAG	80747	TCAGCCTTGAUTGCAAACCCTUAT
234741596	80748	ACAGTTTUAACGCCTAAAGTAUCACA	80749	CTTTACTGAGGCUTTCAAAACATTCCUT
234743582	80750	CCAGGUGAATUGGGACGAAGAA	80751	CCAGTGTGCAUCACCACTGUA
234764991	80752	CACACTTTGTCTUTGACTTCTTTTTCTUCT	80753	CCTGTACACAUGAAGCCATCGTAUAT
234768466	80754	TCCACCAATUAAAAGATGGCCCUT	80755	CATCCAGCCAUGTTATCCCTTATTUGA
234770646	80756	GGGATCTAGCUCTTCGAGUGGA	80757	TCTTTGCTGGCUAGCATCATGATTUAT
234773109	80758	AGGAATAAGCCCUGCCCAGUA	80759	GTGAATTGAGGCAUTTTCTCACTTUGAT
234776515	80760	GGGTTACAGAAACUGACTGTGUGT	80761	GGCTTTCUCAGAGATTTCCCCUT
234781199	80762	GGCUTCCTGAAGAUAAAGGGAAAGA	80763	CACATGACTCTCUGGAATCATTCACUAT
234787278	80764	GGGCTTTGAUGTTCCTGATTGUAAAAA	80765	CTCTTTCACATCUTCTTGGCTGCTAUA
234792805	80766	CTCAGCCATCAACUTCTAGTAGCATTAUT	80767	GGTCGACCUTGACAAAUCACACA
234797841	80768	GCCCCTUAATGCCATUGAACCT	80769	GCACAATCATTUGAATTGGTTGTCUACA
234819805	80770	TCTCAGCCUGGAAGCCTTTUAG	80771	CTGTGCTTCUGATTTGCCCTUG
234826403	80772	ATTTGUCTGCCCUGACCACAT	80773	TTTACACCAAAAGCUCCCACTUGA
234832176	80774	AGGTGGCCUACTTAACTACACUT	80775	GCAAGCUCCATCAUGCCGAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
234913782	80776	ATGGUGTCAGTACUGCAGAAGG	80777	TCTTACCAGCCCACAUCTATUCCA
234913839	80778	GGGTCAAGTGAGUGGATAAAAATATUGT	80779	TTCAGCTCUGAAACATCACACAUCT
234913890	80780	AACTTCCAGCUGCTTTGAUGGA	80781	CGCTCGAGUGCCCATTUGA
234914154	80782	CACACCUTCCGCCUGACA	80783	CCCUGACCCCTUCCAACAC
234914302	80784	GGAGCUCTAGCUGGGAGACC	80785	GCCAAUAAGGCGGAGAGUGT
234914319	80786	CACAAGTUCATGTGTCUGACAAGGT	80787	GCTCCACAAAAUCTTCATCATGAGUGAT
234914454	80788	GTTACACAGGTUTTTCAAGGGACUG	80789	CCTGTTCAACAAGCAGUTCTGATTUT
234916217	80790	CTGAAATAAGTAUCAACCTCACCCCAUT	80791	AGAGGUCGACAUCCACACCT
234917691	80792	CGACAGCCUCCGATCTTUCAG	80793	AGTTAAAAGACUGGGAAGGATGCAATUA
234918963	80794	GGAAGTAGTCGCUTACTCATTTCTCUT	80795	GGTTTGAGAGAGCUTGAAGAAATGTTUT
234919866	80796	TGTGACAUCCTCUGCAACCAC	80797	TGAAAAACTAGTCUTGCCAGCACUT
234920036	80798	TGGAGCUGAAGCTACACUGACT	80799	TGGTAACUGGCACCATCTCUCT
234920506	80800	GGTCTGGUGAGTCGAGAGGUT	80801	GGTCGGCUTGTTGGAUCGT
234920707	80802	AAUCACCAGAGAACAGUAAGGGAGA	80803	GTCCUACCCTGTUCAACAAGCA
234925104	80804	CTTGACTCTUCCTCGGTACCTUG	80805	CAACCGCCGUGCAAGAUG
234925392	80806	GGCATAGGCCUCTGGGUAGT	80807	GGGTACCAGGUGATCAGGAUAG
234927801	80808	CCCAGCUTGCTTCCUCCAT	80809	CAGTAAGAAGCCUCTAATCTGTTTUAGCA
234928292	80810	GCGTAACTUCCAGCTTCTGGUA	80811	GCTAACACTGCAUTTCACAATCTCUG
234929551	80812	CATCAGTTTTGGUGGGACATCUCT	80813	AACTCAGGAGGCUACCAAAUGAC
234931385	80814	AGTATTGGCTUACGCTTCAGTATTTGUT	80815	CCAAAATACATGUTTGTCTCCTTUCACT
234932132	80816	AGGATTAAAAAGAACAUCGATCAGUGCT	80817	CACTTTCTGAGGACCUACATTTCTAUGG
234932399	80818	TGCTCTGTGAGUCAATGCTTAGUC	80819	GTGAGUCAGCTTGGAGUCAGT
234934204	80820	GGTGCTGACCAUGTGGACAUT	80821	CCAATCATGGAATUTTCTTTCTCCTCCUA
234939106	80822	CCTTCCAACAUCATTCCCCACAUT	80823	CTCACTGUCACCTGGCTTCUC
234941827	80824	CCCACACCCUGTGCTCTUA	80825	CTGTAACACCUGCTTCTCTUCCC
234942390	80826	AGAGGCCACUTCATCAGCTTUG	80827	CTGGGCAAGAACAGGUTCTTUT
234945360	80828	CGGACCAAUCCATGGGTCAUA	80829	AGAAACCCCCUCAGGUACAGA
234947083	80830	TCCGCAAACTUCTGACTCTGTUAA	80831	AGGAGGAAGCAGGUGGUACT
234948002	80832	GCTATGCUGAAAGGAATTTGACTUCCA	80833	CTTCUGGGAGCAGTACAUCGG
234949586	80834	ACCAAGCAGAGCUTCTUGCAT	80835	ACTGCTTTAGUGCAAAGTACTGACUT
234950021	80836	CACTCACAUGACTTACCTTCUCAAAGT	80837	ACTAAAGAUCGAGGCCCUCCA
234950438	80838	CAGACTATAAAUGCACTACATGACACTUG	80839	AGGATGCUGCAGGACCTTCUA
234952730	80840	AGTCATCCACGUTTTCCCTGTTUT	80841	CCUCCACGGAGCGAAACUG
234953554	80842	CTTCTCCAGAUCTGTGACUGCAC	80843	GGAATGTGCCAGUTAGAATGAUCCT
234954334	80844	CCAACACCACGCUGAUGAAC	80845	TCAGACTTTGUGGAGGCAATUGA
234958934	80846	TGGCCAUCCGCATCTTUCAG	80847	CAAGGAGGCCAGCAUTGTGUA
234960414	80848	TGCTGCAGAUGGTCCTTACTTUT	80849	CTAACCTGUGCCCTTCTCTGUC
234961752	80850	CATGTTCCAGCACUTGTTTATTUCGAT	80851	CCTCCAGAAGCUTACAGTGUCC
234966282	80852	CTCAAATATGGAGUCCACGAGATCAUT	80853	CAAACTTGGGCUCCATAAAGUCAC
234971181	80854	GAGCCUGCGAAAGCCTTTUG	80855	TCATCCCACCCUCTTTCAUAGAAGAT
234989587	80856	CTCTTTTGCCTTUGAATTTCTGAGGUT	80857	CAGGGAAGTUCCCTACCTTTGUC
234990716	80858	CCAAUGCCCAGGAACAUCCT	80859	AUGTCAAGCUGGGAAGCCAT
234992496	80860	CCCAGTGGCUCAACAACTTTUT	80861	CAGAGGCACUTGGACTUGAGAG
234994316	80862	GAAACCCGCUATAATCACUAGAGCAAT	80863	GCATCCGUGTAAGTUGCACCA
234995979	80864	GGACTCTGUCAGAGGCUCCAT	80865	TGTTGGCUGCAAGGTUACAAGA
234997753	80866	AGGTTGUGGCTTTATGCTUAGAACA	80867	ACCATATTCACUGGACATCAUGCAC
235002827	80868	GCCTCTGAGAGUGCTACCCUT	80869	GCATAGCCATTCAUTCGTTGATTCATUC
235003725	80870	AGCTGTGAUAACCTCACACTCUCT	80871	CAAGGAAATCUGCTTAGGGTTCUCA
235004173	80872	TCGTTTTCCUTGTCCAAGCUGAT	80873	TGTTGTAACTUGAGCTGTGTAATUCCT
235008195	80874	TGTACAGTTAAATAAUAGTAAGTTCTGAGTGUC	80875	AGGATGGUCACTCTUCAGGAAGT
235008307	80876	AAATTCACCUGGACTTCCUGAAGAG	80877	CCACTGUCAGCGCUCAGT
235011344	80878	GGTGGUCTGGAUGAGCAGA	80879	GTCCTCTCCUTCAGGGCCUAT
235012735	80880	CTGTTAAGTTTGUATGCAACATTTCUAAAGT	80881	TGGGTTATGGUCTTCAAAAGGATATUGT
235012738	80882	GAGGTTATCTUTTTACCACAGTUGCAC	80883	GTGAATTGCUGCAACATGATTGUCA
235014277	80884	AGCTAGAACTTAUCAAACCCTTTTGUGA	80885	TGCCCCGAUGTAATAAATAUGCACAT
235014683	80886	GAAAGGGACGAACUGGTGTAAUGAT	80887	CAAUAAATTCTCAGAUCCAGGAAGAGGAA
235015095	80888	ACACACAAGACCCAUTAAAACCTATUCC	80889	GTTTTTCCAUTGGATTCCTUCGCAA
235017110	80890	CCCACAUCGGCCTGTGUAT	80891	GGGAGATTGAUAACTGGTGTGTTTAUGT
235019026	80892	ACAAAGATCACUCCTTGCCUCAAC	80893	GCAGTUGGTGGACUGGCAT
235019721	80894	AAAATTCCATCATTUAATTGTAAACGTGTUACT	80895	GCCGCCTTUGCACTGAATTUG
235021056	80896	CCAGGGAAUATAGCTGAAATUAGGGT	80897	AATGGGUCAGAGAAGCCATATTUCC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235021062	80898	GGATGAAGGAGUCTGCTUGGAG	80899	TGTTTGACGAAGUCCATAAACCCTUA
235021741	80900	TTCTCTGACCCAUTAACCTTCAGTUC	80901	GGATCTTGTCUAAACATCGTAACUGGAT
235022560	80902	GTGGTGCGAAAUTCTCACACTATTAUG	80903	ACTCACATTTCUCCTTTGTTCTTGUCT
235023347	80904	CACACACTACAUCAGTGGCUCAA	80905	TTCTAACUCAGAGGAAUACACAAACACC
235023816	80906	CCTATTTCTGTTUGTTTGCCTCTGUT	80907	CCTCUCCGAACACTTUGCCT
235025130	80908	CCAGCCTTUACAAGCCCUCT	80909	GGUCAAATTTCTTTUCAGAGCAAGAGT
235029520	80910	TGTCCCGGAGUTTGCACAUC	80911	TTTCCCTGTCCAUTCCATCAAGUC
235035286	80912	ACCAGAGGCUGCTTTCTCTCTUA	80913	CAAGGTGGUGGAGAAGATUGGG
235035547	80914	TCTTGAAAGGAACUGAAATACGACGUT	80915	GCTTGAGCTUTCCAATCTGCUC
235035859	80916	CTCCCGCAAAAUGTGCCUAC	80917	GAGCATAACAUCCGCAAUGACAAAT
235035972	80918	TTCATCCTGTCAUTCCTCTTCCTCUAT	80919	CGGGAAGGACUTTATGTATGAGUCA
235039262	80920	GGCCCUGGCAAAACATTTGUA	80921	CGCCUCCCCCAAUGAAGAC
235040578	80922	AGGGTTCUGGCGTTTGTAGUC	80923	GCTTATTGGGTAAUTCTTTGGGATTCUCT
235040988	80924	CTATCAUTCCCTCTUCACCAGCAT	80925	GUTCTTGAAGCUCGAGAGCCA
235044412	80926	CTCAUGGAGCACTCAAGUGACA	80927	GAGGGTTCUGGCTGTGTGAUAG
235044843	80928	GAAATATTAATGCAUGGAGCCTGGGAUA	80929	AGGAGCUAAAGGCTCAAATUGAGG
235045412	80930	CATAAATAGGUCACAAAGTCTTCUGCCT	80931	CCCTTTTCUACCTCCCCCUCAA
235047653	80932	GGUGAAAGCAGACATCUCGAAGT	80933	CTTCAGAAUACCTCTGACAGUGACA
235047858	80934	CCAGAGAGGCAUCAGACCATCUA	80935	CCUGGCAATTGUGACCCAGT
235048587	80936	GACACTGAGGAGAAUCCTGCUT	80937	GGGACAGUAACAGGTGTCTUCA
235053623	80938	CATGCAGGUGTTTGUAGAGGCT	80939	AGTAGACCUCCCTGAGCACUT
235056744	80940	CCTCCACGGCUACTTTCCUCT	80941	CAGGAAAGUGAGATTCTAAGUCAACCT
235057537	80942	CCTCAGGUGGAGCATTTCTUCC	80943	GCCTAACTTCTUCAAACCATGATTTUCT
235061529	80944	GTTGCTTCCAGGCUAAGACTCUT	80945	ACTTACCAGCAAAUGAAAACCAAAACUT
235062367	80946	CAAGAGTGTCACUGGGAGATTTUAAAGA	80947	GCCCACAAGUTCTAATTUAGAGGCAAAT
235062549	80948	GCTGGTAAGTTAUTGTAGGTGAGTUCAT	80949	GACTGTCTCTACAGAUAACCTCCTTGUA
235065617	80950	CAGTTGGCCACUTTTACTTATAGCTUT	80951	GTAGCAGUGAACTTACTACUCACGA
235067513	80952	CCTCCAAACTUACAGGTGAAGTAAAUCT	80953	CCTAATTUCACCAGGGCGACUAC
235068746	80954	CTCCACTUCAACCTTCAGCUCAA	80955	TGAGAGGCUGUGGACCAAGG
235068956	80956	CCGCTATCUGATAGAGTCTGUAAAGGAA	80957	CAGATTCUCCAGAACCAGTUACAGAAAT
235070609	80958	TCCCGAGCUCCACGUAAAC	80959	TUGGAAGGAGTUCAACAGACAGAC
235071919	80960	GATTCGTTCCCUCATTCACTTTAACTUG	80961	CTAACTTACCGGGAGAUAATTGGCAAUA
235072234	80962	CCAGCGAGGGAGACUAUGAG	80963	CGTGGTGGAUGACATAGACTATCUG
235073014	80964	AAATGCAUGAGACTCCACUCACAT	80965	CTCTTGUCTCTGCUCCCCAAC
235074018	80966	CCAGAGCCACGCGUCAUAC	80967	GACCTGGUTGTTGATTUGGACAA
235074202	80968	CCAGTGGUGAGTGTGAGTUGG	80969	CCTGTGGCUACTGAGGTAGTUG
235075389	80970	ATAGGAAACTCAGUTGTAGAAAACUCCT	80971	GAGAACAGGCUCACGGAGAUG
235077422	80972	GGACTTGGGUGTTCAATTCUCCAG	80973	CAAGAATAUGGACCCGCTGAAUG
235077668	80974	AGACAGACCTUGGTCTCAGTAAUACA	80975	GATTCTCACCUTCTTTAGCGCUCT
235077810	80976	ACUGGTUGAAAGCGGAAAAAGAGA	80977	TGATGGCCUTGTTAGCAUGGG
235078160	80978	CAGAAUGGAACAGATGACUGGAAAGT	80979	GGTAGGGCATTUCTCCCACTTCTUAA
235078261	80980	AGCACCCUCCAATCCTTCCUA	80981	GTAUGCAACAGGACATUGAGCAAG
235080126	80982	GGGCAGACCAGUGTCATUGAG	80983	GAGACCCACUTGCCTUCCAA
235080295	80984	CTCGTTTTGATTCUTCACAACAGGATUT	80985	ACCAGACCAUATTTGTUGGACACA
235080783	80986	CAGGGUGAAGTGGCUGCAT	80987	GGGTTGGTTGUTATTACTTAGCUCA
235083434	80988	CAGCCCUCCCAACACATTUCT	80989	GAAGCCUCCGTGCUACACAA
235084449	80990	ACUGACACCCACCUGAGACT	80991	GCATGTCTCUACCTCTATCTCCUCT
235084924	80992	CCGCCGGUTGAUAAAGAAAAACT	80993	TCTAATCCCTTUCACTCTGGAAUCCT
235085500	80994	TCACCGGUACAAGTTCTTTTCTTUGT	80995	ACTCTTGUGCGTGCCTTCUC
235087070	80996	CACTGAGUCCCCGTGCUT	80997	GUTGUCGGAGACGCGGAT
235089199	80998	GGAAGGAAAGGCCGAUACUCA	80999	CACTTCUCCCCAGTTGTCUACT
235090119	81000	AGGAATGGAUAATAGCTCCUCCCAAA	81001	CCCAGTCTUCATTGCTACTAAUCAGG
235090322	81002	CTTCGGCUCGGTCTACUCAG	81003	CCAGGGTCUCCGTCAGGUT
235092690	81004	TCCAGGTUGGACACGAGTUG	81005	AGGTUCCAGAAGGAGAUCGAGAA
235093047	81006	CCAAAGGCUTCGTAUGCAGGT	81007	CCCCTTACAGUGCAGCCAUAG
235093133	81008	GGAACGCUCGAGTCTGCUT	81009	TCCTCTCTCUACTTTGCAACAUAAACC
235093374	81010	TGGGTGTATCUGGTGTTGAAAATTCUAA	81011	CCCAATTTTCUCCTGATTGTUCCAG
235095019	81012	GTGCTATATGUCAAAGTGCUAGGCT	81013	GGGAACTCAUGGTGTACCCCTAUT
235096903	81014	GAGCAGGGAAGUCACGTUGT	81015	GCCTTGGTTTCUAAGTTTCTAGTTUCC
235098163	81016	ATGTGCTTGCUTTACATCGTCUACT	81017	CCAAGAAGAUGCAAAGTAAAAAGCACUA
235098976	81018	TGGCAAACAAUACCAAATTTACTTCAUGT	81019	CGGTGCUCTGCGUACCAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235099809	81020	CCTCAAAAGCAUTAAGAAAATGUGGACT	81021	TGAAAATGACAAGCUGGTTGAGACUA
235100920	81022	AGTATGAGTTTUAGAGGCTGTTAATTUGCT	81023	TCAGCTGCCUACTTCCUCCAT
235101088	81024	GGCUTCTGGACTUGGAACCAT	81025	AGAGATAAGCCUGAAGATAATGUGGGT
235101674	81026	GGAAATGUGGGAGGAGAGAATTACUG	81027	CAAGCATGTCCUAGTTTTGCAGUT
235101719	81028	TGGACAGTCUACGAAAAGCTCTUG	81029	GGACTGAACAAGUAGGAAAAUGACAGA
235102726	81030	CTATTACGTTACGAUTTCCCCCTUGAAT	81031	CGAAGTTCCUGATGGAGCTGUAA
235107329	81032	GGTAGTTTGUTTGTGGGUGGCT	81033	CCTTTTGGATGTUGTGCTCTTGTTTAUT
235107485	81034	TGAGAAGUACCGCTCCCUCA	81035	GTTGUGGAGCTGGUGGAGAAT
235108616	81036	GCTGACAGAAAGUGCTGCAAUT	81037	GCATGUTACCTTAAGAUCAACCACCA
235109734	81038	TGTCATTTTCCUACTTGTTCAGUCCAT	81039	CAAGTCCUATGAACTTAUCAACGAAGAG
235110912	81040	TCCTCGTACUGCTGGGUGA	81041	CCTGGACGCUGTCCTTGUAG
235112686	81042	AAAAGGTCGUCTACAGCUGCAA	81043	TTTCACUGAATGGUCCACGCT
235113886	81044	GCATTATCGGCAGUTTGATCTUGAGA	81045	GCCAAAGAAAAUGCTAAAATGTUGGAAT
235114450	81046	CTTTTGATGACATUGCTCATGCTAGUG	81047	CTCUGGGAGCTACUAACAGGAGT
235116476	81048	CTTAGAGGUTAGTTTCTTTUCCACCCT	81049	TGAAAGAUCCAGACCCTGAUCCA
235118885	81050	CTTTCCCAACCGUGACCTTCUT	81051	AAAAACTTCAUCAACAGCCCAGUG
235119720	81052	CAACAGAAGTUTCAGGTGACUGAG	81053	CCTGTTGGUGGAAGACTCATAAAUCA
235121199	81054	GGACATTATTGAUCACACCTGGGUT	81055	GAGATGGTCTCTUGGGTGAATTTTACUT
235121433	81056	GGCAACACAGCUAGAATTGGAUG	81057	CCATCAGTTGGUTGGCAGTTTTUG
235124393	81058	CACAAACUTGUGAGAGAGAGACAAGAA	81059	TGCCAAAAUGGAGUCCAACCA
235126076	81060	GTGGCCCCCUCTUGGAT	81061	GCACUCCCAGCCUCGAA
235126962	81062	CATAGCAGCUGACTTCUCACCAT	81063	AAGGTACCCUGGTTATTGTGGTATUG
235126969	81064	GCTUCGAGGCUGGGAGT	81065	CAGGAACUACGCCTCCAUCA
235127840	81066	GTTTACTGCUGCAGCTACCUCT	81067	TGAGGGCAAGACUGAGGACUT
235128370	81068	GTTCCUGCCCCAGCCTUT	81069	GAAATTCGAGCUGGTGCCAUC
235129035	81070	CGGGATUCCGCTTCGUCT	81071	CCAGCGAGGACAUCUGGAA
235129090	81072	GGGACCCAGACGAGUCTCUT	81073	GTGGTCTGATUCTGACCCTGUT
235129332	81074	GAAAGACATTGAGAAUTATATTCAAGAUGGGA	81075	TCGCATTCACTUAGTTGAGCTATTACUT
235129682	81076	AGATGGGAAAGACGACUATAAGAAGGUAA	81077	TCTTTTCTTTGUGTTTCTCGCATUCAC
235129748	81078	CGATGGCACCAGCUCGAAUT	81079	AGGGAGCGGACAUGGACUA
235129989	81080	CCCCAUGACGCCCTUGAAAA	81081	CTCTCTGTTUCTGGTTCCUCACAG
235130386	81082	AGTCATAGTCGUAGAAATAGTGCTGGUA	81083	CGACUGUGCCGAGGGAC
235132256	81084	AGAAAAAGAUACAACCGTATTCAGAAUACT	81085	TTAGCTGAGTAAUGAACTGGGAGUAAAC
235132261	81086	AAAATAGCCAUGCTGGCUGGA	81087	ACTTCTTGTAACUCAGCCTCTGUCT
235136880	81088	CCACCTAGTUCCGTGCCATUG	81089	TGTCCAACTATGTUAGCTACGACTCTUA
235139142	81090	AGCAGTUGTTCAGGUGGCAT	81091	TGACAAATACTGUGCAGACCACTUC
235141580	81092	TGTGAAAGAACAACAUGAACCCAUAGT	81093	CAAAATCUCCAGGGTGGCUCT
235144027	81094	GGATTTGGCUGAAACAAAGCUGT	81095	CAGAATGGCTUTTCCCGAACTUT
235145652	81096	AGGCACAATCAUGAAGTAAGCCAUA	81097	ACGTGAACUCAAGGAAGACUCAC
235145869	81098	CTGGGAGAUTCCTTTACTUGAACCAT	81099	CCTCTTCCUCTGTTGGTTGAUGA
235146310	81100	CAAAAGTAATACCAUCCCCCGACUT	81101	TCAAACAGAUGAAATCCCTGTATUGACA
235147324	81102	TGTATACATTUGGATACCAGTGUCCT	81103	ATTCGAGCTCUGCATTCTTCTUCAT
235148313	81104	GCCTCUCAGGACUGACCCA	81105	CUCCAGAAGCCACGTUACGA
235149460	81106	AACATGGUAGTTTTCTTGUACGAGAGAG	81107	ACATCTUGCCAGACCCATTTTUCA
235150326	81108	AGAACCCCAGGUACATGGTCUA	81109	CGACACUGTGGTCATUGGCAT
235151286	81110	CGGGAAAAGCCAUTCTGCATTTUT	81111	TCTGAGAAGTGAAUGTACTGAGTGGUA
235152124	81112	CGCTCUCCACCCATCTCACTUA	81113	AGCUCAGAGAGGTTUCAACACAC
235155127	81114	AGCTCACAGACUCAATCACCTUC	81115	TGUCCUAGACGGACGAACCT
235156026	81116	GCCCCGTTUGTCAGAGAGTTTUT	81117	CATCACGCCGCUTTTCCTTTUT
235156091	81118	CCCUAGCCAACAAUCGGGAAA	81119	TTTATTGAGUGCAAGTCCTCUCCAC
235159279	81120	CATTGTGCCUCTCTCTCTTGUCA	81121	GCTTGTTCUCATTGGCTUCAAAGAT
235160819	81122	GTGAATGAGTATGUGGGTGAGCTTAUAG	81123	CAGTGAAAACAGCAUTTCCCATTACUT
235162257	81124	GTTCTCAAUGACAGGGAUGCGA	81125	CAGGTCCUGCGTCTCTCTUG
235165652	81126	CCTGGTCACAGUGGTTGTCTUT	81127	GGTAGGAAAAUCCACAGTAGTUCCAAAT
235167881	81128	CACTCATCACGAUTTCAGGCCUA	81129	GTACCUGGGAACAACCTACTTUGAG
235172038	81130	GCCAGCUAGGAAGAGCCUAGAAT	81131	CCTCAAGCUGCGCATCUAC
235172751	81132	GTGCAACTCUCTGGCTTAAUCACT	81133	TCACAGGTATTAUTCTCACTAAGGTUGGT
235173295	81134	GCCAGTGGGAUAGTTTTTCTGGAUT	81135	CGACAAGGTAUAATGGCAGAATCAUCA
235180559	81136	AAACTCAAGUCAACAGAATCAGAGCUAAA	81137	AGGCATGAGAUGGGTACCTTTUAC
235180806	81138	TTTTCCATUACAGCAAACACAAATUCCA	81139	GATACTAAGCUGGCTCUGCAGT
235181399	81140	GCAGAGAGACAUGGCACUCA	81141	AGTAUCGAGAACCGAGUGAGAGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235184812	81142	CATGCGCUCCUCCAGGAA	81143	AATCGGGCACGCUCCUC
235186235	81144	CCTGGTTCUGCAGAGTCACUT	81145	CCGACUCGGAGTATAGTUCCCA
235188251	81146	ACGGATTATUTAGTCATCGUGGAGGA	81147	AGGGCCCUACAGUGAAGGT
235189467	81148	CATGTGTGGCUTAATCTTGCCTCUA	81149	GCTACAGTAUGGACCCTGUCACA
235190667	81150	TCATTACCTGTTCUTTTGTCTGAGCUT	81151	TCACGATGTTUCTTTTCTCCAUCCAG
235192189	81152	GAGGCCUGACACTGUCGT	81153	CATGGAATCCCCUTAAATAGGTGUCT
235194079	81154	GGCGACAUGGCCCCTATUG	81155	CGGGTUACACCACTTGTGTCUG
235195444	81156	GCAGGAACAAAUTCTCCAGGTUG	81157	CAGACCCCUGTGATGCTGTUA
235196344	81158	GCATTTCACAUCACAGTAGGAGCUT	81159	CAAACAAGAGAUGGCAATGTTTUCC
235198390	81160	AGGCGGTUCAAGCCGUT	81161	GGAACAGAGGCCCCUGAAAAAUA
235202074	81162	GCCCTAGGATUAACTTTTTCCCGUAA	81163	ACGAGGAUCAGACAGGTAAGTUGAT
235202208	81164	ACAGCAGACAGGGCUTTAAUGG	81165	CGCACCTTAUGATTTTGCCTGUT
235203153	81166	CCACATCTCCUTACCCTCCUG	81167	CAAGGGAATTCCUAATGTTGGTGUCT
235203593	81168	AGGGCAAUATTGTGCCTUGGT	81169	AGTAATGCTACUCAACACAGAGTCTGUA
235204393	81170	TCTGGCUTCTTACTTTUGGGAACAA	81171	TGACAAAAGCCUTCACCTACUGAAAAA
235205672	81172	CTTTGTCCAUACTGCCCATATUGGT	81173	GAACCUACCACCACGGTGUC
235206695	81174	GGTGGGCACACACUACGUC	81175	AGAACCUGCCCATCTACTCUGAA
235206860	81176	AGCAGAUGACCAAAGATACAGUGG	81177	TGAAACCCAAAUGTAACTCTUGGAACA
235210417	81178	CTTCGAGATAUAAGGTGCTGAGTUGT	81179	CTCAGAATUGCAGAAAAAGAAAACUGGA
235211354	81180	AAUCAGCCUGCAAGCCAGAT	81181	GTGCATTGUGATCGGGAAUGAG
235211457	81182	CTCCCTGTCUCCTTTCGCTUT	81183	GCTCCGTGCUTTCTAGGTCUT
235214512	81184	TGAAGGCTTTTGUCATTTTCTCCTTTUT	81185	CTTGCATTAATUCGGGATATACGUAGGA
235214651	81186	CTGAAGGUGAGGCTTAAUAGACAAGA	81187	TGACCAGCTTUCCTTTTCTGTTUCA
235216895	81188	GCTCTTCATATGGUCTAGTCTCTGACUG	81189	CCTCTTCCCAAUCTGGCTGTTUT
235218925	81190	TGAGCAGCCACUTTATTCTUACCC	81191	TCTCCATAUCCCATTCCCTGUAGAAAAA
235221814	81192	TGTCCACUCGAAGTUGACCAC	81193	GACCTAAGCCAAUCTCTCTCUACCA
235222326	81194	TGATGGCGUGATCCCCAAAUT	81195	ACAGGTTGCCUTACTGGTTACCUA
235225467	81196	CTCCACTCAUTGCCATGACUCT	81197	CCTCCACGGUACTCCTGTCUC
235225796	81198	TGGGATCTTTUCTCTGAGAGGUT	81199	TGAACCGAGCAUAGTTTCCTTUGG
235228116	81200	GCCCTTGTACAUTTCCACAATCUC	81201	GAGAATCAAACTUCCTAACCTGTTCCUA
235232963	81202	CCCUGGGAAAAGCCTCAUCAC	81203	CTGGAAGTGTAUTTTGCTCTGGTUT
235233459	81204	CCGGTTGAUCTTCGGUAGAGAGT	81205	GACCCAGGUCCTCTACAAGAUG
235237916	81206	TGTCTGGCCAUGAGGAAATGUC	81207	GCCUAACCCCGTATGUGACC
235239707	81208	TCAAACATCAUCACGGAGAUCCAC	81209	TGTCCTGACUGTTGAGGAACUCA
235240300	81210	ACCGAATCAUTGATGCTGGUC	81211	TGTCAGCUGCAGAATCCUGAAAT
235243339	81212	GUCTCTUGGAAGAGGGCAAGAC	81213	GGCAGCTUGTTTGTTCATGUGA
235243961	81214	GCCCCUCCCAGATCTCTUAAAGT	81215	GCTTTATGAGAUGCTGAGUGACCA
235243982	81216	GTGATCACAGUTGACGAGCUT	81217	GAGAAGAACCUGGUCCCAGAG
235244146	81218	TTGAAGUCAACAACAGGGAGGTUAAT	81219	CACACCAGAGAAAGAAUTGCCTGUA
235247847	81220	ATCAUCAAAGGAGCGGAUCGAG	81221	CUTGGAGCTTUCCACAGGAGAAA
235248469	81222	CCCATCUGAGACCCGGATCUT	81223	CTCTCTGTUGAAAGTCCCTAAUGCT
235248988	81224	GGGAGAGGUTAATGGGCCUAGT	81225	TGCCCGCCUGTTCTCTUAAAG
235254155	81226	GGAAAAGTGAGGUGTGGAGCUT	81227	GGGUACAGCTCUCACCAAGG
235255911	81228	CCAACGUACATGTGATTGUGAAAG	81229	AACCCATCUGGGCCATUACAG
235258061	81230	CTCTATCCTTCAAUTTCCCCGTCUT	81231	CCTGTAGTATCUTGCTTGGTCAUAAAGG
235261220	81232	CCTCATTCACAGGCUGGCTTATUAG	81233	ACTGAAUGAGAACTTAAGUGGGAAACAAA
235263129	81234	CCTCCAGCUATTACGGGTGUAGAAT	81235	GCAAAGCCUAAATCTCAUAGAACAGAAAG
235266540	81236	CAAACUCCACATTCCUGGCAAG	81237	CGACAUGUACAAGGGCAAGAAGAG
235266569	81238	GCGGCTGUGTCTCCTCTCUA	81239	CCTCACAGGCAUCACTGAAGUAT
235270493	81240	GGAGGUCCCAAATCCCAUGAG	81241	AGCAGCUGGUACACGACAAG
235271482	81242	GTCTACATGUGTTGCAGCTCUCT	81243	TGGGUGGGAAGCCUCCT
235272916	81244	CTCUGGAGAGGAGGGUAGCA	81245	GUCUCGCCCCCGAAACA
235273298	81246	CGGCGTUCAACCACCTUCT	81247	GGCACCACUGAGAUGGCA
235273681	81248	CCACAUCAUCGAGAACCCACA	81249	GAGAAAGGGAGGGAUCGTUCAG
235273751	81250	GGTCAGGGACCAAAUCCCAAUC	81251	TGACTGAGGGUGAGGAGCUT
235277065	81252	GACAAACCCUCTCCAGUGACC	81253	GGAACTGAGGUTTTCTCCAGUGA
235277634	81254	AAAAACGAGATCCUAGTTACCCAACTUT	81255	ACAAAGAGGAGGCUAGTTAGUAGCA
235281037	81256	CGTAGATGUGAGGCGGCAUC	81257	GTCTGGAAGUAAGCTGGGTUCT
235283041	81258	GAAGCCCAUGAGATCTTTGCAGUA	81259	CCAGTTTGAAUGCCAGTCATAAGUAAAG
235284518	81260	CAAGAAAGGGCACUGGCAUC	81261	GTGCUAGGCAGCAAAGGTATUC
235285458	81262	ACUCATUGGAGAGCCCCAGAT	81263	CAAGATCCUGTGCAGGUACCAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235285964	81264	GGATAAATCCAUAGGTGCUGCCA	81265	TGGGAGUCTCUGGGACAAAGA
235289799	81266	AGGACGTAUGGAGCCAGUCT	81267	CGGCGGUGTTTTTAUCAACGG
235290452	81268	CCATCCCUCCAAAUCCCCAAC	81269	GAATAUAAACGCCAAAAUCCCACCAT
235291554	81270	GCCUAGGAGCAGUAAGGGAGT	81271	AGGACUTGCAGAUGGACAAAGG
235292280	81272	TGCTGCUCCGAAGCUCAT	81273	TTCUATGCCTCACUCACAAAGGAAG
235292994	81274	CTTGTTGAUCAGAAAGGGUCCCA	81275	GTTACTCCUCACATCACCCCAUT
235298329	81276	ATCTTGUGGCGGATGTGGUT	81277	GCGAAATTACGUGCTGCTGTUC
235299066	81278	CCTACUGACAAACCCCAUGCC	81279	GATCCAUCACCAAAGCAGCTCTAUT
235299806	81280	TCCCUGATCUCCCAGGCAAA	81281	GGTTCCTCAUGGCTAAGCTUCT
235300136	81282	GCAGAGATATGUGCTTGTTTAAAGUCAA	81283	TTTCCATGTGTATAUTAGCTACAGAAGUCAAG
235303894	81284	GGGCGAAGGUAATGAAUGAAGA	81285	CGGCGCGCUCGATCUAC
235304633	81286	CCACTTGCTUAGGACCTCTCUT	81287	TCAGAGTAGCUGGAGAAGCUGT
235308464	81288	ACCAGCUCTGCCUACGGA	81289	GCTGGGCUGAGACCACCUA
235309467	81290	AGCACCTGAGCUTATAAAACAAATCUCT	81291	GGAAATGATACGUTTGTAACACTCGAUG
235310012	81292	GGAAGACAAGACGUGGAGAGGUA	81293	ATTTGGAGGAUCTGGUGCAAGAG
235310363	81294	ACAAACCACACUCACTTCATTTUCCT	81295	AAAATATTAGTUGCAACAGATATTCATCTUGG
235312777	81296	TGAAGCTCTGCCUAAAAGTCCCUA	81297	CTGGAGGAAUCCATCTGCAUCAA
235315006	81298	AAAGTAGAAGCAAUCTGATGAACUCCAA	81299	CCTGTACGAAGUGGACACTCUC
235316396	81300	CACACATTCTCUCCCTGCTCUC	81301	ACAATGGGCAGUGTGTGGAUAAA
235321911	81302	CCTUCCACGAGCAGUAGAGGT	81303	CTCTCTTCATGUCCTGGTGGUT
235323189	81304	GCTGAGTGAAUGGGAAGGAAGUC	81305	AGATCAATGAAUGCAGCTCTCAUCC
235325808	81306	AGCAUAGTGCTTCUCAGCAAAAGA	81307	GUGACACAGGACACCCUCAG
235326041	81308	CTGTGGACCAGAAUACTCAGUCAAAA	81309	ACTTGACUCCAACACTGGCAUC
235331991	81310	GTGCTCTCUGGGCTCUGG	81311	CCACAGCUTTGCCCAUGAA
235335742	81312	GTGAACGTTGUTGGACTCTACUGT	81313	ACCCUCCAGCGAATTTCAUACC
235337345	81314	GGGAAGUGAGAGGAAAACGAGUG	81315	ATTGACCUGGACTCGCTGAUG
235339417	81316	CAGGCACUGGAAACGATUGAC	81317	CACCTTTCTCTCUCTTTAAGCCACUT
235340993	81318	CACACCACAGGCUGAUGAGAA	81319	GCTTUCCCAGATGTCUGAAGAGG
235341253	81320	CACGTUCCCTCATUCAGGCAT	81321	CTGATGTTGCUCTGTTTGCTTCTUAG
235341576	81322	GGACTGCAUGGTAATCUGCGT	81323	CAACATGTTUCCCCTCCTTUCAG
235343396	81324	CCTTGUCAGCGGGCATGUA	81325	GGTGGCAAGAAGGGUGAGUG
235343819	81326	TCAATUGTAGTTCTCTUGCCAGCAAT	81327	GCAAAGCCUCATTCCTTTTGTUCAG
235345048	81328	CTTCACACACGGAGUCACUAGG	81329	TTTTTGCGCTTGUAATGTCAATAGCUT
235349131	81330	GCTCGCUGTCGCCATUCT	81331	GAGAUCCACCCCCUGGAGAT
235349704	81332	TGGAGAAGTTAGACAUGTCAACCTTTUG	81333	ATTTACCTGGGCUACTTCATCTCUAGAA
235350858	81334	GTTTGCACAGUGCCTTUCAGA	81335	TGTTTCAGCUCATTGTGATUAACCCT
235351598	81336	CTGTCCUGGTCATTTAUAGAAACCGA	81337	GGAGGTUACCCCATGGAACTUAC
235352525	81338	CCAAATTGCTUCTGTCTGTTAAAUGGAA	81339	TGGACTTTCUGAGAGAAAACAATTTAAGUGA
235352841	81340	GCTGGAUCTGCGCCUGAA	81341	GCATCATGTCUAACTCTACCUCGAC
235354152	81342	CCGCCGUAGCTGUCAGG	81343	CAACCCCCAGGCACUAGUT
235356758	81344	ACAGCACCAAAUAATACAGAGCAGTUAT	81345	ACCACAATCTUCTGCCCATCTUC
235357198	81346	CUACACCCACCCCAAAGUAGA	81347	GTCCTCAUGCCAACCCCTUT
235359975	81348	GCATTGGAACCAGUGCAGTUT	81349	TTTCCCTCTUAGAGCGTACAACTTTUT
235366141	81350	CTACCCUACGCCAAGCAUGA	81351	CCAGAGAGUATCCCAGCUGGAG
235367443	81352	CCACGCUGAGAGTCGTCUT	81353	CCTGACATACTCUTGACAGTCTATTUGG
235370584	81354	GACCTTTGAACUCTTTGTTTTCATGUCT	81355	TGATAAATCUGAGGAACATGGCACTUC
235371715	81356	AGCCAGCTUCTCTTCTAGUCCAT	81357	GGGTCTUCACCTCATAGTGUCC
235373297	81358	CAGAACAGCAUCGGTGCAGUA	81359	CTTTGACATTAACUTCAAGCCCCUT
235375004	81360	AAAAAGCCACCACCUAGAAUCGAA	81361	CAAAAGCACAUAACTGAAAACCAUAGGG
235378816	81362	CTGAAGCCCUGGAGAGUAGAAAG	81363	CCCTCTCAGUTACAAGTGATTATUCGT
235380215	81364	CCTCAGCACUTGGCTCAAACUT	81365	TGTAATGTCCATUTCAGGATCCATUCC
235380681	81366	CATCCAGGTUGATCTCGCAGUT	81367	GCGACAACGCCUACCTCUG
235381427	81368	TGGUCCCCTUCAGGCAGAA	81369	CCACCTUCACCTGCCUCT
235383157	81370	CAGTGGUGGCCCGTGUA	81371	CCGCCAGUCCTAAGTCTUCC
235388069	81372	GTCTGAAGCUGAGGUAGAGAAGG	81373	ACCTTTGCUGGAAAAGAAGAUCCA
235389091	81374	CCTCTUGGCCACGTTCATGUAG	81375	CGCAATUCGAGTATCCCAUCCA
235389989	81376	CATACTCAGUAGACAACATAAAGCCUCAT	81377	GAAGTCCCAGCUTGGTAGAAAAUACT
235390321	81378	AGGCAUCAGGTACAUGAAAAAGAAGAAT	81379	CATAGTATTTCUTACCTCCGUGCAACA
235391229	81380	GTGCATGCUCCGGTTCUC	81381	CCACCCGGGCUTCTAGUC
235391473	81382	CTCTCAGCTUCCAGGGTCUT	81383	CGGGTATATGGAAAGUCAGAAAACATCUT
235391588	81384	GACTTCCAAAGCUGGGAAUCCT	81385	GGAAAAACCAAACUTGCCATCTCTCUAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235392346	81386	GGCGGGCACGAAUTTTGUC	81387	GGGTCUGGAGCCCUCAGT
235393372	81388	CTTGCCCAAAGUACCAGGTAATUG	81389	CCAAGAAGTUTCTCAGTTGUGCCT
235394591	81390	GCATUAACGGGTGCCUGGA	81391	CATGGUGGGCTTGUCCAAAAT
235395596	81392	TTTCUGGCCCCACUGAACC	81393	GGCATGGUGGGCTTGUC
235397145	81394	CCUGGCCCCAGAGGACAUA	81395	GTGTCCCATCUCTTGGGTATCAAUG
235398587	81396	CTCGGCAAAUTTAGCTTCUAGCAAC	81397	GAACACTGCTUTCCGGCTTATUC
235399150	81398	GGCTGGGCGUGCATTTUG	81399	TCGCCCUCTGACUCCGA
235404687	81400	GATTCCTCUGGTGAAATCGGUCA	81401	CCTCTCUGCTCCCAAGUCAAG
235404741	81402	AGGCATGAGUGGTCGAGGUA	81403	CATCTUCAACAGCCTCUACACCA
235404766	81404	ACTTGTGCCCAGUTTCTAAATCAUCT	81405	GCCAAGGUCCCCCTUCT
235405311	81406	CCTTCAGATCTTUGATGTCCTTTCGUA	81407	CUGTGCTCUGAGCAGGGA
235405862	81408	CCCUGGATTTAUGCCCAAGAAGG	81409	ACTGCUGACACACACACTAATTUCT
235406697	81410	CTCACGCTUCCCCAAATTTCUT	81411	GCGATTCTCCAAUATACTGAAACTCCUC
235409404	81412	GCCAAACUGTCCCCCAUGAAA	81413	CCCCACCACACCCUATCACUAT
235411576	81414	CUCCAGGACACTCUGGAACAAC	81415	GAAAAGGAAGCUCTGAGTGAGGAATUA
235412439	81416	TGAAGAUCUCCCAGAGCAGGAT	81417	CTGAGGTCCUTCCTTGCACUC
235421010	81418	GCTAAACAGAAAGCCCUGGAACUT	81419	ACTATGAAAACAAACUGACAAACCTCUCT
235423712	81420	ACTTCTACTACCTUATCGACACAGCTAUT	81421	GGAGGGCTCAUTTGTTTATCTCTUACAG
235430726	81422	CAGAGGACUGACTTCTCUCCCT	81423	TCAGCCGGGAUGCGATUG
235432260	81424	CCATACACAAGUAATCACTCACUCAAGT	81425	AAAACATTACATACCUGCCTCGAGTUAT
235434292	81426	GGCCGATCACCCAUACAATATTTTCTUA	81427	CACCTTTTTCUGTTGATCAGGUGG
235437417	81428	AGTACTAGCAUCCTTACAGTCTTCUAAA	81429	GAAAGACCAGUTCTTCCCTCAUCA
235438071	81430	TGAATATCUGCAACAAGCAAGTCAUCT	81431	AGTGAAGAAACGUCTTTTCATGAUGAGT
235447043	81432	CCCCAACCUTAAGUGCACCAG	81433	TTCCCTCUCACCCCAGTTTTUG
235447238	81434	GTGCCCCAGGUAGCTTCAUT	81435	GTGAGAGGCUTGACUCAGGAAC
235447984	81436	AGATCCTGGCGAGUAGTAAAACTTUC	81437	GCTGTCATAAAUACACTTGGGTTTGUT
235452841	81438	TGGGTUAGAAGAAGAAAAGUGAAAAGCA	81439	CCTGCCTUCCAAAGCAGATACTUC
235458671	81440	CTATTTCTTCTCGGUCATCCTGAAGUG	81441	CCTATTCCUCAAACCCCAGAAAGUG
235461221	81442	GGAAGCCUGGTCAGGTAUGAG	81443	CCCTGUGTGGAGGUGCAG
235462079	81444	GAGTCUGGGAGAACAGATTTCTUGA	81445	CTTTTGATTCUGGGAAGCACATTCAUT
235463674	81446	CTGCACGUTGCGGTTGUT	81447	GGTTCCCUGACCATTGCUGAG
235468355	81448	TCTTGCACUCGGCGAUCAT	81449	GGGTUGAAGGGCGUGAGAAA
235472176	81450	GCTCCTGGUGAAACTGCTCUA	81451	GCAACAUGAGATGGAGCUCAAGG
235477606	81452	CACAAGUCCCTGGCAGUCA	81453	TCCCCTCCUCAGACTCCAUC
235480103	81454	GTTGCTGTUGCTGTGTTTATTUCCA	81455	TCCTTTGCAGAUTTAGTTTCCUAAGCA
235482505	81456	GCTTGAGCCUGTGTCAGTCUA	81457	GCUCAAGGAGGCACATCAUGAG
235483117	81458	ACTGGAACAGTGUTTCTGTCTTTTTGUA	81459	GTTCATTACUGACCCTGAUGGAGAAAA
235483554	81460	GCCCCAGGAAGGUCAUCAA	81461	CTGTUGGGCAGGAAGACCUC
235485169	81462	GCAGTUCAGCAAGCCTTTCUCA	81463	GGTAAGAACTCUGGGTTCATACACATUT
235486033	81464	TCAAGCTTCACUTGCAGTTGTTTUT	81465	AGAACAUGAAGCAAAGGCAUGAGA
235486084	81466	GGAGCCCCGUCAUAGGAAGT	81467	TGGCTTUGGGCTTTCUGGAT
235488274	81468	CGCTTTCTAAAAUGTCAGTTGUCCA	81469	CCGCACCTCUACAACAAAATGTUT
235489147	81470	CTACTCUCCCACCUCCACCT	81471	GGCTCAGCUGCCTTCUCA
235491997	81472	GCTGCCUGCTGUGGAGAC	81473	GCTCACCCUGTGATTTGTUGCT
235492806	81474	GTTTTTCTAAGGUGTGCGTTUCGT	81475	ATCTTGTGGUGGTGTCACTCUG
235495770	81476	CCTTTGCTGGAAUTAATATGGTGTTCUC	81477	TGAAACACACUGCAGTCAGAACAUA
235497549	81478	TUTATGACUGGACAGGGCAAACA	81479	TCCGUAGGACACCAUCGCT
235498907	81480	CCTGCGUGCAACUCCGA	81481	TGAGCAUGAACACCCACTTUAAGG
235501145	81482	GCTGTCAACCUGCATGAAGUC	81483	GCATACTUGGGCAGAGAGTTTCTTUAC
235501300	81484	CGCTCAUAGCAGGAUCCACAG	81485	AAGTATGUTTGGGCUGGACCAAT
235501994	81486	GAATGCCTTCTCTTUTGTCTATATCTGATAAUT	81487	CTCTCCTTGCCAUCATTACTTCAACUA
235502541	81488	GGCUCTGCCCUCGACAAAG	81489	TGAGACTGACCUCTCTTCTCCUG
235503357	81490	CUGCAAGGGUGACCACACT	81491	GCUGAAAAAGCUGGAGGAGGA
235503863	81492	TCCGGTCUCGTTAAAGTTCCUCT	81493	TCCTGGGCUGGAACGAGUA
235504565	81494	AGUTGAAGTAATGAUGGCAAGGAGAG	81495	CTCCTTTCTACCAAUAACCGCATATCUA
235506419	81496	TTCTGGTCCUCCAGGATGAUCT	81497	TGCTGTCCUTACCGTGTCUCT
235508140	81498	TCTAACACAUCCACCTCCUGCT	81499	AGGGAGCATUGTTTTCACCTTUCA
235513636	81500	ATTTCACUCCATCCCACUGAGA	81501	GGUGGAGGAAGCUGACAACA
235515069	81502	GAGAACACCUAGAAGACAGUGCAT	81503	CACCGGCACUCAGCTAUACC
235516511	81504	GCAAATGTTTUGTGGTATAGCUGAGT	81505	CAGCTTGTATGUCAATGGATACTCTUGA
235516957	81506	CTTCAGAGUTTGTGCTTTTUCACCAT	81507	GGTGAATTAGCAUCCTGCAGTUAAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235519965	81508	AGCCCTACTUCCTTAGCACTGUAT	81509	CATCCAGATUGATACCTGGCUACA
235523337	81510	CAAGCTGGCUAAAGCTCCTTCTUA	81511	CCAGCACGUCACGTTCTUC
235523412	81512	AGTGCAAAGAUGCCCTUGAGAG	81513	CCTGGACUCGGGTCGUAAGA
235523599	81514	AAATCCTTCCTCAUGTCCTGAAAGUAAC	81515	TUGGAACACCAUCCGCCAA
235525634	81516	AGTAAATCTTTUGCTCATGTGCATUAACC	81517	GCGUGCAGCAGTTATTTUCCA
235526495	81518	GCAACACGACGAAAUAGCCAUAC	81519	GATTTTGGCUGTGACACAGUGAA
235528206	81520	TGATGTTGAUGATCTGCGUGGT	81521	CCAAGGUAGAATCCCUGGAGAGT
235530627	81522	CACAATGCUACTATGCCCTUGGA	81523	GCATGCUGTCCACTUAGCC
235530862	81524	ATGTCACCAGUGACCUCAACAG	81525	TGAGGGAAGAAGAGAUGAGUAGGG
235531311	81526	CCTTAUGGCGCACAGGTAGUG	81527	CGAAGGTUGGAACTCGACUGA
235531762	81528	GCAACTAGCUGGCAGTCTCUAT	81529	TCCAGCAAAAUCATGUCCCAGAG
235534256	81530	CAGCGTTAUGAAGTAATGCAGUGT	81531	CCTCTCTUTTCCTTAAAGUCACAGAAGA
235535331	81532	TCAAAATCAACCCCUTTCGATACTUGA	81533	CAGAAAGGCACACUTGATGAATTAUGT
235535964	81534	CTGCAAAACACGGUGAATGACUT	81535	GGCCAATCTGACAUGTCTGATACTTUA
235537334	81536	GAGCCCAGTUTTCATTGAAATCAUGT	81537	AGCAGCUACAAGAAGAATUGCAGAA
235537909	81538	CAGGGAUGGGAGTGAAGUAGAG	81539	CCTCAGCAGGUTTCCTTTCCAUAG
235538631	81540	CACCTGUAACCAAGTATCCUCACC	81541	GCAGGCAAAAACUGGGAAACUAA
235538801	81542	CACCCTTACCUCCTGAAGATTTUCAT	81543	CTCACTTTGCUTCTCTTTTGACUGG
235540590	81544	GTCACTCTCCUCCCCATCUGA	81545	AATTTGUCAAAAACCTGCUGCCA
235542358	81546	CCTCAATAGGUGCCATCAGUGT	81547	GGATCTGACCUCGGTGCUCT
235544452	81548	GGTTTTCTGGAUAATTTTCCCATTGUGA	81549	AGUGCCCAACATCAUGGGT
235545543	81550	CCGAAAGACCUATCCCACUGT	81551	CCAGGUCCACCTCGATCTUG
235549618	81552	GAGGGTUCACTAAATGTTTUAACAGCAA	81553	TGCTACUCCATAGAAUGGGAGACA
235550790	81554	ACCCAGCAGACAUTTACCTATAGACUT	81555	TGUAGTGAACCUGGAAGGCAAC
235552029	81556	GCACGAAGCUGTTGGCTCTUA	81557	GCCTCTGTAUCTAATAACCATGUGACAAT
235552766	81558	GGCAAAGCAUAATTGATTUGAAGGAGAA	81559	CAGGCATTATUGTACCCAAGAGUGT
235552965	81560	ACAGGTCTUTCTGTGCATUCCT	81561	TGTTCACATGGGUCTCATTTACUCC
235553834	81562	GGCATTGCUCCTGTTCTTTUGA	81563	TGGCAGAAUATGAGAATCUGACAAACAA
235554666	81564	ATGTGGATUGTGCAAAATUAAAACGACT	81565	AGTTTGGTGTTCUAGTTCAGCACAATUA
235555845	81566	TTCATGGCGUAGTAAGGTTTUCACT	81567	CCACTGGTUAACAAGTCTTTGUCCT
235558608	81568	GCCUAAAGAACGACAUAGAAGAACAAGAA	81569	CAAGCCACCAUGGAACAAGTTTUAT
235559334	81570	TTGCTGAATAAGUGTAAAACCCCUCA	81571	GTATAATCATGTGGGUAACTGCAGGTUA
235561468	81572	CAGGTTTACCTTUTCTGCTAACACATUT	81573	ACCACATTTAATTUCCCCATACTTGTUCA
235562527	81574	ACATTTGAGCAAAGACCUGAAGGUAT	81575	AGAGCCAAGCAUCATTGAGAAAAGATTUA
235563881	81576	CCTTCCTGGUGTCAACCACUT	81577	CTGCTCCUCCATCTTUCCACAG
235564745	81578	GUCACATTCTCUGACACAAACACAAC	81579	GGATCATTCCCUTCTTAACAATUGCAT
235565116	81580	CATGGCTCAGUCTGCTTCUCT	81581	TCCAGUACCAGGCAGGGUT
235566054	81582	CACTGAGUCCTAGAGAAGUCACAGA	81583	CATGGCCTCUTCTTTTTAACTTUGACA
235569124	81584	TGTCTTCAUCCGAAGGGUGACT	81585	CATTACAAUGACATGTGGCUGAAGG
235569608	81586	AGGGCUCCAAGGACTACUCA	81587	GCTAATGGAUCATCTCUGCACCAG
235576359	81588	AGCAGTCCUGGCAAATGGTTUA	81589	GTGCTGAAUAAATCTCTTGCUGAACAAA
235581427	81590	CGACAGCAUGCCAATCTCTUCA	81591	TGAAATACUCCAAAGCCTCTTGCUC
235581910	81592	CAGTACCUGGGAACCTGCAUC	81593	GTCAACTUGAAGTGTTCUGAAAACCAT
235583861	81594	GGGAAGGGAUGATGCACTAUG	81595	AACTCAAAGCUTCCAATGTAGUCAGT
235585454	81596	GCGAUCCCAAAGAGTUAGAGGA	81597	GCCGGACCGGGACUAUCT
235586113	81598	CCTCGTCTCCUCTAGGTCCUAT	81599	CCAGTGACCACACUCTCTGUG
235586242	81600	AGTCTGAAAUGCACCTTGGAAAUCT	81601	GCAGCGGCUGTAUCGGT
235586852	81602	GGCCGGUGCAGATAGUCC	81603	ATGGCCUCGGCTGGUAAC
235587712	81604	CCACTCTUCCGTTTAGCCUCA	81605	CTTCCAAAGGGUTGCGTGTTUA
235589069	81606	TTGAUGAAGACACAGUCGCCAA	81607	TTTCTTCAGCCAGUTTTCTTUACAACAG
235594429	81608	ACAGUCCTTGTACUCCCCACT	81609	TTGCACTGACUGCCAACTAATTTUG
235594750	81610	CTGCCCCUGTGACACCTUA	81611	GTATGCAGAGGCUGAGGAGAUG
235595589	81612	CCAACTGGCUTAACACAGGUCAA	81613	GCUGTATAUGCCCCGAGGGA
235596049	81614	CTGCAGACCCAGGUTAGCTUA	81615	AAGAGATTTACCUGATCACTTTGUCGAG
235598029	81616	AGTCCTAACCCUCTAGCTGCUT	81617	TGTCTACTCCTAUGGCATCGTATTGUAT
235598597	81618	CTCCATCTCAUGCAGTATCTCCUC	81619	AGGAGAAGAACCUGCUACAGGAA
235599637	81620	CCTCTGCAUACAGCTCTGTCUCT	81621	GAACAGAAGCACUCGCAGGUA
235600016	81622	ACATAAACCCAAACUGAACCACTCTAUC	81623	GCACCAGTGUATTACTGCTAUGAAAGAA
235600121	81624	AGAAGCACUCATGTGGCTTUAACA	81625	GGATGGGAGAAAAUACCTCUGACC
235602326	81626	TCGAAAGACCCUAGCCTTAGAUAAAACT	81627	CCAGAGTGAGCUTTCATTTTCTCAGTUA
235602904	81628	GTTTTATTCGCTUCCTCATGCTGUC	81629	TGTTTTCTCAGAUACGGCGATUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235606585	81630	CTTTCTTGUCTCTGCCCUGGAG	81631	CAGACACTTCAUCATCAGCTCTCUT
235607483	81632	ACTGACCTCTAGUGACTTGCTTTCAUA	81633	AGAGAGTAGGAAUGTAAAACTUGGACCT
235610924	81634	AATGAGTCTAGAAUCCAGACCTGUCA	81635	GCACTGUAGCACCAAAGUACCT
235611339	81636	GGCATTCGUTCACCTGUGAGT	81637	TGACTAACACUGTCCCCCTUCT
235612876	81638	GGCTTACUACAGGAGGCTCUGA	81639	TCCGUCCACATTTGTUGAGCA
235613485	81640	GCTCCCCCGUCATCAGTUC	81641	GGTGATAAAUGCACTTTTGTCATAUGGT
235618914	81642	CTTCTTGATCAUCTCCTTCTTCTUCAGA	81643	ACCTAAAAAGCAGCCUAAGAAGGAUG
235619062	81644	GGAGGTTGAAGUAACCCCTGUT	81645	GGAAAAACAACCUAAAAAGCAGCCUAAG
235620632	81646	TCCTTTCUACGCTGCTCCTUG	81647	AGUCAGGAAGAGCCAGUAGGAAA
235621812	81648	GAGGGCCAUCCTATUGCGA	81649	ACCACTUGACTCTGAUGCAGAAG
235629082	81650	GUTGAAAGAAAAATUGCACAACAAGCA	81651	GUCTCTATGAGUACAGAAGGACACAGA
235630364	81652	CATGGAGGTAAGUAAGGGTCTGTUT	81653	CTTUGGCCAACAGAAUCAGCAG
235630572	81654	TGTTACTCCAGUCCACACACAUAGT	81655	GCATAATTTACACCUGTGTTCTTGTUGT
235633011	81656	CAGGAGCUCAGTAGGGTCUCA	81657	AGTCUCCAAGCCAGGAGUCA
235634279	81658	GCTCCACACUCATGAUCCAGAT	81659	GAGTTTCCUGAAGTGACGGUGA
235635266	81660	CCCAGGUGCCAUCGAAGAAC	81661	GCAAGAUCCAAACTTUCACACCAT
235636895	81662	AUGTAGAACATGUAGGAAACACAAGGAA	81663	GUGACCACCGUACCACCAG
235637041	81664	GTTTGCUGAAGAGGCTGGUAGT	81665	CAACAACTGGAUAATGGAAGGTTTUGT
235637180	81666	GCATGCUCAAACACCUCCAC	81667	GTTTCTTCCUGGACCCAAACUACAT
235638295	81668	CAGCAGCAGAAGCAUACTTAAUCAGA	81669	GCUTCUCAGCAGCAGCAG
235641061	81670	GGACCCCAGUATCATTUAAGCCA	81671	GAGCUCTTCATUAGGGCACCAA
235644275	81672	CCCACCCCCAUTTAGATCUGA	81673	CATGACTCACUGGGTTGUAGCAA
235645150	81674	GCTCTCUGGGTGCUAGGCT	81675	AGAAATCTCTGCCUCACTCCTCUA
235645223	81676	CTGAAAGTAGTUTCTGATGGAGTUGGT	81677	GGAGTCCUGCAAAACAAGCTCTAAUAAT
235648879	81678	CCUAGCCCAGAGACAUGGAGAG	81679	ATCTGCGAGCAUACAGGTGUAAG
235649323	81680	CAGCTGCGGUGTGAAATUCC	81681	ATCCACAGGCCUATTUGAACCC
235654051	81682	CCTGACATUGTGAGTAGGUGGT	81683	CCTCAGGUGACCTATGCCUACAT
235654215	81684	CCACTGACCUCAGTCTGTTUCT	81685	GGUCCCAAAACCAGAAGTCUGT
235657283	81686	GCTTCTTCAUCCAGTGGCUCAA	81687	CCTCAACTCTUGTCTCCTCTCUCA
235657309	81688	GTTTGGGATTCUCATCTTAGCCAAAGUA	81689	GGCCAAAAGAAAUCAAAGTCUCCAA
235657431	81690	GTGCATCTTGUGAAAGCATTCTGAAUT	81691	ACGATCTTTGTTTCUCTATTAAAGTTGCUGT
235659832	81692	GCTTCGAACUCACCTUCGCT	81693	TCTACACTGGCUTTCTGTTCACTTUT
235660535	81694	CACTTTCGGAUCACTGUCCCA	81695	AAGAGGGACCCAUTTTGCTUGT
235661448	81696	GCATAACUAGGCCGCTGUCC	81697	AGCAGTAGAUCCAGAACAGTTCUCA
235661489	81698	CAGGCCUAAAACCCUGGGAA	81699	CGGCTGCUCTTTTCGTTCUGT
235664071	81700	AGAAAGGCCCCUGTTTGTGAUT	81701	GGAGGAGCGAGAUTTGAAGAUCA
235664696	81702	GAAGTCTGACCCUTTTTGTCTCCUA	81703	CTTCGGCUCCACCTGGUC
235665327	81704	AAGGAACCUGTTGAAGCUGAACA	81705	CTTACTTTACGACCUACACAGGAGTTUC
235665606	81706	AAGAAATCTATGACUTTTCCACTTCAGGUT	81707	TCTGTCGCCCUAATGCCAAAUT
235667676	81708	CAACCCTAUAGGAGGCGUGA	81709	GTGGAAACUCACTAGAGCATUCCT
235668046	81710	CATCAGAAGTUGGAAGAGAACAUAGACA	81711	CGAAATTGTGGTUCTCGAAGTTCTTUC
235669577	81712	GGCGACAGAAAGGUTAUGAAGAAGAAA	81713	CACAAGTTCTGTUGTCCTCATAACAAUC
235670531	81714	GGGATGCUGAGGAAAAGTAUAGAGAAAT	81715	ATTAACTGCAAUAAGAAAATCCCCAGUCT
235671193	81716	CAGCATGAUGTTGGAATCCUGACT	81717	GAGAAAACAGCCUTATATTGACTCUGCT
235674202	81718	TCACTTTACTTUGGTTTTGAGTCUGCT	81719	AGAAGAAGAUAGTGAGGTCATUGAACCT
235674308	81720	CCAGGCCACAUCCAAGTUCAG	81721	GTCTCUGCAGTGCUGGAAGT
235677538	81722	GGGCACTCTUCCACATGTTTTUC	81723	GTCCAGTTCTGUCTATAACCCAGTTUC
235679711	81724	TTGCACUGGCTGUCACAGT	81725	GCGGGCAACAAGGUCUG
235680759	81726	TTTTGAGTCUGAAACCCCCAUGA	81727	TTCTUGCCCACCAGAUGACC
235680989	81728	CCCAGTTGUGGTTTCAGUAGGA	81729	CGGGAGTTAATCUGATGTCTTCTTTGTUT
235682733	81730	CTGGCGGCUGGGTCTTUA	81731	CCAGCUGUGCCAGCCAA
235683531	81732	CCTGCUGGCTTGGCUGA	81733	TCACAGCUCAGTCAGGTTCUCT
235684100	81734	CGCGTGGUTGTTGCACUG	81735	CCAAATUCAACGGGCTCTTGUG
235685746	81736	TGGAUAGCCUCCACCACCT	81737	GUCCTGCCUGACCAGCAAA
235687627	81738	CGAAGCTGUAGTCCAGGAUGT	81739	CCCCGAAUGCCAGTUCCC
235688412	81740	GGAAGGCCAUGATGACAUCGG	81741	AGGAGCTCTUCCTTTCCTTCCUT
235688709	81742	AGGTCCCCUGGTTGUAGCA	81743	GTGAGAAUGACGCTCGUACCT
235690796	81744	GGGACUGATCCTCCUGCAC	81745	GCCCATUAGCAGCCCAAGUC
235691810	81746	TTCCAACATGACAUACTTCACGTUACT	81747	CGGACAUTGTACCUCGGGAAA
235692106	81748	TCTTGCACATTGUATAAACATTTAATGUAGGT	81749	CTGTGATCAGAAUTCCTCCTCTTUGAA
235692136	81750	ATTCAAAGAGGAGGAAUTCTGAUCACAG	81751	TCCATTTCUGGCAATACAGCACUAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235692404	81752	CAAAGAGGAGGAAUTCTGAUCACAGA	81753	GTACCTGATUCTCCATTTCUGGCA
235692657	81754	AGTGCTGTAUTGCCAGAAAUGGA	81755	CACAGTTTAGGUTTTGAGATAAATAUGACAGA
235695451	81756	ACACCGACCCUCTGTGAUGA	81757	GCUGGAGCGGCUCAACAA
235697908	81758	TCATAAGGUCCTCCATCUCCGT	81759	GAGAAGACCAUCTCTGCCAAGTAUG
235702106	81760	ACAGAGCCUTGGTCTCCTUCT	81761	GTAGCTCUGAGCCTCATGGUG
235707658	81762	GGGCACGGACAGGUCTTUA	81763	TCGCUCATTTGTUGGCGACT
235708083	81764	GTGCAGCAAUAAAGTCATATTCTCUGG	81765	CTGACCTTGUGCCTCTTCTGUT
235710247	81766	ACCACCCUCTTGTCCCUCAA	81767	GGCAACAUGGAGGCCAUGA
235711596	81768	CCTCCAUGTTGCCCUGCT	81769	CCCUGAGGCATGACUCCAA
235716971	81770	AATAAAGATTCCUTCACAAATCCTAUAAGAACA	81771	GATCGGGTAGCUAATCCAAAAGACAUT
235717175	81772	TTTCCTTTTGTUCTCTATGCCUGAAAA	81773	GCAAATTGTTGUTTCCTAGCGTUCA
235717531	81774	AAATCTCTTGGUAGCTGGTTTACCTUC	81775	GGAGAGGAUTAGTGACTUAACGACAAAT
235717580	81776	CGCGATTACUTTAGGCCCUCAA	81777	CGCCTTAGUGAAGAGCAGTATGTUC
235718920	81778	TGGTTTACCTUCCAGTTCTGAAAUCAT	81779	TUCTCTTUCCCCAAAAAGGAACGA
235719601	81780	CGTTAAGTCACUAATCCTCTCCUCAAG	81781	AACTCTAGTTGUATTTTGTTATAATGUGGGT
235721974	81782	GCCGCAGGAUTCCAGAUCA	81783	GGCCCCAUCACCUCCAT
235727263	81784	GGAAAGAAUGCTCACAGCUCACT	81785	CCAGAUCGCGGAGCUCA
235728187	81786	TCCTCTGTAAAUGGTGTTGTTTUCACT	81787	CAAAGCACTTCAAACUTACTACTGCAUT
235729152	81788	TTCTUGGCCAGCTGCAUCT	81789	GGGCUCCCCCTGCATUG
235731344	81790	ATCCCCTGAACACUAAGAATGGAUT	81791	AGGCACCTGUATTGACCTTGUG
235736180	81792	TTTGGGTGACCACUAATTAAAGTGUGA	81793	CATGAUAACCAGGAAGCTCAUCAGAAAT
235742125	81794	AATGCCAAAGGCUTTCGTTUGT	81795	CAATGGTCTCGUCCTCTCTCTUG
235743010	81796	CCAGGAGCUTTGCATACUCACC	81797	GCCCTATCTUCTGCAGAGACUT
235749304	81798	TTCGTTGTCAGUGATTGTTTTCATTGUT	81799	CAGCACAUGAACGTGUAAACAGG
235752028	81800	TCCCCTGAACUCCAGGTAAAAGUAA	81801	TCTGAGTTTCCUCAAAGATCTCCTCUA
235754789	81802	GGCAAGAGCACUTGAAATGGUT	81803	GGTCTGTTTCCAGUAATGGTCCAAUAT
235755040	81804	TTGCCAATGUCCGCTTCAAUG	81805	GGTCAAAGAUTAAGGUGCCCACAA
235759170	81806	GCGAAGCACUGCATAGTTUCAT	81807	CTGGATTACTUTTGCCTTGCUCAG
235760009	81808	GGCAAACAGUGCCAAUCCAAA	81809	GGACTATGCCAUGGACGAACUG
235766723	81810	TTCTTTGTAGATAUGATGCAGCCATUGA	81811	AGAGAAAACCAUTACTTGTCCAUCGT
235767608	81812	AAAACAACUAAUAGGCCCAAGGGAA	81813	GACCTUCCGACGCATTGUAGAA
235772241	81814	GTTCCAGCAGUTCCACCTUCAT	81815	GGAAGGAACCCCUCGAAUCC
235772323	81816	CCACCTAAAGCUTATCAGAGUGGAT	81817	GGTGGCACAGGUGGCUT
235772800	81818	AGTAAAGTGCACAAAUATGAGTGUACCC	81819	AAGUGACUGAACAGCGACAGAA
235773041	81820	CCAGCCTCUCGGTTTGTGTUA	81821	GAACATATGAGCCUTTCTTCCCUACAG
235773943	81822	GTGCTTCUGGATGTACUGACCA	81823	ACTGTCCTTACUTTTCCTTTGCTUCA
235775103	81824	CTGATAATGCTAUCAAGAACCACUGGAA	81825	GGCAGGGAGUTGAGCTGUAG
235775595	81826	CCUGUGCCACCCCCAAA	81827	CGAATAGGCCUAAGTTTGTGGAATGAUA
235781911	81828	GCAGAUAGGACTGGGUAAGGCT	81829	TGGTGCTGAGUCTGCATCAUC
235784652	81830	GCCAGUCACAGAGGATGAGAGUA	81831	GCTAATGGCAAGAAUGGCGAUT
235785665	81832	TTTGTAACACACUCTCACAGUACCAC	81833	TGGTAAATCTTACAUCCGTCTCTCCUT
235786133	81834	TGUGATTGAUCAAGGAGAGACGGA	81835	GGGATGTAAUGACCCTTCAAAATCACUA
235789742	81836	GTCATTTGAUGGGTTTTGCUCAGG	81837	CCTGGAGCUAAACTAACCGTCUCT
235793748	81838	CAGAGAAAGAGGAGAUGAAGCTUCT	81839	CCATCAUCAACCAGTGCATCUCA
235801541	81840	GCTAGGAUAGTGATTATUCCCCAGGAT	81841	CAGAAAAUAAGGAAAAGTAUGGCAAACCA
235802952	81842	TGAGUCGGAGGTTCTAUCAGGAG	81843	TGATTATUACACCCCACCCUCAGT
235803433	81844	GCACCCTGGGUAAGATTTCTCUT	81845	CTGGATGTCGGAAUATTTAGAAACCUCT
235803778	81846	ATGCTAUCACACACATTCACTUGAGT	81847	ACCTGGUGCAGGCTGUC
235804118	81848	ATCTCAACUGAATGGAAUGAACGACA	81849	AAGCTGTGTTACUTCAAAGGAGGTTUAT
235804125	81850	CGTTGAGTCUTATTTCCAGTCUGACC	81851	GCACTTAGAGGCCCUTTGCTTAUT
235804680	81852	TGCTGTTGGAUTCGGCCTUAG	81853	CUGGGTAAACAUAAGGCCAGGA
235804875	81854	CGTGAAGAUGAAACAAGAATTGUCCAT	81855	CTTACCTCTTUTTCCCTTCCUGAAACA
235810701	81856	GAGTAGACACGGUGCAGUCA	81857	TGTTTGTGUCTCCTAGUGAAAAGGG
235811629	81858	TCCTGCCUGGGUAGGAAAAGA	81859	GGCAAGUGGGATGTGAUGAGG
235812061	81860	AGGAGGTAATTTTUCTTCTCTGCTGUT	81861	AGTCAAGATGTTUCTGGTTCTGTTUCT
235816422	81862	GGATCCATGUGGACACCTCAUC	81863	ATGGAGUCCATTGUGAGAACAACAT
235818276	81864	AGTATGUCCCCATGCUAGAAAGGAA	81865	CACCCAGAGUGAGTATAGACACTTTUAC
235819686	81866	CTGACTTGTTTUATGCGGTGTACUT	81867	TGCGGTUGATGCATUCAGAGT
235823180	81868	GCAAUGAAAAAGCAGCCCTTCUC	81869	GATGAAGTTCCAGGUAATTCTAGCAUGT
235827061	81870	GGAAAAGGCUGCAAGACCCUT	81871	GACTGGGCCUGTGCTCAUT
235828506	81872	AGAGATAAAGACAUTAGTCCCAGAGUGT	81873	ACAAACTCUCAGAGCCCAUCC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235829250	81874	GGTTCCAGUGCTCAGCCTUA	81875	AATCTTGGGCUAAAGAGACTTTCCTUAC
235832644	81876	CCAGATTCCAGUACCAGTACATUAGGAA	81877	CAAGTTTCCCTTUAAGTGGCCTGTAUAT
235840214	81878	GCTGTAGGCAAUGGAACUGCT	81879	CAGCAAGAGGUGTGTATGGAUGT
235840608	81880	TCCCCAGAUACACTCCCTTUCT	81881	TGGAAGCCGACUCTTCCUACT
235842889	81882	TGATGAGAACCCCUGTGGGAUAG	81883	ACCTCTGGAUATTGGCGCTUG
235845092	81884	TCACCTCTCAGUGCACTCATUG	81885	GGATAAGUGCCAGACAGACAUGAAT
235845407	81886	GCAGCGUTAAAGGAAATUCCGAT	81887	GTTCTGUGCCCCCATTGTUC
235849170	81888	CAGGUACACGGAGCTTCUGG	81889	CTCCATGAAUGAGGATGGGATTTATUCT
235851738	81890	CGCTGUCAAAACCAGTGCTTTUC	81891	AAGCAACUGCAAAGAGGAGAAAGTAUAT
235852487	81892	GGCCAGACCUTGGGACTUA	81893	CCACTGCCCUCTTTGACCTUT
235854962	81894	GTTCTATGGUGCCCCTUGGAG	81895	CTGACACCCCAUTTGCTTCTTACUA
235858166	81896	CTTACAGGGTUCACTCAGACACUC	81897	TGATGCTACTCTUCAGAGGTCTAATUCT
235860581	81898	GGGACAUCCCCGTGTCACUA	81899	TGTTCCCGTTUCCTCTTGATCUC
235863494	81900	CTTCTAGGAAAGAUCATAGGCCAAUCT	81901	GTTTAACTTATUGAGCATGCCTGGTTUT
235868201	81902	GCCCAUCUCAGACAACCAAGAC	81903	GCAACATAUGAGCGCCTTTUCC
235871506	81904	AAAGCTACTGUGTGAACCTCAUCAA	81905	TTTTAAAAGGUGTCCAACCAAUGCAA
235873922	81906	GCCTCCCTUTCCAATGGACUA	81907	ATGTTCCATGTAAUACTGGACCAACUC
235874062	81908	CTTTGCATTGGUTGGACACCTUT	81909	GCCTAGTTTGCAUTTAAAGTAAGACAUAAG
235874208	81910	GTCCTGGUAGTGTCTUGCAGT	81911	GGTCTGGCACUGTTCTTCAAATATTTUT
235876260	81912	ATGACTTUGCAGAAAAAGAGACTCUGA	81913	TCCAACTGCUGTAATTCATACTUCACAT
235877850	81914	GGACAGCTAUTGAAGCATTTAAUGAAACC	81915	GAGGATTTUGGTTATCTCUAGCACAAGA
235878631	81916	CCTAAGUAAGAAGCAGAATGAGCUGAAA	81917	TATTCAAACAATAUCTTACAGCTTTTAUGAGCT
235880810	81918	TTCACGCGGGUGAGTAUCC	81919	ACCAGCCUGGCTTATGUGAAAAT
235880812	81920	CAGCTCGUTCCCGATAUCCA	81921	CTGGCTCCAGGUAAAGAAAATAAACAUT
235880822	81922	GTGTAAGCAUAGATACTTGAUCAGAGAAGG	81923	TGGCAGACAGUAACTCAGCUAGT
235882050	81924	CUTTGTGUAACAGCACGGAAAAGA	81925	TTGCATTTGTCUGGTTTTACACUCAAG
235884794	81926	TGAGAGGGCACUTCTCTTGCUA	81927	GCTTTTAGGACAAGCUCCCTTAAUGAAT
235884867	81928	AGAAGAGGCCAUGCGTUAGG	81929	CTGCTTTTCATUTTATTAGGCAGUGGAA
235885514	81930	TGCCAACAUTAGTGACATUGACAG	81931	CACACAGCCAUGGGTTTTCTTUT
235886703	81932	GGCCUGCAAGGATTCCCAUAG	81933	CTGAACTTCUGGGCCACUCA
235889035	81934	GGCCTTGGCUATTGCATCAUC	81935	AAAGTGGGCUCCAGTCUCAC
235889826	81936	GCCAGGAGACUATTACGTTCCTCTAUAA	81937	TCTCTTGCTTTUCTATGTCCCTTTUGAA
235891398	81938	CTTGCTAATCUCCCAGAGGAAGTUA	81939	CATCATCCCTUCCCCTTTTACTGUT
235892116	81940	AATTCCUGGAGCCCAGUAGGA	81941	CGAGAAGAAGCUGAAGAGCAUGG
235893903	81942	CAAATACAGCAUGAAGGTGTACTAUGGT	81943	GCTTATTGTAGAGCUGAGTCTTCUCA
235894567	81944	CCTCCTGCAACUGGATCATCUC	81945	GGGUGCCAAGCCTCTGUC
235896708	81946	TCTTTCACTTGTGUTTCTTTCTAAGTGUGA	81947	GCCTTGAUACCCTCCCCGTUAT
235896720	81948	ACTATGGATTUGATAAAATTGAGGUGCGA	81949	CCACGAAAACCGUAAGTTGTCAAAUT
235899743	81950	GCACCTGTAAUGGCAATGAAGTACUA	81951	ACCTTACCTCAGCUATACAACAAATUGAC
235900009	81952	GGTTTTCGUGGAGAAGCCTUG	81953	CCATACTTCACCAAAUACTGGGTUAGT
235904102	81954	GGAAGACUCAGAUGCCGAAAACT	81955	TGTCCUCAGCACAGCTUGG
235907293	81956	GGGTCCUCTGTCCACUCA	81957	GACGAGUGGCAUGGAGGT
235914054	81958	AAAGTCAACTTGACUTTTGACTCAATTUG	81959	TCCAGTGTTTAGUATTCATGGCAAUCAT
235916094	81960	AGCCTGCATCUCCACCTTATTATUC	81961	ACCUTGCATCCTUCACAAGCA
235916666	81962	ATGACAAAAGGCUACAGAGCAUAGG	81963	CAGCATCACCACUCGGTAGTUAT
235917102	81964	GGUAAGAACGGUCCCACCAA	81965	GTGACTTCUGCTCTGTGTTUCAAG
235917643	81966	GTGTGUATATGTGTGUGCCAGAGT	81967	GACTUCGGCATGUCCAGAGAT
235918954	81968	CCCATACUGAGCCACCAGGUA	81969	GCCTGTTACUTGGAGTTCCUGAAG
235922099	81970	GGGUAGCTGAUGGCCCAAG	81971	TGTTTCTCTCUCCACCCACCAUA
235924030	81972	CAATAATTACCCCUGTGGGATCGUC	81973	ACAGCTTTTGUCCCGTATGGAAAUT
235927943	81974	GCTCGCCCCCUTAATCTCUT	81975	GGAATAAGATGGCAUTGTAAAACAGUCC
235935034	81976	TCAGCTTCTGAUAAAAGGCGGAAUT	81977	GCTCCCCAGGCUTTTGAGAUAC
235935272	81978	TTTCTTTGAGTCCUCAGTGAAAGCTUAA	81979	CCTTTTAGGAGCCUTTGTGTCTGAUA
235935639	81980	GGAACTCCTUCAGCTCCTCCUT	81981	CTGTTCTCUGCCTGCCTGAUAC
235936473	81982	GAAAGCCTUTATTCTCAACUGCCAAT	81983	ATTCACGTAGGTUGCACAAAGAATTTUT
235938569	81984	GGAACAAGGAAAAGUTTTGATCACTUGA	81985	ACCCATTTCATAAUCAGTTTCTGCUACT
235940833	81986	ATGGAAUCAGGGAUCACAACACC	81987	TGACTTTCATGUACTCTCCCACCUT
235942028	81988	CCTTTGGGTTAUAAATAGTGCACUCAGA	81989	AGGTCAACAGAUTACTGTATAGUGCAAG
235943014	81990	CCCTGTAATAAUCCGTGCTGUAGAC	81991	GCTCCACAUTGCCAGUCAGAT
235948521	81992	ACAGAGTAACAGACUAGCTAGAGACAAUG	81993	AGCACTTACCUGTGACTCCAUAGAA
235951539	81994	CGAGATCCTCUCTCTGAAATCACUGA	81995	GTAAAAACAUGCTGAGAUCAGCCAAAT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
235952365	81996	CCAGCUCCACCAGGAUACAT	81997	CAGAAGUCCTUAAAACAGCAGGAAAG
235955471	81998	CTGGACCACGCUTTCCUG	81999	AGAAAATGGAGGAAGUCACTGAAACAUT
235956752	82000	GGGAGGCCAGGUACACCAUA	82001	CTCTCTTCUCCCCATGCTCTUG
235960673	82002	GAGGCTGCUGATGTCACTCTUA	82003	AGAAGGCCCUGGAUGAAGAGA
235972250	82004	AGAGGCCCAATAUATCCAGAAAATTGUG	82005	TTTTGTGAAAUGGTCGGGUACAGA
235975527	82006	TGUCCAGCCAGCAAAUGAGAG	82007	CAGCAATCUTGACTTCUGGAACAAT
235979011	82008	CGTAACTCTUTTCCAGGCUGAGG	82009	CGAGAAAAUGACTGCCTUCAGGAA
235980602	82010	GTTTCTGCCUCATCTCCUGGAC	82011	AACTGCCAUTCACTGTGTUCCT
235983247	82012	CGAGAAGUAAGTCCCAAAUGGCA	82013	GTTTTGGGAACAUGGTTTTGACCUT
235984107	82014	CTATCACTGUCCCAGGUCAGGA	82015	CTTCAGACCUCAAACCCATCUCA
235985044	82016	CAGTGTGAATUACAGCAAACCCCUA	82017	AATAGCCGTATCUGGAAGGAACTTUAC
235988482	82018	GGCTGAUGCACGATTTGCTUT	82019	GAGCUGGAGGCCCUAAAGAC
235992734	82020	GAAGAAGACCUCAGCAGATGCUT	82021	CACAATTTCUGTGTTTGTUAACCAGAGT
235993981	82022	CACTCCUCGCCAGUCCA	82023	CGCTGUGAGGCUCAGCAT
235995878	82024	CCTGCCCUGTGGCACAUA	82025	CGAAGGCGGAUGGCTCUC
235996736	82026	GGCATCCTUCACCTGCTATTGUT	82027	CUGCTAAGUAGGCCACGCT
235997411	82028	CACAGAGCGUGGCCUACT	82029	TGTGAACTUTCTGCTCUGCCA
235998976	82030	CCAAACCAGUGGTTAGAUGAGAAACT	82031	CAAGAAUTGAUACGCCCAGACC
235999342	82032	GGAGAAAGGACAUTTGTGAUAGGAGAA	82033	GAUTTCTGTACCATUGAGGGCACT
235999363	82034	CTGTGCTGUCCAGTGTGTCUT	82035	AGAAGAACAAUGCCCUGAAGAAGAT
235999576	82036	ACTTCTTTTUCAAGCAGGACGAUCT	82037	CACAAACATUGCAAGCTGAATTUAAACA
236000518	82038	CGTGTCTCCAUCATTCTCAGCUC	82039	GGACCTACTTTTUGATGTTTCTGTGCUA
236003482	82040	GTGACATTCGUGCCTTGCUT	82041	GCUGGAGGACGCCACUG
236003797	82042	CACTCTATGCAUTCATCTTCACGUT	82043	CTCATAAATAGAUCATGGTTCCCGAUACA
236005921	82044	TGAAUGAGACGUCCCACCAAG	82045	CAGAGCAUCAACCGAAACAAGTUAAAA
236009437	82046	ACAGCTTTGTUTGCACTGTTGUT	82047	CCCACGTGUAAATGTAGCCACTUA
236009827	82048	AAAGTCAAGCUGTGTCACTUCCT	82049	TACAATCCACUCATTCTTTTGTCTUCCT
236010692	82050	CATGGCAUCGGCCGUCT	82051	GGGCCACACGUCCATCUC
236012201	82052	AGCTCTGUTCAGAAAUGGCAGT	82053	TGCTATGTCTTCCUGAAAAGGGAATUT
236012554	82054	CCUCACACAGGAAAAUGGGAGT	82055	ACCUCCCCAACACCUACAAGT
236012826	82056	CTCCTGGAGGUCTGAGATGUG	82057	ACTGTCTGGUCCCAGAAAAGTTUT
236015033	82058	CGGCCCTUACCCTGAGUG	82059	AGGGCCCCUCGTTCUGT
236019764	82060	GCCGCTCATAUTCATTTCTCATCUG	82061	TUGGGUCAAAGAAGGGCACT
236020284	82062	GGATTCTCUCAAGCATCTTCAGTTUCT	82063	TCCTGGGAGCUGAAGAAUCAGAT
236020792	82064	CCACTTCCCAUAGCCACGUT	82065	GGAGGAACUCACCGACCTTUG
236024721	82066	CATTAGCTGTUCCTGAAGCTGACUA	82067	GGAAGUACAGGGACGAGCUCT
236025900	82068	TGGCCACAGAUTCTCCAGCUA	82069	CATCAGTUAAAACAAGGTTGTGCUCA
236028696	82070	AAATAATGAAGTGUGAGGCTGCCTUA	82071	AATGATGCACATAUCCTGGAGAAGTUAC
236031502	82072	TCCTCCAAGCUCAACATGUGG	82073	CTTACACACAGGUGAGCACUGT
236034284	82074	CCAGTGGCUGCACGUCT	82075	ACUTACAGAUGCAGCAGCAGAA
236037082	82076	CTTTGCTGCUGCTGGATGTUT	82077	GCTGCACAGUAGCCTUGCT
236039709	82078	TCTGTCUAGAAACACGGGACUGA	82079	GCACGAUTCCTUCCAACCCA
236040694	82080	GGTTCAACGGCUTCTCACUCA	82081	GCTGAGGGCUCTTAACUACACC
236042712	82082	ACCUTCCTTGAUCCAAACAGAAAGAT	82083	CCAGAGTCACGAUTTCTTTCATTTTGUT
236042835	82084	TGGTAGCUCATCATCUGGGACA	82085	GCAUGGUGCCGAACCAA
236043910	82086	CCCCGCAGAGGGUTGUA	82087	TCTCUCCCACCTGCCUGT
236044556	82088	AGTTGCAAATATAUGTCTTCCACCCUT	82089	GCTTCAGUGTCAGGGTUCCA
236048289	82090	CUGGTGTUGAGGAAGCCAGA	82091	AGGTAGCAATUGTTACATGAGCTUGT
236049186	82092	CTGAGCACAGUGCTGGAGUA	82093	AGCATGCAGCCAAUCCAGAUAG
236053466	82094	CAGTAGGCAGAGCUGCTGUC	82095	AACTTTCTCUGCTGGCCUAAAAGAA
236053538	82096	GCTGCCGGGUGGTGAUG	82097	TCCATACAGCUATGGTCCACUGA
236053758	82098	AGTGGCCCUGTACATGTTTCUG	82099	AGAGGCAAACUCCATGAATGTGTUAT
236054430	82100	TGTGTGTTUGCATGGTCTUAGAAAGT	82101	CGAGTGACAAUACACAGCATCAAUC
236057679	82102	CAGTCUGCCTCTGGTUACCAAT	82103	GAUGACTGCCCUAACCACAGG
236058540	82104	CTGAGATGGGUAATGATGTCTUCCA	82105	GCCAACCCTUTATCCTTCCTCUCT
236061864	82106	CTTCACACUGCGCUGAGAGAT	82107	CGTCTCCUGGCTGTGTATGTUG
236064411	82108	GGCAGTCAAACCUTCTCTCTTATGUA	82109	CTCTTCAAUCACTGACATATCUGGGAAC
236067958	82110	GAAGCCAAAGGGAAAUGCACAAUT	82111	TGGAGGCUGTATTCAGCUACCT
236069946	82112	GCAGGCAGAAACCAUGTAAUCC	82113	GGTUCCAAGAGAAGAAGAGCUACCT
236070143	82114	ACTGGTUCAGCAGTGTGGUAAA	82115	ACTCAGTGATTUGCCTTACCAGUC
236070736	82116	CCCGAGAAGCAGGAUTTAGCTATUC	82117	GGTCCTAGAGUTCATAGTATCTAUGCCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236072010	82118	CTCAGAACCAACACUGGTGCTUA	82119	TTTGCTTTTCUGAGTACACACCAUAGAT
236072083	82120	TGAAGTGTCAGUGCATAACCTCTUG	82121	CCAUGTGCTTUGAGGCAGACT
236072329	82122	CGCATTGGAUTGGTGGCCUAA	82123	AAGGAGGTGAGAUTCAAAATTCGUGAT
236077162	82124	CAATGGAGAACUTATAGCTGUGCAAAG	82125	CCATCAACTUACAGACCTAAAAGACUGA
236081261	82126	CACAAACCCCUCCATTCUGACA	82127	CAGGTCGTTTCUTCTGTATGAGATTUC
236085027	82128	CATCATCAAAGUCCCCGCUGA	82129	GTAGCAGGUGTCCAGCUGAAG
236086000	82130	CTCACTGAUCCTTTTGCCTGUG	82131	CCAGCTAAAUGAACCCCGUGAAT
236088874	82132	GAAGCCCACCCCACUCUAC	82133	TCCCUAGCAAAUACCAAAGGCAA
236092939	82134	GTTATACTUGCCTCTGCUGAGCAT	82135	CTGCCTGUCCCCTATGAUCAC
236093811	82136	GGCTCACUGAACCATATCCCTTTUA	82137	GGGAUCTGAAAATUCCCAACGGT
236097291	82138	GAGACTCUGCACATGTTCUGAGA	82139	CTAACTGTGCCAUTGCATTCTGAATUAT
236100338	82140	TCTTCTTCGCUCCAGAATTTGAAUGT	82141	TGAAGTTGTTGUAAGACTTTGTCTCGUA
236100522	82142	GUGCTTACTAGTUCCAAAGGCAGT	82143	GGTACCACAACUGGCTTGTTUG
236103901	82144	GCCTGCTGCAUTTCCTTTATTTTACUC	82145	TGGAAAGACUAGAAATGGAACAUGACC
236106254	82146	CTGGAAGUGGCUGGAGAAGAC	82147	AATATGTTTUCCCTCCCTUCAGGAAC
236108869	82148	TCAAAGAUACCAGAAAAGCCACGUT	82149	CTCACGGAAAUAACTGAGAUCACCA
236111424	82150	GTCCAUCCAAGGCAUCCGAAT	82151	GGCCCTTGAAAAUGAACTTTTGGUT
236113776	82152	CTCTTGTTUCAGCCCACGTCUA	82153	AAGTGACGCUTTCCAGACTUG
236117111	82154	GGACATCATUTCCTGCCTTUCCT	82155	CAGATACTTGAGCUGAAGAGCAGUC
236118403	82156	GGTCTGTUACTCGGCAUGGAA	82157	CCTGATTTATUCACGGCTCCACUC
236120687	82158	TGGCTTATUGGCAATGCCTCUT	82159	GCGTAAGCAUGGCTCTCTCUG
236121503	82160	AGCTTTAGAAGCUGTTTGTACACTGUAT	82161	TGTTGGCAGTTUTAAAGACCTCTTUGA
236130391	82162	ATGACTATGAUGGGCTGCTUCC	82163	GCTTGAGCACCUGTAGTTTAGTUGAAAT
236135209	82164	GCTCCCUCAGTTCCCTTTUGT	82165	GAGAGAGAGAUGCUGGAGAAAACAT
236139599	82166	CCTGGTGAAUGCTGTTCTUGGT	82167	TGAATTTACGCCUTGCTCTGATTTCUA
236140634	82168	GAGGUTTGAAATGUGAAAAGACAGGAA	82169	GCCACCACUCTGATACTCCUACC
236144827	82170	CGAAGAGUGAAACCTUCAGGCA	82171	CCCTGTCUCTGTGGACTTUCAG
236148340	82172	CCTCCCTAUCCTTCCCTGTUGT	82173	CGTTGAGATUGAATTCTGTGTGUGG
236152793	82174	GTGATTUCAACCCCCTTACUGGA	82175	GTTGAGUACGTTGTUGGAAGGAAAA
236157757	82176	GACCATGCTGUTCAAATGTTCTTUGT	82177	GCGTGAGGAGAAAUCCCAGUG
236159641	82178	CCTTCAAGAUAGCCATUGGGCAA	82179	GTAAAGGCAGCCUTGGUGAAGA
236160438	82180	GATCATTUTCAATCAGAAUGGCACAGT	82181	TGTTCGTGTACAUGTGTATGTGTCTAUC
236162756	82182	GCTGAAACUTGACTUCACACCAA	82183	CAGTGAAGUGATGCTGUCCAC
236163715	82184	TGAGCTCGUCCTTCTCAAATUCC	82185	GCCCAGTTUCAGTCTGATTGUCA
236165362	82186	ACTCACTTTCTGUTCAACCTCGAUT	82187	CGTTACACTGUGTCTGGGTCUG
236167611	82188	GATCUCACCCAGGAACTGGUC	82189	TGTCTGCCUCTCCCTCTTCUT
236170473	82190	CGGTAATACTTGCUAGTGGGATTTCUC	82191	GCACTCTAATTUCAGCTACCAAGTTTCUA
236172524	82192	GAGCACTCUCCTCACTACTTTUCAA	82193	GGUAATTCUCACCAGCCAGAGAAG
236173397	82194	TTAACCATGCAGAUCCTCAGTTUGT	82195	AGCATCTTGUTCTGTTTGUGGAAGA
236174169	82196	AGAGCCUGACCCAAUCCGA	82197	GGTTGATCCTTUGATGCCCTCATUAT
236175521	82198	CTTACUCGCAGTCGUACAAGAGG	82199	TGCTATTCAGCCAAGUTAAACTCAGUT
236178457	82200	GTGGTGATAUCAAAGTAGAGTTCTUCCA	82201	AGCAAAACACCUGCAGATCTAAUAGAAAA
236181961	82202	AACAATTTTGGCCUGTGGACTCUA	82203	AAAGAATTCUCGTCCACCUGCT
236182614	82204	TTGAGGGATGAUTCAAAGGTGGTUT	82205	TGCATCACUACACCUCAAAAGGG
236182835	82206	GGAGTATTUCCAGCATCCCUGAAC	82207	CTCCCTTAATCAUTGTTCCCTATGTUCT
236184850	82208	CCATUACAAAGAAAGCCGGACUCT	82209	CCTGGTGGGUCCATTTCTATAUAAAACAT
236186027	82210	GACAGATATAAATUGTGGCACAGACTUG	82211	CAAAAAGGATCTUTTACAGTAGCTTUCGA
236190837	82212	AGGTCGAUCTAGTGCUCAGAACA	82213	GCAACTCAGCAUGTCCACCUC
236194072	82214	CUCCCAGGGCCACGUAA	82215	CGCAGAUGCCAACAUCCAG
236195969	82216	GTGCGGCCCAUGTTGUC	82217	CGTCATCUCCGACTTCATCUACCA
236198019	82218	GTGCGGUCTGTCTGGTUGT	82219	CAGACUGAGCACCCGUCT
236199404	82220	GTGGCAGCUCCAGTAAUAGAGAAC	82221	GUCAAGAGUCCAGACAACAGAAGA
236201541	82222	CCATTCACACCAUGCACATATGAUT	82223	CCTGTTUGCGCACTTTCATCTUC
236201712	82224	TGTTTTCTTUCCTGCCGUCCT	82225	TGTCAGATAGTCACUCCGTTTACAATUT
236202098	82226	CCCTTGGCUCAGTCAGAACUT	82227	TGCUCAAATACUGAGACCCCAAC
236207033	82228	CAGGTUGTACTCGUCCAGCA	82229	GGAGGAGACACCCCUGTTUCT
236207114	82230	CCTGAAGCAGUCCAGGACTTAUG	82231	AGAAATGTATGGUCAGAAAACACTGUGA
236213226	82232	CACCTUGGCGGTCTCGUA	82233	CTTCCTCTGGUGATGGAACCTUG
236214556	82234	TGACUCAAGGGTUCAACACAAACT	82235	CAATTTGUAGAGGCUGCAGCAC
236216934	82236	CAGCAACACUTTAAATGGACUGGAA	82237	GACAACAGCAACAGCAUCTGTUAA
236218670	82238	ACCTGGGUCCCCTCCCTAUA	82239	GAAGAGGCUGGTAGCTGACUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236220075	82240	TCGTCCTCTTTUAGGACTCACTTTUAGA	82241	CCATCGAATTAAACUTTGAGTGCCUACT
236222301	82242	GATTTGTTGCAGGUTTTGGTTTTAAUGG	82243	TGTGTGTTCTUAAAGCAGGCATACUAAT
236223903	82244	GUTCAAAAUCAAAGGAAGCCCAGA	82245	CAAACTGCCAAUTCAAGCCTCTUAA
236227221	82246	GGCACATGUGTACCCCTTGUT	82247	GAATGACAACAUCGCCACACUG
236227630	82248	CCTTTTGAATGACUGCAGTGAAGUT	82249	CACTGTCTACGUTGGCATTGAGUA
236231008	82250	GCCACAACCCUTACCCUAGGA	82251	CTACACAGGCAGCUACTGUGA
236233222	82252	GTGAGCACUCGUCCACCA	82253	CTGGGCCUCACCTGTCUAC
236236010	82254	CCTTGTTCATGAUCAGTGGATGTAAUCT	82255	GCCATCATUGGGTTCATGTTCUGAA
236238761	82256	CTCTTTCTGCUGTTCACTCUCGT	82257	GCTTTATTCUGCAGCCAACTUGAAA
236240960	82258	CAGCUCCGAGACAAACTTGUCA	82259	GAGACCCUGUGAGCACACAT
236245499	82260	AGACCGGTUGGCTAAATCAUGG	82261	AGATGATGTUCCCGTGTCTTUCAG
236246420	82262	TGCAGAUGAAGCCTTAAAUAAAGACAAGA	82263	CCCCAUCACCCTAACATAAAUAACAACT
236250927	82264	GGATGTCCUTCAGCTGUCACA	82265	CCGAAUGGCACAUACACAGAGT
236252383	82266	ACTGTGAAGTCUGACCCCTAAAGUA	82267	TTGCTGGAACTUTTCCAATGTTGTUT
236252415	82268	TGTACGGUCCTTGCAATGUCA	82269	CTCTTACATGCCAGUTCTCTAGGTUT
236253255	82270	GAGCACAAGGAGUACACAGTATUCA	82271	CACTUGGCAGAACUCCAGGAA
236253784	82272	AAGAGCAGGUAAGCCCTTUGG	82273	GACGTGGTGCUATGAACATAAGTTUAAT
236254926	82274	GCCTCGGUCCCAATCTCUT	82275	GGACCAGCCUAATTTCTTATCGTCUC
236255129	82276	GCCTCTCTUCCTTTACTTTCTUCACA	82277	AGCTCAGCTGUTTTCTTTCCCTUAG
236255845	82278	CCAUGCTAGCCTTUAAAAAGAACCC	82279	GACTGCUCACAGAAGGAATAUGCT
236259532	82280	AATTTCTTGGCAUAACCAGCCATTUC	82281	GTUGACAAGCAAGCCATCAUCAAT
236261891	82282	TGTTACCCAUCTTTGCTTTCUCCA	82283	TGTTGTACUGCTGGATGTTUCGT
236262341	82284	GCTTCTTTCTCAUGTTGGCCTTUC	82285	TGCTTTUCCCCCAAGATTATAATUCCAT
236264855	82286	CATGGCAGGUGGAAATACGAAUG	82287	TCAGAATTAACUGTGATGTGGTGUGG
236268705	82288	TCAAAGGTACAUGAGAAAGGTGAAUCAA	82289	CACCACTGAGCAAAUGTTTGAAATTAUGT
236272952	82290	CCACCCTCUGGAGCTTCTGUA	82291	CTCCTTGTGATTGUGATTTCTACTCTCUT
236273997	82292	CCTGAGACUGTTGCATCAUGGG	82293	ACAGTCTCTTTUGGATTTCTGTTTCUGT
236283564	82294	AGCTGTGAGUTGCATGAGGUC	82295	GAGGAGATUTTGGATGATTUGCAGAAT
236286849	82296	GAGCCUGGACTCCCCUCT	82297	GAUGAGACCTUGGCCAAAGAGAA
236287132	82298	CCCATGCUCAGACATCCUCAA	82299	GTTTGCAUGAGTGAAGCAUGGAT
236293900	82300	CAAGGAGAUGGAACAGGUAGCA	82301	CCTCTGACAGGAUGATCTGACTCAUAAA
236294835	82302	TGGGAAAAGCUGTGGTAATUGACT	82303	GGGCTTGTGGUGTCTACTCTUAGA
236296564	82304	AAAAAGTCATUCCTTGTCCUCCGT	82305	CTCACTGAGCAGGUACATTACAUGA
236296853	82306	TGGCCTCTGUTTGCTGGATTUT	82307	TTTCTTCCTUGCCGTTTCTTCCUA
236298246	82308	GAGCCCCACACAGAUTTCCUAT	82309	CGAGACATCAUGCGGGACUC
236300614	82310	CATGAGGACACUGCUGACCT	82311	CCCTCCACCCUAACTCCTCAUC
236308354	82312	CCGATCAUCCCGATTCAUGCC	82313	GATGGGAUGGGCCTGTATTCUT
236310760	82314	CAGCTTCAGGGUATATCATGGTAAAAUGT	82315	GCGACCAUGAACACACTCTTTAATUT
236311791	82316	GGACATCCTUCCGGCAAGUC	82317	GCAGCUTGCTGAUGAGAGAAGT
236311842	82318	CGCTGCCTTUGGAGATGTAATUC	82319	TTTCCCCACAAUTGUCCCCAA
236314691	82320	CCCGUCCCAGGCTTCUC	82321	GCUCCGAGCCAUGCAGAA
236314777	82322	AGAATGAAGCACCAGUTTGGAAAUG	82323	CTCATGCTGTTTUATGACAGAACCAAUT
236315401	82324	GACCTCCCGAUAAAACGCTACUT	82325	TCATTAATCCCAGCGCUTTCTACAUC
236317926	82326	GCTTTTCATTTTUGCTGTGCTCCUAT	82327	GAGAGCUGGTTGCAGUAGAGG
236319071	82328	TGAAUTCAUGACCACCAGCCA	82329	CCCCAAAGAGGUGTACGAUGT
236321132	82330	GCUGGTCCUCAGAAAACCGA	82331	GGAAGCUGTGGUAGAGGAAGGAT
236323750	82332	CCCCTTGCTUCGAAAGACAGUT	82333	GUGATUAAGGCCCAACACCCA
236324463	82334	ATGAUCCCGCACUGAGACAC	82335	GTACATTTGACAGCUCTGGGCTUA
236326670	82336	GCCTCAAAAAUGACAATGUGCAGA	82337	GTCCCAAGGGUTGTTTCTCTTCUA
236328456	82338	CAGGGACUGCACUCACCAA	82339	CCCTGACCACUGCTTTTCCTTTUA
236331089	82340	CAGCTCCAGCUCATCCCTAUT	82341	CCAATGCATAUGGGCCTTCUCC
236333256	82342	TGACCCAAGCCGUCAGGUA	82343	CCCCCAACCCCAUTCUCAAAG
236334375	82344	GATTCTTTTGCUGTGGGATCUGAGA	82345	CTGCCAUAACAGGGCTCCAUAAA
236336144	82346	GATGTUCAACCGCTGCTGUG	82347	AAGGCTGAGCUTTGGGTGUAA
236338744	82348	GAAAAGCACCCAGAGAUATTTGUGAAC	82349	AGGAAUGCCCTGUCCAGACT
236340208	82350	GAGCUCCCCGAAAGAGTAGUC	82351	TTGATGCACCAUAAGACCTTTCUGT
236340778	82352	CGGCCAUGCAGAAACUGAC	82353	AUGCCAAAAGAAAAAGUGCCCAAT
236341395	82354	CTCACCCGUGAGCUGAGAA	82355	CAAGAACAAGCAUGAGGCAAUGAT
236352526	82356	AGTTTAAACATUTGCTGAGCUCAACAG	82357	CCAACCCCCUAAATGGGCAATAUA
236352665	82358	CCCTCACCUTCCAAGTCAGUG	82359	CCAACACTAAAUGCCAGCCUACT
236352716	82360	CCTTGCTUCGGCCTCAGTUA	82361	GGGCTGAAGAAAGUGATAATTTGCTUAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236354637	82362	GGTTCUCCAGAGAGCTGTGTUT	82363	GCATTTCTAGCUCTGTGACACUCA
236356680	82364	CCTCCTUCGGGCACCUCT	82365	GCTUCACGGGCAGCUACT
236358602	82366	GCACTCAUTGACATCGUGCT	82367	CACCAAUGCCCTCCACUCA
236360765	82368	TGTCATGGAAGAAAUGTTGGAUAAAGCA	82369	ATGGATCCUCCTCCACUCACAT
236362649	82370	GGGTCCCUCAGGTACCAUCA	82371	TGTTTTCTACGUTGTTGTCATUGCAG
236363213	82372	GCUGAAAGCCTUCACAAGACCAT	82373	CCAGGCCAGAAUTGCTTCUCT
236363607	82374	CAGCCCCUTTGTAGCCTUGT	82375	GACATTTTCTCUTAGTTGTCCTTUGCC
236364596	82376	AAAAGCCTTCTAAAGUGACTGACACTUA	82377	CTGGACAGGCAUCTTTGTTUGG
236365247	82378	CTGAGATGCACAAUAAAACAGTUAGCC	82379	GTTTCATCCTUCTTCTCCTGTTUGAGA
236368953	82380	GGGTCAGAGUTGAGATGGGAUA	82381	GAGGACTUCCTGCCTUCCAC
236369236	82382	CGGAGUTTTGGAAUAGAGGACAAAG	82383	CCTGTAAACUGAAGGCGGCUA
236372734	82384	GCAAAATAATGAUGTGCCAGTCTUCA	82385	TCATGGCCUGCTCTCATCUCT
236374135	82386	GTGGGATGTATTUGAAGCACCTGAAUA	82387	TCTCAAACACAAACUAGAGUCACACAC
236378571	82388	CCCTCCAATCUTAGGTTGGTTGTUC	82389	GUAACTGACCTCUGGCACAACAT
236380415	82390	GGAATGGAUCAACATGACUGGCT	82391	GTGTATCTGCGUTTCCCTCUGAA
236380636	82392	CAAGTAGUAAAGACAACAGGGACTUCAG	82393	CATCTCTUCCCCCTCCTGTTTUAG
236384813	82394	GCTGGCTCUAAATCCCACCUAA	82395	GATCCTCUGGGAGATCTUCACCT
236385605	82396	CAGTCAGUGAACGTAAGGGTUCT	82397	CAGATCCTTAACAUTGGTCCGTATTUGA
236386263	82398	GGGAAGCUGCACGCUGAT	82399	TGAAGACCCCUCCCAAGCUA
236386925	82400	TGGCCCCCAUGCTAATTUGA	82401	GGTGTCTGACUGTGACTTCUCCT
236387002	82402	TGAAAAGATCATGUCAGGACTGCUT	82403	CAAGGCAAUGAUGCCACAGT
236389810	82404	CTGAGACUCAGGCACUGACAA	82405	GAACCTGCTTUGATGACATAAGUGG
236390124	82406	TCTAACCAAACCUGCAACACUAAAACT	82407	CAGTTGCUGCAAACTGGTTUAAGA
236390724	82408	GCAGATACACCUGTCAGCAAAUT	82409	GTUAAATAGCATTGGAUACAGAGCAGGA
236393544	82410	TGTTGATTGGUAGCAGAAAGUGAAACT	82411	AAAGCCTGCCUACTTAAGATCAATTUACT
236394283	82412	CCATCAGUAGCATCACCCUCT	82413	TCCTTTTCTTGTUCCCTACCTCTTTUT
236394928	82414	CUGACAGUAAAAGGAAAAGCAACCA	82415	GAGGACCCAGGUAUGCAAGAAG
236397974	82416	TCCTGCTCTGUATCCAATGCTATTUAAC	82417	AGGCTTATTUCAAACAAGTCACTCTATUCA
236399890	82418	TGATACACCAAAAUCGGCAAGCUA	82419	ACTAATGACGTCUGGTTTTCTCACAUT
236400355	82420	AGCACACAGUGGCAAGTGUAG	82421	TGAGGCTGUCAGAAAGTTTTACTGTUT
236401388	82422	ACGACCTUTTGATAAGAUGGCAACA	82423	CTTCUCAACCAAAAAGAAAGCAAUCAAC
236401551	82424	GGAAAAGUGAUCACCCGGGAA	82425	CCCTGATCTGUCTTCTGTTTCUCAAAG
236402038	82426	ACAATTGGAACTUACTTAGCTACTGCUT	82427	TTGAGCTACAATAGUATAATGGCCACUG
236403266	82428	CAACAGAACUCTGTAGCTUCCCA	82429	TCCAGTCAGAGCUACAAATCUACGA
236405706	82430	GGCTGAAACGUTCTGCCUCA	82431	CCAGAGCATGUGCAAGAGATACTUAC
236409008	82432	CTCCUGAGGAGAUGGAGAAGGA	82433	CATCTGCATTTGGUTCTAGCAACAAUAC
236410744	82434	CCCTGAGAUCAGCUGGAGAAGT	82435	CCAGCGCAUCGTAGACCUG
236410986	82436	CUGATCCGTGCUAAGGAAGAAGA	82437	AGACACTCATCUACAGAGCTAGCATUAT
236416748	82438	GGAACCAUGGCTGCTTUCCAT	82439	GTGCCTCTATCUCAACCCCTTTUAG
236417817	82440	TCTTGGAATUGCCATAAAGUGCCT	82441	GCTCTGGUGTGGCTGAGUA
236418816	82442	TGAATTUCCAAAGAGGCCUCCA	82443	GCCTTTTCATTUGGTCATCTTACGUAGA
236419237	82444	TUGGGCACGCUAGAGGA	82445	GCATTCTUGAAAAGGGAAUACAGCAA
236422771	82446	GATGUCGCAGGGCCTUACA	82447	CCACCCAAACUCCTACCUGAC
236423262	82448	ACTTACCUGAAGGCGGGCUA	82449	CCTTCCCTCUGACTCCACCTUT
236427857	82450	AAAGCCGUGATAUGAAGCCACT	82451	AUGTGTCCAUGGCGACCAA
236432186	82452	ACAGTCCUCCCAATCUGAAGAGT	82453	ACCAAATTUAGCCGTUGGCAGA
236433598	82454	ATTACTTACTAATTAAUCATGGCCAACTCATUT	82455	CAAAGGAAGAUACCGACCAUGAAGA
236434332	82456	AGAACATACCUCATTGCTGGCTTUT	82457	ATTAATAGAGUTGATTGCUCACAGGCA
236437547	82458	ATTTTCTACTCTGCUCATAATGCGTCUT	82459	CAGTAGGUTTTCTGCCUCCACA
236438905	82460	TCATCTGGTUCATGCTGCUCAT	82461	ACCAGCAAGCUGTAACATTCATUCA
236449038	82462	CACTGTTCCUCTCCTCTCCCUA	82463	TGAACTTGUCAGCCACCAUGT
236449228	82464	TCATGTAAGCUTAAACAGCGUGGT	82465	TGCTGAAGTTUTGGCAGGTTTUC
236452546	82466	AGATGGTTUCACCCAAATATCACUGG	82467	ACACTCTCAGGAUCCTCTCTTTTCAUT
236455510	82468	GAAGCTAGAAGAUCCTTACTAGTCUGAAGA	82469	AGCTTGCAUGACTGCCTTAUGAA
236455604	82470	CTGCTGAATGAUACTCTCTTGTUCCT	82471	GACTGATTATTGCUCTCTTTATGGCTGUA
236457248	82472	CCAGGGTTUAGGACTGATGUGT	82473	GGACGGCAUCAATGGCTUCA
236459549	82474	TGCTGTTTGGUAACTTGAGTATATCUGG	82475	TGTTTTGGGUACACTCCAGTTGAUG
236460622	82476	GGACAGAAGGUTGGCTUGAGAA	82477	AAATCAGTAAGUTACCTGCTUGGCT
236461297	82478	GGGAAGUGAAAGAACTTGAAAGATUCA	82479	CTGTGATTTGGCUTCCATCAATUCC
236462084	82480	GCCGCUGAAGACAAGTCCUG	82481	CCAATGGTUCCATCGGCCUAA
236462274	82482	CUCATTGACCUCAGACAGGCA	82483	CCUGCCCTUAGGGAGCAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236462348	82484	CCGCCCCUCCCACAUAG	82485	CAGGUCCCAACUGCCAGA
236466406	82486	CAGCCUGAAGAAGGAGATGGUG	82487	CCTATCCTAGUCCTGTCATGGGUAT
236466569	82488	CACACTCAUCGATGTTGATGTUACAC	82489	GGTTTCUGACACCUGGAAGGAT
236468092	82490	TGGGAAAAUACAACACUGCCCAT	82491	GGCCAAUGGCATGGAGTTUCT
236470262	82492	TTGGGCCAGUTCAATTGTCTUACT	82493	ACAAGCAATGAGUTACAAAATCGACTTUC
236471982	82494	GACGCACACUCGTTGATGTUG	82495	TCTGGCUCTTGGAGAUGAGGAG
236472349	82496	TGGAGAAGUCTGAACACUGCAC	82497	TTATTTCTGUGCCCACCTTUCCA
236474471	82498	CAACCAAAGGACACAAUGAGATTAGAUG	82499	AGCUGAGAGAAAAUAAAACCCCAGAG
236474903	82500	TGCGTTCTCTTUTCAAAACTGTTTTUCA	82501	AACAAAGCAAGUCATGCATTTTCCUAAA
236478867	82502	CACCACACGUACGTTCTUGGA	82503	GTGACCCTCUGCTTCTCCTCUA
236487854	82504	TGCAGCUGAACTTCGGAATUCT	82505	TCATATTACTTCAGUAGTCCCATGUGGA
236488329	82506	TCATCCAAGGTUTTCATCTTGACTTUGT	82507	CCTCTAACTGACAUGCATGGAGATAGUA
236495108	82508	TGTGGTCTAAUGCATTCAACTAUCCAA	82509	GCCCTCUAGCAGTCTGGTUAC
236495223	82510	CATACCCATCUCCTAACGGCTUT	82511	AGCTCTTTCTUTGGCTTCTCUGG
236498026	82512	TTGCTGTTCTTTUTGGCTTCATTTGUA	82513	CCTTTTGGACTUACATTGGTGATGATUC
236499063	82514	TGGCTCAGAATUCACCTTCTACATUT	82515	AACCTTTTUGAAAACCAAGAGUGCAT
236503284	82516	CCCCAGUCTGTCUCCAAACC	82517	GGGAGGTUAGTGAACTTGCUGAC
236505138	82518	TCAAUGCAGCCAGCGCUAA	82519	GGGAUCCACTGUGAGAACAACAC
236507124	82520	CATGCCCCAAGCUCCUAGT	82521	GCUGCAGCAAAGAAGAAGCUG
236507235	82522	CACACCTCUCTGTGCAGUCA	82523	GCACTTTCTGUGAGGAGGACAUC
236510532	82524	CAAGTCATGCUGTTTACATTCACUAAGG	82525	CACCCATTGAGUCATTCACTTTUAAAGAA
236510920	82526	GAUAGCTTCCUGAGCCACCAC	82527	GCCUGTAAGATAATGAUAGACAGCAACA
236511370	82528	GGTCACUGGCACACTCGUT	82529	CTCACACUCACCCTUCCGT
236511584	82530	CCCATUACCAGCACTTCAGUACC	82531	GAGCATTATTTGUGCCAGACTTGTTTUA
236511685	82532	GGGACCACCUTTGTCTTUCGAG	82533	CACACACTUCCAACCTTATTTAATGCUT
236512430	82534	GGGATAGGUGAAGGGCCTTUT	82535	ACACTTAGAGCUCAGACTGACCTUT
236513303	82536	GCCTGAAGCUCCAGGTCTTUC	82537	GGGCAGCACACAUCTCTATUCC
236513480	82538	TGATTTTCATTTTCUGTAGGCATGGUGA	82539	TGCTTCAAAGCCUTTCCTTCACTUA
236514340	82540	CCTTTGGAGCAUATCCATTATTGACUGA	82541	GGAAGCUAGGTTGAUAACAGAAGAGAAT
236516677	82542	TGTTATTCCTGTAUCAACAACACACGUT	82543	CATAAGAAATTGAGUTCCGCAGTTGUC
236516996	82544	CTCTTCTGTTAUCAACCTAGCTUCCC	82545	AGTAGCACCAAGUCTTCTTGAATUGT
236518302	82546	AGGAGTGUGCTGTTGUGCAA	82547	CTGAAGATCAUGAGTCACCTUGGG
236520959	82548	CCCAACAGGUTGACCACGUT	82549	GAGTCAGAAUAGGCTCCTGUGG
236520987	82550	TGTCATCAAGAAGAUTCTAATTGGCCUT	82551	GCATCCAAATUGCAAACACAGTUCA
236521449	82552	AACAGGTTCACUGGTTTGTTGATTUG	82553	CCCTGAACCACACUTCAACCTUAA
236522963	82554	AAATGAGACTAUAACTCTCTACUAAGAAGAACT	82555	GGAAGAGCATUAAGAAGTTGGTTTUGAA
236524480	82556	GGCATGTGTTUCTACAGAGCTGAUT	82557	ACTAAACAAUTCGACAGTUCAGGCA
236525354	82558	ACGATUAACAGGAGAAAAGAGATUGCT	82559	AGTUGAGCAGAAGUGCACCAT
236526400	82560	CTTTGAAAUAACACCACCAGTGGUC	82561	GCAACTGCACUAAAGAGGACAAACUAA
236527079	82562	ACAGTGTTAGAAAAAUGTGGCTCUCAT	82563	CAGGGACCTGUTTTTAGGTACTGUAAA
236528189	82564	TGGCUACGACCCAGTUACCAT	82565	CCACTGGTCTAUAATCCAGATGATTCUT
236528386	82566	CCCCCAACCCGGUCAUC	82567	GGACUGGGCGGUGGAAC
236528446	82568	GGTUCCACCGCCCAGUC	82569	GCGCUTGTUCACGGGAAA
236529710	82570	GACCACAAGGCCCUCAGUA	82571	AGACAUACGAGCACUAACAAAGGG
236530876	82572	AGAAGAUGAAGACAATGTTCUCAAAGCA	82573	CCAAAGATGACAGUTTTTCAGTGAAUGA
236533874	82574	TCCTTAGAAGUACACCUGAGAAGAAACA	82575	CCACAGAGCAAGAAAAAUTGAGCTUAA
236535492	82576	CTTGACATTTAATUGAAGCGCAGGUT	82577	CACATTCTTTTCAAUGGCTTTGGCUA
236536646	82578	CAGTCAGAGGCGCUATGTGTATTATTAUA	82579	ACATGGAAGGAUGAGAATTUCAAGCA
236539485	82580	GAGCCCCCAGUGCTTTUCT	82581	GAGUCCCAGCGCAUCAAC
236541239	82582	AGTTGTGCUGTTGCTGAUGGA	82583	CTTCTCTTGAUCTCTTTTCUCGGACA
236543000	82584	GCAGCTUCCTGCGGTUG	82585	CCTAACCACCCCUCCAACUCT
236543106	82586	AGATTACAAGACAAUGGCCGCUT	82587	GGATCACACCCUTACTTGAAAAATAGUG
236544179	82588	TGCTUGAAGGAGAGGAAAUGCAA	82589	CCGCCUACGACAAGCUG
236544422	82590	GGTAAACTTCUGTGGTTCTCTTAUAACGA	82591	CCATTACCTUGGGATCGTGUACAAA
236544450	82592	TTGCAGGGUGGTATGTGGTUT	82593	GCCCUCAAGGCTCCTAUGAAAAAG
236547781	82594	GTGCTTTTTGAUGCTTTTGTTTATUGAG	82595	CCAGCAGCUCUCAGGGA
236548198	82596	GGGAAGATTTAGUGAGGAAGTGCATTUA	82597	AGATAAGGGUTAATGAAAATAATUGAGAGAGAA
236548237	82598	CCAGGAAATGAAAUAGAAACAGGACCUT	82599	AGAGGCUCACCAGCAAACUC
236554257	82600	GCCGCGUCTTGGTCTTCUC	82601	CCAGGUGGCCGACAUGAA
236555372	82602	CTTTCTGAAACUGATCACACTCTCUCT	82603	GGCTGGGTGAUTGTATTAGCATTTUT
236558450	82604	ATGTGAAGAGCAUCAGCCTGUT	82605	TGAAAGGAGACGUCAAATAUGCAGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236561258	82606	GCCTCCUAGGATGCAACTCUA	82607	CGAACATCAUCTGGTCUGCCT
236562974	82608	CCACACTGUCCTCCATCTTCTUT	82609	TTCATAACUGGGCAGAUCCCT
236568832	82610	AGCCAGAGGAAAUGGGTTGTUT	82611	GAGCTGTUCGGCATGAUGG
236570762	82612	CCATGTAGUTGGAGGACUCGAT	82613	CTCCTGTGAUGCTCCTTUACCC
236572151	82614	TCTTTTGCAUGCCGGGUGA	82615	CCATAAGTTAGCTUCCACTCTTTCCAUA
236581146	82616	CAGAACCAUCAGGACCCATGUAA	82617	GCTCAGGUTTGGGTUCCACA
236586117	82618	TGCTCACCTUTTGAGGTCTCUG	82619	TCCTAACUCAGTGCTCTCUCCAT
236586583	82620	TTCGTCCAGCAACUTCTGTAGAUG	82621	CGGGCCTTTCTUCATCCATATTACTTUAT
236588734	82622	GCACTGAGCUTGATTCCGAUGAG	82623	TGATCUGAACCGAGGACACCUT
236593112	82624	CCAGTAACTUACCTGTTGTCTUCGG	82625	TCCTGAAGACAUACCAGCTAUGGAA
236594430	82626	CCAAUGGCTTCCTUGAGGAAGT	82627	TGTATCATAGUCCCCATCATGTTCTUCT
236594684	82628	GTTGCTTGGUAGAGCTGCCUA	82629	GTAGCAGGTTGUCTTGAATGTCTUCA
236601663	82630	CTGTGCCCACUCTTGAGTUCT	82631	TTUCCACCCACAGAUCCAAACA
236605072	82632	CAACTTTTUCCCGAAGAAGTAAGACUT	82633	TCAAGACATTTGUTCCCGTGCUA
236607679	82634	GGCTCTGTAUAAGTGGCTTCUGAA	82635	CCTTTGGTGCUTTAGTTTGTTCTATUACT
236608020	82636	ACAAGCACAGGCAUTTACCUACT	82637	TCATTCATGACTAUGCAGATTGGGTUAA
236610199	82638	GGGTGTCCUGCATGTGACUA	82639	CTTCCAUGAGCACCUCCCAT
236611759	82640	GUTTGCTGAATGUGAAGCCCAT	82641	GTGTTCCGUGACAATCTGTCUGA
236613578	82642	GCGCAACCGUATTUAAAGGAGT	82643	CATGGATACAGAAAUGGAGGACTUAGA
236621504	82644	CTGAATATGUGGCTCTGTCCUAGAAAAG	82645	TTCCTTGGGACUTCCTTCTTTGTAUG
236626272	82646	AAGCTGCUCCAGAAAAUGACAGA	82647	GGAAGAAGGGAAAUGTUGGCAGT
236628343	82648	CAGGUAAAGCCATGUAGGGACA	82649	GCATGTTTGAAUGGTGTAGGAGTUC
236630706	82650	CTCCCAGGCACUTGATGATACUC	82651	CATTTCTAGGUTACAGGCCUGGAT
236631350	82652	AGGCAGGAAAAGCAAGUTGAGUA	82653	CAAACUTGUCCCCGAGCGA
236632063	82654	GAACAGCCCCUTGUCGGA	82655	CCCAGUCAGCTGTGTUAAAGGAA
236633461	82656	TTGCTATCAGTTAAUGGAAGTGCTCUT	82657	GCTTTGUGAGAGCCGCUACA
236635075	82658	GTAAGTCCCUGTAGTCCCCUCA	82659	GAGCCACCUCCTCTACUCAGT
236637644	82660	CAGATCUGGCGGATGATCUCT	82661	TGTCTTTTGGATUGTTCGTGCAGUA
236637797	82662	AAAAGGTCAATCUTAGAAAGCTCUCCAA	82663	CATCAGAGAGAACUCCTAATGGGACUAAT
236638986	82664	TCTACGTTGTTUCAGGTGAAAGUGT	82665	ACCATCCAUCCTGTCTGTCUCA
236639674	82666	TCTGGTAAGTCUCCTGATGCTUCT	82667	CAAAGAAAGCCAGAUGAAGACATGAAAUT
236639693	82668	TTCATCTGCUTGTCGCTCUCAT	82669	TTCTCTTUCAGGAAAGTGTGCUGT
236640700	82670	AGUTGCCATAAUCGGGAGAACC	82671	GACTGTACACUGCAACAGATUCAC
236641827	82672	GCTCCUCTGCAGGUAAGGG	82673	CGGCAUCCTGGGCAUCA
236643006	82674	GCCTCTCTTACCUTCGTCTCTCUT	82675	CCUGACCGCCCGTCTTUC
236643853	82676	ACAGAAGTTUAAAAGCCCCATGAAUACT	82677	CCAGTGCTATTUTGATGTTTATGCUCA
236647397	82678	GCAAGCUACAGAAGCATACATCUAAACA	82679	TGUGCATAUCCGGAGGAAAGAAG
236649203	82680	GTGTGGCATGUGATTCTGTAGTUG	82681	CATTCTCACCCUGATACGUCAACAT
236649472	82682	CAAATCTTTGAUAATGAACCCAUCGCAA	82683	CTTGACCAAGAUGTGAAGGTTTCUG
236649993	82684	AGCUGACAGGCAGACCUAGAT	82685	CGAGGGAGAUCCCATCAGGUT
236651142	82686	GGCAGUGGCCACATACTTUCT	82687	CCCAAAGCAAUATATTTGTATUCACCGA
236651988	82688	GCACAGTUGCCAGGCTTAUG	82689	TTTAAAAUGAGGTGTTGUCCCCAGAA
236652232	82690	GTCCCCTGAAGAUGCTAGTAAGTTCUA	82691	CAGATCTTCTACUAGATGAGAGGGTGUC
236655957	82692	TGAGCTCCAGAGGUGTCTGAUAT	82693	CCTAGCTTCTGUCTTAGGTTCATTTUCT
236661574	82694	GGTTTAACTGUCTCCCTCCTUCC	82695	GCCCAAAUAAGCAGCAATGUCA
236664818	82696	GACUAAAACAACCAAACCAAACUCCA	82697	GTCGCACAGAACUCCACUCAA
236666148	82698	CAGCCUGGCAACTCCTACUG	82699	CTTTTATCTCCUCCCCATCUCCCT
236670853	82700	TCTCTTCTATUCCCTTGGCUCACA	82701	TGCUCGAAAGGAATATCUCCACAC
236678229	82702	CCTACCAAGGAGAUGAAAAGUGAGAA	82703	TCATGTTACCACUGTCCCTTTTUGAG
236679736	82704	GGGATCCUGCTGTATGATAUGGT	82705	GAAGACTAAUAGCCCCATUAAGACCAAT
236686923	82706	GGTGGUGAAGGAAAGCACCUT	82707	GCTGTGTCACCUGAGATCTGUG
236695415	82708	ATGTUCACAGCAGUCCCAAGAA	82709	AGGTAGAUGGCAAAGCGGAUG
236695701	82710	GACCCAACAUACACATCCAUACACA	82711	GAUGACACCGAUGCCAACAG
236696430	82712	CTGAAATTTTAAGCUGAGGATGAAUGCAA	82713	CATGAGAGCCAUCTTGTGATCUGA
236698582	82714	AAGAGGCTTAUTCGGCAGGTUT	82715	TGACCCTCUGCTTCTACCTCUG
236699373	82716	CAGTTATTUGGCAGAAAAGCAGAGUA	82717	TGTGAACAGCUTCATGAGTAAAUCAGAA
236703185	82718	GACTCATTGCCACUTGAACCATUG	82719	ACATGAGUGGCCCCCUAGAA
236705068	82720	CCCCCAGGACAAAAUGATUCC	82721	ATCTTCCACCUCACTCCCUCA
236707970	82722	AGCACTAAAAUGAAGATGTGCUACCT	82723	GCACTGCCATTUAATTCACACTTATGUT
236708352	82724	CTGACGCTUGGTTTTTCTGUGT	82725	GAGGTCTGUCTTCTGCTUGGG
236712519	82726	GGACGAGAACCUTGCUGACC	82727	GCACTTCTUTTTGGGACUCAGAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236713033	82728	CGCTGAGGCCCUCCCTUA	82729	TGGATATAATTUCCGAGCGAAGCUG
236716112	82730	TTTCCUAATGCCTUGCAGCCT	82731	CCCACATCATGUCTCATCTTATCAAUGT
236721179	82732	TGCAGAAAGACUTGAAGGCGUAT	82733	CATCACAAAGTAUCTTTTTCTGTGGCUT
236728736	82734	TCCTCGAGCUGTTCCTUCCA	82735	TCTTATCCTUGCTGCTCACGUC
236728810	82736	TCTCTGUGGCCGGGTGUA	82737	CTGACCGTUACCTTTCCTCCUC
236731278	82738	TTGCAGTTTTUAAACCTTTTCCTUCCAT	82739	CCAAGTCTGUCAGCTACTTUCAGAAA
236734860	82740	ACCATGGAUCAGCCAGTCTUG	82741	GGCCAAAGUCACAGATCTUCACAAT
236735027	82742	GCCCACTUCCAAAGCTGTAGUT	82743	GGCAAGCAGCGUTTAGAACTUG
236737901	82744	AGTCTUCCCTTACAUGGAGGGT	82745	ACAGAUCAGACACTCAGGUAACAGA
236741237	82746	GGTCCCAGTUGAAGACCCTCUA	82747	CTTCCACCUCTACCTGAUCCCA
236745812	82748	CCCTACCCUGGGAGAUGCT	82749	ACCTGCUCGAACTTCTGCUG
236748733	82750	GCCCACAGAGGACCUTGAUG	82751	CCAGTACCGCUGCGAGUG
236751123	82752	CCTCTGACCUCCCTCACATCUT	82753	CCTTGGGAUGCCACACTUCC
236751142	82754	GGAGCGCGAGUCCTCTUG	82755	CCAGUAAGAGCAGTUGAAGGGA
236752686	82756	TGGGCACGUCGCAGUAAA	82757	CCAGCUGACCCCAATCTGUC
236752957	82758	AATGTGCAGGGCUGATTGUCT	82759	CACTTCAAAGCUAACATGTUGCCA
236756004	82760	TCTGTTTTTGCCUTTTCAATTTCCTGUT	82761	CAGCTTGTCCAUTTTTCTTCGTUACAG
236757599	82762	GUCCTCCUGGCACAAGGAAAA	82763	GAATCTCUAGAAGCAACACCUGACT
236760309	82764	GCACTTUCAGCTCUGGAGGA	82765	CCCTAGAGATGUCTCCTTCCAGAUAT
236760864	82766	TTATCCTGTGAUCCTAATTGCCCTUA	82767	GCTGTGTCAGCAUCTAGAAATATGUCT
236762074	82768	CTCCTGGATCCUTTATTACGAATTGUGA	82769	GGAGAAGGUGCCTTGCTUCAT
236763350	82770	CTTCCGAAUGGAGCAGUCACT	82771	CATAGTTCUGGAAAACCCCAGCUT
236768155	82772	AAATCCCTGTGAAUCAGTTGTCTAAUGAA	82773	GACGTAGAGCUCACATTCUCGAA
236768945	82774	TGATTCTGGTUCTCTTACCCTUACCT	82775	CGAATTGAUGTCTGCCTUCAAACA
236769665	82776	AGAACCATGGAGUCTGGCAGUA	82777	GGUCTCTCAGGUCGAGCAGT
236770477	82778	TCACTTGCAGTCUATACTCACCATCUAT	82779	GAAATAAACCTUAGCTGCTGAUAGGCT
236772462	82780	GUTAAGACACCUCCACAACCAACA	82781	AGGGCAUCGAGTGGAACTUC
236775332	82782	TGGCUGGAAAAGCAATCGUCA	82783	TCTTTTTCTTACTUGCTTCTGTCACUCA
236775892	82784	GGGTTACUGGAGGCTACAGUG	82785	CTGCACAAGCUTCTACTTCCTAUCT
236776767	82786	GCTCAAAGATUCTATTGTGCAGTUGT	82787	CAACTGTCACAAUCACCTCATCAUCT
236777546	82788	GCCTGTCTTUAAGTTGAACATGAUCCT	82789	GACAAGCAACACUATCCGTGTTTUC
236777598	82790	GATCATTTUCAGGAGGACUCCCAAG	82791	CTGTGCCTCTUCAATCCATTCTTUT
236778526	82792	CAAGACAGUCCCCGCUACA	82793	AGGAGGTUGTGGCACUCAG
236780496	82794	GGGUCACACGCTGUCAAG	82795	AATTACAAGAAUGGATCAGACGAUGGAG
236783252	82796	GCCTTTGGGAAGGUCTTCCTUG	82797	CACTCTGUCCTGATGTGAUGGA
236784511	82798	GCATTTGTGGATUCCATAGACCGAUAA	82799	ATGTTGAATCUGTTCCTGCUGGT
236786720	82800	GGUCGAGGCCAAAGUCGAT	82801	CTGACATTGUTTTCTCTCCTUGCAG
236787506	82802	GCTCCATCUGGCACTTCAGAUA	82803	CAUCGCCGCUGCAGAAG
236788575	82804	GCTTTUGGGCTTGCTTUGAGT	82805	TTTACAGGACGUCCGUGCAT
236788686	82806	CTGTTCTUTGCTTGTUCGGCAA	82807	CCAGCTGCAUCTCTCCUACAAT
236791255	82808	CCGCCACUGGTTGUACCAAA	82809	CCAACCCAGUATACCTGAGGUAAC
236791511	82810	GGGCTGUTCTCGGUGCT	82811	CGATGAGAAGAAGAAACUGCGUCAT
236793103	82812	CCAGGAGUTTGUAGGCAAGGA	82813	GCTGCGAGTUATAATGTGTTACAAUCAT
236794546	82814	CCTCGCTCUCACTGTTGCUG	82815	CGAAGCTGUGCTACACUACAAACAT
236794681	82816	AGGCAGAAAGAGUGAGGAGGTUA	82817	GATTAATTGGCTUCTCTGCTTCTTUGT
236797775	82818	AGAACAAAUCACCTUGCCACCA	82819	AGAATTUAGAAGACACCGUGCAGAAT
236800513	82820	TGGGTGUAGGTTCCAUGGGAT	82821	CTGCTCCUGTGAAGGTACUCA
236800945	82822	GGGAGCTGUCCAGTGACTTUG	82823	GCGAGTGCUCGTGTGAGAUG
236801565	82824	GCTGAUAGCCAAACTGCUGAACT	82825	CCAGGTTTAAGAAUTGTTTAAGCUGCAT
236801740	82826	TCCAGGUCATUGAGGAGGGT	82827	CCACAUCCACCGAGGCAUT
236803779	82828	TTAAGGAACACUGTCCATUGGCA	82829	GGGTTCAGCAAAUCTTCTAATCCAUGA
236804359	82830	GCTTTGAATCUTTGGCCAGUACC	82831	AGAGAGAAGGUTTGACTGCCAUAAAAA
236804566	82832	GACAAGGCAGUGGAGTCCTUA	82833	CCTTCACAGCACUGGACACUC
236805398	82834	GCATGACGCAGUTTCTTCTTCUCA	82835	GTCACAGCUCCAGTGTCTGUC
236806692	82836	CACGCUGAAGGUCCAGGT	82837	GCCAGCGAAGGUCTTCUCA
236808323	82838	CCGGGACAUTTGCAGGTTUAC	82839	GTCCTTATTCATUCCTGAACATGCUAGA
236809345	82840	CCCACCAATAAAGUAACAGTGCATUT	82841	AACAGTAGTCCCUACTCAGTGAUACC
236810767	82842	TCCCAGTCUCTGGAGAGUGAAG	82843	CCAGGUGAAGAACCAUGAACCAG
236813210	82844	GTGTCAATTUACAGGAATGGTUCCC	82845	GCUGCCAGGCCTTCAUGT
236813774	82846	GGCCTCTTCUCCGTCTGCUA	82847	CCCAGCUAGACCAAAAGGAGUC
236815163	82848	ACTTTACAUAGCCCTGGCUCCT	82849	GTGACTGUCTGGCAUCACCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236815587	82850	ACAGGCTAUGTAGAACCAAUGCAG	82851	TTTCTCCAAAAUGGCTGGTCGUA
236818060	82852	TCAGCTTUGCTCACGTGUCAA	82853	TGCAATTTCAUCTTGAACTUCAACACAA
236818943	82854	CTGTACAGTACUGAGGTTCTCAUGT	82855	GGAGACAGAAAGCCCUGUAGAG
236820759	82856	CTTGCCAATAUCCCTTCCTCTTGUAA	82857	CAGCAGCTUTTGGAAGACTUGAG
236823376	82858	AGAAATCTCUGTTATGCCUGGCAA	82859	AAAGCACGCTUAGATTGGAATACUGA
236823725	82860	CTGGAGGUGGAACUAGCACA	82861	GTTCCTCCCAUCAAACTCTCTGTUAC
236826296	82862	GCAGCACCUTTTGCTAAATCUCAC	82863	TGGTGTGACAGUATAAGACCCAGTUA
236829186	82864	CAAGACCTCUTGCTGCTTCUC	82865	AAATCAATCCUGTGTTCCTCUCACC
236831140	82866	GATTACCCAUCATTCCTGGCUGA	82867	TTATTGCCAAACCAGAAUTTACCACTUG
236831541	82868	TCAGAGUTCTCTTCUCCAGCAAAC	82869	GGATTTATCACAGUATCAAGGATGCUCA
236835983	82870	GGUCAGCCAGAGGGAGTUCT	82871	CGGCTCCCUTTGTGCTTUCA
236836287	82872	GTTGGGCTUTGCAATGTGAUGT	82873	CAGACATTGTCCCUAAACACTACTGTUA
236836354	82874	GCUGCCAAUCGCAAGCA	82875	ACTGGCCCUCTCCTCCUT
236838687	82876	AGCAGGGUGCATTGGATCTTUA	82877	GGTACCUGGAGAGCUGCAAC
236842413	82878	GAGACCACUGGTGTCUCACA	82879	CCTAGGCTTUCATTTTCACTCCAUACC
236847672	82880	GAGGAAGGCUAGCCAGCUT	82881	GGTGAUGTCTGGUCAGGGAAT
236848499	82882	GAGGCACAUTTACGCTTAGUGG	82883	CTGGACAGCAUCCTCAGGUAA
236849837	82884	GTGATCTTCCAAAUCTACAGAGTUCCC	82885	AGTCCTGTACUTCTGGATCTTUAACCAT
236853594	82886	GCATGCCAGUGTGTGAATTUGAT	82887	AGACATACATTGCUCTACTATGAGGUGA
236854141	82888	TTTTTCAGGGACAAGAAUCCTUCAAGA	82889	AAACCAGACACGUGCAATTUGAG
236855933	82890	CATACGAAUCAGGAGAATAACGUGT	82891	GCACAACCAGUGCACCTUCA
236856970	82892	CTGTGGATCUTAGGGACCUCAAT	82893	ACAGGTAGAAGACUGCACTATAGTAAUGA
236859715	82894	GTCACTAGTTGUACTGAAATGCCAAUG	82895	GGCTGGGAACAUTTGTCATTTATTCUT
236859943	82896	AGAGAAGTUGAGAGGACCCAUGA	82897	CTCAACGTGUCTACGAAGCUG
236865027	82898	AGGTAACTGCCUTTAAGGAAACTUGAC	82899	TTCTCGCGGAUGAATGTUCCA
236866863	82900	TGGTCTUGCAGGCTGTUCC	82901	GTGTCCUGCCACATCAUCCA
236868194	82902	GCCTGUCGCGGAGAGTUG	82903	GUCGCUGAAGCAGAAAGACAAG
236868846	82904	CATGGGAGGUGCTCAUGGAA	82905	AGCCGCACUATACTCAGAUCCA
236869106	82906	GAUTAGTGUGGCCAGGGAAGAAA	82907	CCTCAGCUCTGCAAUGAGAACAG
236870605	82908	GGCCAAAGAACUGAAGAAGGUGA	82909	ACCCCAGGCAAUCAGGAUACT
236870789	82910	ACTCAGGTUAGAGGAAGAACUGGAA	82911	CCCTATGACACUCAACCCTGUG
236874615	82912	ACTTTTTGCAAAUGTTTAACATAGGUGACA	82913	AGGTTTCCTCUGGTCCTGGUA
236875490	82914	GCAGTATAGAGCGUGCAGATAAUGA	82915	CAUACAAGUCAACAACCCCCACA
236876211	82916	GCAGCAAGAUTTCCTTCAGCUT	82917	AGGAAAGCACUCAAGAUGCCA
236876743	82918	CCAGAUAGCACCGAGTCUGAAC	82919	GACCGUGAAGAATGACAACUCCT
236877524	82920	GCCGCGCUACUCACGAA	82921	GCCTUCACTGCGUCCCT
236877645	82922	CTCTTCCUCCATGCTTTCUCCAT	82923	GACTATGAAGCCAUTTGTAAGGTACCUC
236878686	82924	TCGATTGUCTTCCCUGAGGACT	82925	TGAGAGATAACGAAUGGGAAACTTTUGA
236879263	82926	TGCAAACAAGGUTTTCCATCCUG	82927	TTACGCAGUCGGCUAGAAGAAG
236882906	82928	GCACTUGGCCTGTGCTUCT	82929	ACACGGAGCUGAUCAACGAC
236883988	82930	TGCAGGTUGGCCTTCTUCA	82931	AGGTGTGUCCCCAGGGUA
236885923	82932	TGGTTUACAACCACCCCTTUGA	82933	ACACATGGCAGUAGTGACTCTUAC
236887217	82934	AGTCAATGAAAUCAGGGCCTTUGA	82935	CGAAGACGUAGGTACCAAUCCAC
236889408	82936	GCCATTTCACGAUGACCTCUCAT	82937	GCATCCTGACUGGGTTTTCCUC
236894174	82938	CCACCUAGAGCCAGCACCTUA	82939	TGTGAAAAGUGGACCCTGGTTAAUG
236894655	82940	ACCCGCCCUGACACACTAUA	82941	CAAAGATGACUGGCTGGAAUGG
236895167	82942	GCTGCTTCCAUGTGTCATAAAGACTUA	82943	TCTGAAACCGACAGUACTGACATTTATUT
236895448	82944	TGTCTTTCAGUTCTGGATGUGCT	82945	AACAATGAAATTTCUTCCACAGGCAUAC
236895503	82946	GGAGATACTTCUGGCCACCTTUC	82947	GTTTGAGUGCTGGGUGGAGAAT
236900732	82948	ATGATGAGTCCUTCAGCAGCUC	82949	AATTGGCCCTUGAAACTGATTGTTUT
236902818	82950	CGAAAGCAGAACCUGGAGATUGAG	82951	CCATTGAGUGGTCACCCAGUA
236903470	82952	AATCTTTTATACCAAUATGTGTAGCTCAUGAT	82953	GTGCTGTTGCAUGCATGAGTAUG
236904400	82954	TGATCTTAACUGTCGGAUCCACAAAAA	82955	TCCACTGGUCTGGCAGCTAUA
236905420	82956	CAGCATACUCATGCAUGCAACAG	82957	TGCGTGCTCUAAAAACATTCATATTGUT
236906083	82958	CTGACAACAUAAACCACAACAUCAGAG	82959	CCATCCAGGGCAUTGTCTTAAGTTAUA
236906628	82960	CGCUCCAAGCTTCTUCCAAGA	82961	GGCTAATCCACUTTCCTTCCAUGT
236907273	82962	CCATCTTGGCUTGGGTCUCAT	82963	GGAAGATTGGUAGTTTAAGGAGATTUGGA
236908539	82964	CCCCTTCCCUGTTTATCCUGAA	82965	GCAUGGGAATGCAUCAGCCT
236908758	82966	GGAGGTTTCTUCAGTGGCCTUG	82967	AACACCCTAAGAAUGACAATGGCATUA
236912127	82968	TGCTATGTCAGUCTGAAACTTTCTUGT	82969	GCTGTUCAAGAAGAGCCTTCUCA
236912167	82970	TCCCATTUCGAAGATTGGUAAAACCA	82971	GAATGGAGGGACUTGTGCUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
236920537	82972	GACCTCCUGCTGTTGCTCUT	82973	CTCAGTGAAGAUGAAGCTGGTCUC
236920642	82974	TGTGTGGCUCCTGGATCUGAT	82975	GTATCGGAAGAAUAACGATGACTCUGG
236921093	82976	CCACAACAGUAGAAGGGAGAAAUGA	82977	GGGCTCCAUCAGTTAAATAATGTUGACT
236923511	82978	CCTUCAAGCCCCCTTCUCAAC	82979	GCACAACCUCAAGGAGCGTUA
236927713	82980	GTCTGTCTCTUCACCCACACAUC	82981	GTTCTGCUCACTGTGGUGCT
236928233	82982	TCAATGGCUCCGTGCUCAAT	82983	CGTGTAGTUGCCGTTGTUGAC
236928340	82984	TGAAACCAUCAGGCATGTTACUGG	82985	TTGCAGTGACUACTTCTGCCTUT
236933520	82986	GGGTGTCUGCGCCUCAA	82987	GGGCAGGGUTCAGGAUGG
236935865	82988	ACTTACGTAGAUGAGCCCTGAGUAG	82989	GGGAAGAAGGUGAAGGUGAACA
236936286	82990	CCAGCUTCCUGAAGGGAGGAT	82991	CTGGGCAUAGGTGATCUCCAC
236937241	82992	GGCGGCUGCAAAGAAAAAUAACT	82993	GCAGGTAGTGUTCGAGGCCUA
236941231	82994	GGGAGUGAACACGTCCTCAUT	82995	GCAAGGUAGCCTTCGTGTUG
236942817	82996	GGGUCGCGCATTTTCTUCAA	82997	GUCGAAAAGGCGCACUGT
236946028	82998	TUGTCTTUGAACCACAGGACAGT	82999	CCTGACGGUCACCCCUT
236947138	83000	GCTTCGUGCGCTTCTTUCAG	83001	CCGGCCCCAUGTACTUGAT
236948093	83002	CCCGGGAGGUGTUCAAGAC	83003	CACUCTCUGAGGCGGGAAA
236949611	83004	CACTTACGUGCGTACTTTGUGG	83005	CACTCCCCUATCCGCTTCUG
236949929	83006	GGACATGUCAACCGTCCCAUT	83007	CGACACAGUTATUGCCCGGAT
236950240	83008	GGTATCUGCTGAAGGUAGGAAACC	83009	GGAGAGGACUGCCAGTACUCA
236950519	83010	AAACAAGAGAAGGCUGTGUGGAT	83011	ACAUCGCTGAAGUCACACAGAC
236953598	83012	GGTTCATCTUCTGGATGTCAUCCT	83013	GCCAAGAAGCUGGTAUGGGT
236956067	83014	CATGGTGACAUACTCCCCGUT	83015	GCCTTGGTCUCCTGGATCTCUA
236961869	83016	ACATTCTGCACAUTCAGTTTCTCTTUCT	83017	CCAGCAGCACAUCAATAGTCTAACAUAC
236966293	83018	AGAGGAGAGUCTCCAAAAGGUGA	83019	CGAGCTCTGUGTTACAAATGCATUG
236973066	83020	CGCTCAAUAGAAAGCGCTUCA	83021	TUCCACACGGCGUCCAA
236974462	83022	TCAAAGCCACUCTTGUCGGAAG	83023	CCCGCTTAGGUCCTGGCTAUA
236975765	83024	CCATGAATUCAGCCAAGTTUAAGAGG	83025	ATTTTCCACCUTCTCTGCCTUCA
236977505	83026	GCACGGGCGUGCTTUAG	83027	CCCCACCCACUCATCCUG
236981632	83028	GCTGTTCCTGUAGCAGGTTCUT	83029	GAAGGCAGAGAAUGAGCTUAAGGAG
236983558	83030	CCUTTGGAGAUGGACGAGCA	83031	GGTCTGTGATGGUCATAATTTGCTGUA
236986252	83032	GAGGTGAAAGUTGTAAATCTTTGUAACAC	83033	TTTGCAGAGGACAUAATUCGACACT
236986278	83034	AAGGCTTGAAGAGUGTCGAATTAUGT	83035	GCTCATTAATACUCTTCCTTACCAUCCC
236986582	83036	GGCGACCUCTCTCTCCCUAA	83037	TGAGACUAAGGAAAGAGCCUGGAAA
236986754	83038	GGAAGCAGGACAUTGGAGACATUT	83039	CATTGTUTCCCCCUGCAAGAG
236986781	83040	GTACCTGCGAGUGCTTCTGUT	83041	GCCACAAAAACAAAUGATGGGCUA
236987977	83042	GACATCATGUCAGAGTTACTGTTUCAGA	83043	TGGCTTTCAGUAGTTTTCATGGTUCA
236988768	83044	ACCTTTTGTATTUTCCTGTTCTCUCACC	83045	GGAAGGACUAGGUGCACCAT
236999718	83046	GCTTCTCTUCACGCACUCCAA	83047	GCUGGCGGCCTUCAGAG
237004269	83048	CTUGCCACGAAAACCGUGAAA	83049	CCTGTGACUCAGACAGCTCAUA
237005787	83050	CCTCTUGGGACACACCACTUA	83051	TCAGAAGGAACUCAUGACAGCAC
237005879	83052	GGTCCAUGGAGCCUGCAC	83053	GCTTAACCCCAUCATCCCCUAAC
237006004	83054	GGAGGTACCUTGGCATTGUGG	83055	TGTCUCCCCAAAGAGGGACUT
237006286	83056	GAAAAUGAAGAATTGCAUAACCAGCGA	83057	GGGTACGAGUATGTCUCACACAT
237009052	83058	CGCCTTACCUGCTGCTCATUA	83059	CAACTCATGAUACAGACCCCUAAAGAAG
237012448	83060	GTCGAAGCUTGAGCTCUCGAA	83061	GGCCACACUCTGGGACTAAUG
237021950	83062	GCTTTGTCCUCGTTCCAGTUG	83063	ACTGATGATGUGCCTTCCCTUG
237022187	83064	GGTCAAGACUGTGGCTGUGA	83065	CCAGTCATCUGCAGCAGCUAC
237023515	83066	GTGGTCAGGACAUTAGCACCUT	83067	CATGAGTTTGCAGUGATTTTGCTATTCUA
237023973	83068	AGAGTCTUGGCCAAACCTATAAUACAGA	83069	CTTCATTGACUGCCAAAGAGGAUG
237024698	83070	CATCCTGUCCCTGAGTGGUG	83071	TTACGGGUTCTGGTCAUGCAA
237026902	83072	CTAATGTGGAUCTGGGTATGCUGA	83073	GTGATCATAGTUCCTGCATCTTCCUAAG
237028820	83074	TCAGCTCAUTGAGGGCAUCC	83075	GTTTGTAGAGGGUTGGCAGGAUAA
237032468	83076	GCCACACACGUGUACAAGGT	83077	CACCATGUTCATCCUGGAGCA
237033733	83078	CATCUAGGGCACAGCUACACAT	83079	ACACTATAGGGCUTGGGTCTCUG
237036021	83080	GCTGAGGAAGCAGCUTCTTCAUA	83081	CAAAGATTGCTGAAUACTCTGGTCCUAA
237036970	83082	GCCGAAGUCTCCTTTTCUCCAC	83083	TGGTGGCCAGAGCUTATATTTTCUT
237041445	83084	GGTAGATTTCTUACTGTTGTCCTUCCT	83085	TGCCAAAAATAGACUAAGAGGAGTGTUC
237041724	83086	CTCGCGCUGGTACTCCUC	83087	GGCTCCTTGUCTTCTGACTUCAT
237042741	83088	TGAAAGCUGCTGACAGUGAGT	83089	GGAAUGAGCTATUCCCAGGAAGAAG
237045698	83090	GUCCACCTTCUGGGAACCT	83091	GTCCATGGUCCTTTGTGTCUCC
237062840	83092	CTTTCAACTTCGGUATCACGGATUC	83093	GGAGCATCCGUCTAAAACTAGUACAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237066023	83094	CATGGCATAGAAAAAUGTGTAACTTUGGA	83095	GTAGAUGAATCAGATGUGGAAGAAGACA
237069981	83096	ACCATGGUGGAGCTAUAAGCC	83097	GACATAGUCAGCGAGUACACACA
237072724	83098	CTCCUCCCCACAGAACUGG	83099	AGGAGCUGCAGTCCAAGUG
237073441	83100	CACCUGCAGCTTGUGGACT	83101	CCAAGCAGGAGGUGGAACAUAA
237076108	83102	GCAAAGGAGCAGUCTTCAACTUCT	83103	CAGGTATUGGGAAAGCATAATGTTUAAGT
237076660	83104	TTCTGTTTTCCUAAAAGGCACTUGAGA	83105	ACACTGAUACCCAAAATGAAUGCACT
237077862	83106	TCCTCAGCUACCAAGCTAGUT	83107	CAGGAAAACCACCUTCTCAAAGAUGA
237078653	83108	GCGCCUCCAGCTTCTTCTUC	83109	GTTATCCCUCCCCTCTGCTUC
237079459	83110	GCTTTCTATTATGUGAACCTCCACTGUT	83111	GUGATGAAGGUGGCAGAGAGG
237082665	83112	AAGGCCATGTUAGTAAATTTGCATCUG	83113	CTCTCAAACCGAUCAGCCAAUACT
237085294	83114	TGGAGGCUACCTGAGTGACUG	83115	CAGCCAUGCCTTGTCUGACT
237086719	83116	TTCTGACTUCTTGCTGCTUGAGT	83117	ACCGCTTTCCAGAUATACTTAAGAGTTUC
237086914	83118	CCCACAGAAACUGGATGCTUCT	83119	CCAGTGACCGUAGCAGAUGAC
237088586	83120	GTTCTCCCAGCUCCTGGUT	83121	CCUAGAGGCCAGGGUGGA
237091653	83122	AGAAGAUGAAGAGGAGGAGGAUGT	83123	CAAGAGCTGTUCTATCACCAAACUAAAAG
237092059	83124	TGTTCTGCTGCAUCTTCTTCTTCUC	83125	GGCAGAAACCGAGCUGUGT
237093681	83126	GCTCTCCTGUTATGTGCCCTUA	83127	ACCTTCTTATAGUCGTCTTTCCCAUCT
237094635	83128	TGTTCTCCTTUGGTTCTTCATCTTUGAA	83129	GCUAGGGAGGCTTUAGAAGGG
237095395	83130	AGAGGUGCTGCUGGGAGA	83131	TGACCTTGGUTTTACCCGTUGT
237096079	83132	TGTTTTTCTUCACCCCUCGCA	83133	CCCAGCCCCUCAGAAAUCAC
237099287	83134	GCCTTACCUGTTTCATTTTCUCCAGT	83135	CCCCAGCCUAAATATGTATGTCTGUT
237102665	83136	ACTATCACTCUTTACTCCCATUCAGGA	83137	ACCTAATTGGUACTGGAACAAGUGAAC
237103071	83138	CAGATCTCTTCUAATTCCTGCTTCTUGG	83139	AGGAGCTTGUGTTTTCCACTUGT
237105765	83140	GCCCATCAACCUTCTCTTTTGUT	83141	GCTATATTUGGAGCAGACACACTUGG
237112721	83142	ACAGAATTUGACACACTUGCAGAAAC	83143	CTTCCCCGCUTACTCTAATCACTUAC
237114548	83144	ATCCACUAAGAAGGCATTUCGCT	83145	ACATCCTTCCCUGTCTAATTGCTTTUT
237118247	83146	CCUACCCUGGAAAGCACACC	83147	TCTACCCAACUCACAGAAGAAUCAAAC
237121169	83148	CCCACAGAUGACAGGUGAGAGA	83149	CTGTTAGACCAUTTTGCCAAUCGAG
237122141	83150	CCCUTCATCAUCGACCCAGT	83151	CATGGUGGAAAGTGTUGAAAACCA
237128232	83152	GGGTGATAUGAGGGATAGCAAAUC	83153	TCACATTCCAGCUTTAACTCCAGUT
237131370	83154	GACGATCCAUATGGTCTGTGAUGT	83155	TTCTGTGAUGGGCCTTTTCTGUAG
237132072	83156	ACGAGTTAATGGCAAUAAAGGGATGUAA	83157	GTGAAAAGGCTUCTTCAAGAGAAAGUG
237135601	83158	TTCTCCCTTTCTUCTGTCCTCTCTTUA	83159	GUGGTGTTCUCCCAAACAGGA
237139050	83160	CTGGTTGACAATAUATCTATGCCACTTTUG	83161	AGCTGCCUGGAATGGATATGATUAAG
237140469	83162	GGCACAGACACAUTGCAGGUAA	83163	GTGGUGCACACUGGAAGAAAG
237141662	83164	CTGGCCAUCACCTCGGTUA	83165	TGTTTGUGGCTCTGAAUGACCA
237143564	83166	CTCACAGAGTAUCATGTCTCCCTUG	83167	CCAAATUAACGCCCAGGAAAAAUACAT
237143684	83168	TTTCTTACCCGUGTTGTGTCUCC	83169	TTTTCCAGUGCACTCTUGGACAT
237144528	83170	GCTCACTTGTUCTTTGAGCTGAUT	83171	ACCAGTGTTTUCAGTGTGACAUGAT
237144676	83172	CCCCTCCTCUTCTTGTTCTCUCA	83173	AAAACCACCUCCCAAGAGUCC
237144687	83174	GTGGCAGAATATUTCTACAGGGTTAUGT	83175	AGGCATCUCGTTTGTACTTUGGG
237146843	83176	CATGGAGACAGUGCACCTGUT	83177	AGTGTTTCTGCAAAUTCTAAGAGGTUCT
237151370	83178	CAGGTTTTGGGUCTAGTAATACTGGUT	83179	CAGTGAAGAAAACUGAATGGGTTUGAT
237151736	83180	CAGGGCACCAUTCTGGATAATGTUA	83181	GCTTGGCTAUAGAAAATGGCAATGATUT
237151966	83182	CGCAGAAGCUCAGCTGUAAC	83183	GCATCAAUGAGAGCACAAUCCC
237158015	83184	CCCCACACUCGACCAUAGGA	83185	TCCTGTUGGAGCCGUACAAC
237158839	83186	GCATGACACAAUAACTGGGCUCAA	83187	CTCCTCCAGCUCCTCCGUA
237159717	83188	GCUCCCGGATCUCAAACACC	83189	TGTTCAAAGGCUCCATTGCTCUT
237161024	83190	GGCTGCUGGCACCCTUA	83191	CGTGGTTCUGCCTGACCUG
237163908	83192	GGTGGTCUGTCTGGTCGUC	83193	AGGACCUGGAGACCAAGAAGUT
237164446	83194	CTTCUCCCAGCCCTUCGG	83195	TCCTCCACAGCUTCTCTUACCT
237165980	83196	GCTGTAGTACUGCAGCACTTUG	83197	TTTTGAGGAGGGAAUGTCAUGGG
237167296	83198	CCUTGCAGAAUCCAAGAAAACAGG	83199	CATTTTCCCCUTACCTCCATUGCT
237168083	83200	TGCACAATACUGACAGAGGAAGUC	83201	GAGTGCTTCUGGAGCACCTUA
237168735	83202	CGGGACCUCCCTGTCGUA	83203	GCTCCACCCCUTCCTCTTTAUC
237168797	83204	AAACATGCCTTUCACGTTCCTTUC	83205	TCTCTCCTTCUTCTCTTGGCTUCA
237168971	83206	CATGCCAGAGAUTGCUCAGGA	83207	CCUGTTACUCACAGAAACCACACA
237169128	83208	CCATUGGACAGGAAGCGGTAUT	83209	TGTCCCAGTCUCTCCAACCTUT
237172749	83210	CAGAUCCAAAAAGGCGGAGCUA	83211	ACACCCCUCTCTCCTTGTUGT
237173770	83212	TGTGATAGAAAGCCUCCCTTCUGT	83213	TCTACTCATGCCCCUCAAACTTATTTUT
237177776	83214	ACACAGCAACUATTACATCCUGAAACA	83215	CCTGAAAGCAGUTGAGUCCAAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237178442	83216	ACGACTTGCCUGCATGAGAUT	83217	GAATGUGGCAAGAACTACAAUACCAAG
237180090	83218	ACGUCCACAAATGAGUGCACAT	83219	TGGATGTAAACAGCCUCTTTGTAGTUT
237190087	83220	TGGGUAGCAACUGGCACAAA	83221	GCAGCCUCAACATCCCCUAC
237190476	83222	CCTAAAACGUCATGATTTTCAAUGGCA	83223	ATTAGACATTCCUTGTTGTGCUCAGT
237192792	83224	AAGTGTATACUAAGGCCTTGTGAGGUA	83225	CAGCCTAAUTCAGGATUGGGAAAC
237193438	83226	CTGCACGGCCUCGATCUT	83227	CAGCCCCUCTCTGATTGUCC
237194048	83228	GCAGAACACACAUACCAAAGUCAGT	83229	TUCCCCAAAACACAGUAACCCAA
237196610	83230	GGCCAAGUGACGTTTAAAUCCAAG	83231	TGUGAGAAAATGTTUCACCGGAAAGA
237197086	83232	CCUTAGAAACACTUCGGCAGGT	83233	CTGGGCTTCCUTACTTGTAATCUGAT
237197404	83234	ACCTCUGAGCACAGUGCAG	83235	ACGUGCCACCCCTUCAG
237200288	83236	GTCAGACACAAGGUCAGAAAGUAAAAGA	83237	CTTTGAAGATGUTAACTGGGCTUCC
237203098	83238	AGCAGAAATTATATCAAUGAGAAAATTCATGUT	83239	GCCGCATAUGTTCTTCTTTTGUGA
237203200	83240	ACTTCAGAGTATUGCCAATCATGTTCUC	83241	AGCAACUGAGTAAGUGGCAAGAAA
237210508	83242	CTCTACCAGAGUTAATCAACTGAUGCAA	83243	TGCCAACAAGGACAGUTGAUACAA
237214547	83244	TGUCCCAAAGCAGAAGUAAAACCA	83245	CCAAGCCUGGGACCTCTATTAUCAT
237215211	83246	GGCTGGCCUGGTGACUG	83247	AGTAUGACCAGCAGCGTACUCT
237215886	83248	GAGTCUCAAACAGGAAGACAACUCAA	83249	AGGAATATCACAUCCTACCCCGUAAAA
237216370	83250	CTGCAAAGAAAUATACAUGCGGGAA	83251	CTTTGGAACCACAAAUACCACCTCUAA
237216613	83252	GUCCAGGUAAACAAGCCCAGAT	83253	GCAGACATTGUGCTCAATACTTTGTTUC
237217291	83254	CAGAATATGGGUAAAGATGAUCCGACAA	83255	CACTGACAAUCCAGCTAAUCCAGAA
237224709	83256	CCAGAUGTGCUGCCAAAAGGA	83257	GCCCAATTCCAAUGCATCTTATACAUT
237225205	83258	CCACAGCCCUGCCTGTAUC	83259	GGCUTCCUCCCCGGAGT
237227347	83260	GCCCCAUGGGCTGCUAC	83261	GTGCCCCGGAGUCCAUA
237228343	83262	AGATAGAAGTTCCUGTCACTTTCTCCUT	83263	AGAAAAAGUACAGAAGAAGCUGACCAT
237228504	83264	CCTGATCACUTCTCATCUGAAGCA	83265	GAGCACAACUGAGCATCUGAAGA
237230465	83266	CAUGTGTGGUGCAGAGGAGAAA	83267	CATCACCTUCATCTTCAAGUCCCT
237235325	83268	CTATCTTTGGUTGAGTTTCTUAGAGAAGT	83269	GGACAGTTGAAUCTTCAGGCTUAAGG
237236540	83270	CCCAGACUGGGCAGTTUGAC	83271	GCCCAGTGAAGCAUATGAGATTACUC
237240658	83272	GACAGCTTUGAGGAAGCATGTATTUC	83273	GUTTGTAGCUCCCCCACCAAA
237243672	83274	GCCAGTTCGUGGGCTTGUT	83275	ACCCAGCCTAAUCTTGTTTTTCTTAUGT
237245300	83276	AGAGCAUAAAAGTUAAAAGCAAACAGCA	83277	GCTACCACCAGUGCCAUGAAC
237248971	83278	GGTGGGATCAUATTCATCTACAAAGUGG	83279	ACAGGTTCUTGCTGGTGUGAA
237249120	83280	AACTGTTCCAUGCTCTCCTTCUG	83281	CTTTAGGCCUTCTGCCUGGT
237250850	83282	GCTUTGAGATTCGUCGGAACAC	83283	GATAACTTGAAAACGUGCCTGCTUT
237255384	83284	GGAACUGCACACATTTGAGUCC	83285	GAAATGCUGGTCAACAUGGGAAA
237261421	83286	AGGTAGGCCUCTGAGUGAAGAA	83287	CATGTGGTCCUGTGCTCTTUCA
237266818	83288	CGAATCATACCUCCTTGGACUGG	83289	CAGTTACTGCAUCTCTCAGTTTTCTTUG
237273712	83290	CCAUCUGCCAGGGAGCAAA	83291	CUCCCCACCCATTUCACCA
237277788	83292	GTAAACCCTTUAGCCTTCCTGGTUA	83293	CUTAATTTACATGTAGUGCCCAGGACT
237283168	83294	GCTCTAGACUAAGTTGCTTTCAAGUGA	83295	GCAGATCAGTUAACAGACAAAAGUCAAC
237285690	83296	GATGCCUGGCAGGCCTUA	83297	GGTTCUGCTCCCGUCCAG
237286655	83298	TGGGAAUGGAGCCATCTCCTUA	83299	AGCAAGUGCAACCCTTCTTUGA
237287930	83300	GGUAGAACTCAUCCAGAGGCAAG	83301	CTAACCAUGCTCTGCCUGAAGT
237291537	83302	CCCCGACTUTGCAGTCCTUAAT	83303	CTTCTCAGGCCCUTCAGAGUC
237293263	83304	CTCCTCAGGUATCCCAAAGATUCA	83305	ACGGAGACCUGGTGGACUAC
237296461	83306	CCUCAGGGACCAAGGCUAGT	83307	CCATGTGAGCUTGAGAAGGCUAT
237298095	83308	CCCCTACCCUGCCTCAACAUA	83309	GCCCTGACCCUTCTCCCTAUC
237300703	83310	GCTTTATCUACAGCCTGUCCGA	83311	AAUATCGUGCACAAGGCAGAGT
237301468	83312	CTGGCACUAATGGCCTTTUCC	83313	GTCTCCTGGCUTGATGGAGUC
237301619	83314	CCAACTCACCAGCUGTTCCTUA	83315	GGCACAGUCCAGCACCUAC
237301899	83316	CTGCAGGAAGGUGTGTTTGTUG	83317	CCACAUCCAGCCCCTGATUA
237305760	83318	CCCCTACCUCTGATAGCGACUC	83319	AGCCTGTGTCUTTAAGTCCAGAUACT
237306504	83320	TCGGCCACCUCCATCUCA	83321	GGGUCCACGCTGUAGCC
237306608	83322	CACACGGCCACAAAAAUGTUG	83323	CAATGAGAGTTCUCGGTTTGCTTUT
237308365	83324	GTTGGTCTCAUGCCTCCTUGT	83325	AACUTTAAGCTGCAUACAGGCAAAG
237308552	83326	CCTACUGCCCACCCACCUA	83327	GUAGCTCTCCAUAAACAAGCAGGA
237313575	83328	CAGATTCTTCAUATCTAGGCUGCGA	83329	AGCTGCGUGTGTTTCCTUACA
237314829	83330	CTTCTTCUGACGGTGAGTTCTUCAA	83331	CAGTGTUGGTTTTTAAAUCCCAGGT
237316341	83332	GGGCCCTAUCCTCCTGATTAGTUT	83333	GAGAACAGCUGAATGGCTCUCA
237317048	83334	CCTCCCUGCAGTTTGTGAUCT	83335	CAGTGAGCCAAGUATGACTTCATATGUA
237320198	83336	TCATGGUGAAAGACGAUGGACAA	83337	TCTTCTTGTGAUCCAAAAAGTGUCCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237322555	83338	GATTTTGGACACUTTTTGGAUCACAAGA	83339	GCTCGAGCUCACCTCTCAAAUT
237325070	83340	GCCATTTGTTTUGACACAGGATTTCTUA	83341	TGAUTGTTTCTAAUAGAGCAGCCAGAAC
237326341	83342	AAAAGCACAAAUACCTACCGAGAAUACA	83343	CCAUCTTCATUCACCCAGAAGAAAC
237327379	83344	GCAGGTTTCUTCCAGATTACUCAGAA	83345	TCCTCCCCAAGAAUTGAAAAAGTAUGG
237328237	83346	GCTCUACCAAGAGAAGTUCAGAACA	83347	GACCTCGUTGTGAGAUGGACAT
237328549	83348	CTGAGAGAUCTGGGTGCAUGT	83349	TGCTTTCTGTCUATGTGTGTGTGTAUAG
237329147	83350	CCATAAAAATAUGCAGCTCCATCUCGAA	83351	CAGCCAGUGAAACTCCTCUGA
237329729	83352	CTGTTGGATTTUCATCAAGTCAAUGGG	83353	TGCTCTGUCACTTGGAATGTUGAA
237333164	83354	ATCGGCAATCUGATGATTTTCTAGTUCA	83355	AGGCCTAGUCCCTCGUGAAA
237337100	83356	CTGACCACACCGCGUTCTUA	83357	ATCGCATCUCATGCCCTTCUC
237339717	83358	CCCTCGGGAGAUGTCCAUAAAAG	83359	CGGATGCCAAUCACCTCGUT
237340319	83360	TCAGGTGGCUACAGGCCAUA	83361	AAAACCAGGAAAAACUGCAAGAACTUAA
237341087	83362	TCCCTCGUCTCCCCCTUG	83363	CUGCACUCCGCCGAAAG
237341397	83364	GGGTCTGAAUGGCACTCATUG	83365	TTTGATCCCAGUAATTGGTACTTGUGT
237342173	83366	TCATUCCCTGGTUAGCCAGAT	83367	GCACAGCAGUTTCCATTTCCUC
237344220	83368	GGCATAGCATTUCTGTTAGACGTUGA	83369	GCACAAGUAGGGTAACAAGTTUGAAAAA
237346051	83370	GGTTGAGCAUCCTGCATCCUT	83371	CTAGATGCAAGGCUGTTCGUC
237347538	83372	CCTUGCCATAGGUGACAGACT	83373	CAGAGCAGCAUCTTTAATGAATAUCCC
237347917	83374	ACATCATCTCUAACCTGGACTGUGT	83375	CTCCTCACUCACCAGCTGUC
237349937	83376	GTCTTUACAAAAGGAACGGAAAGUGT	83377	CTGACAGGUCCTGCCTAUGG
237351262	83378	GGCCUGCAGCATAAGAGAUCA	83379	CACACTAATCTTCUCTTGCCTTCTCUA
237352417	83380	CTGGATCUGCTGGUGGACAG	83381	CACTCCTUCCACAATCCUCAGT
237356033	83382	CATTGAGTACAUGCCCCTCCUG	83383	CAGTTGUCACAGCCTCCACUA
237357763	83384	TCCAAGUCACCCAGCAAGUG	83385	AGAAGTAAATUCGGGAAAGGUGAAGAG
237358500	83386	GGATCTAAGUCCAGTACCGTAGTTUG	83387	AACUTTGATGAUGAGAGGACAAGGG
237358588	83388	GATGCCUCTGCCTUCAGGAA	83389	TGGACCGCGUGTTUGAGAG
237358820	83390	CTCTTTGCCUGGCTCUAGGT	83391	TTTCCACGUCCGGTGUGAG
237359819	83392	GCGGCCGCCUGACTUAC	83393	GCAAAUTGTGTCUGCAGCAAGA
237362388	83394	GCCGCAGAACUTCCUGGT	83395	GAGCGGUGCUGGCAAAG
237363403	83396	CTGATGCCUCCAGTUGACAAGA	83397	CTCACACUGACCAACCUCACT
237363624	83398	CCAATAAAGAAUAAGGTTTGCCCCAUT	83399	GGAAGCACAAAGAUTGCGCUAT
237366859	83400	TGTTTGGCCUTCTTCTCGCTUT	83401	CCCTGCTUGTCTCAACCAUGT
237368063	83402	CTGTCTTACCUAAACCATAUAGCGCAA	83403	GGACATTTTAAGTUGTGCTGGATTTGUA
237368433	83404	TCCACCTUCGAATCCCUCCT	83405	GCTTCUGCCTCCGUGACT
237371289	83406	GGGUAGCCUGGGCAGAGT	83407	TTCUCACAACCCUCGGAACC
237371812	83408	GACAGACCAAGAGGAUGUGGAT	83409	CCTTCATUCCCGCTTCATTUCAG
237372755	83410	CCAUGGCAGUGGACGCT	83411	CCCCCAGAGAAGGCUTGUG
237373093	83412	GGTGAAGATGUCTGAGTAGTGCUG	83413	CCTTCCTCUCTCCTGCTCAUCAA
237373600	83414	ACAGACATTGAACGUCCAAAGTGAUT	83415	AGGTGATACGAUATTCATGCAGAUACCT
237376025	83416	GCTGGGAAGUTCTGGTTAAUGGA	83417	TGGCAGAGGUACGAGCUCT
237379635	83418	CACCATGCTUGGTGTCATATUCAA	83419	CATGTGTUGCCCCGGATTUC
237380853	83420	CCCCCACCCCCAGUAACUAAA	83421	AGAUTTGATGCUCCGGGACAC
237380984	83422	CTTCAGTAGAAAUTTCAAAAGCGTCUCT	83423	ATCCCGAAUCCAGGCAUCAC
237384592	83424	AAAAGTATTCUCCCGTGTCUAGCC	83425	AATGTCUCCAGCACCTTCGUT
237387152	83426	CCGCCGGCAAUTGATCUCA	83427	GCGATCGGAGAUGGATGUCT
237387880	83428	CGCAGACAAUTGTTCCCCUGAAT	83429	AATGTTACCAGACUCCTTCTCTCUCA
237390027	83430	CAGATUCAAGAGCTGUGGGAGAA	83431	GTCCACCUATACCCUGGAGGAG
237390403	83432	GTTGTATGCTUGGCGAATGTUGAG	83433	TCCAUTTGUCGAAAGAACAGGAGAG
237395866	83434	CTTTTCAGCCAGUGAGAGGGUAG	83435	TCAGACCTTAGAACUGAGGGAAATTTUG
237396779	83436	CACUTGGCUGGGCAAAGAG	83437	CUCGGCGTTUCAAAGGCA
237399394	83438	GCUGAACCCGAGCAGGUC	83439	GAAGCCCCUGTTTCCTGAUGT
237399437	83440	CTCAUGCACCAAGACTGGUCA	83441	GCCTCATCTCACUCTGTCTCTGUT
237400814	83442	CTCAGACGUGATGTGCUCCA	83443	CCTCCTTACUGAATGCCUCACT
237409001	83444	TGTGGAATCCUGATGCTCCTGUA	83445	CAAAACCATAAAACCUTTGGAAGTGUAAGT
237411139	83446	ACAGGCTTCAUGAGAATGTAAUCAACAT	83447	CAGAUAATCCTAAAGUAACCCAAGCCA
237412111	83448	CAGAAGCTUTGTATGGCTUGGG	83449	CACTTCAGACAUGTTGGTTUGCT
237421255	83450	GCAGTGATGAGUCCCTTCCTTUC	83451	GATGCATCTTCAUCTCTGTTTTCCUC
237422949	83452	TGGCAGGAGGUACTGTTGTCUA	83453	GTCTTGTCTATUAAGCCTCACCTUCAG
237423394	83454	CACTGTGUGAAGAGGAATTTTATGCAUAT	83455	TTGCACATCACCCUGAGGAAATTUA
237428388	83456	GGTCTACUCAGGCCTCCTUGT	83457	GTGATTGTTCUCCCTCCATUCCA
237430981	83458	GGGAAGACCUTTGCAGTGUAAA	83459	GGATGGTUCTGGATTTCTUCGAAGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237431039	83460	CTGTTGGGCUCAGATTGTUGG	83461	CGAAGUCACAGCGAATCAGGUA
237433713	83462	TGGTCACTAAACCUTAAGATGAGCATUG	83463	CCTAATTTCAGCUATATTCCCTGGCTUA
237436378	83464	GCGAAGAAUCCACUAAGGGAAAGT	83465	CCCAGGATGUGGGAGTCTUCT
237437042	83466	CCTGAGACCAUCAGAUAGGCCAA	83467	CCUCGGGCATCUGACAAGAG
237439208	83468	GAGAUGGAGCAGUGGAACCAT	83469	CTTCTCAGUGGCTGTCTCCTUC
237439377	83470	GUAGTGACATTUCGGGAAGGCT	83471	ATCATTCAGTTTUGCAGATAGGACUCA
237439469	83472	ACTTTAAUGCCAGGGATTTTGTUCCT	83473	TCTGGACACAAGAUAAGGAGAATGATTUG
237441721	83474	CCAAAGAGAACAAUGCCTAGAGCUT	83475	CCGGACATUCCAAGCCTCTUA
237442591	83476	CAAAGAAUCAGAACAATGCCUCCA	83477	GAGGCATTCUAAAGTCACTATCATUCCA
237444341	83478	AGCAGCAGUTTGGCCACUA	83479	CACCTTGAGUAAAATAAACTGCTUCACAT
237445497	83480	CCCAGCTTUCAGGTAACCTTUGA	83481	TGAATACTCUGGCAATGCCTAUGG
237445932	83482	GATAGTGACUTTAGAATGCCUCCGT	83483	CCCTTTCTGCTUCTTGAGTAACACTUA
237445936	83484	CCTGCTCCGAAAUGTAGACGAUT	83485	GAGTACACACTUCAGAACCAGGUC
237449633	83486	TTGAAATTTGGUGGATCTATGTCTUCGT	83487	GACTACTTGAUGAGATGTCTGATTTCUGT
237450466	83488	GCCTCGCUGTAGGAGGAGUAG	83489	CCCCAACCAUTCCTGAGCTUG
237451028	83490	AGAGAAATCAACAACUGATGACGAUGT	83491	CACTTTCTGAGUCAATGAAGACACCUA
237452245	83492	AAAACAGCCTCUCTCTTACCTCUCT	83493	GCGTATTGCTUCCTCTCTCTTCTTUA
237452875	83494	CCTCCATCAACUTCTTCAAGATGAAUCT	83495	CGGTTGCCTACUGGTTCAATTACUT
237453745	83496	CCTTCGGCTTUTTCAACCCTTTTUAA	83497	AAGGGACAACAGUTAAGCTTTAUGGT
237455830	83498	CTGTGATUCAGGTGCCUCACT	83499	GACATATTGGCUGGGTCCCUAC
237460755	83500	GATCAGCAGGUGGGATUCCAA	83501	GCAGCGCAAUCGAGTGUG
237461314	83502	CAAAGUCATTGGTCAUCAGGAAAAAGT	83503	CATTGACCTTUGTGTCTGCTCUG
237462153	83504	GGGATAGCAGGUCTTCAGAUGT	83505	CGACTCCAGGCUCATTTGTUCC
237462561	83506	CCTTCTCAUCCTCCAAGACAUAGGA	83507	CCCTTTUCAGTCCAGAUGACCT
237463182	83508	GAAGCUGUAAGGAGAAACGGGAAT	83509	CAATAATGUGGAGGCAACTCTTTTGUT
237463193	83510	TCTTCTGCAAUGTTTCTGAAGGAUGA	83511	TTGGTAGCAGUGACAGCTGTUT
237468729	83512	CAGGCUGACCAGAAGAGUCC	83513	TCGGAGGUGGATGAUCACCAT
237471074	83514	ACATCTUCCCCCAAACTAUCAGAAAAAC	83515	TCTTTTGTUCCAGATGCTGAUCCC
237474279	83516	AGGAAGCCAAUATTTATGCUGCCA	83517	CCCAATGUAGGAACAGCCAGTAUAAAA
237477988	83518	GAAGACTTCTCAAAUTGTTGCCATTUCA	83519	ACGGACATGAGUTTGTTTTCCTUCT
237478313	83520	CGGTUGGCCCCATTTTUCAAC	83521	AGATTTCATTGUGCAAGTCATAGTGUCT
237478406	83522	CCCATCUAACCCATGCTUCCT	83523	CUGACTUCCAAGACCACCACAA
237480904	83524	TCATUCCGCCGCTCTAUGG	83525	TGCTTAGAAACAGUTTCCCATTAACUCA
237481091	83526	CCACGCCCAGUATCCAGGUA	83527	CCCTGGGAGUGGTCAACTUC
237481914	83528	ACCGUTCCTGATGUACCCAGAT	83529	GATACTCAGCUGCCTGCTTCUT
237483254	83530	TGTGTGTGAUAGATCTTATTGGTTUGCT	83531	GAACTUACAGGAAGATACUGGACCAC
237483551	83532	CTTGCGGCUGGCCTTUC	83533	GGCCAAAGCCCACUCUCT
237489917	83534	GACAGTAGAAGAAGAUTGGAAGAAGACUT	83535	CAAGTATTGGTCUCTCGTCTTTCUCA
237490590	83536	CTTCTCCAGGCUAAGACAUGCT	83537	GCAAGATGGUACAATTCAGAACCUCA
237490930	83538	GGCUGCAGGCCAACTACUC	83539	CCAGCTTGTGUTGCTCCTTAATATUT
237491009	83540	GGGCAAGGUAATGUAGACAGAGG	83541	AAGCAATUAGAGCCTTTAGGTUGGT
237498725	83542	TTCAGATGAGUCCCTTAAACCCUCT	83543	GACAAAGCACACCAUCTGTUGAA
237500383	83544	ACAGCATUAAACCAGACCTTAUCCAG	83545	CGAACACCUTTTTGAGUCAACCA
237502624	83546	CGCAGATCTUCATGGCCTTUT	83547	GGGATCTCTUGAATGCAGTGGUG
237503920	83548	TTCCCTGCUTTTCAGAGTTUCCT	83549	ATTTGAGGCUAAAAGACATCATTGACCUA
237504870	83550	AAGAAGTAATGCUGATCCAGGCTUT	83551	CTCTTTTCGGCUGTAGAGAAGTTUG
237505475	83552	TCTCCTTUCCCAGTCACCUGAA	83553	GGAGGATCCTTUGATTTACCAGCAUC
237509378	83554	CCAGACACUACAACAACAGGAGUG	83555	AGGTACAGAGGUGCTAGGAAUCAAA
237511209	83556	GCCCAGAGCUCTTTGTTTGAUT	83557	CACGTTGGGUAGAGGTCCUG
237512401	83558	CAGGCUCAGCCACAACAAAAUAAAAT	83559	AACCTTTTUACCATTTGCCTUCAAAGAA
237516735	83560	ACACGAGCAUGTGTGTGTAUCC	83561	TCATGGCCTUTCTTCTCTTCAUCAC
237517874	83562	GCCTTCUGGACGGCTCUC	83563	GUACCAGGACACCAUGAGGAA
237518084	83564	GGTUGGCGCCGUACCAT	83565	CGCCGCCUACCACAUGA
237518808	83566	TTGGCCACUCCTAAGCAUCC	83567	TCTGCACCUCCCAAAATTTAAGGAUAT
237519534	83568	GCCGCCGUCATGTGGUA	83569	CTUGAGTCCCCUGGAGGAAAG
237519695	83570	GTGATATGGGCAUTTTAATTTGCTGGUAA	83571	TCAGCTTTAUGACACAGTTAGGAGTUG
237521751	83572	GCTGCCCUTGGTTATUCCGA	83573	TTCTTTCTTCATCUCATTCGTCCCTUT
237521999	83574	CTTCCUGCTGGACUCAGAGAAC	83575	AAAACTATACTUCCCGAGGCAUCC
237522143	83576	CCTCCAUGCCCACTTTCTTGUAG	83577	TCCTCTTCCUTCCTCCUCCAG
237525900	83578	CCTGCTCCAGUTCTCATGTUACT	83579	CCCUTACTGAUAAAGCAGGCAGA
237530969	83580	CTCTTTGCAGUGCTCCCCUT	83581	TGACGACTCUTTGCTGTATTTTUCCA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237534122	83582	CCCCAAGCAAGUAGGCCTUAA	83583	TCTGTCGGUGCTGTTGACUG
237535029	83584	CGAGGAAGAAAAACAAUCCCACTUG	83585	AATGCAGCCAACAAGAUTCUGAAG
237537191	83586	CAACGUCAGCGGGAACTGUA	83587	CCCCATTUGAACTGGTAGUCCA
237537220	83588	CCTGCUCCTCTCCUGGGT	83589	CGUGAAGCUGGAGAAGGAGAA
237537864	83590	CTTGCCTCCUCCGGGTUT	83591	GGGCUAGUGCCCCAAGG
237538587	83592	GTTGCTGTGCUCACACATGUT	83593	TCCTTAAAATTCAUACCAGCTCTUCCC
237538795	83594	AGGAGGGCCUTGGAAGCTUA	83595	GCAAGCCCUCATTUCACCAG
237540399	83596	TTGGCATCATAAUGTGTTTTGGCTUT	83597	GAATGAACUGCAAGCCCAGTUG
237540516	83598	TGGAGCAGAAACACCUCCCTUA	83599	GCTGCGUGGACUCGACAG
237541465	83600	GAACAACCUCCCTCCCTCAUC	83601	ATGCTTCAGGAUTTGCTGCUAGT
237541503	83602	CUGAGGGAGCTGUGGAAGAG	83603	CAGACGCCUACCGUCCA
237541513	83604	CGTCTGGAGUTTTTGGGTGUT	83605	CCAGGAAGGAGCACUTACGUT
237543586	83606	GCTTATAGUGCTCAGCUGCCT	83607	TTTCCTGAGUGGCCTTTCTTCUC
237544405	83608	AACTTCAAACAAAUCAAACCAGUCAACA	83609	AGTTGAAGTAGCUTTTATGCCCUCAG
237544747	83610	CCTGCCGCUTCCAUCCA	83611	GTCCCCGUGCCGCAUAT
237545172	83612	AGCACGGCCUTGGUCAG	83613	CCTGAAGTGGUTCTGATGACCUT
237547338	83614	TCTTCCTGTTUGGCTAAGGTTTUG	83615	CGAGCUGAAGACAATTTTAACTUGGAAA
237548388	83616	GAACTAGGCUCCAGGGTTGUT	83617	CAAGGAACUCAGAGAGGACUGG
237549836	83618	CCCTGCUCATGGTCTTUGAGT	83619	GGGAUGTCTAUAGGGAAGGGAAGA
237549971	83620	GTGTTTTGCUCTCCACCCTUCT	83621	GAAATGCTGAAUAAGGCTGAGGTUG
237552668	83622	CAAGACCGCAAAUTTTCCCTCUT	83623	CTGGATCACCCCUTCCTGAUG
237552947	83624	CTGTGTGGCUATTATCTGCAUACCT	83625	GTTCGCGUGGCCTCTGUAT
237553879	83626	CAGTGTCTGCUCTCCATCCUC	83627	GGTGGGCCAUCTCCACTAUC
237560815	83628	CCUAACCACAUCCGCCACAA	83629	GGACCCGGUCTCCTGGUAG
237562108	83630	ATGATTTGTUGGCAGAATTTGTCTUGT	83631	GACAACTGCTCUTCCTTTCTTTTTAGUT
237563902	83632	GCGGTCCAUGTAACCAUGAC	83633	TCTTTTCATGGTCUCGTCTCCTAATTUC
237564353	83634	CTCTGAGTTGTCUGTATTCTTCTCAUCA	83635	ATTAAACTGUGGACCAUGCCCAT
237565403	83636	GGAACTAGCTUCATCTGAGCAGAAUAAA	83637	GCCTGTCTAAAUCACTTTCAAAATCCUG
237565508	83638	TTCUACCAGCCCGTTTUCACA	83639	GCTGCATCUGAGGATTGATUCCAG
237565516	83640	CGAGGGACAAACCUGACUGAG	83641	CCAGGAAUACTTTAAGTTAUGCCCAGAA
237567115	83642	GCGTCUCCAAGATTCTTUGCC	83643	GGAGCCCCCGACUAUAGGAA
237568846	83644	GCCCAGUGACTATCCAGUCCA	83645	TGCCTGTCTUTTCACCCACTUT
237572719	83646	GCAGGCAUAAGTGAATGGTCUAGAT	83647	GCTGTTTTUGTCTCCTCUAGCGT
237572732	83648	GACAAGCTGTTUGATGTTTGTGGUA	83649	CCCATCCTUAACAGTTACCTGUGA
237573610	83650	ACAAAAACATCCUCATCTCGGAAGUT	83651	CAGTTCAGCTTUTGTTTGGTTGGUT
237579843	83652	ATGGGTGUAGATAGAGTGAAUGGAAGA	83653	TTCAUGCGACGCUGGGT
237581611	83654	GAAACAUAGGAGGACAGTTUGGCA	83655	AGAGAGACCUAAGCCTGTATGGATUAC
237582536	83656	CTGTTGATTATCUGGCCAAAAATGUGA	83657	GTTAGGGTUGGGCTGGGAAUT
237582644	83658	CTGGTCTTUCAGTTCCATGUCGT	83659	TCCUGAGCGAGCGAGGUAA
237590480	83660	GCCACAGCAUACATCCTGUCC	83661	TTCCUTACTTTTCCTUACGCACAAGA
237591111	83662	GCTAGTCACUGGTGCGGTUC	83663	TGGCTTTTTGGUGTTTGAATTTTCTGUT
237594248	83664	CTTGTTTTAUAAGTTCCGTUAAGCACAC	83665	GTATATTTCCCCUGCTCCACTCAUC
237596265	83666	CCAACTGAAGUCTCTCCTGTCCUA	83667	CCCTCTCUCATTTTCAGACUGAGG
237598127	83668	CAGGTCTTGAAAACUCTTCGGAAAUT	83669	TCATTAAGATTCAUTTGTTCAGGGATUGGA
237601009	83670	ACTTAGCAAUCGAGTAAUCAAGAAACCC	83671	ACTCAATGTCTUCCACAGTTCTUCAA
237601541	83672	GGAACATGAGAGUGCCAGCTTUA	83673	CCTTTAACCACUGGGTUGGGT
237602572	83674	CACAAACTUGAACAGCUACGGAAC	83675	GGTTGTGAGGUTGCATTTGAUCAT
237603280	83676	CACTGCAAAGAAAGAAUTTGAGACTUCA	83677	CTTTTCCTCAUCACCTGCTCCAAUA
237603917	83678	TGCCAACAGUCTGAAACATCUGT	83679	GATGAATGTUACAGCAGCCCTUG
237607361	83680	CATGGGUGGGUGGACAGT	83681	CTTCCATGAGGAUGCTGAGGUC
237614401	83682	CATTGAUCTGTAGCUGGAAGGAGA	83683	CCTTTCCTGCUCCCCAGGUA
237614436	83684	TCCTAAGACUAGTTTAGAGGAUGCAACA	83685	TGGAAATAGCUGAACATTCAAGUCACA
237616127	83686	GCAGACCGUGGAGTACCTGUA	83687	GTATCTGGCCUTGCGGAATTTUG
237619351	83688	AGACTCAAGGGAGGAUGAGATTUCT	83689	CCAAGUGGGUCCCAAAAGCAT
237621847	83690	TGGTTCAAAAGUGAAGCTCTGCUA	83691	GACTCTGAGCUGTGTTCTAUGGG
237627770	83692	CAAUGCAGCGACCATCGUT	83693	CATGGTCAGUGTCAGGATGGUA
237628281	83694	GGGTCTGUCTTGCTCAAUCAG	83695	CTTTCTGCCACCCUCTTTTTCAUT
237629333	83696	CATAACTCTGUATTTCTCCAGCUCGT	83697	ACCCUGGGCCTCAGUCA
237633763	83698	GATGGAAGCAGUGACCUGGAT	83699	CTTCTGTTTTGCUTTTACCCTAGTGUT
237636338	83700	TCUATCAATCTCCUCCAGGCCAT	83701	GCCCAAGGUGACATTTCTGTCTTUA
237636363	83702	CTAGATCCGUCCTTCTGCUACCT	83703	AGGCTATGGCUGTGTATGTGUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237640009	83704	ACACCAAGAAGCCACUCTUCC	83705	GGACGACAUGAAGGCCAAUCT
237641132	83706	GGTGGACCCUGGTAGGCUAAA	83707	GAGTAAAGUCCACAGGGTUCAGAAG
237644166	83708	ACTCTCCUGCCGAUGCC	83709	GCTGACGAGGUCTTTCTTTTTCTUGT
237644417	83710	GCAGATGCAGGUGTAGGAAUCAA	83711	CTGCCTTGGUCTTTGAGAAUCCT
237645114	83712	CTACAAGATCUGCTAACGGAUGGT	83713	GCTGGTGGUTTCTACTCTGUGG
237646732	83714	CACACTGCUCCCGATGUCA	83715	ACGTGGAGUTGGCATTUGACT
237648822	83716	AGGGAAAGAAGAGAGAAUAGGAGUCAA	83717	GTCCAAGGUAAAGCATUGCAGT
237652368	83718	CATCTCCACUCCAGCCGUT	83719	GAGACUCAAGAGCCCTAAUCAAAAGT
237653717	83720	AAAGTATTCUAGGTTTGCUGCCACA	83721	GTGAACAAGAGUAGATGCCTUCAGA
237654770	83722	GCTGCTTTATTTUTAACTGCAGTGUGT	83723	TGCGGUACCTGCTGAAUACAAG
237655143	83724	TTUAAGGAGCAAAGAATCUGCAGAGT	83725	GCCAAATACCAAUCATTCTCCTUGGAT
237657285	83726	CGGAAGCAUGTTACTTATUGGCAGAA	83727	GGCTGGGAAUAAAGGTUGGGT
237658519	83728	CTTCTTTGACTUTAGTGGCACTUGG	83729	CTCAATCAGCAGUTCAGCTCUCA
237659175	83730	GCTGCAGCUTGATGAGGUCAA	83731	GTAAUCTAGGAACCUCAAGGCAAAGT
237660525	83732	AGACCTGAUCCTATGCAAUGGAGAT	83733	CCATGTUAGAAGAGAGCAUGCCT
237661102	83734	GCCACCUTTGATCAUGGAAGAAA	83735	CCAUGCCAGGUGAAAAAGCAC
237661409	83736	CCTGGAUCCCGCCAAGUA	83737	CGACCUGCTCACGCUGAC
237662469	83738	CUGAAGTGCCTUAGCAGAGACC	83739	ATCAGCAATGUCACAGCCTUCT
237663341	83740	GGCAGCGGCACUTGUACT	83741	ACAUGCCACGTGGUGGAC
237664764	83742	CATAGTCUGCCACGCCTCUG	83743	AACTAACUGCCCUGGCACAT
237667648	83744	AGACGTCTCAGGUTAATCTCTCUGA	83745	GTTCTCACUGGATATGCTTGAUGACA
237667756	83746	GTACAGAAACGCUTTAAGTTUGCACA	83747	GAGTGGTTCUCAGCAGGTUGAA
237668837	83748	GGGATUAACGCGGCCAUGA	83749	CACGTATCUGCTCACACAGUCT
237669460	83750	GAGTGAATCTCUCACGTATTTGGAUCT	83751	TGGTGGCAGAACUGATCAACUG
237671425	83752	CAGACACAGGUTCCTGATCCUC	83753	GCTTTCCTGAUCTTTCTGCTGTCUA
237673045	83754	CAUCAUCCCACCAAGGCCAA	83755	GACTTCCTUGCCTCTCTTGGUA
237674806	83756	GACGATGCCUGTTCAAGUAACAC	83757	AGTATCAACTGCUAAACAAGAGCACUT
237675781	83758	GAGGACAGAGCCAGUAGGTUG	83759	ACCAGAGTCCUTAACAAGCATUGAG
237676414	83760	GCCTGUCCAGGTCCATCUCAT	83761	TGCUAAGCTGGUACGACCAAG
237679676	83762	CTCCACATAAUCAGGCCAGCUT	83763	CCATGGGAGCCUTCTGUGAG
237680230	83764	TGTTAATGGTGGCUTTTTGTTTGTTUGT	83765	TCTACCTCACUCTAACAAGCAGAUAACT
237686202	83766	CATGUGGAACAGAGGCTCUCT	83767	TGTTCCTTCTTUCCCTCCCTTACTUA
237691270	83768	GAAGCAACCCACAGAUGTUCC	83769	TCAACGAGUGCGTCUCGAA
237691345	83770	TCCATGGUAGGTCCCGTTUCT	83771	GGGATGATTGCUGAGTGTCCUG
237693257	83772	CAGGTGGCGUCGTTCUG	83773	CAGCCTCUCACCCGUGT
237694948	83774	GTGACTTCAGCUACGTCTCUGAAT	83775	CTGTGUCCCAAGACCCTGAUG
237695837	83776	CTGCATUCACATCCGCTUGG	83777	CAGGTGACTCUCTTTTCTGTACTTUCT
237700511	83778	GGUCCGAGCCGTGAUCAG	83779	TGCTCTTCAUCCTCGATGGTGUA
237702371	83780	GATGGAAATGAAACAAUTTGTCACTGUCT	83781	TGTTTCACCTUGGACAGGAACUC
237702477	83782	TCAGGAGUTCCTGUCCAAGGT	83783	ATTCCATTACUGGGATTTTTCACGUAGT
237703486	83784	ATGCCCTTUACTGAAATGUCAGAAGAA	83785	CCTTCATTCCAUTACTGGGATTTTUCAC
237703933	83786	ATGACTTGCAGUCTTGTGATCUGAAT	83787	TTTCCTTCAGGGAUATCAATGTUCAGG
237704592	83788	TTTTCACTCAATCUAAGCCCACACUT	83789	TGAAAGAAUAAACACAGAACTGGTUGGT
237713225	83790	CAAGACCCAUCCTGGCUCAT	83791	GTCTTCUACTTCAGCUGCAGAGAG
237716399	83792	CATTCCCCUCCTCTTGGTGTUG	83793	CCACAATATCAUCAACCTCCUCAAAGAA
237716507	83794	CCCTGTGCUGGCACCUA	83795	ATCAGCAACCCCUGUAACGAG
237717598	83796	GGTTGGUGTCGCAGTUGGA	83797	CGTGGGUGGTGUGCCAT
237718482	83798	CCTGCTGCTUTTCATCGTGAAUG	83799	AGAGATGAGTGCUATTCTTCAGGCTUA
237719798	83800	GCCACGGGCUTCTTAAATTUCAT	83801	CAGAUGCCAAUGAGAGGAAAGGT
237721437	83802	CGAGACUCACCACCTUGGACT	83803	CCAAGAACCUCGCATAGTCATACUG
237721702	83804	CTTAGGCTTCUCCTGGCAATCUC	83805	GAATTCACACAGUCCTAGTTTCCUCT
237725262	83806	GTTTTCTUGCCGTGGUGCAAA	83807	GGACGTAGAGTUATTGAAAATGCAGAUG
237731334	83808	GTGTCCGUTTCCTCCUCAGAAC	83809	TCCCAACCAUGAAGATTTCTTTGCUAA
237736320	83810	CUTCCTTGCTACUCAGCACAAGT	83811	GGTGATGGTUGAGACTGTGGUAA
237736714	83812	CATCCTGCCAGUGCCTCUA	83813	TCAAAGAAGGCCCUGUCCAAG
237736906	83814	CCTTACCTAUGGCCAAGAUGCC	83815	TCCCACCACCACAGUTAGAGAATTATUA
237737626	83816	CCCAGCCUAGACATTTTCTUAAACC	83817	GCATTAAGCTGUCCTTTTATCTGTTCCUT
237740556	83818	GGTTCCACUGCGAGTGTUG	83819	CATTGGGUCTCCCGGUCT
237741017	83820	GTTGACUTCCCAATUCCAGCAG	83821	CCAAGAUCCCCTGGUCAAGAG
237742914	83822	CATGCTUCAGGCTCAGGAUACA	83823	CCAGCTTCGUCTTGCTGUGA
237744065	83824	CCCTAATTCTGGUGCCTTCACTUT	83825	TCACAGTCTTUCATCAGGTTCUGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237745484	83826	GGCACAGGGUTGAGTGUCAT	83827	CCACAGUGTGUACCCCACAG
237748202	83828	AGTTGUACAATCTCCUGGGAGGT	83829	CTGGGCTAUACTGGGAGCUACT
237750565	83830	GCACAGGCUCUCCACAGG	83831	TGCAAAGGAGCUCTGCTUCA
237751853	83832	TTTGATGTCACUTGCACTTTAGGUCT	83833	CGATGCCCCACAAUTTCACATUT
237753037	83834	ACACTTGCCUAGAATTTTACTAACUGGAA	83835	AAATGGTTGTAUGGCTGTTGGTTTUAC
237757670	83836	GGGATTCUCAGGAGTGTGUACC	83837	GCCTAACACCUAAGTGATGCTCTTTUT
237759237	83838	CAGCCACUGUCAAAGCAAAGAC	83839	GTTACGTAGATGAGAAUTCTAAATCACACUCT
237759472	83840	TGGAGTTGGGUATGTGGATTCCAUA	83841	TCCTCCGGGUAAAACACATUCC
237760425	83842	GGAACTGAGAUGTCCCCAGCUA	83843	CAACTCCTGAGAUCTGCTCTGTTUT
237761719	83844	GGGCCUGAGAUCACCAAGAC	83845	GATGTGCUAGTTCCACCUCCA
237762210	83846	CCTCACAUGTGCACTCTUCCAA	83847	CAGGUAAAAAGAATTTCCTUCAGCACT
237764564	83848	CTGAGCCUGGAAAGGTGGTUA	83849	CCTCCAGGUGAGAAAGAUCGAGA
237764726	83850	TCTCTCTAAGTCAUGATCTCGCTCUC	83851	AGAGCTTTAGGAGUCTTCCTTTCCUT
237764910	83852	ATTTTTCAGUGACAGACAUACAGAGAGG	83853	CAUCCGGGACUACAGGGAGAA
237768698	83854	CTCCTCAUCCAGATUGGACCAAA	83855	CCTTTCCUAGGCCTGGAATCUC
237768779	83856	ACTCATCGAGUTGCTCCUCAC	83857	TGTTCTTCTAUGACATTTCTCCCUCACT
237770513	83858	CTACTCTCACUCAGACCCTCTTUG	83859	GAACACCAUGCTGAGCCTTUG
237772923	83860	GTCGTTTGCCCUCTCCAGUT	83861	CCGTAGAUGGCGTGCAGUC
237773299	83862	CCGCATCTCUTCCCGATGTUT	83863	TCGCACAUTTCGAGAUGAAGAGG
237773994	83864	CUGTGGTGTTUGGGAGGCT	83865	GCCCTGGCUATGCAGGUA
237774165	83866	AGAUTGGCTTCTUCCGCACAA	83867	CUCCGGGCTTUCGAGGAAA
237777185	83868	CCTTCGCUTCGCTCTTUCC	83869	CCTCGGCGCUTTAACCCTUT
237777336	83870	GCAGGTACTUCTGTCAGCTGAUT	83871	CCCCUAGCACGTGCCUAC
237778006	83872	GTGATGAAAUGGCCAAGAATCUGG	83873	TGCTGGATCTCUGTGATGAAAAACTUAA
237778242	83874	GATCTTTGCCAGGUTTCCGTTUAT	83875	TCAGGTGGUGGAGAGTTGTTTUT
237780168	83876	GTGAGGCATTUTGGAAAGTTTCTUGT	83877	GCATGACATTUGCTTCTGCTAAUAACT
237782565	83878	CGCUCTTACCTUCCACCCA	83879	GAGAGCGAAGTUTCAGAGACTCTTAUT
237782721	83880	ACAGATTTCATGTUAGTAACTTGGTTATTTTUG	83881	ACCTGCATTUGACCCATTTCCUT
237782758	83882	ATCTTTTCAGTAGUGTGATTAGGCGUT	83883	CAGACCCCGCAUTATTTCAATCUC
237782771	83884	ATTCUCAAGTGGTUGCGGGAA	83885	GGAGGAAGGAGAAGCUGAAAUAGAAC
237785195	83886	GUGGACAGATCUCACGGGAAT	83887	GGTCAGGATUGAATGGGAAAUGAAGA
237785329	83888	CCACATCAGUTCTTCACCUCCAAAT	83889	GCCCACTCCUTCCCAAACUT
237786090	83890	TCAAATTACAGUCAACTGCAGAAACCUA	83891	CCTGGAGGUCTTTTUGGGACAG
237790388	83892	GCTCTGUCCAGGTGTCCTTUG	83893	TGAAGGAGAUAGACATCAGCCAUCAT
237791372	83894	TCCCAGTGCUGGTGTTTGUAG	83895	TGAGATTCGTUACGGAAACTATUACAGG
237793618	83896	CCAAGAACTUGCCGCAGTTTUT	83897	ACTCCTCCCUTCTGCTUCGT
237794475	83898	CAGGCAATATTUCATGTGGGAGATUAGA	83899	GTTGGAATATTTCUGGTTGTTACAAUCCC
237794627	83900	CTTACCAAAGGUCAGTGGGATUGT	83901	CTCTGTGTGCUTAGGTAGAGCUG
237796245	83902	ATCTGTATGUTCCTGGUCAGAGACT	83903	GGCAGACATUGTTTCCTCTTTUCAC
237799191	83904	TCAGATTAATTGCUGTGCTTTTGGATUC	83905	GGCTCAGAAAAAUTGGATUGACCAT
237799313	83906	GCTCGATGTUGAGAAGGATCTTCUT	83907	TTTACGGTACACUAACCCTGCTTUT
237801648	83908	GCAACCUGAAGAAGCTAGUGGAA	83909	CUAGGGAUGGGCCAGCAG
237802439	83910	TCTCCATCUTTGCCTGUGAGAT	83911	TGAAAAAGTACUCATTTGGTGCACUCT
237803449	83912	AGTGGGUCAGGAAAACATTCTTGUT	83913	GGGUGGAAGTUAAAGAAGGCAT
237807561	83914	GAGCUGAGGAATTUGCAACGA	83915	TGGGAAATTCCUGGAACCCTUG
237808863	83916	AGGCAGAGGUCTTCTCCAGUT	83917	CTTAGTGGATUCTTCGCAGCCUA
237810345	83918	TGTCTCACAGCGAACAUACTCTTUC	83919	CTACGGCGAAUGCTACTGGUA
237812542	83920	CCCCCTCAUTGGTCACAAATUG	83921	AGTGGATCAGACAUCTGGGAACTATAUT
237812660	83922	CAGCAACCACUAGCCUCCT	83923	GCGAGUCGGAGGACAACUG
237815087	83924	CCCAGGCAUAGCCTUCGG	83925	AGGUGGGCAAGCGAGUT
237818440	83926	CTTGGATTTCUCTGGTGGCAGUA	83927	AACAGAGUCAGCAUCAGAGCAG
237818987	83928	GGAAGUCCCAGACCCUGAC	83929	GGAATCACTTTTCUTTTCTGGACTTGUT
237819391	83930	CAATGACCCCGCUCTTAAAGAUG	83931	ACAATACCTGTTCUGCTGCAAATACUT
237821735	83932	TGTTCTUCCACGCCATCATCUC	83933	GATTCCUCCCAAGCCUACAGAC
237822098	83934	TCAGCUCCGCATTCUCAAGG	83935	AGTTAATTGCGGGCUGAGATGUT
237823848	83936	GGCGGTGUAAATAAGAGGGCUT	83937	AAGCATCTGTTTUCTCTCCCTTTCUT
237824275	83938	CACCTGAUTGGAGUGCAAGAC	83939	TTGACCUCTGATCCUACCCACA
237825634	83940	GCUGCCAGCACUAAGGAAAGAG	83941	CGGAAGCAGCCUCTCGAUAT
237826280	83942	ACACTGGUCCCCCUGAGA	83943	AGCTCATTGTCUAATGTCATTCTCCTUT
237829691	83944	GTATCTTAGAAAGUGAAATAACTAACCUCGCT	83945	CATAGGGATTGUGGGCATTTAGUCA
237831689	83946	ATCTCTCUGGAGGATGACGUAGG	83947	TCAGAGCACGAUCATTCTTCTCATUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237832277	83948	AAGCGAGCTAAUTTGTCTTCTTTCUCT	83949	CATCUGGAGCTAATTGUGAAAAACAGT
237833419	83950	GACGTCTGAGAUCGTCAGGUT	83951	CTGAAGUGCCCATTTCCCUGT
237833444	83952	GCAGAACTUGGTCCCCUCAAT	83953	GCTUCCCAAGGAAAUCAGGCT
237833750	83954	CACACUGAGAAAGCGGAAGAUG	83955	CCCAAGTCCAUCCAATTCTAATUCAGG
237833804	83956	GCAAAGGTUGGACTGAAUGGG	83957	CCTTTGGAGGGAAUATTATCCAGCAUT
237834866	83958	CCTTCUCAAAGCCCTCCTUCAC	83959	CCCAGCUCGTGGTAAACUCA
237843874	83960	GCTGGTTGUGGCCCAGATUT	83961	AAGTACAAGGCCUCCAUCACC
237844563	83962	CGTTCCTTCTUCATTTTCCCTCCUG	83963	AGCTGACTTCTUTCCTATGCTCTTUG
237845317	83964	GCACGTACUTGGTCTCGTUGT	83965	CCAGAACAAGGAGCUTAAGGUCAA
237849574	83966	GTCAATGAATGUTTTGGCCCATUGT	83967	CTCGGCCAAUGGACCUACAAA
237855594	83968	GAGGGAAGUGGCTTTUGAGGAA	83969	TCATGGCTTAUCCAGAAAGTATAUGCAC
237856977	83970	TTCCTCCAGGAUGGGTCCTTUA	83971	CTGTACAUGCTAACATAGUCCAAGGG
237857203	83972	TGATTGTTTCCUGATGCTGCUGA	83973	AUTGAGAACATGTUGCAGAACAAGAAAA
237857475	83974	GCCCTGCUGTCCGTCUC	83975	GCUCCAGCGGCAUGGAAA
237857533	83976	GACTTGACAGUGCCCUCCAT	83977	AAGGTCACUGGCCCTTCTUC
237861438	83978	TCCTTCTCAUCAGGAATTTCCAAAAUGA	83979	ATTGACAATGAGGAUCTGGTGTAUGG
237861943	83980	CCTTCAAGGUCAGGGTTUGGT	83981	CCTCTGGCTUCTTGAGGTCTUC
237862032	83982	ATGAAAACCATUACAAACTTCTCAAGUG	83983	TTGTACCTTUCCCCCTTTTCTUCAG
237865860	83984	CCCAAGAGCUACCACAATTUGCT	83985	TCATCAGAAAGGGACCUGACUCA
237868220	83986	GGGCTGCCAUAATTCCAUAGCA	83987	ACAGGUGTCAUCAGGGAGGA
237873847	83988	GGGAGCGUTGAAGGAATUGG	83989	CATCCCCAGUGCCGAGTUA
237876672	83990	CGTGGCUACAGTTGGUGAAGAAT	83991	CCAGAUGAAGCAGTGGGUGAG
237881176	83992	CATCCCAAAUGATATTGTCCUCCCA	83993	TGGCUTACAATGTUCAGCAAGGT
237881643	83994	GCTCCUCCCATTCACGUGAC	83995	GTCAGCGUATCTTTGACCUACAGA
237882152	83996	GAAAAAGUCGGTAAGAAUGAACAAGGG	83997	CATCCCTACCUTGCCTTCACUT
237882402	83998	CTGAGACAUGTTCTGCTGUGGT	83999	GGCACTTGAUCCCAATGAUGAGAA
237884501	84000	GTAGAGGCATUTACGCACATTTUCA	84001	GGTGACGCUGTCATCCAUCC
237891453	84002	AAAAACCAGGAAGCAGAUGUCCA	84003	GTTAAACTUGCCAAAACAGCUGACT
237894640	84004	GTGTAGGUCCCCGAGTCTUC	84005	GCTTGCAGGCUGATTTCUCC
237894790	84006	CACAATCAACUCCTCCUGCCA	84007	GTGACCTGCCUACTAATTCCCATAAUT
237894933	84008	CCCCUCGTCCCAUGAAGGA	84009	CCTCCACCUTGGGCTACUCA
237896052	84010	GCCCTGGCACCUTCATATGUA	84011	ACAUCGACUCGGCCAACAAG
237896197	84012	GGUTGGGUGGCCCAGAC	84013	GGATAAAGAACAGGUGGCATATACUCA
237899254	84014	GGTACTGCUCCAGAAGTGGUT	84015	ACTTAGGAAAUAGAATCCUGACCCACAT
237899918	84016	TGAACTCCCUGACGGGUCT	84017	CAGGAAGUCGCGCUCCAA
237901881	84018	GATGGCTUCGTCCCGGUT	84019	CTTCCCAAGTUGTTGATGTTCCUT
237905828	84020	CATCAUCCAGAGTGGGUGCAAA	84021	CACAGCUGCATUGGGAGGAT
237906436	84022	GGAAGCUGTGATGUCCCCAAA	84023	CACCATCCTCUGTTTTTGCTGUAG
237910368	84024	GCCGCAGUCUGACAGGAAA	84025	CCAAGUCCCCCGUAGCCT
237912034	84026	AAAGGGTGTGTAUTTGGAAGATCTCUC	84027	TTGGAACCACUGTTCATTGTGACUAT
237913176	84028	CATGCCTCUGCAACCTGAUGA	84029	TGATAGGUGAAGCTCAACAAAUCCAAT
237914002	84030	CCTCAGTTGAUGACAGAACCTUGT	84031	GAACAGGCUCATTCUGGAGAGG
237914369	84032	AGCCATGCUGGTTACATTTUCCT	84033	CCTCAATUCCCAGGTGGACCUAT
237920365	84034	TTTTTGCATTUCCCAAGACAGTGUT	84035	AAGCTTAAGGACUATGGAGTGGATCTUA
237920522	84036	GGGUCAGTGCUCACCAGT	84037	AGCTCTCCACUCCAGCUCAA
237922146	84038	GGCCUCCUGCAACAGCA	84039	TCGCACUCCCCTTCUCCAT
237923738	84040	CTTGAUCCACGGGCAAATTTACUC	84041	GGTGTGCCUGAGGAAGAGATUAAAAA
237924233	84042	CTTCTTCUACCCCACATCCATTGUC	84043	AAAAACTGAUAGCATGGGUCCGT
237924767	84044	GCCTGGCTUGGTATTGCAAAAUAT	84045	TCTCTTCTTUGGCCGTGGTUC
237925161	84046	AGAGAACACUGGGAGAGGGUAG	84047	ACACCACUGCCGAUCCAAAG
237925481	84048	GGTGGATGGACUTATGAGGTATATUCAA	84049	GTCTUCGGGAAACAGCTAATUGAGAAT
237926434	84050	GAGACAUAGCAGGGCGCUT	84051	GGGTACUAACCCCAGGTUGA
237927515	84052	CTGATCAGCCUTAAGTTAUAACCCAAA	84053	GCTCATTATGUCACCATTATCTCTUCCA
237927525	84054	ACTCACTUGGGCATGAAUGCT	84055	AGAAGGCTCTTACUACACCTACTCATUAT
237928974	84056	TCCAGAGCAACAGCUTTATCATGTAUT	84057	GAAACTATTTTTGGUCTCAGGAATTUCGG
237929352	84058	GCTGCAUCTCGAGTUGAACAGT	84059	CTAACTATCTGTUCCCAACCCCAUC
237929810	84060	TGGTTTTATTTTAGUGCTGTTCCTTUGG	84061	CCACTACCUCTAGATTCTCUGGCT
237931184	84062	TTTUCAGGCCGCCCUCA	84063	ATGATCCAAAUGGCTGGTGAGAUT
237932183	84064	TCTGGAGUGCCCCATAAGGAUA	84065	CCCTACCCUCTCCCAGTGTUC
237932366	84066	CAGATGATAACUCAGAAGGCCTTACTUT	84067	GGGTCTAAAAAGGUCTGTGTTCCUT
237932822	84068	CCTCCCCAUCCCAGATGAUAGA	84069	TGAGAAAGACACAACAUGAACCUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
237933219	84070	GAACAGAUAGTUAGGGAGCACCAA	84071	CTUCCCAGCGGTTGUCCA
237933606	84072	GGAGGGAAUGCGAAGAAACTCUT	84073	CGTCGTAUGCGAGAGTCUGT
237933750	84074	CCCTAACACAAUCCAGGUGGAA	84075	CCAUGAAGGCCCAGTUCGAG
237936866	84076	CTGACCAGCUGCTTCTTCTUCT	84077	GAGAUGAAGACGCAGCUGGAA
237936877	84078	CCAGAGCUCAAGGCTGTCTTUC	84079	TCCTCACTGUCATCGTCACUCA
237938099	84080	CTTTGGCCGGACUCTAGUGG	84081	TGTGATTTTUAAGGCCAGTGCAGUA
237938149	84082	TTACCCACAUTCCTTTATAAGUCCACAG	84083	TCCTGCAATTCUCAGCATGGATTUA
237939245	84084	TCTTTTCTGGTUTTTCTTGGCTCUACT	84085	CGGCCCUGCATCCAUGAT
237940466	84086	GCAGCTUGGCATCTUCGGT	84087	AGGTACCUGCCAGTCCCTUT
237940525	84088	AAGAUCAAGCTUGGCCGGAA	84089	CGGCCUCACCTCCTCTUG
237940579	84090	AAAAATTACCUAACAGGCATCCUGGAA	84091	GTCTCTGTAAGAUTACTGCAAGCCUAAA
237942000	84092	TCAGCUGGCGCTTACAGUAG	84093	ACTGTACGAGAUGTTTCGGATTUCA
237942008	84094	GAGGUGCACCAUAAGCAGGA	84095	TTAAAGAGCUAGGAGTGGGUAGGT
237942399	84096	AAGATCTGUGACGTTCCTUCCAAAT	84097	GCTCATGAGGAGAUCTTGGATCTUT
237943523	84098	AACAGGTACAACUGTAACTGCTTUAAGA	84099	AGGAUACCAAAGCTCAUGAGGAGAT
237947873	84100	GGCCTCACCUGCCTCUCT	84101	GCAUCCUGAGCACAGCGT
237949576	84102	GGTCTCACCTUCTCTCTGCTCUT	84103	CAATGTGCUCACGGATGCUG
237949761	84104	CTCAAGTTTCCUAAATTCCTCCATCATUC	84105	GAGTGGCUGAGTGGCGTUAT
237949874	84106	CGAAGCUGCTGCCTTGUC	84107	CCGCUGCAGACTCUCGAA
237951243	84108	CAAGATCUCCTTCCCGUGGAA	84109	GCCTGGGAAUTAAAGGACTCTAUGAAT
237951564	84110	GGATGACAGGGCUGGAATAUGAC	84111	AUCGATGCCTUCCAGCACAT
237953277	84112	TCCTGTCCUCGCGTCGAUA	84113	GCATGTTGGUGACCTCTGAATTTUT
237953328	84114	ACACACGCCUCTAAATTATTATTUGCAC	84115	GCCACGGAGAACACUACUGAA
237953344	84116	CCGCCCUGGATAACGTCTUT	84117	GTGTGCCUCGAAGCACTUG
237957004	84118	TCTGGUGCTTTGAGUGCGA	84119	GGAGCAGAAGAUGTTGTTGGTCUT
237957637	84120	ACAGCAGGCACUCCAUAAACAG	84121	CAAATTCCAGGUGGCAACUGA
237958271	84122	GATCACACATCTUACTAGAACACACUCA	84123	TGTTTGAAAAUGCCAAACGCTATAAUGT
237958497	84124	GTCTCUGGCAAAGGTGTTUGG	84125	TGAGTAACCUGAAGACCAUGGGT
237961228	84126	GGTGCGUGAGTTCCUGGAC	84127	GCCCTCUACCTGGTACTUGGAT
237962204	84128	GCATGGTCUGGACAAAATGCUG	84129	TCATTCTGTGCUCTAGGGTATTCUGT
237963221	84130	CAGAUGAGACAGCUCACGAGAA	84131	GCAGCAUGAAGGAGAATCTGUG
237963975	84132	CTGAATTGGGCACAUTATAGCGTUT	84133	CATTGGACTTUCAGGAAGAATGTTUCAT
237971446	84134	GTGGCCUGCCTGATGAUGAT	84135	GAGTCCATCACUGTATCCTCCUG
237972800	84136	AGAGCCTGUCTTTGCGGAUAG	84137	GTCTGCGACUTCGGCTTUG
237973507	84138	GGCUCACGGCTCTTUAAAGCA	84139	GCTGCCTUAGGCTTTTCTUCACT
237976051	84140	GCCATCTCTCUCCTCCTTTTTCUT	84141	GUGACAGAAAGGUAAAGAGGAGCA
237976541	84142	CGTGUAGCAGGGTGTCAUGAG	84143	GCCTTCTGTCUTGCAGGTTGUT
237980419	84144	ATTTTCUGCGAACCTCAUGCAC	84145	ATGUGCCACCTUCGAAACCT
237980984	84146	TTGATTGCTGUTGTTAGGAAAUAGGACA	84147	TGGATAGGUGGCTGCAAGGUA
237981490	84148	ACTCGGCUTCAGGTCUCGAT	84149	GCAGGACCUGCUAGGAAGAC
237981580	84150	AGAAGCTCTTUACTTGATAGCTUGCAAT	84151	CCAGAATUAGTGTCATCTUGAGGAGAAA
237981708	84152	CCCUAGGGAGCACAGUGG	84153	CGGTTTATTCTGGUGGATACCATGUT
237982360	84154	AGGAAAUACATGTGUAAGCCACACT	84155	AGCATGGCTGUTTTTGTCTCTTTCUA
237982785	84156	CCUGAUGCCAGGACGGA	84157	GTGGTGCUGGAGGCTAUGG
237984110	84158	GGGTCTTUGGACAGACAACCUT	84159	GCACCAAAGACACUTCCACUG
237986190	84160	CTTCGCCAUGTTAUCAGCCAGA	84161	CCCTATGGCTTUGAAATAATTGGTAGUG
237986575	84162	TCATGATGAUGCCTCTTAGCAUAGGA	84163	CATGTAGGTATAAUGCCTGCTGTTACUT
237988103	84164	CCTGTTGGUCAGGAATGCTUAACA	84165	GAAGTGATGAUCTGAGAACTUGAAAGGA
237989195	84166	GGTCCUCACCAAAGTTCTCUGT	84167	CCAGGTAATCUTCTGCCTCCUC
237993791	84168	CTCUCCCAAAGGTTCUGAAGGA	84169	CTAACCAAGCAACUTCTTAGTGTUGG
237994613	84170	GCCGUCGAAACATCAAGUACC	84171	TGTTGTTGGUGAGCTGGTUGA
237994921	84172	GGCAACCUTCUCAGGCCAA	84173	AAAAACTTTGCUACACTGACAUGGAAAA
237996715	84174	GCCCTTCTTUTTCGGCAACAUC	84175	GGTGTAGUGGTGTGCCTUCC
238000818	84176	GCTTCCUCCACTCCCACAUC	84177	CAGAGCCUCCCTGUCCAAA
238001198	84178	CATGAGTGAUGGGCTTTATTUGCT	84179	GCGTAGGUGCCATTCAGCUC
238002517	84180	GTCATCTTTTGCUAAATCCAACCCAUT	84181	TGTGATTCCUGAGGGAGGUGA
238002595	84182	GCACACCACUACACCAUCGAG	84183	CCGGTUGAAGGGCTTCTUGAG
238003298	84184	CUGCGGCAACAGTUCGAC	84185	GTATTTGGGTUCTCAAGGACACUCA
238006007	84186	GAAAAAGAGGAAGAUTCTTCTGGCCAUA	84187	GCCACTAGAGUCCTAAATCUCGAACA
238007286	84188	CTGGCATCAGUGGCAGATCUT	84189	GAAAGGTTCAUGTGGTTCUGCAC
238012538	84190	AGGAAGUTCUAGAAACAACAAAGCACT	84191	GGCTGGUGCACACGTACTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238012575	84192	GGTGATTAAAGUCCACCCAUCCT	84193	CACAAAGUCCCAGTUCACCCA
238013374	84194	CTACCACUCCCAGGAGTCUGAT	84195	GCAGGTTCCAUGTCTGCTUCA
238014183	84196	CTGCCAGTUCTAGCTCAGCUT	84197	GCTGGCTGUGCTACCAGUC
238018062	84198	GGTCAGTUTTCAGATGAUCGCCAT	84199	AAAACUGGGAGCCGGGTAUC
238020841	84200	CTGCTCUTCTGTCAUGGCAAC	84201	GAAAATGAAAGAGCGUCCTGACCUA
238021669	84202	CCTTCTTAUGAGGCCATTCCUGAAAG	84203	CCAGCTTACUAGAGGTGGUGGA
238022124	84204	GTCTTGGAGUGGCTGTTTTGTTUT	84205	CATCCGCUCTCCTTTCTCUAACA
238023895	84206	CCCTGUGACCCTGCTTGUC	84207	GGCGTTUCCAGGGCTUAC
238024164	84208	GTTTGAATUCCCGGCAGGTUT	84209	GAAAGCCAGGAAAUGCACTCTUAC
238024680	84210	CUCCTGCTTTUGGGCAGAGT	84211	AGAGGGAAACAAGUAAAAAGCTUCCA
238026020	84212	TGAAGGAAAACCUCATCAGGGAATAUG	84213	GTTGCATGUAGCCAGGAAGUCT
238027284	84214	CACCGCACCAAGUCTGTTUG	84215	CGACUGCCCAAAGACUGAGG
238030869	84216	GGCATGACAAGUAGTGCCTGTAATAAUA	84217	GCTAGGTGAATUCTGTGAGCTCAUC
238032241	84218	GTACCAGCCCCAAGUGGAUG	84219	AACCTCATTCUGTTTTGTTCTCTAUCGT
238034820	84220	CAGGGAAGGGUCATGAUCAGAA	84221	CATTGACGUAGAAGAGAAUAACAGCAG
238035113	84222	GAAAGGAAGUGAAGTCACCGCUA	84223	TCACAGTCAGUGTCAGGTACUCA
238035319	84224	GAGGCUCCAGGACTTCGAAUT	84225	GGAGACUCACUACCCCGACA
238036994	84226	CACATGCCCCACAUTTCAGTUT	84227	GGAGGATUCAAGAGCAACUGAGG
238038895	84228	CAAACACAGUTACCUGCACGAT	84229	CATCTGAACUCTGCCCCTGUC
238042039	84230	AGTTCATTGUCCTGTTCTCTUCAGG	84231	CCCAATGCCAUCACTTAGCTTUT
238044968	84232	CACATUGCCACCAUCCAACAG	84233	CTTGGTTUAAGGCAACATTGGCUA
238046811	84234	CAGCTCCUCCCGAGTGUAGA	84235	GTCTCCTCTGUCATACTCTAGTTCCUT
238046994	84236	CTTCTCTGCCAGUTCTCCAGUC	84237	GAATCCAGAGGUTTGCCAUCACT
238053321	84238	GATAGCCTUCCCCACAUGGAA	84239	CTTCGTGCGCUGCATCAUC
238053843	84240	GCACCTTCUGGAACTGCTCUT	84241	CGCAGTCCUGAAAAACTUCCC
238055250	84242	CTTTGAGAACUCTCCTUGAGGAAGAAT	84243	AGGUAGAAGACACAACCACCUAGAG
238055360	84244	CTCCTTTTCCUGGTTCCGCTUAA	84245	CGCATACGGACUACAAAAGAUGAGA
238055908	84246	TGUAAGACACGAGACACUGGAAGA	84247	TGGGTAAUGCAGGCAGACATUAT
238056291	84248	CUTGGGCTTCCUAAAAACAGCAAT	84249	CCTGTGCACCCUCACCTUG
238058188	84250	GCCAACTTGAAAUGAAGACTTTUCCT	84251	GAAAGAGAGGUAGATTTCAATGGCTUCT
238058943	84252	CTCACCCTCUTCTCGTGGUT	84253	GAUGGCCAAGAUGACGGAGA
238063591	84254	GGAGTATCUCCCGGGACUCA	84255	GGAGCUCGACAGCAATCTGUA
238065039	84256	GGAAAAGTUAGCAACACAAATGAAGUCT	84257	CCTCCTCCTTUTTGTGTTTGGTTUT
238068373	84258	CGTGGTCCGUGAAGAGTTUGT	84259	TGCCGTAUGACCTGACCTUG
238069400	84260	GGTGAGAUGGCCTACATCGUG	84261	CTGTGCTGAAUCTGACCTGTCUT
238071583	84262	GCGGAACUCGAATCGCUACC	84263	TGGGUCCCCAAGACACCUA
238072323	84264	TGCCUCCATUGACACAAGGT	84265	AAATGTGAGACUGATGTCAATGAGUGT
238073127	84266	TGCCTCCATUGACACAAGGUG	84267	CAGAAATGUGAGACTGATGTCAAUGAG
238076498	84268	GAGAAAAGTGAAUTGGCCCTCUCT	84269	TGATAGGCTUTGGTGAAGAUAGCAC
238079093	84270	TTCCCTGGUATCCCATTCTUCCA	84271	CTACAACAUACGTAGCUGACACAGAA
238079289	84272	TGACCTTTTTGGUTACCCACACUT	84273	ACTGGTGCUCATTTTCATCATTAUCCA
238079347	84274	CATGCCCUTCTTGGTCTUGGA	84275	GCTGAGCCUCTGGCCTATTUAG
238080927	84276	CAGATAGCAUCAGGGCCUCAG	84277	TGCUGTCTAAAAATUAAGGCCCACAT
238082176	84278	AGGCCGACAAAGAUTATCACTTUAAGG	84279	AAAGTCUCAAGCCACATGAAUAGAAACT
238084206	84280	CACACTCATUGACATCAGTCUCACAT	84281	GGAGUGCCAAUGGACGGA
238084618	84282	GAAGACTTTGCUCTGGCCAAUG	84283	CTCGUCAGCCAGUGAGAAGAA
238085432	84284	CAAGUTCTTTGGCUGGAGAGACT	84285	TCTTGGTTGGCUGGGTACTAGTUA
238086816	84286	GTCACTTUGAGAGCCCCACUC	84287	GAAATGTTTTTGTUCCTCCTGTGCUA
238089891	84288	AUGAGACAGGCAGGCAUCC	84289	AAGAGCTCGCUGATGTCAAUGA
238091230	84290	GCTCACCCGGAAGUCAGAUT	84291	TTGCCAAUCCAGAAGTAACCUGT
238091709	84292	TGAAATGATTCAAUCTGACAACAGCUCT	84293	GCATGCCGUAACTGCTGTUC
238099926	84294	CTTTACCATGTAUCTGCTTGCTCUGA	84295	CAGTTGTGATTCUTTCTTTCTACTTGUGT
238102632	84296	CTCCTTCUGCTTCAGGCUACT	84297	CACACTCAAUGCCACCAUCC
238104976	84298	CAACCAAUAAGGCTTCAUCCACAAG	84299	CTGCTGGUGGTGCTACUGAG
238114052	84300	TGTGTGTTTGTUTAGCTTTTTGGUGA	84301	CACTGAGAGGUGACTUAAAGAAACCAT
238116451	84302	GCCAGTTCUTGATCCTGTUGCT	84303	GTCTAGCCUGATCACTGACCUG
238116712	84304	CTTCCAAGAGCCCAUCCAUCA	84305	GATTTGTACCTUCGAACAAGAAAUGAGT
238117251	84306	GTCATTGTUGTGCCCCUACCT	84307	CGUTGAAGUGGAGCAAGAGGAC
238117364	84308	CAGCCTUGCCCCTTCAAACUA	84309	CCAAGATCTUAGGCAGAATGAACAATUC
238117887	84310	GCACAGUTCATGTCUCCAAGGA	84311	TTACTGGGATGTUTGAATAAGATCGGUT
238127121	84312	GTGGUCCCAGCCAGTCATUAC	84313	GTTTGTTGGAAGAAUGTGATCAGCTTAUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238127313	84314	GCTGAGAAAGCUGAAGGTCCTUA	84315	GACUTCAGTTCCUGCAGCCA
238129047	84316	CTGGTCAAUGACTCAGACTUCCAG	84317	TCCCCAGACAGGCAAUAGGUA
238129858	84318	TGAGGTUGGAGATGGAGCUCT	84319	CCACUCTTGCUGCAAACAACAC
238130907	84320	TTGCATGGUCATAGCUCCCAAT	84321	TGTAGTTTCTCUTTGGAAAGCTCUGG
238138488	84322	CTAGUGCAGCTTTUGACAACAACT	84323	TTTATGCCGTTCUGTCAATGAGCUA
238139142	84324	GCUACCTGTTGUACAGAGCACA	84325	GCATUGGCAGGATGGTUGAG
238140375	84326	GGGAAGCCUTCCTTTCAAAUCC	84327	GGCCTAUGACAAGAAAAUGGACAC
238143557	84328	AAGTGCTTAAUGGCTAGACAAAUAGCA	84329	TCCCGGGAUCGTGTTCUACA
238144512	84330	TCGGGUTATACUGGAAGCCACT	84331	GCTGAGCCAUCCAGAACCTUT
238144974	84332	TCAAAGCATUGCCATGGAAAAUGG	84333	AATCCAGUGCTTCCUCCACAG
238146745	84334	GTCTCCCCAUGTGGUCCAA	84335	CGCACAGCCCCUCGTAUC
238149566	84336	GTCATCTGCUTCTCCTTTCUGAACAA	84337	GAAACAGGUGCTTTAAAAGUAGCAACT
238156385	84338	CCAAGGAGACUGTUGAGGAAGG	84339	ACACAAGUGGGCAAACATTTCTCUA
238157881	84340	CCAGGUAGAGGGAGUACAGAGT	84341	CAGGGCTTUGAAGGAAGTGUG
238160056	84342	TCAGTCUCCAGCATCTCUACCC	84343	GGTTCCTGGUGTTCCTCCATTUC
238160464	84344	GCTCCCTCUCCGCTACTCUC	84345	GGCTGGATUCACTCTTCACTCUAC
238161337	84346	TCTTAGAACUAGGATTACCTGUGAAGCA	84347	AGACAAGGATUGGCATTCAGUCAAAT
238167004	84348	GCCCACCCCAGUTCACAUA	84349	GCTGACACCUGAGGCACUG
238168384	84350	TCACCCCAGGAUGAACAATGUG	84351	CCTCAACTTTGTUCACTTCTCAGGAAUA
238172418	84352	GCTCTGGGUCGTCCTTGTUG	84353	ACAGCAGTCTUTCTTTCCCATGUAA
238175328	84354	AUCAAUGCAGGCAAAAGCAACT	84355	GCCTCTGAUCTTGCTGCCTUC
238176328	84356	GCCAUCAGACAAGGAAAAACGAUAG	84357	TGCTGGTGGGAAACUATTATGAAACUT
238177503	84358	GGAGGTTCTUGTCCCTCTTCUCA	84359	TTTCCTTGUACCTGTCCAGUCAC
238179129	84360	CCGAAUCUGAAGGCAGCAAGAT	84361	TGCATACACUCGGGCAUGAC
238180496	84362	CCACCGUGGGCCTGTUA	84363	AGCCGCCUCCGAAGAUG
238192268	84364	GUTTTTCCCACUGCCAAGCAT	84365	ACAGAACTGTUGCCATTGTGUCA
238194370	84366	CTGCGCTUCTTGCATGGUT	84367	TTTGGTCACCACGUAGCTCUC
238195566	84368	TTGGTTTGTGGUCCTCACCTAUG	84369	TCCCGTTCCUACCAGTCACUAT
238202758	84370	AGAAAAGGAAGUGCCAGGCAAAUA	84371	TTGTTAACAGGUCCAAGGAAGAAGUC
238205322	84372	CTTCGGAGUGATTGCAAGGTAUCA	84373	CGAUGCAAGTGCUCAAACACC
238205876	84374	CCAAACGAUGAAGCCTCACTUT	84375	CGTGATCCUTTAAGCTCUAAGAAGGG
238215553	84376	TTCGTGCUGATATTTGTGUGAGGT	84377	AATGACTTGTCUAGGAAGGCAGTUG
238222715	84378	GGUACTCTCTGTUGACCACCCA	84379	GCUCTCUGACCCAGCACAAAT
238226054	84380	TTTTTAGCCAUGAGTTCAAGTTCCUCT	84381	GAGGCAGCAGAUACCACATTATGTUAA
238228637	84382	ATTCTGTUGCCGGAAGAUACCC	84383	TUGGTCCAGUAACAAGCACACA
238231328	84384	AGTTGGTGGAAUTAATACACTGTCTUCA	84385	AAGGAACAGGAAGAAAUCAGUAGCAAA
238235502	84386	TCAGTTACTGGUGATCTAGCAGGAUT	84387	GAGGACAUTTATTUCACAGGAGAGAGAC
238236064	84388	GCAGGAAAAUGGCAAAGCCUAT	84389	ACTGTGTTTGGAAAAUGATCACCTAAGUA
238236245	84390	TGAAAAATTGGGUGAGCTGCUG	84391	TTGGAGGAAGACCGUTCGATATCUA
238237084	84392	GCCTCCCUGGGTGCTTAUG	84393	GCUACAGUGGGCGCAACT
238237165	84394	CCCGACUCCCGCCCUAA	84395	CCAGUCCAGGAGCCTAAUGAC
238237773	84396	GAGAACAGGAAGUTGGTAGCUCAG	84397	CCAGCAAGTTUACAATGTTCAAATGUG
238238929	84398	GCAGTCGUCGATGUCGGT	84399	ACATCAACGAGUGCGTTCUGA
238240250	84400	GUGGGTGTTCUGGCAGGAT	84401	GGUCGGGAGAGGCACTGUA
238241292	84402	GTATCTTCUACCAGGTGCTUGGG	84403	CAATGAGGAAACUGACCAAAGUGAAA
238241534	84404	GTCCCCTACCUTATCTCCCAUCT	84405	GGTGGTGAGAUAGCCCCUGT
238243120	84406	ATTTTATTCCTAGGGAAUGAGTGAGACTTUG	84407	CCACCTGGCUACACGAAAATTTCUA
238245429	84408	GUCTTCUGGCCCCAAGAAAGT	84409	AGACATCAGCAUCAACTTGTUCAAAAG
238246970	84410	AAGAAGGUGAGCTCGGGTTUC	84411	CTCCCCUTTCCGTGAUGAAGT
238248381	84412	CCGCCCTCUTTCACTTTTATCUCT	84413	GATAGCGAAAGCUCCCCTUCC
238251018	84414	AGUGAATCAGUGCCAAAGACACA	84415	CCAGGAGGAUTACCTAUACAAAGAACAG
238251442	84416	GCCCACCAGCUGATUCACAG	84417	CCTCCACCGCAGUGCTAAUG
238253203	84418	GAGCCGGUGCAAGATCTCUT	84419	TGAGGTCGAUAAGGATGTTTTCGUC
238258168	84420	CCTGGCTCUGCAGTTTCTCTTUA	84421	CAATATAATGCUGGACCGCCATAUAGAT
238258529	84422	GTCTGAACTGAAGAUAATGACTCACCUG	84423	AGAGTGGAGGAUTTAAGCCTGATUG
238258736	84424	CAAUGGCTUCAAACAGCCAACAT	84425	GCCCUACAAGTGCAUACAACAAGA
238258779	84426	TCTATTCTTAGATAUGAAGAGAAGGCTACUAAA	84427	CATGCGCUGGTGGGTTTTAUC
238260775	84428	GCGGCACCUCATGACCAUAT	84429	CTCGGTTGACAUTAGGAGCAATTCUAA
238261997	84430	CUCCACCGCGACAUCAAG	84431	GCCTGGCUCACCAUCGAA
238263939	84432	GTTTTGUGGCACCGCTTCUC	84433	GAAGAGAGAUCAATGCACUCCCA
238264710	84434	AGTATCTGGACTUAAAGACACAGGCTUA	84435	GGGATGCCUGATGCTTCUCAC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238266569	84436	GAAACAAAGGCCUTGGUGCAG	84437	CGUGGUGAAACCAAACCAAGAAAA
238268147	84438	CACAAATGUCACTAAAAGAUGGCAGAAA	84439	TTTCAATTTGGGACUGAAGGAGTUCA
238268210	84440	TGCATGUGCCAGACATCCUAA	84441	CACGAAGCAUGTCCAATUGCC
238272444	84442	TCAACCAAAACTUGATGAACTCCTUCA	84443	AAACCTGAGAUTGTGGAUCAAGCA
238275826	84444	CCGGCAAUTCATGGAUCCAG	84445	CCCCTCUGATGTGTCUCCAA
238276216	84446	GGGAAAATGUTCTTGGGTGUCAT	84447	TGACAAGTTACACAUCAAAACCCAUCT
238278369	84448	AGTTGACTUAGAAGAGAAGGAUGAACCT	84449	GCTCTGCAGGAAGUTTATGATTCUCA
238284235	84450	AGTACTCTTUAGAGGAGGUGAAGGAG	84451	CTTAGCGCCACUGCAAAGAUG
238285758	84452	TTCCACTCAACUGCCAAGUGT	84453	GGCTAATGACTCUGATGATAGCATCUC
238288038	84454	CCAUCCCTGCTUCAGAACAGAA	84455	CGUCCTCAAGGUCACCAGAAAC
238290218	84456	GAAGCCCTGCUATTTAAAAGACTUCT	84457	CCCAACCTTCUACCTTCGATTTTAAUCT
238297245	84458	CAGACAGAAGCACAGUACCGATUT	84459	CTAGCAAGAGAAUGAGAAUCCGCAT
238298078	84460	CCUGAGAAGGAAAAGCGAAUAAAGGAA	84461	AAGCTGCTAUCCCCTCATUCAAG
238301937	84462	CCTCAAGGCCUGTTTGTCTGUT	84463	CAGAGAACCUCGGAACAUACGG
238302713	84464	AGAATTTTCAUCCCATAGAGCACUGG	84465	CTTGGCCACACUGTCCTCUAAG
238303733	84466	CACACAGTUGGCAAGGAAAGUT	84467	TCCAACAAGAAGGCCUGGTTUAG
238308177	84468	CACTTAGGUCCAGCTCCTUCAG	84469	ACACATCACATCUCTCCTGTCCUT
238318029	84470	TCTTCCTTUGTTGGTTGCUGCT	84471	TGTACTTTCTCCUTCTTCTCCCTCUT
238324054	84472	GCTTTACTCAUAGGTGGGAAACUACCT	84473	AAACCCUCGUGAAGACGCA
238324782	84474	CAAUAGTTGCUGGGACACCAAAG	84475	TCATAGCCCUTAGCTGGGUCAT
238333067	84476	TCAGCAGAAACAGCCUTAATTATTUGGT	84477	TGCATACTTGGAAUGAATCCTTCUAGAGA
238333128	84478	ACATACCGUGGACGTCTCUAGAA	84479	TGTCAAAGCTAUAAAAATCTCCAGUGCT
238334068	84480	TCATATTGATUAGGCTGTTCCAAUGAA	84481	CCTGTTGCACUGGTTTTGAUGAA
238334827	84482	GATCTGCTUGATGTTGTACUAGACAGT	84483	CTTGCTTGAAACCAAUTTCACATTUCC
238336948	84484	GATACTGCTGUAGCTTTGGCTUCT	84485	ACATGGGACUCAAAGTTTUAGCACAA
238340206	84486	GATCTTCATCUCTTGTTTGCUCCACT	84487	AGCTTGTGUGAAATGCATTAUGCAA
238350885	84488	TTCAAGTGACTCUTCTCATGTTCTTUACC	84489	GCCAAGCGUCTCCUGGAT
238352888	84490	GCAGUCGCUACCGGGAAAAT	84491	CGTATCCGCGCUCGTCUA
238353484	84492	CCAAATTATTAGAUGCAGAACTCCAGUGA	84493	GGTACGUCAACAGGAACAGCAAAUA
238357367	84494	CAGCACTAAAGAAUTGGGATGTTTUGA	84495	ACAAAGGAGAGUGATTGATTTTCTUCCT
238357654	84496	CATGTTGUCCTGGGCATUGG	84497	AGAGGACTCTUCTGCTAACATCAUCA
238364112	84498	ACCCCTAGCAAGUATATGAGTAACGUA	84499	CTATTCCUGAAGCAGAAATTGGATUGG
238364889	84500	CCGCCAAUCCAATTTCTGCUT	84501	AAAGAGGTTGCTTUATCTTGACATTATCUGA
238367077	84502	CCCTCTTCCUCCATTCAGTTTCCUA	84503	CCUTTCCCUGGCAGACAACAG
238369458	84504	ACATTGCTTTTUCAGAAGGCTAAUAGGA	84505	CCCAGATGAGAUCTCCAACTTCAUACT
238373365	84506	GGCCCUTCUAGCACGCA	84507	GACCAUGTTCCUCACCACACA
238373880	84508	GCTUGCACGAGCCAGUCT	84509	GGCGAGUAUCGAGCGGAA
238374239	84510	TGAAGTCAAATAAUGAAGTCCCAAGUGA	84511	GGCTTTTTGUACTTGTTTGTCCUCAA
238374676	84512	CCUGGCGCAGCAUCAGT	84513	AGCTGGGAGCUAGGTCCUC
238375387	84514	GCACCCTGGUAGACCAAGUCT	84515	GGGTTAACTACCUTCTCCTTCTUGAGT
238375735	84516	CCTAAGAAAAAGUCTACGCCACUGA	84517	GCAACTGCCUTTAACATGTATAAUCACT
238376416	84518	CCTTGCATTUTCCATTGCATUAGAGG	84519	CGTUCAAACCAAGAGCUAGAGAGAT
238378845	84520	GTCTTGGGTAGAAUCATCTTGTCTCAUT	84521	GGAAGAGAAAGAAAGACUTTTAGAATGUCCA
238379074	84522	CCCCCAAATUGAACTGAAGTCAUGT	84523	GGGAGGCACCUTCAAGTGUC
238380979	84524	GGCTTGTCCUCTTCCCTCCUA	84525	CTCCTGCUCGATCTTCTGCUG
238383974	84526	CACTUCAGGGACTTCTUGGCA	84527	GAAGGTCTTCGUTGGAAGGGUAA
238390829	84528	CCACUGCGAAUGAGCGAAT	84529	CCACGAGCAGAUCGCUGAC
238391369	84530	GCATCACUGAGAAGCUGGAGAA	84531	GCAGCAUGTTUAGGAACAAAGCA
238399756	84532	CCTTTTCCGUCAGGGCAUGAG	84533	CTGACCUTGCCCUGGAGAA
238403461	84534	TGCUTGCAGTUCCAAACAAGG	84535	TGACTTAGTGGCUCTGATGTACTUAACT
238403967	84536	CCAAGAAACUGACCCTGAGCUT	84537	ACTTTTCUCCCACTTCATTTTUGCC
238404187	84538	GCCAGCAGUCAGCCTACUT	84539	CCTCCAAAUACTGAGACTTUGAACACA
238404364	84540	CGCATCUCAAGCTCTGCTCUG	84541	CAGATGGGCAAUGAGCUGGAA
238406511	84542	GCTTCACGGGUATAAGAATCTTCTGAUT	84543	CAAAATGGTUTGTAGCAGUGGAAAGG
238406953	84544	TGCCCCUGGCTCUCCAT	84545	CCCGAGUGGCUGGAAGAG
238409648	84546	TGTTTGCATGUCTGAGGGAUGT	84547	CTGGUCTTCTTCUCAGAGCCT
238410971	84548	TGTCCATCGTCUTGCAAGTAAAAAUG	84549	AATCCACCCTTUGGTTTGTATTGTAUCT
238413411	84550	CAGAACUGGCGTCCCTGUT	84551	CACTCUGCAGGAAAAGAUGGCT
238414740	84552	CUTCUGCAGGGAGCCAGA	84553	GCCCCACUCACCTGCUT
238415755	84554	GCATCTTGAGCUCTGCGATCUG	84555	CCCTTCCUGAAGAGCACCTUG
238416100	84556	CGTCCTGCUGCAGTGCUT	84557	AGGCUCAGCTCUGAGGGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238420729	84558	CGTCCTTCCUCTCCAACCAAAUG	84559	CTTTCTGUGGCTGTGAGGUCT
238421227	84560	GCCCCAUGTCTCAGACUCAAG	84561	GGTCTTGCUGACATTCTTTCCCTUT
238425414	84562	TGUGCAAGAACCGTACUCAGG	84563	TGAAGGACAAAGCUGATTTCUGCAT
238430074	84564	CCCTCTTCUTTAAGGTCAUCAAGGA	84565	TGAUCGUCAAGGCCAGAGAAAC
238431698	84566	CTCCTCACGGUGGCGUT	84567	GCGUGGCAGGAGAAGTTCUT
238433624	84568	GTATGTGCTGUTGTCACATGTUGAT	84569	CAAGTAGUCCCACCAGTTAGAAGUAGA
238433664	84570	GCCUGCGUGAAAGAAGCAGAT	84571	GGAGGACCUCATCAACUCACAC
238433972	84572	GGCCACCUCTTTGCUGGT	84573	CCACAGCGAGCUCCAGAUAAG
238434888	84574	GGAATGCCGUGGGTCUCAAA	84575	GAGCCCUGGAGGGAACTTUC
238437323	84576	CCTTGCCGGCAUAGTGGAUA	84577	GGACGAGGAGUGCTGGTUC
238439241	84578	CCAGGTCAUCTACGGCGTUG	84579	CCTGAGCCUCTCCCTGUT
238439385	84580	CGCUTGGTGGTUGGCAAAAAG	84581	CCTGTTGUCAGGAAAAGUCAAACAAG
238440324	84582	GGAGAGGGCCUGCTCTUT	84583	TCUGCTCUGCGGGAGGA
238449326	84584	CTUCCCACCTGUAAAGCAGACT	84585	CATTTCTCTTCAUGTGTTTTCCTUGACA
238450256	84586	CGCTGTTUCTCAGCCUCCT	84587	GTTGAAGCGGCUGGTGAUG
238455935	84588	CCACGAAGCUCTTGUCGGT	84589	TCTGATGUCCGGGCTTUGG
238456991	84590	AGCTTCUGGCTCTTCTCUGACT	84591	GAAAAATAGCCUCATCAGCAGCTUG
238457845	84592	CTTTAGGAGTCUGCTTTAAGTACUCACA	84593	TGGAAAGCACCAGACUAAAUGGG
238458768	84594	GCGAGGCAAAUAGACCTTAAACUC	84595	GCTATCTACTTTGUCTTTTCTGTGCUCA
238458948	84596	CTCTTCCUGCCCACAUCAGAT	84597	TGTGTGGUACGCTGGATUCAAG
238461555	84598	CCAGCAAUCAGCTTTGCCTUAG	84599	ACTAGGCTGUTCCCTTTGATTUACAG
238464266	84600	GGGACGUCUGAACGGAAGT	84601	TGAAACUGCGCCATCGUCA
238464412	84602	CTGGCGAUTCAGGAUGGACA	84603	CTUCCGCACCAAGGUACAAGA
238464566	84604	ACUTGGCATGGUACAGAGCAAAT	84605	GGCTGTCAGUGTTGGAGAGTUA
238470625	84606	CTGTGTCTGTAGUACAAGGGAACTUT	84607	CACGTGAAGCUATTGGTGAAUGAC
238471614	84608	GCCACCUCACGTUCCACAT	84609	GCATCCCCAUTCCTTTCATCUG
238476825	84610	CCACCCACUACTATCTGCCCUT	84611	CCTATTGUGACGTGCCCAAUG
238477567	84612	GCTATATTAATCUCACTGACCTCCUCCT	84613	TGGAATGCUGCCTGCUGAT
238479377	84614	CCTGAAGACAGGUGCAAAGUCA	84615	TCTTCCATUGAGCTGCUCCAAC
238479961	84616	CATGCAUGAGAAGGGCATGUC	84617	GGACUCTGGAGTAUGACAAACACA
238481521	84618	GCGGTAGAUGCGGTGCTUT	84619	CTGGCCGAGGCCUTGUT
238482716	84620	GGGAATGCGTUTTAGATACAAATGUGAA	84621	TGAGAUAGACACAGAAGAAGGGUCT
238483218	84622	TGTGCACAUGTTTTTGTTUGGG	84623	CTCATTCCAACCUTGATGTGTUAAACT
238485366	84624	CACCAACUGAAUCCACCACCAT	84625	AGCCATTAACUGGCCATACAATTATGUT
238486223	84626	CGCUGAGTGAUGCCAACA	84627	CCGTTGAGGUTCTTCGCCUT
238488115	84628	GTCTCCCUCCTGTTUGCACAT	84629	AGAAACTACTGUAAACCTGGTGTTUGT
238489534	84630	AAGTGAGTCATCUCTGTTCTCCTAUT	84631	GGCAATTCAGCUCGACTAGAAUCC
238490871	84632	GAGCCUCGCGGTCGAAUAAT	84633	TUTATTTGCAGCUCGGAGCCT
238495867	84634	CGAGCAUAGCAGGTACTGUGA	84635	AGGAATCAATGTUCTTGTAATGTGACUGA
238502596	84636	CCAGCCTUGCCACATCAACTUAT	84637	GGAAAUGCAGACAATGCCTUCA
238504964	84638	GGCCTTGCAGUAAAAGGAGCUT	84639	TCCGTTGGGUTTTCTCTUCCAG
238505227	84640	TTTACTATGTGGTUTCCCATCTGGTUAC	84641	GGCTTCCUAAGGCGTTTCTTCUC
238508034	84642	CAGCUTATGUAGCCAAAGAACACAA	84643	CTTCCGCUAACAGCATGTTGUC
238508169	84644	AAGGCCTGTUGCTTGGAACAUA	84645	CAGUCACAACCAAGGAGTCTUGT
238516790	84646	CCCATAGUGAGTGCTCCTUGA	84647	TCGUGTATTUGGACGAGAAGCAG
238518160	84648	GAGGCUGCTATGUCACAAGAGA	84649	GTATGTACACCCCUGCCTCUG
238518468	84650	TGTTATATAUAGCCAGACCCGUGGA	84651	TTCTGGTGTUGAAAGACTAGUGAAAGAG
238518712	84652	GATCGAACUGCTCGTUCAGGAA	84653	GCCCAGUGACCCTCCTAUGT
238523219	84654	CAGAGGCUGAGCCATAGACUG	84655	TCCTCCCAGCUGATCTGAAGUT
238523315	84656	GATTAATTGGGAAUCTTGGCTACUGGA	84657	GCACTAACUACCAGGCTACACTUAC
238523441	84658	CACAGACCCCCAGCUGAUG	84659	CTGTGAGAGTUTGGCTCTGTAAUCT
238523658	84660	CTGGCTGUACCTCGATGGTUAAG	84661	CTTGAGAGGCUCTGGCTCTUG
238526316	84662	TTCCAAAGUGTGAUGCAGACCA	84663	GGAAGCAGUCCTTGTTACAATGUGA
238527794	84664	ATCATCTTTUAGCTGTGCGGUCA	84665	GGACCAGUGAAAGTTTGCTGAAAUT
238528568	84666	GATGGCTCCUGCACTCTTCATTUA	84667	GAAAAGTGCCAUCTCGCTUCC
238529896	84668	AGCCATTGCUCCACTTAACUCAAAT	84669	TTGGCTACCAGAUGTTCTACTACAGUA
238532025	84670	CAGCUCCAGACTTTCUAAACACAAC	84671	AAGCACAAAGUGAACATUGGCAT
238535271	84672	CCUGCAGGGUCCCCAGA	84673	ACCTGGCUGTGGCUGAAG
238537422	84674	TCAGACAACUCAGTGGAGCATUC	84675	GCTTCCUCCACCCTTTCCUAAA
238537438	84676	TGCAGGTUGGTGGGAACUG	84677	GGCGUGCACTGCTUCCT
238537993	84678	GTCAUGACCGCGTTCTUGT	84679	GGTTGACGUACTCGCCCTUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238538049	84680	CAGTATCAUCAAGGCCAUGGGT	84681	AGCAGGTTUCTGTGGCAAUCA
238538521	84682	CAGAAGCAGGUGTTCCTUGGT	84683	TGAGCAGGAAGAUGAAGTACUCAGA
238539831	84684	TCTTTTGCTTGUCCCTGATTTUCCT	84685	GGGTAAAGTGATUAGGGCAGATGATACUA
238541001	84686	TGTGGCUGTGGCTGUGAG	84687	CGTCTGCAAGGUGAGCCAUA
238542166	84688	CGGTGCAAGGUGTGACTGAUAA	84689	GTTGCTCTGCAUTAGAAACCAATATTUGA
238548246	84690	ACTGGUCCCACGGTCAUACA	84691	GGGCAGAAGAAGGUCAGCAUA
238549363	84692	GCTGGGUCAAAGATCCTUGCAT	84693	AGAAATGATTUCTTACCTTCUGAGCACA
238549388	84694	CATGTTAATGTUAGCTGGTGCTTUGT	84695	CCAGTGGCAATAUGATGAAAAGTATTTTUGT
238551717	84696	GCTGCUGAAAACCTUCAACGA	84697	CCTTCCTTCUCCTCGACCUG
238555045	84698	CAAAGCUGAAAACCTGTUGCGA	84699	GCCCCCAAAACUCAATGAAUGAA
238556063	84700	CATCCCGGGACUGGTCTAUC	84701	ATTATGTAACCUGAGAGGAGTAUCCGT
238557550	84702	GGCCTCCUGACTGACUGACT	84703	CCTTCAGAAGAGCUCCTTUCCC
238562983	84704	GUTCATTUACAAGCACCAGCAGAA	84705	GAGAGACGCGUCCAGUACC
238563169	84706	CTGAAACUCAAAAGCCTGAAAUGACT	84707	TGGATGUGAAGACGCAATCUAGG
238564925	84708	GGGCCTUCAGCTCCTUCT	84709	CCTGACCCUAGGCCTGTUG
238568546	84710	TTAAACCUGCCATAACTTUCCCAAGA	84711	AGTTACAACTAGAUGAAGAGACAGGUGA
238569789	84712	GCAGTGAGCUGCCTTTTTCTTUC	84713	GCTTUCCAGAAGCAAGTCUCCAT
238570345	84714	AATTTACAAAACUGTACCAGAUCCCACA	84715	TGACACCAGTUGACAATAGAAGATGUA
238571478	84716	CATACCTAGCUGAGTCACUGACAAAT	84717	CTGTTACCTAGTUTAGTCATGGCCUT
238572411	84718	GGGCCTTCCAUATGATCTGAUAACC	84719	GTUCCCCAAACCCTTGUGAGA
238575716	84720	TGGCATTGUTGGAGGAGUCAG	84721	TGAAAAACTGAGGUGCTTAAGGAGUAAA
238577035	84722	GGCUGGCTGAATUGGGAGAAAT	84723	GGAAAGAGUATGAGCUGGAAAAACAGAA
238582171	84724	GACUCTTUGCAAACAGCAGCAT	84725	TCAGAGAACAUCCTTGGGAUAAGGAA
238582189	84726	TGGAGTTGTTCUTGTCTTTCCTTTUCAA	84727	TTTGATTGACATACUTTGGAGGCAAGAUA
238586175	84728	GTCAAATACTUCTCGACTTACUCCAAGAT	84729	CCCACTUCCCACCAUCAACAG
238586183	84730	AGTGCTUGCAGCTCACAGAUT	84731	GATGTCCUGGAGCAGCTTTTUG
238592482	84732	GAUTTGGATACUGAGGCCACCA	84733	CTCTCTUCAGACGAAAGGUCAACT
238594455	84734	CCCACGUCTGCACATCUGT	84735	TCTCAUCCCCACCCCATCUC
238596346	84736	CCCUGAAGAACCTGAGUGGAGT	84737	CTCACCCTGGAUCTCTTTTCCUT
238596959	84738	CCTTTTAGAUGTCCTCCTTUGCCT	84739	CAGTUCCCCAACCACTCATUCA
238597033	84740	TGCCGGAAAGCAUGUCAGAT	84741	GCTCCGUGGAGTTTGACAUGG
238598915	84742	GGCTATGGGUTTGCACAGUGA	84743	CGUAGCAAGAGAGGAAACCUCAG
238599629	84744	CATGGAGUCCACCAGCTUGA	84745	TGTTGGCCACAUGTCCCTTUT
238601645	84746	CTTTTCCCUGGGATTCTGGACUT	84747	CCTGTGTTCUCGTACACTGUGG
238601985	84748	AGGTCTTTGAUTTGCGTCAGUGT	84749	GGAGCTATUCCACCTACTGAUCCT
238603145	84750	CCCATGGGAUCCTCAUGCT	84751	CGCTGACACUGTGCTTCTCUC
238603833	84752	TCAGCUCTCUCAAGAGGAAGCA	84753	AGAGAACCUCTCGAGCTUCCA
238611281	84754	GGGTGGGCUGTGAGAUCA	84755	TCTTGAGTCTUGCACTCCAAUCAG
238611376	84756	GAUCAACCAGGAGCTCAUCCAG	84757	ATCTGAAAACTUTCTCCACACTUCCA
238611800	84758	GGACCTAGUGGTTTTGGCTTUG	84759	CAACCAGGCUCAUGGCAAAAG
238616212	84760	CGAGGUAGGCACGTGCUA	84761	GAAGGTGUCCAGGCCGUT
238616560	84762	GACACCTUCTCCGGCTUCAA	84763	TGUGGCCAGAGAGGGUCT
238617532	84764	CTCTGAGGCUCCAGGACUCA	84765	CGAUGTUCGACGGGACAC
238620393	84766	CTUCCCGGAGGCCUACAAG	84767	CAGAGUAGCACAUCAGCACCA
238625175	84768	TGGTGCCUGCATGCUGAT	84769	TCCGCGUCGTCCTTGAUG
238628352	84770	CGAGCUCCCCTCGUGGAT	84771	TGGGCCTCUCCAGCATGUA
238628669	84772	CATTCTCTAGGAUCGAAGCTCATTUCT	84773	AGTGTTCAGAAUGAAGTACAAGAAGCUC
238630712	84774	CAUCCCGCCTUCCCAACT	84775	GACGUCACCCACGAGUGT
238630960	84776	GCACUACCUGGCAGGCA	84777	ACAACGAGGUCGGCTCCUA
238631254	84778	GCUGCAGGGCACGUAGG	84779	TCAACGAGUGUGGCCAGAAG
238632111	84780	GTAGGAGCCGACCUCGTUG	84781	CTTCGAGGCCUCCTACATCUG
238635218	84782	TCAGCTCUGTTTTAGCAAUGACAGT	84783	ACTGCATCGUGCTTTCCACTUA
238635270	84784	TGACGCCUTCAGAAGCAUCC	84785	GTACAGGGCAAGUTGCTCCUA
238635564	84786	GCCACACUCGTTGACAUCCT	84787	GACCCTCTUGTCCCCTTGUC
238640358	84788	GGACUGACCCATUCACCACAT	84789	GCTCAGAGUCATCTGGTUGGG
238644032	84790	GTGCCAATATCCGUAATAACCCTGUA	84791	ACAGTTTTATGGUCCTTTACTCACCTUG
238648460	84792	GCGTCUCGTGCCUCCAAGA	84793	AGGCTUTGCTGCUGAGGAC
238651096	84794	CGCCTTCCUACCTGCTGUA	84795	CTCAGCTGTCUTCGGTTCTCUC
238651312	84796	GAAGCCTGGAGUGGAGAATGUT	84797	CTCACCTCCCUGTCTTCTTGTCUA
238653132	84798	TCTTCCCUCCCCTCGAAAUGA	84799	CACCTTUCAGCAGGUCAGAGA
238659833	84800	TGUTTGAGAACAUCGGGAAGGG	84801	CCAACCCUACATTTCUGCACAAAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238667783	84802	ACCTTTTTCUGGACCTGTUGGG	84803	ACACGGAGAAUGAUAGGAGACACA
238668874	84804	ACTGGCTACUCCCAATTGTCCUA	84805	CCTCCAUCCACCTCATCAGUG
238669801	84806	GCTGUGGCGCAGGTATAGUG	84807	CGGUAGTTCTTGUAGCCCACAAA
238670567	84808	CTGCGUCTGTGGGUCAGA	84809	CCUGGCAGAGGGUACGG
238672207	84810	CTTCTCACCTCUTCCAAGCTCTUT	84811	GAGUACCCCACCUACCACAC
238674262	84812	GGACTUAGGCTGTGUGGGAAT	84813	TTGTACUGGACGTTGAUGCCA
238676901	84814	GGGTGGGAAUTGTCGCCUAA	84815	GGCTACGCUAAGCACCUCAG
238676907	84816	CCTUGGGCCACAACCTAGTUC	84817	GGGTCTTTTTGUTTCAGGCCAUC
238679589	84818	CCTCCATCAUAACCCTGTAACTGCUA	84819	TGTAACAACAGTUCCAGACTGACTTUG
238684044	84820	GTGAGAAUGACCGGGUGGA	84821	CCTGGACCUTGTCUCACAGA
238684295	84822	TTTGCCTCUTTGTTAGGUGGCT	84823	TCTGCCTCTAGAUGAAACCTTGATAUCT
238691315	84824	GGACTCTGUGAGTGGGATTUGT	84825	CCCAGTATATTTUGTTGCCCAACUG
238693151	84826	ACTUCCCCACCGAGCTACUA	84827	ATGTGCTTTCCUTTCCTTGTTUGG
238697450	84828	GTCCCAGGAACUGATGCUACA	84829	CACGCAGCAGCAAAGUCTUAC
238699253	84830	GGCCCAATCUCACCTTCTCAUA	84831	GUGCCGCCGAAAGAACUAC
238699336	84832	GAAGTCAGAUGATGAATCCUCCCAAAA	84833	CAGCTTCTCAAGUATGTTTACCTAUGGA
238699348	84834	TGTTTCACGTAGUACACATTGCTUCT	84835	TGACAATTTCTTUAACAATGGCATCCUG
238700031	84836	CGGTTTTCTUCCCCTTTTGCTGUA	84837	CTTCATTTCTTUGACCTCCCUGGT
238701795	84838	GGAAAACUGCCAGGCATUCAG	84839	ATGTAGTGAAGUTCGGCACACUT
238702010	84840	GCCUGCTGCCUCAGGAT	84841	ACTCTTGACGUTGTCCAGCUC
238702685	84842	AACAGAATAUGAAGAAGCCCAGGAUG	84843	CTTGCGAAAAUAACAAAACACACTUCAA
238707579	84844	AGTGGAAUAGGAGTGAGGUGAGT	84845	AAAACAAAGAGCUGCGAGCUG
238709446	84846	GGGATGAAAUAGAAAGTCAAUGAGGAGAA	84847	ACCTGAGTCUCCTGCTCTUGT
238709495	84848	ACAGTTCCUCACAGCCTGTTATTUC	84849	TGCTGGCAAAAUACAGAATTTUAAGCAT
238709653	84850	GGGAGTTUGCCAAGGUGCT	84851	CCTTGCTGAGCUCTGGGATUC
238711791	84852	TCTCTGGAGAGACUGAAGCAUAAGA	84853	GGAGGAGAAUGGAGACCTTUCCT
238715650	84854	CCACTTCAGCUAAGAGCACUGT	84855	CCTCCGUGCGAAUCGCT
238716325	84856	GTATCCCGGGCUGGAAAGAUG	84857	GCTGGCCATUGTCTATCTCATUG
238718325	84858	CTGTTCAGCCUCCTTGGTCUT	84859	AGAAAGCCAAAACACAUTATGAUGCC
238719671	84860	GGATCCUGTTTGTGAAUGACACCAA	84861	CCCCUCCACTGTUACAAGCAG
238725791	84862	GTGCCGAACUTCACTACAUGGT	84863	TGCUTTTCUCAAAGGGCAGGAG
238725795	84864	AGGTTTCATTGTAUCTACTCTCCCUCAA	84865	CAGTTGACATAACUACTCCAAAAGCUG
238727223	84866	GTCTGGCUAACCACAUGAGCAT	84867	CTTTCTAUCCAGGCCACTCTCUG
238728051	84868	GGATGATGUGGCAGGACACUC	84869	ACCAGTCTCUTGGCACCCTUA
238729811	84870	AGGAAAUGCAGCGCAUCAAG	84871	CCTCCUCGCCAGTCUGGT
238731741	84872	CTTTCTCTTTCUCCCCCTTCUGG	84873	AATGCTTTCAGTUAAACGTGCTTGUAA
238733857	84874	GCTCTTGGTUCTGCTGCTTCUT	84875	CTGAGCACTAUAAGCTGCAGGUA
238736337	84876	ACAGTGGAGAUTACGAATGTGCUG	84877	TCTCTGUACAGGGAAGAGTTUCCAT
238737627	84878	CACCACCTUAACACCCACCTUAA	84879	CATACTCTCTUCTCACTGCTUCCC
238739778	84880	CAAGGGUTCGGUGGGACT	84881	GCAGCAUGAGCACATTGUCA
238749069	84882	CCATGTGTGUTCCCAAGCTUC	84883	GTTCTCACCCCUTTTGCTTCUAAC
238753363	84884	CAGUGGCGAACAAATUGGGT	84885	AGTAGCCTCAAAAUGGAAAATTCAGCUA
238755874	84886	GCCGCACACUCCAUAGAACT	84887	CCTGTGTCCUGCATTGTTCCUA
238764877	84888	TGCTCTTTAGCUGTAACTTGTAAAUGCT	84889	GTGTTTATGTCUGTTGGTGAAACUGA
238765100	84890	CCTATCCCCUCTCCTTTTCTTGUT	84891	GGTCCCGGUGCACAAAAUG
238766724	84892	CTCTTTCCATCUAGAGTTATCCUCCACA	84893	TGTGUGAGGCAGCAACGUAA
238769513	84894	GTCGCTTCAUCCCCCTUCAG	84895	TGCCTAACTGUCCTCTTCTCCAUAG
238774506	84896	AGTCCCGATCAGAUTTAGAATAGGAUGA	84897	GCGCTATUCTCGGCCAUACAC
238775348	84898	GTGTACCUGGCGGGTCUG	84899	ACGGTAATAGUCGGTGCTGUAGAT
238782752	84900	GGCAGUACCAGCAGTUCACC	84901	GGGTCACUGAAAGTCCACAAACUT
238784852	84902	TCGGATGATCUCAGATTTTTAAGCCTUC	84903	AUCTATCGAUGGGACCCAGACA
238787110	84904	GGGAGGAAGUTTGCTGUCGAG	84905	CCCGGTTAGUCTCTGACCTUCAT
238790181	84906	CGAGATGGAUGCCATGATUCCC	84907	TGTGAACGCGGUAAACTGUT
238791843	84908	TGTTACTTTUGACAGGACTTUAGCAGAA	84909	GTGGCCGAUGTCCGTTUG
238792478	84910	GGACAUCGGCCACAAAGUC	84911	GGAGAATTCTTATTUGCCATTATGTGCUT
238792819	84912	AGAACTCTCUCGTGCTCTGTTAUCT	84913	CCTATTCCAGGUCAGAACGATCTCATUA
238797056	84914	CCTCAAATGGUGGTGATTTCTCCAUA	84915	GAAAGGAUCTTGCATUCGCCAAT
238798543	84916	TGAUTTTGGCAUGAGCAGGGAT	84917	ACCAGAGCCAGUGAATCUCAGA
238803728	84918	GGTAACGCUTGCTTCTCCUGT	84919	GCTCCCCUCAAAACTCCAUCA
238809192	84920	TGTCTCCAUGTTCCCATCUCCA	84921	GGGCCTUCTCACTTGUAACCA
238809746	84922	TGGTAGCGACGAUCAGAGTCAUAA	84923	ACTCGGTATGTAUCTTCCCGATGUAG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238812205	84924	CATATGAGGUTTGTCUCCAGCCT	84925	GTGCCAGCAAAAUGGAATTATCTTGUAT
238812706	84926	GGGAGGCTAUTCTGCCCATTUG	84927	GCAAGTGGACUTCGGTGCTUA
238814598	84928	CTGACCUGGTATGGTCAUGGAA	84929	TGATGACATGUGGGTGGTUGAC
238816521	84930	GAAACAGGAAUCCAUAGCAGAACCA	84931	GTGAAAGACACAUCTGAAGCUCCT
238818346	84932	CAATGTGAAGCUGTGAGCAAATUC	84933	GCCATTTCUGTCACCGTUCCAT
238818575	84934	CTATGCUGCAGCTGTUACCCA	84935	CTTTCTCUCCTGCCCUCACAAG
238822505	84936	GCCGTCGCUCTCTTTCUGAT	84937	AGAGATTTTAAAAAGAGCUCAGCACCUT
238824466	84938	CCTUACGCGGCTCAUGGAC	84939	GCCCTGAAUCCATGAGGCATUC
238824520	84940	CAGAGTUCAACGTCCUGAAGCA	84941	GGAGAACAGGGCUGTAUGGAG
238824990	84942	TTTTTCATCAGAACUGCTAGGAGCUT	84943	GGACATCAUGCACAATTTCTTTATUCCT
238829899	84944	CAGGCCAUCATCCTGACGUT	84945	CCGGAAAGGAUATATTTTCTGCTTCUCT
238830951	84946	GAAGGTTTCCCUAGATCCTCACTTTTUA	84947	TGAAGGCAUCTTTCTTGGTUCAGAA
238830974	84948	CCCTGGCUTCCTCAGAAAUCAT	84949	GGCCAGACGAUACCCCUGA
238833111	84950	AGAAGTCCGUACAGAATCTTCAUCAGA	84951	GGGAAGGAUGAAGAAATTCCAGATAGUT
238833563	84952	GCTGGUGGATGTGTTAUACAACGA	84953	CGTGTGCCAGUCTCCTUCAAG
238835142	84954	GGCCTAGUGACAGCAACCTUG	84955	CGATGGAATTGUGGCCTACTCTUA
238835635	84956	GCAAGGAGAAGUCAAACAGTCATAUCT	84957	GTAGCTTUAAAAACAGCATGTACCAUGT
238836233	84958	CGAUCCGCGCCAGAATCUC	84959	GGGAGAAGCAAAGUGCTATUCCT
238839772	84960	CAGCAACCAAUTGAAAATAAAAUGGGA	84961	GCGGTTATCUTCTCGAGTUAAGGT
238840274	84962	CAACCAGCATTUCACTTAGTCTTCTCUAT	84963	CATCCTGCUGCTCTCAGTGUT
238841446	84964	GGGTGCUGGCTGTCCUAT	84965	CGTCGCUGTCTCGCTUG
238847556	84966	GGGACAGCAGCUCAACUCA	84967	GGGTAAAAUGACCAGGCTTCTCTUT
238848030	84968	AGGTTCCACAUAGACGTAATCUCCA	84969	CCCTTTGGTGAGUACCTTTTTCCUT
238849816	84970	CAGGCAGCTAUAGAGGAGTCGUA	84971	GTCTTCTGGAGUTCTCTCCCGUAT
238851990	84972	GTGTGCUGAAGTGTTTTAUGCAGAA	84973	TCAUCCGGACAAAAGUACAGCAG
238852418	84974	GGCAGAAGAAAUCAUCACGGAAG	84975	TGGTGAGGTUGGGTGGGTUA
238853072	84976	CGCCUGCCGAGAAACUC	84977	GTGCAGAGUCAGAGUGCAGAT
238853469	84978	AGGTATCTCTCUCGGTGTATTTCTCUAC	84979	ATCATGUCCCCAGAAAATCCAGTUAC
238856536	84980	CAAGAACCCCAUCAATCAATCAAUAGAAT	84981	AAGGAAACAGGGAGCUCAATUCAA
238857483	84982	CCTATGCTGUGACTGGAAGCUG	84983	CTTGGGTATGAGUTTTCTGGTTGUCT
238858612	84984	GGAAUGAAGTUACACAAAACAACAGCAA	84985	CTTCTCTUAAGGCAGGCUGCT
238862774	84986	CCAGTTUCAGGCCGGTATUCT	84987	GCCAACAGAUAAAACATCTCGTTGUT
238864921	84988	GTTTUAGAGAGGAACCTUAACCCCAA	84989	CCGTACTUACCTGGCTGAUGT
238865858	84990	TTCATGTTTTTCUCCCTATCAGGTTUGT	84991	CCCAGATTUGATCTTGGCTUCCAT
238874601	84992	CAAGGCGATCUGGGCTCTTTATUA	84993	CTTTCTGGTCTTAUATATGAAGCGCTTUT
238875930	84994	GGTGGGCAUGGGAACUCAA	84995	ACAGTCCCCGUTTCCCUCA
238877237	84996	GTTACTTACCTCCUCATCGATTTTGUCT	84997	CAAGAAUTTGUGGACAAGGAGGAGAA
238880401	84998	GCAATAUGCGGAAAGCTGUGAAG	84999	GTCGAUGAGGGCTTTGUGGAT
238882482	85000	GAGUTTGGCUCCAAGGAAGGA	85001	TCTTTTCCACUGCCCTTATCTTATGUG
238882536	85002	TCUACCCGACAUCCCCCAAT	85003	GTGTCTTGGCUCCACCGUAG
238882920	85004	TGGTATTTCACUAATTCCTCAAUGGCA	85005	TCTGCATCCAGUGATTTGTATCTUACAG
238886124	85006	GCAGACUCCCGGUGAGGAT	85007	GCAUGGCCAGCTCUGGT
238888040	85008	CACTTUGAAGCCCUCAGGGA	85009	CGCAGCUGCACTTCAUGT
238888294	85010	CTCTGCCCUAGGACCTGCUA	85011	AGATGCCAUGGAAAGCTCTCAUAC
238889089	85012	TGCTTAAAAATTAATAUGTTCATCTGCAAAAUG	85013	ATTTGACGGCUCCTCTACTGTTUT
238889133	85014	ATTTTCTTTCTCTAGGUGAAGCTGTACTUC	85015	ATCAGAGTCAGUGGTGTCAGAATATCUA
238894549	85016	CTTCCACCAGGGUAGGUCAAA	85017	CCGTAAGGGUGAACTAGGAAACTUG
238894902	85018	CTATCCCATUCCTGTCCCCATUT	85019	GCAGGCAGCAGGUCAGUG
238899873	85020	GATCGAUGCAGGACCAUGAGA	85021	GGCUCUGGACAAGACCAAGAG
238904882	85022	GATGAGCUGCCTGGCCTUA	85023	CAGGCUCAAGGACCTGCUC
238905395	85024	CTGAGTTGUATCTAGTTGUGGCACAT	85025	GGGCAUTATTACAGUCCACCAG
238909628	85026	CCTTATGCTCUCACACACGTUG	85027	TCAGACTTGAAAUGGGTGAGAUGAAG
238909849	85028	GTTTTGUCCTCAGTTUCGGGAGAT	85029	GAGCUAUCACCCAGGCAAAAGAA
238913142	85030	TGCCCTTCCUCTTCCTCAAAGUA	85031	CCGCAGUGATCAGCTCUGAC
238915636	85032	CTGCCCUGACCTTTCTCGUT	85033	GGACCTTCUTACCAGGGUAGGG
238916496	85034	GATGTTTTTAAUCGACAGGCACCUT	85035	CATACTGTCTCCUACATCTGCTAGAAUG
238920328	85036	AGGCACCTTCUTACTGAGATACGUAAT	85037	AGCCAAATTGTTGUCTTAAAAGAGCAUC
238922335	85038	TGCGATGAUGACAGAGGTTCTUG	85039	GCAGAGATUACCAGGTTCCAUAGG
238924827	85040	AAAAGTGAAATGCUGTGCAAATCUCA	85041	GUGGACACCAGGTCUACGAA
238926081	85042	CTCACATTCCUCGAAGCCCTUA	85043	ACUACTTCCCUAAAGAGAAAACACACAC
238926165	85044	GATTTAUGACGACGGCCTCUCA	85045	GAGAGGAAGGAUAGUGCAAAGGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
238938203	85046	GCUGACTGAGCUCACCACAAA	85047	GAGCCTAACAUCAGACGCUCAA
238939266	85048	CAATGTCCAGGAUCCCGAUGAA	85049	CCUTTGTATCUGACACCACGCT
238947202	85050	CCUCCCCTGTUCACGGAGAT	85051	GCTTTTACTTCTGAUAAGCTCCAATGUG
238949359	85052	GCGGCUAGCTCUGCACT	85053	GAAGTCCGAAAUGATCCCAUCCA
238951854	85054	CAGTGCGTUTTTCATAAAGGUCCAT	85055	GTGACTTTUGGGAAGATGUCAAGAAA
238955987	85056	AAGCACAUGGTCACCAUGGAT	85057	CGACACUGCCGTTGATGTUG
238956749	85058	TCCATCCCCUGTCCGAUACC	85059	AGCCUGAAGGAGCUAGACCT
238959080	85060	ACTCATCUCCCTTTAATTTUGGCACAT	85061	TGGATCTUGGCACAATGAUAACAGG
238961013	85062	TGGACTCTAAGAUCAACACCCUGT	85063	CATCAACCATCCUTCTCCAGATACATUT
238964042	85064	CAGCTCACUGCGGGATCTTUA	85065	CTGTCUCCAGGCATCCTUGT
238968319	85066	GAGUACTTUCACAGACAGAGGCA	85067	TGACACGAGGGAUTTAGGACUCT
238981724	85068	CAACGTCAUCCAGGTTGTTCUG	85069	CCUGAAGAGCGAGCCCTUAG
238984110	85070	GGTGGAUGGTGGTCTGUGT	85071	GCCAGGUATCCAGCCUGT
238984450	85072	AGGUGGGACAGGCTGGAUA	85073	GCCAUCTCCGUGGGCAG
238985136	85074	TCCCATATTUCCAGTGAAUGAAAGCA	85075	ACGTTUCGGACCGTATTTCUGT
238986016	85076	CACGTGUACCCCAGTUCAGT	85077	CGTCTTAAATACUGGTAAGGTCTTUGGA
238986358	85078	CTTGCTTCUGAGCCTTCCTUGA	85079	GCTGGTTGACCUCTTGTCCATUT
238988956	85080	CCGCGGCUTTGTATTCATUAAACA	85081	CTGATGCACGUTGGCTTCUC
238989438	85082	GTGCTGUCCGGGUCAGT	85083	GCCAGGUGTGGTUCCAGAA
238992810	85084	ACATAGUAGAGAGGGACUCAACAAACA	85085	CTCTTGTGGUGCCACATCGUA
238992850	85086	GATACAGGGCAAGCUCAGGUT	85087	CAUTTCTCUACAGGAGGCAGAAGG
238992936	85088	GTGTTTATCTGAAGGUGATAGAGCTUGT	85089	TTCTGTCCAGGAGGUTTTCTTAACTUC
238996847	85090	TGAATTGCTUCAGCAAATCCAUCAG	85091	TGTGGTGTTTTGUTTGTTAACTCTGTUT
238998048	85092	CGGCAGATGUGCAACAGTTUC	85093	GGCUAGGTTUACAGGAAGAAAGCAA
238998592	85094	ATGACATTCAUCGGCTTCCAUCT	85095	TGTGTCTGGGCAGUTTATCAAAGUC
238999868	85096	TGCACTGCUGTATGGAGCUG	85097	AATGTAGGAGUCAGTCTUCCCAGAT
239009272	85098	CATTGAAAGAGUGACCGTAGAGCUT	85099	GTCATTGCAAGAACAGUTGAATGTAGUT
239019050	85100	CACAGCCAUCCCCCACAAUAA	85101	TCAACTTGACGCUGGTGAAUGT
239026460	85102	CTCCTGCUTGCGAAACTUGG	85103	AGGGTGTUAAAACAAGCCGAAGUA
239027529	85104	GCUATGGCUGGCAAGGGT	85105	GCCCCUCCAGUCCACAA
239031429	85106	GAUGAGAAAAAUCAAGACCCGAGACA	85107	TCAGCAGAUGGUCCAGCAAAA
239032028	85108	CTCUCAGGGTTTCAUGAGGAAAACA	85109	ATCTCTCUCGGTGTGATTTTUGCT
239033263	85110	CCCAATTCUCCTCTTCTUCACGA	85111	TGATTACUGGCAAGGCAAUGGT
239033906	85112	CCTTUGCAGACACCCCUGAAG	85113	CTAACTCTTUGGCCCCTCTGUG
239035173	85114	ACACAAUGAGGGUACAGGGAGAA	85115	AGAAGCGGAUGCTGGAAUCAG
239035544	85116	CAAGTGAAGACUGTGGCAUCCA	85117	GCCTGAGUAACCTGCTCUCCT
239035665	85118	AGGCAGGCGAUTATCTATTTGTTTTCUA	85119	GAGTCAAGGAGACAUTTGTAUGAGGAAA
239043292	85120	GGTGGCAUAACCACTTGAAUCCA	85121	CTCCCTCAUTCTTCCCGAUCAAT
239045841	85122	CAGAGGGUGCCCTTCAAUGT	85123	CGCATCTCGAUGGCAAGGATTTUA
239046000	85124	CAGTTTCAUCCCTTTGCTUGGA	85125	GGGAAGGUGGCTTCTTCTTGUT
239053496	85126	GGGAGTTCUGCAGCGAAACUT	85127	CTCTGACCAGGAUGGGTTTATUACC
239056689	85128	CAACACCGGCUCTTCTTTUGA	85129	GGCUACAGAGGACCCCCUAC
239059105	85130	GCACAGGAGGAAGUGCCAAUA	85131	TCUCAGGATAAAATTUGGCCAAGAAGT
239059191	85132	AAGCCATTGUCCTCACTCGUC	85133	GCCATCCTTGUAGAAGCTATCTGAUT
239062394	85134	GGAGAGGACAUAAGGGTCATTCAUCT	85135	CCCTGACCUCTCCAAGAAGGUA
239063150	85136	CAACAAGCTGAGGUATGTGACTACUT	85137	TCATCTGAGGTAAUATCACAGCATCUAGT
239063567	85138	TTCCTAAGGUTGCACAUAGGCAAA	85139	CCCAGCTTCUCTGTCTAAGTAGUAACT
239064384	85140	GAAGGGTTUCTGTCCCCAUCAA	85141	GAGTCACCCCAGUCGGATUC
239064543	85142	AACCAACACAACAUCAGCGTTUT	85143	TTCGGTTTCACUTTTTACTTCAGGTUG
239065059	85144	GGACAGGCTTUACTTGCTATACTTUCAAA	85145	CTTTGCCCAUGGAAGAAACAAGUC
239065210	85146	AGTCACCTUGGCCACTTTCUT	85147	CACCTTATGTTCUGTGTTGTCACCUA
239075640	85148	GGAAACATCAUTCTTTGGGATUAACACT	85149	CCTGTTCAUACAGCCATACCUCAC
239075894	85150	CACTAAGAGACGUTGATTTTGTTGTUGA	85151	AGAGTGCTTUTGATGGAACTUGAAGAA
239078147	85152	ACGAATTACGUGGTTACCCCTUG	85153	ATTTGAGGCAGUACAAGTUGAAGGT
239079411	85154	GCCTTCAGATTGUGAGGATTTCTTCTUA	85155	GAATGAGCAAGCAGAUATTTCCUCAAAA
239080008	85156	TGGAATTTCTTCAUCCTTCCCAATAUGG	85157	AGAAGCAGATACUAAGCAGGACACUA
239080321	85158	GAAGTAGGACAUAAATCCATCATACTUGACA	85159	CCTTCAATTCCUACACCTGCCTTUT
239080634	85160	ACCACGCGGUCTTTGUACAG	85161	CACCCAGAUTTCAATTCTTTUGACAACA
239081306	85162	GGTCTGGGUTGAGGUACAAAGG	85163	TGGAAGCCACAAUATGACATUACGAT
239081515	85164	AGCUCACAACCGACAATAUGCT	85165	CCGCAGGUCGCTAAGGAATTUA
239081546	85166	TGAGGAAATATCUGCTTGCTCATUCAAT	85167	ACCAGTACCCUTACCAGTAGATGUAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239082857	85168	CCCAGGGATUAAAAATGTTGCTUGAA	85169	CAACATCTGUCAACTCCACAAAATUCT
239083028	85170	CCTTCCUCGGTTAGGGUCGAT	85171	AGCATCATCAGCUCAGACCTUC
239084035	85172	CAGTGGAAACTTCUACGTGACTTTGAUA	85173	AAATCTAACATTCAGAUAGAAAGTACATTCUGT
239084111	85174	CTTTCUCTCCAAGUCCAGCGT	85175	GCAGCCUGCTGTCGTCAUA
239084421	85176	GGTAACTTUCACTGATACCAUGACAAGG	85177	CTCTTCTTGTUTAGATGTCTCUGGGAAA
239086176	85178	TCAAAGGAAGAACCAGUCACCTTUC	85179	ACTCCUGGGCAAGTTCTCUCA
239086483	85180	TGGACTCUGCAAATAGGACATTUCAA	85181	CACCCAAAAGAAUAGTCAAUGAACAACA
239086549	85182	CCCATTGAUGGAGTAGGUGGA	85183	AGTCCCCAGCUCAACTGTAACUA
239087853	85184	ATTGGTGGTTCTUTCAGAGATCTAACUG	85185	CTCTCAUCACCAGCACCAGUAA
239089045	85186	GTCTACCTGATCUTGGATCCCAGUA	85187	CTCAGAAACTUAGGTTGGGACTTCUC
239089702	85188	AGGGAGUAACACUGAGACCGT	85189	GGTGTGGCUGAAGCAGTCUT
239092654	85190	TGACUGCUCCGAGAAGAACAAG	85191	GTGATTCAGAAGAUACAGATTCGGAUGA
239093243	85192	CUAGATCTGTAACUACGAGGGACCA	85193	AGGCGUAGAGGGCACCUA
239094877	85194	CTCCAGCATTUCCTGTTTCACUG	85195	AAGGUCACCACGAACTTCTUGAA
239097318	85196	ACCCCATTTCUACCACCAGCUA	85197	CGCTGACATTTGUTTTATACTGTGTTGUT
239099062	85198	TCCTCCAAGTUGCAATATAGCTTGATUT	85199	AATTGCCATCUCTGCAACTCUGA
239102154	85200	GGTGTGUGTGTGGCTUCAAAAAC	85201	AGACATTTTACAUCATCATCTGCUGCT
239103139	85202	GTCACCUGGAATGTCTUAGAAGCC	85203	ATTCTAGCCAUGCAGTCACCTUAC
239105187	85204	CCCTGACCAGACUCCACUGA	85205	GTAAAGGCGGAUGAAGUAGGACT
239108362	85206	GAGACGGTTTCUTGGAATACTGCUA	85207	CATGGAAGACAGUGATGGTGUAACT
239110577	85208	ACTCCAGAGAAGUTTGCAGATTUCC	85209	ACTCTCTUGCGCTGAUGGAC
239111343	85210	CTGTTATUGGTGTATGUGGCAAGG	85211	CACCUACTCAUGCAGCACCAT
239111517	85212	CCTACAGGAAGCUATCCTCTGCUT	85213	TCCTCAACCAUCTCCTGUGACA
239116087	85214	GAAAGAGGCAUCTCCAGGCUT	85215	CATTGGCACCACUGAGTCTUC
239116303	85216	GCTGUGGGAAAACCAGGCTUAT	85217	ATTTTCAGCCUCCCTGACTCUG
239118617	85218	GCTCTGGCUCTGGTUCGT	85219	TGCTGCUGGAATCCTCCUG
239122081	85220	GACCACTACTGUCACACTTTAATGCAUA	85221	CCAUATTGCCUGAAAGAAGAGGAAGAC
239125173	85222	CGCCAGGUTCTTUCCGAAAC	85223	GAATCTUCAGCTCGAUGCAGAC
239125971	85224	TCGUGAAGGAUAACCCCCAGA	85225	GGTCTGAGGUCTTGAAGCTAUGGA
239128751	85226	CGAGTTTTATUGGCGACACACUGA	85227	CGCTAGAUCTTCTTCCCUAACCC
239130126	85228	GAGAAGCUCCAGAGCCTTTUAAAGA	85229	CAACTCCCAGUCCCACUGAAG
239131541	85230	GAAUTTGCTUGAAGGCCACCAT	85231	AAAACTUCCACACATCATUGGAGGA
239132213	85232	GATACGTGGUAGAAGGCTTTTCTUGA	85233	AATAAGTCTUGGCAACAGACCACUT
239134837	85234	GTTGATTCTGCUATCACTGCTGGUA	85235	GCAGAAGAAUCTUCCCCACCAAA
239135386	85236	CAGCCUGGCUGACAGGAA	85237	GCUGGAACAGTUGCCGGAT
239137380	85238	CCACTGUACGATGCCTUCGG	85239	CACCAGUGGAAGGCUCAGAAT
239142882	85240	TGTCCTCCTTCUCCTCTTTCATCUAAA	85241	TCAGGAAAGGGAUTTGCTUCCAG
239143980	85242	GAAGGAGAACGUCTTCATGAUGGT	85243	CCAGGUGGACCTGCTUCA
239144275	85244	AAAATGGGATTGUTTGCACTAACCUG	85245	CATGGAGTCUGCCAATTCTACTTCTTUA
239147154	85246	AGGAAUGCAGGGAGAGCTGUA	85247	ACAGAUAGCCATGAUGCAGCAG
239148283	85248	CTCCTATACTGACUGGGAGGACUT	85249	CUCTTCTTGTCUCGGCCCAT
239149627	85250	TCGAGCATGAUGAGCTATTAGATCUGA	85251	CACTTATGCATGAUTTACCATCTTTGCUT
239150870	85252	AGTCTACTATCUGGCCTGTTTUGGA	85253	TGGGUCACCCAAATUCAGAGG
239159418	85254	CTTCTCATUCAGCAGGGCUAGG	85255	CCCCTTGUGCACATAGTTCUGT
239159964	85256	CTGTGAUGGAGCCCCTCATUA	85257	GAATGCTGCUCATCTTCTTCCATUG
239164556	85258	ACCCATTATUACGCCTGTTCUCC	85259	TCTGGATGCAGUGCTAAAGAGUAAAAA
239167801	85260	GCUCCACAACCAUCAACAGGAA	85261	GCACAAGGUCAAAGCAGAGUG
239168699	85262	GAAGGTATTTUGGCTTTCACGGTUT	85263	CCGGAAATTUCTTTTACACAGUCCAG
239172825	85264	CCATGAATAGTCUAGCAGTTTGATTGUCT	85265	AATCATTAAACTUACTTGACAGCCUGGT
239172883	85266	CCAACTGCTCUGGAACATGTTTUC	85267	GACATACCUCAGCACACACAUACA
239174145	85268	CCTCAAGACCUTGCCTCTTCUC	85269	GATGTGCUCACTGTCUGACCAAT
239176080	85270	AAAACTCACAUTCCTCTTUCACCAGAA	85271	CATTTTTAGTGGACUCTTGTGGGCUA
239178416	85272	TTCATTCAAAUGGTTCTCACAUGAGAGT	85273	TTCTUGGGACGCACAGUGAT
239181039	85274	CCTGCATGCTTUAAAAACTCTGAACUT	85275	TCTTCAGAGTCUTCCACCAGGAAUA
239185226	85276	CAAGGTTCUGCCACTCUCAGAC	85277	AGGACAAGACUGAGTTCTCCAUCA
239186428	85278	TCAAGAGAGTUAGACTGTCCACCUT	85279	CAGATCACUCAAAATTTGCATGUGAAGA
239187331	85280	GATTCUCCAACCTCGTCUCCAA	85281	CCAGCCAUCGAGACTTUGCT
239187339	85282	ACCAAGGCUGTCACCACATUC	85283	ATAGTTGUGCTGCTGGUGGAT
239188133	85284	TGGTACCTUCCCAGCATAAUGGA	85285	CTGGACGAGGAAUGCTGGUT
239191013	85286	TGCAGCUCCAGGUAGCAC	85287	GCTTACCGUACAGGCTTUGGA
239191641	85288	TTACAAAGAATGGUTAGTGGTTTAACAUAAACA	85289	AAGCTTTGUCACCAGATGATAACUGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239193281	85290	GTGCTACCGAUGCTCTGCTTAUAT	85291	ACTCTGAAGCUGAAAATATTGAGCCUT
239193372	85292	CCTTAAGCCAUCTGGGCCUAC	85293	GACTCCUGTTTCCTAUGGCAACT
239196385	85294	TGATCCUCAAACGATGCCTUCC	85295	GGGCTCAAGCUCTTAGCCTUT
239198234	85296	CGCCAAGGUGGTCATTTUGAAA	85297	ACUGTCCAGTTTUGAGAAGCGT
239199100	85298	AGAAATUGCCCCACATTGAUGAGT	85299	GGGTTGGAUGATTACGGTUGGG
239199535	85300	CCAAACTTTAUAAGATCCTGGCTAUCCT	85301	GTTTCCCCTGACUTATACACGGTTTUAA
239203333	85302	CGTCCGCUCAAGAGTGUCAT	85303	CGUGAGAAAGCUGGACCGAAG
239206598	85304	TATTTTCTGTCTTTACUTGTTCCTTTATTCUCT	85305	GCAGCTGACUTGACTTTGCTAAUG
239207701	85306	GGCTCCTUCCTCACCCGAUA	85307	CGCUACCUGCGGACCAC
239212134	85308	GCAGCAUCAGTGTGTCUGAACAT	85309	GCAGACGAUGAGGTCAUGCAA
239213121	85310	GTCTGACAGAGTUCTCATTACCCAAAUT	85311	CUCTCTCTCAUAGGAGCCAGGA
239213918	85312	AGACTTGUCCGTGGCTTUGG	85313	GATGCCCAUGCGTTGTGTAUAG
239216152	85314	CACGCUACCACTCCTGTUGA	85315	AGCTTCTTTAGCCUCAAACTTAATCTUGT
239216566	85316	CGUCGCAGAAACCACAACAUC	85317	GTGGACATACUCAGTGGCCUT
239218253	85318	TCTTCTTTTGCUTCCCTCTCTTUCC	85319	ACCATCAGCAUCTACTCCATAUAGACA
239219354	85320	AGCTGGATCUAGAAATGGAAGCUC	85321	ATTGCACGTTTUGAGGGTACCUA
239220201	85322	TCATTGCCTUCCGTTCCAGTUAC	85323	TCATTTTGGCTUCTATACCTCCAUGAT
239222218	85324	AGAATTCGCUAGCCCTGGGUA	85325	TCATGGUCGAGCATTTTUGCAAAG
239224463	85326	CCCGGCCCACAAUTTTATTCTUAA	85327	TTGCTGGAGAACUTGTAGTAGTTGAUG
239224564	85328	GCATGGAAAGGUGCCTTTTUAGT	85329	TCTAGATGCUCGAGGAAGTATTCCAUAA
239228613	85330	CTACTGCATTUGACATTCCTTGTTTUGT	85331	TGCTGGGTAUGTAAGGAGCTUG
239230016	85332	CAAAGCAGAGGAAGUAGCTACGUT	85333	ACTAGGATATUAACACATGGGCUACAGT
239231892	85334	CTCATTGUACCGTCAGGAUCAAGA	85335	GTACTGATTACTACUGGCCGGAAGTAUA
239233519	85336	CTTGCCTTUGCAGCCATUGAT	85337	GCGCGUCAATGACTUCCACT
239233765	85338	CTCAGTTGAATTUGCTGGGTTTTATUGT	85339	AACATCAGCTGUAGGAACATCGAUT
239234199	85340	AGCCCCAACAUGGTTTTGAACUA	85341	GGTTCAATTCATTUACTTCAGAGGACUGT
239234799	85342	CACCGGUGUGACCAGCA	85343	GTGGGUGAGCGCTGUGA
239238083	85344	GGACAGGCACUCGTTGACAUC	85345	TCAACGUGGACGACUGCAAT
239238296	85346	CAGGCAGCUAATGAAGGUCCA	85347	AAAGCCTUCAGACCCAATGGTTAUAG
239239197	85348	AGCAAACCUGCCAGTGGTUAT	85349	ACCTACTGCUGTGTCTACTGUAGAAA
239239668	85350	CAGGUGCCGTTGTUAAAGCA	85351	GUCTUCCGGGACGGACAC
239240505	85352	AAGTGGTACGCUCCGGAAUG	85353	AGAAAAUGAAGCAGGACUGGCT
239245378	85354	GCUCCCUCACGACAGGAT	85355	CTCGAGGGCAUCCGTATCUG
239251089	85356	CCUGGAAGACCACCCTGTUG	85357	CCCTGACTATUCTCCGACTGTUCT
239251433	85358	CATCTGAGUTCTGAGAATUGGGACAT	85359	AAGGCTUCAAGCTCUCAGGAC
239254211	85360	TGTGCCUCCCACATTGTTUCA	85361	GTTCACCCTUGGGCTAGGTUC
239261820	85362	GCCTTCTTCCUCCTCCTCCAUA	85363	CTTCTCAGAGCUGGATGGACUG
239263457	85364	TTCCCCCAAUTGACACTCTUCC	85365	GCCAGTGUGTTCAAGACUCAGA
239268489	85366	TGTCATTTTCCUTAGGTTCAAAACUGGT	85367	CGATTGCUAGGCCCGGTAUG
239270819	85368	CCTCTUCCATGGGCUCCAG	85369	CTGGCAGGUTAGCAGUGAGA
239275849	85370	GCCATATGAAATUGTAGTGGACCTUACC	85371	ACTCCCUGACCCAGGAGTUAC
239276738	85372	AGCAGTUCCACTTACGUGCAT	85373	AGCATGGAGAAGCUTTAGAAUGGG
239278102	85374	CAGACGAGCUGGAUCGCA	85375	GTTCATATATGTUCTGCCCTTGTCUCT
239281758	85376	TGGAAAACCAAAUGAAACCATUCAGG	85377	CCGTTCTTUAGCGGTCATGUCAA
239287296	85378	CAATGGGACUAAACCUGCAGGA	85379	CTACAGTCUCCAGTGGCUAAGG
239287620	85380	CCAGGCCUAAAATAUACCCAACCA	85381	TCTCAAAAGUACAAACCAAAGACAGCTUA
239289337	85382	TCCGTGTTCUTGAAGCAGUGG	85383	CCTGACCUGCACTCTTCTGTTTUA
239293657	85384	CCCATCUCCCAAGCTTGUAGA	85385	CACTACAACAAUGGCAACTAUACCCT
239298248	85386	TTCCATCCTUCACATTGCCCUT	85387	CAACAATGCAAAAGCACUTCTTATCCUA
239301823	85388	TTCCACUGGTCATCCTUCGAAAAA	85389	TGAGTAACAGCUGTGCAGAAATUGT
239311557	85390	CCCACCACCAUCTCCTCTTTUC	85391	TCCTGAAGGCCUCTGTGGATUA
239312901	85392	AACGTCTCCGCAGUCTATATCTAUAACT	85393	CAGGTAGTTTCUGTTGTTCATGCUC
239315061	85394	CCCAGTGGGUTTTTGGCAAUG	85395	CACTGGCUGCACAAUGGG
239317146	85396	CCTTCTGCAGCUTGCGGAUA	85397	AGCTCCUGAGAAACTCCTCAUGT
239317698	85398	GGTCAGAAAUGACCATGTGTAAGUCT	85399	CACTGTAAUGAGGGCTGTCTGUAAA
239323364	85400	GCTGGAGGAUCGGTTGUCAA	85401	GCTGTCACCAAUGAGGTUGAAG
239323860	85402	TGATCTTTTUCTCCCCCUAGGGT	85403	GAAGACTACUTGCAGAGAATUACCAACT
239326308	85404	GGGAAACUGGCTGAGCACAUA	85405	TCGTTUACAAAACACAGACUGGAACT
239327716	85406	CTGCCAGUTAGCGGUAACCT	85407	GCTCAGTGGUTACTTCTCTTUCCC
239330191	85408	GTAGTATTCCACAUGGATGATCTUGGA	85409	GCAGGCUTCTCCCTUGACAG
239332380	85410	AACACTCACTUCTTTACAGCTTCUCC	85411	GGGCCAUGAACATGAGTGUAAAAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239338049	85412	CGTTGCCUCCTGACAUACCAAG	85413	CCCAATCACUCAGTCTAGTUCACA
239338431	85414	CCATGTGGGUGGGTGGUT	85415	AATGTUCCAGGGCUGCCA
239342461	85416	CACCAAAGCUTTTCTGGAAAAUCCA	85417	GGTTGCTTTCUCCAATAACTAGATGUGA
239344631	85418	CACATGTGAGUCAAATTGTUCAGAAAA	85419	GCACATCGAUCATTTCCAAGUCC
239346364	85420	TGTTTCCUAGATACACCCUCCGT	85421	TUCAATGAGGTUCCCAGAAGAGAAAAA
239347884	85422	CCACGCCUCCCAGACTUA	85423	GCTCGGCUGGAGTCTGUG
239350135	85424	CTCCCAACAAAUACCTCATTCAUGGA	85425	AGTCAGAUGAATTCCCTUGAACAAGAAT
239350190	85426	CCCTCCGUCCCAUAGCAAA	85427	TTATTTCACUGACAGGCAAUACCGT
239350990	85428	GUGCTGGTUCCAAGAAGGAGAG	85429	CCCTGGGUCCTCCAGTGAUAG
239351398	85430	GTATCCATUCCCACATGGUAAGACA	85431	ACCAAGCUGAAACAAAATCAAAAUCACT
239353953	85432	TCTGCAUCACCCCCGTUG	85433	CGGGUCAAGCCATCUAACCT
239356288	85434	TTTCTTTTUCAGGCCTTCATTTUCCAA	85435	AAGAGUTGAGATTTCUGACAAGCACA
239362747	85436	CTTCTGCAGATUCTCTACTTGACTTUCA	85437	ACTGTTTGTUGTCTTAGGTTAUGGAGAC
239364419	85438	AGGAGGCAGCUTCTTCTCUACA	85439	CTCTGATCTCTUGCTATCCTTTCTTACUT
239364548	85440	CCTGAAGCAUATGTAGCCCUGA	85441	GTGGTGCTTUGAACAGTGAAUGAT
239368878	85442	GCUACGCCUCGGACCAG	85443	CCCCUGGGTGAUGCAAGAG
239370527	85444	CGTTTUAAGAGGAAAAAGUCAGGAGAGT	85445	CTGGATCTCUGCGCTGAUGT
239371364	85446	GCTTCGACGAGUTCAAGGUG	85447	CCAGTTTTCUTTTCTGTCAAAUGGAGAT
239372670	85448	GGATGGGUGTGTATUCAGGAACT	85449	AACCACACAGGUAATCGTCTCTTUC
239372821	85450	GGCTUCAGCGTCCAGUCAAT	85451	GCTATCTCCCAUCACCTCUGCT
239373717	85452	GCAGCCACAGUGAGCUCAA	85453	GTGCATCUGCGCGUGAA
239374666	85454	CAGGAGCAGGAUAGTGCCTUT	85455	GUCCACAGCCUCCAGCAG
239374885	85456	GCGCCAGGUGGTAGCUC	85457	GCUGCAGCACAGCAUCCA
239375395	85458	GCGCGACUACGAGGAGAUG	85459	AGGAAACCGUGCATGUCCAG
239377327	85460	TCCTACAGACUTCATCUGCAGAGA	85461	CATAATTGTTCTGGUAATTGCCAGCUT
239379034	85462	AAAAGTGTAGUGTTGAGGGCTUCAT	85463	CACCUGTACCAACUACAACAACAAC
239380625	85464	CGGCACCCUTCCATCTCTCUAA	85465	CCGTGAAUGTGGUCCGACT
239381201	85466	TCGGTGAGUCCTGTCUGGAT	85467	AACATGTTATCTGUCGCTCCTCTUAG
239383830	85468	GCTTGTCTAGGAUGCTGTTGTGUT	85469	CAGCUTCGACUCCAGCACAT
239386296	85470	GAACCTGACCUCCCACUGAA	85471	CTCCTCGCGGGUGTATATGUC
239390066	85472	TTUGAGAGGACCCACUACCCA	85473	GCCATCCCAAACUTCTGAATCUCT
239393913	85474	TGATGTTTCTGUGCATATACTTGTTGTUG	85475	CAGCTCCTGGUTATACTCCTAATGUT
239394432	85476	GTCCTGGTGTUTTATTGTTTGGCTUT	85477	CCCACAGACUGUGAACACAGG
239395452	85478	CCGGCCCAAUCACAATGATTUC	85479	GTTUGCACCCGTCCUGGAT
239396320	85480	GAGGCCAUGCCACUAGAGAT	85481	CCTCAUGCTGGCTAUCCACAA
239397856	85482	TGGAGGAACUTGCCCAACUAC	85483	AGAGGAAAACAUGGTGATTACUCAACAAA
239398075	85484	GGCGAGAGGAACUCACTCTUC	85485	GCCACTCUGATGCCTCCTUC
239402030	85486	ACAATGAAGUCGAACTCAGAUCCC	85487	GCAACCTGAUCTTGTGAACAUCCT
239402777	85488	CCTTCCACCUTCCTTTCUACAGAAT	85489	CCATGTGGAUAAGGTACGTGUCA
239404253	85490	TGTTAGTTCCUGAAAACATTGACACGUA	85491	AGAACCGGGAAAACAUCTCCTTUT
239407307	85492	CTTGTGTGACCUTTGCCCTTUG	85493	CACAAACACACCCAUGAGCUG
239408094	85494	CCTCTCAGCUTCTTCTCTGCTUT	85495	CTCTCTTGAUATCTGGTCCAUCCC
239411065	85496	GACTTCAACCUTCATGTGATGUCAAC	85497	GGATATGCAAAUTGAACAAACUGACACT
239414678	85498	AGCATGCUACCAACTACAAAUCAT	85499	CAUATGTTTGAAGTATUGGAACGAGCAA
239415904	85500	GCTTTGAAAACAUACCGATTCATCCUT	85501	ACCACCCCTUACATTTGACATAATUAGG
239419440	85502	TCAGATAGTAGUCAGGCAACUCAGAT	85503	AGGAAGAGUGGCATTTCTCCUA
239426118	85504	CACCACTAGAGUGCCTCAGTUT	85505	CACCAGCCUCAUGCACAAC
239427009	85506	GCTCAAGGGCUTACCACTGUA	85507	GGCUCCCCCTGAUGCAC
239427313	85508	GCTGCATTGGAGUCATGTATTTTGATTUT	85509	CAAATTACTTGGAAUCGTCCCTTGUG
239432856	85510	GACGGTAGCGAUTATTTTCAACATTCUT	85511	TTTGTGTCAGUCATGAGTCAUCAGG
239435289	85512	CGGTGTCUCCTTGGTTGUCAT	85513	CCTGGTGTGUCAATCACTGUCA
239442640	85514	GCTGGCCCAGCAUGTCUAC	85515	GTGTGCACUCAGCAGCUC
239443414	85516	TGGTTTUCAACTCTGTATUCAGCCA	85517	CTGCTTGTGUCCCTTAGCUACA
239443530	85518	TCCTCACCCUGCCCTUCT	85519	GAGCUCAGAAAGCUGAGGAAGT
239445608	85520	GCAGACTGCUGTGTTCTTTGUG	85521	CAGCTGUCAGCACTTACTGCTUA
239446871	85522	GCTGTAGCAUCTTCCCTCAUCAT	85523	TGCTCTTGTTCUACACAAAGTCCUG
239447841	85524	GAGAAAGGCGUCCGGAUGAA	85525	GGAAACCTCUAGGGCTGACUC
239450815	85526	CATCTACUCCAAGGCCGTGUC	85527	GGAATUCCCACAGCCTGTTAAUGT
239451635	85528	CCCTACACAACGUGAGCTUCAT	85529	CCUTCAAAGTAGGUGCCCAGAG
239456244	85530	GCTTAAGCAUAACCCTGTCGTTUA	85531	ACAATTTCATTGUGTAGGCGAAUCAAG
239458969	85532	CCCAGCCUGCTTCUAACCT	85533	CCAGAGACUCCAAGCTGGUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239461955	85534	CCTGGCCUCCCAAACTTCTUC	85535	GCTCATGTTUCTCGCCAGGUA
239464738	85536	GAATCTTCACCUCTCTGGGATATTUCAC	85537	GCTTTTCCAAGAUTCACTGGTTTTUGAT
239468216	85538	CUCAAGAACCUGGCCCAGAC	85539	AAAGCACUGCAGGCTACUGAA
239471359	85540	CCAGGTCUCTGCGTGTTUCAA	85541	GCCAACAAGUACCAAGATATTGACUCT
239474830	85542	ACAGGAAGAATCUAGCTAAAGGCTTTUT	85543	GUCAAGAAGCATUAGAAGAAGCAAAGG
239476554	85544	TTCAGATGGCUTTCATCGUCCA	85545	CTTGAGCTGTTUCTGCCTTTATTTUCAT
239477450	85546	CTCGGTTTUCCTGTCGGACUT	85547	TCTTTGGTACCTUTGGATTTGACAGTUAT
239482302	85548	CAGACGCUGGGCTAUCGAA	85549	TCCAGGGACCUTGGTAGGUG
239482916	85550	GTGCCTTGAAAUCCAGTCAATTGTAAUA	85551	GGGATTACAAAUGAGAAGTGCAGUAAAC
239483569	85552	CGCGATCUCGCTACCGTTUA	85553	GCTGUGCGGCTTTGGUG
239488196	85554	AACAAAGAAAGAUGTTTCACCTUCAACC	85555	ATCTTCCTTCCUGTGGTCTTUACAC
239489141	85556	GCTACCGCUCTCGTCAGCUA	85557	ACTGGGCTUAGGGACTCUGG
239494401	85558	GTCAGTTUCACTGCCCUGAGT	85559	CCAGUACGATGUGGACGAGT
239498335	85560	CACTUGGCACCATTCTUGCAG	85561	CTGAAGGGCCAUAGTGCTGUT
239499951	85562	TATCATATATGCTUACACGATTTCGGTATCUAA	85563	GGACGTAGGUACAAGACTCAATAUGAAG
239500017	85564	TCTTCAAAATACCUTATCCTGTTGUGCT	85565	AGGAAACCAUCCAGAAGGACTUAGAT
239500426	85566	ACATCAUGACAAAGTCCUCAACCAT	85567	GCCATATTTCUGAGGCTTCCCTCUA
239501016	85568	GAGTCTTGTACCUACGTCCAATTTTCUT	85569	TGCATCTTTGACUAACAACCAGAACTUA
239501093	85570	TGGATGGTTTCCUTTTCAGTTCTTACUT	85571	ATTGGACTTCAAACUTTGAAAAATGTCUCA
239502432	85572	CCTCCGCGUCTGGACUC	85573	GAACUGCGCAGCCAGAAAUC
239503262	85574	GCTGATTTAGTUGAGACTTACGTGCUT	85575	GGGAATCGACGAAGUAAATCTTCTTGUA
239503310	85576	CTCTCACCCUCCTCCTCCUC	85577	TGCGUCACUCGCGAAGT
239505349	85578	GGGAACTAGAAAAGUCCCCTCUCA	85579	CCTTATTACCCCUACTTGCACUAGAG
239506153	85580	GGCTCGAUACGTCTTCUCCAA	85581	CCAGGTUTTGGTCCUGCCA
239508301	85582	GGTGAGCAAGUCAGCATTUGG	85583	AGAAAATGACCUGGGCCTGTUT
239509741	85584	AAGATGCAGAAUTGAGGCAGACUT	85585	AGTTGATTTAUACCCTGATAGAGUCGGT
239513624	85586	TGGATGAAGAAGAUCAACTGAAGTTUCC	85587	GCCAUCACAACATGCAUCAGAGA
239513718	85588	TGTGGGCGAGUTCCTCCUA	85589	GAGGAAAGGAAGGUGCAGUCA
239521410	85590	TGATACTCCTCUGTCTGCCAGUAG	85591	CTGAGGAACUGGATGCCTTUGT
239524898	85592	GACAAGCAGCAAACUTACAAGATTGUT	85593	GGACAGCACATUGCCAAGTATATATUGT
239527302	85594	GCATAAGCTTGUTTTAAACAATTCCUAACCT	85595	AGGCTGGAAUGCAAGCUCAT
239529723	85596	TCTTTTCTTUAGGGCCTGTUCACA	85597	GTGCGTTTCAAUCACCACTAAAUCAAT
239530810	85598	AACAGAACTTACUACTGAGACTUGGAGA	85599	CCTGAGTGUGACATGTTCTCUCAT
239534661	85600	AGTCTGTCTUTACTACACTGUCCCAA	85601	GGACTTCCAGUCTTCTCGATACUG
239540037	85602	GTUCTAGCACTCUGACCAGCAA	85603	TCACTCAUCCTCATCUCGAGGT
239542949	85604	AAGGTATCTTGATTUTAAGTTGTAATTCCTUGA	85605	ACCTGAACAGTAUTCTGGAGTTACGUAT
239543300	85606	TGTTTTTACAGAGGUAAATACCGGATUGT	85607	CCAGTGTCCAUCCATAGGTTTAACUT
239552003	85608	CUAAAGGGACAGCCTUGGAGAA	85609	AGGTGAAGGCCCUAAGGAGUAG
239556324	85610	GCATCTGTAUCAGGCAAAGTCAUAGA	85611	GTAGCTAACTAACUTCAGAACACCAACUT
239558795	85612	CCAGCTGGAGUTTGGTCATGUT	85613	CTGACUGGCAATTGTGUCAACAG
239564394	85614	TGGGAACAAUGTCATCAGUGG	85615	ATCCUGACCACCTUGCAAGAG
239565469	85616	GCTCAGAUGACAGCCGGTUCT	85617	GAACCAAGUTCTUCCGAGGGAAT
239566960	85618	AGCTCTGUGCCCTGTGUG	85619	AGCACGUCCAGCACCUT
239567874	85620	GCAACCCUTGCCUAGGAAGAA	85621	CTGAAGCGGCAUCTCCTGAAAUA
239569560	85622	GTTCAGATTUAAGCCTGAGGAGCUT	85623	CCACTGTGTTTUCTCCTCCATTTTUAG
239575754	85624	TGTGUGGACAAGAUCCGGAAC	85625	TCCCTTTGTUAAGCTCAACACUAGAC
239587376	85626	CTGCUGCAGAAGGAAAGCATUT	85627	GATGGAGGGAGUAGAACTGGTAAUACT
239588213	85628	TGCATAACTGAACUGTAAGCCAAGAUAT	85629	AGCAGGAAAAACCCUTGTTAGCUT
239612485	85630	CAGTCUCAAAGTCTGUAACCCCAAT	85631	CTGGAACUGCTTCACTAGAUCCC
239613030	85632	GCUTAATGTTTGAAATUCACGGAAGAGA	85633	GTAACAATAUTGCATGCUCCAGAGG
239617538	85634	TCTCGGGAUAGATGGCCUCA	85635	AATAACATGCUCAACCTTGTCTGUCT
239621783	85636	TCAGCCATUACCTTGTCATGUGG	85637	AGTATCATCCATUGCCCTTTTCTTGAUT
239625181	85638	GTCTACATGUCCATTCCTUACAGCAT	85639	GACATTTTUGGCCGTCTGUCA
239628105	85640	GGCAGACAACUACTGAAUCCCA	85641	GGACTGGATAUGCACATTTTGUAGAGAT
239630595	85642	TCTACTTTGUGACAAAGTUCAGAAAGGT	85643	GCTUCCCAATCGTUCAACACAAAA
239630735	85644	CATAGAAGTUCGTTTTGTGTUGAACGAT	85645	GGTCUCCGCAACTGCATTUT
239633077	85646	TTTTCACTGCAUATGGTCTATGTGUGAT	85647	CCCTTGAUGAGCTCAGGGTTUAG
239633572	85648	ACATAGGAGGAUCCAAAGUGGGA	85649	GCAGGTACCUTTCAGCATCTUCA
239634238	85650	GCTCCTGAGUATTGGTGTUCCA	85651	CCCAAACAAAAGCGAUCTCCUC
239641660	85652	CAGCACCGAUGGCAGAAAGUA	85653	CCATTTTACCUGCTTCCTCAAAUAGGA
239649723	85654	GCACATCCTGAUCTCATTGATTGATCUG	85655	CATTCAGTGGTAUTCCTAGTGACACUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239650035	85656	CUTCCATCUGAAAGGCAGAGCA	85657	AGCCGCTCUAGAACAGCAUT
239650358	85658	GCTAUCACAGAACCCGUAACAGT	85659	CAAGAAGATGTTATUAGCAGGACCACUT
239653958	85660	CCTGAGAUTTTGGCCTUGCAAA	85661	GATCCTTUCGAACCGCCAAAUG
239655775	85662	CAATCATATTCAACUTCTGGCTTUCCAAT	85663	CCCAGUCCAGGGAAGTAGCUT
239660886	85664	TGGTTTCTUCAGGCACCAUGA	85665	CGTTTCCTGUTTGACCTTTTCUCC
239661439	85666	ACTTGCAUGGACTGTGTTATUGGT	85667	GAGCTAGTTCUGTCCACTGGUC
239663045	85668	GCTGGACCAGUGGACAGAACUA	85669	TCCACAGAACTUATAAAAACCTTTGUGT
239680434	85670	AACACCAAGGAAAAUGAGGGACUT	85671	AGTUCTAAAAACTTGATUACCGCAGACA
239683680	85672	GTCTACGAGCUCCCATUCAACA	85673	GAAACCUGCCCAGAGGAGUC
239686636	85674	ACTAGAACTTGTUTGTGGCATATCTUCA	85675	TTGTTGATGTTCAUTCTTCCTTCTUCCT
239686717	85676	ACCTGCCACCGUTTTCCTTTUA	85677	CACCATGATGAAUGGGATATGTAUCCAT
239687739	85678	TTTAGGTTGCAGUTTCATCACTGUCT	85679	GCTCTGACTGCUGCAATATCCAAUT
239691764	85680	TCAAAATTTCCCUGTCTGCCGTUA	85681	TCCTTTTTGCGUTCTCATTACAGTAUGA
239694657	85682	TCACTGTCUGCGGTAATCAAGTTUT	85683	ACCTGAAAAAGGUTAAGGGCTCUG
239694744	85684	TGAAATTGGAUATTGCAGCAGUCAGA	85685	GCTCCTTTATAAGCUTCTTCAGTATATGUCA
239694874	85686	GCATTCUGAGGGCTGTCATCUT	85687	CGAACTTTCUCCCTGGUCACAC
239697470	85688	GCTCATUGCGGAAGTTCCTCUT	85689	GTCGCUGGTTCTCGUGGT
239701397	85690	GGUTTTCCGAUGACCAGGACT	85691	AGATAGUGCCCCTGGAAGUGT
239702231	85692	ATTCCTTCTCUCAACTGAGTCUAAACC	85693	CCACACCAGGACUCATACAGGUAA
239705756	85694	GAGGCTCCAUCGCTGAAGUA	85695	CACAGACAAGGAGCUCAGUGAC
239707106	85696	CTCCCUGAGGCTGAGUGAAC	85697	GTGGAGCAAACAAUGACGAUGAC
239707192	85698	TCCACCCUCCUCCAGGAC	85699	GGAGAUGAUGGAGAGGGAAAGGA
239712250	85700	TCTCCACTUCACCCCGUCA	85701	GGTTAAGGUGAACTGGTTCTCAUCT
239718463	85702	GCAGCCTAAAACAUAGAAAGTCACTUCT	85703	GCTGCTTGCCUCCATTAGTUG
239720969	85704	ACTGGGTAUGGTGGTTTCTCUCA	85705	GACAGAGCUCCAAGAGGUGAC
239725368	85706	GGGCTTGGUAACGTCCUGT	85707	CTCCAUGCCCCTCACUCA
239727682	85708	CAUGCTGTATTCAUGGAAAACCAAGAT	85709	GGAAAGCTAUTGCAGAGAUCAAGAAAA
239729531	85710	AACAACAGGAUTCTCAGGGAAUGG	85711	TCTCCGUGCAGUCGGAAAAA
239730565	85712	AGTTCGUGGACATCTTUCAGCA	85713	CTGACCCTUAGCCAGTATCUAAACAT
239733908	85714	CACCAUGCTGAAGUCCAGGAG	85715	AACTCTTCUCCCCTCCCTGUT
239734819	85716	ACTTCTTCAAAAGUCTCCAGGTTTTCUT	85717	CTCTTCTCAACGGGUTCCTTTTCUA
239742375	85718	CATAGCCTUGGCCCATGTGAUA	85719	GATGCTGCTUACAAAAGGAGCUG
239744790	85720	CTTTCTTCTCCUTATAGGTTGCCAUCA	85721	GGAAGGAGTTUCACCCAAGATUGT
239746111	85722	AATGTGAAGAAAAGUTTACGCACTTGUT	85723	GGCTAGACCTUCTCTGTCCATTUAG
239758603	85724	GGTCATTTAGAAAGUTTGTCAGTCCUGT	85725	CGGTCCUGAAGAAATGCUGAGA
239760064	85726	AGATGUGAGACCGAAAGAAATTAUCCAG	85727	ACTACAAGGCCUCCCTCCUT
239765682	85728	TGTTGGAUGCAAACAGTAATATTUGGA	85729	CTGTTTTTCUCAGCCTTGCTUAACT
239766808	85730	TGACUAGGAACGTGAGTUAAGCAAG	85731	ACTGCTCCAUCTCCTGGUCAA
239766976	85732	ACTCACCCGCUTTCTCGUT	85733	GCCCUGCACGAACTCCAUC
239769572	85734	GTGCTTCUGACGCACACCUA	85735	GTUCAAGACAGAAGGGCCUGA
239776746	85736	TGGCTGTTGTTUGATATTCTCTCCUT	85737	ACUTAGTCTCUGGGACGCCAT
239778898	85738	CAGCCTCCUTCTGTGAGAUGT	85739	CCCAGGTUCCAGAGGATUGG
239780501	85740	TTGAGAAAGGCUGTGTGUCAGAT	85741	CCTGCAGAAGCUCTTCCUGAG
239780944	85742	ACCGGGUGTACCTGGUG	85743	TTCTCACCUGCTGCTUGACAA
239783045	85744	TCAACTCACUAACAAGCATCTATUAGCC	85745	GATCATCTTCUAGAGGTGGAGCAAUC
239786724	85746	CTTAGACAGGACCCUGCGUAAAC	85747	GTGCAAGGUAGGCTATTTTAAGUACCA
239788707	85748	CTTCTCTGCGGUTTGAAAGTACUG	85749	ACAACTTGCAAUGAGTATGCACATTUT
239792247	85750	AGACCTCATUCCTCTGTCTTCUCA	85751	TCCAGGUCCAGATCCACCUT
239793456	85752	CAGTGGUCAGACCTGCTCAUA	85753	GUAAAGATGGCUAGAGCCCAGAAAG
239797121	85754	TGTGTCAAGGAGUTCGAAGATUCAC	85755	ATTGAAAATCUTCCTGCCTUCCCT
239798998	85756	CCAATCTCCCTAUTTTCTCAAGCATTUCT	85757	GGAGAAGUGACTGATCTGTUGCAT
239800737	85758	TTCGGAAATUGAAGAAATCTGCCUAGT	85759	GCGGGUCCGGATATGAAUGA
239807548	85760	CAAGAAGTGGAGAAUGTCAGTCUGAG	85761	CAGACCCTCUCACTCATGTGAUG
239816250	85762	CAGAAGAGGAUAGGCAGAAACUCA	85763	AGTGATGAUGGGACTCAGGGUT
239818584	85764	CTGGGAUGGAGGGAAGAUAAACC	85765	GCCTATCATGUGGCAGCTCUAC
239818754	85766	CTGGTGTTTUAGGACCATTCTGTTUG	85767	TCAATGATTCUGACTCCGGCATUT
239821359	85768	AGACGCAGAGUCAGTTTTUCCC	85769	AATACCAACACAAACUTGTACACCCUAT
239822292	85770	GCCTTTTTATAUGAGCCAACAACUCA	85771	GAGACCTAAAAGAUTGCCCACTCUT
239824520	85772	GAACTGAGGUGACATGGGCUT	85773	CTGTGUCGGGACCCCTUAC
239825252	85774	AGTGTUGAGCAAAAGCCGAGUA	85775	TCTCATCGAGAUATTAAGCGAAUGCAG
239827046	85776	TGTACTGAGCAUGACCCCUGT	85777	AGCAGGAGGUTTATCTGACATTTUGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239838122	85778	GTGTGAAGCCAUTGTCCAGTCUA	85779	ACCTACCGUAAACTCGGGUCA
239839152	85780	GCCAGCAACUACCTGCACUT	85781	GTCTGUCCAGCCACTAUGGG
239852045	85782	GGTTATCTGGAAUTCCCACGGUAA	85783	CACCAACAACUTTCGUCAACACAG
239853329	85784	ACCACACAUGGCAATCCCAUAC	85785	TTTGGATTGTGUCCGTTGAGCUA
239856763	85786	ATCAACAGGAAUGGCTGCUCA	85787	GTCAGTTCTCUCAAGAGGTCTTUCAG
239860841	85788	GGACATCAGTUACATCTTCCCATUGAC	85789	TGAAGGCACUAACUGAGAAAAACAAAGA
239861023	85790	GGATCGGUATCGTCCAUCAGG	85791	TGAAAGTATGCCCUGTCCTTTTCUT
239862998	85792	TGCGATCCUGAGCAATTUCAAGT	85793	TGGCAGTTGCAUAAAAACACTCATUG
239868286	85794	TCGCATTACTTAAUTTAGGCAGTTCUGA	85795	CAACACTGCAUACCTTCCAATTUACAAT
239872671	85796	CACACTGGGACUTGTGTTTAGUG	85797	CCTCACCUGCTACTTUAAGCCAT
239883388	85798	TGACCUGCCTTGGTTUAACGG	85799	CCATCCAUCCCAAGATCCATCTGUA
239883973	85800	CCAGCTCCTCUTCAAAGACTCAUC	85801	ACTATGAGAGCUTCTCCTGTGUCT
239888601	85802	TTGTTTGTTTCCUGTCTGGACUGA	85803	CTUCACAGCAGAACAGCUGGA
239890414	85804	CCAGCCUCACCTUGCCA	85805	GGGTCACGUGTGTCTCCUT
239891166	85806	CCAGCCUCUGAGAGAAACACAAAT	85807	TCTGCATGCUATTGGCCTGUC
239893201	85808	GGAAGGCUCAAGCCAUCCAAT	85809	GAATCCCUAACTCCCUCCAAACC
239899236	85810	CCAGCAGTCUGAGCAGTTAGUAA	85811	CACTUGGAAACAGGCTTUGGAA
239900679	85812	GACTTGUCAGAGGCCATTGCUA	85813	GCCUCTGGCUGGAAACCAAG
239905868	85814	GCTGAUAGCTGTUGCCGACT	85815	GTGCGTAUCGACTCGAUGCT
239906792	85816	CAGGGCCAGAGAGUAGAGAGTUA	85817	CCACCCCUCAAACCCTATCUT
239908628	85818	AGAGGGCAAGAGGGUTTCACUA	85819	GTCCAAGAGACUCTGAAGTTACUCAC
239912605	85820	AAGAAGTGAGUCAAGCAGTAUGCAA	85821	GGACAAAAATGAAUGCCTTTCGAAUCC
239913450	85822	ATATATATGAAGUACCAATGACTTCCTTTUCC	85823	TGGTACTCACCUTGTCCACGAUA
239915118	85824	TTTAAGCTTAGAACTUTAGTCAGTCTAGAATUT	85825	AGGTTAATTCATCACUGTGCCTAGATUT
239915353	85826	TTTTACCTAUAGGCTGACAAAGAUGAACAAA	85827	TGTCCCTGGUCTGATTAATTTCTTTUGA
239915654	85828	TCTCAAAAGCACGCUCCAGUT	85829	TGTTTTGTTCUTCTGTGCTTTUAGCC
239915882	85830	GCCCATTTAGAAGUTCAGAGAGUGA	85831	CAACCAGTUGACAGTGAACTCATUAAA
239917344	85832	CCAAGUGGACACAGGGACUAT	85833	ATGGGCCUGTTCGTCCTTUAG
239918759	85834	GTGATGAATTAACCUCACTGTTGGGAUA	85835	TCTATTACATCUCCAAATGTTGCAACTUACT
239919433	85836	TTCCTGGUAGAACAATAAGGTCCUCT	85837	TGAAAAAGUGAAGTCCTGCUCAGAA
239923667	85838	AAATTATACGUGACCTGUGGCGAA	85839	GGGUCCAGGGAGGTAAUGCT
239923757	85840	GCCCACUTGGUGGAAGAACAG	85841	CACCGCUCAGAUAAGGAACAGAG
239924520	85842	CTGTCCTTTCUGACTGCATCCUAT	85843	GTACUGCCAGCTCACTUCACT
239925003	85844	ACTTGCAACCUTTCCTTGAAGUC	85845	GAGTACTCGGUGTCAAACUGCT
239926012	85846	GCACAGAACGGUGUCCAGAG	85847	CAGCTTGCGGAUCTTGTAGUG
239929896	85848	CTGCAGCGAGGUATGGACUC	85849	GTGACGCCGUAGTCGAGUA
239932589	85850	CCCGTAGCUCGAGAGUACAA	85851	CAGGCCCUCTGTTGCCUA
239932898	85852	AACTTGAGGUTGCTAACTAUGAAACACT	85853	CCTTCAGCACUTCTTTUGAGCAC
239935048	85854	CCAAGGGCCUCAACGUGAA	85855	CCCAGAGUCTGCAGCUGAG
239936250	85856	CACTGTCUCAGCCAGAGGTUG	85857	ACTTCTGUGGAGACACCCTACTTUAT
239938258	85858	TGTGTTGACUGTGGCATCUGAA	85859	CTCAATGGAAAAAGAAGUAGGTAACUGT
239939613	85860	CTCTTCATGGGUGAGGGTAGUCT	85861	AGAAGAGGAUCACCCUGGGAT
239940055	85862	GCCATCGUGTCGTGTGTTUAC	85863	GACGTCCUCCTTTCCAGGAUT
239943702	85864	GAUGGTATGUAACAGCGACCGT	85865	GCTACTGGAAAACAUTCAAAACTGGUT
239945240	85866	GGGTCAGGUTTTATCAACTCAUAGCA	85867	GACTTCAGTTGUCTTTGTTTCTCTUCAG
239948812	85868	CTACCCCCAGAACUTCAGGUC	85869	AGCCTGGTCAUTTCACATATTTUCCT
239949488	85870	GGAGGGCCUTTAAAATGAGGTUCT	85871	GCTAAGCATTGUCCCATCATTCAATAUG
239950912	85872	CTCCGAAACCCACACUCCUG	85873	CGTGACTGUGGCGCTCATUA
239958349	85874	GTAAAGCGGGCUGGGAUGAT	85875	CAGCAAAAATUCCTCCTGGUGT
239960819	85876	ACAAGTTCCUCCATTCUGGCAT	85877	CACCAAGTCCUGTATTTCACTCTAUGAC
239961657	85878	AGTGGCTAAAUGAATATCTCTGCTTUGT	85879	GGTTTTCCAATUTACTGAAAGCAUGAGG
239968651	85880	CCTCCAGCCCCUCCTATAGAUT	85881	CTGTCGATGATAUGAATTCCCATGAUGA
239969009	85882	AGAGAGGGUGGGTGACAGAUT	85883	CACTAACCTUCCTTCTCCCCTUG
239971549	85884	CTCAAAGGGCUCCACTGGTUT	85885	TGATGCTTUCACGGCUCCAT
239973885	85886	GUTGGAAGAGTUAAAAGCCCGAAC	85887	TGCAATTCAACUCAGGAAAAGTAUCCAT
239973944	85888	TCAAAGTCCAGACAUGCAACCUT	85889	AATTTCTGCTTTCUAGCCATCAAGAGUAT
239977367	85890	TGAGACAACAGAAGCAUTATACTGCTUT	85891	CTGGAGTGTGUGGAGGAATTACAUT
239977787	85892	CTACCCUAGGTGCUCAGGACT	85893	CCCTTTCUAGGGCCATCTGAATUAGA
239979260	85894	GTGATGGATCUGGCTAAGCATCUT	85895	TCAAGCAAATTTCUATGAGTCAGCCTUA
239985141	85896	GGACTGACUGGCACCTCUT	85897	GCCTGGAUCACCTTCTGGUC
239985956	85898	GCTTGTTGUTGGCTATACUGAGGT	85899	CTGCTTCTGUGTTTTCCCTTTTUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
239987086	85900	GGACCCCAGCAUCUGCAC	85901	ATGTGCCAGAUGCACCUCAA
239993600	85902	GTTGCCCUGGGTCCTCTTUA	85903	CTGCCTCAUGAAAGCCTTTATCTTTUT
239993724	85904	GGTCUGCGCTTTGUCCGA	85905	CUGTCCCUGGAGGAGAAAGAC
239994214	85906	TTTAAACTCAGCAUTCCATCCCTAUGAA	85907	AGATTGTCTGTTTUGTTGGGTTTTGTUAC
239995827	85908	GCAGCCAAGUACAAGCUCAAC	85909	GCGUCCACCATUCACGCT
239996493	85910	CCCCTGCCAUTTGTATATCGTUGA	85911	CCACUTCAGUAAGACCAGAAAGAACC
239999847	85912	GTTATTTGATGUGAACTTTGTGCCTGUT	85913	GACAGGAAAGAGCAAUCACUAGCA
240002093	85914	TGTGCTAAAACUTTGAGTCCCAUGT	85915	AGCATGTAGCGUGCTAAAATAGCAAUA
240003822	85916	GCUCCCGCGCGTTATUG	85917	ACACAAGTAGCUGGATACCCUCT
240004731	85918	GTTAAAAAGCTUCACAGTTTGTCCTUGT	85919	GGCCTCAGTUCAGTCTCAATGTUAG
240008519	85920	TCATCCTTTTCUCTGAGATGCTTUGG	85921	CAAGTGUACAACCCTGTGUGG
240009248	85922	TCACTGGATCCAUTGTGTATAGTUACGA	85923	CACACCTCACCUGTAAAACTCAGTAUAT
240011200	85924	ACTGAGGAGGAUGATAATTGGGTCUA	85925	CCCATGTTTCAUCTTCAACGTGAATUAA
240019775	85926	GGGAGUACAACAGAAACAAATUAGAGAAC	85927	GTTGTCTTCTACUCCATCTTCAAAUCCA
240024290	85928	CUTGGAAATAAAGUGGAACGAAAAGAAGA	85929	TCCTGAGACUGCTGTTCCAAAAUT
240025344	85930	TCTCCAACTCCUACTTTAGAACAACAUCT	85931	CGGACCUGTGGCTACUAAGAA
240029004	85932	TTTACATAGGUGGAATGAATGGCUGAA	85933	AGCGGTATAAUCAGGAGTTTTUAAAGGT
240029170	85934	GGAAAGAGCTTGUTTGATGTCGTTAGAUA	85935	GTGCTTCCTCUTTATTTAGTACCUCAGT
240037800	85936	TCCAGAUCUGAGAGAACCAGGAA	85937	AGAGTUCACTTACCUCCAGGCA
240038917	85938	CCTACCTCTUCCACGTTGTUACT	85939	TGGTAAACACAAAUTCCTTTCCUAGAACT
240042436	85940	TTTTGTGACGGUCTTGGAAGUGA	85941	AGGAAGAGAAGAAGCUTGGUCCT
240043600	85942	ACTGAACTGUACATGCTCTTCAUCAAC	85943	GCACGGAACAGAGCAUTCGTTAATTAUA
240054812	85944	GGCAAAAGAAGGAGGUTAACTGTAAUC	85945	ACATGTATCGAAGCACAUCAAAGAGUAA
240058778	85946	GACATCTTCTTTCUTCCTGATCAAGUGA	85947	AGATTAGTGCTTATUTCTTCTTTTAGGTAUGT
240058818	85948	CTGCACTUGCATTGTCTUCACA	85949	TCTGTGTACAGUGAAATAGTATATUGAAGAACA
240061071	85950	GAGCTTUGGCCCTTGGTGAUA	85951	GUTCTCATCUGCAGACCCCAA
240062998	85952	GGTGCAGGCAACAUGGTCTUA	85953	CAGCACAUCCGTATACACUCAGG
240066636	85954	CTGAAGGGUCAGCCTTCTCUT	85955	CCTTGGTCAGCUTCTGGATTTUG
240068470	85956	GCAGGAUACAGACGTCCCUCA	85957	AGCCGUGAAGTUGGAGAAGAC
240072080	85958	GTCTGGACAUGATGGCTCGAUAC	85959	CUAGAAGACAGGGAGCGUGAAA
240073706	85960	ACAGGCCAUTTTCCATGTUGGT	85961	ATGACGCCATAUTCTTTTAGAGCAUACT
240081302	85962	CACAGAAGTUACAACTGTAGGGCTUA	85963	GTGCTCACUGACATTCTACUCCA
240081810	85964	AACCUACAACTATTTAUGGAGAACAAGCA	85965	CCCTCCCCUTTAGGTACTGUGA
240083789	85966	GGAATAUCACAGATCCGUCACAGG	85967	TGUAGAAGAGCGCACGUCAAG
240094066	85968	GTAAATGTGTCAAAUACTGGCCTGAUG	85969	ACAGTTCCCAAAGUCTCTAGAAUACGA
240097273	85970	CTTGATGCGUGTTGAGGCTUG	85971	CTGAACTUGCGGTGGATGAUG
240103699	85972	GAGCUGGCCATGCTCUCA	85973	ACGCGAACCCCUCAGUC
240104554	85974	CCATGCTCUCACCTCAUCCA	85975	GGGCTCACUACACGCCUT
240105442	85976	GUCCCCGGACCGGUAAG	85977	CAGGAACCGUAGCTAGGACUG
240106142	85978	AGTGGAUCTGCATCUCCGACT	85979	AGGTGGGCTUCTCTTGGAAGUA
240115136	85980	CAAAGGAGAUTGAGCGGAUGGT	85981	CAGAUCAGGGACUCCCAGAGA
240121645	85982	GATGTATTGUTTGCACTCTUCAGCA	85983	GCTAACATUAAAAGGGACAAGTCUAAGA
240128237	85984	GCACCACAAGGGCUCAGUAAA	85985	CTGACACCACUCAGGTUGGAG
240130721	85986	CTTTTCCTCAAAUTCTTCCCUGCAA	85987	AAATATTTCATCUCCTCCTCUGACACT
240131794	85988	ACAACATGCTUCCACTCTTGAUAACT	85989	GCATGAAGAACUGATGAAGAAAACUGAAA
240137361	85990	ACACACTGUGCACAATTTCCTUG	85991	CCAATGAGGGUGACAACGACTAUAT
240139242	85992	ATGATGGUGAAGGATGAATATGUGCAT	85993	GCAGTGCTGGUAGCATTAGACUC
240139636	85994	GGGCCCUCGUCAGCAAC	85995	GTTCCATGGCCUCCGATCUC
240141039	85996	GCCAAGCTUCCGTTTTCCTTGUA	85997	GTGTCAGTGAGUCCTTAGCCTAATUT
240141288	85998	ATGCCCCTAUGGAGAAAATCCTUG	85999	CCAAACTUGAGAGACTGGACAGUAAG
240144463	86000	TTTCCTGGCUCCGCTUCAAT	86001	CTATCCATCTUTGGTATTTGCTUCCAC
240145155	86002	CCAGGCTCATUATAAGTTTTGGCAUT	86003	TGATGAACTCUCATTAAAAGGAACUGCT
240146408	86004	TGAAUCGCCGTATCUGAGAAAAC	86005	AUGCAACAAGCUCAGAAACACAC
240146839	86006	AGTCTCTCCTTCUCTTCTCTTAGCATTUT	86007	CTCATAGGAACAGGUAGACTTUCAACT
240147005	86008	GCAGTAUAGAGGACGGAGCUG	86009	CAGAAGUACCAGCAGGUGGAT
240149366	86010	CAGGAGTTUGGTCTGCCCTUT	86011	GGUACAACUGGACAAGCAGAGA
240151927	86012	TGAGCTTGUTGCATTGUGACCT	86013	ACTGGTCATTTUGCACTACCTCTTUT
240155197	86014	GGTTTCGCGUTGGTTGTGUT	86015	GCAGTCAGCUCCTCTGUCAC
240156431	86016	TUGACAAAGGCAUCGAGACAGAT	86017	TGGTGGAAUGCTGAGTGAUGG
240161497	86018	GTCATTTGTTUCCTTTTGCTCUCCA	86019	AGTTAATATGAAUCCTCCCCCACUCA
240166378	86020	TGCTGGTGGUGTGTCCAUC	86021	GCCCGATACUGTGGCTCATTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240166773	86022	GAGTGGCUATTGCTTATGTUGCAAAA	86023	CAAATGCAGCUTGTTGATTCCAUAGT
240170708	86024	CAGCTCTGUTAGCCCCAUCT	86025	CAATGATTAGGAAAACUCAACTTGCUGA
240170798	86026	GCCCCUGACACGCATUGT	86027	GCAAGGGACACUGGAGCUG
240170962	86028	TTTTGTGTTACUGGCAGGATCUGT	86029	AGCTCCTGGAUCAGAAGTGACUAT
240178854	86030	CGGTACAUATCACGCUGACGA	86031	CCTGTGAATUAGGCCGACTTTTTCUA
240184627	86032	GGGACTCCUGCTCGCTUT	86033	GGGCCAAGUCGGACAGUA
240186875	86034	GCCCTAGAAAUGGAGGCTGTUG	86035	CAAGGTAGAATAUAGCCATGGTGATGAUT
240187068	86036	GGGCTGTTCAUTTTGAGTGCAUA	86037	GGACATGACCCUCAGTAGCAATATAAAUT
240187529	86038	GGCGAACUCACCCACGTUT	86039	CGAAAAGGCGCUCACGUC
240188413	86040	GTTGGTCUGGGAAGGTGUGT	86041	CTTTAACCCUCAGCCTCAGAGUC
240190110	86042	TGATCTGCCUGTTCTTTCCACUC	86043	AGGGCCCAUCCTCTGGUT
240190149	86044	CCCAGGAUGGCGACGUG	86045	AGCCCUGGCACCTTCTTUG
240190808	86046	GCTTCTCCCAGUCTTTGTGCUG	86047	TAACAGTGTATUAACTTGGGATCTUGCT
240191283	86048	GGCTCACCGGCUCTTGTTUA	86049	TCAAGGAGAAGCAUAAAATTTUGCACAG
240191717	86050	GAGCCGCCGAGUACTUGT	86051	CCCCCAACUACACCCUGGA
240192613	86052	TTTTGAGTCCAAGCUTCCCATCUT	86053	CCATAGTTAUACCAACAGCUCCCT
240195941	86054	GTCATUCCCCGACGUGGAT	86055	CCCGGGCUCGGATTACTUC
240196319	86056	CATCTGGTACUTACCCTGCAUCT	86057	GGGAGCUTGTCCTTTUCCGA
240197591	86058	GCTTUGGAGCCGCTGCUA	86059	CGUGACCTUCAACAAGAAGAACC
240201794	86060	GAGCTCUGCATGGAGTGUCA	86061	GAAAGCATUCGTTGCAGUAGCC
240205811	86062	CAGACUGCCCCCGAACUG	86063	TCTGCCCGCUGACTGUG
240206411	86064	CCTCUCCGGGCATCCUCAT	86065	GACCTGCUGCCCCGUAG
240207117	86066	CGAGCCGCCCAUCCUAC	86067	TUGGCCCAGCCGAACUT
240207454	86068	CTCAGTTTCCUCTTGCCCUCT	86069	TCGCUGGGCTCCTUCAAC
240207799	86070	CCAGGCUCACCATCTTCTCUACA	86071	CCAACTGCUCCAGGTCCTUC
240208065	86072	GCCTGCUGCTCGAAGGUG	86073	CCCAACCUGGCTCAGCUA
240208742	86074	TCTACCUGAGCAATATGCCUCCA	86075	GCATCATCTTCATUCGCTTATGGGATUA
240210093	86076	CCATTTGTTCCUTTGGGCCAUT	86077	GTGTGTGTGAUGAATCCGGAUCT
240211846	86078	GAGTCCTCCUGTTGCTCAGUC	86079	TTCTGACCAGCAGUGTTGTTGTUA
240212302	86080	CCTGCACTUAAAACCAGCUGACA	86081	GCTGCTTTGTTTUATTTAGGTTCCAGUAT
240212404	86082	CCCCUCCGGAGTGTTTUGAA	86083	CCAGTTGAGCCAUGGTGATCAUC
240213014	86084	TGATCATTTUGGCAATGCCAAGUG	86085	TCAGAGGAUAGCACCATGAUGACT
240214997	86086	GCCTTCGCGCUCAAAGTUC	86087	AACGCGGCCCUCATGATUAA
240215350	86088	CGGGCCCAUCCACUCAA	86089	ACATTCGGATUCGGAGCCTUC
240215552	86090	TGAGGGCCUGAAGTGCATUG	86091	CACCAAGGCAUCGCAUGAG
240216090	86092	CAGCTGCUCCAGTTCACUGA	86093	GCCCCAGUTTTAGGAAAUCCACAA
240216378	86094	ATUCCGCGACGCCAUCT	86095	GACCACCAGUCCCUGCAA
240216995	86096	GTCCTUGGAGCTGGGCUT	86097	CGGUCCAGGCGUGAACT
240219357	86098	TCCAGAGACAAAGUTGCAAAACAGAUAA	86099	CAGAAGCCTCAUATGAAGATGGCUAT
240219591	86100	GGCTGGGCUGGAAAUCAGG	86101	AGCCGGGCUTTCCGTUT
240220303	86102	TCAUGAGGGCCGCGTTUT	86103	GCCCGACAGCUTCCCTUC
240222052	86104	TTCCCCATCGUTTGTCCAGUC	86105	GTTCTTTTAAGGUGAAGAGGCCATAUCA
240223410	86106	ACATCAGGCACUGGAACTATCTGUA	86107	GCCTTCAAATGAUGAAAATTATCCTUGT
240225755	86108	GAACUGCTGTCCUGCAAGAGT	86109	GCCAGCTCUTTGTCGGAUACA
240225812	86110	GUGCGGCAGAAAAUCGAGAA	86111	GGAGGGCUGTGAAAAGCUG
240226383	86112	GTTGCAGGGACUGGUGGT	86113	ACAACGGCGCUCTGGAUAAT
240228884	86114	CUGGGUAGGCGGAAGGG	86115	CAGCGGCUGCAGCATUT
240229741	86116	GCGACCCGCUGCATAAUGA	86117	TCCGATUCCCACAGTCUGGA
240230629	86118	CTCTTTCTGAAACUCTGTGAGATUGCT	86119	GGTCTTCCAUTACGGAGAGAUCC
240232017	86120	TCCCGCACAUGTGUAACCAAT	86121	CCTTCGATGGUACCCCACTUG
240233374	86122	GTGCUAAGCAGTACATTUAAAAAGAAAGGA	86123	TCTAGGACAAAGGAAAUTGAAGCCAUT
240233431	86124	CTTACCTCTGAUCTCAAGATTGCAUGA	86125	GCCTACTATTCUGTGTAAACTCAGUGAAA
240236189	86126	GGAAGCGATUTTTGCCGACUT	86127	CCAGCCUGGGCGTTCTUAC
240237906	86128	CCTTCATCCAUTCTGGACTUGGT	86129	GGGAGAAAUATTCUGACCACGAAAGAAG
240238809	86130	GGGCCTGAGGUGTTCTGTTUAG	86131	GCTCTGGTTUCTCCCACGUT
240239955	86132	GACGGCUCCTTGGTUCGT	86133	CGGACTUCCACAGTTCAGGUG
240241497	86134	TTCUGCAGCAGCACAUCCT	86135	CCCTUGCCCCTTTCCUCAC
240242108	86136	CATCGTCAUGGAAAGCUGAAGGA	86137	AGGTAGAAAUCAGCCATCTUAAAGCC
240243282	86138	CTCGGTUAGGGCTCUGGT	86139	CTUCGCCGAGGGCTAUGAG
240243366	86140	GGAAAACTGACUGGGTGGGATUC	86141	CAACCACTCCUCAGGGTAGUAAC
240243667	86142	AGAGGAUCCTUGGGAGGAAGAC	86143	GCAAGGCAGUGGATGAGGTUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240245235	86144	CTGGCTCUCCGCCAUGT	86145	GGAAGUCATCAUCCCCACCA
240246146	86146	GCCATTGCUGAGTCACCCUAA	86147	GAACTCTGCCUCTTGAGACUGG
240248972	86148	CAAGCTACCTGUGGAGTCTTTGUT	86149	GCAGAGCAGACUGCAUGACA
240250230	86150	GGAGTGCAAUCTGTCTGGCTUT	86151	TCAGTTGAUAGAGGACCATCATUGGAT
240250526	86152	GCUGAGATTTGGUGAGACACAGA	86153	GTTTGCATTTCTUGACTTTCATTGCAUT
240265457	86154	GGAGCAAAAGTAAUACGTAAATGGAAAGUT	86155	TGCTAACUGCGCAACCTTCUT
240266433	86156	ATTAAAGATGCCCUGAAGAGTTGUGAA	86157	CAGTTCTTUCAGAGAGCTGUACAAGT
240266483	86158	GCAGTTAGCAGUTATAAATAGCCUGGAA	86159	TCCTGAAAATGAAUGTGAAACTATCACUCA
240266787	86160	CAACTTUGGGATCAGCUCCGT	86161	AATGGAATGTCTUCGTAATGTGGAGUAG
240276098	86162	TGTGTGTAATGUTCAAGCACGTTUT	86163	CCUCAGGGCAGAAAGACGUT
240280763	86164	GAAACAAAUAGACACAGCTCUCCAGA	86165	GTTTTTGTGGUGGGCTTTATGATGUT
240281327	86166	ATTCACCUCCTGTGGGUAGGAT	86167	CTTGACCTUGTCTCTTTCUGCCT
240284872	86168	AATCACACCCACCAUTTCTGUGT	86169	AGGAAACACUGATAGCTGAGAUAGAAGA
240288789	86170	GTAGCTTCTUGATTCTGTCTGUCCAAT	86171	GCTACAAGAGACAUAAGTTTGGATUCAGA
240291536	86172	CACTACTGTTGACUTCTCCAGCATUT	86173	GAGTCCAATTCUAGTCCTAGTAGTCUGA
240293972	86174	TGCCTCCAAATUAAGTCTTAAGTCAUGT	86175	TGGTGTCTCCAAUTGAAAGTATGUGT
240301036	86176	CTTTCCAUCCCCATCTCUGGA	86177	GCTGAACCUGCCCAATCUACAC
240303735	86178	GATGAAUGGATATCTGUAAGGAAGCAG	86179	CGCGGCTAAUCGAACTCACUA
240307429	86180	GCAGGCAAGAACCUTTTGGUAA	86181	AATTTCCAAAUGGAAGGCTCACUCT
240312479	86182	GCCAGGACUCAAGGGUCAAG	86183	GGACCGGAAGUGCAAAGAUG
240318884	86184	GGCTTUGCCGAGCCCTAUA	86185	GAACTUCAGGAGAAGGAUCAAAGAGT
240319482	86186	CAGTGGGTUCAGACGATGUCA	86187	CCACUCTGCTTACAUACAAAACAGGT
240322255	86188	GCCTGAGGUGTCCTGTCUC	86189	TGAGATGUGCGTGAGCTUCA
240322795	86190	CTCTGAAAATATCAAUCGTTGCCTCTUT	86191	CUCCCGGCAGAAGGAAUACAAG
240326122	86192	GACACAGTCGAUGTCCAGCUT	86193	GCCAAATGCUGACTTGCUCAC
240326301	86194	GCCAGAGGCCAGCUAGCTAUA	86195	CCTTAACAGGUCTTTGAAACCCCUT
240330136	86196	GGAGATGCCUGACATCATCAUCAA	86197	GTUACACAGCCCGAACCUCT
240332954	86198	CATGTTTGCCUGCCATTTTCUGT	86199	CTCATCTGGCUGGTCTCGUC
240337490	86200	TTCTTTTGGCUTCTCAGGAAUCCAT	86201	CTGCATAACAGUGGGTGGGUA
240337721	86202	CACAGCAUCGACGGCAUC	86203	GAGAGTTTCUCCGCTGGAGUT
240340809	86204	CCTTCAGGGCUTGGTAGAGUC	86205	GAGTGACAUCGGTGGAGGUT
240344039	86206	CCACCAGACAGUCTAGUAACAAGG	86207	AAGCCAAAUGGACCTAAAGAAUCAGT
240344964	86208	TCCAGCUGCAGTGATTCTGUT	86209	GCTTCTGGCCUGGTGCTUAC
240349234	86210	GCATCTGTTTCUGGAGGCATTCUT	86211	GAGGTCAAAGGUCACCCCUT
240350430	86212	ACGAATGACUCTTTTTCAGCCUCT	86213	GGAAUGCAAGGCCCAACUCA
240355096	86214	GGGTTGCTAUCATACGGTTCTUAC	86215	CCTGGAACGCUTAGTGGUACA
240355595	86216	TTTACCAUGAAGAGTGTGUCCAGAAG	86217	CAATTAGACTGGUCCACATAAGAAAUCCA
240361418	86218	GCCTGCAUCCCTCCUCAA	86219	GCTCCTCUGAAACCACAGCAUAC
240365375	86220	TGTCCAUGCAGTTTGUCCAAGA	86221	CTGTGGTUGGAGCCCTTCTUT
240370192	86222	GTCTATUGGGACAGCTTGGUCAG	86223	CTTTTCCCCTUGAATGCAGTCCUA
240371014	86224	AGGGATAACUCACAGGTGTCTUGT	86225	GGTCTTGATUATAAGCCCAUCCAGAG
240372757	86226	TGTGAGATUGCCAACTGAUAACGG	86227	TTCAGTGCUATTGCAGCAUCCT
240377565	86228	CATGUGCCGCCGTUGAG	86229	CGAGGGCUGGGTGUGAG
240381311	86230	CTACCAACAUGGGCCAGGAAAAUA	86231	CCTTGGCTUTAGACCATCUCCAC
240381740	86232	CTCCTTTACCCCUCCTTCCUAGAG	86233	TGUAACCUCCACCCCAAGAGA
240384360	86234	GCATGAGAAGCUGGTGCAGUT	86235	TCTAGACAUGAGAGGAAAUGAGGCT
240387103	86236	CGCCGCCGAUGTGUAGAA	86237	CGCTGCUCTACAGCCUCA
240388042	86238	GGCTGGCUGAGGCTGUA	86239	CCACCGAGCUGUGCAGAC
240388482	86240	GGTCUGCACAGCUCGGT	86241	GAGCCCCCAGUCAUCGAA
240388560	86242	GCTGTCCCUCAGTCCTGCAUA	86243	GTTGACAUCGCGTTGTGUCC
240388592	86244	TGTTTGUGGCATATCCTUCCCAAT	86245	GAAGTTCCTCTUCCCAATTCATCTAUGA
240389174	86246	CGCGGCCCUTTAAGTCUCT	86247	GCACCUGGTCCTGCUGA
240390110	86248	CGTUCAGCAGGACCAGGUG	86249	CATCCGCTUGTCTGTCTGUCT
240395542	86250	TCUGTAGATGAUCCCCAGGCT	86251	GAGTTCTTUAAAACACACCAGCCAUAAA
240397744	86252	AUTTCACTGGAAUCGGAAGCCT	86253	GAGACUGAGAGAAGUGCAAAGGA
240398814	86254	CUGGTGAAUAGCACAGAGGGT	86255	CCCTUGAAGAGGCCTUGGAA
240405521	86256	TCAGGTCUGCAACCAAAGATTCATUAA	86257	GCAAACAUGCAAAAAGCACCAAUC
240413144	86258	TCCTCCACUGAGATAATGACTTCTUACC	86259	GCTGTCACTGUATTATTTGTCCAUGGAA
240413772	86260	CCAGGAACAGGCGAUCAGAUT	86261	CCACTGTAGACUGAAATGTAGTTUGGA
240417352	86262	TGGGCTATAUCAGAATACATUGCAACAA	86263	GGTGAGTGCUGTGACATGUAGAT
240418729	86264	GATTAAAGGGACUCTGAAGGGACUT	86265	AAACCTGACAAAUGTGCAATCTUAAAAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240419617	86266	GGGACACUGCCCTGGAAAUAT	86267	CACUTCTCCTCCUCAGGGAAG
240420862	86268	TTGGCCAATCAGAUACCAACTGTTAAUA	86269	GGTAGTAAGTTUCCCATTACCAAGTUCT
240421803	86270	GGGATUAAAGCTGGCTAUGGCA	86271	CCTTGTUGGGACCTCAGAUGT
240422418	86272	GATCTGACGAAUTTGCTTCACAGUT	86273	CCCAAAAGGAACACUGAAAAACGUA
240423762	86274	CTCTCTGCUCGACCTGUGT	86275	GCTTCCCTCUGAGAGGCGAUA
240423779	86276	CCGCTCGAGUTCCTCTTUGG	86277	GAAGTCACCUCTGGGTCTTGUG
240423850	86278	CACGATTACGTUTTTCAGTGTTCCUT	86279	TCTGTGTTTATAUAGGTAGCTTTTGTTUGCT
240430143	86280	TGAACAACAGUCACACTTUCCAAGT	86281	ACTUAGCAAGCACAAAGGUACCC
240431165	86282	GCAGATUCAGGTCTGCCUCAT	86283	ACTTCATGUCCACGTCTCTTUGG
240432777	86284	TGGCCCCUTGCCTTCUC	86285	GGGTCUGCGGTGGCAUC
240433430	86286	GCACCCCUCAGAAGCTGAUT	86287	GGTGAUGCGGCTCTGCUT
240433532	86288	CGUGAUGCCACCGCAGA	86289	CCCGCCCUCACCTGUACT
240434396	86290	GCCUCGACCCTGUGGAGAT	86291	GCACAGGGCACUGTTTGCUA
240440308	86292	AGCUAACGGGAAGCCTCCUA	86293	CUGTCCCCTUCGGGCAT
240443752	86294	GTAGTACUGGGAGGTCCCCUT	86295	GCTTCGGCCUTTGCAGTTUT
240460973	86296	TCUGUGAGCCCACGAGGAT	86297	GCCGCCACCUACTTUGCT
240469438	86298	CUGGGCAGCAGCTGUAAGT	86299	TCAUACACACGGCCTUGGG
240471636	86300	GGAGGCCAGUCACAAUGGA	86301	GACAGCCGGCGGAUCUT
240472570	86302	TGTAACTTAUGAGCAGCTGUGACAA	86303	CACAGGGACTUCACAAGTTCCAAAUA
240472739	86304	CGCAGCUGAGCACCAAAUC	86305	CAGGCGUTGUCCCCACAT
240476469	86306	AGAGTGCCCCAGUCCCTUA	86307	GCCCAUCATTTTGTCAUCAGGAAG
240491736	86308	ACTCCCUGGGAACTTTGAGUCT	86309	GAGAAAATGUGCAAATCCCGAATUAACT
240492380	86310	CAAGGACAGCCCUTTCGGUA	86311	GATCAUGGAGGCCAAATCCTGUAG
240494321	86312	GCTGCCAGCAAUGAGAAGUGAA	86313	GAGATCCCCTTUTCCAGTATCATTTUCAA
240498687	86314	AGAAAACCTUCCAAAGACAAAGUAGACA	86315	GGCAACAGAUTTTCACAGCUCA
240499849	86316	TTTTCTTAGTUCATCTTCGGCUGCT	86317	CCCCTGGACTUTTCTATGAGTTCTTUA
240500662	86318	GGAAAGTCUCTGTACGUGAAGAGG	86319	CTGATACUGCGCAUCCAGGAA
240500706	86320	TGACCCATAUAAACCTCATCCTCAUGAT	86321	TGTCAUGGAGAAGAAACAGAACAUCC
240504125	86322	GGGAGCUGGCCGCAUAC	86323	CCAGUGACCCUACGGACAGA
240505270	86324	CTGAGTCCUGACCTTUGCACA	86325	GTTGGUCCCAGGGAUCGAAAG
240505284	86326	CCCTTAGGAGCGUCCAGGUAT	86327	CTCTUGGCCGGTTCGUACT
240507914	86328	GCTTCTCCUCAGGGATGCUT	86329	TCUAGCGCCCGCUCAAC
240508899	86330	GTGCCCCGAGUCCTUCT	86331	GTATGCTGTCUTCTAGCACTUCAGG
240510024	86332	TCTGTAGACAGACCUCTTTTCAAGUACA	86333	TCCCTGTAACAUGAAAGTCACACTUAC
240510235	86334	CTGTGUAGGAGGGACCTCTTCUAT	86335	GAAGAGACGCACUTCCTCCUG
240516615	86336	TGTACCACCACUCCTTGUGGA	86337	GCCAACTTGGAAGUCAGTCTGTTTATUA
240518057	86338	CCTTUGTCAGAGAUGGCACCT	86339	AAAAGACGUGTCCATTUCCAGACT
240520025	86340	TGGCTGCCUTTAAACCUCGAA	86341	TGTATTCAUCGCCGUACACCAG
240520917	86342	GCTGAAGAUCAGGCGGGUT	86343	GCTCCAGAAAACCAGUATAAAGCTUAC
240522554	86344	AAAACAAUTCGACTGAUCGACCCT	86345	GGGACCACGUCTTTACTGAUG
240525377	86346	TTGCTTTCTTUAACAGCTCCUCAGT	86347	ACCAGTATCTUCACTCCCAGUCC
240528309	86348	CTTTGCTGTGCUTCATGATGTAACUG	86349	ACTCAGGACAUGTCAGCCUCT
240529325	86350	GCACCUGAAGTGCUAGAAGACA	86351	CCCCTTCAUTAAGGACUGGAGAAG
240533768	86352	GGGCACAACUTTCTTATTAATTTUCACA	86353	CCTCAGCCAACUAATCUCGCAA
240536427	86354	CCTGGGCAUGCTAACTCCTUT	86355	GGACACGCAGGAGGUCAUC
240536873	86356	GATACGTGUGCCAGTTUCCAGA	86357	GGTGACAGGAGGAUGGCTCTUA
240538425	86358	TCUGCACCGAGGUGAAACAAG	86359	GAGGGUGCATTTUCAGGAGGAA
240542727	86360	CAGTCTGGAAAUGGACACGTCUT	86361	TCTCACCATUTCAGGATAGUCCCT
240542777	86362	AGAGGCTGACAUGTCCTGAGUA	86363	ACCAGGAAGAUACCGGATGTAAATTUC
240544458	86364	GGTGTGAGCCUTTTTGTTATTATTUCCT	86365	TGGCTAACUCCTCTTTGGCTUC
240544696	86366	CGGTATGGTUTACTCTGCTTUGCT	86367	TCCTATCAGGACAAUTTGCTCAGATUC
240546347	86368	TCCAAAGAATCAAUAGACAAGTCTGTGTUT	86369	CCAAATAAACTGUGCCTGCGAUAT
240547892	86370	CTCAGCGUCTTGCCGAUCA	86371	AGAAACTTCUACCAAGAATCCCUCAGT
240549107	86372	GTATGTTCCCUCCACCCACTUC	86373	GTTCTGATGATCAUTTCTGTGTTGTUGAC
240552624	86374	GGGACUCACAGTGUGGCA	86375	GGAGAGCCAGCUGGAGACUAA
240553831	86376	CTTGTTACAUTCCACUGCGGAGA	86377	AGGACUCAAGGAAGUGCAAACA
240554407	86378	CCTGGCCCAUTTTGUCACCT	86379	CGCACCUGGCAGTGUGT
240558315	86380	GCAACCCUTACCCCAGUGAG	86381	TGTCCAGUAAAGCAAGACCTCUAAGA
240559019	86382	AGAUTAGTTGGCUGAGGCAAAACT	86383	GTCACUGCAGCAGCGAGUA
240564374	86384	TCCTCCUCCCAGTACGUCAC	86385	AGTTTCTCCUCAGTTTCCCTGUCT
240564668	86386	TCGTCGGAGGUGGAATTTUACAA	86387	CTTTACACUCCTCCCUGGACAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240566819	86388	CCCAGGCCAGAUGGATAGGUA	86389	CAAGGGAUGCCACCTGGUAT
240574060	86390	TCCAUGGAAAAATCTCUCGGGAA	86391	GCCAGUCACAAGGAAGCTGAATUAT
240574194	86392	AGAAAAGAAAACUGCCCCCACUA	86393	ACCAGGTGATUAAGTACGTGCUC
240574538	86394	AAGCACTTTTTAUAGTATTTCCTGGUAAGCA	86395	TGCCCUGUACACAAACAAGAACA
240574628	86396	GUCACUGCAAGGAGGCAACT	86397	GCTGTCUCGGTCATCCUGAAC
240576606	86398	AGATGATGAUAGAGAACACCCTUGGA	86399	CAAUACTCACAGAUGCCAAAGCC
240576731	86400	TGTTCCAATAGCUGACAGTCTCUACAT	86401	GCTACAGAGUCTGTUGGAGCA
240577020	86402	ACAGGGCGUTGACCAGAUG	86403	CTCCTTCTTTUGCCCCTATAGAATTUT
240577165	86404	GGCTTTTUCCCGTCAGCUGAT	86405	AGGATCTTTUAATGTGGAGUGGGAAAC
240579169	86406	CGGTTCCUGAGGAATUGGAAGT	86407	CTTTCGGACCUGGTGGTCUT
240580071	86408	TCGCACUTGCTGCUCCAA	86409	TGCGGGUCCGTGACAUC
240585439	86410	CAGCTCCTUAAAGGCCTCGUT	86411	ACCTCACTGUCTCCCTCUGG
240586409	86412	GGGCTAAATUAGGCTAAGGACUCA	86413	CTCCTCGCUTGCGTTUCAG
240586717	86414	AUTCAAGAGCUCAGACGCCAAT	86415	GCAGAAAGCCAUTCTTGATAGTCTTUG
240588445	86416	GAGCAGCCAAAUGGGAUCCT	86417	GCCTGACUCCCATTGGUCT
240589268	86418	GATCATGGAAGAUCAACACCUCAGAT	86419	CCTCAGGCAUCAGTAUGGACAC
240589498	86420	ACTGACATGUACCTGTTTTTAACUGCAT	86421	CTCCACATUACCAGTCTTCUCCAG
240590166	86422	GGCCAGCGUGGTAGTTTTTCTUA	86423	GGAAGGACAGGUTTGCTGTUG
240591948	86424	TCAGCAATAGUGGCCCTTUCAA	86425	CATTCTGACAUCTCCAACAGATTUGG
240593833	86426	GCTCCAGGAUCTCCTTCAAGUAAG	86427	AAAAAGTTGCTGUTTTGAATTAGCTCUACAA
240594775	86428	TTGGTACTAATGUGTTCACAGAAUGCT	86429	CATCCCCACAACUAAAACACTCAUCT
240599405	86430	ACGTTTTCTTUGGGACCTGUAGT	86431	AGAGACTTTGTAUAAAGGCAGAACGUG
240601495	86432	AGGCTTGCUTTGGTGTGUCA	86433	CCTCGAGGAGGCUTTGACUCT
240602625	86434	AGTUAGGGCAGCCACGAAUG	86435	AGTGCCTGUCTGTCCACUG
240603573	86436	CTCCCACAUCCCCGAGGAUA	86437	CGGGUACAACGGCTCUCA
240604230	86438	CCUGAGGAGAGGACUCGAGAT	86439	CUCATGCAAUCCACAGGGACA
240605573	86440	CTTACTAGGAAGUTTTTCCATGGCTUCT	86441	CCTATTTGCCAAAGUGTGACTACAGUT
240612755	86442	GCCTGUAACAGTGTTTCUGCAA	86443	CTCTTGGGACCUTCTTCUAGCC
240615227	86444	GTCACCCACGUCGTCUGT	86445	GCCACTTUGGCCCCCATUAT
240617009	86446	AGCTGGTCUGACTTGGACUCT	86447	CGAGAACACAAUGTTCAUCAACAAGAT
240621248	86448	GGAGACUGTCTCGGUAAAAGGG	86449	ATACCGACUGCCATTTCTTTTGTUT
240626366	86450	CCTTCTCUGGCAACAGCUGAT	86451	GAAGTGCUCATCCTTGAUCCCT
240628014	86452	GGUGAAAUCACAAAGGAGCGAGA	86453	CGAGTAGCGGUACAAATGGATTTUG
240629784	86454	AGCCAATGAAGGUGAGTCCTCUA	86455	GAAGAAUCAGCACGCACCUC
240636079	86456	AAAACCTGAGGAUGAGCAGCUT	86457	GGCAAGTCTUGACTGGCTCUG
240643515	86458	TCACTATGACUCCTGCTGUCCAT	86459	AGTCCAAGTUCAAGTCCACCAUC
240645872	86460	CAGUCCCUGAACCCAAGCAT	86461	CAGCUGGTUGGCGAAGG
240646660	86462	CTCCTCCAGCUGTGCAATCUT	86463	CGGCCCAGAAGAAUGAGAGUG
240648438	86464	GTCTCGAGUGGCCGTUCT	86465	GGAAAAGGTGUCAGGTGTGGUT
240651787	86466	CCTCACCGACCUGGTCTUT	86467	AGCTCCCUGGAAGAGACUCC
240652682	86468	CTCCGGAGCUCCTTGTTCUG	86469	GGTCTCAGUGCGCTCTCTUG
240666010	86470	TCCCTGGAUCTATAGCTCTUCACC	86471	AAAGGTAUCCCTCTTTGUGCAACA
240666205	86472	TTCGGCGAAAAGUCAGGATGTUA	86473	GTTTTCAGTTTGUTTTGTACGTGAUGG
240672581	86474	CTCCCUGGAGAACAGCTCAAAUAAAA	86475	CCACACAACACAUTTATCTACAAAUGCT
240673548	86476	TCCTGGAAAUAACCTGGGUCCT	86477	TTACCCAGGCUGCAATAAGAGATATTUT
240698061	86478	GCATCTGTAAGUGGGACAGCUT	86479	TTAAAGCCTCCCUTCCTCTTACUCT
240699467	86480	GCTATATGCTAUTCATTACCGTGUGCT	86481	AACGGAAACTGUAAAACAAGAAAAUGCT
240701448	86482	GATGTCTATGAAGUGTTGTGGTUCCT	86483	ACAGCCAGAUATCAACTGTUACAGAAAT
240703072	86484	AGTGAGAUCCCAGCCCAGAUT	86485	CAGCATGTGCUGAATTCTTGACUC
240709322	86486	GGGTGACCCCUATGTGGTACUA	86487	TGAAACACTTCUGGCAGTATCCTUC
240709447	86488	GCACAGCCCUTTGGAUAACAGT	86489	CTUCCCACAGGAAGGCTUGA
240718058	86490	GCACCAAGACCCCUTTAACUCA	86491	GTAGAAAUACGGCUGCACCGA
240719158	86492	GCCAAGCUCGTCUCAGAGAA	86493	GGGTCGAUGCACTCUGAGG
240720488	86494	CCAGCUTGTACCUGCAGGAT	86495	GAGGACUCCGUCGAGGAGA
240722804	86496	TCTGAGGUCCCCCTTCTGUT	86497	GGAGGGUGCAGTGTUGGG
240724714	86498	CTCTCCGUCCTCGGATTCUCT	86499	GCCAATGAAAAUGGGAAAGGTAUCCA
240725334	86500	AGGAACTAUGACCTCGACUACGA	86501	GCAGCAGCUCGAATTTCTUCC
240725368	86502	ACCCTUGGAAGCACCATGTUT	86503	CUCCAGCAAAAAGCAUCGAACA
240726027	86504	CACTATTAACCACAGAUTGCTGATTUGG	86505	CTTTCAGTTGUTTCATGACGAUCAGG
240726145	86506	CTGGUAACACCGCCCUGAT	86507	GTAGGAAACATTUACTAGGACTTGAACUT
240726215	86508	GGATAAAUGACCGGTAUGCCCAA	86509	GGCTTCAGUGGTATGGACUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240727865	86510	CGCCCAGCGAGGAUAUCT	86511	GUCGTTGTCUCCCCGAAGG
240731575	86512	CCTCCUACGTTGCGGUCAC	86513	TCGCAGAUGAAACTCTGGTUCAC
240733064	86514	TTTTGTCCTUGAAGAAGCCTTATTCUCA	86515	GGCAUGGACGUACAGCAAG
240736615	86516	AGCUGCUGGGAGGAGACAT	86517	GGGCUGCCGCTGTCTUT
240742669	86518	CTGGGAGAAGCUGTATGUGGAC	86519	GTGTCCUCCTGGAUGCAGAT
240747929	86520	CGGCTGCAUGAGAACAACUG	86521	CTGTGAUAAGGGCGGCTUGA
240752289	86522	GGCAGTCAUCAATGTCCTCCUC	86523	GTCATTTATUGGCCCTGTGTTCCUA
240757346	86524	GGCUCCCACATGGGUGAC	86525	TGCCCTGATUAAACCCTGCTUAC
240761684	86526	CATTGCATTCAAAUTTGGCATACTUGT	86527	CCACACCAUGAUGAGCACCA
240769424	86528	CACTGTCCAACUGCTGTGAUG	86529	ACTTTTCATUGAGGGTGCATCTUCT
240769484	86530	CTCTAGTGAGTUTCCACTTCAAGUAGT	86531	GACCAGGCUGGTTCAGGUAAG
240770544	86532	AACTGAAACACAGAGUTTTCTGAGTATUGA	86533	GGTCCTGCTUATGTCTGTAATAUCACAA
240771526	86534	CGACAGAAGAUGCACCCUCAA	86535	TCCACAATACUCAAATCCTATTCUCCCA
240773269	86536	CTTTCTGGAAGUGAGGTGCTATTTUCT	86537	CCATGUTAAAACTTCAUGCAGCCA
240773779	86538	CAGGACCUTGGCTGCAUGA	86539	CACTTGCTAUAAGCCTATACATTTTTGUGT
240776088	86540	CTGACGUCCAGTGTACAGUGAA	86541	GGTTATTCAGUCAGTAGCTGCUGAAG
240778363	86542	CCAGCAGAAGAGCCUCCUT	86543	GAAGAATGGCUGCAGATTGAGATAUCA
240780532	86544	CAAGTACTTUGCAAACACACAUACCT	86545	TCCCUAAAGCTGGAGUCCCAA
240782358	86546	GGACCUAGCGTGGACUCACT	86547	CATCTGAAUCGGGCUGCGA
240783064	86548	TTCTAGTAATTUGGGAATGCCTGGTUT	86549	CCCGCCTCUGAATATTTCTTTAATGTUG
240784107	86550	CCTGGCGUAGACTGUGGAC	86551	GCUTCUGCCGCCACAAC
240784630	86552	TCCUACGGUGGAGCCAAGA	86553	GTTCUCCAGCAGGGCUGT
240785971	86554	CACCGAUGCCGUGGAAGAT	86555	GAGCUCAGAGGAAGCCTGAUG
240800175	86556	GUTAGTTTCTCUAGGCACGGCAA	86557	AGCTGAAGGCAAUGATGCAUGA
240802338	86558	GAGGGAGGAAUGATAAAGGTTAAGUGA	86559	GGUCGGCCAAGACACCTAUAAG
240810403	86560	GTGCTACUCTCGGUCCCAA	86561	GATGGACAGGACGAUCTCAUAGGA
240812979	86562	GAGCUGGGAAACAGAAGAATGUG	86563	CTATCTCCAUCAGTGACCCCCUAA
240813108	86564	TGAATCCTTTTACCUCCTGTTCTCUCA	86565	GAAACGAGACGAUGGTTCUAGGG
240818195	86566	AATTCAGTCCUCATCAGCTGUCT	86567	GAGGTCCTUCCCTTTCCACTUC
240819467	86568	CATGUCCGAACGAGGUGGT	86569	GCUGAAGGAGCCGTUCGAT
240819645	86570	ATTGGCUGCAGAGTUCGGAT	86571	CUACTATCAATACUCGACCAGCAGAAAA
240823090	86572	GCCCGTGUTCTCTCCTTTUG	86573	CTCACCTTTUGGCCACCTTUG
240823447	86574	CCTCTATTTTGACUTCCTGTCTCUGAAC	86575	TGGAAAUACUGCGGAACAAACAGA
240829013	86576	CCCAAGAGUACCTGCCATGUG	86577	CTGCTGATCCUCTTTTTCTCTCUGT
240829792	86578	GTCAGCCAGCUGCTGTTTCUA	86579	GTTCTGAGGCUTCATATCUCGGT
240831716	86580	CGTGGGACAUTCTGCUGAACAT	86581	CCCAAGGUACCATCTTCUGAGT
240832073	86582	CTGGACATGGAUGCTGACCUC	86583	GCTGCTGGGAAGUAAATTAGAGGAUAC
240836244	86584	GAGAAAAATCCAAUGCTGGTGUGT	86585	CCCTCTTCAUCCCAAGATTCUCA
240836543	86586	TTGTGAACACAGUGTCUGCCT	86587	AGAAGCTCTTGGAUAAAGGACAAGUG
240836757	86588	GCTTTCACACCUCTCAGTGACTTUC	86589	GGCAGTTTCAAUAATGCTGTATGTUGAC
240838357	86590	TGTGTATGGAGGUGATTCTTCAGAUGA	86591	TTCCATTTGAAAAGUGAATACATGCCAUT
240840772	86592	CCAAAGAGGCAUCTATGTGAUCCAG	86593	TCTGTGAAGAGCAUAGGTTAGAAGUCA
240841640	86594	GGGCCACAACUGCTGCUA	86595	GCAGGAGCUGCAGGUCAAG
240845538	86596	GCGCTCUCCCTCGTUGAA	86597	AGGUGAAAGCAAACCUCGAGAAG
240845699	86598	GCTCTAACUCCTCTGCTGTUCCT	86599	CCACGUAGCCGAAGUCCAC
240850314	86600	CUGCAUCACGGAACGAGAAG	86601	GTTTCCGGCAUTGGTUGAGT
240854577	86602	CATACUGCCAGGGTCCTGUC	86603	TGCTGTGTUGGAGCAAGUGT
240855631	86604	CCUGGCGUGACCACCAA	86605	CCTGUCCCACCAGCUCAC
240857828	86606	CTCGTTCUCCAGAGTCTGCTUT	86607	GAAGCAGCGAUGTCTGGAUCT
240858263	86608	GCATUCCCACCGCATCCUAC	86609	GTGGAACUGGAAGCTTAGAUGGAT
240860912	86610	CCTAGCTTAGAUGATGACGAUGCT	86611	CCCTCUCACCACCTTTCTTUCA
240862655	86612	GCTTCGTUCGGTTTTGCTGUAAAAA	86613	TCTAGATUGCAACAGAGGCUACAAAAG
240866038	86614	TCCCCATUGGTTTGTTATUGCAGAT	86615	AGTTTCAUCGAGTTCUAGCCCAAC
240866303	86616	TGCGGGCACACACUTAUAGG	86617	CACAGCAAAGCUGGCACUG
240868327	86618	AACTATCTTGTUTATTTGGAGCTUCCCA	86619	GAAAGCCCACGACAUGAUCAC
240868639	86620	TGUCTCGGGTUCGAGGGT	86621	CAGGGTUGACTGAGTCTTUGGT
240869925	86622	GGGTGAAGUGGACTGTACTCTUA	86623	GATGCAGCCUCACTAGAGGUG
240872336	86624	GCTTGGAGACAAGGAUCCTGUT	86625	GCCCAGAGCUGATGCAACAUT
240872942	86626	CCGTGGUACGCTUCAGAGT	86627	CCTTUACAGGACGACGUGGAG
240873483	86628	AGAGTGCGGUATTCCCGGUA	86629	CTGACGCGUTCCCTTUACAG
240874975	86630	GTAAGTCAUCGAAAGCATCATAGTUACT	86631	TTCTGCCAGTUTCTGCTGAAATTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
240875639	86632	CAGTAAACATCUCCCAGGAGAGUC	86633	GCATAAACAAACCUGCCAACUGAA
240878212	86634	CCATCTUGGCCCTCTCTGUT	86635	CTTGTCTGGUTTGGCCUGACT
240881104	86636	AGAAGACATTACUAACCCTGGCTCUAA	86637	CCTGUCCCTGCTUCAGCAAG
240885974	86638	CACUGTGTGCGUAGACAGGT	86639	GGCAGGAGGAAAGAGUACAAUGT
240894156	86640	GCATATGAGGUAGAACTGAACGGATAUT	86641	GCAGTTAAACCUCTACAACACUCCAT
240904201	86642	CGTCCCCAUTTTCTUCCAACAG	86643	GAGCACAGAAAUCTCCAGACTUCA
240904645	86644	GGCCAGTUTCTCTGCTUCAGAA	86645	TCAUCTGCTCUGAGGCAAACC
240906065	86646	TGACGGCUCCCTTCTCCUT	86647	GCAGCCAGAGACGGUACUC
240910644	86648	TGTGTTTUAAAAAGGCTCCTCUGGT	86649	CAGAUCGCCCGCATUCC
240911940	86650	GCGCGCCGUTTACTUGAA	86651	CTGACCAGUGGTCCAGCUC
240916162	86652	CCAGUCGGAGACGTUGGAAT	86653	CCCUCGCAGCACAGCUAC
240916946	86654	GUTGUCCACAGGCGAGGA	86655	CCTGGCGGUGCACACUA
240917184	86656	CAAAGGACCCCGUCTGTCUG	86657	CTTGAGAGAAAGGGUGTTGUACCT
240921248	86658	CAAAATACTUGCGAGAACGGUGT	86659	TGACATTUCACCCGAGAUAGGAGAA
240921691	86660	TGAAATUCAGGGCCCCUCC	86661	GCAUCGGGCACCUGAAC
240922854	86662	GGUGGGCCAGTCUCAAAGG	86663	CAGCAGUCTCCGUCCGT
240923175	86664	CATCCCAGGCAGGUGGUT	86665	AGCTCCGGCAUGCTCUC
240923315	86666	ATTCTCUCCAGCTGTTUCCCAAG	86667	TCTTATGATAGTTCUCTGAGGTCAGGUT
240923842	86668	CACGTCUGACAGGUAGCCAT	86669	GGCCUGUGGAAGCAAGGA
240924470	86670	CCGTCCUGGGACTTCTUCCT	86671	CGCCCAACGGCUACCUG
240924785	86672	CGAGCTCUGCATGGACUGAA	86673	ACCAGUGGATTTCCTUGACCCAT
240926801	86674	GGGCTUGCGGACCTTCUT	86675	GCGCATGCAUCACGACAUC
240929067	86676	CCACAAGUATCUGGAGCCCAAC	86677	GGGAGGTUGAACGTTACATAAAUACCA
240935006	86678	ATCTGTGGUCTAATTAGCUCAAAAGAAA	86679	AGGAAGAAAGUGAAAATGATUGGGAAGA
240942348	86680	CTCGAGCACUGGCAGUGT	86681	TGGACCGGCCAGAUGUG
240942888	86682	ACCATGCUGAGGAGACTGTTUT	86683	GCAGTATCTCUTCTGGGAACUGAGA
240943413	86684	CCTGCACGUAGCTCUCGAA	86685	CAUGUGCAGCCGGGAAC
240944402	86686	GTCTATCGAGTGUGTGCATATGTGUA	86687	CTTCCTUACCTGGGATUGGAACA
240947865	86688	GCATGAAGGCUCGCTGUACC	86689	ACATGGUCCCATCCCACUGA
240948996	86690	AGGGCCAAAGAGUCCATCAGUA	86691	GAAUACACACGCACGGTGUC
240949849	86692	GAACGAGGGUGCGAACUCT	86693	GCAATGGGCCUTCCTCTTCTUC
240951845	86694	GAAAGTGAAATUCTTCCTGAAAUGGCA	86695	AAAGTCAUCCAAAGATAGCUGAGGAAAT
240970430	86696	GCTCACCUGAATGCCTCUGAA	86697	TGAGCCTTTTUCCCTTCTTTGUGT
240975931	86698	GTCAAGATGAUACAGGTCAGTGUGG	86699	CAAGTTTTCAAAUCCTGTGGAAUGGT
240978961	86700	TGUTGATUAGCCAGAGAGGAGGA	86701	ACTTCCTTCTGAUTTTGTGCTCTUGA
240984644	86702	CAACACCATACCUTAGAATGAGCACUA	86703	GGTTATTCCAGAUTCTGTTCAAGAGUCT
240985825	86704	CCATTCCACAGGAUTTGAAAACTUGAA	86705	TTTCTATGATTTCUATATTGGTCAATAAUCCCC
240999353	86706	CACAAAGAATUAGGCTATTTACUGACAGGAT	86707	AGTCCAAGTUGCTTCTCAGTCTUC
240999385	86708	ACCTTTACCAGUTCTCTGUGAAGACT	86709	CAAAGAGACAACUGGAUACAGAGACA
241003926	86710	CCCTTCCTUCATCTGCCGTUA	86711	GCTTUGGAACAGGGCTCCUC
241005601	86712	AAGATGCATAGAUAGGCTCATCTGGUA	86713	CACCCTCTAUTAGTGCACCUCAAA
241006745	86714	GAAGATTTGTCTCUGTATCCAGTTGUCT	86715	CCGAGCUCCAAAGGTCTAUAAAAAGAT
241008021	86716	GCAAAATTCAAUGATCATAATGGAUGACA	86717	GGGCAAAACTUACTGCTAACTAAUCT
241008367	86718	AGCAGTAAGTUTTGCCCCCTUT	86719	CACTTGACACCAUGTTTTTCAGCAUT
241010738	86720	GTGTGCGUCACGCTUGAA	86721	GGACGGGCUGGACTGUG
241012687	86722	CUCAGACAGTUGGCAAGAAAACC	86723	CAGCTGUGCAGTGAGATTTUCC
241012723	86724	GCTGAAGTGGUCCTTGCAGUA	86725	ATGCAGTTCUAAGGCTCTGCUC
241012838	86726	CCCATTGTATGAAUCAGCCACAATUT	86727	CAGGGATACTTGUTGGCTGAATTTAAUG
241012843	86728	TGTGAATAAAGGGUCCTTAGTAGCTCUT	86729	GGTGUGGGAGGCGAGATTTUT
241020386	86730	AAGGCACCAUATATTGTGTTUGGGA	86731	TGCCATAAGAGUGGACAGGTTTUG
241022784	86732	AGGAAGAGAAACUGGAGTCTCATTUG	86733	AAGTTGTTACAATUGCTGCCAATGAUT
241025997	86734	TCCGGGAACTUACGTAGAATATATUGGA	86735	AAAGAAAGGGAGUCATUAAGCAACCA
241028034	86736	GGTGTGUGGCTACTTTUGGGT	86737	CCAGATUGACCAAAAACAAACAAACUCT
241028486	86738	ACTTGTTTUGCCCTAAACCUACACA	86739	CGAAGAATGUGGGAAAGAATTTAUGGAT
241029567	86740	GCAGTTAUCACAAGTTGGCAAAUCAAA	86741	AGTTCATTTTCCUTTTCTTAGGACCUGT
241031717	86742	TCTTTCCCACAUTCTTCGCATATUACA	86743	TTGTCTTTTACTUAAATGTATTTATGUCAGGCA
241032033	86744	CCTCTTAUCCCCTGTGAUCCCT	86745	CATGACACUGCAGCTTCTGTUC
241034855	86746	AGCTGGAGCUGGGTCUCT	86747	GCTUGAGGACCAAGGGTGUG
241036377	86748	CATGGCCUACCAGAGTUGCAT	86749	CTAACACGUGTGTGTUCCAACAG
241038032	86750	TGCTTCCAAGUGGACTGATTCTGUA	86751	ACTGGAUCCAAGGACCAUGAAC
241038413	86752	TCATGAACAGAAAGCUTTGGUGGT	86753	AAGCTGGTACATUTCCTTAGTTGTAGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241040592	86754	GGAACCCTCUGCACTGTTCUT	86755	CCTTACACCACCUCCCUCAC
241051217	86756	CTAGTTTCTAUACCTTCGAGGGUCCA	86757	GTTCCACAAACAUTCAGCCCTTTAUAAT
241054915	86758	GUACTGGCCUCAGGCCAAA	86759	GCCAUGAGGGCGTUAGACA
241056948	86760	CTAGCTUCCGCCTCTGUCT	86761	GCTGGUCCACACUGCAAGG
241059125	86762	TTTCTCCUCGGACAUCAACAACAT	86763	CTCACCUGTGTUGGAGCGA
241060589	86764	CAGCCCTGUACAAGTCACUGT	86765	GCCACAUTGCCGUCACC
241064397	86766	TGCGCTATAAAGUGCTCATCTTTACUT	86767	CAGAGGCUCGCAGTCTTTUG
241066932	86768	CAAGAAGAAAACGGCAUTTTGAGUGT	86769	CACCTTTCCTUGCCTCTTTCCUA
241075551	86770	CCAACTCUGCCCCCUCAC	86771	GCTGCCTTUAGGTCACACUCT
241077399	86772	GAACTATGAUCACAATGACAGTACUGAG	86773	CCCACUGGCTGTCTUGGA
241077756	86774	TCUGTTTUCCAAGACAGCCAGT	86775	GCAAGCCTUAATGGAAAGAAATUCAGAA
241080421	86776	GGTAACTUCAGCTTGTTGGTUAGAGAT	86777	GTGATTTCCUCTTACTAGGCUGCT
241080619	86778	GTTTTAATTGCUCTTGAAAATCTGAUGACGA	86779	GCACATCTGTTUCTGCTGTTTTACUAAG
241082013	86780	GACTTGTTAUGGACCATTACCTAGUACA	86781	TTGGAATGGAAUGACTGAAGTAUCAACA
241082238	86782	GAAGACCCGCCUAACUGCT	86783	CCCUGGCCCAGCTUGAC
241083391	86784	CTCAGAGCUGAAAGAATCAATGAAGUG	86785	CAAGAACCTGGGACUGAAGATGAAAUA
241084245	86786	CACCAGATAAGUATTGGTGACTTUGGT	86787	TCTGAGAGTTCUCCCATGATACATUACT
241084674	86788	GGGAGAUCCCUCGGGAGT	86789	CAUCCAGCAGAGGCAGCUAAA
241089026	86790	CACTAAGAATGCAUTTCAGGACATTUCA	86791	GGTCTTTATUGCCATTTTCTGACUGG
241093452	86792	CTGATTTGAGAUACCTTGTGTATUCAGT	86793	GCCTCCTGCAUCTTTCAAAAGCTUA
241093629	86794	CAAAAACGCCCAUTTGCCTAUCA	86795	TGACTUGCAGGACAGCAAUACT
241097631	86796	CAACGGAAGUCTCUCCAGAGT	86797	CCATGAAAGGAAAAAGGUTCTCUGGT
241101424	86798	TTGTTTTACACCUCCTGAAAAGCUACA	86799	TGTTGTTTCTTAUTAGCTGTGGGUCAT
241103511	86800	CCAGCCCCCUTCTCATCUCA	86801	CUGGCCUACCGAGAGACAC
241111211	86802	AGGTTGTTTGCAUTAATCACTTTCCAUC	86803	GAATTCCCCAGCUCTGGTCUT
241118515	86804	CCTTTAGTTGCCAUATTTACCATTUGCT	86805	GGGCTCCUGAAAACTGUGGT
241120916	86806	TCAACTGUTGCATGGUAGCAGAT	86807	GCTTCCTGUCCATCACTGAAUCC
241121618	86808	GCAGTTTGUCTGGCTGAUGGT	86809	TGCTACAGTGUGAAAGCCTTTATTACUC
241134966	86810	GCAGAGAAACGACUGAAGGCUCT	86811	CAACTTTGUCCGCTGCATCAUC
241137234	86812	ATTCAGTGTUGCCCCCUACC	86813	GCTGCTCTUCAATTCTGAGGCUAA
241138180	86814	CGCACCTTCUTCTCGTGGUT	86815	AAGGGCAUGTUCCGCACT
241141553	86816	GTAAAGGCUTCTGCAAGUCCCT	86817	CAGAGCCTCUGTGAGCATGUA
241147907	86818	GCCAGCUGCTCCTTGUAAAG	86819	GGCACUCACGTGTTCTCUGT
241148461	86820	AAGUGGATTGGUGGGAAGGAC	86821	AGGATCAATGAGUCCCATGTGTTUT
241158331	86822	GGCCACUCCTCAGGAAUCAAG	86823	CTTTGGCUAGAGTTAAAGATGUGCAA
241159884	86824	GGCCCCAGAACUAACAGGTUA	86825	GGGAGAUCTCTGCCUCAACCA
241160235	86826	CACCTCCUGTCCCAAATGUGAA	86827	CCATGAAGGTGAUTCAGAGGAACUG
241162426	86828	TTATTGTCTCTUAGGAGTTGGCATCUG	86829	TTGTCTTUGCCCAAGAUGGGA
241166866	86830	GCTCCTCCCUGTAGACACUCA	86831	GTTGTCAUGGAAATGGCAUCCAA
241167943	86832	AGGAACAAGCCAACCUGUGG	86833	AGGCAGUCGAGGAATGGUACT
241169387	86834	GTGAUAGCCGCCGGTUCT	86835	GCAGGTACAACGUCAGGGTUAC
241169869	86836	CGCCCCCUGAGCTUCAC	86837	GCTCUGGGCAGAATGGGUT
241172995	86838	CAGTTCCGCAGCUTGAGGUA	86839	CTGTGCAGGUTCAGGAUGCT
241173339	86840	GCGTGGACCCUGGTCUC	86841	GAGTCTGCAUCCATGAGTTCUGT
241187296	86842	CCUATTCACUCCCGCACCAAC	86843	TTCTCUGGAAGACGGGAUCCT
241187681	86844	GCCTCAGTCAUCATGGGTCUCT	86845	CAAACCCAGAGCUGAGAUCCT
241192326	86846	CAUGGCAAGACGGCCAAUG	86847	CATCATCACCUTTTGCCTTCCUCT
241197219	86848	AGCAGCAACUGGUGGGT	86849	GCCUCAAAACCGAGAAGAUGAAGAA
241203147	86850	TTCTAATGUAGTTGGGATUGCGAACA	86851	GTACCATTCAGCAUCTTGTAAGGACAUAT
241212885	86852	CGGCGACAAAUGGCACATTUA	86853	GCAGUAGGCTGTUCAAACACAAG
241216202	86854	CCACCCTUCAGCTTCTGCUT	86855	CCACCACUGCCACCTGUC
241219798	86856	TGTAGCCAACAACGGUATGAAUAACA	86857	GCAAGCTGGUGCTTTTCTTTCTTTUAAT
241223223	86858	GCTGACTGUTGCTTCCATTUCA	86859	TGTACCATTCAUGTTCCAGGUGAAG
241226921	86860	GCAACACTATUGCAAATTAGCTCTUGAA	86861	CAAGAACAAGTUACAGATTTGCGAUCA
241227261	86862	GGTATTTTGTGAUCGCAAATCTGUAACT	86863	CACAGTGTTACCUTCTCATAATCUCCAA
241229935	86864	CACTGACCTCUTGTGATACAGTUGA	86865	AGGATGATAGUGAGATGCTUCCAAAAA
241230625	86866	CTCTTGTGAUACAGTTGAAATACCUACCT	86867	CAAACTTCAGGAUGATAGTGAGAUGCT
241232257	86868	CTGCTGGGUCATGTTTTAGGTCUT	86869	CCGCCAGAGGAUAGUGGAAC
241232803	86870	GGACCGTTTCUTGAGGAGGTUA	86871	AAGTGAACUCCAGAACCACAUCC
241238070	86872	CAUGGAGATCGAUGGGCAGAAG	86873	CTGCGUGTCAGGUCCAGAAT
241239949	86874	TCACTAGAGUGGTGCAGCCUA	86875	GAAGCTTAUCAGCAAAACCAGTAUCAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241241894	86876	TGTGGAGTTTTAUGTGGCGATCUC	86877	GGCTTCCAUACCCGTGUCAA
241244671	86878	GAGTGGUAACGCAATCACGTUT	86879	GAGGTTTCCTUTCCCACCTTCUC
241247830	86880	CAGCGGCCAUTGUGCAG	86881	CTGGAGGCAGGGUTCGTUT
241248460	86882	CGGCCCCAGAGCUTAGAGAAUA	86883	TGAGTCTTCUGTCCTCCTCTUCC
241252046	86884	AGGCCAUGGAAACAGAAAGTUCT	86885	GTTTAAAGAUGCAGCUCAGAAGCAT
241252626	86886	GAAACTUGGAAAATTATGCUCAGCAGAT	86887	CTTTCCACUTATGTCCUGGAGGAG
241253947	86888	GAGCTCTCGGUGGATGGTUT	86889	GGGCCAGAAUGAGAATCTGAGUG
241262201	86890	CAGAGAUGCCAAGGTTCCTTCUC	86891	GCAGCTCUCAACTATCCCCTUAC
241264293	86892	GCCUGACACCTTGAUGAGCAA	86893	ACTGGTTCUAACTACCCTTUCCCT
241264888	86894	CTCCTAGGAUCACTCCTCAGUCA	86895	ATCTCTGTGGUTGGCGTCUC
241268004	86896	CTTTTAGTTGTGCUGAAAGACATTAUGACA	86897	TCTCACTCGATAAUCTGGATGACTCAUT
241268471	86898	CCTTGCCTUTCCCCTCAAUGG	86899	CCAAGCAAGAUCTGGTGAAACTUGA
241269118	86900	TGGACGGCUCAATGTGUGG	86901	CUGCGGCAGCAGCTAAUG
241269419	86902	CCTGTUCCCGACGCUCA	86903	CTACACTCTCUGCATCGTCTUCT
241270596	86904	CGGCUAAACGACTTGUCACAGAA	86905	GCAGATGGAGUGGATGTUGAAGA
241272058	86906	CCATTTGGGUCCCTCTCAUCT	86907	GCCUAGGAGCUCAGCAGACA
241276589	86908	GCTGCTGCCUAGTCATTTCUGA	86909	TTGATGGAGAAGGCGUACACUG
241277623	86910	ATGAAGAAGAUGACGACAUGGCA	86911	AGACCCTTUAGGCTTGGGAUGA
241278551	86912	CTATGGCUGTGGTACAGUCAGT	86913	GCTCACTTTCCUGGTGGAACUC
241279252	86914	GCCCAGCUCCTTCATTGATTTUCT	86915	CCAGCTGTUCTCGGAGTTCUAC
241282020	86916	GACCATAUGGCAGGCCATTGAUA	86917	GACGUTCCACAUGCAAAAGACAG
241283727	86918	GCGGAAAGAAGCCCUCAGUC	86919	GCCGCCGAAGUAGAAGTCAUC
241286465	86920	CUGCTTCUACCCGGACGAA	86921	CTCAAGCAGCAUCTCCGUGA
241286496	86922	GCCAAGAGCAAGUCGGAUCA	86923	ACTCTGCGUGCTGGTUGAAAT
241288233	86924	GGAGGACATCUGGAAGAAGTTUGA	86925	CCACAGCUCGTTCUCAAGCA
241288575	86926	GAGCTGGGUCACGGAGAUG	86927	TCCACAUGCAGTCCUGGAG
241291593	86928	CAAGGCCCACAGCAUCCTUA	86929	GGTGTCTUCTCCTCGAUCCCT
241292336	86930	GTTCTAGATGCAUGAAAAAGCCCTUT	86931	CTTATTCCTTGGUTCCAGAGAACACUA
241294377	86932	TCTGAACUGCAGACCCATUCC	86933	GAGGAGTTUTTAGAGCATUGCCAAAT
241298434	86934	CCTGAUCCCAAGUGGCCAAC	86935	GAAAGACCTUCCATGCAAGAUGAAC
241304372	86936	TGGAGCCUTCCAATTAAATUGCAAAC	86937	GCTCTCAAAAGGUTAAGCAATTGTTCUT
241304667	86938	GTAAAACTCCCCUTATAGTGGCAACUT	86939	CATTGTCTUACCTCCCAACUGGA
241310393	86940	CCTTCTGGAUCTCGAGCTGUCT	86941	AGAGATCACTGAUCAAAAATGTGTGUGT
241319323	86942	GACAAAGACTCUACAAGTAACTGTUCCA	86943	GAGGAAAAAGCUATGTATTCTGCUGAAC
241320099	86944	GCTATAAGCTGTUTTTGCTTTTCGAGUT	86945	GAGACATTTGAACUGTTTTCGTTGGAUT
241320313	86946	CTCTGTCCGUGCCTTTATGAATAUCA	86947	GCTTAGTTCTCGAACUCTGCTTTCTAUT
241323204	86948	TCCCTTGAAAAAUGAAAGAGAGAUGGT	86949	ACACAGTCAUGGTTGATTTUCAGAGT
241325709	86950	GGTGATCUGGGTAATAGTTTCUCCAAAT	86951	AGAGGATAGCAACAUACTTCGAGTTTUT
241327232	86952	CCAGAACAAGTAAUTGCTGAAGCAAUC	86953	GGAAGUATTCATCACAUCCACACACT
241329778	86954	ACGACTCGUATAAATGCTGCUGA	86955	AGCAACTTCUCCTCCACTAAAAAUAGG
241330530	86956	CTTGCGAAGUTCCCACTCUCT	86957	GGCTGTGCUGGCCTCTUAC
241339083	86958	ATGCAAAUGGGAATCCTCTUACACA	86959	TCACTCACCATUGTCTGTTATTGTCUC
241342629	86960	AGGCCTTTTUAAGCCCCTUACAG	86961	TGGATAACUAGGAGATTCACGGTUGAA
241344217	86962	GAGCCGTGUCTCACTGTCUG	86963	TCTTTCAGTTUCAAGGCCTCGATUT
241344438	86964	GCACCAUCCCCAAATTCAGAUGAT	86965	CAGTAGTATTUGGCAATTGTTTGGUAGT
241346645	86966	GTTAAGACAGACCGAGUTTCUAGGG	86967	CATGAAGAACCAGGUTGCAAGATTUA
241349010	86968	GATTGTGCUCCATGCTTTCTTTUCT	86969	GGTACATACCACAGUGCTTCCATUAT
241350429	86970	CTTACTTGTCTUCATCTATCAGCCAUGT	86971	TTCTCCATTTGCUTCTTTCGGCUA
241351770	86972	GACAATGAAATUAAAGCCTTGGAUAGCC	86973	AATGTGGAUGGCAAAATGGATUCAAA
241352636	86974	CATAAACCUGGGACGCACUGT	86975	CCACCAUAGAAGAGGGAGCUCA
241357747	86976	CCACAGGGACAUTCACAACAUGA	86977	ATTAAGATTTTUCACAGTAATAGTCAUCACAGT
241358173	86978	GGGAGCUGAAAGCACCATCUG	86979	ACCTCACAUCTTTCTCCUCCCT
241359350	86980	TGCUAGUCCCAAAGAGGAGGT	86981	CACCATGCTUTTGCTCCCTTUT
241360432	86982	CTGGCUCACCCTGCTTUCA	86983	GCCAGATGCAUGGCTGAGUC
241362320	86984	GTCATAATGTTTTTCUTTTCAGGACATGUGA	86985	AGCCTGCTAUAATCGATCAAACUAACC
241362738	86986	GCAGCUCAATGAACUCAAGACAG	86987	TCCUGATCAGCAAAAUACAAGAAAGAGA
241363321	86988	CTGCTGGAUCGGCAUGGA	86989	CCCCTTAGUCAGGTGAGAUGG
241363958	86990	GACCGACAAACCUGAGGUCAT	86991	GCATTTGTCCTUTGACTGGTGTTUAG
241364904	86992	CTATGTCAGUGTAAACCUACGCGAT	86993	CACCCCAGTTUGTCGAATATATGTUGA
241374390	86994	GTATGTGUCTCACCAGUCGCT	86995	AAGTTACUACAGCAGCAGAAUGACAT
241374655	86996	TGGUGGGCUACCAAAAGCAA	86997	AACGTGTTCUCTTTTCTCUGCCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241375102	86998	CGUCGGAAACGGAAACACUT	86999	CGGGCTGCUTCCGAGAAAUT
241375823	87000	AGGCCCCAAUATGGGAGGUAAA	87001	GGGCUAAGATGCAGUCCACAAT
241378032	87002	TTGGTCTCACUCAACTATGCCAAUT	87003	GCTGCATUGGATTCAGCAUCA
241379674	87004	AAAACCAATGATGCUTAATCAATATTTTCAUGT	87005	GCGGCTUGAGCTAGAGAAACUC
241380195	87006	GACTGUGGGACAACCTCTTTTCUA	87007	TCTTATGTGGAGCACAAUTCTAATACUG
241380240	87008	CTAACTGTTCTGUAAGTCTTGATGCUGA	87009	CAGCTGAAATGUAGAGGTTGACUCT
241381215	87010	GAGTCAUCAGCGGCACTCUAA	87011	GGAACAACAGGCCAGUAUGGA
241382681	87012	TTTCAGATTGAGUACTTCCAAAGAACCUT	87013	GTCTTGCTCAUCCTCATGTGGUAAT
241384248	87014	CCCAATTTGTGAAGUTCATAACATGCUT	87015	CATATGGAATTCUACAGCGAAGCTCUT
241390437	87016	ATGTGAGUCAGCAGAAGTGUCC	87017	TCAAGGGACUAGGAGATGCACTUA
241390613	87018	CAGGGCUCTGTGUGCCA	87019	GCCCTGUCCAGGCACCUA
241392505	87020	GAAAGAATGGGUTGGGCTGGUA	87021	CGTCCTTGAUCCTGACAGCTUC
241393260	87022	GCCCTCGUGAGCATTATGUGT	87023	CTTGTCCTTCUCGGAGCCAUC
241395251	87024	GAGUGCTCUACCGCCACAT	87025	AGATCAUGACCCGATGGUCAGA
241398159	87026	CAAAGCAGUCATAATTGTTCUGGCAAA	87027	TGGAATGGCUGTTACACTTTTGAUAACT
241398926	87028	TTGATAAGGGUGAAAAUGGCCACT	87029	ACAGTTGATGAUTCAGAGACCUAGGAT
241399526	87030	GGGTTGGCUTTTGAGCTCGUA	87031	ATTCAATCACUGACCACCACUCC
241400507	87032	CCCGGCCCUTCTTCACUT	87033	CTCCGCAGCUCCGAGUC
241400582	87034	ATGAGATCTACTUACCTATGGCCTUGT	87035	CCTTCATCTCAUTTTCAGGATCTGUCAAA
241401874	87036	TTTATTCCUCCTCTCCCUCCCAT	87037	CCCAACAGTTTTAUATCCACAATGCCUA
241404270	87038	TCACATCACUACATTAACAACUGCACA	87039	ACCCCCTUCCCATCCTTTTCAUA
241405421	87040	GAGCTGTUCCACTTGTUAACAGAGA	87041	ATGAGATGAGUTGTGCCAUGGT
241410487	87042	GGTGATAGAAAUCCCCGUCCAAG	87043	CAAATCACTCUACTGTTGAGCTUCAG
241411031	87044	AAAACTGGCUCCTCAAGAGUGAAA	87045	CATCTCATCTUGATCAGGAAGCUCT
241419122	87046	CATTGAAAUGGAAAAGGTTGGAGAUCA	87047	AGAGCTTAAACUTCTCACTGGTTUCAC
241419544	87048	CCCUCGAGUCCCAGACAGAA	87049	TCAAAATGCGGGUCTCTGUCC
241420276	87050	GCTACGAAGAAGUTTTCTCUAGACGA	87051	GGACGGACGUCUCGAGAGT
241426372	87052	CACCCTCATUCCTGTGTAGCUAA	87053	TGTGAAACACGUCTCTCCAAATUGT
241433419	87054	GGAAGCCUGAGAATGGCAGUC	87055	GCACTTCAGAUTGCCCAGGTUT
241439744	87056	GACTGGGAGGCUCATCAUCAC	87057	GTGAGGCUTGGAGAAGUACCC
241440252	87058	CGTGTUTCCATGTTTUGGAAGAGT	87059	TCAGGTGAGGAAACUGGAGTTAGATAUT
241442042	87060	AGTGGCAUTTTCAACACUGGACT	87061	CCCTCATGACTGUATTCTAGTTCTTGUC
241443488	87062	TTCTGTGATAUCGCTCAGCGAUT	87063	ACTGAAGAUGGAGAGGCACTAGAUT
241445317	87064	CTCACTTTAGCAUGAGTCTATCAGAUGG	87065	AGUAACATTTGCTCUCAGAAACACACA
241446669	87066	TCTGGTCTCTUCCTCTCTGCUG	87067	ATTTAGGAATGUGCTGAGGAGCTUAG
241449553	87068	CAGCCCAAAGGUGTGGAGAUT	87069	GCTCUGCACACCTCCTCUAC
241450232	87070	CCCCAGCUCCAGTTACCTTGUA	87071	ACCTTTGTGUCCTGTGTTGGUT
241452310	87072	CTTGGCAAAGUTGCACTAATUCAGT	87073	AGAACGGCCAGCUAATAAAAGAACTUA
241452361	87074	CGTCTUCCGGCCTCTTCTUAC	87075	GTGTUTCTGTTTTTGGUAGCAAGAAGAT
241459122	87076	TCAGCATTTGCUTCTTGTAAGGGUAA	87077	TTAGTTATCAAGAGUGGAAGCATGTUGT
241466854	87078	CGGATCUGAGCCCGGAAAAUG	87079	CCCCATAGGUGTGCAAATCCAUA
241473524	87080	GACTCTCTACTAUGGTGTCATCTTTUCC	87081	CATACCTGCACUCAAAGCAAUACC
241475892	87082	TCTCTTCCCAUGGCGATGUC	87083	GTTCCCTCUAAATCAAGTGCUGAGT
241479159	87084	TCTGATTACACAGUATCCTCGACATUGA	87085	CAAGTTACCUGTGATCCAATTUCGAC
241481319	87086	ACTGCCGCUCCGTCTTTUAG	87087	AACUGCAGAACAAGCACUCAGA
241484257	87088	GCTGUGGGACAGGGTUGT	87089	GCAGCAGGGAUATAGTATCTGACAGUAT
241485053	87090	GAAACAAGCAAGCUAAATGTGAACUGA	87091	GTCTCCCUTCCCCCAUGAAAG
241487484	87092	GTAGCCAGUGAGGTATGCAATUCT	87093	CCCAAAGUAGTGATCCUAAGCAAGG
241493432	87094	GCATTCCAATAUAATCCATCCCUGCAA	87095	AGUGAGGGCGGAACAGGUA
241496606	87096	CCACCAGGGCUTGCAAGTAUT	87097	TGAGGAUGUGACCAAGAGGAAGA
241500160	87098	TCTGTTTGTCAUCTGCTGGAAAUGT	87099	ACAGGATCAGGUTTATCGGGAUCA
241501340	87100	CCCCAUCCCGAGGGACUT	87101	TGAGCGUGCTUCCAGGAAT
241503590	87102	CCCTGGCAUACCTTTGTGGUA	87103	TCGGATTTTTCACUTTGCTCATGTTTUT
241504553	87104	TGTGUCCACCCCCTTACUCAT	87105	CCGTATTUGGCGTACUCCAC
241505752	87106	GGGTGGTGUCTTTTCCTGCUA	87107	CAATCTCCAGGAGCUTCTGCUT
241506126	87108	GCCCGCUCCTCCTCAUC	87109	GTCCAGGGAGCUGGAGUT
241508632	87110	TTTCTTTCAGCTUCTTGCCTTCATUG	87111	AAATTGCATTCUCGATTTTGTCTUGGT
241509966	87112	GCGCUCCAGGAAGTTGUGAT	87113	CAAGAAGAGGTUCTGGAGAGAGAUG
241510364	87114	GCTACCUGGGCAGUGGA	87115	GCTGGGUGCAGAGCCAUA
241514371	87116	GCAGAUCAGCUGAAGCAGGAC	87117	AGGAAAGAGAACAUCACCAGGACUA
241518871	87118	CCCGTTTCUGCTTCTCAGCTUT	87119	CTGATGTTGCUGGTCGCTTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241526442	87120	AGAAAAGCTUCACTTGGGTCUGG	87121	CACCAATGACUACCTGTGTGTTUG
241527099	87122	GCACTGGCCCCUTTTTCTTCUT	87123	CTCTCTAGUAGCTCAACTGGAUAAACCT
241528708	87124	TCTCTTCATCCUCCTCATCTTCCTTUT	87125	GCATGAAGCAUTTCCACATCUCCA
241541321	87126	GACCCAGTGAUGTTTGTCTGTUACA	87127	CUGGCCAGGAACGCATUAC
241545370	87128	GCTTCTCACCAGUAAAGGCACUA	87129	GCTACAGTUGTCGCTGCTUG
241554803	87130	CTGTCCCACCAUAACCAAAATGUG	87131	ACAGAGAAAAGACAGCUCCGAUG
241559951	87132	GGGAGACGGGUGCAUCA	87133	GACAUGCACACGCUGCT
241560149	87134	GAUGACCCAACCGTCUCCAC	87135	GCACGCGUCATCCTCATUCAA
241560220	87136	CTCGTTGAUGTCTCCCUCACAA	87137	ATTCTGTACCUCTTCTCTTTCCUCCA
241560385	87138	GTGCAGTTUAGTAAGTGGGUAGCA	87139	TGAGGAAAATAUCGACGATTGUCCAG
241560861	87140	GGGCCGGUGAAACCUGAG	87141	CCACCCUGCAGCAGAGUA
241561944	87142	TCGTCCAGGUGGTCTTCTAUCT	87143	CCTGGCAUATGCAGCTUCCT
241564195	87144	CCCAGGCAAUCGACUGCAT	87145	CGTGCACAUCCTTGAUGCT
241564438	87146	TCCCTUCACCCCTAAAAAUAGAGAAGT	87147	CTGATACAGAGCUGAGGGCUAAAG
241565599	87148	CCCCGTTCUTGCAGTTGTTUC	87149	CTTGTGUCCAGAGCAGTGUGT
241566602	87150	ACCAGAGGUCTACGCCAUCAT	87151	CAGTATTCCGGCUAACCACUCC
241566768	87152	GAGCUGCACGCGCAAUAT	87153	CCCCCAACACACAGUGAAAUGA
241572645	87154	GATGATGCAGUTCCATCCTCUCT	87155	AGCTTCCCTGUCTTGTCTTTGUC
241576957	87156	GTCGTGGAAGGGAUCCTGTATUT	87157	CACUTAGTUGGACAGCAAGCAG
241577803	87158	AGGTGCUGCACTATCGCAUC	87159	TGCCCUGTACTCUACCCACAA
241585717	87160	GCACACGCUCTCTGGCTUA	87161	CATGTGTTTCTUGCCTTCCTGUG
241587222	87162	CCTGCAGCUGCCCTCTUA	87163	GCAGGGAAGGUTTCCTGGUG
241589297	87164	CTCATUGAGAAGGUGCGCAAA	87165	AGAGAUCTTGCCUGGCACAAG
241595689	87166	TTGGTACTAAGGAUGGCGACCUA	87167	CTGAGGACUTGTCCUGACAGAC
241596789	87168	GCCTTCUAGGCTAGTGTCUAGGT	87169	CGTCTGTGAUGTGGTTCAUGACT
241601785	87170	GTGGCCCAUCTCTCTTCUGT	87171	TGGCCTGGUCAGTAACTCUAGG
241607470	87172	CGGCACUGACAGTTUGCAAT	87173	GCAGAGUGGGATGCCUGAAC
241611179	87174	AUTCAUCGACAGAGACGGCAA	87175	GGGAAAGAAAGCCUTCCACUCA
241611325	87176	CGCATCUACAAGCCTTGCTUT	87177	CATTGACCTCAUCAAGCTGTCCUT
241616453	87178	CGTCTCTTTUCTCCGTCCCUA	87179	AGGTGCTCAAUGAAGTTTTCCATAUACA
241617783	87180	CGCATUGGGCAGAAAAGAAAUG	87181	CCTTCTTGTUTGCTGATGGUAACCT
241621238	87182	GCAGGCCUGATTCAATGACUCT	87183	CCACAAGGATGUGAATAATGCTGUCA
241622028	87184	GCCTCAUGGGAGACUCCAGAA	87185	AAACTGCUCGAACTGGGUGAA
241626667	87186	GCCTGACGACUCGTGCUAT	87187	TCAUAAACATCUCGGGACAAGCC
241627155	87188	TCCTTTAGCAAACUTCTGAAUGACAACA	87189	CUCUCCCCCGACCAAAGAA
241633877	87190	GCGGAAGAUGAAGATTTCGGATTUC	87191	GGTATCTTUCCTAGGCTUCCCAA
241634684	87192	CTGCCACUTCAAGUCACGAAA	87193	GTGGGAAGAAUGAGGAAGAAAGTTCTUA
241639949	87194	TGATCATTGUCCCTTCATTAUCAACACA	87195	GGTGTTTACTACCUCCTTCTTCATTUCA
241640254	87196	GCCTGACCGUGTCTCTCTCUA	87197	CCTTAGGGCUAGCTTGATACTUCCA
241642285	87198	ACACCATCAACCUGAACAGCUT	87199	GCTGGUGGCAAGCCTGAUAC
241649273	87200	TCTTTTGGTTUTGCAGGCTTUGG	87201	GTATGCTGUAGACGCTCGTATTCAUT
241650333	87202	CCCTCUCCGGGCCAGUA	87203	ACCGCAGCAUGGUGGAG
241651493	87204	CAGCACCUCCACCAUGCT	87205	CCGUAGAUGCCAGCACGA
241653498	87206	GCTACCTCUGAGTCACCTGGTUA	87207	CUCCAGAGCCGACTUCAGAC
241654465	87208	CAGAGTTUCTCCACUGGGACA	87209	CCGCTGUAGGGCCCTCTUA
241654701	87210	CAACGCCUCGCTCATCTUG	87211	GAGCTGTTUGCAGGGTCCUAA
241656078	87212	CCTCUGGGCAGGAGATTGGUA	87213	CCTGAACTGUGTTTTCCTGTUGG
241658440	87214	CACACUCTGUAAGCAAAAGCCAA	87215	GAAGAAGAAUCCACATCATTCACAAUGG
241658590	87216	GTAGAGTTTCATAUCACCCCATTGUGA	87217	AGAGATGCTGAUGATAAACACAAGCTUA
241658901	87218	GCTACTTAGGTUACAATCAGGAGGAAUT	87219	ATATAAGGAGAAGAUACAGAGAGCTAGTATUC
241659859	87220	CCCTCCUGATCCCUCGCA	87221	CTACCUCGGAGCCGAUCAT
241661028	87222	CTCATCTGAAGAAAAGUTACCTAGUGCAA	87223	CCGTACUAAGGCGGTGUCAAG
241663938	87224	CTGATUACCCACGTCAGUCCT	87225	ACTCCCCACCUCTTCTTCTTTTCUA
241664054	87226	GATATTCTTGTTTUGCCTCTGTTTTGGUT	87227	GCTGTGTGUGCCCCTAAGUT
241665505	87228	TCTTTGCTTAAUGGGTGTCGTATAUCA	87229	CTGCATGACUGGTCCUGAAAG
241673388	87230	TGCTTTAAUCCAGCGCCTCUC	87231	GCTGCAAUCTTCGGTAGUCCAT
241675149	87232	CTGTTCTUCCTCAGACATUCAAACG	87233	CCTGGTGGAAGCAUACTGCAAAAUAT
241675304	87234	CCTGUCCACAGAACTTTUGCGA	87235	GGTGGAUCCAGAAGCAGAAUAAGAG
241677346	87236	CGGTCTTCAUGCAGAGACUGAAA	87237	GTGAGGTATUGGTGACAAGGUAGG
241679670	87238	TGACAUAGGCCAGCGGTTTAAUT	87239	GCACCACCUCACCTGTUGAC
241679980	87240	ATTCAATTCTUCCCGGTCTGCUT	87241	TGCTCTTCCCUATTCTCCCCTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241686339	87242	GTGGCTCTAAAGUCAATCTCTTCTTUCT	87243	AGAAUGGCCCAACAAGCAAAUG
241689145	87244	GGAGUCCAGCAUGGCAAGAAG	87245	GGGCCATTUAGTGACTGTUCAT
241689534	87246	GGTCTCCTAUGAGTGAGAACUCCT	87247	CCCCAAAGGACCUAAGTCTCUT
241690821	87248	GACTCCTTUGCCCCTGTGUT	87249	CTGCTGCCAAUAGCTTAGUGGT
241692652	87250	ACCCUCAGACAGAGTCTGUCAA	87251	CAGCTTGAGAUGAGGTGGAAUAGA
241695176	87252	AACATGAATAGGAUACAGTCTTCTACTTCUCA	87253	ATTCGTTGATCAAACUCATCTGTGGUAT
241700476	87254	GATGTUCAAAGCCAAAGCCTUCA	87255	CTTCTTTACCGGUGTACACTACTATTUCT
241703952	87256	TTGGCAGGCUACACTGGUAAAAT	87257	GCACGAAGGUGAATTAAAAUCAAAAGGA
241705064	87258	CACAUCGAGAAGCAGCTCUGA	87259	TCATTCCTGUCATTCCCTUGCAG
241706064	87260	GGUCAAAAAGGAAACGCAAUAAGGAT	87261	CAGCTCTGGAAUAACAAGCTUCAAAAA
241709768	87262	GTGTTATTGACGUCATAGAGTGACUAGA	87263	GCACUGACCTCTATGUCCACA
241711920	87264	ACATUGCCAACCATTCCUACCT	87265	GTAGGGUAGGGAAGTUCACAGAGAA
241715498	87266	GGGCACUCAGCTAGTCCTCUT	87267	CTGCAGAGUGCTATGAAAUACAAGG
241716240	87268	GAAGCACCAGCCCUAUGAACT	87269	CCATTGCATTGAUATGATGGATATUGGG
241721407	87270	GTCCGCCUTCTCTCCUACCT	87271	GGATUCCCGCCCCUCAC
241725482	87272	TGCCUACCCCAAAATGCTTUCT	87273	AGCATTTATAAGUCCAGAGAUGAAGCAAA
241726314	87274	CCGGCCCCUACTCACTTTUG	87275	CUCTTTTCCCUCCACAACAAAGGA
241726831	87276	TGCTTGGAUCATATTGGCCUGT	87277	ACTTTCAGCUTGTGGGAATUGGA
241730990	87278	GCGGTGTCUTGACTCTCUGAAG	87279	ATGCCGTUCAGGTTGTTGTUG
241734255	87280	CAAAGCTTTCATTUATGACTCCACTGUT	87281	GGTGGAATTUAATGACCCAGUGCT
241740937	87282	GGTCTTTGGUCGGGTTCTUGAG	87283	AGGAAAACTGGCAAUAACTCAGATTCUT
241743680	87284	GATGACTGACCCUCCCTCTUG	87285	CTGAAGATGUGAGCATGTTCTTTGUAAA
241747361	87286	AGTGGCTGGUGTCCCTGUA	87287	TGGCAGCGGGUACUCAC
241749424	87288	CTTACCCTGGGCUTTTGAATCAGAAUA	87289	TGGTAGACUGAGCTUAGACAGAGG
241751409	87290	TTTGGAGAACUTGCTCUCACAGAAA	87291	CAGAACUGGACCTATGAGGUGAAAG
241751419	87292	CTCCUCCAGCTGTTCTUCAAGG	87293	CTACAGAGTUCTGGGCATCTUCAG
241766339	87294	GTTAGGTGAAGUGATTATCCAGGUGT	87295	GGATCTTCGGAUCAGTAAGTACTTCTUC
241773106	87296	ACGGGCUCCTCGAACUACAT	87297	GGACGACAACCAGAAUGAGUGG
241773827	87298	AGGCAGAGAAGAGAAGUGAGUGA	87299	TGCATTCTTAGAGCUGTGGAAATTACTUT
241777431	87300	AGTGTCTGAAUCAAATGTTCTCTUGGAT	87301	GGCCTCCUAAAAGTAGACTGGAAUAAAA
241777763	87302	CGACUCACCCGGAACTTCTUG	87303	TCCTAGGGAGCUCGCUCAG
241779987	87304	AAAAGGTGGCUCCGAGAAGUT	87305	CGATCAGUCACATCCCUACCCA
241784484	87306	CAGGAGGGUCTTGGGTGGAUA	87307	GAGAATCCTUGGTTTGCCCTUG
241785959	87308	GAGATTCATUGACGGGACTTACAUAGA	87309	CCACATTCCCAAAUCAGATGCTUT
241787011	87310	GCAGTCATCAAAGUACAAAGCATCUGA	87311	ACATCAATTATTGAAUATTTAGCTTGGCAAUGG
241790569	87312	GTGCAGTAACTUGATTTGCTGTTGUAT	87313	AAGAGGCUTCCAAATUGAGGGT
241798612	87314	TTCTTCTAUCCTTCCTTCUCCACAGT	87315	ACCTTCCTCUTCTAGGTGGTUCAG
241807793	87316	CCAGTGCTTACUCCAGAAATGAUGAA	87317	AGAGGAAATCUGCAGCTCTGUC
241808858	87318	GGCCAAUAACTCCCUAGCCA	87319	TTGAGTGTAACUACCTTTTCCCTTTGUT
241812122	87320	CCTCGGUTGAATACCUGCAAGA	87321	TCGAAGAACTAGUTTCCCATACTUCCT
241817164	87322	CUTCTCACUGCCCCACCAG	87323	CTGAGCCACCUTGTCTGUCAT
241821278	87324	CCTTGTUGCCACCACTTCUCA	87325	GCAGTGTACAGTUTTAAATAGCTGCCUA
241828787	87326	GACTTACCAGATUAGTTACACACGACUT	87327	CATCTAAAAATCUGCCATTGGTGAAGUG
241831145	87328	CAGGCGCCCCUGGAAUT	87329	GGGCTGCUTGCCGUAGG
241832858	87330	TGGTGCTCUGGGAGATCTUCA	87331	GAACCGAGUTCCCUGAAAAAGG
241838789	87332	AGGCACUGAGAGGGACAGUAG	87333	CGCAAGUTCTCATCUGGCCAT
241839100	87334	TGCTTTTAGACGUGGATGTACUAACC	87335	TTGCTATUGCCGTCCCAUCAA
241841870	87336	CTTUAACAGGAAGAGGTACUGCAACAT	87337	CGCACAGCAACAUTTTGAGAATAATCUT
241845298	87338	GCAGTTGTTAAAGAACUTGCTGAGACUA	87339	GCAAGAGAAGUGCCCTCUCAA
241850726	87340	CTTTTCCTGUGCTTGCTUCACA	87341	ACCTUAGGCAGAGAGGAAUGAGG
241851452	87342	TCACACTGAGCAUTTACTACCTGAAUG	87343	CAGCTTUCACCGCTTGGGAUA
241851713	87344	TGCAAGTTAACACUGATTGACCAUCAT	87345	AAAGACAGAACUGGGCAAAGACUT
241852237	87346	AGAGCGUACATCTGAAATUCAACCA	87347	CTGAAGUGCCCCCUGGAG
241864381	87348	CTCATGACAAUTGGCAUGCACT	87349	CAAGTCATTAAGGGUGCAGAGCUA
241866608	87350	GGGCUCCAATAATCAUCAAAGGGA	87351	CTCAAGCTCUTGGGCCAUCT
241869507	87352	GACUACACGGGCAGCTUCA	87353	CAAGCGACUCGGGUAAGGA
241880803	87354	GCCCATCTCUCTCCCTCCTUAT	87355	CCCTGGGAACAACAUCCTAGUG
241897440	87356	CGCCCACCUCACUGACC	87357	GGGCTTCUGGCTCCTTCUC
241900387	87358	TGUGAAGCGCCUCAACGA	87359	GGGACGGAAAUGACTUGGG
241906883	87360	CGCTACCCACAGUGACACUC	87361	GGAAGTATAGTTUCTTTCAGGGCUGAAT
241921610	87362	ATGTTACATTGGTTUCCTTGACATTTTTCTUT	87363	CACAACUGCATCAUGAGAAAACAAGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
241921917	87364	TUTTTCCUCCCACAGAACCAAACT	87365	GTGCCATUGAGGCATGATGUG
241931093	87366	TTGCTGCTUACTCCCAAATATUGGA	87367	CAGGAGGCACCUTTCTGACUT
241931182	87368	GGCCCATCUCAAGTGGATUGT	87369	GGATACCTTGCGAAUTAGAAGGAAGUG
241932108	87370	GCAGAUCCCTUGCAAGCAAAAA	87371	AGCAAGGTAAUACGGAACACTUGAAAT
241942552	87372	CCCCAGACCCUCAGTUACCAT	87373	AGAAAGGTTTTCCUCACTCAAGACAUAC
241942829	87374	CAAGGATTUGAGCACTTTCAUCCAAT	87375	CAACTTCAUCCCAGGATGGUCAA
241945435	87376	CCCACUGAGTAGTTTTUCAACAAGGA	87377	CCATATAAATCUGCTGATGGCAUGGA
241945722	87378	GTAAGAUAAGAGCCAGCAAAATCAUGG	87379	AAAGGATCTUCGCTGGGATGUT
241947393	87380	CAATTACAATGACAUCATCTCCTTUGCC	87381	AAGGGAGTUACCCAGGGAGAUT
241949775	87382	GTTTCTTCACTGUCTTCCATAGGTGUAT	87383	GCTGCTAGTCCAUAAGTACTCATTATTCUT
241953402	87384	CTCACTGTCUGGGTGTGCUC	87385	GCCGTACCUCTTGGGTCUCT
241954369	87386	GTAGGGTTUTCCACTGCUCCAA	87387	CCCGCUCCACTTCATAACUGAT
241955285	87388	TGTTCCTTTCUTTACAGCGGAUGAG	87389	ACACAGTUCCCTTCATTTTAUCCAAGAT
241957860	87390	GCCCGGAGUACTAGTCUCAAC	87391	CACAGGACCCAUTTCCACUCA
241960860	87392	CATAGTCGGAAUGGAAGCGUCA	87393	GGGTTTUCAAGATTCATGCUCAGAAG
241960906	87394	ACGGAAGGAAUTCCAGGACAAUC	87395	TGACGTCCUGTGCACCAUC
241964125	87396	CGAGGTCACUGAACTGCATGUC	87397	TGACGATCUGCCGCTGAAUC
241966660	87398	TGTGTGTAAGUCCTGGCCTUC	87399	AGGCCUCGUGCAGAACAC
241969549	87400	GGAGGTAGUCCATGGTCTUGGT	87401	GCAGGTCTAUGATGATGGCAAGUT
241971098	87402	GCAGGAGUTCGATCUGGAGAA	87403	GCUTGTUCACAACAGACACACC
241975315	87404	GCATGGGAGAGACUGATAAUCCAAGA	87405	CAAATGCAUCTGATTGUGAAACAAAAAC
241979902	87406	TCAGCTCCAUTACCAGGUACACA	87407	CCTCTGACTUCCCTCTCCTGUC
241982994	87408	TGTCCCTTTUAAGTAAACACAUGACACA	87409	AACCTGTTGTATUGCTCCCATTCTUA
241998221	87410	ACTCCCAGAGGCUGGTUAACA	87411	CCAAGAGGGAGAUTCGCTUCC
242001174	87412	GCTCTGGCAUCCCAAGGUAA	87413	AGCUCAACAGCCAGAACCUC
242004903	87414	GGAGGCAACCUTCTGTAGCTCUA	87415	TGCAAATCTTUACACCTTCTTACUAACCT
242011113	87416	GCCATCAGCGUTGATGCAGUA	87417	GCCATCTUCGGTTCAGAGGUT
242014400	87418	GGGCCAAGACCCUATCACCUA	87419	GGTGGTTCUCTGCCCTCUCT
242016876	87420	ACAAAACACAACUTTGCAGATTGUT	87421	CAACAGGTGAUGATGGAGATGAAGUAT
242019466	87422	GCCACACUCCTGGCAAUCAT	87423	CCAUTGAGCCTTATTUGAAGAAGAAGGA
242025027	87424	CCTTCAGAUTCTGCCUCCACAA	87425	CTGTATTTACUGAGAGCACCACCUC
242027077	87426	AATCAAATCAGTAUCAATGGCTCCTUCA	87427	GAGTAUGCACGAAACAAAAACAUCCAT
242031286	87428	CCCCAACTCUGACCCTTCUGA	87429	TCCAATTCCAGAUGCCCACUG
242031500	87430	TUGTGTCAGTUGAAGAAACAGAAGGA	87431	CCATGTGCUGTGTTTGTUCCAG
242031628	87432	CTGCTTGCCUTCCTGAGATUCA	87433	AGGTGATGATGGAAUCTGATCCTTTUC
242033059	87434	AGGCATGTUCCGAAGCAUCA	87435	GGCAGATAGUAGGTTCTGTTTTATUGGT
242038760	87436	CATCATTCTUCAGGGCCATGAAATAGUA	87437	TGCTCCTAGGUAGGAAGTGCTATTUT
242042504	87438	GCCCCUGTCTGCTUGGT	87439	GGGCACCAUCACCACCUC
242042773	87440	GGGAGAAGUACGAGCUGGT	87441	ACCTCCTUCCGCTTGAACUC
242042980	87442	CCCTGCCCUGGGTCCUA	87443	CAGCCGAGCUCTGGAGUC
242044200	87444	GTGCTGCUGCTTCCACUG	87445	ACUCGGCCCCCACCTUA
242044298	87446	ACTCCAGAGCUCGGCUGA	87447	CCCCAGCAGCACCUAUCC
242044564	87448	GTGUACGACGAGGACGACUC	87449	GGTGGCUACACGGACACUAAA
242045868	87450	CAAACUTGCACUGGAGGGAGAT	87451	GTAGTGAGGUCTGTGGGCATUT
242048475	87452	GCATGUGACAGGAGCCUAGAA	87453	CUGGGTGACGUGAGAGAAAGT
242049018	87454	TGACTTGGGUACTTTTTAACTTGCUCAA	87455	CCAGACAAGCAAACUCAAAAUAAAGAGA
242053016	87456	AAGGCTTCTTUCCATATACCTUGCAAT	87457	GCATCTAGTAAGUCAACAGAAAGAUCCA
242053305	87458	GAAAGGAGCTUCCGATATTCTTCTGUAT	87459	TUGATTACTTTACAUGCAGGACACCT
242056841	87460	AGAAGAGAUCGAGAGAAGGCUGT	87461	ACUTCCTCCTUCCCAGCAGAA
242058885	87462	GAGGGAGCTUCTTCGTTTCCTUT	87463	GCAACUGAACGAGGAAGGGAUG
242061294	87464	AAAAGCACACAGUTATGACCUAGCA	87465	TTCCATAGAACUCCACTTTGACAATUGA
242063723	87466	TGCTATCGAGUAGGTAATTTGCTTTTGUT	87467	GGACUTAGTGAUCACAGCAGACAAG
242064024	87468	GCTTCTTGCAGUTTGGAATGAAATUCT	87469	TGGTTTCTGTCAGUATGTTTGCTTGTUA
242064652	87470	GUGTTTGATCTCUGAAGCCAACAG	87471	CGGAGGAGUCCATAGATACATTTGUT
242068271	87472	ATTTGCGGAAAUTTGGCAUCGT	87473	CCTTGCCUGAGCTGATGTUCC
242070584	87474	CTGATGGAUGACTTTTGGUGGACT	87475	AGACATCATCTUACCTGATCCACUGA
242070942	87476	GTGTCAGGUAGGGATGCUCAC	87477	GCAGGTAGCUCAGACCATTCUC
242072133	87478	TCCCUGCCCAGCUAACAAAAG	87479	CCAGCGAAGGUGUGGAAGAAG
242072236	87480	CTUCCCCCACCCCACUT	87481	CUCCTUCCGCCAGCACT
242076872	87482	CCCUGCACGACCTCAUGT	87483	GCCGAGAAGCCGGUCUG
242082040	87484	CCTTGGCUGTGACCTGTUACAC	87485	AGTCTTGCUGAAGACAATCTGAAACTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
242083990	87486	TGTACTCACAGCUTGTCTACUCCA	87487	GCTTGGCAGUCCTGCACAUA
242084209	87488	CACCTTTTCTTGACUCAGTAATGACTUC	87489	AAACACACAAUTGTATAGATUGCCAGC
242087973	87490	CCATGATGUGCAGCTTCUCCAA	87491	TCAUCTGATGAAUGAGGAACAGCAG
242089236	87492	CACTGCCUGGAGACACAAUGT	87493	ATGCCCAGCAUGCACTATCUT
242090206	87494	CACCACCTUCCCAGAGTCCUA	87495	GTTTTCTCAGAACACAAUGGAACAGUC
242095150	87496	CCAGTCTTCUGATGCCCUGAT	87497	CATCCAAGACAACCUGCTGUG
242095193	87498	GAATTCAACUAGAGGGCAGCCUT	87499	CAGAGGTTCUGTCTGGCAAAUG
242098368	87500	GGCCCUCTGCACUGAGAAAC	87501	GTGGGACCAACUGTGACAUCA
242099919	87502	GATTCAGCCCUCACGTCUCC	87503	AACCTACCCCAUCTGCTTCTTUC
242103129	87504	GCUGGGAAAGGATGAUAGGCT	87505	TGCCCACCAUGTACCAGATUC
242103345	87506	GGAGAAGAGAGGUCATTTTGCAUGA	87507	GCATAUGCCAAAGCACTACACUACAA
242113245	87508	GTCTGCCAUGGTAAGAAAUGCC	87509	GAAGTGTACTACUTGCCTTCTTTCUCT
242113770	87510	GGTTGGATUCACACTCATTGTUGT	87511	CCCAUAGGGCATUGCAGACC
242114724	87512	GGCAAACGGGCCAUTTCUG	87513	CCCATTGUGACTTTCCAGCUCAT
242115218	87514	AGTATTCAAAAUCAAGCGAGTUCGAGA	87515	CCTGTATTTTGCAUGCACTTGATTUCA
242118719	87516	GAAGACTTACUCCCTTTGCCUGT	87517	GGCTTACCGTTTUCCCATTGTAGTAAUA
242121248	87518	TGTCTCCTCCUGACACCTGTUT	87519	TGTCCTGTCGUTCCCTCCUA
242121580	87520	GTGGGUAGAAGACTAGGTUGGAA	87521	CCATTTGAUGAACTCCAAAGGUCAGAA
242123593	87522	GGGAATGUGGGAGGAGGUT	87523	CTGAGGCUGCCCACACUAC
242128641	87524	GTGCTTAUCCTGTCCCUGGAAT	87525	AAGCGAGTAATGUATACTGCTTTCCTUT
242128816	87526	CTCTGAGCUGGACCCGAUG	87527	ACAGUACCTGUCCACCACACT
242132358	87528	CAUAGTCAGAUGCACAGGCCAAT	87529	TCAATGATGCUCTTTTGCUGCAC
242133132	87530	GCCUGGGAAGCCAGCTUG	87531	CACCCCTTUGAGTCCTGTUCT
242133528	87532	CGTAGAAATUCCCCTTATAGUCAGACCA	87533	GTGATGCAAGTUTTGGGTCTTGTUT
242134062	87534	GCGGUCUCAGGGAGGCT	87535	ACGUGAGCAGGAGGUGAAC
242135314	87536	AGGCTGCATUTCATGAAGGTUAGAA	87537	CTCACACGUATGTTUCCGACAC
242136767	87538	TGTGTCCUTTGGTTGTUGCCT	87539	GTATGCGAUGGTGGUGACAAAC
242136822	87540	CUCTCATTCTCTUGCCAAAGCAG	87541	TTTAAGGCTTACACUCTGCAATTCTCUT
242140449	87542	TGGTTGGGCAAUACTGCCTTUAG	87543	TGAGACCCAGUACAATGAGATGTTUG
242140500	87544	GACTAAGTCCAUTCCTGATACCAUCAC	87545	GCTTCCCTTCAUACAGGGTATTCCAUA
242142842	87546	GTTUCCACACCAACCAUGAGAGT	87547	CAACAUGCAGGCGCUCAAG
242143163	87548	CCTCCAGGGUCTTCTUCAGGAT	87549	GGTAGAAAAGCUGCCTGGAGUG
242146499	87550	TGAATGUGAGGCCCAGAAGUCA	87551	CTTCAGGAUAGCGCTCTTCTUCC
242148700	87552	GCCTTTCUGGAACTCCAGTUCT	87553	GCTGTGAGGUTTTGCTCTTCUC
242150889	87554	TTTTACUCCAGCTTGCUGACGA	87555	AAGTAAGUCAAGAGAACCTCCCTUCT
242152677	87556	GACAUACAGACUGCAGGGACAAT	87557	GACCCTTCAGAAUCTCTTGCTCUT
242155874	87558	TTGTCTTAGAUGGGACCCACAATUC	87559	ACCCTAGTCACGUGTTATAGCCUAC
242157302	87560	GGGATGTAATCAUTGGAGAGGATGUG	87561	TCCCUAACCTUGCCAAGGAG
242157897	87562	GACTACACAUCCTGAACTTTTUGCAG	87563	TGACTTCTGCUCCTGTTCTUGAAAG
242158020	87564	GCTTGGAGAUCCCTTUCGAACT	87565	TCCATGAGCUGGAGAAGUCCA
242158034	87566	CCTCCACGUACCCCTCUCAG	87567	CGTCCUGGACGAUGCAGAAG
242158130	87568	TGTCTGTCCAGACUCCCATCUT	87569	GGAGTCCCUGGATTTCACUGA
242160928	87570	TTGGGTTACTGUGTGGCATATGUT	87571	GGAUTCAAAUAAGCAGCCGGAAG
242161604	87572	ACAGAGAACGCCGUGUGT	87573	GGGACCAGGGUGGAAAUGG
242161672	87574	ACCAGAGAAGUTTGCCCUGAAG	87575	CTCAAAACAGTTUTGCAGGGAGAUG
242165703	87576	ATCCCAAAGCAAGAUCTTCTUCACA	87577	GCACAGGAAAAACAUTTGCATGGUT
242169295	87578	AATCCACCUGCAAGCTGTGAUAAT	87579	CCCTGACATTUCAACTTTTACTTGCTUC
242170242	87580	AGCUGGAGCCAGGACCAUA	87581	CTCAGUGAGCCAGTTGCTAUCC
242175178	87582	ATCCAGAAAAAGUTGCTGAAAUCAGA	87583	TGACAGAGUCTTCCCGAUGAGT
242175293	87584	AGGGACAGGAAGUCTGACUGA	87585	CTTGAGGTGCUACTGAATTTTCUGAAG
242178813	87586	CTGCGTCTUCATCTCCTCCAUC	87587	GGTGGGTTUCTCAATCGTCTUCA
242179242	87588	CTCTACACUGGAGGTGGACUCT	87589	TCAAGTTCAUCACCCCACTCUG
242180376	87590	TCTTATTCCCACAGUGTATCGGCUA	87591	TGCCTGTCTCUCATGAGTTCAUACT
242184044	87592	GGCTGTGCTTUGTCTTTTAAAGGUG	87593	CCUGGCCAAGAAUCAAGAACCT
242184051	87594	CATCCTCAACAUAGATGCCAUGGT	87595	CCCCTCCTAGUTTTGATCTTCTTUGG
242189409	87596	GCCGCTUACCAACCTCCTTUAA	87597	GGTAGAUGCTAGGGUGAAAAGGG
242191185	87598	CCCCACAGACCUGACTTCUCT	87599	GCUGGAAAGGAGGTGTUGAAGAA
242193785	87600	AGTGTTTTGCUCCTGGGTCUG	87601	CAUAAGACAAGCUCACAGCAAACAAA
242194873	87602	TTGGGTTTTCCUTAACTTTAGGTUGGA	87603	CTGTCUGCATTATTTCUGAAAACCAACA
242195741	87604	CTTCTTCACGCUCCTTCCCUAT	87605	CATGCUGAAGGACAGCUCCT
242201305	87606	GTGAATGAUCCGGGAGGCAUAG	87607	CTTCCTTGGAGAUTGTATGTTAGCAGTUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
242202654	87608	TTGCTCAGCAAAGGUACTTGAUACAT	87609	CTTCTGTAAGAGAUGCCACCTUAGAG
242202824	87610	CCAAGTGGCACUCTTTCAAAAGTUAT	87611	TGAUCUGAAGGAGCCCAGAGA
242203356	87612	GCTTGTCTCCUCGCCTTATUCC	87613	CTGGTCCTCAAUGAAGTCGTAGAUAA
242205246	87614	GAACATATCATCUGGACCCTTTUCCA	87615	TCAGUTAACAAGTAAGUAGGGAGGAGAG
242208771	87616	TGTGCCCGCGUATACTTCUC	87617	CAGGCGGAACUGGUGGAA
242210546	87618	TGCCAGCAGUTGAUGAGAAACA	87619	GCAGTGATGCCUCATTACGTTTUAG
242210853	87620	AGATGATUGCCAAGGCCTTCUC	87621	GCUGGGAGAGACUAGCACAT
242214148	87622	CCTACTACCCUTGGCATCCTTUG	87623	AGGCACCGUGTTGACTTCUG
242215151	87624	GGTCACAUCTGACCAGUCAGAA	87625	AAAUGCTGCUGAGCGAACAC
242218663	87626	CCUTCCGCATUCGGGAGAA	87627	CCACAAGGUCGGCACUCAC
242223119	87628	TGTACCCUGGTTCTGCUCAGT	87629	AATCGTGTTCUTGTGCCTAUCCA
242223332	87630	CCATAAGGCUCTTACTCTCAAAUCACA	87631	AGCTGTTCTTUTGGTTGGTGUCT
242224871	87632	GAAGGACACUCAAAAGCATGCUG	87633	CTTGCATCCAGGUTCCACCTUA
242233032	87634	CGACGCCGAGACCUCUAAAC	87635	GCTATGAGCUGCTTGGGCUA
242239227	87636	GAGCAGCAAACAACUTCTUCAGAAA	87637	GGCACTUACCTACACATCUGCAAG
242243722	87638	CCTGTCAAGACUCAATATGATTUCCCAT	87639	CAAATTGCUGCCAGACTCAAGATTUAA
242253254	87640	GCTAAGTAGCUGCTTCTGGTUGA	87641	TCTTGTTCAAUGGAAGCCTCCUG
242255840	87642	TTTUCACAAGCACATUGACAAACAAGA	87643	CCTGTGATUGCTCCTGTGAUCAAA
242257004	87644	ACGCACAGTUAGTGAACCTTCUC	87645	TTATCACTCAAAUCGGAGACATTUGGT
242257182	87646	TCTGTTGAGAUGAACTAAAUGGCAACT	87647	AGAAGAGCCAUAGAGAGCAUGGA
242257244	87648	ACGGTTAACCUATTTACCTGTTGTUCC	87649	TGAAGTTCGTTUAAAAGAGTCAGCUGAA
242259751	87650	TTGGATGCTAUTCAAGGTTATUGGCT	87651	ACCACATTGAGGUCACAATCTUCAA
242259948	87652	TTUCACCAAGCGGAAUCCCAT	87653	GTGCTCCAGCUGTGTTGTTTUC
242261527	87654	GGCTCTTCTTTUATCATCCTGAAGTUCT	87655	AAAGGUGACAGAAGAAGUGCGT
242266370	87656	TCTGCCUCCCTTCTGACUGT	87657	GAGAGUCCACCCAGCAUAGG
242266984	87658	AGTCCCUGAAAAACAGCTGAATGAUA	87659	AGTACTTACGGTUGTCATAAATTGGGUT
242268366	87660	CCTCCCUACGCCTTCTTCUT	87661	CCACCCUCCACAGUCCCT
242274751	87662	GCUCGGAGAACACCCTTCUG	87663	ACGGTCCTCAUTTTCTCGTATTTUGT
242277756	87664	CAUGGAGAAGAAGGCCCUCA	87665	CTTGGCGAACUCCACAGTCTUAA
242278796	87666	GGGCTGGATUTGGAGCTAAAGUA	87667	GCTGCAAATAAAAGUCCAGATACGTTUT
242282859	87668	ACTCACUGGCTCCTAUGGCA	87669	AGTCACAUAGAAGAATTTGGGTTUGGT
242283169	87670	CAGGUGCCACCTGATAGUGA	87671	CUGAGGGAGCCCCATATUCC
242286369	87672	ACACCCATTTUTACAATGACGUGACT	87673	CAGCTACAGUGATGCCCACUAC
242287217	87674	CTCCCTTAGGUTCCCTACUCCT	87675	CAGAGGAAAUGGCTCCAGGUA
242292875	87676	CTCCUCCACCGCTTCTTGUC	87677	CTACUGGGACGGAACAGCTUT
242295437	87678	GAACTCUCCACCAAGTGCAUCA	87679	GACAUCUACCCAGGACACAGG
242305483	87680	AGTCAAGCGGACUTAAAACTTCTUACC	87681	GTCTGCTATACUGATTCCTGACTTGTUT
242310698	87682	CTAACCTTCCUGTGATTCCACTUGT	87683	GAAATAAGUCAACACCCAGGGCUA
242312366	87684	TGCGAGAGCAGAGUGAGGAUA	87685	GGAACAACCAAUTGTAGCUCGGA
242315995	87686	AGAAGGCAACTUGACAAGAGAAATGAUA	87687	AGGTAGATGTUAAGAAACACCTCUCACT
242320957	87688	TGAAATACCUCAGAGCUAGAGCGA	87689	TGUGGACGTTTUCAGCAGAAAGA
242324749	87690	TGTTTAAAUGCAGTCTAACTUGGAGAAGT	87691	CCCAACATCUGACAGTTCTTTCTCTTUA
242326507	87692	GGCTTGATATUGGCTGTTGGUG	87693	ATTCAAAACAGCUTTAATAAGGCTCUGA
242326573	87694	CUCCCAAGGCAAGCTUACAC	87695	GTGAGGGUTTTTGGAACUGGAGA
242329242	87696	GGTCCUGAGGTAAGACCUGCT	87697	GTTGAAGGTCUGTGCGTTCUG
242338282	87698	CATCTCATTAUCAGCTGTGUAGCAAAC	87699	CTCACCTCAUAACTCTTCTTGGUAACAA
242340127	87700	GAAGGACGUCATGCTCCUGT	87701	CACAGCUAGCGGGACTTGUT
242342378	87702	GTGGTCTUTCTTTCTGAUACAGCCA	87703	CGATCAATGCCUTCTCTCTCTCUCT
242344565	87704	GGTTCTTTCUCTCCACCTTUGAACT	87705	CAGAAAGGAUAAACCAGCACCUG
242353642	87706	GCTGTGAUTTCACTTUCGCAGAA	87707	TTTCCTCCTUGGAGACATGCUG
242355829	87708	GTCCACACAACUTGATTTTGATCCAUAT	87709	TGCCAGATATUAAATCGAGACTTUGCT
242362523	87710	TGAGCTCAGTAUGGAAAGAAATAACUCT	87711	TCACTTTGCAUATGCCATACAUGGA
242362921	87712	CATGTATGGCAUATGCAAAGUGAAGAAT	87713	AGATCAAATGAATUACCTATGTTATGTTAUGGA
242363876	87714	CAGGGCAUGCATTTCATUGGA	87715	GCAGGTATTUCTCGTACTGGUCA
242365080	87716	GGAGGTCCUGTTTTCAAGTUCCT	87717	GTCCACUGCGACGCCUA
242366362	87718	CCCATGGAGUGTCCTTCGUG	87719	TTTCCUGGAAGGGAGGUGAGA
242371116	87720	ACAGTTGUGGGTGGCTUCA	87721	GCTCCGCCUCGTGACUC
242377525	87722	GCAGCCCAUCATGAAGTTCAUCAA	87723	AUGAGGACGCCGACACUG
242388834	87724	TCCTAGATACCUTCATTCCTTUCCCAAA	87725	TGTGGGCAGCAUCACTCTUG
242398855	87726	CCCCAGCCUGCAGAGUC	87727	GUGGAGGACGAGAAGAATUCCT
242399640	87728	GTCCATGGUTCATGCATCTUCCT	87729	CAAAAAGGACAAUCAGGCCTGUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
242402961	87730	TGCTTCUCCAGGTTGTGCUT	87731	CCTCUCAACCCGCGAGUAG
242406478	87732	GTGCCACCACAUTGCAGUAAC	87733	GAGGTUAGCCACGTACTCGUC
242421295	87734	CCUACCTCTUGCAGCAGACA	87735	ACGUGAAGACGGCTGCUC
242422869	87736	GCUGCCAAGCGTUCGGA	87737	TCAAGATGGGCUACTGAAAAUGCT
242431688	87738	TCTGCTGGAGUTCATCCTGCUA	87739	GTCAGAACUGGGATCUGCGA
242431976	87740	ACTCACTGGUCCTTTCACTCUCT	87741	CAGTTGTCUGGCCTCUCCAT
242435711	87742	CTCCACCACGUCGCUCT	87743	AGCUCGCCCTCCUACCA
242436622	87744	GUTTGTGCAUAAGGACCAGGGA	87745	CTTCCCAAGAACAGACUGAGUGT
242436890	87746	CCCACCAUGGAGAACTGGUA	87747	CATCGGCAUCGGCATGUC
242440737	87748	CGGCAGGUAGGTGTGGUA	87749	CTGCCCUCCATCUCCGA
242442006	87750	CAAACTTTCUCACCATGGTTTCAGUT	87751	TCCTTTTCTTTCUGCCTTCTTAGGUG
242444313	87752	GTGAAGGCGCCUGGAUAGT	87753	CCGCAACCUCCTACTCACTUC
242446520	87754	AAATAGTTGATCAUACTTTGTAACAGAAUCACA	87755	GGTACAAGTUAAGGCACACAGAAGATUA
242447158	87756	AACTTCATTTGTGUTTTCTCCTAGGUCA	87757	GTGTTGTUGGCAGGGATACAUAAAC
242450407	87758	CACCCTACAGAAAUTCAGAACTCUGAT	87759	ACUGGAGCGATCUGAAACAGAAAC
242451684	87760	GCGGCTCUTCAACCTTCUGAA	87761	GGAGGGAAUGCACACAGATGUC
242459536	87762	TCTATCTGGCUACTAAGCCTTTGTTUG	87763	CTGCTTCATGUAGAAATGGGTTGUAAT
242464216	87764	AGGCCCUAAGCCCTCUGT	87765	CCGGCAGGAUCAGCUCA
242466922	87766	AGCCACACCUCACGTTAGAATUT	87767	AGTAAAAATGTAAGUGAAAGTCTTCACUGGA
242471288	87768	GTTCTUGGAGAGCACATCCUCA	87769	GTCGCCCUGGGCCTUAC
242473896	87770	TGAGAAAGCCAAUTGAGCACTATCUT	87771	GCCGAGUGCTACAACCUCAG
242478303	87772	GATGCCAGCUCACCAGAUGA	87773	CTTTCAGTCACUCTAGTCAAGCACTUAT
242479542	87774	CAAGGAGGGAGAUCACATTAGUACA	87775	GCAATGGUGTGTTTTAACUGGCAT
242481641	87776	CCACATGCTTTUGAAGATGTTCATTUGA	87777	GGGAGTTACUTAGCTTTTCCTUAGCA
242490772	87778	GAAGCCTCAUTCAACTCAAAUACAAACC	87779	ACGAGCCCUACTACAGCAACUAT
242494828	87780	TGCCCTUCCAATGGAUCCAC	87781	TCATGCTGGAUCCCCACTTTUC
242509307	87782	TCCTTCUGCAGGCCTUAAACAG	87783	AAGCAUTAAAGCCUGCAGGGA
242511159	87784	CCUCGCCGCCACACTUT	87785	AGGCACUCAGGUGAGCAG
242511282	87786	AGCTTCTGATTUCATCTCCCTTTUCC	87787	TGACCCCTUGGGAACATCAUACT
242518778	87788	TCACUTCGTGUGGAGCACAT	87789	CAAGTCAGACAGUACAGGTACATUAACT
242521245	87790	GCCAGUGGCCCGTCTUC	87791	CCCUGGCCAGCATCTTGUA
242523472	87792	ATTTGTCTGTTCCUTACCTTGACAAUAT	87793	AGGAAATUAGCAGAGCGATUGGT
242527953	87794	GACCTCGGUTTGCATTUGCC	87795	GCGATTCTGGCAGAUCAAGTAATGAUAA
242542626	87796	GCTTTGACCUAAATCTGTTGCTTUGT	87797	CCCTATCUGGCCAAGCAATACTUA
242550361	87798	TCAATTCAAACUATGGAGGAUCAAGCC	87799	TCAGTCTTUGCCTTCCTTUCAGAAA
242558690	87800	TCCAAGTGUGACTCTTGATGCUG	87801	CTTGCTAUCGAAATGCACAUCAGAA
242560505	87802	TGATGACTGCUCAAAACCTGGUC	87803	TTCTGAGTGCCAUCTCCCTTTUT
242565948	87804	CTGGAGAACAUGGCTTCTGTTTUT	87805	CCTTCTCAGTCCUTCTTACATTGTCTUT
242569747	87806	TGATGCTCUCTCTCCAAAATUCAACC	87807	TCTGCCATAACUGGATTTTCTTTGUGT
242571315	87808	ACUTATAATGCAAGTUGGACAAGGGAT	87809	GAAACTCACUGCCACAACUCAAAAG
242571562	87810	CTGGGCCACGGUTAAATGTUT	87811	GACAATGTTTAUCAGCACTTTCUCCAAT
242573832	87812	CTAGCTTCTCAUTTGCTCCTCUCAAA	87813	CCAGTTATGAAAUGCTGCAAGATAAUGT
242575364	87814	TTTGTCCAGAGACCUTTCTAACGTATUC	87815	GCCTCTTTUCCACAGAAACAACAUC
242578052	87816	CTCAGGTCACUCGGGCTUA	87817	GCTCTTAGUGTGCACTTTCUGCAT
242581871	87818	GGAGGAACAAGAAGAUGAGGAAGAAAUC	87819	AGTTGTGCUGATGTGUGGAGAC
242583475	87820	TGCGATTTTCTCUCATACAAAGATCUGA	87821	TGGTTCTTUGAGCAACAUGGGA
242587898	87822	AACUCTCTATTUCCCAAACAACGCT	87823	GAACCACAUGCAGACAAAGATTTCUG
242588044	87824	CCCCCTGCUAATGACTCCUGT	87825	CGCCTTCACAGAUCCAAACCUAA
242589314	87826	TTUCGGGACCTCUGAACCAAC	87827	GCGGGACGAUCGAGUACAT
242589434	87828	CTTGTCTGCCUCAGGGAUCAG	87829	CGUGTACCTGUAGGAGCCAT
242589945	87830	GGGCCUCAAGGCACUCA	87831	GTCAACGGCUGGACUGGT
242591678	87832	CAUTTCCUCCCCGGCCAA	87833	CTTCGAAAUCGCCTGCUACAA
242596342	87834	TCGCCAUCCTGTCCAAUGAG	87835	CCUCACCACACACGUCCAG
242596413	87836	GTTTACCUGGACCGAAAGCUG	87837	CATGTCTAGAACCUGAGCTCATGUG
242597530	87838	TCACAGAGAGCUTTGCCCTUT	87839	GCATGACCUGGAATCAGAUGAACT
242597787	87840	TGTTCTCGCUGCAGTCCUC	87841	GGCCGACAGCUCCTGTUC
242598516	87842	CATCTTTCTGAGAAUGGAGTATCATGATUCA	87843	TGGTACTTGATTAUAACAATGCTCTTUGGT
242598639	87844	AACUGTATCTUCGGGCACCAAA	87845	ATGCCATTUTCTCTTTAATUGGAAAGG
242601234	87846	CCAGCCGGACAAGGUGUA	87847	GGTAGCAGGACUGGAUGGGA
242604823	87848	GGTATTGAUGAAAGAGGAGGUACAACA	87849	CGTAGTCTGCCAAAUTACAGCTTTAAUC
242605495	87850	CCCACUGGTCCUCAAGAGGT	87851	GCTGGTGCAUTTTCGGTTGTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
242608952	87852	CGAGTTGTCUGCTTCCCUACC	87853	TTTACGGTUCACTGTGTTCTTUACCA
242609458	87854	GTGGTTCTAGGGUAGAGGTAACCUT	87855	AAGAAAATACUCACCCCGAATGATUCA
242611032	87856	ACCCCTTUAAGGTGGCTCCUA	87857	CCATTGCTTTUGAAGAAACAGTTGUGT
242615893	87858	GCAGTAAGCCACUTGTTTTTCTUGG	87859	ACCGAGAAGGGUTAAACTATATGGUACT
242616297	87860	AATACAGTTTTAACAUAGTATCCAGTGTGUGAA	87861	CAACTGCTGCAAUAAAGATACAGATUCC
242619885	87862	GCTCTGATAAUCCAAAAAGGACTAGUGT	87863	GGCTATTTGCTAUCCTGGAAAGTTCAUT
242621141	87864	CATGCATATCAGCUATTTCCTCATCUCT	87865	AGAAGGACATUGCATCTTGCAAAUG
242621354	87866	CGTTUAAACCAAAGGCGCACUA	87867	TCAAGTATGCTUGCTGAAGGAGTUC
242627940	87868	TGTCAGAGUCCTGAGACAGAUCA	87869	CGTTTTAGCUCGTTCCTCCUCT
242632724	87870	CAGAACACAAAGAUCATCCTTUCAGAGA	87871	CATACUGGATACAGCUGGACAAGAAG
242633431	87872	GGTTTTCCAAUAGTTCGGATTUCCCA	87873	CGCCGCTUTCAGTTTCCUAGT
242641813	87874	CGAACACACAACGUCTUGGA	87875	CTTTTGCUCCTCTGCTUGGAC
242642962	87876	CCTTGGCCACAUTCTGUAGCA	87877	TTTCACAGGUGAAGAUGGCGAT
242643780	87878	GGCCUGGAAGGCUGACA	87879	AAAUGGCCACAUCCCCACA
242644655	87880	GGTTAACCAAACUGAATTATTTGUGCCA	87881	CCTGTACTUACCACAACAACCTTATCUT
242651455	87882	GTCACTTUGTTCTGTTUGCAGGT	87883	TCCAACCUCCAATGACCCATUC
242653825	87884	TCTTCTATTATCUCAACAGAGCAAATTATUGAA	87885	GTGCCTTTGCGUTAATTACCTTUCT
242654504	87886	CCAAGGUACAGUGGACCAACA	87887	GGACATAAGTTTUTCAGTTTGGGAAUCT
242658095	87888	CGGACACUGTCCTCCUAGCAT	87889	AGGCCTUCCCAGAAACTUGAG
242658097	87890	TGGTCTCTCAUGGCACTGUACT	87891	GCATTGCATUCCCTGTGGTTUT
242661219	87892	GTGGCAGCUATTAGAGAAATCAUGGA	87893	GCAACCCTAGAAUAGCTAAGCCTACUAA
242661804	87894	GTATGTTGGAGUAGGGCUGGT	87895	GATAAAGCGTTUCTGTCTCTAGCTUCA
242663757	87896	TCCACAGUGTCTGAAGCUAGAGA	87897	AGCTTTGATATTATTCUTGTTAAAAATCTGCUT
242667489	87898	TGCAGAACTTUTCCAGAATCCUGA	87899	CATTCCCAGAGUGGAGTUGGA
242670631	87900	AACATGTTTUATCCGAGTUGAAGGA	87901	AGCAATGTACTGAAUTTGTAGTCTGGUT
242671895	87902	TTGTAGCCTTTAUGTTTCCCATCACUT	87903	CGGATTCCATCUTCAAAATCTGTCUGA
242673416	87904	ACGAATACAGCCAAAUGTAAAATCCUCA	87905	CTAGGACTTCCUACGTTTTGGGTUT
242674741	87906	GAAATAATGGUGCAAGTCTUCAAGCA	87907	CTCCACCUCAGCATUACCGT
242676343	87908	GTGTCCAGTATUCTCTCCACAGAUG	87909	CCTGGAAUCAAGCTAGGCTUACT
242678647	87910	GACCUGAAGUGCCCCCAT	87911	CAGTCTCCTUACTTTGCCTCGUA
242686025	87912	CCAATGAAGUCTACACGTUGCAC	87913	GAAGGAGGTUCCGCTGGTUT
242688090	87914	TTTTGTGGAUGAAGAAAAACAACCTGUT	87915	GTCCCTTGAAUGAAAGGAAGTCUCA
242692069	87916	CGUCAUGCCGCCCAAAA	87917	CGGCTCUGCTCGCUCAC
242697182	87918	GGCTGTAGCUGAAAAGAGUACCT	87919	AGTGGAAAUGCCTCTUCCAAAGA
242698868	87920	AGGAAGTCACAUATCTGGTCCTUCT	87921	CCTGCATCUGACATGCTTUCC
242701781	87922	AAGCTTGCTGUGAGTAAGACAUACA	87923	GGUAGCCTAUACAGCCAGGAAAAG
242714492	87924	ACCAUCAGAGAGCCTUGAGGA	87925	TGGTATAAACAGUGGCACACACUT
242716979	87926	CCTACAGGUGTGACACTTTUCAACT	87927	CAGUTCTTCTTUGCCAAAGCGT
242717481	87928	TTAGCTGTTGUTTTTCACTGTTUCCAAA	87929	ACCTTGTCUATGGCACAUCAAACT
242721006	87930	GCTATCCTCTUCCTCTTCACGUGT	87931	CTGTGTTCUCCTTTAGTTAAGUGACCAT
242724574	87932	CATCAGTTCCUCCTCAGAATUCCC	87933	ACACCAUCAGCAGCTAGAUCCT
242726967	87934	CAAGAACGAGAAACUGAAGTGUGT	87935	CCCACTTCCCUGCTGGGATTAUA
242728936	87936	CCATUGGAGAGGAAGGTGUAGT	87937	CCTTGACCAGAUCTCGGTCUCAT
242731302	87938	CAAAGAGUACAGCTGGCCUGAA	87939	AACTGTTACACUGGAAGTCACUGG
242731871	87940	CCGTCUCCCTCUCCACCA	87941	CTUCCAGAGCAGTTUCAGAAACC
242733483	87942	GCTTGAGTTUCAATTTCTCTUAAAGCA	87943	GCCTCTCTUTTCTCCCCAUACAG
242734403	87944	GGGCAAUGGCCATATCAUCCAA	87945	CAGAGAGCCUTTGCACUCAGAA
242737641	87946	TGGCACUAGATTTCATTTUCAACAAAGAG	87947	ACTCTGGGAUGGTTGTGTTTGUG
242737916	87948	GCCTGTCUGAGCATTGUGCAT	87949	GATGAGCTCCAUTTGTAGTTATAGCUGT
242742173	87950	AAAATACCAAAAAGUTCATGGGATUGCT	87951	GCCCCACCUCAGGAGTUG
242742258	87952	AGTACTTTTAATACCUGAACTGGTGGUC	87953	ACAGCCAUCATCAGCATCUGAAA
242742426	87954	CCTAATCCCUTCCTAGTGGUGGAT	87955	CCCCUACAACAGCAGACUGAGA
242745839	87956	GCATGAAUGGTCAGTCTUGGG	87957	CAGGTGCUGCAGAATCTTCTTTUT
242751048	87958	CTCAAATAACGGAGUAGAAATTGCAGUT	87959	CTGATGTTCCGUTTTCTCTTGCUAAG
242753058	87960	CTGTTGTTCTCUAGAAACCTCCUGA	87961	ATTCGTACGGUGAACATTCCTGUT
242753333	87962	CTGCCAGACUCCTTCCTTCUC	87963	GAACAACCUCTGGCUGAGACA
242755858	87964	TGATTACTATUAACACCTCCAGCCUCAT	87965	GAAAGTAGUGGCCAAGATATGTTUAGAGA
242765384	87966	CTGACTTAGTGCAUCTATTTCGATGUCT	87967	GATGGAUATTGTTGCUGCCAAGG
242766062	87968	TCTTGCAGTTUGATAAGAGCTGCUT	87969	GGCTTATGCTAUGGAAAGAGAAAAGGUA
242776336	87970	CATTTTTCCTGTAUCTTGCATGTTTCUCA	87971	AGCAGGGAACAAUCACTAATACAACAUT
242778418	87972	AGCTCAUCACACTGGTTGTUGA	87973	GCCAGUATTGUGCCGACAAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
242778937	87974	CCTTTTGCAACAUAAGCCTCAUAAACAG	87975	TGATCCTTCTCTUTGCTGATCATTGUT
253626535	87976	GGACTGTTGCCUAAGGGATTTAUAGT	87977	TGAUCCAUCAGGCAAAAGCCAT
253629987	87978	CCUAUCCCACAGCACAGCAT	87979	GTGGUGACAAGGGUGAGACAG
253630819	87980	GCATGGCAGUTCAAAGGTUGG	87981	TGACAUACACATCATAUGCGCAGAA
253634254	87982	GGTGACCCTUTATGCCTCTGUC	87983	GTGTCCCCCAUGCCTTUAGAA
253634967	87984	GGCTGUCGGCGCAGUAG	87985	CACAGGAGCUGGTGTUCCA
253635139	87986	AGCCAUGGAACACCAGCUC	87987	GGACCUCCTTCUGCACACA
253641636	87988	GCTTTAGGAGAGUTGAAAGATGCCAUT	87989	CTUGAGGGAACACATACUCGCT
253642417	87990	CCCTCGGUGTCCTACTUCAAA	87991	CAAGTUGCAGGGAAGTCTUAAGAGA
253652619	87992	CCACCACGACUTGACCTTCUG	87993	AGCAGGGUGAAAGCAAAUCAGT
253654556	87994	CGATTATGUGAGCAGTTUGAACCA	87995	CTTTACCTGTUTCCATCTCAGUGAGG
253655145	87996	AAATACTTAAGAAGAUCGATAACTGCCUCAC	87997	TCGTGGTACCAACAUTCTCTACTGUA
253660947	87998	AGCTCTACUTCCTGATTUGGGAGAA	87999	CATTAAUGACAACCCUCCGGAGT
253667298	88000	CATGAUAGGTCTCGUGCAGGA	88001	ACATTCAUGCCACCAAGACGUT
253668904	88002	ACTCTAGGAAUGAAGGTGUGGGT	88003	CTTGTCCUCAGACATUCGGAACA
253668988	88004	GCGTUAGAGCCAAGGTTTGCUA	88005	CGAGTGCUGTCCCGUCT
253669697	88006	GGGCAGUTCTTGGTCUCGT	88007	CTACUGACAACGCCCCTCTUC
253671035	88008	GAAAGAAAGCCAUTGCTUAACAGACT	88009	GATCAAGACTUGACCACTTACTUGGA
253674340	88010	CACTCCAGGCUCTGGAACTTUA	88011	TGCCACCTACUTAACCTCTTTGTTUT
253675711	88012	TGGGCTCUCTCTTCTCGAUCC	88013	TGACTCTGGTGAUGGGAACATTAAAUAC
253679742	88014	AGCTCCUTCCCCUGAGAGAAT	88015	GTAAGTGAGTTUCCCCACTGCUT
253680963	88016	CGACATAUGCAGCTGCTGTUT	88017	ACCAGATAAAUAACTGCTCACATTUCCC
253687433	88018	TGATTAACCUTTGTTCTTUCCAGCCA	88019	GGTTGTUCCAATGGTGGUCCAA
253693017	88020	CGAAGCCGAAUTCCTGGTCUG	88021	TCCATCACUCCCACGTGGUA
253699002	88022	GATATGCATGUCAGAGGAAAGUCACT	88023	TTCTTTTAGGCCUCTTTTTCGUGGA
253699548	88024	TTGATCAACAUCTGAACTUCCACGA	88025	TTTGCTTCCTGUGAAACAATGATAAUGG
253699893	88026	GTTCAGTTUGGGTTGCTTGUCT	88027	CCTGCCCAUCATCGATGUG
253702885	88028	CCACCTCCCAAUCTCCCAGUA	88029	CTGGAGAGCUCTGACGTTUGA
253704306	88030	CAGCACUCACAUCGAAGGGT	88031	CTCACCAACACCACCUGATUCT
253710385	88032	CCTAACTTGGUCTCCTGCTTCUT	88033	GCTGCCAGAGUAAAATGCTGUT
253710778	88034	CCCCGGAGGUCCTGUCAT	88035	AGAATGGUGGCTGCAGGUG
253711113	88036	CAAGCCTGGUCTACACTGUGG	88037	ACTCACTCUGCTCTGGGTUGA
253712561	88038	GCATCATUGGGTCCTCAGUCA	88039	CTGTTCCTAUGTTCTCTCCTUCCAG
253715312	88040	GGGTCAGAUGGTATCTTCTUGCT	88041	TTCCCTTCAAUCCCAGCCTUC
253732414	88042	CCTGCACUCCATGGCTCAUA	88043	GAAAAAUGCCAGUGACAAGCGAA
253738432	88044	CAGATGCACUGGAAACUAGGCA	88045	GAGCATGUAGACCAGGACCUAAG
253743100	88046	CCGTGCUCACTTACTTTGTUGGT	88047	ACATCTCGTTGUTTTTCTGGTCAUAGT
253749736	88048	GGGTGCCTUGTCCAGATATGUC	88049	GGATTGAAAAGUGAGCATTTACTCUGGT
253753394	88050	GTAAGGACAGGACAAAUTTTCCTCCUA	88051	AAAACGCCGUCCTTTGAATAACAAUT
253754328	88052	CTGCTTAGUGACAGTGCAATTUCAG	88053	TGGGTCCTAAAAACUCTTACATTGCAUA
253755754	88054	CTGTGCUCCCCACCGTUT	88055	GCTGCUCCGTGGGAGUG
253756214	88056	TCCATTGCCACUGTGATCTTCTAUG	88057	GAGAGCTGGTAAUTTGGTCATTGTTUT
253756551	88058	CCCCAGGUCCCUCCACA	88059	TTUACCCGGGAGGAGAUAACCT
253761334	88060	AGGGAGGCCUTCAUGCAAAAT	88061	GCATCCAATTTGGUAAAGAATCGTGUC
253763316	88062	GCAGCGGUTGGUCAAAAGAAT	88063	CACACCTGATUCATACAACTTTTCTUCC
253763811	88064	CTCAGTGGCUTCACTGGUGAT	88065	ACGAAGGCAAGCUTAAAAGAACUCA
253767227	88066	CTGAUGGACTGACUGAGGAGGA	88067	ATGTCCAUCATGGCCTUGCT
253770012	88068	CTCACCTGCUTATACTTGTACAAUAGCA	88069	CTGCTCACUGCTTTGCTUCAT
253777269	88070	CCTTCACGCCCUGCTTCUC	88071	CGTCCTTCAUGAGCCCAAUCA
253777424	88072	CAACGUGAAGAAGAGCTCUGG	88073	AGCACTTCUCCACCATCTTCTUG
253778207	88074	CTCAUGAAGGACGCCTUCCA	88075	GCUCAGCCGGCCTTUCA
253781081	88076	GCACUGCCCCCTTAACUCAC	88077	TCCTGCTTUTCCACATGUAACCAT
253781261	88078	GGGACUGCTGCAACUCAAACT	88079	CTGCCCTUTGGCCACAUAC
253781762	88080	GGCCAUGCTGAGGGUACT	88081	GCCTGACTCUTTCTTCTCCCUT
253787706	88082	GCTGAATTTGAAAGAACUTAGGTCCAUT	88083	GTGCACAAACUCTCCTACTAUGAGT
253829947	88084	AACTTACCCCACGUTCAAAGUCAT	88085	ACAGGUGAACUCCAGAAAGAAGAAG
253941736	88086	TCAGTCTTUGGTGGCTGAAUGG	88087	CTGCUGAACACATUGCCCAAG
253964048	88088	GUGAGGUGCCAGAGAGCAG	88089	TGGACGTCCUGGTGAAGTUG
253972931	88090	TGAGGCCUGTAGAGACGUAGG	88091	ACTAGGACCCCUGCTAUCCAAA
253976729	88092	GGAUCCTTTCUCGCCAGCA	88093	GAGTCUGACAGCCCCTCCUAT
253986811	88094	AGGGCUAAGCAGTGCCTTUT	88095	GGTCGATCUTGAGTTCGUCCAG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
253992510	88096	CCTCGTCGUGGGTTCTGUA	88097	GCAGTUACACGTTTTCCUCCAAG
253993637	88098	CGACUCCGACAGCCAGTUT	88099	CCATCCGGAAGGUGTCCUC
254000374	88100	CAACGACCCCGACAUGGUT	88101	TCACAAGCUCGGCCGUT
254157667	88102	CTGAACAUAGCCCTGTGTGTAUGA	88103	GGACACTCAUGAGGGTTGGUG
254170750	88104	TGAAGTGACUCGTAACGACGTUG	88105	AGCTTAGAGAUGAGCCATGCTTUG
254198832	88106	ATGAAAGCAAGAACAAUATCTCTGUGGA	88107	CAAGTUCAGCAGCAAATCUGACAT
254241303	88108	AAUCTTATCCACTUACCAAAAGCCCAA	88109	TCCTAATGCAACAAGUCCTGAAUCC
254456538	88110	TCAACCCGUCAGUACCCAGA	88111	CGAAGTAGAGCAUCCTGGAGUT
254463962	88112	ACAGACCCUTGGGAGAGUGAT	88113	CTGCTCUCAGACAGCCAAAAAUG
254496744	88114	TGGCGATCCUTCACCAATGUC	88115	AAGCTTCACUGTCACCCCAUC
254507753	88116	CTCCAAAATTUGGCAGCCCAUAG	88117	TGATCTCTCTCUTCTTTCCTGCUACA
256744700	88118	GAGAGAGAGAGUTCCTCCUGGAA	88119	ACTGCCACAUTGTTTCCTUCACA
257231228	88120	CACCGTTTUTGAGCTGGUGAAT	88121	CTGAATCCTAACUGCTGAAGTCUGT
257366070	88122	GGACCAUGCTGTGGTGUCAA	88123	CCCCUGAGGGTGAGACUGA
257415226	88124	GCTGCAAAUCCCAAGCAUGAG	88125	GTCTTCATTACUCACTGCCUGACA
257426404	88126	AGGGCCAGUTACTAGAGACAUCAG	88127	TTGCTAAAUCCAGAAATACACTCTUCCAA
257444649	88128	GGCTUGGACCCUGGCAA	88129	CGACTUGCAAACCTGTUGGT
257450849	88130	CCACAAGCAUCTTGTCCTUGGT	88131	CCTCCTCTTUGTCCCCATCCUA
257481829	88132	GATAAATTCAAGUCTCTCTTCCTUCCCA	88133	GGGCTGACAUTCATAGCCTUCAA
257507147	88134	CAGAAGCUGACAGTGUCACACA	88135	GCUAGAGAGCAAGGCUGCAAA
257509184	88136	TCTGCTTCTAGUCAGAATCACAUACCT	88137	CGACCAGGACUCCGGUAAGA
257520581	88138	CCAGTGUTGGACTUGCAGAAC	88139	GCCAGUGATTUCAAACAGCCAT
257544121	88140	GUGCUGGACACGACAACAAC	88141	CCCTTATCTCAUGCTCCCACUT
257549696	88142	GAGGCUCCACACACAATUCAGA	88143	CTCTTGUCGGACAGUAAGCCA
257556167	88144	ACTTAACAAGTGAAGAUGGTGACCATUT	88145	CCATTGAGTTCAUCATTCTCACTGTUC
257572069	88146	GAGTCAGAACAUGACCTGTTGCTUA	88147	GCTTCAAATTGTAUGTGGCCCTTTTUC
257578711	88148	TCACGUGGCGGCTGAATTUA	88149	CAGCCACACUCTCTGGAGUC
257581111	88150	TTCAACCCTTCUCCAGTTTGTCAUT	88151	GTCTTCTCCUGCCTGGATGAUG
257588464	88152	CCCAGAGCUGGACTCTGUAAT	88153	TGTTCATGCGCUTACGAGGUT
257590446	88154	CCCAAGTUCCGAAGTATAAAGUGCAA	88155	GTTTTAGACCAUCCACTTUCCCACT
257604762	88156	GAGTCTCGUACAAGCAGUGGA	88157	GCAUCAACCACACGTTUCCT
257621190	88158	CAAGCTACCCUCCAGACUCAAG	88159	TGCTTTUGGAGGGCTUCAACA
257624546	88160	CCUCATCACTUAACAGGCCCAAT	88161	TTTCCAAGAGTUCTTTGCAGCAAUG
257626179	88162	TCTCCTTUGGCCAGCATTTCUAAA	88163	CCTCACCUAAGGATCTGUAAGAGAGT
257630711	88164	CCAAGCACCUGCCCCATTAUT	88165	GCTTCTGAGCUGCCTCTGATUG
257633669	88166	GGATATATCTGAUACGCAGGCCUCT	88167	GCAAGCCCAAUAAAGAGTCACCAUT
257654704	88168	CGGGATGAGUTTCCAGAGCAUA	88169	CAATGCUGGCACTGGATTTAUCAC
257655352	88170	CGAGAUGCTTTTUCAGCCCAAA	88171	TTCTCGGTCUCCCTGCAGUA
257669324	88172	CATTCCTGAATTAUACTGCGAGGCTUA	88173	GGATAGAAGAGAAACUGCAAGAAGTTUG
257686635	88174	GTUGCAGGCCTCAUCACAGA	88175	CTCCTTATTACUCCTGCCAGTGUG
257692662	88176	CGGCUACCCGAGAAUGGT	88177	TGCTTCUGCCCCAGUCC
257696780	88178	CTGCACCCCUGCACCUA	88179	CTCACUGCCCTGCTCTUACC
257697991	88180	CTACUGGCACAGCCTGACUC	88181	GCCATTTTTATTUCCTCACTGATTUCCA
257703329	88182	CGGGTGAUCCCCAAATCTUCA	88183	GTGCAACATAUGCTTCTCTCUCAG
257712554	88184	GACAGTGCAUCTACTTCTGTGUCA	88185	GCTCAGGTTUGGAGTTGATCTTAAAUCT
257713066	88186	TGTTCTGUAGGCAACTUGCCA	88187	GAAGGTCAAAUAGGCTGAAGTGAAGAUA
257718834	88188	ATAAACACAAGAAUTTGCAGCAGAAUAAT	88189	GGCAACATGTUTGTGATTTACTCUGT
257726201	88190	CATCAGCTCCUACGCTATCTTTUAGAT	88191	GGGTTGGGUTTGTATTACAUGGA
257731000	88192	ATCCCAAGCCCACGUTAGUG	88193	AATTGAGGAAAUCCTCAGGCACAUAG
257731081	88194	AGATTTTGAAGUGACTTGTGCTGUCT	88195	GGTCCCCCAAGAUTTTCTCCUC
257731522	88196	TGAAAGUGGAAAAGAAAGAACAGAUGGA	88197	TCTGUGAAGCAAGCAGTUACCC
257735044	88198	TTUCCTTGCCUGGCAGGT	88199	CTCAGAATCTGAUATGACCCTTCGTUT
257742460	88200	ACACAGTCAGCACUACAAGATCUG	88201	CTCTCTAGUAGGGTTCCTTCAGUAGAA
257746144	88202	GCTAATCUCATAAATGCUGAAGAACGG	88203	CAGCACTACUTATCAAAGCCUGAGAA
257752696	88204	CCCCGATTUTGATGCATCUACACT	88205	CACTGACUCCAATAAGAGCAUCCA
257755837	88206	GCTCTGGAAGGAUTCAAAGTAATGTGUAA	88207	GGCTGTAUCCCATCGGTUCA
257758179	88208	CAACTTGGAGAUTTTTCTGAAUGGAACA	88209	GTCTTCTATGGCAUCTAGACGATCAUT
257765576	88210	GCGAAGUAGCCGCCAAAUAAAA	88211	ACTCTCACTAUCCCCCACUCC
257775564	88212	CCCCACTCTGUAACCATTATGCTAUT	88213	TGAGTAGCCUCTCAAGATCUGGAAG
257789735	88214	CTCCGAAGTUGTAGAGCTTCUAAAGAA	88215	TCTTCATACATTAUAGCCCTGCTGUCT
257795953	88216	GGTCGTTTTCCUGATTTGACTGUAGAAT	88217	GGAGGCTCTGTUCATTTTCTCTTATGUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
257801277	88218	GGGAAATTTUATGAGCTGUACCACA	88219	GTCTGTUCCACTCGTGCUACT
257801983	88220	TCCCCUGAAGAGUCAGAACCA	88221	TCAGCAACTTCTUCCATGATCCCTAUA
257802730	88222	AGGAAGCAGUGATGAAAUAAGCAGT	88223	CGTTTCCTTCCUAGAGCTTTTCCTTUT
257831625	88224	GGTGACTGGAAAUGGCTCTCUT	88225	CGACTACTGUCATCACCACCUC
257845858	88226	GGGTGTAAAAUAGGTGGAACUCAAAAGT	88227	GCCTTCGTAAUTCATTGCCTCUG
257855790	88228	CTCTGATTAUGACCAAGCTCTUGCT	88229	GGCAAATUGCGAGTGGUGAAAT
257858086	88230	AAAGGATGAGUTGCACATTGTUGAAG	88231	CCTTGACACAACAUCCAAAGTATGUAAG
257868066	88232	GGAGAUCGTGGCUCAGCAAG	88233	CAGCTACCACUACCCCATTUGT
257878744	88234	CCTGGUGCAGAAGGGCTAUAA	88235	GTGTACCCTUGGTAATGATCCUACAG
257904070	88236	ACTGAAGGCAGCUCTGAACAUC	88237	TGTGCAGUAAAGAAUGGCCAGT
257916240	88238	TCTATTTTGUAGCAAATTCCUGAGCACT	88239	CCCAAAGGAAGUATAAGCCAAGTAAUGA
257920839	88240	GTTACCAGCUGGAAATTCCUGAGA	88241	GCAGTCCTUCAATGATACAUCCCT
257923164	88242	GAAAAACCUACAGACCUGGAGACA	88243	GGCGTTTCAGCUAAACCCAAUT
257927083	88244	GAUAGAGTGGUGAGGAGGGAGAT	88245	GCACACACCAUAUGCACGAG
257965684	88246	TGTCTGTATGUGTGTCCCCCUAA	88247	CACTGGGUGAGGTTGTCTGUC
257971131	88248	TGGTTGCGCAUTTGTGGAATUT	88249	AGGATCTCAACUTACCAGCTTATUAACAC
257978516	88250	GCAGCCUGGTAGACACGUA	88251	GTCTGAGUCATGGTUAGGGCAT
257994467	88252	GTCTTCAAGTTUAACTCCTCAAAGCTUC	88253	GCCAAGTGAGAUACCATTCTATACTUCA
258000163	88254	TCAGAGUGAGGTCGGGUCA	88255	ACACACACACUTGGTGCTCUT
258000703	88256	CAGTTUCAAAGCAACAGGUAAAGCA	88257	AGGACCAAGUAGTGTGTCTGTUCT
258011862	88258	GCAUCAAGGAGCTATUAGGAGGGT	88259	AGACAGCTTCUTTTTCGTTGTTUCAG
258080174	88260	AGTAACTGGCUGTTCTCTTTTTCUCC	88261	AGCTTCACACGAUCTTCTTAAUGCT
258106547	88262	CGCTGGCAGUTTCAAACGUAAT	88263	GGGTTCATTAUAAAACAGGAAGUGCAG
258118626	88264	GAGCCUGCACUCCACAGA	88265	CUGACCACGGCCUGGAC
258121305	88266	CACAGGCCGGUGGAAUG	88267	CTCCTACCUCCCCTCACCUA
258132064	88268	CACTCATCTUCAGCCTTGCUGT	88269	GGACAGTGCUCTGGAGACUCT
258135082	88270	CTGGACACAGAGGAUCGAUGT	88271	CTGGAGGUGATGACUGCCAA
258140673	88272	CCTGGGCCUTCTCCTCUAACT	88273	GCAGAGGUGAGCAAGCUG
258156745	88274	CTGCTTCUGGCATTGCTGUT	88275	CAAACCGUGAAGCAACUGAAGG
258168828	88276	TTGACCTUGGCACCCTCAUAC	88277	AGTTTCUGGAAGTGGAGTUGGAC
258176054	88278	CGCTUCTCCTCTUCAAGGCT	88279	GCCCAGGUTGCAGAGCUA
258176544	88280	GGAGCTCAGCUAGTTCGTUCT	88281	GTUCCAGGAACAGCTGAUGACT
258182700	88282	TCCTTTTCTTTCUTAGCCAGCTGUT	88283	GGAGTUCGCTACCCUGCAAG
258184281	88284	GCTGCCAACUCTTGGACATACUT	88285	AGAGAAGGCCAGCUAUGCAG
258186555	88286	CTCTGCAUAGCTGGCCTUCT	88287	CACCGUGAGGAGCUGGA
258188852	88288	CCUTCUGCCGCAGAGGAAT	88289	CAGCUAAGCACCTCUGCCA
258191574	88290	GTACCTTTTGGAUCAAATGATGCTUGT	88291	TGGAGAAGUCAGAACGAAGAUCAGT
258193740	88292	TGTAACAAGGGUATACCTGTATUGGGA	88293	GGCTGCTCAACUCTTGTCCAUT
258199336	88294	GACCGCAGCUGCAACUC	88295	GCUAAUGAAGCCCGGGACA
258201628	88296	TCTTCGTTCTGACUTCTCCAAGTTUC	88297	TGTCCACAAAGGUGCTACAATUAGAT
258203202	88298	GCCTTCTCACAUTCCTCCTUCAA	88299	TGAGCAGCUCGTCAAAGAAGUAG
258213716	88300	CTGGGCCUGTGTCACUGA	88301	GGAGCGAGAGGCCUCCTUAA
258215667	88302	GGCTATCCUCATACCGCUCAC	88303	GAGGCTCGAUTACAGCAGCUT
258224394	88304	GCUGCTUGAGAGCCGCAT	88305	CACCAGGUGGAGCAGCUAA
258225961	88306	AGGACTTCAGUCTCAGCCUGAT	88307	GTTGTATCUCTGAGCUGAAGGCA
258234352	88308	CTTTCGTUCCCGCTTATGCUG	88309	CAAAGAGUCCTTGAAGGUCACCAA
258245320	88310	GCTAAAGGGCUCAGAGUGCAG	88311	TCCTCACGGUGAACGTCTUG
258370730	88312	TTCATTGACCAUCACATGCTAATAGUGT	88313	GCATCAUCATTATGCTUGCAAAAACGA
258378481	88314	GACTCCAUGGCTGTCAAATCUAGT	88315	AGCAAACUCAATACCUGCCCAA
258489720	88316	GCAGCTGGAUTTTACTGCCAUT	88317	CAGGCTGACUGCCTCTUGA
258512573	88318	CCTGCTTTTTAAUCCAAGTAAGCCAUT	88319	AACCAATGCTCUCACCTTAAAGUGT
258513834	88320	CGUATAAGCCCUCACAACAACCAA	88321	GTCTTGAAACGAACAUCAATACATAATAGUG
258566881	88322	AAGAAAAACAAGUCAGGTGAGGUGA	88323	CTGCCTCCUGTTTGGCTTCUA
258584191	88324	AGGCCTGUGGATATAGCCUCAA	88325	GAGTUCCCGTCCGUGACC
258590893	88326	CCCCGUTTTCCTAAUCCACAA	88327	CGCTTCCTUGGCTTGTCAAATAUCT
258600971	88328	GCCCAACGCUGTAGTTCCUG	88329	AGTGGCATGAGUAACAAGAGAGAAUG
258615367	88330	CTATTTTCCTGUCATAGGCACUACCA	88331	GAAGGTGAAAAGAUCAGGAACTGAGUAA
258651309	88332	CGCUGCCCACGGAGAUG	88333	GCCGGUCCTGGUGAAAGA
258656292	88334	TGGCCUGGCGCTTCAUT	88335	CGGGUGCTCTTCUCGCA
258662099	88336	GTCGCUCCAGCTCGUACA	88337	CTTACAGTCUCCCGCTTCAUGG
258663329	88338	CCCAUGCCGCTCATGTUCAT	88339	CTAGGCUGCCTGGGUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
258676704	88340	CCUAGCAAGGCGAGGCTUT	88341	CCTCCCUGTTGACTCAUGCAG
258685330	88342	GATGCTCATACUGTCAATACAAAAUCGAA	88343	GCCAAGGAUGGATATAGAAACAAAUGAC
258687897	88344	CTACTTTCTGGUACTGCTTCAUCACT	88345	GACACAAAACCAGAGUTAGAAATTGAUGT
258689379	88346	CTAGATGACAGUACAGGGCTAGUG	88347	TTGACTCUGAGGCCTGGAGUA
258706709	88348	TGACATCTTCCUCCTGTTTTTGAACTUT	88349	CATGCTGCAGAAAAGCUAAGATCAAAUA
258715494	88350	TGGGAAUGGCAAGCAGTAATTUCA	88351	CCAATCATUCGCATTCAGUCCAT
258728496	88352	GGCCACATCAUCCATTTCCCTUT	88353	GTGGAAAAAUAAGGAGCAGCATCTAUCT
258729776	88354	GTATGTTGCCUTACCTGTGTUGG	88355	AGGGCAGTUACTTGGGAAACTUG
258736567	88356	TGTTCTCTUGGGAGTTGGTAUCCT	88357	CAAGACATTCUAGGTTGTAGTUGAAGGT
258743804	88358	TTGTGUCCACAGGCTCATTCUC	88359	GTCTTCATGCAAAUCAGCAAGAAUAGAA
258749617	88360	GTCTCTTAUGCAGGCACTGAACUT	88361	AAGCAGAAGTCUAGAAGGGTGGUA
258761299	88362	AGCAGGTUGTGTTTGTTCUAAAAGAGA	88363	GCCAAACTAAAUGGTTACTTAGCTGUGT
258773859	88364	TGACTUGCAAAGACGGUGCT	88365	AGGCAGAACACUAAATCCTTTGGTAAUT
258783469	88366	CCCACACAUCCCACAAUGACT	88367	TCTAGCAATGUGAGCGTCCUG
258796578	88368	TTTCCTCATUCCGGCTCTTUAGG	88369	TCTCTCUAAAGAACCUCAGGGCAA
259126143	88370	GTCATCTTUAAGCCTCAGUGGGT	88371	ACGTGGCCAUCAAGATGAUCAA
259163945	88372	CATCTTCAGACAUGGAGCCTUCT	88373	CCAAAGAAUCACACCAAGACTTTATUGT
259664452	88374	GCTGGCTTUGTACCGGACUT	88375	ACAACACTCACUACCCTAGAAACUGA
260221995	88376	TCCCUCCAGAGCCCCTTUT	88377	GCACACUGGGAAACGCTUCT
260241491	88378	AGGAAAUGCUGGACAGCGT	88379	AAAAACTTGGGCCUTCATGTCAAUG
260285074	88380	GGATGAGCCAAAGAUGACCAAGUT	88381	TCCCCTTTGCUGATGTGAAAAGUT
260331512	88382	CACCTTCUGGGCCCAATCUC	88383	TGGCAATGCUAACCATCTTTAACATCUA
260341866	88384	AGCCAGCACAUTGTCACAGAUA	88385	TCCACUCTCTCAGUGACAGCA
260379124	88386	CCTGTTCCATUGGGTCTCCATUT	88387	AGATGCTUCAGGATGGACAUGAG
260390550	88388	ACAAGAAAGUCATTGTTTUCACAAGCAA	88389	CGTTAAAGGACUTTGCAAUCAAGCC
260397183	88390	GTGGCCUGCAGTCCTACTAUG	88391	CACCACCUGGGAACACCUG
260403479	88392	GCCCAGUGAGGAGTAAACUGAA	88393	TGGCTTAGGUCACGGUGAAAC
260410323	88394	CCTGTCCCAGCAUGGAAGTAUC	88395	GTAACTTCTTTCCUGCCTTCTTCTTUCT
260464926	88396	GAAGTAAATGATUCGCTTGGCTUGT	88397	TGAGGTTTCTTUTGTTCCTGTGUCA
260467679	88398	GGGAAGAGGCUGTAAAAAUCACA	88399	CUGGCCCGGAAGACAUCT
260488279	88400	ACCAGCUCAGAGCTCAGAUCAT	88401	CCUGTUGCGGACACCGA
260496390	88402	GCAGAUGCCAACGCUACCT	88403	CAGCCAUTCGCTCUGAGACA
260537218	88404	TCACTATTCCUCTTTAACTTCUCGGACT	88405	GCTGCCAACAUGTCTGATGTAUCT
260545990	88406	CGGACTAACCAGUTCATCCAUGAT	88407	CCAGCAAATUGTTTATTTCTCUGAAGGA
260579401	88408	GCCCCAGGUCGTATGTTTCUT	88409	AGTTCTTTGUCTTCCAGCGUCAG
260590774	88410	CAGCCGACGACCUTGTTUT	88411	CGGGUCAGCCCTGGTUC
260595572	88412	GTGTCCUCGCCGGTUCA	88413	TGAGUGUGGACCCCCGAA
260627711	88414	GTTCCCAGGGAGGUTATATUCAAAAGAA	88415	CGUTTCCTTTTAUGGCAGAGGCT
260644344	88416	CAGTTTCUGCAGATGGCTCUGT	88417	TGGAGAACCUGAGGGTAGAUGG
260669812	88418	ACATCTTGUGAAAAGACAAAGACCACUA	88419	CAAACCTCACAUGGTATGGCAUC
260714479	88420	TCTCUGGAAAGACCACGGTGUAT	88421	AGGATGGAGACCUTCAGCTTCUT
260714778	88422	ACUGCGGGAGGGUGGAT	88423	GGGACTUGACCGCUGAGG
260716363	88424	CTGCTCCAGUGTGCATUGT	88425	GGUGGCACUCACCACACC
260752233	88426	GGGUGGCCATUAACACACAAT	88427	CCACCTUGCATGGGTACUCAC
260756130	88428	CAGCUGCTCTGCUCGGAT	88429	CAGGCCCGGUTCTGGTTAUAAAA
260772398	88430	CAAAAGCCGAGCUGTGCAUC	88431	ATTUCCCACAGGGACACGUT
260795354	88432	CATGGTCGCUTGCTTGGAUG	88433	AGTGACTGAACUGTGCTGGTUT
260795918	88434	CCCAGGUGACAAGCTCACTUA	88435	GGTCATCUAGACCCCAACACTUAC
260824106	88436	GTTUGGTAAAGAAGCUGAAGGAGAAAAA	88437	AATCTGCCACCAUAGAGGGTAUAGAA
260933423	88438	CCTTACTGTUGCCCACCCTUT	88439	GGGTGACAGUGCTTAUAAACGAAGA
260940878	88440	GCAGCUCAGCCAACTCTTUG	88441	CACTTCAAAUGCACTGTTAACATTUCCT
260961762	88442	GCTGCGCUACAACGUGT	88443	GCUCCGCCGCACTUACC
260964772	88444	CGGCAAGCUCGTGCUCT	88445	TCCCCGCCCUCUCCAAA
260967304	88446	CTCCCCUAGACUGAGACCGT	88447	CGGGTCACCUTGTTGATGAUG
260973611	88448	GGAGUCAGCAGCAGGGUT	88449	CCGGCUGAGGTGTUCCA
260975900	88450	AGGAUCCGCATGACUGCAC	88451	GGGTGACUCAAGTCATGGUGAT
260993146	88452	AGCAAGCUCTTCTUGGAAAACCT	88453	ACTCTUGAGAGAGGTGCCUCAT
261007470	88454	CTTCAACGUACCCAACCCUCAT	88455	GGTGAGCCGAAGGUTCACTUAC
261007968	88456	TGUCACCGGGACAAGAACUG	88457	CTTGGTCTTUAGGAGCATCUGAGA
261054286	88458	GCCCCCUGCCCTGATUG	88459	CTTGTTCUGCAGCGGTGUG
261070779	88460	GTACAGCCAGUGTGUCCGA	88461	GCAAAAGTGGUCCTCTCTGAAUCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
261072067	88462	CTCTGCUCCGGTTTGGGAUAT	88463	CTCTGGAGACAUATAGAGTGGTGUG
261080083	88464	GGAAGGGAAAGAAUGACTGAUGGAAT	88465	CTGGGAACCCUGATGACUCAC
261096127	88466	GCUCAACACGCACTATGUGG	88467	CGTUAAACCACTGCUCGAAGGT
261103039	88468	GCUGCCCACCATCTUCAAGAG	88469	AGCTGGTGCUCAACACGUT
261106648	88470	AAACAAATGCCCUGTTGGTAGTUA	88471	GCAGTTUCAGACACACAGUCAGG
261119226	88472	AGTAGAATGTTACCAAGAUTATTTTTGACCUA	88473	CCGTGCACUCCTGTTCUGA
261120733	88474	CCACAACAAGCCCAUAACTUACC	88475	ACAGGAATTUCAGGACAGTATAGCUCT
261131852	88476	GTCATAGGTTUGGAACCCGTUCT	88477	AGTAAGAGACCCUAGGGCUCAC
261136969	88478	TGGTGCUGACATCCAUCAAAGG	88479	CTGACCAGCUGAAAGATGCTUG
261158262	88480	CACATAGGCCUGCATGGGAUAA	88481	GGAAGTTGTTUGAGCAAGAGGUG
261162984	88482	CAUGAACAGACCAUAAAGCAGAAAAGAA	88483	CTGTCAGTGUACAGCAGCAGUA
261167079	88484	GGAGGCCTUGTCACCATCCUA	88485	ACCTTGTGTGUTGACTCCACTUAC
261174156	88486	GCACCCCUCCCTTCTATGCUA	88487	GAACAGAGAUAGAGGGAGACAGATTUCT
261184968	88488	GTTTCTGAGCCUCCCGTUGA	88489	TTTGATTGUGTCTATGATTUAGGGAGCA
261192714	88490	GCUTGAGACTGUGCAGGAGAG	88491	TGGCCCAGAGUGATGGTGUA
261203560	88492	CCTCATCATCAUACCCTTCAACAUCC	88493	GCCTCTGTATTUCAAGATGAGAGCAAUT
261212029	88494	CATTGUGCGCACCACAUCAAT	88495	CAGAAGGAUGAUAAAGAGCCACAGG
261230442	88496	CAACGCTGGAGUCTTGGTGUA	88497	TCTCCTGCUCCTTATGATCAUGCT
261242926	88498	GCTCCUCACAGCTCCCAUAAC	88499	TGGAAUAAGACCCAAACAACCCUT
261244802	88500	GTTCCTGUCACTGTCTTCTUCACT	88501	GCCAUGAAGGGCAAGTGTCUC
261245009	88502	TTTGAATCCAUCCCTGUGCGT	88503	TTTATTUACCGCCTTTTCUGGAAGAGT
261250832	88504	GCAGUGGAAATAUCCAAGACAGACA	88505	GAATTAGAAAGCCUGGACCCAAUGA
261261263	88506	GGTTCUGTAGAATGUCCCACCA	88507	GCATCATCCCUTTGCTGGTUAC
261265676	88508	CACCCAGCAUATCAUACCACAGT	88509	GCTGATGAUGAAATCACGATGAUGG
261271903	88510	TCTGAAUGGGAAGGAAAGGCTTTUT	88511	CCTAACUCCAGAAGGGCCAATAUG
261281126	88512	CATCCTCAGAUTCTGCCTGUGT	88513	GACCAAGATGCUATTACCTGTGUGT
261293407	88514	GAATCCTUCACCACACCCUGT	88515	CCCAGAAGAAGAAAAUGAGGAAGATTUC
261293654	88516	GGTATCATACAUATCAGGAGGCUGAGA	88517	TTGUGAACATCTGTUACCAGACAAT
261296169	88518	CACUGATGTUGCCGAAAAGGAT	88519	CTGTTGTTTTAUTTCCGGTTTAUGCGA
261297042	88520	GGCGGTAAAUAAAAACCTGTAGAAAGUC	88521	ACAAGACAGGGUTACTATATUCGGGAA
261317962	88522	GGGAAAAUTTGGACUCCACAGGAA	88523	AGCAGAUCCAGGAGGUGGAAT
261340568	88524	GCAAGATGATGUCTTCTCCACTTUCAG	88525	CCTTTACCACUCGGATTATGAUGAAGAT
261345239	88526	TGTTCTCCUGAAGCATGCUGAAG	88527	AUGCTGGGAGUGACGAAGAAG
261354776	88528	GCTGTCCGAGUCTGACAUGAT	88529	CCCCCGCCUTTATTCAGCUT
261356293	88530	TGGCCAACCACAAAAAUATCCACUAA	88531	CCAATTACUGCAGGCACTUGAGA
261360222	88532	CTCAAGTTGAGUCAAATGCTCATCAUAC	88533	AAGTATCAGAGUCGGGAGAGTTTTCUA
261379135	88534	CAGCGTGAACUTCATCATCAATCTUC	88535	TGTGCTTATTAUAGCATGATAGCUGCAA
261400233	88536	ACUGGAGCACGAAAAAGGTUGT	88537	GCATGGCAACCAAGAUAAAGAACTAUT
261402290	88538	ACTGTTGGCAAGAAUAAGGTTTACAUCA	88539	AGTTCCAGATUCTTGGCCATTUCAT
261403500	88540	GCCAGCAUCCTTCAGTCGUT	88541	CTAAAGCTCUGCGCTGACTUC
261407053	88542	CTGGCTGACUTCTGATTCTACUGAG	88543	CAGAATTTCGACCUGGAAAAGTGUT
261420334	88544	CAGCTGGAUAGCAGAGAAAGGAUT	88545	TGAAGAGGAAGGAACUGUACAACAAC
261422429	88546	CAATGTCTTCACAAUCAGCATCATAGUC	88547	ATGAAGGGUGGATTAGGAGUACAGAA
261447187	88548	CCTCAUACAGGACACTGGCTUC	88549	GCTGGGUGAGGAAGACTCUGAT
261451075	88550	TCTATAGCTGGAAAAGUCATTCCTCUCA	88551	GGTCGCGGAUCTTCTTCUCC
261455594	88552	TTGGAGATGTTCTUACGTATGGTCTCUA	88553	TCACCCAGAAAAUGATGGCAGUT
261469284	88554	AGACTCUGACAGACGCUGAGAT	88555	CTGTCUCAGAGACCAUGGGAGA
261471352	88556	GGUCCAAAAAGATGUAGGAAGCGT	88557	AGAUGGGACCUCAGGAAGCA
261471365	88558	GGCCCCAGACCCAUTATTTTAAUGA	88559	TCCACUATTCGGUGAAAACCAACAA
261484241	88560	CACTCACCUGCTGTTTTGTACUC	88561	ACTATTGUGGCAGACAAATGTGUGAA
261493209	88562	CTCATTGATGUCTGAATAGTCUACAGCA	88563	TTGGATGATGAGUGTAAGAAGCACUT
261498793	88564	TGTACTCTUGTTGGTTTUCACCGA	88565	ACACACACAACUGGAGCAGAUG
261502879	88566	ACCAACGCCCUCUGCAT	88567	GGUCTCGTUGGGCCAGT
261505861	88568	CAGGUGGTGAGAUGCCAGAAA	88569	TGACUTCUACGACAGACAGCAC
261508003	88570	CCAGTTGTGTGUGTCTTTCTTTATCUGA	88571	AGGATGAAATTUAATTTTCTCTCCAUCCAGT
261518628	88572	CAGACCUTCCGGGUGGAAC	88573	TGAAGAGCGAGCACCUCATTUC
261541258	88574	CCGTGAGUTCAGTGATUAGGCT	88575	CATCTGGAGGUGGCCCATTUA
261562283	88576	CCTACAGCGAUGCCTGUGAA	88577	CTGATTTCCUTTTCGGTGUGAGAC
261578668	88578	TTACTTCATTTCACAUTCAAAATGATAGCUACA	88579	CTTGGCUGAATGGAAAUAGAGAAGAAGA
261631832	88580	ACCCTGTCCCUCTGATGTCUT	88581	GAATTTCAAUCCAGCAAGGTGTTTCTUT
261660527	88582	GGTGTAACCAUTGGGCGGAUAC	88583	TCTATAAGUGCCAGCACAUCAGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
261669586	88584	TGCGGAGATUCTCTTCCTCUGT	88585	AATGGGACAGGUAGGACCUGAT
261679091	88586	CGGATUACCCAAGACAGAGCAUC	88587	TUAAGGGCCCCAACGGUAAAA
261686408	88588	ACAGAAGATAGCUCATGACTCCTGUT	88589	GGACTTGCTUGATTCCACCCTUAC
261728092	88590	GGGATGUGATGAGAGGUGGAT	88591	CCATCCTCACCAUCATCACACUG
261731104	88592	GTGAAATAACAGCUTCGTAAGTGCTTUA	88593	GACTGGAAGAACAAAUGAATGGCTUAAAA
261746128	88594	GGCTCCUGACCTGGAGTCUT	88595	CTCATCTUGGGCCTGTGTTAUCT
261746947	88596	AACGAAATTGTGUAAGGATCATGTCUCT	88597	CCATCCAACTCUGGGTGTAGATUG
261778873	88598	TCTAGGUGGCTGGUCGGA	88599	AGGTGATACAACUCGTTCGTAGTGAUA
261793303	88600	GGTCTGTTTUCAGTGACCTTGGUT	88601	GCGAGCUCTCTUCAAACGGA
261794479	88602	AAAATGTGATAGUGTCTGTGTGAAUCCA	88603	TCGCGGGCTAUCTTCCAAATTTATAAUT
261797677	88604	GGAATCTUACCCAGCCGGUT	88605	GGCCCTCTTUATAGCTTGTCCUT
261797703	88606	AATCTAACAGAUGCCAGCAAUAACCA	88607	AGGCAAACUGGTGGAAGGUC
261802015	88608	CTGCAGCTGUCCTCTGAAAGAUA	88609	GAAAGACCACCUTCTTTUGGAACAG
261803704	88610	CCAACGCACACUCTCTCCUC	88611	GCTAAGGCCUATGCCATCUCA
261810380	88612	AGACTGGATGAUGCAATCCATGUG	88613	CTGAUCGACTGCTUGCAACAA
261810639	88614	AAATTTUGGAGAAGGGAAGUCGGAA	88615	GGTGGAUGAACGTGTCCAUACC
261814797	88616	GGAGGGCGAGCUGATGUC	88617	GAGUCCAGCACCTCCTUCAC
261816662	88618	GCCTGGAGTTUGACATCCTCTAGAUAT	88619	CGCCTAUCGGAAAGAGCUAGAA
261827469	88620	GGGAAGGCUCTUACGGCAA	88621	ACCCCAGCAAGCCAUACTUAC
261829633	88622	CUCTUCCACGAAAGCGCAAA	88623	GTTGACCACUTGTUCCCCAAGA
261842869	88624	GTCATTGAAAGGGUATTGAATCUAAACAC	88625	GCCCCAAAACAUCTCTGTCACUT
261844125	88626	CAGATTTTAACCCCUGTACCTGTTUCA	88627	TTTAGTUCTTGGCTAGUGAACAACACT
261850969	88628	CACCGGUGTGGCTCTTUAAC	88629	GCTGTCCGUCAACATUGAGAGA
261867178	88630	GCAGCAACUTCACGAGCAUT	88631	GATGGGAGTCTGUACAGCTTAAAGATUT
261882862	88632	GTGCTTTCUCACCATGTTTCTTUGT	88633	GCATTTTAACCCAGUGCTGAGATGTUA
261889368	88634	CATGGCGTUTATCCAGAATUAGCAAAT	88635	CACAAGCAUCGGTAACTUGACAAAAA
261917790	88636	CATCCAGAAUGCCATGCTTUAACT	88637	GAAAGGCGACGUTTTTGTGUG
261929876	88638	CAGAUGAGCCUCACGCACAT	88639	GGGCAAGUAGAGATGGAACCCUA
261942226	88640	GAGATAUCCGTCCCATUCAGCAG	88641	TGTTGAGGUGCAGATGTGATTUGT
261949816	88642	CCGTGGCAUTTAGTCGUGAG	88643	CCUGAAAAGACUGCCCCCAAA
261953775	88644	GAGAGCAGGCACACUAGTUGA	88645	CCCCTGTGTTCUTCTCTTCCATTTUAG
261955270	88646	CGGCUGACCCCAAGGTAUG	88647	CAACTTCCTTUCCTCCCCTGUG
261976420	88648	AGACUTTTCCUCACCCCCAAAG	88649	TCCAGTCCCAUTTGGACATTAUGAG
261992674	88650	GGCTATTTTCCCUAGTCTTCTCATUCAA	88651	AGCAGAAAGATTUGGAGATACAAGCUC
261992705	88652	CCTGTCTGAGUAGATCTCTGTGAGTUT	88653	GTGAAGGAATAUGCATTACCAATAGGUG
261996895	88654	AGGCAAGGGUCTCCTAUACACA	88655	GCCTGGAGUCCAGTTACAAUGAT
261998692	88656	GCATGCGGGUTGTTGUGT	88657	GGGCCAAGCCCUACAACUG
262000221	88658	TGGGAAGTUGAAGAAATTCTAGCAUGAA	88659	GAGCGAGAACUGGAGATTAAACTTCUAA
262002097	88660	TTCATCTTTGGACAACUGATCAATCUGT	88661	GCATGATUTATCTAAAGCUGAAACGGAA
262004398	88662	AGGCCTUCTGGCAGUAGGAA	88663	GGCAGGAUCCACTCCAAGAUG
262016396	88664	GGCTTGATGGUCTCCGTGUG	88665	CATCCGUCAAGCAACGTCATUT
262019467	88666	AUTTAAAGCACACAUACACACACAAAC	88667	GGCTATTGUAGCAGCAAAGUCAAAAA
262026988	88668	GGGCAGAUAGCTGAGCATTUC	88669	CACATTCCCCUCCCAAATTCTTCUAA
262027693	88670	GCAGCCCCGUCTGTGUC	88671	GGCTCUGAGCCACACUCA
262030444	88672	GCATGATCUGGGAAGCGCAUA	88673	CTCAAATTGUAGAAGGAGTGTGATUCCA
262033805	88674	CAGGCATAUGCTGGTCCCTUT	88675	ACCAUCATGAACUGCACAAGGA
262040681	88676	CCCTACUCTGGGCUAACGCT	88677	AACTCTGTACCTUTTCCTCTTTTCGUT
262042257	88678	GACTCUGCAGCAGCUGGA	88679	CCATCUGGAGCCCCAAGATUAT
262048751	88680	GCCAGGGCAUCUCCCAAT	88681	CCAAAGGGCUGCACCUAC
262053097	88682	AACAGATATTUACCAGCTAAGTGUGCAA	88683	GGAACAGACUGTGCAACTUCAGT
262053249	88684	CTTGAAGAACAAGUGGATTGGUGAAAT	88685	GTAGCCCTUGGCTCTGACAUC
262063828	88686	CGCTTTGTGACUTAACTTTTTACAGUGA	88687	CCTCCCCTACUAGAAAACTCTGUACC
262063993	88688	ACCTGAAAACAGGAACUGATTTTACUGT	88689	CTTGTCTTUCAGGAGCTGTTUACCT
262064950	88690	CGTGAGGAGCAUGGTTGTTUG	88691	GCCAGATCTCUGTGCACAAAATUG
262065201	88692	ACCCATGGUAGCTGTCACTGUAT	88693	GCCAAAGUACATCTUGAGGCAAGT
262068915	88694	CCTGACGAAGUCGTGAAAGTUCA	88695	ATATTGAAATGATTGAAUTCCATGGTGAAUAC
262080378	88696	CCTTAACAGTCUGGTTAAACACCTCUT	88697	ACATAAGCAUCAGTGGCUGCAT
262084495	88698	TCAAUGCCAUGGAAGGGAAGAAA	88699	GAAGAGCCUCCTTCTGTTUCGT
262086869	88700	TCTCACUGAGGACCAGAAACUGT	88701	AAATATTTTGGTAGAGUTTCTGCCACUA
262093424	88702	AGCACCCAAUGAAGAGCAAGUT	88703	CAGGTTATTTGCCUTTTCCCTTGUT
262096080	88704	CCTGTCTACGUTCCCTCACUGT	88705	CTTGGUCCAGACCCAGGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
262109848	88706	CGTCCGAACUGCCGUCAA	88707	CACCAAGCUTTCCTGGCTUC
262112505	88708	CCCACGUACCTUAGGACAGG	88709	CAGCTAATCAUCCCTGGTTTUCCA
262117124	88710	CCACTTGCCAACUTACCCAGUA	88711	GGTGUACACAGTGUCCACCAA
262123737	88712	GTCTGCAGCUCCCGUGAA	88713	GGGCCCCAUCATGCUGT
262126135	88714	GGAACTGGCAUCGCCAUGA	88715	GGACCCGACAAAACCUAAAGAUGG
262127475	88716	CCUTCCCCUGGAGCCAT	88717	GGATCCCUACCTTGTGCATCUG
262130001	88718	GGGUACCCUCAGGACAACAT	88719	ACACCUCCAACAAGAAGGCUT
262138043	88720	ACTGUAGGCAGGATATUCCAGCA	88721	GACUTTAUACAGCCCCGCAGAA
262141959	88722	CTGTTTCUCTTGCAGGUGAGACT	88723	CAGAAACCTGGUCACCCTACUC
262143308	88724	TGTGCACACCAUACCUCCA	88725	TGTGUCCAGACCGTCCTAUGT
262143870	88726	GGCAUGAAGTACTUGGAGGAGAG	88727	CTGCTGCTCUGAATATTAGCTAAGTUGT
262162995	88728	GTCTCTCATCUGACTTTAGGCGUT	88729	GAAAGCAGTUGCATTGTACTTUGAAGAT
262165652	88730	CTAGGTATGTGUGCCATTTACACUGT	88731	CTCCCTCAGUGATGTCTTTUCAACT
262166401	88732	GAGGGCCUCAGCACUGG	88733	CTCACCGGAGUCATTGUAGACA
262168487	88734	CTGTCATTCAAGUGAACAGAGGACUT	88735	AAACAGCTAGUGAACCACCATTTAUCA
262174235	88736	TCGGAAAAUGTACTCAGUGAAGGG	88737	CATCTTCTCUGTTGAGCCAUCCAT
262175904	88738	GGCAACGACUTTGTGUCCAT	88739	CTCCTCGUGACCGAAGCUC
262185555	88740	CAAGCUCTTUGCACCGACAA	88741	CCCCTTCATUCCCAGATTTTTCACUAT
262194042	88742	GATTCCCCAUGGTTTCTACTGGUT	88743	GCCUTCAGTTGAAUAGGCACAGG
262196327	88744	CTCCCGCCGCUGCTAAAUA	88745	ATGCTTATUCCCCCAGGCAUAAAT
262197189	88746	CCTTCUCAAGGAGCGTCUGT	88747	TCACGUCCCCACTCCCUT
262203681	88748	TTGGTGAAAAAGAUACGACACTGUCA	88749	GTAGGAAGACCCAGAUTTCTTTCCAUT
262204318	88750	CATCTGGGACUCATGCCTUCA	88751	GGUGGAATTTAGGUGGAACAAACCT
262212932	88752	GUATATAGCAUCCAACCGAAGGCA	88753	CTACCTGTCUGCAAATTGTGTTGTUT
262215139	88754	CAGAGGCAGCAGCUCTTGAUA	88755	TGAACTCACTGUGCTCTGTGTUG
262248491	88756	CGGTAGAACCAACUCATTCTAAATGCUT	88757	TGGTAGGTAUCACAGGTGAGUCAT
262251545	88758	ATTTTGTTAACACCCCAUTTTCATGCUT	88759	CTCTACCTGUGCCTCTACTTTUCAG
262255709	88760	GGCCTAAGUTTGTCCCTUAAGGAA	88761	CCTGCGGTTAUGGTCATTATCAAAAUC
262255776	88762	CACCTGCUAGAGACCACUGAG	88763	TCCACAGTGTCUTTCTCCCCATUA
262260924	88764	TCCTCAGACAUCCTCGUCCAG	88765	AAAGACCATTTUGATGAGGCTGUAGT
262269542	88766	GGAGAGGTTUCATGCCTGGAUT	88767	GTTTTGTCCAGGUAGTTATGGUAAGAGAT
262270242	88768	CGGCTGCCUACTCAGATCUCT	88769	CACCUCATCUAACACCACCACA
262271608	88770	ACTTTGUGCCAGGGACTTAAGUT	88771	GACTTGGCGAAUGTCAGCTTTAUT
262276465	88772	GGAACAACUGCAGACATGATCTACUC	88773	GCTGGCCAUCCACCATAUGAT
262283259	88774	GGAAGGACCUGCAGCAGUA	88775	GGCCCAGUTGGAGAUGCC
262285544	88776	TCAATATACUCACCTGCCUCGACT	88777	GTGACCGGUAGGTAGAATTCCAAAUAT
262290081	88778	AATTCTUCGGGCTTCGUGACT	88779	CCAGAAAGAUGTCCAAAGCTUGGAT
262293123	88780	GCAUGGAAACAGGCAAGAUGGT	88781	TGACAAUCAGGCGGAAGTUGG
262296591	88782	GCAAAGCCUTCACAGACCUCA	88783	CCGGATCACUCAAGCAATAACTUC
262298381	88784	GGTTCCAGUGCTGACAGCATUA	88785	GGCAGAAACUCGTTTATGAGAAAAAUGT
262299624	88786	GGGUAGAAGGGCUGGACGA	88787	GGGAUGCCCUCGGCAAA
262303185	88788	GUTCTCTAAAAACCUAACCCAGGACAAA	88789	CAAGTACAUCACAGACTGTTUCCAC
262303528	88790	ACCATAGCTTTUGGAATGGGCAUT	88791	GTGACAAGAACUTTGAAGTCCAUCAC
262306715	88792	GGGCTTUCCTCTGCTTUGGA	88793	CTTATAAAGAGGAGAGUGGGAGTGAUGA
262310223	88794	TCAAUAACAGGTACUGGAGCAGGA	88795	GCTGATTTAUGAAAGCCAACAAAGCAUT
262310836	88796	CCACUGGAGAGCTCAAAAUCAGAG	88797	CCUCCAGCGAGGAAGAUGAG
262312386	88798	CACAAAAAGGUCGGCTUCGT	88799	CAAAGTACCCUTGGACUCGGT
262312722	88800	GGUGTCCUAGAGCGGAGAGT	88801	TTTCCUAACGCGCCCUACC
262314705	88802	GTTGCCTTCUCCTGCTTGUCT	88803	AAACCUTTGCUAAGGGCACCT
262315530	88804	CAGGAGATTGGUAGAGCTGGUC	88805	GGATACTGGAAAUAGCCTCAAACACTUT
262318506	88806	GTTATGGCATTAUTTAGCATCACTTUGCAT	88807	CACAGGAGGAGGCUTCATTTUAGAA
262319133	88808	GAATAGCGGGCUGGCUCT	88809	CCTGAGCGCCUTCACUGT
262322666	88810	CCTGGTTGAUGAACAACTTTTCCAATUT	88811	ACAGGCTTACCUACTTCAATTGTUGAC
262322849	88812	CAGCCTGTCUAGTCAGCAGUAA	88813	GGAGAAAGAUGGCCTCCUGAAAAA
262325189	88814	AGUGAACUGGCCGGAAAAGT	88815	CGGCTUACGGGTCGTUGG
262327650	88816	GCTCCTGTTUGATGAAGGAGUGA	88817	CTGTGCCCUGCCTGUGA
262327761	88818	GCACGUCGGAGCCCAUT	88819	GUGCCUACAGCAGCCAGA
262327837	88820	GCCACUGACAACCACCCTUAA	88821	CGTGTGGAGUATTTGGAUGACAGAAA
262329174	88822	CTCCCTTGTUCCTCTTCCCTTUG	88823	CCAAGGAAAGAUTGACUGCGGAT
262331143	88824	GCGTCAAAUGTCGGGTUCAC	88825	CCAGCACCGUGTTGATAUCCA
262331865	88826	GGAACTTCAGUGGCAAGGAUGA	88827	CCTTCUGAGAAGGCCCAAAGAUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
262337816	88828	AGCTGTAUCAAAGAAGTCCTGTGUG	88829	CGTCTCCTCCAUACTAACCCTGUAG
262345739	88830	GAAGTTTCUGAGGAGCCTCCUG	88831	TTCTCTAGCTGGUGACTTAACCCTAUT
262347540	88832	ACCACCACACUATGTCGAAAAGUG	88833	AGGCCTCUGATTCCTCACUGAT
262349949	88834	CCAGAGUACACAGGAAAUCCCA	88835	TCTCTGAAUCAAGGAGTCTCCTGUT
262352475	88836	CCAUGCAGCTGAUCAAACAGAA	88837	AATAATCTCCGGCUGCTGGUC
262353292	88838	CCUATAATATCAGCUGCACAGCCT	88839	TTCTGGCAAACUTACATCCATTGUAGT
262367284	88840	TCTCTTTUGGTTGTTCAUGGAGCAT	88841	GCGATTATACAUCAGGAAGUAAACAAACC
262367434	88842	CTTACGAAGGAAGGUCTTUGGCA	88843	TTTCAGTTCUTCTCGGTGUCCAAAT
262372888	88844	CTGCATGCUGTTTTCTCUGAAACC	88845	AAAGTTACTTTGGUTCTTTTGCTGCUT
262375644	88846	CTGCTTCUGCTTTTTCTTCTUCAAGT	88847	CTATATTCTGGCUGGTCTGTATCTTUCA
262377757	88848	CCGTTTGGAGUCAGCTGGTUT	88849	TGTAGAGCTTUTCAGCAACGUCA
262379084	88850	CCGGCUGGAGAAGCACTAUC	88851	CGAGTGGUAGCCGAUGAAGAC
262386513	88852	CATGGAGCUGACAGGTGTCUA	88853	CAGGTUGCACTCGTAGUCCAG
262389373	88854	AGATCCUGCAGCAGACATTCTUC	88855	GUTCTGCAGGTUGAGAAGCAAC
262389934	88856	TGTCCACGUGATCGUCACC	88857	GCUCTUGGCGCCACACT
262401572	88858	AGCTATGTGUTATACCCCCUCCA	88859	GGGCAAUCCCCAAAGGUACAG
262401646	88860	CCTGGACAGUCAGCACCAUC	88861	AGUATCCGTUGGCCAGCAA
262402238	88862	GGTAACAAGGGUCGTTCUGGT	88863	AGTGGUCCAGAACGTCCAGUA
262402469	88864	GGTCCACUGCCCCCTGUA	88865	GGCAGTGGUCCAGAACGUC
262404898	88866	GCCCAGCUCCGGGAAUG	88867	CCTCCAUCCTGCCTGUCCT
262410295	88868	AGCUATCATGCUGACCCAAAACA	88869	CCAGTTACTCUATGAGCGTTTUAAGAGG
262420854	88870	GGCACAAAUACAGCCCCUCT	88871	CAGTTCAGCAGGAUCGATTUGG
262430759	88872	TCCCACAACTCUTTCATGTGTTTAAUCT	88873	CAAGCAAGGGAAAAUGCCAUGT
262431796	88874	AGATCAAAGUAACATGGCATTTUCCCT	88875	GUGAGCTUCAGGACAGAAAGAAAGT
262432715	88876	TGTGGGACUTTGGACAACUGAG	88877	CTGACAAAGCUGCACTCATCUT
262433061	88878	TGGTTTTGATUCCAAATGCACATUCAT	88879	GCUGCAAAACCAAAGATUCAGACA
262437218	88880	GGGACAGGAAACUCAGGGUCT	88881	GGGTGACCCAUAACTCTCTCUGT
262438602	88882	CTTCACCAGAAGGUGTCUGAGG	88883	CCTGAAGGAAAUCTGCAAAGGAGUT
262446132	88884	CUTTGATCACCTUGCGGAGGA	88885	CACCCUCCCTCTGCTTUACAAT
262446282	88886	GACGTCCUCCAAGGCUAGG	88887	AGCCGTGUTCGTGCTGUT
262448152	88888	CGCACCUGAGCAGCUGA	88889	CCGGGCGUCATGTCUCAT
262449287	88890	GCCAUCCCGAGCTGGTUC	88891	GCGCAGUGCTAGCUCCAT
262451759	88892	CUGGAGACCCAGCCTTTUCT	88893	CCTTTCAAAACCUATACCCAAGTCUGAT
262454104	88894	GGGTTGCTATCGUTCAAAGTACAGTAUA	88895	TCACCACACCAAGAUAAACTCATGUC
262455562	88896	GCAGAGGUGTTGCTCAGAUGT	88897	TCCCAACAGAAUCTTAAACTTCTCCTUC
262464947	88898	CTACCTTTUGAACAAGGTGTCTGUAAAC	88899	GACGAGGGUCATCATATTCUAAGCAT
262467588	88900	CCCTGCTCUACCTCCACTCUA	88901	GGACACTTUAGCTGTGAAUGAAAAGAAA
262468359	88902	GTAGATTTAUAACGGGAAGCACTACUGT	88903	ACTTAGAGAUGGAAAGAAGAGGCAAGUA
262477106	88904	GGAATAATCCACAGUCATAACTGGCAUA	88905	GCATGCTTTCAUCAAATGGATTUCAGAA
262478576	88906	CAAGGCCAGCAAAGGUAGTUT	88907	GCATGACCUCTCTCTCTGTTUCA
262481083	88908	GGGAGAACAACAUCTTTTAATTGCTUCA	88909	TTCCTCTTCTUACAGAGACCUAAGGAC
262487350	88910	CGCCCATCTUTGTGAGATACCUA	88911	CCTTCCCCCUATGAGAUGGAGAT
262487797	88912	CCCTGCUGCCTCTCCUT	88913	CGCTGGCUGGCATCCUT
262489980	88914	CCAACAAGCAAAGAUTCAGGCUT	88915	CAAAGACACAGGUAGCTCACUCA
262501849	88916	CACTCTCTATTUCCTGCCTCCTTTUT	88917	GTGCAAGCACCUGAAAUAAGCA
262505892	88918	CACAGCTAAAGUGTCCTTAATGGAATUG	88919	ACAAGTACCAGAUTCCCTAACAGAUGA
262508669	88920	GGGCAGACUCACCATCAGUA	88921	GGATCTTGTGAUCTGCCCGTUC
262511146	88922	ACCTCUGCCCCCTCCTUT	88923	GGCTGUCCGCTCAGAGUG
262516884	88924	TCCAAGTCTTTTUCTTTGCACCTACUAA	88925	GGGCAGAAUCTGATTUGGCA
262516899	88926	TCAGAUTCUGCCCCAGGAGAT	88927	TCCGAATTTAUAACACATGATAGCCAUGA
262517465	88928	CTGCCCCAGGAGAUCCATTTATATTUAA	88929	GCTAGATGAATUGCCTATTTTTAAGUCCGA
262518096	88930	AGAACUCAGAGGGCCUGGA	88931	CGAGGGCUGTGTCCATGUG
262530648	88932	TGCCCAATUCCACCCTUGAC	88933	GCAGAATAGGTUTCTCACTGCACUT
262533692	88934	CACCACCCCUTCTAATTGTGTUACA	88935	AGCAATGCAUCAACCAATAACCATTTUT
262539419	88936	TCTTGGACTTGUAACATCTAATGGACTUC	88937	TGGCTAGAUTCTTCTUGGGCAAAA
262540959	88938	GGTCTAAATACUAGTGAGTTTTCGGUGT	88939	GAATGGACGGCCUTCCTUCA
262550671	88940	AGAUTGAATAUGAACACAGAGCACCA	88941	GCTGTCCUCAGCCCAACTUA
262553226	88942	CCTGCCAUGCTACCTAGAUACC	88943	GCACTGGCCUGAACTGTUGAA
262556941	88944	GAAGGTATAGUGGAGTAGGGUAAGCA	88945	GAAATAGGUCAGAAAACCAGTGTCUCT
262560298	88946	GGAGTATCACUTTGCTTTTCATUGCC	88947	GACCAATGTUCAAAGGTGTUGCT
262562639	88948	CAATCAUGGGAGCCGAAAUGG	88949	TGAAATAGGATUAGGATCAGGACUGAACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
262573009	88950	AGCTTCCTUGCTTTAAGTUGCCT	88951	CATCTTGGAAGCAUAAGCTCTCUCA
262577279	88952	GTGTAGGAGUCTGCCTGTTUGA	88953	TCTTTGGACACAAUTCTTCATTAGCTUGA
262578967	88954	GCCAGACCUAAGAGCAAUCAGT	88955	GGCCATCUACAAGCAGUCACAG
262582706	88956	ATTCTGTCAGCAUTACTCTGTGUCC	88957	GGACUCGCCAGAGACATCTAUAAAAAT
262583639	88958	CCAGAATGAGGUGCAGAACAUCAA	88959	GATGTAGCTGUGCATGTCCUG
262585531	88960	CTGATTAAATCUGGCTGGTUCCAAAAC	88961	TCTGAAATTUCCCAGAATGCACUGA
262585883	88962	CCCACAUACCACACGTGCUC	88963	GCTACGAGAUCAAGGAGGACAUC
262586114	88964	CCAGTGUCCCCUCGGAGA	88965	TGCAUGGAGCAGAGGUGAAC
262587464	88966	GAGGAGAAGGAGGAUGCAGAUG	88967	CCAGCACGAGCGUATGGUA
262589944	88968	TTAGUAAAGAAGGCAAAAGAGGUGCT	88969	GACTGCCCTUGTTCTTTTACATTTUCA
262591353	88970	ACAGAATCUCAGAGCCTCAUCCT	88971	ACTTGTGAGAGGCCUATAAACTGGTAUA
262597423	88972	CCCUGGGAUGGAGGACAGAT	88973	GGAGCGACUTCTCCTCCUG
262597430	88974	GCCTTUGGGCAAAAATCGACUAGA	88975	ACTGTGCAGUCCATTTGAAAGTAACUAT
262601651	88976	AGAACAGCCGACCACUATAGUACA	88977	ACCACUCCAGAAACACACACTAAUT
262603904	88978	CTCTUCACAGAGGCUGAGCA	88979	CCCTTCCCUCTGGCTCTCUT
262604122	88980	GACTCTTTUCTGTTGCCTUGCAG	88981	TGGACUTTTCCTTGUACCCAACAA
262605694	88982	GTCCTTTCTAGUCGTCCTCAGUCT	88983	AGAGGAGCUGGACTTGCUCA
262608447	88984	CGTCATCGUCTGCTGCTGTUAT	88985	TTCAGAATTGCUGACAGAGCAUAGAA
262610068	88986	CCTCACAACCUCCGTCATGUG	88987	CAACTCTGTCUCCTTCCTCTTCCUA
262611399	88988	TCTGTGGACCUCTCCTUCCA	88989	AGCACTTUCCCCGUCCAG
262616247	88990	CAAAGATTACUGGGCAGTCAGGUT	88991	CAGGAGGACACUGAUAAAGCCA
262619219	88992	CCCGGUCACAGUCAGGGA	88993	TCTTGCCCCUGCGTGAUG
262623865	88994	CTCTCTCAAGUACAGATGATTGCTUGT	88995	TGGTGGTGTTUGAGTATTGTATGTCTUT
262624798	88996	CGAGGTUACACCATCUCCGACT	88997	CCGCAGGAGAGGUGUCA
262625807	88998	CGCTUGCACACTGAGUAGGAG	88999	CCACATTCUGTGTGCGTGUAG
262632891	89000	GGCCTTCCCCUCTCTTTCTATAGTAAUC	89001	GGCAGCUAGAAATTGCCTTGUT
262633509	89002	TCGAGTGGGAAUTCCTGGGUAA	89003	CAGUGACTGATUCCCCAGAGAG
262636340	89004	TCTATGGCTGTTATUCAGATATTTAAGTAGAUG	89005	TCAACAGTATGUGGGTTCAATUCCAAT
262646118	89006	TGGACTGGUATAGTCTTUCACGGA	89007	ACCTACTAGGGCUACTTCTTTGATTUCT
262658266	89008	CTCTCTGAGGUATTGTAATGCTTCAUCA	89009	AUACTCCAUGAACAGCCAAAAGAGAA
262661399	89010	CCAGAGACUTGTGGAGCTUCA	89011	ACATGUAAGGGAGAGCTUGGA
262664342	89012	GACTACAGUAGATGTGGTCAUGGG	89013	ACTAAAATCTCCTUTCACGTGATCAGUT
262672324	89014	GAAGAGAAUCTGGGUGACAGCA	89015	GTCAAAAGCTUGTAGAGTCTCTUCCT
262678224	89016	GUGGACACAAAACAAGAAAUCACAGT	89017	ACATGTTTAATGCCAUTTCTTACGGTTUG
262685175	89018	TCCTCTCCACCUAACCAGUGT	89019	CCTGAGAGTUAGTGCTGACUCC
262688650	89020	CCAUCAAGAGAUCGGCGGAAA	89021	ATCATGUGGACAAAATUGCCCAAAAT
262690411	89022	TTCACACTCCAUCATAAATCATCAUGCT	89023	CACTTGCTCCAAUGTTAATCTCCTAUCT
262690718	89024	AAGAAACGAACCAAAUCTCCAAAATTGUT	89025	TCCAATGTCTUGCCGAATTCTTCAAUAT
262691230	89026	GCCAGUGAGAAACTATCCTUGCT	89027	AAAGAGCUGGCAACCAAAGTUG
262692944	89028	CATATGCAUGGCCCCAATCUCA	89029	GGCCTTGGUGAAAATAGCAUAGAGG
262701792	89030	GTACACTGUTTACCAGCUGAAACAAAT	89031	CTCCCCTTGAGAUGATCACAACUC
262707280	89032	CAAGCATCCACAAAGUCACATGAAUAT	89033	CACTTCATTATTTCUTGGTGGCAACUG
262707737	89034	GTTGTTATTUCAGACCAAAACCTTGUGT	89035	GACTAATCUGGAAGGCCTUGCAT
262708254	89036	TCTTGACAATUGTTCCAATGATTUGCAT	89037	CAACATCTTCCUCAATTTGGGTAUGG
262724007	89038	GCTATGAGCTCUGTTGCTACTGAUAT	89039	TGGTTGATCACCUTCATTGTGTAUACT
262724139	89040	CCCAGAGUCCTTAACCUGCAAT	89041	ATCACAATCAUGTTGCTTTTCUAAACCC
262725402	89042	GAUCATTGGTTTUGGCCAGGAG	89043	CAATTCTCAGGAACUTGTAGCCCATUAT
262730460	89044	CGTTCAACCAAGUCTCTTATCGTTAAUGA	89045	AGCTATTAAGCAAACUGGCTGTUCT
262731591	89046	CAGATGATCTAUCATGTCAGGAUGCAA	89047	AGGCTTGTUGGTGTACTTUCAACT
262738213	89048	GCGACATTTGGAUAGCATCGAAAUT	89049	CTGAGTGAGUGGTGGAAATACUGT
262755540	89050	CAGTTGACACAACUTGCTTCGATAAUT	89051	ACTTGAAGGTGGUTTCTGTTGTATUGT
262757383	89052	GGTATCTCTCAUGAAACACCCTUACC	89053	TTTCTGTGCACUGTCCACUGT
262760138	89054	CCTTCCTGUTCCTCCAAAUCCAAT	89055	CTGAGTTTGATGAUGATTGAGGAGUGT
262763395	89056	GGGAGTTTUGCCAAGGCCTUA	89057	CCAGTGTTAGUGCCATCAGCUC
262765572	89058	TGAGTUCAACCCGTGUGAAGAC	89059	TGTAGTGGCUGGTGAGGAGAAUA
262767522	89060	CCAAATCCAAAAAGGUTCCACTTTCUAA	89061	AAGGACTUGGGTGTCTUGCAT
262770683	89062	CAGCAAAAAUACAAUCAGGAGAAGGG	89063	TTGATAACTTACAACUGTGGGCTTCUT
262774095	89064	TTTTCCTACTCUGTAGCTATGTCUCGAT	89065	TTCCAGGGCUTAAAGTCTTGACUG
262781003	89066	GCACTCAGAAAAUGATTCGGTUCCA	89067	CCACTGTGGGUAGGGATATTGATCUT
262785569	89068	CGAGGUCCATTAUGCAACCCAAA	89069	TTCCCGTUGGATTCCGTTTUAAGA
262787059	89070	ACTTAACTCCUGTGCCAATCCAUT	89071	GTGGGTAACCTUTTGAACCTGAATAUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
262790432	89072	CTTGCAGUCCAGGGTGCTAUAC	89073	GTGTTAGCUGGCAGGAAGCTUAT
262791917	89074	GAGCCAACAAAAAUGTGGCAUCA	89075	CTGCUCCAGCTCTTGUCAGAA
262798603	89076	GTTGGGTUCACGAGTAGAATCTCUT	89077	TTTATTACAGAGGUAGGAGACGUAGACC
262800778	89078	AGAGAAGGAUGAGGAAUCAGAGCA	89079	CGTGTTGCAUGAACTTTGTTTTUCC
262803246	89080	GTTCATCCAGTTUTGGAACATCAGAAUT	89081	AGAACACAUGCACACAAGTACUCA
262809742	89082	TTGGTCCCAAAGAGUTGAGGATUC	89083	CACACUGTGTCCUGAGCAAAC
262811566	89084	CUAAACCACCCGUGCCAGT	89085	CTTCGUAGCGCCATTGUAAACC
262812737	89086	AGAGTCCUGTACCACUCACGA	89087	CCCTTGTGAGUCCATTACCTTUCA
262814177	89088	GGGCAATGUCTTTGTCCUGCT	89089	GCATGGTTGUAGTACTCAGAGUGA
262827457	89090	CACTTGGCUGCCCTGUAGAG	89091	CCAATCTTCUGAGATGCUCCGT
262830009	89092	CAGTGGGAUGGGACCATGUG	89093	ACCTCGATUCCATTATCATTTACUGCAA
262831543	89094	TCTGAGACAGGAACUGTTAATGTCCUA	89095	CAUAGAGGACAACACAGUAAGAACCA
262835372	89096	GUGCAGGCAGGTUCGGA	89097	GCTCCTCAUCAGGCACUGT
262836600	89098	ACCAACUGTGGTGAAUGCACT	89099	GCCCCTUGACTGTTTGCTUAC
262837793	89100	CACAGATGUGGGACCUAGGAAAAG	89101	TGACAAACAGAAAGAUGGGTGAAUGT
262844720	89102	AATGAUACCAGTGGTUCCCCAAAAA	89103	TGGGATCCAGGUAAGAATCAGAUAACT
262846572	89104	GGUTCCUCCAAAGAACAGCAC	89105	TTCTGAGATTUGGCCTTGCTUCT
262848358	89106	CAATGTAGAAAAUGAGAAGCAGGTUCAT	89107	CTCTGTCUGATTTGCUAGGACCA
262854137	89108	GAAACTGCTUGGCTCTTGGUG	89109	CAAAGGCCUGTCCUAGGAAAGA
262859114	89110	CACCAAAACTTAAUCACTGTCCATCTUT	89111	CATGTGACTTUGTGGATGCTUGG
262859166	89112	CCAACTCACATAUCAACTCAGCTACUAA	89113	TGAGCAATACTTUTATTGGTGTCAAUCT
262865126	89114	CTGTGTCAUCGTGCCTGGUA	89115	GGGTCUCACAGGCCUCT
262869728	89116	ACCATTGGATUCACTCAGCTTATTUCA	89117	TCGCCUGCCATCACGTUAG
262878343	89118	GATTGAAAACUCCCATCUAACCCCAA	89119	CATGGGATUGGAATGCATATUCAAGAAA
262880172	89120	TCCTTCACCAAGUTTGCAUGGT	89121	GCCAATCCTAUGCAGTCTCATAACTTUA
262886432	89122	AGCAACGGUGTGGTACTTUAGG	89123	ACCCTTCATCTACUACACTGATATGGUT
262890925	89124	TCTCATTTGTATUGTTACCACGGCUAAA	89125	ATGAAATAGUGAAAGAAGUGGAAGCCA
262895190	89126	GGTAUAGCCCAACTCTCUCAGG	89127	TCTTCTTTUCCAAAGTCGGUAGCAA
262904909	89128	TGGCGTTUCAAAATTGGTGCUT	89129	ACAACCCTTTGUCTACTTTCAGCUC
262907864	89130	GCTACTGCAAAUCAACAGGAAGTUT	89131	AGACCTCUCCTTGGACUGGAAT
262935731	89132	GCCCTCUCACCCTTCACTGUAA	89133	GGTACTTCUGGCGGUGGAA
262941862	89134	CCTUCACACGCCUGCAGAT	89135	GGTTCUGGAACCAGGTTTUGAC
262942459	89136	CCCCAGATCUACCAGAGATUCCT	89137	ATTTGGAAGGAGCAUTAAAGGUAGCA
262943493	89138	GCCAAGGCGCUCAAAAUGA	89139	CAAUGAACCGAGAGCUGCCT
262960694	89140	GTACCTCCUCTTCTTCCTAUACCACT	89141	GGCTGTTCTTUCTGTTCTTGCAGUA
262964260	89142	CCAAACGGGUCTGAAGCAUGT	89143	TCCACAGGAUAGATTCAGTTTCCUAAGT
262965872	89144	CTTTAACATTCUCTCTCTTTCCUCCCA	89145	CTGCATGCUGCTGATGTUGAA
262969364	89146	TTCAAGGATAUGGAAAGAGTTTGUGCT	89147	AAAGAGGGTGAUATTGTGGCAATGAUAA
262977071	89148	GGTGTTTGGGAUGGAATGGUGAT	89149	GUAGAGTTTGUCAGCCAGAGACAG
262978854	89150	GAAAAATGACACAACAAGUTACAGGUGA	89151	AGCAACGGAGAGCAAUGATGAUT
262988662	89152	GCTCCTUCGCAGCTTGUAGAG	89153	CCAATGTGTATCUTTGGACAAGTGCUA
263000601	89154	GUGACGGGTTUGGACACACT	89155	GAATUTGACCAAGTUCACCAGCA
263012473	89156	CATCCTGGTGUGGGAAGGAAUC	89157	TUTCCTATCAGUGGCCGCAAA
263019020	89158	ACCTGTTTTTCCUTGTTCAGGGAUT	89159	TTTUAGGTCAGCCUAGCAACAAAGA
263022772	89160	GCTGACTCACAAGAUCATCCACAUC	89161	TGTATTTGAACCUTAATGCTAATTTCAUAAGCT
263024893	89162	TTGTCCUCGGAATTCCTTCUGG	89163	AGGACCATTAUCAGAACAGGATCUCAA
263040682	89164	CACTGTCTCTAUGCACATAACATTTGUC	89165	CACTTTAATTGGGUTGCATTTCTGAGUT
263042228	89166	GGAGAAAUAGCCCCGAGUCC	89167	GTTGAATATCCUTGCAGGTGACUCT
263052808	89168	GCCAUCAGGAGGAGGACTUC	89169	GTTATTGAGCUGCTTTTGTGCACUT
263088536	89170	GTCAAUGAGCCAACCACCCTAUT	89171	GATCTTCTTCTUCCCTGAGCGTUT
263120098	89172	GGACCUAGCCCAGCTGAUAAG	89173	TCAGCTGUCCACTTGTTCAUGT
263130522	89174	GAGACTTTTACUAATTCAGGCCTAUGCT	89175	TTTTCUGATCTAGACTUCCAAAGCACAA
263131013	89176	GATCAGAGTTATCUGTTCCTTGTGCUT	89177	CGGAATCTGUGAAAATCCCCCTUT
263144145	89178	CCAAUACACACAAAGCATCAUGGT	89179	TGTACACAATGUCCACAGAAGTTTTUCT
263152168	89180	GCACCACTUCTCACCAGUCAC	89181	AGTTTTCATGGCUACCCTTGACTUAC
263178386	89182	CCGTGUTGGCCTUCAGAG	89183	ATGGCGAACACACUGGCAUA
263179203	89184	ATTACCUGCAGCTCTGTTUGGA	89185	CGGAAACAAAAUAACCCAAGTTCATCAUT
263179840	89186	CCGCACCUCTACAGGAACUT	89187	TTTCUGCCGCAAGGCCUA
263209938	89188	GGGACTGUAGATGGGUGAAAAGA	89189	GGGACTGACUTTCTGCTCTUGT
263213093	89190	GTAATACCCGTUTGCTTTACCTGAUG	89191	TTCAGTUGGAAGATGCUGGCT
263219607	89192	GATTATCTAAACTACUTGAGCCAGCAUCT	89193	GGCTCAGCTTGAUATTGGATAATCTGUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
263230987	89194	CCCACAGGAUTTCCTCTCCCUA	89195	GAGTGCAAUGAGAATGUGAAACACAAA
263245987	89196	TGCCTGGUGCTGCAGTTTAUA	89197	TGGAAGGUTAGTCUGCAGAAAGAAC
263254464	89198	GGTAGTTGTUGGCAAAGCCUCT	89199	GTAGAGCGACCUGACGAUGT
263297186	89200	TCCTGGAGCUGATTGTATCTAGCUT	89201	GTTGGAAGACAGCUAAAATGATGACAUT
263298288	89202	GCATGTACTTCUTAATGTACTCCTUGGT	89203	CCCTCATATAATUTCTGCTCTGATUGGT
263315434	89204	GCCTGAGAAUTACAGGAGACUGG	89205	CAAAAGCTGAGAUGAAACAGTGTAAGUT
263321902	89206	AACAGAAAUGGGCTGAGCACUA	89207	GGAAGAAUTAGAAGCUGAGAAAAGAGACT
263331493	89208	GCTACAAGCACUTCTTCATACCTGTUAAG	89209	TCGCTTTCCTGUATTGCTCTACTUG
263355930	89210	CACATGGCUGCCATTATCATTAGUT	89211	CAGACTACATUGGAAAGGAGATTTGCUA
263363234	89212	GGCATCTCTUGCCTCATGACUA	89213	ACCCGGGAAGGUTTTCAAGTUC
263378136	89214	GCAUCGCACACCGAATUCAG	89215	CAGCAGUGTTGGUGACAAAGG
263384504	89216	TCCTCATCATCUCGAGCAGAGUAAA	89217	ACACAAGGAAUGCCTGCTTUCT
263408977	89218	GCUTTGTCCTCUGAGCACGA	89219	CCATCCAGUTGGGAAGCTUCT
263414015	89220	AGTTTATGCATTAGGAAUCATCTGGTACTUG	89221	CCATTCTAGAGGAUGTTAAACGTCUGA
263421752	89222	GGACAAACGCCCUAATAUGCAG	89223	CGCTTATCTTGGCUGATGAGATTATUCA
263422510	89224	ACUTGCGTGUGGGAGACAAAT	89225	GTCTGTCTCCGUCCTAGACTCAUAG
263425494	89226	GTTCACCCTTTGUTGTATTGCTTTCUT	89227	CAGCTGTGCAUACTTTGTATUAAAGGT
263434637	89228	TGTAAAGCCAUCAACACAGAGTATCUC	89229	ACCATTUCCACCCTCACTAAUAACC
263442726	89230	GGGTGGTUCTGCTTCCUCA	89231	ATGCTTCGCAGGUCAGTAATCUT
263447769	89232	CACCTTTGUGGCCCTCTAUGA	89233	CTGATGCCAGAUCCTGCAUGA
263452725	89234	CACATGTUCCCCAAGATGCTAAUG	89235	TCGUATTGTCCUGGCACAAAGA
263463824	89236	CATCTAGAUAAAACCCTUCCCACCA	89237	TCTTTTCCUGCAGCTCCAAATCTUAG
263521408	89238	GGAAAAGTGUGGTCCATUGCT	89239	GAGCCACAGUAAGCCAGACAUA
263539942	89240	TGCTACTTCUGAATTGAAATGGTUCA	89241	GATTACCTACCAUTACTCTGCAGTGUT
263540385	89242	AGATCTCUCAGGATTAACACUGCAGA	89243	GCCUGCCGCUCACACAA
263560236	89244	GCTCTCAGUCACTATTTGTCTATTUCCT	89245	ACTCCAGTGUCTTGGGAACUCA
263563567	89246	CTTCTCCTTUCCTTCCTTCCATUCC	89247	ACTCTCAUACCTGGAGTUGCCA
263585145	89248	CTGCCCCAGGAUATTTCTGUCA	89249	GCCCCACUCTTCAGATCCUCT
263597230	89250	AAACGGAUTCGGGCUCACA	89251	ACACUGAGGAAUCCGGAGAGAA
263667014	89252	AGCGCCCGCAUGUACAA	89253	GTCCGGGCUGTTTTTCUGG
263668375	89254	GACAGTUACGCGCACAUGAA	89255	GGGCGCUCACGTCGUAG
263669558	89256	CATGAUGGAGACGGAGCUGAAG	89257	GGACCACACCAUGAAGGCAUT
263670306	89258	CGUCAAGCGGCCCAUGA	89259	GCTTCUCCGTCUCCGACAA
263674303	89260	GCACCCGGGCCUCAAUG	89261	CGAGTAGGACAUGCTGTAGGUG
263678611	89262	GGCGCCGAGUGGAAACUT	89263	GGGCAGCGUGTACTTATCCTUC
263680581	89264	CCAGCUCGCAGACCUACAT	89265	AGUGGGAGGAAGAGGUAACCA
263687220	89266	GGAAAACCAAGACGCUCAUGAA	89267	GTAGCUGCCGTTGCUCCA
263687508	89268	GTTCGGUGGTCAAGUCCGA	89269	GTAGTGCUGGGACATGUGAAGT
263691844	89270	CCGGGACAUGATCAGCATGUAT	89271	CCGGCCCUCACATGUGT
263699335	89272	GGCCATUAACGGCACACUG	89273	TCTTTTTGAGCGUACCGGGTUT
263722695	89274	TTGGUCGAGCCAAGCTUGA	89275	CTCUGAGGAAGCGGACTTGUT
263730624	89276	TCATCAATTTCCUGACTTCGGTUCT	89277	TCAGCCTTAACAUGTTCTGAGAATTCUT
263736118	89278	CCCACCAAGGCACAAUTTTAGUAG	89279	CCTCTCCUCCCCTCUCCAAAG
263737237	89280	AGTGTCTCUCTTTCTGTTUAGAGCAAAA	89281	CCUGAGGCCACGGGTTUG
263740247	89282	CCCTGTCACCUGACTTTGCTUT	89283	GGGCTGUCGCCAACCUC
263741475	89284	GCTGGUGAAGGCCATTCUAGG	89285	CCATCTCUCCCGGATGACUCA
263744303	89286	GGAGGGUGACGGCCUCT	89287	TCCGTGTGGUCCTGGAATUG
263745509	89288	CCACAGGAAGUGAGGCUCAG	89289	CTCCUGGGCAGCATCTUCA
263757129	89290	GAUACGGCCAGGCATUGAAG	89291	TCATCTTCUGTCCCTUCCCAGA
263758827	89292	TTTCCTTTTGGUCTTCAGGTUGGA	89293	CGGAAGGTUCCATGGGATUCT
263763446	89294	TTGGAGATCCUCAGGCTGGUAT	89295	GTCTCCACAUGCCATTTCUAGGAG
263769320	89296	GTAGCTGCCCUGGTAGGTUT	89297	AACAAUGGTTCACUGAAGACCCA
263771837	89298	GAGUACAAGAAAUGGCAGGAAAACAG	89299	GCATAAAGGCUGGGTGTUCACA
263772176	89300	CCCGGCCAGUTTTTCAGATTTUAA	89301	CCUTCTCCAATUGAACCGAGGA
263772589	89302	TTAATTTTCCUGAGAGACCAAGACCUG	89303	TTGTGCAAAGUACTGGTCTTTCUGAT
263778772	89304	GCTGTTACAGUGCGAAGUACCC	89305	GGCCCTGAUCATCATGGTUCA
263779137	89306	CATTCUGGGAGCTTCATCUGGAC	89307	GGTCCTCUGACTGCTCTTTUCA
263782414	89308	GAGGATTAAAACUGTAACACCUACCCA	89309	TCACTGGTCUCTGTTTGCACUAC
263783514	89310	ACACUGAATGUGCAGCACAAC	89311	TCCTTTUGAAGCAAGTACUGCAGAT
263784219	89312	CCAACUGCCCCTTCTTCAUGT	89313	CTCAUAGGCTTCUCCCCGAGA
263788163	89314	AAACTCCCAAAGCUGAACUCCAA	89315	TGGUCTCACUGAACAGAAAAGGG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
263789696	89316	GGAACCCUGAGGAGUCCACT	89317	TGTGGCAACGUTCACAAAAUCC
263790945	89318	AGGATGTUACCAGGACATTTAAUGGG	89319	TTTCCAGCUCTGUGGCAAGAAT
263791196	89320	GACAGATUCCCGTTGCTUCCT	89321	CCTGAGGGACUAGGAUGGACAT
263795758	89322	CACCAGCGUTCCAAGUCAGAT	89323	GCTTTTCUGCACTTGCTCGUC
263800053	89324	CTGUCTCAAGCUGCACGGA	89325	CAGCCGCUGTGTUAGGAAGT
263822180	89326	CAAATCTGCUGTTCCCCATCUCA	89327	CTCCATTTTCTUCCTCATTCTACTTCUCA
263830694	89328	GCAGCCAAGTUATCTGTATAGTCTUCT	89329	CAAAGGTUAAAGCTGAAAGUGCCA
263835681	89330	GCTTCTACCCAGUATCACAGGGAUT	89331	GAGCTCAUTAACTACCAUCAGCACA
263842989	89332	CCATGTACCUGCCACGUAGAAG	89333	TGATCGUGGTCCCUCCGT
263851301	89334	CCTGGUACTCACCUGCAGAGT	89335	AAGTTACTGACUAAGCATCCACTTCTUC
263859809	89336	CTCTTATCAGAGUTCAGCCUGGT	89337	GCAGACCUCUCGGGAGACAA
263862448	89338	GCUCACCUGGCAGGGAT	89339	AGCAGCACCUCATCGTAAGUG
263863699	89340	AACCTCATGGUTCTGCCTCUC	89341	ACCAGGUCCAAGCCAAAGUC
263864993	89342	GAAGACUACCAGCTCGTCAUGG	89343	CGGTAGTGACCUGCCAGGUA
263865234	89344	CTGGCUGTCTACAUGCAAACC	89345	GTAGCUCAGCTGATCUGCGAA
263868042	89346	CCCUCGAGGCCAUCCAAG	89347	ACCCTGCCGCUCTCCTUA
263869423	89348	GGCACAAGGUCUACAGCCT	89349	TCCCAGUCCCCAUCACAGA
263875756	89350	ATGGUCAGAACAGCAATCGUGA	89351	CCAGATAAUAGATGCCACUCAAAAAGGA
263877317	89352	CTAAGGUTTTACCACUGCAGCCT	89353	GGAGGGAGGAGACCUTCTUACT
263879861	89354	AGGGTGTGUCCCTCCAAAUG	89355	AGGTAAAAGTGCUCCATTCGCUT
263880674	89356	CTGTGATTCAUGAAACGAGAGCAAUT	89357	GTTAGGTTUCGCAGCACAATCTTTUT
263887200	89358	GCAUCCGGAGATGTTUGGCT	89359	CAAACGUCAGCGGGTUCAAA
263887680	89360	CCATCCGGGCUTTACGCAAAUA	89361	ATATCATCCAGCCUGTGTCTTUCC
263900655	89362	TTGACAGCUGGAAGAGATTTGUGA	89363	CTCAGGGUGCAGTTGCTTTUG
263910382	89364	CAGCTGTGUGCTCTTGAGTUC	89365	GCTGAGGTCUTGTGAGTGTCUT
263915276	89366	AGAAATCCTCUGTGACGATCUGGA	89367	CAGTGCUGGGTGAGAAGUCA
263938063	89368	GCCCTAACGAUGCTATCCTUCAT	89369	CCATGATGAUCCTCAGCTTGUCC
263944337	89370	GAUCAAGGACCGAGUCGAACAG	89371	CCACAGUCCCCAGCAAATAACTUA
263948069	89372	GGACTTUGGAGTGCTUGCAGT	89373	TGGCTGTCTCUGAGCAAGTCUA
263975593	89374	GTCCAAGAAAUGGCUGGGAAGA	89375	AGCTCAAGGAUGTGCCTTTCUG
264003670	89376	CUGAGUGAGCCCGAAGAAGAAT	89377	TCACAAAGTCCUTGAAGATGACAUCAA
264029401	89378	AGGCTTAAGGAUTAGAAAACTTGTUCCA	89379	CTAGTAGTAGUCAACCAAAGCCTTUCA
264029419	89380	CTGAAAGGCTTUGGTTGACTACTACUA	89381	AGAATTGAAATCAAAUGAACAAGTCTACATCUT
264038785	89382	CAGAGCAATUGGAAGCACGUT	89383	CACACATCGAAUACCCAAATTTUGGA
264039859	89384	ACCTGACAGTTAUTGACAAAGATGCAUT	89385	TCTCCCCTTAAUGTCTCCATTTATUCCA
264042734	89386	AGAGGUCACCCTUGCAGAGA	89387	GTGCAGGTGAUGGTATTCCTUGAT
264053729	89388	GTGGTTTTCATTUCCATCTTTACGCUT	89389	CTCTCCTTCUCCCTTTCTATCTTCUGT
264055210	89390	GGTCACUGGGCGGGAAAUAC	89391	GCAATTACGUACGGCUCAACAT
264055490	89392	CCGACUCACCAGGGAUCAGAA	89393	CTCCCTAGAUCCTGGCTGGTUA
264055689	89394	ACCGAUAGAGGGAACCACUGT	89395	GCCCTGTCTUGCTTTCCTTGTATUAA
264057049	89396	CTCTGTCCGUCCCTCTCTUCT	89397	CCTCCCCCGGGUTCACTUA
264058006	89398	TTTGCTAATTGTAUGTGTGTGTGTTTCUG	89399	ACCAAAGGCUTTATCAAGUCACACT
264063192	89400	CTAATGAAGAUGAGGATTTGAACCCUGA	89401	GCCAAGCTCTUTGAATGCTTCATUAA
264063512	89402	CGGUGCCAAGCCUCACA	89403	GGGUGGCTTGUGGGCAA
264063961	89404	TCTGGGACCUCACTGUGACAT	89405	CTGTCCCCUCCTTUGCAGAA
264064519	89406	AGGAGCUGGGUCGGAAAAC	89407	CAAGUACGGCACCACAGUCAT
264065193	89408	CGCACGTAGUGTTTCTGCUT	89409	CAUCGAACCCCAGGUACCAC
264073738	89410	CCTUCCCAGCCCTAGCUT	89411	GCUGGACCCCCAUCGGA
264076303	89412	GAAGAAACAUCCTCCGGCUGAA	89413	ACCGTGAAGUCCTGAGTGUAGA
264076697	89414	GCAUCCACTGCUACCACAAGT	89415	TCACCAGGAUCTTGAAGGCAUC
264078010	89416	AGGGTCTUCCTCAACTGCUACA	89417	GCCTTCCAAGAAGUCAGCAUCC
264081824	89418	CCCTCGCUGGACUCCAT	89419	CTCGTCUGCCCAGCGUT
264082771	89420	GGGTUCCAGGAATTUCCCAACC	89421	GAGAAGTUGAAGGCAGAAAGCAUAC
264082996	89422	GTGGAGGCUCATCACTGACTUT	89423	CCTCCTGCUGTTCTGTTGTUCC
264089017	89424	CTCGTTCCAUCTCCGCTTCUC	89425	GATCTAGGCUCAGAGGAAUCACAAC
264095394	89426	AGCTAGTGTGUAGACAGACAUGGT	89427	TGGAAGTCCAAAAACCUGAAAGGAAUAT
264105590	89428	CCAAACCCTAGAUTATTTGCAGCTACUA	89429	ACAGAACCAGAAUTTAAGGTGGAAGAUG
264108923	89430	GCTTACGCGUGCGGGAUA	89431	GTTATACATCUCGGCTGAACCTACTUAC
264121766	89432	AACACTACUGCAGGATCCATTAAAUGT	89433	GCGTTCAGTCACUAAGAAGATCTAUGAA
264125420	89434	GTGAGUGGCGCCCTCTUT	89435	GAGGCCAGCCCAAGUACUC
264133768	89436	ACCACAGAAAUGAAGCAGUAAGAACA	89437	ATTAAGUGACAAGGTCGTUGCCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
264146108	89438	TTTACAGGTAUCACGCTCATUGCT	89439	GACATCAGACUTGGCAAAGCTUAC
264146363	89440	GACCTTGUACACCTTCCTUCACA	89441	ATTCTGATAGACUCTTGGCTUGCAG
264168458	89442	CAAGTTGAAAUGAACAAAAGATGCTUCCT	89443	TGAAGAGGAGGGUGTGTCUGAT
264178054	89444	AGAUCUGCGAGGAGGACCA	89445	GGGCCUCACCTCTCTUCAC
264189430	89446	CCTGTGCGUGGGATTCTCTUC	89447	GGCUCACCCGACAUGGAAC
264190201	89448	GCAUGUGAGACAGACCAAGGA	89449	CUGAACACUGGGACCAGCA
264192094	89450	AATACTCAAACAAAUCCTGCCCUGA	89451	CAAAAATCTACCCUCTTCCACACATGUA
264194321	89452	TGTTCTTGGCUCCTTTCACTCUC	89453	ACCAACAUAGAAGCTAGTAAGCUACCT
264195189	89454	GAGCACGCGAUGTATTCTCACUA	89455	AGACTTUGGAACACTUGCCCAT
264210570	89456	TGCTGGTUCTTGGCTGUGT	89457	CTGGUGCTGCCUACAGGT
264214685	89458	GCTGGUAGCACAGGGACTUG	89459	CAGTCAUGCGGATCCTGUCT
264232370	89460	CTGTGGCTUACCCCAGGUT	89461	GGCCTGUGCCCAAGUACC
264233808	89462	GACACAGATGUTGATCACCAUGACT	89463	GGTTCCTUCACCACAACCUGT
264234263	89464	TCATTTGGUAGGCTTGAGTTUGAAGA	89465	TCCACAGAUGAAACTTTCUCCCAAG
264236203	89466	CAGGCGCCAAUTCCAATACUACT	89467	CATACTGCCAAUACCTGAATACTGACUA
264236629	89468	TGAGTTUGAAGAAACAGAAGAACCUGAT	89469	GAAAATCCTUACCAATACTCCAUCCACA
264240877	89470	TCUTCATTCATTCATUCCCACCACAA	89471	CTTATCCCGGCUAATGGTTAGAATUGAA
264243674	89472	CTTGGTGGCUAAGCTGCUCA	89473	GCTGUGAAGAGGCTGGUACA
264243893	89474	CACGGGAACAAGAUCCTTTAUCACA	89475	GGATGTGTTAAAUGTGTGTCTCTTUCAG
264245598	89476	GUGCAGGCUGGGAACAC	89477	CACCCCACCCUCATGAAAGUT
264248305	89478	AGGCACUGCTGAATCUCAGAC	89479	GAAGAGGGTGTUGATTAAGGTGGAUT
264249865	89480	GUAGAGUGGCAGCACGGT	89481	TTGTGGCCAGUGGTTGTCUT
264253301	89482	GACAGGUAAGTTTCTGCUCCAAAGT	89483	GGTATTTTTATTUGCTGTGGTAGGUGGA
264255626	89484	CCAAACAGUCATGGTTTTGTUCAAGA	89485	TGCTGCATCUATATAGGTGGTAUCAAGA
264258644	89486	CGTCAGCTUCTGGTTCAGAUGT	89487	GGATGGCAAAGAGGAUCTTGAUCAAT
264260707	89488	GCAGAGCGGCUTGGGUA	89489	CTGACCGUGCGTGAUGGA
264271689	89490	AGGTTUGGGTCAGTAUCAGCAG	89491	AATGAATAGTATGCUGTCCCAGGTTUT
264285123	89492	ACAAGTTTTCTTCUCAATCAATTGCCTUT	89493	CCTCAGTGAUGGGCTCCTGUAT
264291684	89494	GTGAATACAUTGACTGTCTUGAACCAAC	89495	GACCTGTUCACAAAGTTATGCTUCAAA
264294442	89496	CCAGCACAGCUATCTTCTUCAGG	89497	ATGGGATTTGTUGTGTGATACACUCA
264297447	89498	CAAATTAACCCAUGTGGGCCTUAA	89499	GCCCTUACAACAAAAACAAGAGCTUAC
264306922	89500	CCTGCAGGGUTCCAGGTTUAA	89501	GCTCGGAGTTUGGGAAGAATTCTAUC
264307250	89502	GGAUGAGGAACAGCAACCTUCA	89503	AGGGACAACGUGGAUGGG
264308558	89504	AUTGCATGUACGCCCCACT	89505	GCCTTCUAGCCCTTTGGTGUA
264312633	89506	CCUCCGGACGAGGAUGACT	89507	TTCGGATACUGCTTCCTGCUG
264319593	89508	CCGCCGCUTCCTCAUCCT	89509	GGCCGAGUGTAGCCGUA
264322175	89510	CCTCTTCCTCUACAGGGACATTTTCUA	89511	CAAGAAACTAAUGTTTCGCAGACUGAAA
264326647	89512	CGAGGCGGGAGCUGUAG	89513	CCATTTCGCUTTTGACACAAGUGG
264338487	89514	AGUATTCCCCTTUCAAGGGAGGT	89515	CCAGTGCUCCGGACTTGUAG
264338736	89516	GGGUAAGGGAAGTAGGUGGAA	89517	GCCCGGGUTCTGGAUCA
264343357	89518	CAGAGTGCCCUATCCCAGUC	89519	AGGUAGGAGCCGCTAGAUACC
264347207	89520	AGCAGGGUGAGGATGGTUCT	89521	TCUGGGACGCAACCTCUCT
264351064	89522	CATGCAACUCCTUCAGCAACA	89523	ACCGACACUGCCTUACACAAC
264351153	89524	GCCTCGGGUAAATTTGAGCTTCUT	89525	GCCTCACUGGCTCATACUCAC
264351722	89526	TGCCGTCUACCCTGTCUCT	89527	CCGTAGUCCAGCGGGUT
264358460	89528	GCTCGCAUCAAGCUGGAG	89529	CTTCGGCUGTGAAGAGAGUGT
264363696	89530	CTTTCUCCCCAAAGGCCACUT	89531	CCCACATUTACACCTTUGCCA
264366735	89532	CCAUTTCUGACAACGCCAAGGA	89533	GCGGGUGGAACUCCCAAA
264368162	89534	TGCACTGTCCAUGCTATTTTCACTTAUA	89535	CGTTGAGUGAAGGAGATGGGTATUC
264370105	89536	AAACAGAGGCUCATTTTGCAATTUGAT	89537	ACTCCAAAUATACCCAAGUGCAGAAAAA
264379712	89538	GAGCGCGUTCCATCCTCUA	89539	CCTACCUCGGCCTCGUC
264381571	89540	GAAGAGUACGGCCCUGAAGAA	89541	GATTGCAGAAGAUGACCUGGGA
264382426	89542	CCCAGCACUGTTGTCAGGUAA	89543	CTGGUAGAAGAACAGATGTAAAUCCGT
264382579	89544	CACTGTCTUCAACAGACCCTUGA	89545	CCUGUCACCAACGGGAAGG
264382687	89546	GCTGCGCUCGGUGAACT	89547	GTACCTCGGUAGCTGTGGAUG
264388649	89548	CCTACCUGAACCTCCGAACUG	89549	GGTTUGAACCCGGGACTGUA
264389311	89550	GGTTTCATTCATCUATGAAGATGTTGCUT	89551	GACTTGTACTAUGTGTGGCCAUGA
264389483	89552	TTCATATGUCAGTTCAUGGCCACA	89553	GAATUGCGGCGAGCAGUAAG
264393987	89554	CCCGTAUGGCTCAACTUCGAC	89555	GGGCTUCAGACCGTGCUAT
264397356	89556	CCAGCTGGGUTAATAAGAGGUACAG	89557	CTTCTTTGTGAAAGAUAGGAGACTAAAUCCA
264415393	89558	GATAGCAGGAAAAACAAUGCCTUCA	89559	CUAACAGACAGAGAAUGGGCAGAAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
264420877	89560	AGCCTTTCCUAGAATGATCCACUAA	89561	CAGCTGUAGCTAAGATAGUGAAACCT
264426887	89562	GCAAGCTCTUCTTCAGACAATAUGG	89563	TATAATGTACAGTACAUGTCACTTACCTUGAAA
264430446	89564	CTGAACAGCCUATTTCCCCAUCA	89565	GGACAACUGAGGGTTGGGTTTUT
264430561	89566	ACAATCGUCTCCCTTTUCCACAC	89567	ATGTACATGGCUGAAAGCTUGAT
264434346	89568	TGTGGUTTATCACATTTTUAGCCAGAAGA	89569	TGTTCCCACUACTCCACUACAAGT
264435251	89570	GGGCTGCUACTTGTAGUGGA	89571	TTCTTTCACAUCCCTGACTTGTUGAT
264446807	89572	GTCTTACATGGUCAAGATGTTUCCACT	89573	GCTTTAGGGTTATUCAGCCTTCTCTAUT
264447142	89574	CTGAAGGAACCAGUTTGGTGGUA	89575	TGAUGATCTTTATATAUGCGCACACACA
264481507	89576	GTGGAATAGUCCCACGCUGAA	89577	AATAGCAGGGAUGCGUAGCC
264499296	89578	AGACTCTAGTGUGTTCTTAGGGCUT	89579	CCATATCATCACUGGCTTCTTGTTTUG
264504908	89580	GGGAGAAUGACATTGATGUGGAC	89581	AGAGCCTUCCACAGCTTTTUCA
264509540	89582	GCTCACATUCCGTCTCTCUGG	89583	AGAAACCGCCUTACCTGGUAAAA
264510772	89584	TCCAACAUCCCAGCTTGCUT	89585	ACATAAATTACUCACAACTTCCUCAGCA
264511104	89586	ACATGTTGGGAAUGAATGAGCUCT	89587	CCAGTACAGGUGATCTGAGGATTUC
264520055	89588	CCGACATCUGTGTTGCCAUCA	89589	CTGGAAAGGCCUAGAAAUGCCA
264524057	89590	CTCAGCCTCUGTCTTGTGTUCT	89591	GAGCCAAGUGAGTGAGUAGCC
264527360	89592	GAAGACATTGUACGTTGCTTAAATCUGA	89593	GTTTTGACAAGAAAUGGCUGCAGA
264527429	89594	CCTTCAGGAUCTGCAGCCAUT	89595	CCAAAACTAGGUGGAATTTGAAATATGUT
264530127	89596	GACTTCAGUGCATTCAUGAAGCAT	89597	GCCACCAUTTCCACAGUCACT
264542583	89598	CCAGTGGTCUTCCTCCTTAUCC	89599	AGAAGCGAAAGCAGGUTCTUAACT
264579210	89600	GTGCTUGGGTGTATTUGCAAAGAA	89601	TCTGGGCUTTGAAATACUGGCT
264585728	89602	CCTAAGCAAATGUGATTTTACCCAGAUG	89603	CACAATTCCAGAAUTCTCCAGAGGUT
264586289	89604	GAACTGACCUCACTTGCCUGA	89605	GTAGTTCAUCCGCTCCACGUA
264588366	89606	CGGGCUTGUCGCGAACA	89607	AACUCCCCCACCAACAUGG
264595318	89608	AGATCGCCUCAGGCAUGG	89609	CCGCGCCGUGTACUCAT
264609210	89610	CATGCCTTUGCTAAGCTTTCTUCAA	89611	CUAAGATGUCCACAGCAGACAAAAG
264616739	89612	GGACTTTGGUCCACAAGCATTUAAG	89613	ACTGCAAACCUCTGAAGAAAAGTGUAAT
264621182	89614	CATGCAGATAACUTGACTTTCCTTCUCT	89615	GGAATTTAAAGTUGCGTGTGTCTGTUT
264633381	89616	GGACAAGGGUGCTGTCTUAGG	89617	CTGTGCTTGUAGTGGAGCUGA
264644990	89618	AGTATTTTCTCCUTCTAATTCAGTGTUCCAAG	89619	CTGTCCCUGCTGCTAAUGGA
264645373	89620	CCTAAATTGACUACATTCTTUGCCCAGA	89621	CTTTAAGATTACTUTCCAGTTGCGUCAT
264648339	89622	GAGAUGCTGGUCAGCCACAT	89623	TCUGCAGCTUCCAGGAACC
264656455	89624	GGATCACACCGUGCTTUCAAAAT	89625	TGACACTGTGGGAAUATATGTGCTTTUT
264660059	89626	CAACTACTATGCAAUGAAACAGCAAUCT	89627	AAGCAAAGUGATACTAUGACAGAAAAGGA
264666529	89628	GAGCATCTCUCAGATTTTGCTCUAGAA	89629	AGACACUGAGGCGCATCTUG
264667248	89630	TGATGCACTCUGGGCAAGAAUT	89631	GAGAACAAGAACAGCUAAATGUGGAAAAG
264667922	89632	AAAGGACTTTUCCCACCAAGAGUT	89633	GTAUAAGACGGCGGAGCAUCA
264670224	89634	CTGTUCAGCACGCUCAAGG	89635	CACCATGGAGCUCTGTTAGTAGATAAUT
264679607	89636	TGACAGUGAGGCAGATGTCCTUA	89637	CACCACCACACUTCCAGTCUC
264684273	89638	GGAUTGCTGUCCCCACCAC	89639	GGCCUCCCAGGCAUCAC
264687061	89640	CCTGTTTTATAGAAAUACTGTGCACUGG	89641	TTCATCTAACUTGTCATGTUCCAACACT
264692816	89642	AGCCTCTTTCUTGCGGGTAUC	89643	CTCCTTGCTUCCTTTAGTCACAGUA
264695053	89644	CACAGUCACCGCCGCTUA	89645	GGAATCGTTGUGGAGGTGGUC
264695625	89646	AAGAUCAUGCCCAAGAAGCCA	89647	AGAGAAGTTGTUCCCAAATCATTUCCT
264696291	89648	CUCCGGGCCGACAUGAG	89649	GGCUCCGGCCTGUCAAA
264697035	89650	CCCTAGCCAUCCATTCACCAAUT	89651	CCACAGUGGCTCGGAGUAG
264697653	89652	GCUGTTGCUAAAACAAAGAAAACAGAGT	89653	GACCCGAAGGCAGUCTGUAG
264698791	89654	CCAAGAGGGUGGAGAUCCAGAT	89655	GUGTAGCCUCAGCCACAGG
264702024	89656	AGACCUTGGAGAATUCAGAGCCT	89657	CCCATUACCACAGCAUCCAAGA
264702858	89658	CCCAGCUCAGCUGCAAAGAAT	89659	CCTACGATCAGUCCTACCAAUACCT
264703299	89660	AGTCAACUGAAGGCCACGUC	89661	GCAGCGTAATAAGCUGTATCTGTTGAUA
264707391	89662	CACTGGTACCUTGGAAAGCUAAGT	89663	TGGCAACAAUAAAGATGAUGACCCA
264708743	89664	GUCGAGACACCCAACUCCAC	89665	GTTGGCUTAGGGAGUCCACAT
264714311	89666	GCCTCACCUTCCCCUGGAT	89667	AAGAGCUGGGCGACCUG
264715987	89668	CTGGGCGUGAAGAACUCAGAA	89669	CACCTGCTUGGACGAGAUGT
264716282	89670	TCAGGUAGUCGCGGAGGA	89671	CGAGCTGCUGGAGCACUA
264716728	89672	GGAUGCGAGCCAGGTUCT	89673	CCGCGAGAGCUTCGACUG
264718505	89674	GCUCCAGCAGCUCGAAGA	89675	GTGGGCACCUTCCUGGT
264720059	89676	CCAGCAUGGAGCACCUG	89677	AGCAGCCAAGGCCGUAUT
264720484	89678	GAAAGAACCCACACUCCGTGAAUA	89679	TTGACCCGGCUGGTATTGUC
264720895	89680	CGCACUGAGCTGTCCATUG	89681	CGGTGGGCUGACTCCUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
264723004	89682	GACCAGGGUGGCUGCAT	89683	CCGGGACCUCCAGTACCAUAG
264724490	89684	GCUAAGGGCGAAAAAGCAGUT	89685	CGTUCGCACGCCGATUA
264724734	89686	CTCTGCTGCUGTGGAGACUG	89687	CCAGCTCACCUCTTTGTCUCT
264725010	89688	GCGTGAUGCGCCGGUAA	89689	CAGAACCTTCCUCCTCTTCCUC
264725705	89690	CGGAGAUCACCATCGUCAAACC	89691	TCAGCAGGCUTGGGCAUC
264726008	89692	CGGAGGCGCCUACACTUAC	89693	GCCUGCCAAGGCCATGUT
264729265	89694	GAGAGAATCATUAGGAAGCTGAACAUCA	89695	CCTTCAGAAACACCAUCAATCCTTUT
264730437	89696	GAACGGAAUGTGCGGAAGUG	89697	GGUGGCAGCCGACAAUG
264733509	89698	GAAGGAGAGGCAAUGGAUCCC	89699	AGGGCCACUCATTTCTTATUAAAAGACA
264734158	89700	GAGCCATTTTUCCTCTACAGCUCAT	89701	CCCAACTTTCACAAUACCAGGTACAUA
264743988	89702	AGACAGCACACCAGUCTTCAUT	89703	CCATGTGAAAATUGAACCTGCAGATAUG
264754199	89704	CCACATGGTUCCAGGCAAGUA	89705	CGAGAACCUGGCTCGCAUC
264763371	89706	AGACCAACUACGGTTGAAAACGUA	89707	AGCTCCUGCAAACCACAGTATTUT
264768949	89708	AATGCATAGGTCUACTCTGACTTCATUT	89709	TTGUGCAACCCACUCAACAGA
264777981	89710	AGGAAAAATGTGGUATCTGAAGCTCUAAAA	89711	GCATGTTTCUGCCTAGCTTCUAC
264785472	89712	CAATAAAATGGATGUTCCCCCAGCUA	89713	GACAGTGGAAGCUATGGTCATATTAUCA
264790777	89714	GTAATCATGTGGAUAGGATTGAGCCUT	89715	GTGATGCCAGGAGUTAAGAGGAUT
264799403	89716	CCTGACTGTTUGCAGCTTTCAUT	89717	TTTGTCATCGUTTTGTTTTAGTUGAGCA
264809639	89718	GCAGGCUCAATCTGAGGAUGA	89719	CAGTTTTUGGAAGCACAAGUGGAT
264817832	89720	GGGAGTACAGGAUACATTCAAGCTUT	89721	GGATGTUGCAAAGGACAAATATGUGT
264820706	89722	ACCUCCCAGGCCCTAUGAAG	89723	ACAGGGCAGCAAGUAACUCAG
264830392	89724	GACAUTAGGACTAGUAGAACGAACGG	89725	TGACATGTACCACAGAAUAGGAAGGAUA
264830407	89726	CATTTTCACTGAUCACCTTTCCAGTUC	89727	AUGTTGGCCCUGAAACAAAAACAA
264835303	89728	CTCATTCTGUAGGGCAGTATTTUCCAT	89729	GCAAGACTGGAGAGUTAAATCAGCTTUT
264841781	89730	GAAAGTCACCUAAGGGCCUCAT	89731	GCTGTCAUAGCCGAGAACAAUGG
264843680	89732	CTTCTCCTGCAUTGATTTAACTGCATUT	89733	TCGGGAGGCUGCCCTATTUA
264859916	89734	GCCCAGGAAUGCTACAGAUACC	89735	AAAACCCTGATGUTTCAGTGTCTAGUT
264860488	89736	GACTTCAGUACAACTCACUGGAAGAAAT	89737	GCTGAAAGCAUTTAAGTACAGAUCCGT
264894959	89738	GGGCUTGUGGAGAAGAGAAGT	89739	TCTGGATTCUAGCCACTCTAACACTTUA
264905162	89740	ACTTCACTTGCCUATTTCTGCCAUT	89741	CTCCACAGAUCAGGCAGGUC
264911362	89742	AAAGTCACTTTUAGAGCCCTTAATGUGT	89743	GGACCTGCUCCTAGATGGGTAUAAA
264924043	89744	GATGGCCAGGCUCTGTGUT	89745	GCAGCAGGAUTGGCTTGTUT
264929391	89746	CCCUTCTTUGGCGACGAGT	89747	GCUGCCACAGGGAGCTUAG
264961066	89748	CACCTCCTTGUCAACCCTGTUT	89749	CAGAAAGGAUCTTGGGCACTUG
264967340	89750	CAUTGACTATTACTTUCCACCCCAGAA	89751	GTGCATGUGCAAGACCCTTUAC
264968415	89752	CGAAAGAAGACAAAGGUGUGCAT	89753	GUGCAACAAGGAATUCCCCAAC
264981924	89754	CTTTCTTCTGUACCTAATTCTGUCCCA	89755	GCAGTAGAGGAACUACACAAACTTTUGA
264984139	89756	ATCGTGACTGUTGTGGGACUC	89757	GCCTTCCAUGCGATCATTTUGT
264985314	89758	AAACACTTACCTUCACCAGCTTCUT	89759	GTTGCATTGTTGACUGTTAGGTAACTUT
264989434	89760	GTCAGGGAAUTCCTCAAGUCAGG	89761	TCCCTCCCUTTTAACTCTTACUGAACA
264991937	89762	CATGGTTGAGCUGTCCACUGA	89763	CATTTGTUCTGAGAGTTUCCACACAG
264993661	89764	CCGGAAATGAUGGCAGAGAUCA	89765	TGCAGAGGAGUAGTGCAGAGTUA
264994341	89766	CAATGAACCTGUCTAATATGCTCTUCCA	89767	CCGAAGTTGUCAACGACCUCA
265005986	89768	CAUATAACCCAATUAGAAGAGGCAAGCA	89769	ATGTGCAACATTUTTCGTCTTGTGAUAT
265006874	89770	GTGCTTCTCTUTTGATTTAACAAGUGCT	89771	CGTTATCGACAAAGGGUTGAACTTTUA
265010091	89772	CAGCATTTAGACUATCTTGCAGTUCCT	89773	ACGACGAGAAAAAGAAAUTGCUGAAAC
265010200	89774	CGAUAACGCAGACTCUCAACCT	89775	ATTAAAGTCAATGAUTTTTGTCATCTUACCAAA
265020783	89776	GTAACATGCTUCAGCAAGGATTCUT	89777	TGCACGTCCCACUGGAGAATAUA
265026366	89778	CGGATGTGTUCCTGAAGAGUGT	89779	CATCTTAAGCAAGUGCATGAAGCUC
265032170	89780	CATGTGGCUGTACAGTTCCUCAA	89781	CAGUGTGTCTACUGCCACGAG
265039407	89782	ATTCATCACCTTTUCATATTTTTACAGATCUGA	89783	CAGCAATCUACAAGTTACCGAAAUCAAC
265039724	89784	TTTCGGTAACUTGTAGATTGCUGCT	89785	CGTTTTTCATAAUGCTGTGCACAUAACT
265049388	89786	TCAAGACTCTTACUATGCGTGACTTUG	89787	CTCTCGAACCUTCTTCUCCGA
265053900	89788	CAGTGTTTTTCUCGCAAGTGTTTTTCUA	89789	GAAAACCAAGGGAAAGUGCATAAGUG
265057178	89790	GAAACAAUCAGACCTGGGUCCT	89791	GCAGATTCACCUGAAAACTATGCACTUA
265061481	89792	TCTCCTGUCCCCTATGCAATUCT	89793	ACAGGGAAGCGUATTTCCUCAC
265066688	89794	GGGAGGUCTCCTCUACGAAGA	89795	AGGACUGGAAGAUGAAGGACACT
265070203	89796	GTGTACTUAGCACCACATTGATUACAGA	89797	AACATTCCCTUGGCCCTGAATUAT
265096247	89798	CAAAGGACUCACCGCAGAAAAUG	89799	AGCACAGUAACGAAAAGAAAGTCTAUAGG
265100247	89800	AATATGGGCCUGTTCTGGCTTAUC	89801	ACATGACTGGUCCCTCGAGUA
265102577	89802	CCTGGATTUCTTCCCATTGUGGAT	89803	CTCCCAAAGAACCAGUAGTAGAAGTCUA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
265116526	89804	CCTCACACUGACTGCACTTCUG	89805	TCACACGUCCAACAAGCCAUA
265120495	89806	CATATGTUCCCGGAGGCCATUT	89807	CTATGGAAACTUTGCTGCAGAAUCAC
265124832	89808	TGGCGAAUTTGTACAAUAGGAACAAGAA	89809	GGGTTTCUCACTGACTCTUCCC
265130523	89810	ACAGCTGTAGGUAACTTTTGCTTGUT	89811	GTACGACUCCAGATTCCAACCUC
265136893	89812	CGGGCUCCTCCGTGUAG	89813	ACUGGCAAGGACCCTGUG
265140470	89814	GTCTUGCAGGAGGTCATCUGG	89815	CCGCCUGGCCATGAAGTAUAT
265141815	89816	CGGAAGUCCCAGTUGCAAGAT	89817	CCTUCAGAAACACCTGCUGGAC
265147229	89818	CTCCTGGTCAUTGAGCAGCUT	89819	GGCAGCAGAAUGUGAACGG
265159899	89820	ATCTCATTCTUGCTGAGCTTCTUGT	89821	TTCTCCTAACTCTUGTCCTCCTAATCUC
265161744	89822	GTCTGATGUTGTGGTCUCGGA	89823	GCAGACUTTGCUGACCAACAG
265168325	89824	CACAAATTAAGUGATGCTAATGGUCAGG	89825	AATGAGAATUGACCCATGAGTUGGA
265184509	89826	GAUCTGTATAGGTAUCCAAGCCAAGAC	89827	ATTTGGTCTAAUGGTACAACTGCUGAA
265186657	89828	GCTTTCTGGAUCCTGACATUGGG	89829	TGGCTCATUCATGCTCTTAUGCT
265217081	89830	GCCCTCCUGGCTGAUCCT	89831	CGGCAGCUCCCTGGAUG
265223429	89832	AACCAAAATAUGCAGGGAGAUGGT	89833	GGATTGCTCAGAUTGGGTGGTAAUC
265226917	89834	CAGGATCUCCCTCGTCTTTUACC	89835	GGGCCATACUTTTCACACTCTUCC
265250376	89836	ACTTCAUGGGAGCCACCTCUA	89837	AGCATGTCATUCTCCTTGTTTUGGA
265253714	89838	GCUGAAAAAGCCCGUGAGAAAGA	89839	GTCCTTUCGGCAAGAGACTUGAT
265285371	89840	GCTCTCTTCAUGCCCTGCAUC	89841	ACTAGTGCCAAUGGCTGCTTUT
265286355	89842	AGCCCACTUACCTGCGTTUC	89843	GTCTTTUCAAGTGAGGUAACCAACAAAA
265394942	89844	GGGAAUCTTGGCTUCCACACC	89845	GGGCTCACUTCCCAGTUCAAAA
265423383	89846	CGAAATAACTCUCGAGCCTTCAUACC	89847	GCGAGCUTTCUACCCCAGAGA
265437079	89848	CCCACCGACUGCTGAAUGG	89849	GGCACAAUGAAGAGGCATCUG
265456452	89850	TCTTGGTCUCACCGTTGUGG	89851	CAGTGTGAGUGAGTGTCAGTGUAAT
265466525	89852	CTGCUGGCCTUGGAGACA	89853	CUGGGAGACCCCTUCCAC
265471474	89854	CCTCCAUCAGAATGTCCUCCAG	89855	CGCAGCAACGUTCCATGUAG
265479047	89856	GGAGCAUTCUGGGCAGGT	89857	CTCCAGGGCUGCTTTCCUT
265496437	89858	TGTCAGAAGCCGAAGUCGUG	89859	CTGAGGGACUCTGAACCCTACTUA
265502151	89860	TCATCCTGACUGGTCCTCCTUT	89861	CCCTGCTCUCTTCAGTGUCC
265677264	89862	AAGAAATCCAGGUGAAAGCAGUCA	89863	TCCCCUCCTGCTCATUCAGAAT
265681463	89864	TCCTAGGCCAAUCCTTCUAAGGT	89865	CTGAGTACAUGGCCAAUGGCT
265686344	89866	GGCCTGAAAAUCCAGAGCTUCA	89867	AGTTCACCAUGTGTGTGTUCCA
265694111	89868	TGCTACAGTUTCTGCCTCTUCC	89869	GACAACTCATTAGUAGCCTGACTGUT
265699905	89870	TGATAATGCCAGUAAACTAGCUGCAA	89871	TGGAACCUGAACAGAATTCTUCACC
265700190	89872	GCATCTCCCUCAGGTAGTUCAG	89873	GACTAGTTCCTUGCCTTTCCTGUAG
265716641	89874	GAAAACCACATCUCACATAAATGCCAUT	89875	TGGAGGCAGCUCAGAGTUAGA
265719730	89876	GGAACCACAAAGCUAGCGUCT	89877	GTGGCAGAAAAGGAAUCCTTAGUGA
265722007	89878	CCTGACCTGUGTGTCTGTGUAT	89879	CACCAUGUACACCAGAAACACCA
265728198	89880	CAGAUCAATUCCGCACAGACC	89881	GGTTTCUGAAAGGAACAGGTATTUAGCA
265734166	89882	CTTACTUCAAGCAAAGCTCAGUGT	89883	CACCATTCAGAGUGCTTTTTCCUT
265751107	89884	CAGGTTCCUCAGCTTCCTUCAG	89885	GGCTGCAUACATGTGTAGAUGGAT
265753258	89886	TCCATGTTUGGGTGCTTTGUGA	89887	GCAAACCTTUGCACAGTATCAUCC
265754052	89888	GAGATTTTGGAUGATACTGUGCAAAGG	89889	CAGGACUGCTCAGACATUCAAGAA
265767832	89890	GCCAAAAUTCACUGACAAAGGCT	89891	GGAGCAUCAAGAGAGACACCUT
265779583	89892	CTTGAGGCUCATCTCTCTGCUC	89893	GAGCCTTAGAUCAGCAGAAAGAUGAA
265785073	89894	CCAGTCCTCUGCCCTCTTCUT	89895	GUCTTCTCCUGCACAGGAACC
265786460	89896	CGAAACCUGAGAAGGCCUCA	89897	CTGUGGGTGACUGGCAGAAA
265787695	89898	CGCAGTAAUGCGAACAUCCAA	89899	GTGCCAATTAAGUGCATAAATGCUGT
265810330	89900	CGTGCAAAGAGUAAAACATGTUCCC	89901	AATCACTGAAGTUTGTTTTCCCTCUCT
265878357	89902	CGAAGAAAGAGACUCTGGAAACUCA	89903	CAGAGTCATCCCUGCTTCATAACATUT
265884179	89904	TGTCCATCUTGTCGTCTUCGG	89905	CCCUTGGAAGCAUCAAAGAAGAAAAT
265895719	89906	AGCCATGATTUATGATTCAGTTGUACCT	89907	TGATTTTGGUAAGCTACUGGAGCAT
265942848	89908	CTTTCACCAUCCTCTTCCUGACA	89909	GTAGUCGCAGACGCAGUAGG
265944117	89910	CCCAACAAGGAUGGAGTCGUG	89911	CCTGGGACAUCCCUCAGACAT
265951022	89912	AGTACTUGGAGGGAGAGCAUGT	89913	CATGGUGGAGAGCACGAGAUA
265956189	89914	TGGTGTGGACUCACCCATTUT	89915	GCCCTTTATGATUACATGCCAATGAAUG
265958773	89916	CTTCCGCAGCUGTAGATCATTUG	89917	CCCTCCTACCTUTTCTCCTAACTACAUA
265964450	89918	CTTTTATUGACTCAAAGUGGCAGGAT	89919	TCAACTGTTCCUCCAGTCTCUGA
265981573	89920	GTAGTAGAGUCAAAGAAGAAGGCUGT	89921	CTCAAGGAGGGCUCAACACTUA
266112012	89922	ACAAATGCACAGUCCCCTUCAA	89923	GAGUGCCACTCAAUGAAGGAGA
266120212	89924	GCUGTUCAAAAGCAAGAGCCT	89925	GGACAUTGGCAAACUAAAAGGAGAAAAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
266124842	89926	TCCTTTCCCCUGTATGTTTCCACUAT	89927	CCAAAAGTGAUCAACTACTTTCTUCCAA
266126580	89928	TCAGACTTACTUGCTCTAAGACACUCT	89929	CACAAGTUCAGCACAGCATUGG
266129093	89930	GAAGATCCTTGGUATTGCAAAGCUG	89931	CACAGGTTTTGGUTGACAGTGATAAUAA
266131321	89932	TGCCTCAAAAGTUCGTTTTCATTTACUT	89933	AACACGAACAAACCGAUTCAGAAAUC
266131393	89934	AGTTCTCGCTCUTTTATTCCTTTCACUAA	89935	CAAATCAAAACCCAGUTGCAUGAAGA
266132462	89936	CAGAGTTATCTGUTTGAATGTCCTGUCT	89937	GTTTAGATACCAGCAUGAGCAAAUGAAC
266132617	89938	ACATCTTGTTTCUCCTTTAGCTGCUT	89939	TGCAACAAUTAGAACTCUCCAGGAAAAT
266136322	89940	CTTCTCUAAAAAGAGCTGGGTGUGT	89941	AAGAUCAAAACCAGAGTAAGAUGCAACT
266143461	89942	CAATCGAAUCAGACAATCTGTGGUT	89943	TCATTGCTUACTCCCCAGUCT
266147562	89944	GGCCAGTATAGUCCACTTGTAATTUAGAA	89945	GCAGGTGAUGACCACAGUACAAA
266148776	89946	CATCCATTTCCTUCTTTTGCTCTTGUAAA	89947	AGTGTTACTGAACUAGCATCTGAGGUAT
266151312	89948	TGTTCCTTGAUCGTGTTCAGTUGAG	89949	CAAGAAGAATUGGAACGACUCAGG
266152301	89950	GGGCTGACUCGTGTTGCAUAT	89951	AGTTTTACAAACAUCCAGCACTGGUA
266154838	89952	GCGGTTCGACUCTGCTCTUC	89953	GCTGCAGGAGGAAUTGGATAAATATUCT
266158967	89954	GGTCTTTTTCCUCTATGGTCTGTCTUAA	89955	GUCATCTAGTTUAGAAGAGCAGAAGCA
266158982	89956	ATTTATCCAATTCCUCCTGCAGCUT	89957	AACTAAGGACGUTTTGTCATCTAGTUT
266159706	89958	GTGTCAACUGCTTCTGCTCTUC	89959	CCTTACAGCUGGAACATGAGCATTUA
266161373	89960	TGAGTTCTGCTAUTTCCATGTCTTTCUT	89961	AGGCAGAATUGTGTTGGGCUA
266164756	89962	TGCTTCTUCCAACAGCCTCTUT	89963	TGAGGCATCAGUTAGAAGAATGTCTUG
266164941	89964	TTTCCAGAGAAAGCUGATTGTUACCA	89965	GCAAAATCTTUCAGAATTAGAACAGCUCAA
266165492	89966	GAGCTGTTCTAAUTCTGAAAGATTTUGCT	89967	GGAGCAUATTAGACAAAAUGAGGAGGA
266165505	89968	TCATTCCTTATTCUAGAAAGCTCCUCCT	89969	AGCAGAAACTUGAGGACAAAGUAGAAAA
266165999	89970	CTCCTTCTGGAUGCTTACATTACTTUCT	89971	GCTAATTCAAAGUGAAGTGGCCCUA
266166160	89972	CAGTTTACTGAUGATGCTATCTCCTUCA	89973	TTTTCTTTGAGTACUAAAATGAGAACATGTUGT
266166547	89974	GACATTCTTCUAACTGATGCCUCACAT	89975	GCAAAATCTTUCAGAATTAGAACAGCUCA
266170791	89976	TGTCCATTTTATCAUCTTCAAGTTGAUGAA	89977	ACCATGCAAAUTTTTCTTUCAGCACAT
266221729	89978	GCAGCGCUCGTTCAGTTTAUCT	89979	GAGGAUGCGGTTCGCTUG
266222200	89980	TGGCAGGUAACGGCTUGT	89981	CGAAGAGCGACGAGUTGUG
266222728	89982	GCTGACCCUCTGUGCGT	89983	GGUCCCACAGGGCAGAAUG
266225755	89984	GCGTCUCCTGACTGAUGGAAG	89985	CTGGCCAGAUATCAAACTTUACAAAGG
266231828	89986	CGTGCCCUCCATCAGCAUAT	89987	GACCGGGUCGTTCTCTAAACUC
266246394	89988	CUGGCAGCCAAGGCCTUA	89989	GGGUCCGAGATGUCACACA
266253379	89990	GGGTCUCCACGATTCGUGT	89991	CCCGTGAAUGAGGGTATTGUCT
266254908	89992	GGUGAGGCCACAGTCATUGAG	89993	CAGGUGGACAGCCTCTTUCAG
266257695	89994	TCCAGACUGGGTCGTACCUC	89995	GUTCTGUGAGCAGGAGGAAAAGT
266264558	89996	CGTGCACACAGUCTACACAUACC	89997	GUAAGGACCCAAGCTUGCCA
266269175	89998	TTTTACTGCUTGAAGAGCTUGAGGAT	89999	CTCTGATGAGGAUTCCGAACCUG
266279987	90000	GCAGTGTTTUCACAAACAAGTTTGAUG	90001	CUAGAAATTGAUAGCCAGCAGGAAGA
266281015	90002	CAGATGCTUGAACCGGCUCT	90003	AGGGAGCTCUGGATTACTTAAGTGAUAA
266290079	90004	AACAGATTTAAACUGGACCCACTTCUT	90005	TTTCAAAAUCAGAAGGGTGCAATUGAG
266291585	90006	TTCTCAAGAAGTUTCGCCAGTAGAUT	90007	GTTTCAAGATTGACUCATTTAGCTGTUCT
266299590	90008	GGGCCAATCUCTTTTTACCAATUCAA	90009	AGAAGAAAGTAUGGGTGGAGGUGA
266318562	90010	CCAACATATTGUGAAAACTGTCAUGCT	90011	TGGGCAGAUTAGAAAATGCAUGACT
266318680	90012	CCGAGGAAAAACAAUGATGGTUGA	90013	GTGTCAGATGGUTTTCTACAATGAAUGG
266318770	90014	CTGAGAACTATUCCAAGTCATGCATTUT	90015	ACTGCCATTGAUTTATGCAAGTATAAUACCA
266319755	90016	TGCAACAUGAACCTGAATAUCCCA	90017	GCAACATAGGUAAGATCAGCATCUCA
266346407	90018	CGCCTAACTUGGCCCAGAUG	90019	GCGATCCUGGACTTCCTCTUG
266351607	90020	CTCCUCTAGGGTUGCGCAAAT	90021	GCCCTGTCUTCACTCCTTCUG
266351742	90022	AAGGACGGAAAGAGCAUCUCAC	90023	GCCCAAGUCTGUCCAGAACAA
266354582	90024	TGGATGUCGCCGTUGCT	90025	CAGCCUCGCTCCUGGAC
266355283	90026	TGCAAGCUCTGCUGACACA	90027	CTCAGUGGGCACTGGAGUT
266355648	90028	CAGGUGUCCAGGAGCGA	90029	GGCCCAGGCUGCTUCAT
266356714	90030	GAACAGATACGGAUGCATTATAGUGACT	90031	CAGAAAAGTAGGAUGGGAGAGGATTUAA
266359771	90032	CAGGGATTUGCAATAAGTGUCAAAAA	90033	CACACCCTUACAGTAAAGTCTTUGGT
266371269	90034	CTGAUCAGCAAGGAACTTTUCAAGT	90035	GCCTTTCTUCTCCGCTTCUACC
266382136	90036	TGTAACTCTAGGCAUACTTGTCTTUGGA	90037	CTTTTCAAGCCCAUCAGAUGAGACT
266387738	90038	GCTCACTGCCUCTCTGCATTUT	90039	AAGGAAACUCAAGGAAAGUGGAAGT
266405516	90040	CCTGGTATTCUGGCAGCATUCT	90041	AATTTCTACTTTTUGTAGCCTCCUCGAT
266406814	90042	CCAACCTAAGACAUACATACCAGTUGT	90043	CCACTGCTGAUGTACTTTATTAACTUCC
266460279	90044	CTCATCGCCUCTGTAGACCTCUA	90045	GCGAAGGUGATGGCAUACCAG
266487335	90046	GCAAGAAACACCUGGACTCTUAAGAA	90047	CCAAGGTCUTTTGTCACTTAUGCC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
266489845	90048	TGACGGUCATCACCCUGGA	90049	CAGATACTGACUTTGGCATAGCUACT
266518026	90050	CCTGCTTCCUTTGGTGGGAAUA	90051	ATTTCGGACTGUGATGTAGATCTUCAC
266705515	90052	CAGAACAGGCCCUCAGTUCAA	90053	CTTAUGACCAGGAGCCACUCAAG
266929317	90054	CCCATTCUGTCTTCAUCCCACA	90055	GAGCTTGGUGAGCTGGUAGAAG
266958813	90056	AATCCCACAUCCTGCUCAAGAC	90057	GGAAUGGAAGCACCUCCCAAC
269459408	90058	GCAGAAATAAGCAAAUTCCCCAAUGA	90059	AAAUGGGCCAGAAGAUCGCA
269460282	90060	CCTTAGGGAAAGGUTAGATTCUGAACA	90061	GGGACTTTUGGAGAATGATAUGGGAAC
269461790	90062	GCCTCAGGGCUTGTACUCAT	90063	GGGCGCUAATCGTACUGAAA
269462910	90064	TTAATTTCAACAGAGUAAGGTGCGAUCT	90065	GAGTGACTCCUCTTACCCATATTUACAAT
269467294	90066	CCGGAAGGAGUGGCACAUC	90067	ACCCTCUGTTCTCCUCCACA
269467762	90068	ACAACTGUGGCACTCCGUT	90069	CCTGGTTGAAUAACACTCCTTGTTTUC
269469367	90070	CTATTTCTGGAGGUTGTTGAAAGUCCT	90071	GGGATUGGAGACAGACATCUGA
269469554	90072	GTGAGATGTCUATTCCCAGCTGUT	90073	GCAACAUCCAGGGACCAGUG
269469898	90074	CTGTTCTGAUACCGTGUGAGAGAG	90075	TGAAGTACUCCGGGTUCACAGA
269471541	90076	TTCTCGTTTTCUAAAAGACGTGACUGT	90077	CTTTGCCTCAGAGAGAUCATCAAGATUA
269473453	90078	CCCUGTATGGCUCAGAAGAGACT	90079	GCTTCTCCCCAUTCATTGTCUCC
269477748	90080	CTCTTCGUCTTCTCCAUCAGCAT	90081	CCAGAAGGTUCCAGCAGAAUCT
269480384	90082	GGGAATGGAGUGCTGTAUGCC	90083	GTAGCTCAAAATAAUGCAAACCTCCUT
269482531	90084	TCCAUGGCCACCATAAAGTUGT	90085	CTCTTTTGUAGGCGGGCCUT
269482545	90086	CCAGAAAGTTUCCCTCCTCCAUC	90087	TGCTTCTGCUGGACACUAACAC
269482576	90088	GTCTCTCTTCCUCCTCCAGGUA	90089	ACTTGCAGUTGTCCCTGUGG
269485586	90090	TGATCAAACCUGGGATCTAACAAAACUT	90091	AGAAUGGGCAGGAAGAAAAGUGG
269490178	90092	AACATACCTUCCTCCAGCCTUAGA	90093	ATAAGGATTTCCACUTTCTGTCCUCAG
269490339	90094	GACAAAGTUCAGTAAAATCTUGCACAGT	90095	GCAACCAGAACAUAGATTGUGCAG
269496234	90096	TCTCUGGGCAAGCCGAUG	90097	CAAGGCGCACCAGUTCCUA
269499037	90098	TGTGCAGTAAGUTGAGGATGCUT	90099	CAACCCAGCUCTCTGTTTUCCA
269503718	90100	CTGCAGTUCTTTTCATCUGAAGCAT	90101	CCATCTTTGCAUTTGTTTATGTACCUGT
269506531	90102	CCAGACTTTUCACTGCTTTCUCACA	90103	GCTTGCUGCCTTTGGUAAGAAC
269516602	90104	TTAACATAAACACUGTAGAGCACAUGGT	90105	ACTGTGAGGAUGGATTCGAAAUAACAG
269519924	90106	CTTACCTTTACAGCUTCTCCCATCUT	90107	TCTCTACAGAACUGTTATCCAATUGCC
269520344	90108	ACTGACAAUTCAGCTGTUGGCA	90109	TCTGGGAGAACAAUCAAGACTATAGUGT
269522045	90110	CCTUGGGCAAAGGUAGGACAT	90111	ATCCGAAGGCACCUCAACUG
269526427	90112	GCAGTCACUCAATCACACCTGUT	90113	GUGTTGACAATCUCCGCAAACC
269532916	90114	CCATUGGCAGTCTCUCAAAGGG	90115	CCCAGCCAAAGGCAUGTATTTACUA
269533796	90116	TGAAACCACCCUAATGCATTTTAUGAGT	90117	CCGACCCAAUGGCAGUC
269533978	90118	TGCGACUGCCATUGGGT	90119	GAAGACAGTGATUCCTGTAAACTCCUAA
269537809	90120	AGCTCATGCUGGACTGTUGG	90121	CATGAAACCAGCCAUATTTAGGGAUCA
269541644	90122	TCTGCAATGCUTGTCTATGTUGGT	90123	ACCTTGACCUTGCTCATCUGG
269547606	90124	GGTGUGAAACAGAAAGAUAAAAAGCCA	90125	GAAAATGAUACCATCTACUGGACAGACA
269549550	90126	CTCTGCTAATTTUATTGAAGCCCAUGT	90127	CTGTTGCAATATGAUCCTAACACCGAUA
269551133	90128	GAAAATUCCCCGGCAACUCC	90129	GGTTACTTTCCUGTCTGCTCUCT
269552602	90130	TCTTGGTTCUCCCAAACACATTUGT	90131	TGAACUCCAGCGCACACTUA
269553606	90132	ATTGTTCAGUCCATCCCTTUCCAA	90133	CUCCAUGACGAAGCGAAGGA
269558510	90134	GGGCUTGUCCAACGAGCAA	90135	GTATTUGAGAAGAGAACUCAGAAGAGCA
269560459	90136	GTAGTTTCCUCCTATCCCTACAUGCT	90137	GGGCCAAUGGAGGCUCA
269560786	90138	GGGCCACCAUCAGCTATATUG	90139	CCAAATTCATCCUGGATTCTAGGACUT
269562787	90140	TTGACUGAAAGGGACCACGUC	90141	GCTGTGTGTAUAGTCACCCTCTAAUACT
269562850	90142	TGTCACAAGAGUACAAAAACAGCAUCT	90143	GGTCTTGGUGCGATAACUGGT
269564100	90144	GCCCCUCCTGTGTCUGAAGA	90145	CTCTATGACTATUCCAAAGGGCATCTUT
269567412	90146	GCCAGGGCAUTCTCTGCUAAA	90147	CAAACCCCCUACATCCCUCAG
269571036	90148	TGGACACAUTGTGGCAUGGAA	90149	TGUATACATUCAGCCAGGACACA
269572519	90150	ACTGCAAGAUACATGGCUCCAG	90151	CAATGATGCUGGTCCACACCUA
269573648	90152	AGTTTCCCAAGUGTAATCCTACAGGUA	90153	CCAATTTTGTTAUGTTGGAAGTTUGGA
269575352	90154	CTGGCUCACAAGTCCCTCUT	90155	GACCTGAGCUGGTTCCUCAC
269575787	90156	CTCATCTCACUGGGTTGGUCAA	90157	CCCTTCUGCCTCAGCTTAUAACC
269581181	90158	GCTCTGGUGGCAGACTTTGUA	90159	CCGCCAGAUCAGAGAAGGUG
269582581	90160	CATAAGAAATGUGCACTTGGUAAAACCC	90161	GGTAGTGGTTUGAATCTGACCTUCA
269582769	90162	GCAACCCCAAUCACCCCTTUA	90163	CTTTGUTTCTGACGUGCCACAG
269585238	90164	CAGAGCAAUGGGCACGATUAC	90165	CCTTTGAUACCACAGACTTCCTCTUAC
269585357	90166	GCCTCCCUGTAGAATCUCGGA	90167	CACCGUGGCCGTGAAAAUG
269585490	90168	CAGCUGGAGATGAGTUCGAGAC	90169	GGGCCCCCUTGAAAAAGTUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
269585806	90170	GGCGTTTAAGUCCCCTGACUAT	90171	GGACGTGAUGGAGCCACTUAC
269588483	90172	CTUCACCCAGGTCUCCGAT	90173	CCATCCACUCCTGCACTTGUC
269588655	90174	GCUGACCCCACACCTTUCAG	90175	CACGCUCACCCCGUACAG
269590379	90176	TGACATGTUAGGACACTTTCCAATGUT	90177	GGGCTUGGCCTAAUGGAC
269590690	90178	GCATGCAAAGGGAAUTTAATTCTGUGT	90179	GGACAACTACGUGTCTCTATTUGAAGT
269595909	90180	GTAACCCCUAGCAGGAAAGTTUGAG	90181	CAGATCAACCUTCTCCCTCUGG
269596117	90182	GACCUGCCACUGGAGAAGT	90183	TGTTACCTUGAAGGACCTTCTTTUGAA
269596128	90184	CCTTTTCTCAAAGUGGTCCACAGTUA	90185	GAATTCTTTTCUGGACAGACUGGGA
269599584	90186	GTGUCAACAAGGAGAUGGAACCA	90187	CUGGAGACCAGCTTUGCAGAA
269600827	90188	CTTCTCCTCTUGGGACATGGUG	90189	AAGAGCAGTTUGGGTTTACTCGTUAA
269603279	90190	GUGGGCACACCACTTUAACAAG	90191	TCTGTTCTGTGTUATGTCGTCTGATTUT
269606739	90192	CACAUAGAACAGGCCCGUCT	90193	CAGTTCTGCUCCATGCTGTTTUT
269606807	90194	AGTGACCUCGCCTCCTCUC	90195	GCTGCCCCUGAAGUGGAT
269609519	90196	CCCAGTCGUAAATACCGACTTCUA	90197	GGAGCATTGTCAUTCACATCTAAGACUT
269613190	90198	CCCTCTCCCCCUCTTCTCTATUT	90199	CCATATCTGCATUCGGTAGGAAGTTAUT
269615314	90200	GGTCUGGTATGGUGAGCGAAA	90201	GGAGACTTTUCTGCGGTCCUC
269615805	90202	CACAGTTCCACAUGTATATTCTUGCC	90203	TTCAGTGAUGAAGCCCAGATCAAUT
269616350	90204	CCTTCTTTAGTACAAUTGATCTGGGCUT	90205	TGTGTTCACTCUTGCTTTGATAAUCAGT
269616440	90206	TTGGAAGTGTUCCTGTCACAAUCA	90207	GGTUAAGCAGAGUGCACCAC
269616513	90208	GCTCAATTTGCUTCATTTCTCCTGUT	90209	ATTTTGGCCTGUCCCGAGTTAUAG
269618428	90210	GGAGGCTGGCUCCAAGATACUA	90211	GCCTTCUCCCAACACCTTUCA
269619802	90212	GUAAGGAAGAUGCAAACCCAGGA	90213	CCCACGCCAGUAGAGAAAAGUG
269622083	90214	CCCGGCCACUGUCACAC	90215	GCTCACGGCUCCCCTTUC
269623113	90216	GCATCTGCCACUGGAACAUCT	90217	ATGGTTCAGAUTTCACTGCCUCAT
269624201	90218	TGTATAGACAGCUTCTGGATCAUCCT	90219	GCTGGAATGAGAUATTTGGCTGATAUGG
269627245	90220	GTGTGAGCUCGCCGAUGAT	90221	TGCTCATGUAAACCAACCCCTUC
269630298	90222	AGGATTGGTAGUGATTTTCATGAUGCT	90223	AAGAGACTUCCAGGACAUGCAAAA
269630797	90224	TCATAATGCACUGAAAGGAATUCCAGA	90225	ACCTGCAGGAUTTGGUAAGCA
269631191	90226	CAGGCTGUGCCAGTCCAUA	90227	TGACAGGATUGGAGCAATGAUGT
269635376	90228	CCCCTTGUACTGAGTATGCUAACC	90229	ACACCTTCUACACCTGGCUGA
269636126	90230	CTAAACTGACUCCAGCTGTATCCTTUC	90231	GGTGTTTUGGACAATGGACUGGT
269637793	90232	TGGTAGCTCTATUTAGTAACTGTCCUGT	90233	CCCCAAGTTCUCATGATTCTCTTCTTUT
269638396	90234	TTCACAGCUGCTUACAGCGA	90235	GCCATTAGCAUGCAAAGAGACUGA
269638656	90236	GGGTTTTTGCUAGTTCAGCTCUT	90237	GGCTTCTGGCACAUAAAACATATAAGUT
269640072	90238	TGGCCCAGAAACAUTTGUAGCAT	90239	TGACCUGCCTCCCTAUGACC
269641833	90240	TGCAAGGTCCCUGTGAACATAUC	90241	AGTTAACTGGGCUTTTATTTTTGTCTUC
269643913	90242	TGUTCGAGCTGUGGCAGAAG	90243	CACTTTGAACAUTGAGTCAACCTUGA
269646455	90244	TUACACCAAGUGAGCACACAGT	90245	CCTAGGAUGAGGCGAAGGTTTUT
269647802	90246	CAUGAAAGCCCCCGCUGA	90247	CAGCGACAGGGUCCTCUT
269651002	90248	GTGCCUGGGCACAUGAAC	90249	GGAUGGAGCCGAUCACCA
269651552	90250	GCCCUCGGTCTUCGAGAA	90251	CCUCGAGCCAGCTUCGT
269652441	90252	CTACTCTGGAUGCCACACUGT	90253	CAGTCTCAATTTUCTCCTTTGTGCUT
269653501	90254	CCTTTACCTTATUGACTGGTTTCTACUGT	90255	GCCAGTGGTUCACCTATTCTTCUA
269654586	90256	CCAAGAGCAGGGCUAGTGTUC	90257	GCTGCCAAAAUTTCATGGAGTGUT
269654623	90258	AGCTUCCGGAAAGACTCUCCT	90259	GGTTTGGCUGTGGAGTTAAUGGT
269656673	90260	GGACAGCACCUCGTTCAAAUC	90261	GGGTGGTCTTUATGCTCATGATAUAAAT
269657676	90262	TGTATTCTTTCAAGAGUGCTGACCTUT	90263	ACATGCAAACGGGUCTGUCA
269662169	90264	CCTTGGTCTCCUTGTCCTTCCUA	90265	CTCAGCAACACAGUTTCAUAAGCAC
269666423	90266	CCTTTGTGUGCCCAGACAUCT	90267	CTACAGCCACAGCUCAGTACTUA
269668401	90268	CATCATTCTTGUGGCCCCTUC	90269	TTTCTTTCCCUTCTGTTGGUCCAT
269669232	90270	GGCCUCAGAGGCTGUGAC	90271	TTGGCTTUGTAGACGUGACCAT
269671511	90272	CCACCUCCAGACAGAGTGTTTUC	90273	CCCTCCTCTUGCAGACAGGUAT
269675474	90274	CCTTACATTTTGUTGCTGTTCTGCUT	90275	CTGCTTTTCTGUGTAGCCAACTTUC
269675595	90276	AGAAAGAACACAGCAUTCAUGAACCT	90277	GAGGACAAGTUTATTGTGTGCTUGAAC
269675746	90278	AAGTUGGCCGAGGCACUT	90279	CTCTCCCUCCGGGCUAC
269676123	90280	TGAAAATAAUGCCCTCAGATGUCCA	90281	GGATTGATGAAUGCGGTGACAAUT
269683621	90282	AGCTGTUGGGCCTAAACCUG	90283	ATGCCATTCTUGATAGAGTTGCUGAT
269685346	90284	TGGTTCUAAAGCGCTGCTTUCT	90285	CCAGAGCCACAGACAUGTACAUT
269686336	90286	GTACGAACUCTTCTGGTUACAACAGA	90287	TGAAGTTGATUGATTAAGTCAUGGCGAT
269686489	90288	TCCTGGAACCCCUCCTTCTUT	90289	GTCATCACAGCUGCACACTUG
269687060	90290	GGCACAAGGACCCUGGTUT	90291	GAACTCUCCAGCATCCUGACC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
269688617	90292	AGCGAAGUCCCCATGTGTTUT	90293	AGGTCCCTGCUATTTCCCATAGUT
269688668	90294	GATTTCAGUGGCCATUAAGACCCT	90295	CGGAAACACAGGUCTTATGACTACTUT
269689358	90296	GCTGGCUGACGTTGUGGAT	90297	GGAGGUGTGCCTUCGGT
269692076	90298	CTTAGGGUGGCCCATUCACT	90299	CATCTCAGGTCUCTGATGAAAACCUT
269693347	90300	TTTACCACCACAGUGATCTTCATCUG	90301	ATGTACTCGAAGGAGCUTCTTTGTUT
269693888	90302	AGGCTATTTTCTAUCGTGAAAGTTGUGT	90303	TGCTGAATTGGCAUTATAGGTTGTGAUA
269694019	90304	CATCCAUGATGTACTCUGAGAACGAC	90305	GGGAUACCATTCCUGGAACAGA
269697698	90306	ACCTATTGGGUGGTTTACAACTTCUC	90307	AGGAACUCCGCGGTTCAATAAUT
269698278	90308	TCTTCCCAAUCCTTTTGGTGAUCC	90309	GAGGAUTCUCCCAGCAGCAA
269698358	90310	GGAATCCCACCUTGGCTGUG	90311	CAAGGAGACCUTCACCGTCUT
269699203	90312	CACAGGCACACUGACCAUC	90313	GGGAAAGCAGCCCCUTACUC
269699487	90314	TGTCCTACACAAGAAUGCAGAAATUCA	90315	GTCTTTCAUACAGGGCUGCACA
269700785	90316	TGTCCGCAUCGCTCTCATAGUA	90317	GCTUCGCACAGGTUGGGT
269700947	90318	ACTAACCTTUTTCATGCAGUCCACAT	90319	GAGGCAGTCUGGAGGAACTUAG
269702681	90320	GCAGCAGGAUTCACUCCAGT	90321	AGCTGTCTGATUATCTGAAACACAAUGT
269704377	90322	CGAUGAGCTGCUCCAGAACAC	90323	TAAGCCATAATUCGTGCAGTTTCTUAT
269704559	90324	CGTGGCGUACACGUGGA	90325	CCCTTGCUGACCTCCTUCT
269706673	90326	GGAAACCGUCAAATTGCTTCGTUT	90327	GCAACCUAAAAACAAGTAAGACAUGGT
269708291	90328	CCTCTACUGAAGGAGTTCCUCAC	90329	TTAGCTACAGUGTAGGTTGCTCUAAA
269709359	90330	CTCCAAGAGAGUTGTAGCCCUT	90331	GGGCAGAGUCAATGTTTCCAUCA
269709893	90332	GGAAUGACGCUGAAAACAGGAC	90333	TCCTTCTTCTCGUACTAATGCTTCTUCT
269710926	90334	GCACAAAACCUATACATCCTTTCTUCCT	90335	GGGATAGGCAGCAUGTGGATUG
269712342	90336	CTTCTCTGGCAGGUAAAAGGAAAAUAAC	90337	GCCGCAGUTCATAGGTAUAGGAAT
269713082	90338	AAUTTTGGAAAAGTGUCAGAAGGCAAT	90339	TGGTGATGGAUCTGATGAACCUGA
269715626	90340	GCTTTCCAACAGCCAUGAGCUA	90341	GUATCCAGAUAACAAAAGCAGGAGGA
269716739	90342	TGCCAGTATACUCACGACAGUCA	90343	TCCATTATATAUGCACTGGGTTCTUCAAC
269717300	90344	TTACCCCCUGACTGGGUGA	90345	AGTGGATTGGGUGTCACGTAATUT
269722160	90346	ACCUGAUAAAGAGGCCCGAGAA	90347	CAGACACACCUATGTGCAGUGT
269722190	90348	GATTGTCCATUCATCTGTTAATCCUCCT	90349	ACTCTAAGCUCAGTCAATGGAAAUGAAA
269723131	90350	CAGAGTCTGCUGAATATGATGATGUCT	90351	GTCGTACUGAACCAATTGTATCATTUGT
269723679	90352	CCTCATCTCCUTTCCAGCGTUC	90353	GCAACAGTGCAUGGACAAGATUC
269724225	90354	CGTTTCATCAAAUTCTGAGCTAAUCCA	90355	AAAATAACTACTUGCAGAGCCAGUACA
269724890	90356	CCTCCTGCTTTUGTTATCTGGATACAUT	90357	TGGAAGTAAAAUGGCAACTCTAAGCUC
269725537	90358	TGAGCTTAGAGUTGCCATTTTACTUCC	90359	AGCTTTCAATAACUAGGGCAAAACTGUA
269726604	90360	CCUGGGAACCCAAAUCCAACT	90361	TCAGGTUCCGGCCACTTUAAAA
269727664	90362	TGACACACTCUAAAAGATAGGCTGAAUG	90363	CCTAGUCCAGCCTTCAGAUGGA
269727960	90364	TGAAACAAAGUCTTCATTTCUCCACAGA	90365	CTCTGGGAACACAAUTCCACCAUA
269730311	90366	TTAGAGGCUACAGACTCUGCCT	90367	GCACTAGCUGCCATTAAAUGCT
269731758	90368	CAGCTUGGTGAGCAUCACAAC	90369	GTGTGAGCTTUTGCATGTTCTCUAAAT
269732277	90370	ACTTTCCCCUACCCTCAUGAAGT	90371	TUCTTCTTCAGUACCCAGGACAGA
269732650	90372	CACAAGTGTUAGAATCTGATCTCUGCAT	90373	GATGAGACCAAGAAUAACUGGGAAGT
269732920	90374	CCCGAGAAAGAGCUGACACTUC	90375	GTTTCTATTTGACAAUATAGTTTGTTGCCTCUA
269733428	90376	CCAAGGCCUGAAAACTCCAUCT	90377	CATATGCTGTCAAUGGATGGAAGUACAT
269733843	90378	ACTGGAAGCUCATTTCCCACTUC	90379	TTGCTACCAUAGGGATATGTGTAAUCCT
269737704	90380	TGATGACTUGGAGGTATGGTCUCAT	90381	CCAATCAACUTTCTATCATCUGCAGGA
269739012	90382	GAAAGGUACATTGCTAUGGAGGACA	90383	ATGATGCTACCAGAGUCTACCTAATUCT
269745170	90384	AAAATCTGCAUTAAGCTGCAUGAAACA	90385	CGCTCAGAGAACAAGUTTTACTTUCCA
269746437	90386	CCTTTCTUCAGTGGGTCUCAGT	90387	CATCCATGTACUCATAACCCAGCUC
269748813	90388	CCTAGGGAGAAUGACCTTAUGCCA	90389	CGGCATACAGAAUTTCCTTCACTUAC
269750797	90390	CGCCAUGGCAACTGTCAAAUC	90391	GTTCTTTCCTAAUGGTGACTGTTUCCT
269750958	90392	GGGCCTTATTTAUCATCTGTTCTGUCT	90393	TGATGGTGTCUAACACAACCTTTGUT
269750987	90394	ACTGTTCCAAGUGGTGCATATUCC	90395	AGCTCCAAACCAAGUGTTAGAATGTTUA
269753164	90396	AATGGCCACACAGUTGAUGAGAT	90397	ATGTGTCCAGTUTTCTTATTTTGCTTUCA
269759504	90398	CCTAGGCCAAGUTCCCTUGAG	90399	CCATCTCGTUGCCGATTCATATATUCAT
269760417	90400	CTTCTCCCCAACAUGCTCTGUT	90401	GTCCTGCACGAAUGCAACUC
269761753	90402	CAAACAGCCGUGCGTCAUAAA	90403	CAAAACGGGACUGGCTAGTUAAAC
269763311	90404	CTGAGTTGCAGGUGAATTTGTAAUGT	90405	GGGTAAACCCGGUCATCATCUT
269763532	90406	GTGAACTGUGACGCTCTCUCA	90407	TTCAGATCCTUGAAGCTCCATTTGAAUA
269763727	90408	CCTGACCCTCUGAGTCTTTCTCUT	90409	CTCCATTUCTGGCCUCAGAGAC
269769478	90410	CCGUAGAAGCCCACGATGUA	90411	CCCAAATGCCUTCATCCCGUT
269774413	90412	GGCACAACUCCAGAUGAAGACT	90413	GCCCCUGAAAAGCTCTCATCUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
269774675	90414	GTATGCCUGCCACAGAGATUACC	90415	TCGATCCCCUTCTTCCUAAGCA
269775341	90416	ACCACUCACCTAGGTTUGCAAC	90417	GACATGCTCACUTGTGGTACTATTTUC
269779186	90418	GGGCGATCUCAAAAGTTATCUCC	90419	AGAAACACUGGATGCUGGAAAGT
269781602	90420	TGAUCCCCACACCUGACAAAG	90421	GTAAGAGACCUGGAAGCCATGUG
269783789	90422	CAGCATCUGAGCAAGGGTAUGAA	90423	GCTATGCCAGUAATCAGGGTTAUCAA
269783908	90424	CCTAGACCTCAUCCTCTTTGAGCUT	90425	TCAGGTGGAUCAAAGTGTCTGUG
269787200	90426	GGCAAACTUACCCAGCCTCTUT	90427	GGATTGTGACTCUCATTTCTTTTGGUG
269788816	90428	GCUCTGAAAGTCUGGAAGAGAAAGA	90429	TGACCCTTGUGAACAGCTUGG
269789333	90430	GGCCCAGCACAUGTAATTTUGT	90431	CTTGGAAAGTGAUGCAAATACTTCAGUT
269795813	90432	CACCGAGUCCUGGACAAGAT	90433	CTTTATGUCTCTCCTGUAGGAAGCC
269797772	90434	CAAAATGACCAAGUAATAAGCTGUCAGT	90435	GACCTTTGCTGUAACATGCTGTATUT
269797825	90436	CCTCAGCCAUGTTTCCUCACAT	90437	CACGGAGACCUTCCTGACAUT
269799570	90438	CGACAAGACCAACCUCCAUGT	90439	GGTGGCTTTGTUCAAATTAAAGGTTCUT
269800873	90440	CTGAGGCCAGGUGGTTUAAGT	90441	AATGCTUCACAGCAAACCTGTUC
269807753	90442	ATGAGGCUGCTGTGCTUGAT	90443	AGCTCAUGCACGACTAGTTUCC
269809920	90444	CAAUGAGCCAGACTUGGAAGAC	90445	TGATGAATGTCUGCCAAGCCTUT
269811759	90446	GUCTTCAAGTGTTUAGCCACAAAGG	90447	GACCTGCAUGCTTTTCTTTCUCA
269815641	90448	CAACAGCCTUAGATGCTCTTAGUAAAGA	90449	GCCAGCCTAAAUTAATTCACTCCATUT
269816666	90450	CATCCTTTATAUTGCCATTTTTGUCCCA	90451	GCACGATAUAACAGGCCAAGCATTUA
269819689	90452	GATCCCAATGCCCUCTATGTCTTAUT	90453	TGCACACCAGGUTACTGTUGAC
269819757	90454	CCAAGUTTTAGGAGATUCAGAAGGCAAA	90455	CTAACAGAACUTCCGCCTCUGG
269822068	90456	GTTTTCTGGAAUGGAGTGAGTATAGUCAT	90457	CTCTTTGCCATUAACTTGGATTTCTUGA
269823251	90458	AGAGUCCCCGGUCCAACA	90459	CCAGGGCAGGUGGAAGAAUC
269825104	90460	ACAGGATTCCUGAAAACCAACTGUA	90461	CTCGAUCACCGTGCAGTUCT
269826635	90462	GCCACGGUATGTTCCUCGT	90463	AAATTCCTGGUCCCCGATCTUAAAA
269827132	90464	GGTCTTCACCAGUACATTTCATTCUCA	90465	CCTCCACCAGUTTCTGTATTUCCT
269827770	90466	AAGTCATGCUAACAGAGTGUCAAGAG	90467	CCGACAGAAAAUATGTTACGCUAAGAGAA
269828795	90468	CAACGACTAUCAGCAGCUGAAG	90469	CACUCGGAACAGCAGCAAGUA
269830478	90470	GTATGTTUCACTCTATGUCCCCCAAA	90471	TTCCTTCTUGGGTTGCTGTUGA
269831716	90472	TGGTCAUGAGGGAAAAUAAGAACCC	90473	GCAGAATGTUAAATGAACGAAUCCCAAA
269832136	90474	CCTGGCTGCUAGGAACATTCUG	90475	ATGCTTCUACTTGAGAAUGCCAAGAA
269832760	90476	CATCAACUCGCUGCCCAAC	90477	AGACCCGGUTCTCGACCUT
269834686	90478	AGATTTACCTCCCAAAUGTCAGATGAUG	90479	CTGTGCUGAAAACAGTCTCTTTGUT
269838052	90480	TGGATAAAAGCGGUCAACTUACCC	90481	TGAAGGAGCUGCATAAAGAGUCAAAA
269838076	90482	CCCTATTUCCCTCCUCAACCAA	90483	ACAATGTAGCUGACAGCCAAAUCA
269838560	90484	CTGGATUGGCACCTGCUAACT	90485	GCCGGGAAAAUCATGTTCTTTTCTTCUA
269839453	90486	GCAGTCCATUCTGCCTCTGTTUT	90487	AGAGTTGCTTUTTGACTGTCTUCACA
269840156	90488	CAAGCUCACGGTCATUACCGA	90489	AAGAUGACCAGGGCGTAGTUG
269840573	90490	TGTTTAAAGAGAAUACGACCAAGCCUAAC	90491	GGCCAGAGACUTGCAGACAUT
269842026	90492	CCCTGCAGUGATTCUGAGGAC	90493	GGAGCTTGTGAUGGAGGAAAGUT
269842266	90494	GCAGGGAGCGGUGAGUG	90495	CCGCCGUCCTCCTUCAT
269842916	90496	GGUCCACAGGGAUGCGAAG	90497	CTCCCCAACCUGTCTCTTTTGUA
269844764	90498	CAGTTGCATUGTTCCACAAAUGGA	90499	TUTCAGGUCCCGAGGAGGT
269844984	90500	AGGAGTGGAUACAGGAAAUCAGAAGAT	90501	GAACCTGCAUTGTGACTGCUG
269846173	90502	CCAGCCAAUCGTCTCUGGT	90503	CCAATTAGAAACUTCTGTCACTTGUGT
269854377	90504	GAACGUTCAUCAGGACAGGGA	90505	TCCTAAGCAAGGUTCTGGTTTGTTTUA
269855707	90506	TCAAGGCTUGCCAGGACUAA	90507	GCGCAGAGAGAUCGAAAUCCAG
269855758	90508	CAGTGGCAGUAAGGCTGGUT	90509	TCCAAUAGGGAGACCCACCUG
269856497	90510	CGCGGCUGGAAACTCTTCUA	90511	GGAUCAGGGACCAGUCCACA
269866011	90512	CATCAACCCAUACTGCAGGUG	90513	ACUTGGCUCGGGAGAAGAAAAG
269869408	90514	GGGCACTAAGUTGCCAATAGUAG	90515	CGAAUGTTGAGTUCGACCACCAT
269870694	90516	GGGACAACUACCTGTATGAGAUCC	90517	TTTGUGGGAAGCCACGGATUA
269872257	90518	TGTTTCTGUACCTGCTTTAATUACGGT	90519	GGCCACTCUGGTTTCAGGUT
269873391	90520	CCAGAGTUCCCACAACGAAATTUG	90521	CTGAGGAGGAACUGGCAUCAAAA
269873503	90522	CTGACCTCUGTTACCTCUCCAC	90523	TGTACTCATTGTUGATGGTGGTCTUC
269879314	90524	GTTGGTGGGAAGUCCAGCUT	90525	TCTCCCACCUCAGAAGCCAUA
269881635	90526	CTTGAGCGCCACGAUGAAAUG	90527	AACCTCTTAAUAACCAAAACCGGTUCT
269889206	90528	TGCTATTGUGTTTCTCAAUCCAGGAA	90529	CCAAGCATTTCAUTACCAGAGTTUACAT
269890290	90530	CCACTGTGUGCCCCTCTTATTUC	90531	GCCAAGGGAUTCAGGTUCAGAAT
269891202	90532	CAGGTTCCUTCCACTGUACCAAA	90533	GGATTATGAATUCAGGGTTGTTGCUG
269894332	90534	AGACAUGGCCAACAAUGACACA	90535	CGTTTTCCTCCTUTCAACTAACCTAACUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
269896136	90536	CCAAGCAAGACAGGUGCTTUT	90537	GGTACCGGUGCCAGGTTAUG
269897900	90538	AGAAATGAAGCUGTTGCTGGAAUG	90539	GTGTGUGACCAGAATTTUCAAGAAAGAA
269899785	90540	CTTACCTTCTGCUATGCAGGTGTUAT	90541	GGGTATGATGAUGCTATTTTGAGCTCUT
269901119	90542	CCCCCGCCCAAUGTTATUGA	90543	AGCATAAACCUAAAAACTCUGAGGAACT
269902530	90544	CCAAGGGTGUGGTGAAAGAUG	90545	CATTTTGGCTTTUCAGGAACTTTCTCTUA
269908799	90546	GCCACCCCAUCAATTTCTTTGUAA	90547	ATCCAAGCCUTACCCAAACCUC
269909812	90548	CCACGUCGAAGAATCGCAUCAT	90549	CAACAGAAUGGCAUCACCCAAAG
269914831	90550	CTCACCTGTGCUTGAAAGTATTTCUT	90551	TTCTCCCTCCUCTTCGGTCTUT
269916151	90552	CACCTGTGUTTTCAGGGAUACGA	90553	CAGGCUGTTCTTCTUAGAGCGT
269919979	90554	CCAAGCCCGCUCATGAUCAA	90555	TGAAGGGTCUGGTAGGATCATACUC
269924505	90556	AGCTGGGAGGGACUGAGTUAG	90557	CCCGACGCGUACAGGAUG
269926378	90558	CGAGGCCAGGUAUACGGACAT	90559	GUACCTGUCGGGCCAGAG
269928748	90560	GCCACTGUGCAGAAGCTCUC	90561	GTACCAGGGAUGAGCTTGACUT
269931208	90562	TGAGCCCCCGAUACTCTATUCC	90563	GCTGCGCUTCGCATTCTUAC
269935463	90564	TCAACCACAGCAAUGCCATCUA	90565	GCAGGAGTATUACCATACAAGGAAAUCT
269936381	90566	GCTCTTGCCUCGATGTCCUA	90567	TGCTCUCGCGCCACTUAC
269938245	90568	CCCUCAGGGCCCAAGUT	90569	CTCCATAACUCATCACTUCCCACAT
269940465	90570	TGAGGACTTUGTTAATGCCAAUGCT	90571	TGAGATTGTCACAAAUTTGCTTTCTUCAA
269942705	90572	AAAGCCAAAACCCCUTCUAACAGA	90573	CACCGTTGUGGTCCGGAUT
269945957	90574	ACAAAAGAGCUGATGTTTCACCAUACA	90575	CTTGTGCATGUCCCACTAACTUCT
269946935	90576	GCCTCUGGAGGAACCACUGA	90577	CTTTTGTUGCCGGGUGGAC
269947043	90578	GCAGCTTCUCCCTCTCATTAGUG	90579	AGATTTGGAGTGAUGTCCTCAGTTCUAT
269947325	90580	GCATTGCTAATAUGTAATCCCTTTTUCAACT	90581	CAGACCGGAAUAGCCTGTUCA
269948255	90582	GCAGAGUCGTGGTAAACUCCAT	90583	GAAAGCATTGCCAUGCATGACATUA
269948403	90584	ACCTACAGTATAUGAGAAATGGAGAGCUT	90585	AGAUTCCUCACACAGCCAACAG
269948892	90586	CCACCTACAAUTAATGCTGGTTTUGAAT	90587	ACTTACTAGTTATUGCTGTGCCAAUGT
269949564	90588	CAAGTCCUATTATCAGCUGCCAGAT	90589	TCCTGTTTTGTTGUTGTTGTTTCTTTCUT
269950627	90590	GATGTCTGGAGCUTTGGGATACUC	90591	TGUTCCAACCUGGGAGGGAT
269950911	90592	CCTGAGGCUGGAGCTGUACT	90593	CCTCCUCCCCCAGCAUC
269951298	90594	GGTGTCACUAGAAACATCACAUGCT	90595	CCATTCTGAUGAAGCACCTTUAAACC
269952645	90596	CCAAAGCACUTTTCTGCTGCUA	90597	TTAAUCTTAGTGGAGTUGAAAGGAAGCA
269952998	90598	CGGCTGUGACGCGAGUA	90599	TGGTGAAUGGTAGGUCAGGGA
269953092	90600	CTGTACCUGCACTTTTACACTTUGG	90601	AGGATAUCGACAGTGTGGUACAGAA
269957203	90602	CTCACTGCCCAUTATCTTAAGACAUACT	90603	TCAATGGAGGAAUAAATGTAGAAATUGGCA
269957907	90604	CGACCCUCCGGGAGUCT	90605	GACUTTTGGCUACGGAGAAGGA
269959016	90606	CCTCCCCUCCCCCTAUCT	90607	GGCGACUGGCAATGTTUGG
269959599	90608	AGTCTATAAACTUCACAGGGAGACCUT	90609	TTTACCTCAAGUTTGGCTGCAAUAAAT
269959691	90610	CCATUCCCCAACAGCTGUG	90611	CACCGGGAUGCCAGGAUA
269960447	90612	CGCCCAUCAGCACAACTAAATUC	90613	GGTGTAGTGUACATTGAGGAGAUGAC
269961478	90614	GGATCCTGCUATGGGAGATCTUCA	90615	GGAGGAGGACUGGAAAGUGG
269963235	90616	GCGACACAAGAAAAUGTTGTAAAAACUC	90617	GCCAACCTCUTCCCCCAAUC
269963333	90618	GAGCGGAGCAUGGTAACTUCT	90619	AATCAGTUCCCCGAAGCTGUC
269963370	90620	CGATTACCGCGUTTCTTTUGAGG	90621	CGCCCUAAAACCGTGAUAAAGGA
269966374	90622	CCCAGAAACUCAAUGAGCCCAA	90623	AACGTGTCUGCCATGUACAAGT
269967648	90624	CCAGGUAGAAAGCCGAGUGT	90625	CCTGCTUGACGCTGTCCUC
269969000	90626	ACTCAGUCTCCCCTUGGACA	90627	GUATCTAGGGUGAGGAGCAGACAA
269969607	90628	GCCCCAGCUGUGGAAGG	90629	CGTUGGGCAGGGTAUGGT
269970090	90630	GCCACCGCUACCTCGTUT	90631	AGGUCUACCCCCAGGCA
269971442	90632	CCTTCTCAGCUGCTCTGTTCUC	90633	GCTCTATUCGGAGGCACCTUC
269971951	90634	AGAGUCTTTAATGCCUGAAGGAGGA	90635	TGGGCAATGGUAGAGTAGAGAATUCA
269974005	90636	CCACCUTGTUGGAGACCACAC	90637	GCGACCUCCTUGCAGAAAGAC
269974491	90638	CACAGCTCTACUTCATTTCCTCUGAT	90639	GGAUCCGAAGACAAGCCCTUC
269976725	90640	GTACTCTACUGAACCATGGCCAAAUT	90641	CTTTCATAACUGCCTTTTTAAAATUCCAGGT
269977028	90642	AAATTCCTAUCAAGAAATGGAGAACUGCT	90643	TTCCTUCCAGACAAAAGACCGTUT
269977056	90644	AAACGGUCTTTTGTCUGGAAGGA	90645	AACAATTCTTTTCAUCTTTCATGCTTACTAUT
269977533	90646	GCAGCGCUCCCGCTAUC	90647	AACTGCCUGGAGCCGTUT
269980499	90648	CTATGTCCUCGTGGCCAUGAA	90649	CGTGGCUGGAGTTGGTGTTAUAG
269981169	90650	GGCTAAGAUGAAGAGGAGACCTUGA	90651	GGAGAAGTUGTCCTGGUAGCAC
269981327	90652	CTCTAATGGTGUCCTCCTCCTCUT	90653	ACAACTTCTUACCATCTCCUACCCA
269982710	90654	CAGCUGGACTGGAAUACACCAT	90655	GGAGGCUGCTCTTGUCAAAGG
269984737	90656	GGCCCTTCUTTGTCTGCCUAC	90657	AGGAUGACUGGGAAGACAGACT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
269986456	90658	TGTGATCUGAGCTCTGCCTUG	90659	CCTCCCAGGGACUGACAATTUT
269989120	90660	GCTTTCAGCCAUTGGACUGGA	90661	TTCTCCGAGAUCCCCAAUACGA
269989212	90662	GATAACTGUGAGAAGCAATACCGUCAT	90663	ATGAGTTAACCAACUAGGCCACTUAC
269990307	90664	AAGCACCAUGCGGGAUGA	90665	ACTTTTGGAGAACUCAACAUAAACAGACT
269990714	90666	GCTCAGTCCUCTCCCCCUT	90667	CAAAGGCACCCUCAGAGCUA
269991153	90668	GTTTGCCATCUTCGTCATGTUGAA	90669	GTGAGCAGUCTTGGGTCAUCA
269994217	90670	GGACAGAGCCUGGAGCUAAT	90671	GUCACCAAAGUCCAGCACAGA
269997797	90672	GTAGTGTCCACGUGTGTGCTTUA	90673	TTCCTTCAAGGAUACTTCTACTGGUCA
269998767	90674	AACTGATUGAGGACAGAAGAUACACAAC	90675	TGTTTGTTTCCTAGAUTCTTCTTGCTCUT
269999378	90676	CGCAGUGCTCACCTUCCT	90677	GGCUGGAAGCCTTTCUCACC
270000980	90678	CACTGTTTTCUGCATATTGCUGCT	90679	TCAGTGTAUACCAGCAAAATGGAAAUGT
270004075	90680	CTTTGAGTUCGCCGACCTUG	90681	CCAGATGGAGUCTCCCTAGGUA
270004280	90682	CTACCTTGCCACAAACUCCTTATTCTUA	90683	CACTCTGUGGAAGAAATCACTGAUAAC
270006083	90684	CATATTTGCAGUCTTCATGGCCAUC	90685	TGTCTTTTGAGUGTGTAGAAGTGTTUCT
270006533	90686	GGTCCACCUCAGAGGTCUGT	90687	CCCAGCCAAUAGCCACTCUAA
270008618	90688	AGCAACAAGAAAAACUAAGCAAGTUGAC	90689	AGTTTTTGCUGAGTGCCTAAGUGA
270010294	90690	GGATAAACAAUAGCCTGCGGGUA	90691	CAGCATTAAGTTUCAGCTCTCTGTTUT
270013737	90692	TGCTGACCUCTGCCCUCT	90693	GACTGCCCUCCTTGUACCA
270014379	90694	GCTCTGCACAAAGAUTGCACUA	90695	TGCTTCCAAAGUCACACTGAAATAGUAA
270015340	90696	GCCTGUGCGTCTGUGCT	90697	GGCCAGCAUCCTCAGGUA
270015907	90698	ACTAAGAAATGTGUTGCTTGTTGCTUT	90699	CCCAAGCAAUTTGTTTGUGACCAT
270016113	90700	AGACGGCUGATCCAATGGUG	90701	CATGCTTTTGAUGAATGCTTTCTCUCT
270017832	90702	TTCTTTCCUTCAGCCCUAAGCC	90703	GGCAAAGACUGCACCAGATGUA
270018834	90704	GCCATCUCCACAGTCGTCAUC	90705	GGGAAGATAACAUATGTGCTCATCUAAC
270018960	90706	CCTGCAGTUCAGGCTGAUAAGG	90707	AGCCTTGGAGUTCTTTGCTATGAAUT
270019227	90708	GCCTAGAGAUTGCCAGCTUCC	90709	TCACTCCCUGCTAGAGTCTCTUAC
270023511	90710	AGTTAATGCAUCTCCTTTGTTTUGCAG	90711	ATGTCTGCCAGCAAUTCACCTUA
270024953	90712	GAAAAAGCAAAUCCAACTATTACUAGAAAACAT	90713	GCCAATGGGAAUCATAGCTGTUG
270025021	90714	ACAGCTATUGGTGTCATUGGCA	90715	TCCTCAGTTTGGCUGTTTATGACAATUA
270026210	90716	AGAATGGCCGUGTTCATGCUA	90717	GAATCATGUAGAGTTGCTGAAUCACAGA
270026216	90718	GAATGTTACTGAAAGAUGTTAATGCATTTAUGG	90719	CAGACAGACTCUCACTGATTTACUCAT
270026459	90720	CACCTGGAUATCTGTGAUGGCAT	90721	GGTGATTGCACUAACATTGTTUGAAGA
270028870	90722	CCCTCCCCUCTTCAACAACUCT	90723	GGCCAACTAACAUTTAGCCTTTCTTTUT
270030547	90724	GAAGGCAGGCUTGGTACGUAA	90725	GGGAAAATGGUAGAAGAAGTGGAUGG
270032226	90726	TTCCCCAGUCCGACCAGAATAUA	90727	TGAAGCAAAAAUAGGTGTGGACGTAUAA
270032966	90728	AGCATTCAGTAAUCGATTTCACTUGACA	90729	ACCUGGTTTGAGUGCAGGAAA
270033747	90730	ATTTAATAGTGCCUGCAAGCTTUGG	90731	AATTCCCTGATACUCTAATACCACCUGAA
270035026	90732	GTTGACAATUAACTTCTGTGUGGCT	90733	ACATTTTCCAAAAGCUAGTGCACATUG
270035446	90734	GTTTTCCCATCAGUCCAGTAGATGUAG	90735	TGTATCTGUCAGCCCATGTAGTATUGA
270039550	90736	ACAUTTAATTGUCCCAGCCCAGT	90737	TGACATTTUGCTGTTTTCUCAAGCA
270042634	90738	TCCTCCTATCATUTCATGTAATTAAATTUCACT	90739	TCGAGTGCUGGAAGGATTGTTTAUC
270042734	90740	ACAATCCTUCCAGCACUCGAC	90741	GTCCCTAAAGAUGAAGTGTTAGCAAAUC
270042987	90742	GCCGGTGCUACTTGTTACAUGAAT	90743	ACTCAAATTTACCUCATTGTCCUGCT
270043233	90744	TCAAAAGGAGGCUTCCCAACUAAA	90745	AACGAGAAGCACAUCAACCUGA
270044078	90746	TTTATGACUCATTGCAGCUCGACT	90747	TGGGAGUAGTGGACTAUCAAGGAAAAA
270045915	90748	GTCTAAACACAGCUCTTTTTGGAUGAAA	90749	TCCAGAATGGAAUGCCGCAUAT
270046742	90750	CCAAGAUGAGCCUCAGACACT	90751	CTACGAGGCGCAUGATGTUC
270046793	90752	CCTTTAAACAAUCACGUGAAACCAAGA	90753	TGGAGCAGTUTTATGGAATCAUCAGAAAT
270048462	90754	CGGTCTCAUCTCCGTCTCUCC	90755	ACAGACACCGGCAUAGTAGUAGT
270048524	90756	CTCCCAGGAAUGCCCTTAGUG	90757	TTCGTTGGGAUCCTCGTAAGUG
270049771	90758	CGGATAGCAAUAGATAACTCCTTGTUGT	90759	GCAGGTTUCTAATATGGUGGCGAA
270050024	90760	AUTTCTGCATTTTUCGCCACCAT	90761	AGCAATTGCGUGTAACTATAACAGUACA
270050691	90762	GGGAUGAGAAGCAGGACAAUG	90763	CGGCCCAUCCCTAACTTUCAA
270051480	90764	CCTTGTCAGTUCAAATCCCTGTUG	90765	CACATTCUAGAAGGTGGACCUGA
270052805	90766	CAACGACACGGCCUGTGUA	90767	GATCACAAACCCCUCGGAGUC
270053136	90768	ATTGTGCAUCGCGACAUCAAG	90769	CCAGGTACUCCTCAGUCCCAT
270053942	90770	GTAACATGGUTCCTGCUGGGAAT	90771	TGATGTCUTGCAGAGUGACCAG
270054738	90772	TGATGAGAAGUTCGTCTCGGUCT	90773	GAGACAUAACTCCTGUGGAAGCA
270055294	90774	AGCAGTGAUGACTCTCUGGGA	90775	CCTGGAGTUACGGGATTGUGA
270057810	90776	TGGUGGAAGCGCGAGAUG	90777	CAGAGCCCCAAGUCACUGA
270057907	90778	CTGTGCAGAUAAAGTGGUAACAGA	90779	CTCCCTCCTCCUATTCCCATTTCUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270058596	90780	ACTTCUGCGCCAACAUCCT	90781	GGCGGGUAGUGACCACAC
270059322	90782	GCAAGGGCUTAGCAGGAUCAG	90783	CTCTCCTGGGUCTCCGTGAUA
270059854	90784	CTTACTTGCCACUGAAAAGTTGTUGA	90785	CATGCGTGCUTTCCTCATGUAG
270059944	90786	CTGCCTTGAAUGACAGTGTGTCUAT	90787	ATGGGAUGAACCGAACAAGGATAAUT
270060550	90788	CTTTGTGGATTUGACCCTCCAUGA	90789	CTAAGCUACAGCCAGGTCACUT
270062058	90790	CCTCUCCAGATGCUCCCAAAA	90791	GGTTACTGGACCUTTGGAGCUG
270063110	90792	GGATGAAGATCUACATTGACCCCUT	90793	AGAUGTTUGGACACCAGGAGAAC
270065220	90794	CCAAAUGACATCACCUCCCACA	90795	CCAGCTCACCUTTTCTCCTTTTUCT
270067593	90796	CTGGCTGCUCTGTCTTTGAAUC	90797	TGGCTCCAUCAAACGTGCUT
270068802	90798	CCUCATCAAACUCCCCACCAA	90799	TTGAAGGUAGGCCTCUGGGA
270068877	90800	CAAATCTAGCUACAATTGCGCCUT	90801	AATTCCTUGGCAAACTCAUGAACAG
270069802	90802	CATTTCCAGAGACUTCAGACCAUGAT	90803	TTGTTCATGUGATGTGCTGCUG
270071303	90804	GGCTGAUGCGTGAGUGCT	90805	CGCGGUCAGGCCAGAUG
270072350	90806	CAGATGCUCGCCTCCGTUAA	90807	CTTTCCGUATTCATACTTUAGGAGGGA
270075827	90808	TGCAUGGACAGCCATAUACAGG	90809	CCTGGGUGCACAGTCTUGAT
270076341	90810	AGCTGCAATAGUGGTTCTCTCTUC	90811	AGCAGACAGACUCCUCCGT
270078455	90812	GGTGCAGCAUTGGTGAACAUT	90813	GCAAAGCAAGTUTATTCTGGCTCTUA
270084018	90814	TCAGCTTATUACAGCCAAACTUACACA	90815	TCAAAACTGTAUCTACTCACCACUCCA
270085914	90816	GGTTTTCTTTGUGAGCACTTGAUAAGT	90817	TGAGGATCTUCACCATTCAGCTATTTUT
270088150	90818	TCAACCCCCAAUCAAUACAAAGCA	90819	GATCAGTTCAGGGAAUGGAACCAUAAA
270088513	90820	GCCTATTCCUGAGATGCUGAGGAT	90821	GTTTCACUAACACATGCCCUACCT
270089806	90822	GCCCCGAACUTTCTCTGAACTUA	90823	CAGGGCTUCAGCCCATGUAG
270090404	90824	GCCCTGAUAGCTCTTCTGATUCCT	90825	GTTCAAAACTGTAUCTACTCACCACUCC
270091733	90826	CCTGGGTTCUGAAATTGGGAUGT	90827	CCAGCTGGAAAGUTAGCTTGTUG
270092252	90828	CCAGAACAAGGAGGCUGUAAGG	90829	ACGTAACTUAAAACGACCGCTUCA
270092967	90830	CACATACATAUGAAGACCCUACCCAAG	90831	CTGAGCAATCGUGATTCACATACAGUA
270094420	90832	CAGTGTTTTGATCUTGTAAATCGCCUT	90833	GAAGTTCTAAAAGUGGAAACCAGTCTUG
270095264	90834	GACTTTAAAACUGCATAGGCCACAAUC	90835	CATCAGTGGTTUCTACAAATTGCTTUCT
270097980	90836	CCACCAUCCAGGTTGCATCUA	90837	CAGTGGTGCUAGGTGGATATTACAATUT
270100595	90838	CTGCAAGAAAGACUCACCTCGAAAUA	90839	TCTCCCUGAGAAACAAGCAGAATTUT
270102225	90840	TTCTCCAGCUGAGCTTTAAATAACACUT	90841	CTAGGAGGCAGUGGGCTUT
270102696	90842	GTGGAGCCCGGCAUCTUA	90843	GTGCGAATGUACAAGATCTCACTCUT
270102898	90844	TGAAAATGAGUACACCCATGGTUCAA	90845	GCTTAGTTGTUCGATTATGTCCCTUACA
270104775	90846	ACTCATCGTCUGGTGGAGCUA	90847	CAAAGAGTTCAUCTTCAGGCAACUG
270105628	90848	ACUGGATUACAGGCACCAGGA	90849	AGCTTCTTTCTGCUGCTATGTCTAATUT
270106305	90850	CTGTCCACAGCCUCTTGTCUA	90851	TGTTCCTTCCCCUCAGACACUT
270106496	90852	GGCGACCAAUTTCAAAGTCTUCC	90853	ATGCATATTGAGUGAAGTTGGAAUACGA
270115037	90854	CCAUGGUGGAGAACGACCA	90855	GCTCACTGCUAACCCTACAAUGA
270115157	90856	ACTGTCCAUGCATCTCUGCAAT	90857	GGAAGCTGUCCCTGTACUGGA
270117422	90858	CTGGATGCUCAGCTTCTGGUT	90859	GUACAAAGACGAGAGGCUGCT
270119273	90860	CCUCCAGCUACAAGCAGCAC	90861	GGAGGAGGATCUACTTGATTCTAGAGUA
270120342	90862	GTGGAGCATGUTTTATTTGGTAGCUT	90863	ACATGTTCCCCUGAGTTGUCC
270120897	90864	CATGTGAATCAGUTTCCTCAAGTGUT	90865	CAGATCACUGAAGATTCTGTGUCAGA
270121094	90866	CAATATCTACCTCUTGTAACAACCCCUT	90867	CAGTAGCCAUAAAAACCCTGAAAGUT
270121229	90868	CATGAACAACCCUCTTTCCCACUA	90869	AGGAGGACUCACTGGAGAACUG
270122464	90870	CCCTCCCUACCAGACTTTUCCT	90871	CGCAGAACTUGACCGACCUC
270127286	90872	GCACTCACCAUCCTTTTTCCTUAC	90873	AATGACCUGGGCTCTGTTUCC
270127397	90874	CTTGGAGGAAACUGGTAUGCCAT	90875	GGAGACAAGCAGUGAAAACAGATUCA
270127907	90876	CCTCTCCTUGCCTATCCAGGUA	90877	GGAGCAACAUCACCATGGUCAA
270128547	90878	AGTCGCUCACGTUCACCAG	90879	CACAACCCCUAAGTCCAGCUT
270128573	90880	GGTTCTCUCCAGCAGUAGAGGAA	90881	CCAAAAACGUACATTCTTGCTGUGA
270129156	90882	GGCUCAGCGCCATCAAAAUG	90883	ACCAUCTGCAAUAGCAGGGAAG
270129371	90884	CTCTTCUGCAGCTCCTTGUAGAG	90885	TCATCTTTTCCAGCUCTTTTATGCCUT
270129627	90886	GGUGAAGGTCCUGAGCGA	90887	GGCTTCGATCAUATGGAACTACAUGAAT
270130098	90888	AATACTGAAAAGAAAUCCAACAGACCUCA	90889	GACAAAUGCCCTGTATUGGAAAGG
270132124	90890	TGATGCATTGUGTATTCTCCTUCGT	90891	GCAAACGCACCCCUCACUT
270132419	90892	AGTCTCTCCTUTGTTTTTCTGTGUAACC	90893	TGCCTGCTUGTTCTGTTACTUCA
270132918	90894	CAACCTTCUCTGAGCCAUCCAA	90895	GTAATGTCTTTUTGCATAGCTCUGCAT
270133652	90896	CTTGTGCTTTTUGGAGGAGTCTTUG	90897	CTGGGATCUGCTATTTCCUGGAG
270134507	90898	CTATTCCAGAAUGTCAAGAAGTUGCAG	90899	CCTTTTCTAGCTUTCTTACGTAGAGUCA
270136520	90900	ACGCUTGCTGUCCCCAAAA	90901	ACCTCCCCUTCCTGTTGUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270138168	90902	ACCATCGACCUCCGATACAUGA	90903	GTGCCAAUCAGAGGCTTCTUCT
270139196	90904	CGAATACCTTCUGGAGTGCCCUA	90905	CTCATCATTUAGAAAGAAAGCTGUGCAA
270139699	90906	ACTGGGCUAATCTGGAGUGAAGT	90907	TGAACATAGAAUCTAGGAATGAUGCACAA
270140171	90908	GGAGGTCUGAGGCTGGACUT	90909	GGGCCACACUCACCTTUG
270149876	90910	CACUTCCAGCUGAAGGAAAACC	90911	GATTGTCCTUATCATTCTCAUCGACACA
270150115	90912	TCTAGAAGUGCAGAGGAGTCATUGA	90913	GCGGGATUCAAAGGAGCCUT
270151252	90914	CTCUGCCACGCUGAGAGT	90915	CGACAGGAUCTGCTGCAUC
270153612	90916	TCACTGTCUCTTCCCTUCCACAT	90917	CCAGTAGUGGGAAAGAGGGTUG
270155134	90918	CGUTAGGGUGCAGAGCCAAA	90919	CCUCACTGCUCCGAGGAC
270155146	90920	GACCTGUGGGACTCUGCAC	90921	GCAGTGCCUTGCCCTTTUT
270155482	90922	AGAUGCTUACCCCGCAACA	90923	GCCCTTGGUGAGGTGUAAACAG
270156257	90924	CATCGGGAGGGUTACAGGTUT	90925	GCTTGGAAAACAGAAUTTCAGCTGAUAT
270157245	90926	GAAACCUGCGGGAGTUCCT	90927	CTTCCGGGACUCCAGATACUG
270157963	90928	TCTCCTUCCCAGTCCTGGUC	90929	AGAGGGAGAAGUCGGGACAUT
270159115	90930	ACAAACACAUGCACACUGCAAA	90931	TGAAACTACTAGGUAAAGGCACTTTUGG
270160140	90932	GAGCAACAUAGTAAGGCUGAGGAA	90933	TTTTTATCAATGGUGCACTGGTUGG
270160793	90934	GCCTTCTCUCGAACCAAAATAACTTUC	90935	GGTTTTGAGTGGAUATTGCAAACACAUA
270161129	90936	TTTGGTTCTATCAAGUTCCATGTTACUGT	90937	CACACGTACCUGGTCTGTAUCC
270161133	90938	TGGTAGCUGGGAAUACAGACCAT	90939	GGGTAAAGGAUTGTGCTCACGUA
270161268	90940	GAAGACAGGCAAAGUTCTTACATCUCT	90941	GGAACCATTCUCCATGTATTCTGUGA
270161468	90942	CTAGGTAAGCCAGUTATGATTGUCACA	90943	AGGGTGTCTCTAAUGTTTTCAGCAATTUA
270161838	90944	CCUCAGGCCAGCTGTTUCAT	90945	TCTAGCACCCCUCCATCTUCC
270161925	90946	CCTCGCUGTGCTGGUGAC	90947	GGGAGUCGCTGTACAUCCT
270162015	90948	ACAGGCGUCCTCUCCCT	90949	CGTUCCCCGCAGGATCUC
270162442	90950	GTAUGCCCGGACACCAUGAA	90951	CAGGTAGGUATGGTCAGAUGGG
270164267	90952	GCAACACACACAAAAUAGTTACTUACCA	90953	GCAAUCATCTAAAGUGCAGCCAA
270164271	90954	GGAGAAGAUTGCUGAGACGAAGAC	90955	CCTCCTCUGTCGCCAACUT
270169017	90956	CATCCCUCATGCCAUACAGACAT	90957	TTCCAGAAACUGGGAGCCTUG
270169604	90958	CCUGTCCCATUCAGACAACGA	90959	ACACCCATTGUCAATGCAACAUAGT
270170324	90960	CCCCAAGGCUCCCAGUT	90961	ACTGTTGCUGGACTTAGAAAGTUAAAGT
270170327	90962	TGACGGATTAUCAAGAATGCGUGT	90963	GCACCATCTCCAUCCACAATAGTAUAT
270170343	90964	CAGAACTAAAAATUGCCATCCTGCUT	90965	CCTCATGAAUTCCAGTGUAAAAACAACA
270171105	90966	TGATGATCTCTCUGAGGCAAAGCUA	90967	CGTGTGAATAUAAAGATTGGCUGACAAAA
270172444	90968	CCTGCCCCUCTTGGACCTUA	90969	CAAGTCCTUGGAGACCTACUGAC
270176290	90970	GCTGCAAAGAAUCCCTUCACC	90971	TCTTCCTCUCCGCCCTTTTUC
270176645	90972	CTCCAACAUCATGTTTTCCUGACAT	90973	CTTGGTGATCUTTGCCTTTGAAAUCA
270177942	90974	GTGCTTGUGCTGCTCACAUAC	90975	AGGCTGUAGCAACCACTGTUC
270178281	90976	CACTATAAAATCAGGUTGACCTGGGUA	90977	AGACGAUACAGCAGACTCUCAAGA
270178706	90978	CAAAAGAAAACUCCAAGACCCAAUACAG	90979	GGAGAGAUGCGGAACCAGUA
270181083	90980	CATAACGACUATATGTGUCCAGCCA	90981	CCCCUGGGAGAGATGTACCUA
270182242	90982	ACTGAGUTTCCCATTUAAGCACCAT	90983	GCCTCAAATAATGUGGGAGAAATAAGUGT
270182346	90984	GCCAGTGAUCGGGAAUACAGT	90985	GTTGTGAGGGAUGTCTTCAUGGAAA
270182938	90986	GACAAUTCCTCTUCCAGGAACAACA	90987	TGTAGTATCCTGGCUAATTGTAGGCTUA
270183661	90988	ACTTGATGTTCAUAATACTGCAGTGUCC	90989	TGTCTGCCUACGATACUCACAGT
270183689	90990	TGAAGGCAUCAATGCAGAGAUGAA	90991	AGCACCCAUGAAAGTGGTTUAGAA
270189817	90992	GGCTGCGCCAUGAATACUGT	90993	CAGAGTCGAUATCTTGAUGCAGGAAT
270190645	90994	GGTAGCTGCUGGCAAATGTTTUAT	90995	CATCTGTCTACUCAGCAGCAGTUA
270191077	90996	GCAAAACTGUGAGTCTGGUGGAT	90997	CCTGTGACAGCUATTGTTTCCTCTAAUA
270194607	90998	CAGCGACAAGUCCGAGTTTUG	90999	ACTTGAATTUCACGCATGCTGTTTUT
270199623	91000	AATTTGTTAGUTCATGCAUCCAAGCAAA	91001	CCTCCCAACCUTCTTATTCTCAAUCAG
270201846	91002	ACCCCUGACAGTCTCCAUGT	91003	ACAACTCGCUGCAGGATGUC
270202245	91004	ACTCTAUACAACCAGGTAGCCUCAA	91005	CTCACTGUGTGTTCUGCCAAC
270206351	91006	AAATGCAATGTUTTGTGGTCCTUT	91007	GCCAAATTUGTTGAGAAGAUCCACT
270207430	91008	GGCAAAGAGCCAGUCAAAGCUA	91009	ACAAATTTTCUGCTCGAAAUGACCAG
270208838	91010	GACCAGUTCTTUGCGGAGAC	91011	GCTGCTTGGGUAGAGAAGGUT
270210081	91012	TCATTAATTGUGTTACAGGGTUGGCT	91013	TCTACGGTGCACUAACCATTGATTUT
270211972	91014	CATTAGACCCGUCGCATAUCCA	91015	CCTTCTTCTAGAUAACACAGACUGCAC
270213657	91016	CATGACCAACCUTCTCAGUAACGA	91017	AAGCUACAGACAUGGAAGGCAA
270214560	91018	ACTCCAAGCUTATAGAAATGTGUGCAG	91019	CCCTGTTGTGUGGGATAATTACGUAT
270215975	91020	CCACAAAUCCCCAAATAACCACAUT	91021	GCAUTATGGTGGATTUACAAACAAGCA
270216458	91022	GTTTACUCAGGGCCCCUCAA	91023	GACCGGCCUCTCAGTTCTUAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270216500	91024	GGGTTTGGAUAATCTGGGCUCAT	91025	GGAGCCAUGAAACTAGGTTACCUT
270221195	91026	AATTCCTUCAAAACACATTCTACUGACCT	91027	TGCTCCAAUCAAAACTGAAAATGCTUT
270222997	91028	TGTTUGAAAGGCCATATGUGGGA	91029	CTTGCATTAUAAAGAGCCGTTUACAGAA
270223018	91030	GCAACCGGUCCAAGGTATTUG	91031	GCACATTCTTUCCCATTTGCCAUT
270225241	91032	CCAAAAGACCUGCAUCACAAGT	91033	GGCAUCTTCACAUCCAAGACAGAT
270227492	91034	GAAGACATATUCTTGACCACTTUGGAGT	91035	GGAGAUATCUAGGAAGCGCAGAAG
270229852	91036	CCAAGATGGGUATTGGAGGAUGG	91037	CCTGCTTCCUCACCTAAAACATCTUT
270231340	91038	CTCTATACUCCGAGGGTTGTCAAUG	91039	CATACAGCUCCCAAGACCCUAGA
270231771	91040	GGAAGGGUGTTAUCACCAGGA	91041	CCTTGGTGGUGAACAACTCATCAUT
270234188	91042	ATTCAACTTCTCUCCCATAACGGAUG	91043	TTGGGTTGTUCCCAGTTCTGAATUAA
270238026	91044	TGCGGTAAUAACTGGCCCUAC	91045	GACTTTGGGAUGGCACGAGAUA
270238911	91046	GAGTTTGCTAAUTTTCCTCCCCUCA	91047	CCTGTTGCAATGUCTAGTGCTGTAUA
270239777	91048	AATGGAGTAAGUCACTGTGGAATTUGA	91049	GCTCAGACUATTACAAUAACACCACCT
270241826	91050	CACAGGGCAUCAGGTACTGUT	91051	GCGAAGTTGCCAUCGAAGAAGAUA
270242562	91052	CACCCGUCUCCGAAAACGA	91053	AGATGGTCCTUCCTATATGTCTUCCC
270243638	91054	GGGTACTGUCTGCCAAATAUGACA	91055	TCACTGGCTTGAUGAAAACCTTAGAUT
270243847	91056	CATACCCCGUTGATUAAAACAAGCC	91057	GTATGAGTGAAGUTTTTGGAGGGAATUT
270246100	91058	CAACCCAUACATTAAGAAACAUGCACT	91059	CAAATTGCAGTCUGTACAGGCTTUA
270246849	91060	GTTTCTUCCCCTAGAATUGAGCACAT	91061	CTGCTAAAGGCUTCAAAGGTGAATUAAA
270247605	91062	TCTAGTTTGUGGCAGTTTTAAGCAAAUG	91063	TCCACACTUCCACAGATGTTGATTTUAT
270247911	91064	AAGCTGATGAACUCCTGAATTTCUGT	91065	CACAGCTTGAUTGATTTATAACAUGGCA
270249449	91066	ACCTGGAUACATCCAAAUAAAAGCACAA	91067	AGAGTAGTACAAAUGCTTGGATCTCUA
270249605	91068	TTGTCCUCCTAGAGAUCCAAGCA	91069	CAAGTGGGUGGCAAAGAGTTUT
270250182	91070	AACACAACCACAUCTAUGGAAGCA	91071	GGGTGAAGTTCAUCCTAGTGAGATGAUA
270250897	91072	ACATGGGCUTTGCCCGATUA	91073	CAATAGCTTUGGTATAATGCCTUGCT
270252193	91074	CTCCTTGAGUTCCACCCUCAT	91075	GAGGTTGTCTGUCAAGAAGAACTUG
270253904	91076	GCGGAACAGGUTTTCTGCATTAUT	91077	GTAGTTTGAGGCCUTCACTTGTCUA
270255086	91078	GGGAAGCTGTUGATACCAAAAATAAUGT	91079	TTGCCAATCCAGUAATTTCAGGTAGUT
270256348	91080	TGAGTTTTTCAAGUGTGGTTTCTUCAAC	91081	AGAGTGAGAAACUCATAGCATUGCC
270256891	91082	TCAGACCAUTTGGGCAAUGCT	91083	TCATTTTTGGCTUCATTCTTTGCTTCUT
270258525	91084	CCGAGCGGUTCUCCAGT	91085	GGGCGCUTCCUGGAACA
270258662	91086	GCATGCUCTTTCTCUAGGCAGAA	91087	GGCCAGGGUTGCTTCCUAC
270259261	91088	GGCAATGCTAUGAGTTTCTCACUCT	91089	ATTGAAAGAGCAUCATTTTTGGCTUCA
270260255	91090	AAGCCAAAAATGAUGCTCTTTCAAUGA	91091	TCGGCATTAACAAUTATTTCAAGAGGUAAGT
270261792	91092	TTTCATATGGUAGGCACTCAGTTGUC	91093	GCACCTGTUGTAATGTCAACAUAGAAAA
270266316	91094	GUATCCACUCCCGGCAAGAT	91095	GGCTCTGAAAGUCGCATCUCA
270266331	91096	GGGCTGAGUCCTGCTCTAATUC	91097	GCACCUAGAATCCTTCUGCCAT
270272653	91098	GCGUCCAGACCGGAAGUT	91099	CGTCGGAAGGUACCCCAUC
270273188	91100	CUCCCAGAGCCTUCCACAG	91101	CACGAGACCAUCTGGGAAUGAG
270274207	91102	GCTCCUCCTCATTCUCCAAGGT	91103	GAACTTGUCACTGCTTCUCCGA
270275456	91104	CCCCTGCGCUGTAATGAGUT	91105	CACCUGAGAACAGGCAGAGUC
270275877	91106	CTGCCUCCCTGCAUGGT	91107	GAGACAGGCAGAGGAUGAGGUA
270276355	91108	AAGATGGCCUCCAGCTCTTUG	91109	TCTGGGCUCTTTCCUCCCT
270277406	91110	GAAGCAGUGACCCUGGAAGAT	91111	GGAGACCAACUTACTGTGCTACTUAC
270279532	91112	GCACGUACCCGGAAAACGUA	91113	GGAGAGCCAGCUCGTCUG
270279692	91114	CTCTUCAACGGCUCGAGACT	91115	AGCGUGCTTTCCUCGGT
270286743	91116	CCACGTTCCCUCTCCTCAAUG	91117	GGAACAUTCTGCTGUCGGAAAG
270290062	91118	CCAAAGUCACAGATCTUCACCAC	91119	GGAGTTTCGGGUGTGGGTAUT
270291053	91120	GCCCUACTACCUGGAGAACGA	91121	GCTCCCGCAGCUCCCUA
270294657	91122	TCATTTGTTUAAGGACCGTGAUACACA	91123	GCGCTUCACCAAACAAACTACAAAUT
270299257	91124	TTCCCGCACUGAAACAAATUAGAGA	91125	CCAGCCAATAUGCTGTTTCTTTTCAAUA
270302007	91126	GGTTTGAAUGCGCCCCTTTUT	91127	ACTGGAAATGCAUCATATCGCTCTUAC
270303677	91128	TGATTAGAUCCTATCCTUCCCCAAACA	91129	CTAAATGTAAAAUTCCAGCCCUGGAC
270303848	91130	TGCCCAAACCACUTATTCTGTUCT	91131	ACTTGTCACCGUTGACATACAUGA
270305857	91132	AGAAGGUCCAGGGCUGGAA	91133	GAGAAGTAGTTUCAGGTATTGCUGAGT
270308946	91134	CTTTCCTCATCAUGTAAATTTCCTUGCAT	91135	CTCAGCCUCAGAGCCTGTUAC
270315047	91136	CGGCGAAUGGATCTTUGAGCA	91137	ACATCTCATUGCTGGTCUGAACAC
270315674	91138	ATGCCTGGCAUCAGAGTCAUC	91139	GTAACAGGAGUCAGCAGACUGT
270316619	91140	CACTATAAGCAAUGGCAACAGTGTUC	91141	GATGTCATTGCUATGCTGCTUACC
270317423	91142	TGCTTCACAAGUACTACCTGTTTTUGA	91143	TCTACAGCCAGUATAGACAGUGAGAAC
270319415	91144	ACCTGATAAAATGGUTCACTCCAGATUT	91145	CCGAGAAGGAUTTTTGGGAACTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270324312	91146	GAGATAGCGCCUACCATUCCC	91147	GAAAAATUGAGGAAAGCCCUAGGAAGA
270325844	91148	GGAGCAGCCUGGCAGTUA	91149	GUGAAGGGUGGCGAGGAC
270326104	91150	GGTGGTTGUAACAGTCAAGGGAUG	91151	CGTGTTCTCAUTGGTATTCTTUCCAACT
270331990	91152	GATCCCAUTCATGACCUGGAAGAG	91153	CCCTGAGAUGACATTCTGATTTTUGAAG
270333464	91154	GGCACACAUAGAGAAATTAGTAGUCAGT	91155	CTAATGCTACAGUGTCTGCCTUCA
270334089	91156	GTGGCATCUTTACTCACCAUCCA	91157	GTGTTUGGAGCGGGATTTTCUC
270334802	91158	GCCUGCCTTCAAUCAGAAACCT	91159	ATGACTUCCCACATGACGAUCC
270336366	91160	ACACAGCAGCUGAGACATUCC	91161	GAAGAAUGGGTAGUGAGGAAGCA
270337583	91162	GCCTTTCTUCAGATTCATTCTCAUGAC	91163	GCACCGTTGUTGTCAGTGACUA
270340917	91164	TCTCTCTCCUCAGTTAATAACGACAUGA	91165	CTCACAGAUGGAGGTGATGCUG
270342683	91166	CAGCGACGUTTGGAGCTAUG	91167	TGCCTTTGGGAUCCCTTCAAUG
270343848	91168	CAGAAATCCUGCATGAGCAACUG	91169	AGAGATACACUGACTGTGTGTACTAUGA
270343911	91170	GGGATTGAGUGACGAAGTGGUT	91171	TGTTTCCGTCUGACTGCCAUC
270348211	91172	CCACATTCAUCAGTAATTCACUAAGCGT	91173	ACCAGGACCAUGAGAAACTTTTUGAA
270348272	91174	AGATGTTACUAGGTGTTATAUGCCACAGA	91175	CATGGCAAGTTAUGTGATGGAGAAAAUG
270348472	91176	GCCAGAUGGCATGCCUGAA	91177	TCTGCAGGUTGAGCAGGUG
270350449	91178	GCTCCTGCAAAUGCAACAGUT	91179	CGUACAGGCAGGGCTGUG
270353765	91180	GGGACACUGTCACAAAAGUGAAAA	91181	ACCAAUGAAAGAAACGGGCCTUAT
270356841	91182	CAGAGCAGAAUTGGGAAGCUGT	91183	AGCATCACCUAGATCTTCCAUCCA
270357700	91184	CATCTGAAGAGAGUGTTCGAGGAAAUT	91185	GAAGAUAATGACTAUGGCCGAGCA
270359457	91186	CCUAGGCCCCACCAGTCUAC	91187	TCTCAGACTACCUAGGCTTTGAAAGTUA
270360662	91188	AGGCCCAGCAGCCUTATUT	91189	GGTCCUGCCTCTUGGAACC
270361734	91190	CATCAGAGUTGTCUCCGCAGT	91191	TGATCTCTGGTUGTGTGTTTCTACTTUT
270361863	91192	CCCCACTGAACCUCTCTTACATUT	91193	GAGGGAAGGCAGGAUCTCUAAC
270361971	91194	TGATTTTGTCUCAGACATTACAGCUAAAAGT	91195	CAAGGCCUGGAUCAACCAAGAT
270361981	91196	CTTTCTCTGGGUGCACAGCUA	91197	CCTAGGTAACATAUATTGGACAGATCAUGGT
270366671	91198	CCUCAAGGCCAACAAGCATUCT	91199	GAATCAGUCTCTGTGGUGGGAT
270368803	91200	TGCGTGTACCAUGATGCTGUA	91201	CATTTGTGCUCGGTACTTUGAGAG
270371129	91202	CAGGAGGUGACACTGUAGACC	91203	TTCCAACUGGGATTTUCCACACA
270374843	91204	TCAAGGGUCATAACAAAUCAAAACAGAGT	91205	CAGGCTTTGGUGAATAATATGTCCTTUG
270375409	91206	GCAGCGGCAUACACTTCTTTATATCTUA	91207	GGCTGUCAATATGACAUGAGAAGGAAAA
270376873	91208	GGTACGAATGUGAAGAATCTTTUACGAC	91209	AGCCCGTACCUTTTTATTGCATTTTUC
270377443	91210	ACTAGAAGGUGCAAATGCATATCATUGT	91211	GGTGACUTGTGAGGAUGAACCAAAA
270378995	91212	AAAGATTCTAUCCTCTGCCTCUAGCA	91213	GTGATGGAATUCATGACTGTGUGGA
270379172	91214	TGATGAACCTAAUTGTACAACTTGUGGAT	91215	CATCAAACCCCACAUGAATCGTAUG
270380084	91216	GTTTAGGGUTTGAAGAATUGCCAAGT	91217	ACCAAAUGCAGAGAACAGTGGAAUT
270383156	91218	TCTCTGCUGTTATTGGGUGCAT	91219	CGATATTTGTGGCUGGTGGTTTATAUGA
270383857	91220	AATTGAGCUGTACAACTTCUGGGAAA	91221	CAATAAGGAGAUCCCTUCACACCAC
270384137	91222	GTAGAAACAGUAACAAGACCCTACCUG	91223	CTTTGUGCAGCCAGTGGUAAT
270390579	91224	GAGATCTCTCTUCCTTCAGACTTUGAG	91225	ACATGGCAATTCUTGCTTGAAAACTAUT
270392693	91226	CTTCCTUAGGGACTGCTGCUG	91227	CTTCGCCCUGCTCTCTATGAUG
270393452	91228	CACAGTTCUCTTCATCACUGCCA	91229	CTGCAGTGUCCATTTGTATTUGAACA
270396736	91230	TCCACAGGUAAGAAATCTTUAAACCAAGT	91231	GGGCTUCCCTACCATUGACAT
270397215	91232	GCACAUGGAGACAGAAATGUCACA	91233	CTGATGAACAUGGGCCUGGA
270400693	91234	CTCAGTTCUACAGGGTCTGTUGG	91235	AGGTGCAATTCUCTGCTTTTCTAUCT
270405220	91236	GTACGCUCAACCACCTUCAACT	91237	GTTCTCAACAAGCACUGAGTAAGGUA
270406257	91238	CCTACAAUAACAATAGUGCACACCGT	91239	AGCATACAACUGCGCCATAUCT
270411923	91240	CTGCAAACAAAACCACUCATTAUGGT	91241	GGAGGCAGUGATTCCAAGCUG
270416751	91242	AUGGGAAGAGCUACGAGGAGT	91243	CAGTGTGAAUCGAGCCTUGACA
270417167	91244	ACCTGTCTGUGCTTTGTTGUAGAA	91245	GGUTAACGACUGGCACCAC
270423296	91246	ACTCATUGAAGACACAGCAGAUGAC	91247	TGATTGCCATGUTGTGTGAATTGATUT
270426962	91248	CCTGTTCACUCTCTTTTCTCUCCAA	91249	CAAGTGCCUGTGTGGACUCA
270444343	91250	CCTACTCCUCCCGTGCTUAG	91251	CATTCAACCTACCUGTTCTCTCCTUA
270447389	91252	GGCATCCAUCTCAGCGTTCUT	91253	CATGCACUGGAAAGCCAACTUAC
270452960	91254	ACTGAATAACAAACACUTTTAAAGTTGUAACAT	91255	CGATGCATCUGAGGAACGTTTATACUG
270454091	91256	CCAGTTCCGTUAATAAAAGCTCGTTUAA	91257	GTTCTGAAAUCAGAGGAGTGGATATUGA
270455843	91258	AAAAGGCAUCAAGCACAAACCUC	91259	GGCCAUCGGCCCATCUC
270459807	91260	GCCGTGATGAAGUTAAAGTATGGATUG	91261	GCUTGCCAACTTCAUAAGAGAAAAGAAT
270471828	91262	CCCTAACAGCCAUGCTTTCUC	91263	CCAGGCAAUGGAAAGGGTACAUA
270473146	91264	CCATGGCCUCATTCTGGTTCUC	91265	GCATGGUACAAGGTCACUCCAA
270474824	91266	GGATTCAGAGUGCATAGGTTCUCA	91267	CGAACCUCTGCCAUCAGGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270474946	91268	GCCTCACUGCTTCCAACAGUT	91269	CCTCCTGTATUAAAATTGAGCGTGUGAT
270475497	91270	TGACTGUGGATCTCUGGAGCA	91271	CCAGUCCGCCCCATUCC
270479650	91272	CCCACCUGGCAATAATAGGGAUT	91273	TGGAGGGUGTGCCGTTATUC
270482101	91274	TGAAAGCAAATCUCTCTCTTCAAAGUCC	91275	GCUACCTAAUGCAGCCAGACAA
270482952	91276	CTTACCAATTTUAGCCTTGCAAGATCUG	91277	AGATAAAGCUGCTTAGAAATGAUGCCAA
270489206	91278	CACCTCAATUGCAGTGGATCUCT	91279	CCAAAGAGCAGCAAGUCTGAUCAT
270489914	91280	TTGTGCTGAUATGATCAGACTUGCT	91281	GGCTTTGTTATUCGCTGATCTGTTTUG
270490301	91282	CTACAAUAGCCTTACCUGCACCA	91283	TCATCACAGTCAUGCTTTCTTACAUCAT
270491520	91284	CAAGCAUGTGCATUGGCAAGAT	91285	TGGGAGTATUGCACAATTATCTCTTGUC
270506588	91286	AAAGGUAATGGGCAUAGCACAACT	91287	CAAGTATTCCAUGACTACCCATAGTUCA
270507494	91288	AACCCATCGAUTTGAATCCTTTCUCA	91289	CCCAAUAGGTTCCTAUGGAAAGAAAGAA
270507919	91290	TCTCTGGCTTCUTTCCTAATTTCAAUGT	91291	TTGCCAGAUTGCTACUAAAACAGAAAAAG
270515896	91292	TCTTGTTATAGCUACTTGGTGGGUGA	91293	GGTCTTCTCAGCUAGAAATGCTCTATUT
270519182	91294	GTACAGTTGUCAAGTCCACTTUCCT	91295	GACAUCAACCTCCAUGGCAAC
270520216	91296	CCATGTCTTACUTGTTTTTAGGTUGCAT	91297	TGTTTCCAGUCACAAAAAGAGTAUCCA
270522154	91298	TTTTGGTATGCGUCTCAACTTCUCT	91299	GTGAAGAUGGAGAAACAAGUGACCA
270522336	91300	GCACAGGAACAUCACCCAATCUC	91301	GCTCCGCTUCTTTCCTTCACUC
270523442	91302	CCTGTGTCCAUACTTTGATTCAACUGT	91303	GGTAGTGAGAUTATGTTGCAGCUGT
270525592	91304	TATGAAAACAGTUAAAATTGTGCCACCUT	91305	GTAAGCACAGUGGCCACCUA
270526630	91306	GACACACAGGCAGCUCUCT	91307	CCAGGGUTCAGCAUGCCA
270527437	91308	AGCTUCCCCCTCCUCAACA	91309	GTCCGTGCUGTGTGCUC
270529388	91310	CTGGTACAAGAAUGTGCAATGTUCT	91311	TTCCAGCAACCUTATCATACAUGGG
270529504	91312	ACCCAGTCTCUCTTCTGCCTUT	91313	TGTTTCCTAGTACUCAGGAATGTCTUCT
270530972	91314	GCACAGCAUAGAACATAAGTAAGCUACA	91315	ACCCTTATTTUGCCCCCAAUCC
270534371	91316	ATTTTGGTATTAUCCACTGAAGACUGCAT	91317	GGCAGCGUCATCCACTTCUC
270535909	91318	AGTTCCCAGUCTCTTGCAGGUA	91319	CCCCCACCAGUTGATGAAUGG
270536047	91320	GTCTCUCTGATCCUGCCACAAC	91321	CAGCUGGCCATGGCAUAGAT
270538522	91322	ACAGACCGACUAAAGAGCAGUCT	91323	CCCACCCAUTTCCTCTCCUCA
270540787	91324	CCCTTCTTCTUGGCGAATGATCTUA	91325	GCTGCAGAAAAUCAAGUGCCA
270541179	91326	GGCTAACUTTCCTTCUGGACACT	91327	GTCAGAAATGCUAAGTATGCAAAATGUGT
270543661	91328	TGTTGATCGTTTCUGAGAACAAGCTAUA	91329	GATGTGCCCCAGUTATGGUACT
270544430	91330	GGTGCTGAAUTCCCTTGGCUAA	91331	ATGCAAGCAUTCTTATTTCCUGCAAAA
270549085	91332	CAAATGTGGCCUTTCTCTTUGCT	91333	CAGCTCUGATCCTGCUAAGCC
270549382	91334	GACAGTATAGGCCUGACCCTCUAA	91335	TTGAATUCAGTAATGTGUCAGCAGGAT
270551230	91336	GCTTACTCAAUAGTCATCCUGGCT	91337	ACACTCCTGATTUCACTACCTTTTGTUC
270554034	91338	TGGTGCAGAGUAGATGATATGAUCCA	91339	GGGAAGAGGAAAGUACCTGAUGA
270554573	91340	CTTAATAGCTUGTAGCCATTCUCCAACT	91341	TCTTTGGTATTUCAGGATAATGTUCGCT
270555623	91342	GAGTTGGCUGGAACCAGGAUT	91343	TCTGCTTCCAAGUCTAGGTCUAGG
270556299	91344	TGTGATTGTGTUTTCTCCGCCUT	91345	TCTTATAGCUCAGGCCGGATTUG
270563727	91346	CAAGGATGGGUCCCCTTGUC	91347	AAGAGAGTGCAUGTCTGCTUGT
270567417	91348	CTGAGCACACAGCAGUGTCUA	91349	GCTTTGAGAGAAUTCTTCAGCACAAUT
270570880	91350	GTAGAGCUGGAGCCAGAACUAGA	91351	GGTGCAAAGUGTTGGGTAATUAGAAG
270571127	91352	CAAAATTGCAAAGAUCTGCCCUGT	91353	GCCCCACTGUAGCTTTAACTAGTAUCT
270573646	91354	CCTTGCAAGUTCCCAGTACUCC	91355	ACATACCAGGUGTGCCAAGUC
270573664	91356	CCAATAGGCCCAUGCTCATCUC	91357	GGGCAAGUGAACCUGACGAA
270573714	91358	AGTGGGUGATGAAUGAAGAGCAAT	91359	AGGGCACUTTGUAGCACCAC
270581200	91360	TCTAGCCTCACUGGACCTTCUT	91361	CCGGCACUTTTTGCAGAUGAT
270584616	91362	AACCAAGTUACCCATGAUCAAGCA	91363	GCCTAGGAAAGUTAAAATTGUGACAGAAG
270585182	91364	GTTGTTTUGGTTGGGCUCCAT	91365	AGTACTTGCACUTTCAAAAGCAAAAUGT
270586094	91366	CACAUCAATGGCAUCCACCAC	91367	GGCCTTCUGGAAAGCGTGUA
270591010	91368	GCGGGAUGATGTGACCUACAAC	91369	GGCCTGGAUGTCAAAGGTGUA
270592738	91370	GGGTCATCCUTCCTGAACATTUCA	91371	GCACTCAUAAAGTTCCTCTUCAAAGCA
270592827	91372	CCCCUGAGCCTGAAUGAAGAA	91373	GAGUGAAGAGTCUGACCAAGGAAAAT
270596087	91374	GTCTCCAUCAGCAGCCUGT	91375	GCACAGAAGCCUCCAGACUT
270597439	91376	TGAATTGCGCUTCTGGUACAGA	91377	CCATTGGAAAAUGTATCUGCAAAGCA
270598395	91378	AGGAGTTCAAAAGUTGTGTCAAAGAUACA	91379	AGCAAAAGGGCCAGUTCUCA
270598958	91380	TGTTGGUGGCAACACACUCAT	91381	CTTTGCAGGGCUTTTCATATTGTUAAGA
270600037	91382	ACTTACCCACAGUACTAATGCAATUCC	91383	AGATAGACAGUTTCCCACAGUACAGT
270603600	91384	TGTCTCCTUTTTGCTGGUAGCC	91385	AGTGACTGGTUCAGAATTTTCCTCUT
270605492	91386	GACCTGAGCUCTGCAGTAATTUAGT	91387	CCACAAGAGGAGUGAAAGGTUACAG
270607507	91388	TCCTCAAUAGCTCTCUGACCAAGA	91389	AACTATGAACUGGTCTACAAAGAUGGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270609937	91390	ACACACCAGCUGCATTTTUGG	91391	CCTCTAACTCACGGUTTGCTGATTATUT
270615043	91392	ATGTCCCUCGAACCTCGACUA	91393	CTTGCATAGCUTTGGTTTCTGUCAAA
270616609	91394	CACTGACTUCAAGGGTGCUCT	91395	CCTGACCTCUCTGATTGCATGUC
270619718	91396	ACTTAAGAGACCUAACATTTTGCCAUCA	91397	GGACAUGCACGGAGATGAGAUAT
270625116	91398	CAUGAATTGCCUCCCAGGAGAT	91399	CACCCAAAGAAGUAGTGTUGCAG
270626492	91400	GGACCAGCACUTCTTGTAGUACAC	91401	CCTTGGUGAAAGAAAGATGAAGCTUAAC
270630900	91402	AGTCTTACCUCCTCTCCATGCUC	91403	TTCAATCCATUGCCTCCCTGUT
270631219	91404	ACCATCATCUGGTCAGAGCUCA	91405	GGCCCUGAGTCTGAATCUGAAG
270638702	91406	TCATTCTTCACUGTTGCCATUGAGAT	91407	GAGCTGGCCACAUATTGTGTUC
270639785	91408	CTTACTTTCAACAAUTACTTGTCTGTCTUCC	91409	AGAATGTCAUAGCCTTGGCTTTUGA
270641566	91410	GGTCCAATCUCTCTCACCUCAGT	91411	CTGGCAGGAAUATAAGAGAAAACCUCT
270642164	91412	CCAGTTCUGACTTCCCCUGAA	91413	GTCTCCTAUGGGTGGCAGTTUAA
270643416	91414	CCAAAGTGTGCAUCACTGTAAAAGAUT	91415	ATTTAAATTCCCCAAUAAGGCCATAUGA
270645116	91416	GCAAACCTTGUAAAGTGCAAATGTUC	91417	GCCCTGAATGUGTCACTTGTTUCT
270651937	91418	CTGGCTUGTGCAGGUAGACAT	91419	AAACTCGGTACCCUTCATGGATTATUT
270654871	91420	GGCTATGACATUCTTGAAATAACGUGGA	91421	GCCCAUGGATATTUGGCAGAAG
270659008	91422	GCCUCAGGCAAGTAACUCCAT	91423	AGGGACCAAUGTTTGUGCCA
270660716	91424	CTGCAGCAAUGGTGTCTATTTTUACAT	91425	CCTGAGGGAUTGTAACAGTCTUCCT
270665964	91426	GGAGCAGCCAGAUGTAGCAUA	91427	ACAAACAGCATTUAAAAATCCACGACUC
270666198	91428	GATAGTGACCCUTTCCCTTGCUT	91429	TGCCACUGAACTTGCCGUAG
270670335	91430	CCGUACTCGUCCAGGGACAT	91431	CTCCCUGTCGUCCAGCA
270670428	91432	CUGCUGGACGACAGGGA	91433	CGCUCGCACACCCUGAG
270674236	91434	AGTAGGAAUCCAAACCAAAGGCAUAA	91435	GAAACCAGGAACAGUGTATGTTTUCC
270677970	91436	CCTTTTACCUGCCCCTTTGUG	91437	CCTTACCTAUGACACCCAGCTUCT
270678291	91438	GGTATATGUGGTACAGGUGCGT	91439	CATTTTTGGCUAGTGCAGCAUCT
270682057	91440	GTAGCTCATTTGUAGTGCCTCTTTUAGT	91441	CAGCTTCUAAAAGCACTTCTAATUCCC
270682186	91442	GCAGCAGUAAAAGCCCGAAUCT	91443	GTCAAATTGUCTGGTTGCAAUCACAA
270683217	91444	TGGTGGTGGUTGGTTAAAAGUCA	91445	GTGGAGTUCTTCCATGUAGAGGAC
270684202	91446	GTGGUTCCAGTTTUGCCGAAAG	91447	CCACTTCAUCCGCTTTUGGGAT
270685211	91448	CACATTCCTGAUGCCACCTTCUA	91449	CCTTCTCTCUGGATAGTAGTGTTGUAAGA
270685641	91450	GTCCUGGGACTCGTUCACAC	91451	GACAGGCAAUCATATCTGGAGGUT
270686370	91452	GGCAGGAACGGAGCUCAUAA	91453	CGATTTTGGCCAUTTCTTCATCUGG
270686382	91454	GGGAAGCUCCAGCTCUCA	91455	GGTAGCUGCGTGGUGGAT
270688615	91456	CCATCCUCACGGCAGUAGAG	91457	CCCUGCACCTCTTCUACAAAAAGT
270689808	91458	AATCGAGUCAGGTTCACAGUCAG	91459	CCACCGGGAAGGUGAAUGT
270690834	91460	GGCTTCAUGTTAGTTTTUGCAGGAT	91461	ACAGCAUGAAACCCCATGUGA
270691045	91462	CCCAGACGCAGCGUCUT	91463	GGUGAGCUGGGAAGAACACA
270693045	91464	TGACCCCUGCCCACUCA	91465	CCTAUGGGCCCCGGCUA
270699044	91466	CCCAAGAGGGAACAAUGTTACAAUCAT	91467	TGTCCCAUGCAACATCTGGUG
270701686	91468	GCACAGGAGCAGUTCTTTTTAAUGT	91469	TGCAAGCUAAAACCACAAATTTCUGAAT
270703969	91470	GTCTGCTTGCUGTGCAAATAACUT	91471	CTGTCTTGGGAGAUTCCAGAGAATUA
270708117	91472	CCCCATUCAGACCCATTGGUT	91473	CAAGCTTCTTUTGGGCCTGUG
270711249	91474	AATCAGGCATUGCTGGTTAGACUT	91475	CCTGTTCUGGCAGGATGTCUG
270711559	91476	TTGAAAGGCAUGGCGGAGTUA	91477	GGAAAGGACAGGUCATCTGTTTUAAGAA
270712427	91478	CCCACCCCAACCUACACCUAT	91479	CUGGAACUGACCCAGCACT
270712946	91480	GTAGTAGAAAACAGAAGUGAGGCUCAT	91481	AACATCTTUCCGGCCTCCUG
270717446	91482	GCCTGCAGAUGACCTUCCT	91483	CACCCAGGCUGGACUGAC
270720590	91484	CCAGCGAGUCCAGGTUGA	91485	GGCTCUGCTGGAAUGGCA
270720926	91486	GCTCCGGCUGCCATUCC	91487	GCAGCAUGTCUCGAAGGAAGAT
270721147	91488	CTGTTAGAGATUGGCTTTGGTGCUA	91489	GGCCGGAAAAUTCACUGGAAC
270722096	91490	GCUGAAGGACUCGGACGAA	91491	GCTTAACGUTGTCGCTUGCC
270723984	91492	CAGAAGUGAGGACAACCCCUT	91493	TCCATAGATGTGGUTGTGTTTTTCTCUT
270725593	91494	CCTCAGTTATCCUGGACTGGAGUT	91495	TGAGUCCAAACTGUCGAGGGA
270730652	91496	TCAGTTTUCCAGGCAATTGAGTTTUG	91497	CCGAGAAUCACCAAATGUGAAAAACAAT
270733049	91498	GAATATAAAACAGUGTGAGCCAUGCAG	91499	CTCAGCTCUGACACCCCATUAA
270736181	91500	CATACCATTGUCAGAAGCAAGGAAAGUA	91501	CCAATTGGCUAAAAATAGATCCTGUGAA
270738083	91502	GATAACAGTCACAUAAGAGCCACUCA	91503	GGCTTACTCTTTCUTATCTCTCTCTGUCA
270740003	91504	CGGTCCAAAACAGCAAUTGTAGTTATUT	91505	GCCAGTUGCATTTGGAACUAAACC
270744867	91506	ACTAACTACACCUTTGAGATTGAUGCC	91507	TTTUCCACCCAGAGUCAAAACCA
270745251	91508	CATACATGGGCACAAAAUAACCACUT	91509	CTAAUAGCAGGAGCCAUGGAACA
270747942	91510	CCCAUATCTTGGGUCCAAAGCAAT	91511	AGUCGACTGGAUAGCAGGAAAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270748102	91512	TCCATUGGCAGGAGTGAATUCAG	91513	CCCGACCUAATCTAACATCCUGGT
270748461	91514	TGGGCTTATTTUAACTGGCTTTTCTUCT	91515	GACCAGAUATCAACTTUCGGACCA
270750272	91516	CCAACTGCTUACAATTTATTGCCAUCA	91517	TACATGTATATGGCUGGATTATCACUGG
270751543	91518	AAAGTTTCCAATCUTCCAGTGATAAUCCA	91519	ATGACCTGCTTUGCCATATTGAGUA
270753116	91520	TGAAGCACAUAAAATTAACTTTTCAUGCCA	91521	GCTTTTGATCTUCCTTTATCTCCAGUGA
270753588	91522	TGAGAATTTCUGCACACTTACACGUT	91523	TGAAGTTUCCCAGAGACTTGTCTTUAG
270754565	91524	CCCACAAGACCAGGAUGTTAGAUT	91525	GGCATGAACUCCTGCCTCUC
270755081	91526	AGCCTCTTCTUGTTAATTTCCCTGUT	91527	TGGCAAACUGCAGCTTGTTTUT
270758012	91528	GTCTGTGGAGAAACUGAAATACAGTUCT	91529	GAAAAUCGCACAGAGGTTGTUGAC
270759776	91530	AGTTTTUACAAACCCAGCTUGAGGAT	91531	ACTTGCTGUCGATTGGATUGGAA
270762726	91532	CCGAGTGATGGUCCAATTTCTCTTAAUAG	91533	TGACAATGCCCCUCAAGTGUT
270764076	91534	TGTCCCUATAGTCTCUGCAAAAACAAAT	91535	CACACGUTTCTATGGUGCAGAA
270767157	91536	TGUAGATAGUCCAAGGCAGAGACAAT	91537	ATTATTACAATCCUGTCCCTGCTGTUT
270768040	91538	GAGGTGGTGACUCGAAAAGCTUA	91539	GGGAATAAAGTACCUGACTTCTCTTCUG
270768527	91540	TTTTCTGTGUCAGACCAATAGAGGTTUT	91541	GCAATTGCUCACTTCTTATTTUAGGGA
270769702	91542	GGTCCAGATTGCUGTCTATCCAGTAUAT	91543	GCACATGTTGGUTTTCCTTCTTTTGUAG
270770124	91544	CAAGTCTCUGCCTCTUGAGGT	91545	GGAGAGAACTGUTCAGCATCATTUG
270770335	91546	GAAAAAGCCCUAAGTTACTCTCATUCCT	91547	GGCTTTCATTCCUCTGAAGGATTTTUCT
270776726	91548	CAAGAGCACCUGACCUCACA	91549	TTGCCUGGCCAGCCUAC
270778060	91550	CTTGTCATTCUGCTTCATATTTUAGCGT	91551	CTCTGACCCGCUCTCTUCAG
270779535	91552	CACTCTCCUCTGCCTCCUCA	91553	CCTCUGGTGGGUCGGAACT
270779598	91554	CACCTGCACCAAUCACCTCUT	91555	CCGAGTCCAGUGGGAGTTAATUC
270780839	91556	CCUCCTCUAGCAGGCGGAT	91557	CTCCTTGUGAAGACATGGUCCAA
270781461	91558	CTGAGTAACUCCTTCCCATTUGCT	91559	CCAGAATTCCUATGGGTCACUCAC
270782300	91560	CTGCCUGGAGGGCTTCUAC	91561	GGAAAAACAAGUCACTCCAAAUGCAA
270785708	91562	AATTTCAGTGAUGTGTGTGGAATTUGG	91563	ATTATTGAAUGGAGGCTGCCAUGA
270786175	91564	TCCCAGUATCACTATUCCAGAAACCA	91565	GACTTCAAAGUGGAGTTCCUGAGAA
270788021	91566	ACATTATGTTTCUGCACCTAGTTGUGT	91567	TTCCAGGAAGCAUTGCCAUCA
270789174	91568	CCAUTGGGAGTUAAAAGGCACAA	91569	AGAGATTGAGGCAGUCTAATAGTTUACGA
270794573	91570	ACCGGGAAUCTCCAGCUCAT	91571	GGTTCTAAACTACUGAGAATGAAGCUCA
270795576	91572	GGGAAGTGACUGTAGCCTGUG	91573	AGGCTGAAGCUCTTGCCATTTAUAG
270798180	91574	CTAAGGCUCCAAACAATAAGUGCAA	91575	CAGTGTACCUCATCCTGTCUCC
270798884	91576	GCTCACGUCACCTCTTCTTTTCUA	91577	AGCAGTGAGGUGGTACTCUGA
270799056	91578	AGGAGTCACUCCAGGAATAUACAAGAA	91579	CTCTTGGCACUCTCTTAACTTGTTUACT
270802411	91580	CATGTTGGTAAUGTCGTTGAAGUCAC	91581	TCCAAAGTCCAAACUAAACATCAGTCUT
270809089	91582	GGAGAGGAGCAGCCUTGAAUC	91583	GGAGGTGTCUCTCTTTCTCCCUA
270809686	91584	TCACCAGCUACATGGCCTCUA	91585	CTGCTCTTUCCAGTACCUCCAAG
270810451	91586	ACAAGGCTCUCATTTTACATUGCAAAAA	91587	TTCATGGAAAAUGGAGCCCTAGAUG
270811124	91588	CTTGCTCTTUTGGGTGTTATUCAGT	91589	GGTCTTGTGUCCTTCAAATTCTUCC
270811617	91590	TGAAUGGGACCAUCACCAACC	91591	GCGGCATUGCTGGTTTAATTTUGAA
270811721	91592	ATCACTTTGGTACUTACCCTGAGAAAUG	91593	CCTCCAGCUCAGGTUACGACT
270813802	91594	TTGGAGAAUGACAGGAUCAAGAAAAAGA	91595	AATTCGAGUCGGGAAGUCACC
270815091	91596	CCTATUGAAAGACAGCAGAUCAAGAC	91597	GAACAGCUGGAAAAATGGACUGAA
270818401	91598	AAGTGGTUGGGCTGACATUGAT	91599	TGAGGAUAGGAATTCACUCAGGCT
270819491	91600	CAGGCATCUCACCATGCUCAT	91601	TCGATCTCUCAACACGTTGUCC
270819854	91602	TTGCCCTTCACUTCTTCCATGUT	91603	CUGAGGAAAGCTUCCCACAGA
270821157	91604	GGCUGGACCGGGAGAATAUC	91605	GAACAACCGAUGCGUGAACA
270823721	91606	TTTTTCTGGTGUGGTCTCTGAAUGAA	91607	GGAAACACCAAUCATGUGAAACAGT
270824007	91608	GCAAAAUCCTGUGACACAGCA	91609	ACCCCAGUGACAGGAUGGAA
270826529	91610	AAUGGACACAGGGAGTUGACC	91611	GCTTGGGAGCACUTCACATATACTTUAT
270826670	91612	GTCTGUGCCAAGCCATGATUT	91613	GAATACAGCUGACAGTCTCUCAGG
270826879	91614	AAGCUTTTGTGCTUGCAAAGGAA	91615	CTCTTCCATTCUAGGCTACAGCUC
270827588	91616	CTCCGAGGCCCAGAUGTUG	91617	AGUTCGGATCCUACCCGAGT
270828722	91618	TGACTTTGGAGGGAAUTTGACATCUT	91619	CACCCCTATTUGGGCTTCAGAUT
270830634	91620	ACCTTGTTGCUTTCGTGGATCAUA	91621	TCATGGAAATTATGUGTTCTGGACTGAUT
270831079	91622	TGATATCTTCUTCCTGCTCTUGCAC	91623	AGCTTCCTATUCCTGAGTCTGUGA
270832010	91624	AGUTCATGACGUGAACGACAACT	91625	CAGTGAAGUGGCTGATGUGAGA
270832113	91626	GCTGGCGAAUACACTTATTACTUCC	91627	AGGAAAACGACAAACAAUGGUACCT
270833925	91628	CACGTTTUGGACCTCCAACUG	91629	CCTTCCATCTCUTATCAGTGACATUCAT
270834982	91630	TGGAACUCCAGAGCUCCAGAAT	91631	GGAAAAGCTGAGUATAATGCCTCTCUT
270836318	91632	TGCAAGAAGACAGACUCAATTATGUGT	91633	TGAAGATGGUGCATCCTUGGAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270836797	91634	GCTGTCACAGUGATCCGGUA	91635	CCAGUGGAAAAACAGAATGGCAUT
270837606	91636	CGCAGGGAUTTCACAAAGUGG	91637	CACTCAUGTTTCTGACUCAAGGGAAA
270840207	91638	CAATGTCACCUCACTTGTTATCAAAUCT	91639	GGTCAGTTCUGATTTTTCACAATGUGT
270841379	91640	CCCCTGTGUCGAAAGCAUGAA	91641	ACTTGGTTGAAUCTTACTGACCTTUGT
270846660	91642	CCATTGATTCUGTTACTTCTGCUCAGAT	91643	CGGGAGCAUGAAAAGCAUCAAC
270846919	91644	AGAATAAUGAAGAGAGGGCTTGCUG	91645	ACAGACACCUCCTCGGCTAUAAT
270853646	91646	CAGTGTACTTGAUGGAGTATTCAGUGAT	91647	CCTGTCCTTTCACUTAAATCCTCCTTUA
270854537	91648	GTCAGTGCUTGTCCTGUCGAA	91649	CACCUGAACAGTTCCATUGCAG
270860163	91650	ACAATGTAAUGCTTTCTATCUGCAGACT	91651	GAACCAGAGAGUGGGCTTUCA
270864377	91652	TGTGATACCUCTATCTTTAAUCCGCAGA	91653	ATGGUAGAGAGGGCAUCCAGAT
270867194	91654	CAGCCUCAGGGUGAAGAGAAAC	91655	TCAGAAACUGTGCCCTTTUCCT
270868760	91656	ACCTTGGGAAUGGTTAATTTCCUGAA	91657	AGCGAGGUGTAGTTGAAAUGCT
270870435	91658	AGGCACTTCACUTGAGTCTCTUC	91659	ACATGCTTTGTGUTTTCTGTGTTTGUT
270873211	91660	GAAAGAAAAGGAUCCAAAAAGCCUCAT	91661	CACCAGGUTTGGAAUGGGACA
270875825	91662	GGACCCGUACTTUGGAGCAT	91663	CCCAGAAGGAGAACUCCUACCC
270876121	91664	ACGCACCCGAGUGAAUGA	91665	GGAGCCCAGGACCUCAUCT
270879938	91666	AGGCTUTGATCCCUCAGGAAC	91667	GTTGAGGGCACAUGCAGTAGATAUT
270882259	91668	GGGTTATGCCUGAGCAGTTUG	91669	AAACAGAATGGGUAGTCAAGGAAGAUG
270884091	91670	GTACUCCTTGCTUAGCGGACA	91671	GTCTAGCCUTGGCTCACUAACC
270885146	91672	GAAGGGCCUTACCGTCUGT	91673	CTTCCGGCUCGAUCGGT
270887014	91674	GGGTTCTCCACUTGATTTCCAUT	91675	GTTTTTCAGCUGTGAGTTTATTCTUGCT
270887491	91676	TGTTCCCTTCUCCCTCTGTTCTUA	91677	GTCCGATCUTTCTTAATCGUCAGGA
270888256	91678	CCCGCCUCCAAGTCUCA	91679	CAGGCCCUACUGCAAGGT
270889606	91680	AGACACCUCACTTAGGTAGUCACAT	91681	GCTAGCCCACGCUAATTATACTTTUG
270892434	91682	TTTGTTCTCCCUCTGAGCUGAAC	91683	AGGTAGTGGUAGGAGGAACAACUC
270892862	91684	ACCUCGUGCAGCAGCAA	91685	CCACCUGACCACTCCTGUC
270895374	91686	GCACACAAUACACACACATGCAUT	91687	ATCCCTUAGAAAAGGAACAAAAGCTUCT
270899357	91688	GGAGAATCAGAAGCUTTTGTTCCTTTUC	91689	GACTCCTCCAUATAGTCTACTUCACAGT
270901352	91690	GACCCCCGUTGAAGAAAGUGA	91691	CATATGTAAACACUGACATGCAGUCAAT
270901439	91692	TGAATGCTGUGCTGGGAAUAAGT	91693	GACAGAAGCUATCCAGGCTGUAG
270904391	91694	CTTGCCTCUGCAGTCTGUCT	91695	TGTGTTGAGTGUGTTTGATCTCUGA
270904696	91696	GGTAAACCAAACAACUTCCACCTCUAAA	91697	CTGTCTTACTGUCATTCGAAGAGAGTUA
270908173	91698	TCAGAAACTCCAUTTACAGCTTCAACUT	91699	AGAATATTGTGUAAGCGGTGCAGUT
270908397	91700	CCTUCCCCAGGCUCACC	91701	AGCGUGCGGTTCCUGAA
270909250	91702	CTCTCTTTACAGCUCCATCACCUG	91703	ACAGCCCAACCCUTAAACATUGT
270910957	91704	GCAGCAAAUCCATGCCACUA	91705	CCGAUGACTTCACAUCCAGGT
270911584	91706	CTCUGCCCGGTTTTCUGAC	91707	TTGCAAGGCAGGCUAGUGAT
270914187	91708	GATCCAAGAAGUAAGTTCTCTGGCTUAA	91709	TGTGTTCCTTUCGGAAGAGATGUC
270915624	91710	TTTTCCTGTGGAUTTTAATAGAACATCUGGT	91711	CCAGTCATAGUCAAATCGCTTTAGTUGT
270916338	91712	GATACCGUAAAGCGCTTGCUG	91713	ACACCTGCAACUGTGTAAGGUT
270916861	91714	CTGCTCTAGCCUGCCTTCTUA	91715	CCUCCCCACUCCAAACCAAAC
270919466	91716	CCGTCTUCCCCTATGGTCUG	91717	CAGGAGACGAGCUGGUGAAG
270919926	91718	CAACACAACAAGGCUCTGUGAAAA	91719	TCTGGACTTUCACACCAACACATUAT
270920204	91720	ACCCAACTUATATGTTTTATGUGCCAGAA	91721	AGTAAGTTGGAUCAAGGAGGAGUGA
270920472	91722	ACCTTAAAGAGCAGUTCAGGATUAGAGA	91723	TATTGATTTTTGGAAGAUATTTGATTGCCUAAA
270922240	91724	GTTACUCCCACAGGGAACACAUT	91725	CATCUGCACCACAGAACCUCAT
270924938	91726	CCTAACCCCAGGAUGGTATAATTGGUA	91727	GTGTGAUGGAGAGGACGACUG
270928424	91728	GGGCTGTUACCACTGGAACUC	91729	GACGGGTCAGUCCTGGATTUA
270929146	91730	TUTTGAGCAACAUCAACAACAGACAAT	91731	GAACUCACCCCATGTGAUGGA
270930444	91732	GTGAAGUCACTGGCATUGAGGT	91733	GAGGATGAAACUCTGTAAGGTGGATUAA
270934119	91734	GAATTTCCUCGAGAGCUGGACAT	91735	AGTCTGTATTUTGTGCTTCCUGCT
270934637	91736	GATCGUAATAGGCAUCACACCAGT	91737	GATTGAGAAGGCCUGGAUGGAT
270935418	91738	GGAGCTGGGCUGGATCTCTUA	91739	GTCACCAGAAGUACAAGAGTTCTCTUT
270935536	91740	CTTACTGTGGUTTGGTTGATGTUGAAA	91741	GCCCCACACAGAUCCTTTUGT
270940170	91742	AGGTATCAGUGATGTCTGCATTUCC	91743	ACTTGGGAACATUCAAACTTGGAAGUAA
270941167	91744	GGCTTCAUCAGAGTTGTCUCCA	91745	GGCACTGATTACUCTGAATCTCTTTGUT
270943687	91746	GATTTCTCTTUGGGACAACAGUCAAG	91747	CCACAGTATAUCCTAAGGGAATUCAAGG
270944411	91748	CATTCGCGTAUCTATTCTTTGGTTUGT	91749	CTGGTGGTTTUCAGTATTGATTTTGUGT
270946113	91750	AGAGTGAGCAGUCTGAAAGUGAGA	91751	TCACCAUCATCAAATTTAUACCAGCGA
270946346	91752	TGCAATGUCCATTGGTGUCCAA	91753	GAAGGACCAAAAUGTGAGGTUGAC
270947844	91754	TCACAAAAATCUGCCGATTGAAUCC	91755	GGCTGGTTGTAAUAACATGTATGCATUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
270948891	91756	TCCCATTUCAGCATGCTCAAUACA	91757	GTCTGCCUGTAAACAGCTUCAC
270949147	91758	CAACTTACCCUGGCATCTGUGA	91759	GUCACCAATACUGGCCAGCA
270951324	91760	TGTACAAGTACAGGUTTGTCACATUGA	91761	AATTAAGAAAACTCUACTGGACCGAUGG
270951624	91762	AATATATTAUGCAGAAGCCCAGCUCT	91763	AGCTCACCTAAUTTACTGTTTTGUCACA
270951751	91764	GGAATGGUGGAGATGGUGAGAGA	91765	CCTTTTCUGGCGCCTGTAUG
270952182	91766	ATTGTGTTUCCATCGGUCCAGT	91767	GGACAATTTUGGAGTTTTCUGAAAAGAA
270953646	91768	CCCATGGCACCUTACACACUT	91769	GCCACCACTAUTGTGTGAATTCUGAAT
270955602	91770	ATTCAACACUTCCATCAUCCCCAAT	91771	AAATGAAAGGGUCACCTTAATTATGACUGAA
270958700	91772	GGTGGACGCCCUGAAGAUG	91773	TCTCTATGGCAGGUCTGGGUT
270961681	91774	TGCTGGACUGGTGAGCTCTUA	91775	TGCGGATGGUGTTCAGGTTUT
270963172	91776	TCCACAACAACACUTGTCATACTUCAA	91777	TGTAATTCCAACGGUTCTGTATGTGUC
270968799	91778	GAAGCUCCAGATCAAUCAGGGT	91779	GCACCTGTGATUCAATGATTTTGTGUAT
270969962	91780	CTTAATGAGCCUTTACCTACATGTUCCA	91781	TCATGTGGGAAGUTATGTCTTAUGGAGA
270971861	91782	TTGATTTGACATGUCCCAATAAGGTCUT	91783	AUTCCAGTAAGGUGGACAGCAC
270971933	91784	GCTACCUCCCCAGCTTTUCAA	91785	CCATUACAGGACCCGGATGUG
270972182	91786	TTCCTGATCAUCCAATGGCAUGT	91787	CAUTTCAGTTGGUCAGAGGAACCA
270974726	91788	GGAAGAAGUCAGTGGCUACGAT	91789	GCTGCAGUCTCTCACAGUGAAG
270975979	91790	ATTTCCGGTACUGGATGGCTUC	91791	GTAGACCUGATGCTGCUGAACT
270979447	91792	ATGAGAAGACAGUGAATACCTTAGUCCT	91793	GGTTACTCTTGCUTGACTCTATGTUCT
270979703	91794	GTGTATGTGAACCUGTTGGTTTCCUA	91795	ACAUGAUCCAGCAGAGAACCC
270979883	91796	CTGGCCTAATTUCTTTGGTTGAAGUC	91797	TGACTATATCTACUTCCCAGCCUCAC
270981453	91798	ACCAUGAAGATTAUGACCCACAAACT	91799	CCAACAAAGACCAAGCUATACAGTCUA
270982751	91800	CTGATAGCCTGACUCTTAAGTTCATTUCA	91801	GCGCACAATGUAGTAACTCAGGUT
270983922	91802	TCAACTGGCTAUTTTGAAATTCCTUGAT	91803	CAGTCTAGGAAAAAUTGAAAGGTGUGAA
270984674	91804	CCCAUCGCATCUACACAGAGAT	91805	CCUCAGACCAGAAGGCUGACT
270984879	91806	AGCTCTTGGGUCAGTCCTTATTTUC	91807	GCCTGGGCAUAGAGTACCATTCUA
270985392	91808	ACATGTCTCUGGGATCCATCGUA	91809	TCATGAGATCUACTCTGACUGGGAAAAA
270991928	91810	AGCTTGTCACUCAATATTTGCCUCT	91811	AGAATTCCUCCAGGCTTCTCUCA
270995475	91812	CCTAAAGGUAAAAGGUGCACCCT	91813	GGACCTCCACCUCTGAGCTAUT
270997674	91814	GTACUGACCACCACTUGAGCA	91815	ATAGCTTGGTATUGCCATGTTTCTAUT
270997796	91816	GTTTTAAAAGAAGAGAAUCATGAGAACTUGGG	91817	TCTTTCAAGTTCAUCTCCAAGCCAUT
270998080	91818	CAGGTGCGCUAACATCGAUT	91819	ATGCGGTAAATTUCGGAAACACATAAUT
270998513	91820	AGCUATTCCCACTAUAAGGGAGAAAGG	91821	AGCTTCTACAACUTGGCAGTCTUG
270999325	91822	CCUAAGAAGCUCACACCCAGT	91823	GCTCGCAACAUCCTAGUCAACAG
271001230	91824	CACCCCAGACUGCAGACAUC	91825	GCATCTCCUGGCCCTUCA
271001588	91826	GUGCCAGTTUGACCCAGAGAT	91827	AGAAGACATGAAGACAUTGTTCGAGAUT
271001881	91828	TGAAGTGGAACCCUCCCTCUC	91829	GCACATUACAACCACAGGAAUGAA
271002316	91830	GACUCTGTCATUGCCACCAAGA	91831	AUTCCGAGUAAGAGGCCCAAAG
271004239	91832	CAGGGCAAUGGAGATCTUAAAAGAAAG	91833	ACCATTGGACGUTTCATTGCTTUG
271014702	91834	AGACACTTUGCAGACGAGGUT	91835	CCACCCUATCTGCTCUCCAG
271018240	91836	AACACAGAGACAAAACCUTTTCAGGUA	91837	GAGGATCCAGACUGTGCAGAUG
271018508	91838	AATCCTCAGUACACTTACAACAATUGGT	91839	CTCTTCCATUTCTATCTGCUGCACA
271021889	91840	CAACTCACCUGATTTCATGUCCCT	91841	ATAGCCAACCAUCCACCTGATUAC
271022150	91842	TCCCUGAUCGGCCACCT	91843	GGGTGACACCUACTTGATAAACUG
271023250	91844	ATGAAGGUAAACACAGAAGUCAGGAG	91845	TCATAGTCTCUGGAAACACUGCAAAA
271024295	91846	AGCAGGGAAAAUGTACTTTGCUT	91847	ACGGTGTTTUGGATGCTGUCA
271026325	91848	CTGUGAGACCCTGTGUGAAGAC	91849	AGAACCCUCTGGAGUGAGGAC
271026363	91850	TGAACTCTGUCCAGAGGAGGUAAAA	91851	CCAGCCGAAUAAACATTTTUCAAAACC
271033861	91852	GCAGTTGGCCUCGTCTGAUG	91853	CTCCAAAGCTACAUTTTAATGGCAGTUT
271041190	91854	GACTCAAAGCAGUCTTTCCTACTUAACA	91855	GGGTTGGTAUCGGAGGCAUC
271041254	91856	TGCTGUGAGAAAACAAGUGACAGT	91857	TGTATACCCTAAAUTTCAGCCACCTUG
271042002	91858	GGGCUACTUAGACCCAGAGAA	91859	GGCTTGGUGAGGAGTGTGUC
271044401	91860	ACATGTAAATGCAUCTCACCTGTATCUG	91861	CCCGCACTACAUTGATGTACTAATTUGT
271044659	91862	GCCAGTGACAUTATCCCAAGGUG	91863	AGATTCCATCTACCUTCATTCTCCCUAA
271046844	91864	ATGAGACACGUTTCAACACUGACT	91865	GAGACCTUACGACGGGTUGG
271048692	91866	CTTACCTUGGAAGGCCGUCT	91867	GCAGTCGCUGGAGATTATCUCT
271048834	91868	GCCCAATACUTCAAGAAGGUGCT	91869	GGCAAGGCACUGAGAAGUGT
271049732	91870	TGAGGCTTAUGATGAGAGUGAGGAT	91871	CTCCACCCTUGGATTTGTCATACTUA
271050597	91872	CTTTGTGAGTUCCTTTTTGTGACCUT	91873	AATGTGGATATGUTTTCAGTTGCAGUC
271053099	91874	ACAATACATTGACUCCACACTCTTUCC	91875	AGAGGGTGGUGTGACCTCTTUA
271054845	91876	TTTATGTTACUGGACCAACCTTTGUGT	91877	GGAACCAAUCAGAGTGTTGTCAUAGAAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271056252	91878	ACCCGGCCTATUATTTCATTTCTTACAUC	91879	ACTTGCATCCAGCUAAACCTAAAGATUT
271057856	91880	CCACCAGGUTAAUGAAAGCCGAA	91881	AGTGATTCGTGAUTGAATGGTACAAUGT
271059216	91882	TGCTUCACCAGCAGUACCAAA	91883	CGTGUAGAAAGTAATCAUGGCAAGAAGT
271060540	91884	GACCAGUAGATGUAAGCCCCAAA	91885	AGGAAAATAAATTGUACTGGTGTGAUGCT
271060991	91886	GTTAGCTGUCGGTGAAGTTUCCA	91887	TGATATUGTTAGCCCAUCACGGAAAAA
271062752	91888	TGUGCGAGCAUCACACCA	91889	ACTATGAGGTCUGTTGGATTTCTTTUCA
271062811	91890	TCTGGGTGUCAGAGCCCTUA	91891	CCTGAUCAGCAGCCTTTCCTUC
271064645	91892	GTTAGTGCCAUAGGTCTAGAAATCTUGG	91893	CTCCCAGAGAAUCTGTAAACAAAAUCAG
271066316	91894	GTTAAAAGUGAAGCATGUCAGCGA	91895	CTCACAGGCAUCACTATGTAAATCUGAT
271068758	91896	ATTAACACAGAGAAACUTACTTGGGCUT	91897	GGGTGGCAUATTTAGGCTGCUA
271071245	91898	GTGAGGGCCAAGUGAAUGGAA	91899	ACTCTGGTUCAGTCAGCTUCCT
271072795	91900	ACTCTTTTCUCAATGTGGCTCUCC	91901	ACTGUGCGCCACATTAGUGAT
271072888	91902	CTTTGGCAAGUTGCAGACTUAGG	91903	ACGGTCCATTUAGAAACAGAATTTGCUA
271073774	91904	AGACCTGGCACAAAUTCATTAGUGT	91905	GATAAGAAACUGTGGUGGGCAGA
271073809	91906	CACUTCAACACCAUACAAAAGCACA	91907	CCGATTTAAUGGGACTGATATTCACUCA
271074354	91908	GGATTCCCCAAGCAUTCTCAATTTUAAT	91909	GTTTTGCCCTCUTTATAGGTTAGACAUCT
271075402	91910	AAATCAGCCCUCATTTGGATGUGA	91911	CATCGAGUCATCACTGCUCAACA
271076552	91912	GTGGATTTTGAGGAUGGACGTGUA	91913	CATTATTGAGAAGAACUTCAGCATUGGG
271076761	91914	AGUCCCGCACCGGUAGA	91915	CAAGAACTTCUAGATTCTGGCAGUGAT
271077690	91916	AUTTCCTTCTGTAAUACACGAGCCAT	91917	CAAATCACCAAGAAGAUGGGCTACTAUA
271078663	91918	TGGCACCAATAGAUTCATTCAGCAAUA	91919	AACTCCTCAAGUTTTGCGCTTTUT
271078902	91920	CACGAGCCAUGGAAAACTTGATTAATUT	91921	CCTTTTTGAAGCUAAATGAATCTACCTTUGA
271078910	91922	GCCCATCTTCUTGGTGATTTGAGUAT	91923	GCATTTTTGACTGUTAAAATTCTGTCTGUCT
271079628	91924	GATGCACCCUTTTCCCGUCT	91925	CACCTGGCUCCACTGTGUA
271079720	91926	GTTTTGCATTCUCACTTTTATATATGUGCCT	91927	ACAACACATCCAUGGACTTACTUGAAT
271080059	91928	GCCCAGGAACUAGGAAAGCAAUG	91929	TGGUGAAAGGGACTGUCCAGAT
271083103	91930	GGAATTCCAGAUCTCAGTGACUGAT	91931	AATCTGCCACCUGAACCUGAC
271084482	91932	GCCCACCTUTCGATCTGACUG	91933	TCUAATCCCCUGCACCCAAGA
271086330	91934	TGGGTCUAAGGGTACGTGUGAT	91935	TGGUGTCCTCTUACCAGGCA
271087718	91936	TCAGAACATTCTCUAGTACCCCAGUC	91937	GAAAUTGGTGATUCGCCAACAGT
271088511	91938	CTCGCCAGCCCAUCATGATUA	91939	TTTAATTCGCTTUAGGCATTCCATGUG
271088665	91940	GCCTAGAUGGAGGTACCUGGA	91941	CACCGGGUCTCTGCTTTCUAC
271090201	91942	AGTTGCTAATGGGUCAGTTTTGTAGAUT	91943	CGACTCATGTUCATCTGGAGCAUC
271090433	91944	ACACUACGAGACCCAGGTUCA	91945	GCUGGAGATUAAAAACGCCAACA
271090650	91946	AGTATTGTTTCCUTCGCCCTUGT	91947	CCUCCUCCGGAGCCAGA
271091463	91948	TTCAAAATUAGGAGCCAGAUGACCAA	91949	GGGATAAAAGCAUAAACTGACTCCUGT
271093356	91950	AGAGAGAGUGTAAGAAUGAGGAAACCA	91951	CTGGGUCCTCTTGAUAGCGA
271096339	91952	ACACATUGAACACTCATUACAGAGACAA	91953	GGAGAACCCUATGCTATTGCAGUAAAT
271098474	91954	CTAAGCCATUAACCTACCCTCTTTUAGG	91955	CTCACTGGACCAGUCTGAGGUA
271099486	91956	CATCCCAAAUAAAAGGAATGAAGTCUGG	91957	CGGCGGGCACAUACUCA
271099632	91958	TGTGGAAAGCUCATCGCTUCC	91959	TGGACACAGAGUAATCTTAATGGCAUT
271102763	91960	GAGAAAGAAACAUGAGAAAGTCCUAGGT	91961	CGUTCAGTCCTUCCCAGAAGAG
271103391	91962	GGAGGTACTTUTGTTCCCCAAUAGA	91963	GGTTTTGTTGATGUCTTTAGCAGTGUAA
271103840	91964	GGATGAAATCATUCCAGTGCTCCUT	91965	CCTACTGTGACUTGCACTAGTCATUA
271106666	91966	CGTGCUACTCAAGUCACCCA	91967	TCCCTAUCCCCATGCTUCACT
271108652	91968	CGCCTCCUCAGGGCTTATTUA	91969	CGTCCAAGGUTTCCTGACTGUG
271117121	91970	CAGCTGCCCUACGTTGAUAGAG	91971	TGGTGTGTTGUTTTGTTTCCTTGUAG
271117563	91972	ACCTTTAAATGUAGATCCAGCTTTGUGT	91973	AAATGTGTCCTGUTTTTCTTTTCCTUCC
271118143	91974	CCGAUGACGCAGAGGGAUAA	91975	AGCTTCUCGCAGGTGUCC
271119158	91976	GAAGACCUCACGGGACTTUGA	91977	CCTCUACCCCCTTAACUCCCA
271121051	91978	CUCCATATCCTUGCGGCCAA	91979	GTCTTACCACUCCATCCCATGUG
271121170	91980	CCTGTCACTUCTTTCCCTACCUC	91981	GCAATCTTGAUCACGGCCACTUA
271123845	91982	CGATGTGUAGGGCCAUGGT	91983	AGTGGCUGGTGGTTTCUGG
271124280	91984	CACTCCCTUCAACTGGACCUG	91985	CTACATGCTTUAGGTTCTCTGGACUT
271125328	91986	CGCCTGCCUGAGGCTTTTUAT	91987	CGGAGGAUGCGGTCTTATTUCC
271126645	91988	GCCTACGTUGACCAACTCTTCUA	91989	GATTGGCCAAAACCAAAUCAGGUT
271131662	91990	CATGGCAGUAATGGCCTCUCT	91991	GGATGCCGUGAACCCCAUC
271132830	91992	GAAGUAGAGCAGGGAATATUGGCAT	91993	GATGCAAGGAUTCATCUGCAAACAG
271133912	91994	TGAATCAATCAACUGTTCCATGTAGAUGT	91995	AGAATAATTGCUACTGCCGCUGAA
271134217	91996	GCCTTUCACAACACGCUCAT	91997	TCCCAATGACCUCCTCAATCTTGAUA
271136222	91998	GTACGACCUGACTGGCCUAAG	91999	AAUGAACAGACGCCAAUCAAGAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271137283	92000	CTCCAAAGGUTATCCGTGUGGT	92001	GAATTCCCUCCAGTATGCUCACT
271140070	92002	CCAAGUGGTCATGAUCGCCAT	92003	CAAUCAGUGGCAGCAAACAAAG
271140763	92004	GTACCTTATTCTTUCCCTCCACAAACUC	92005	TGTATCCCUGACCTGCCCUT
271140785	92006	CAAGAATUAGGACCACTTGGUCAGT	92007	GATGGCAAGAGUGATGGATTACAAAUAA
271143895	92008	GGCCAGGCAUCTCGTGAAUA	92009	CCCATTGAAAUACGCTCAGGUGT
271144346	92010	CGGGAAGUCGATCCTGCTUA	92011	TGTGTTTGGAUGGGACTCUGG
271144718	92012	TGAGCCAGGACUGCTCCUAA	92013	GAGACCTACAUGGACTGAUGCC
271146404	92014	AGAAAGAGGUAATGCTGAUGCCAAA	92015	TGAAAGGAAAGAACUGCTUCCAAAGAA
271148576	92016	GGGAAAAGCCUAACAAGACTGGUT	92017	TGTCTGCCAUCGCTGGUG
271150687	92018	GCCACTGTCTCUCTTATACCAATTTCUAT	92019	ACAAATTACTCCAAUCCGGTATAUGCAA
271151069	92020	TCGACAGTTTUGCCCATCCATATATAAUT	92021	CGATTAGGAGAUGGACATTCUAGGAAGT
271151827	92022	TGGAATGGCUGAAACATGTTCUCT	92023	GATGTGTUCCTGCCUCGAGT
271153129	92024	GCTGTGAGCGCUAATTCTGUG	92025	ACAGTCACGUCCTCAGAUGAGAT
271153651	92026	CCTTCTGGAAUACGTGAAUGGGT	92027	ACATAAGGCAACGCUCAGUCAA
271154889	92028	TCAATATCTAUGGGAATCCCTGAGUGT	92029	GAGGTAACTGAACUGGCTTCTTGUT
271155646	92030	CCAGGCCACAUAGCTCTTCAUC	92031	AGCTGGCATUAGAAATGTTTTGATTUGT
271157588	92032	TCAAGTTUCACAGAGCTTCUAAAGCA	92033	AAAUCTCTGUGCAACACCCAGT
271157808	92034	AGAGGTCAUGAGAAGCTGGAUGA	92035	CCUGCCCCCATCUACAGACA
271159078	92036	GATGGTATTCACUACCTGCATGCUA	92037	CACTGGTATCUACAGACGACUAGAAAAG
271159558	92038	GCTGAAAGAGGCAAUCGCCUT	92039	CTGTACTTGGUCATCCGGTTCUG
271163409	92040	CACCAGAAUAAGGCAAGGGUGA	92041	CCCAGCCCACCCUCTUG
271163448	92042	TGCTGCTTTCUTATTTCTCATCTUGACT	92043	GCTTTGATGCCUATATCAGGAACTUCAT
271163955	92044	AUGGAAATCTATUCCCACGGCAA	92045	TTATCTCCGGCCCUGCATTUAG
271165808	92046	GGGAGTCACUAAAGGCAACUC	92047	TTTCAGGACAAUTATGCCATCTCUCC
271167515	92048	AAGTCACTTCUTTGTCTGCGUGA	92049	ACCACAATCAUCACCATCTGAAUAAGAG
271168104	92050	CTGAAUGGCCCCCGAAGUA	92051	AAAGGCAACAGAUCCCCTAATTUGT
271168745	92052	AAAACAGACACUGAGAAAGGCCUAA	92053	CACCATCATTUCCTTTGCAGGTUC
271169332	92054	CCTUGAGAACATCTTUCAGCCACAA	92055	CAGTGAAACAAGUTGAATGCGTAGUAAAA
271170233	92056	ACCAGGGUAACCGGAATCAUCT	92057	AGCCACAATGUATAGTGAATTCTGUAAA
271172654	92058	TGTTTGTUGAGGACCCAGAUGAG	92059	CCCAAGCCUCACGTTUGACA
271173197	92060	CCAUGAAAGAGAAAGGAAACATUCAACT	92061	GATATGAAGAAUGCAGGACCTCUGG
271173372	92062	GGUAAGGGACGGACCUCAGT	92063	GCAGAAGGUGCAGGAACAGUC
271173684	92064	GTAGACAAGGTUCAATGCTAAAAGCUAC	92065	GATTGTCCTGAUGGCTCTGAUGAA
271175991	92066	CTCATCAGAAGGACUTTAGCCAATGUA	92067	CCAAGTGGAATGCUTTACTATCTGGTUT
271179076	92068	ACATGCAAUACCACAGAGAUAGCC	92069	GATTGCGAAGAUCAGTCAGAUGAAGAT
271180151	92070	AACTGCAGCCUTATCAAGTATAUGGAAAA	92071	ACTCTGAGUGCTAGCTAAGUAACCA
271184333	92072	TCTTTTTCTTAUGATCAGCGTTTTUGCC	92073	GAAACAAGAAGCUGCTAACAGTACTUT
271185540	92074	TGTTGGAGGGCUTCACATCUG	92075	TGGCGUACCUCCGAGAGAA
271186259	92076	GCCTTACCUCGGTGCAUGAT	92077	CTCTGACUGCTCAGCTCUGAC
271187315	92078	AUGACAUGAGACACACAGCACAT	92079	CGCAAGUGAGTGGAGTAAUGAAGG
271187749	92080	CTCCAGAATAUGCAAGAATGCAAUGAAA	92081	GAATGTGCACCAUAAGAATGAGTTTUGT
271188905	92082	GTATTCTGCUCCCCACCCTTUC	92083	AGATCTUCAACAACCAGGAATTUGCT
271189801	92084	AGAAGAGCAGCAAAUTCCTGGUT	92085	GGAATCAGTAGAUGATTGCATGCTCAUA
271189876	92086	CCACTCCCCUCCCTCATTTUT	92087	CACCATCATTTAGUCTTGTCTGTCTUGA
271191504	92088	TCCUGCGGAUGCACGAA	92089	GGAGTUCTGCAAGUACGGCAA
271192643	92090	GTGGTGTGUGCTCAACUCCA	92091	GCAATCTTCAUCACATTGTCCUCAGT
271193101	92092	TCCACACAAGAAACUGTCACAGUC	92093	ACTGAAGACAAUAATGGCCACUCAT
271193956	92094	AAGAGATATGUCCCCTTCCCTAUAACC	92095	ATGCCTCAAAGGUCCGAGUC
271195694	92096	CACCUAAGGACAGCAGAACAAUGA	92097	TGTAGGUCCTGTCCTUGCAGT
271196139	92098	AGUGTAUCCACCGGGACCT	92099	CATCCAGTTCUGCCCCATCUC
271196296	92100	AUGACCCAAGGGUAGGAGGT	92101	GCCCAGCCCUCATGATTACUC
271198532	92102	CCUTACTTCTCUCACAAAAGCCCAA	92103	CCAGUGGCAGGGCAGAUAAG
271200159	92104	CCCAAGACUGGTACCTCCTUGA	92105	GUTCCTTTCCCUGGAGCAGAT
271200723	92106	ATGGGAACCCCUACCAAAGGAUA	92107	GGTTGACCAUCTCTTCCACGUAG
271201209	92108	ACTCCGCUGCAGTACTCUCT	92109	ACCUTAATGAAACUGGCACAGCAT
271202204	92110	GUTCUGGACGACCAGCGA	92111	ACAGAGAAGUGGAGTCGAATGUG
271203745	92112	AGTGTGAAUAATTACCCUGGAGGGA	92113	CAGTACTACUGCTGGATTCUAAAGCA
271206101	92114	GGAAATCCACUCCAACTCTGTTTGUT	92115	TATGAAAAGATTCACCUTAAAAATGTCTACAUG
271206885	92116	GCAGCTGUGGTTCCCAUCAAA	92117	GCCAAGGAGAAUCTGGGAAUAGG
271207883	92118	CAATTGGTUGCAGACACACTTUGT	92119	CTCCTCAGCCUGACGGUAG
271208936	92120	TGTGTCAGUGTGAAGTCAUGCT	92121	CCATTGATTCUGATTGGCGTTUCC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271211783	92122	GTACTUCGGAAACGCCAAUCAG	92123	TTCAGCTGCAUATGAAGTTATGGUACAA
271212018	92124	GGATGGGCTUTCTAGAGGCAUT	92125	GCTATGUCAACACTGGGTGUCAT
271212045	92126	GCAATGACAAUGCAGATGAUAAAGACC	92127	GAAATAGACUCTGCTTTTCCUCAGAAGA
271212458	92128	CCGGGAGACCUTCACCCTTUA	92129	GGAGGGAAAGCUCTCGTCUG
271215238	92130	GAGTAAGGGCUGGTTGCAUACA	92131	CTGTTTTGCUAATATTGCAUCACACACT
271216864	92132	TGGACCAAGGUGGACACAAUT	92133	CCAAAGCUCCGCTCTTUGAC
271218662	92134	CACGGTAAGTUCTGAAACAAGCTUT	92135	CCAGAATCUCCAACCCCATCAUAC
271220154	92136	CAGTAGCATGTUCCTGTCAGGTTATAUG	92137	CACCCCUGGAUCACAGCAAAT
271222952	92138	GAAAGCUGGTTTTACUGCACACA	92139	GGTTCTGCTUAGGTTTACTCUCCAA
271223793	92140	AGAGTUCAAGCCGAATGCCAUT	92141	CCATGACAAGGUGATGCTCCUC
271224484	92142	CAGCTGACAAUGTTTTGTATAAAAUCCCT	92143	GATTGTGAGGAUGGACGTGAUGAAT
271224511	92144	ACAGTGGAAUTCATCACGUCCAT	92145	CACAGTUCAAAACAAACACAAATGUGA
271224600	92146	AATGCATCTUCCACTAGGACAACUAAAA	92147	AGCTTACTTGTTATUTATCTCTTTCAGTTUAGG
271224741	92148	CCTGACCCUGTGTGACTGTTUT	92149	CGGTATAGCGGGUGTTTCTCAUAG
271227257	92150	CTTCGACTUCCTGACGGACUG	92151	CGGAGAACGUCTGGATTUGGA
271227613	92152	AAAGGTTAAAGUAAAGCCACGACUCA	92153	GCCAGCTAGAAACUTGTATGCCUA
271228660	92154	ACAGTGATCUGTGCTATTGCTUCA	92155	GTCACCAAUGCCTTATGTAAAGUGG
271229686	92156	GGGAUAGCAGTACCCUGCCA	92157	GCCCTGGUACAGCCCCTUA
271235727	92158	TGTTTTGGCAATUTGATGGTTTTGAUGA	92159	CATTTGTTGTACUCCAGGTTGAATUCAC
271241475	92160	ACCGTGGCAUTTCGGTUAACA	92161	CTGCATTTTGGUGTTCGATAGCATATUA
271245798	92162	GCCTTGTUGACCTCATCAGCUA	92163	TGGTAAGATTCUGGGTCTCTCCUG
271246397	92164	CCCTCUGTTACAAAGUCAGGGAAT	92165	TGGAATTCTTUCCTTATCAGCCUGAAC
271247586	92166	TGTAGACUCAGCAAAGAACAAUGGAA	92167	CCTCCACAGUCAGGTTAUACCAG
271248611	92168	CAGAUCTTCUGCCCCCAACAT	92169	GTTATCATTTCCCUTGTGTTTTGTUCCA
271254283	92170	ATGGCTAATTTGUTTCATGAGCAUGG	92171	CCTGAAGATGTTUACAGTGCAGTCUT
271254430	92172	CGTTTCTATTTGUGTCAGCTTCTGAAUG	92173	CCAUGTAACTTTAAUGAGAGCCCAGA
271254661	92174	CACAATATGGUGAGGGTGGAAGUA	92175	GTGGCACTTUGCAGGACTTTUT
271255051	92176	GCACCAAGUCAGTGCCACUAT	92177	CTAGCAACCAUCCAUGGAACAGT
271255197	92178	AAGGTTTCUCCAACCCTCTGATTTAAUT	92179	TTGGCTTGAAUTGTTCACGCAUT
271260107	92180	CAGGGAGACACCUAGAAACCAAUC	92181	GGCTTGGATAAUCACTTCGTAGTATTCUT
271263841	92182	AGAACUGGACAGAGAAGTCUACCC	92183	AGUTTTGGAAGAAUGAGGGAAAAGGAA
271265143	92184	TGGTCTTCTGTUTGAACCATATAGTUCC	92185	TTGGGCTTTTCUTCTCTATTTTCCUCAT
271265303	92186	CCAACAAAGCAUCAAAGCCGTUA	92187	ACTAACATTTGCUTCCCATTTACCUCT
271266554	92188	GTCCTTCAUGCACATCCTUCGAT	92189	AGGTAGCAATCAUTGCACACATTTUT
271268426	92190	CAUGAACAUGGACAGAGAAGCCA	92191	TGTGCTCTCUTGGGTTAGGUACT
271271550	92192	GAGAGAGAGAGAGAAAAUTTGTGTCUGA	92193	CTGTGAUGGAGAGAATGATTGUGGA
271271720	92194	GGGCTAUAAACCAAATTGCTUCAGA	92195	CAUCCAAACGCCGAGAAUCAC
271272618	92196	CCACAGTTGAGUTCATCAGAATTGUC	92197	ACCATTCCACAAUATCTATGCTTTCUCC
271275509	92198	CCTACAGAGAUCTAACCATTAGCAUGAA	92199	CCTGTGGGAAUCCGACGAAUG
271276077	92200	GACGTGGTGUGTCACTGCUA	92201	CUCACTTCAUCAGGACAGACGAC
271276449	92202	GCTTTCAGUTAGAGTGTGUGCCA	92203	CTGGGCTTAACCUCTTCCAATTTUAGA
271278610	92204	GGCGTGGAUGGGTCTTUCAT	92205	GTTGTAATTTTCTAUCTTTGTGCCCAUCT
271279045	92206	TCCCACCACAGUGTCTTCTTTUT	92207	TGCTGATGGUCCCACTUACAAC
271282002	92208	TCUAAGATUCGACAGAGGGCAGA	92209	CCATGCTTCCAUGTTCACATCAATTUT
271283241	92210	CAAACATATTTUGAACACACTGGGCTUA	92211	GCCTGGAUGGATACCUGAAGACT
271283454	92212	CTCAGGATTGCAUCCAGCCTTUA	92213	AGAAAAATAUGGCTGGCCCUGAA
271286903	92214	CTTCTAAACATUACCTGACAAGGCUGA	92215	CCTGAATGCUCTAGAAGAATGGUCAA
271287802	92216	GAGACACCUGCAAGTGACATATGUA	92217	GAGACAGTGUCTGCCTTCUCT
271289107	92218	CTTAAAAGCCACAUTTCTCTCCUCCT	92219	GGTACTCTGUCTCCAGCTCTUC
271289831	92220	AGGCTGCATTACAUGTCTGTCAATAUAAA	92221	TCCTGCGTTUCAGTTTAACTTGTTUG
271290182	92222	TGTGTTCGAAUGGGAGACUCCT	92223	CCCAGGGUGAACGCATUAC
271294055	92224	GAGAGCUGGCUGGCAGA	92225	CCAUGGCCAACTCCTUCGT
271294209	92226	GGGATGCUGAAAGTTGACTCUCT	92227	AAACGTTCCAAGUTTTCTTACTTTGUGT
271294219	92228	CCAGGGTGGUGTACAGCATUC	92229	GGGTCTGTCAUAGCAGCAGTTATAAAUT
271294520	92230	CGAAGGAGUTGGCCAUGGA	92231	CGGCAGGCAACUGTUGG
271296364	92232	CGCAGACACCUACAACAUCAC	92233	GCTGTGGATAUCGATGCGGUA
271296874	92234	CAGCTGCTUACAACTGAGGUCT	92235	GCATTTCAGTGUTGGCTTCCTTTUA
271299871	92236	TGAATCATTCTGUGCTTAGCTACGUT	92237	CTCAAGTAGCTUTTCACGTTGCTTUT
271300540	92238	GTGAGGCTGUTTTTCCCATCUG	92239	CATTCCCCACCCUCCTCCUA
271301469	92240	TGCAGTTCUCCCTGGAGUCA	92241	AACTCCCAUAGTGGGUCGAGA
271302276	92242	AGGTTTTTAGACCUCTTCTCCCUCAA	92243	GCTGAAGAAUCCCGGTTGTTACUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271304540	92244	GGCCTCGUGAGTCTAGATCUACC	92245	TGGAGAAAGUCCAGCCUCAGA
271305198	92246	GAUTTTAAAACCTTUGGCGCAGAC	92247	GCATGTACATAUCCCCTTGTGTAGTAUT
271306890	92248	GCCAGTUGGACAAATGCGAGUA	92249	ATCACTGUGAGCCAGATUCCAC
271308173	92250	CTAACCTUCGGCCTTTCACATUG	92251	GGCCAGCUGGATCATACCAUA
271309736	92252	GGGCCAAAGGCCAUAGUAGA	92253	GCAGCCCACGUGAUCCT
271309755	92254	GGCTCCUCCACTGAGGAUGAA	92255	GCCCGGCCACUGATACTTUAC
271310274	92256	CCUCCCAGGAAAAGGGTCUG	92257	CCTACACAAGGUGAAAGCTCCTUA
271311334	92258	GTTTGAGCCUATAGCCCAACUGA	92259	TGGCATGGTCUAAACAAATAGCTCTUAAT
271316527	92260	CCAGGCCAUTGCTGACUCA	92261	CTCTCTUCCTCACCUGCACA
271316757	92262	CAAAGCAAGAAUACTTTTCTGGGTCUT	92263	GCTAGGAACUACTGGATTGGGAUACA
271317562	92264	CCAGCCCCCAAGUCUCA	92265	GCCCTGGGUGGTGGTUC
271318530	92266	GACAGCAAACAGUCTGCCUCT	92267	CCCACTTTTUGGTGTTGGAACUG
271319549	92268	CCTCCAGAUAGCACAACGAUAGAAAA	92269	CCTCTGTTAGAUATAGCACTTGUGAGG
271320055	92270	AGCCTCACAAGUGCTATATCUAACAGA	92271	ACCCAAATCATUCACCTTACCATAUGAAA
271320502	92272	TTTTGTGTTAGAUCAGGTTCTGCCUT	92273	TCTCTAGCAGGUCTGGTACTUCAG
271321210	92274	CCGCTUGACCATGGTGAUGT	92275	TCATCCAGCCUCCGACUCA
271321976	92276	AAAGGTATAGGUGAAGTCAGGACGUA	92277	GGAGUCTGGUGGCCGAGA
271322846	92278	TCCUCUCGGCCACCAGA	92279	GCTGCTGGUGCCTCCAUT
271323366	92280	GCACACAAAGUGTTGAACCTUCT	92281	AGTGAGCAAAGCAGUACACTCTUAC
271324689	92282	GAAGTCTUGGGAATCTTCAUAACCCA	92283	GTGAATCCATGUGGAGATGATGCAUAT
271325100	92284	TCGAAAACCUCAGCAACATUCCT	92285	TTTCAGTGCAUCAGGGTTTAATCAGAAUA
271325589	92286	AAAUCCAGGCTUACAGCGACA	92287	AGTTAACTCCCCACUTCAGGAATUAGA
271326655	92288	GGAAGGACCACUGGTTUAGAACA	92289	AATTGAGAGGUAAAGTTGGGTUCCAA
271330469	92290	CCATCCCAGGUTGTCCTTCATUA	92291	CAACAGTGTUGTGATGCCATUGAT
271331496	92292	TCCTGTTCAGUTTCTTCCTUGCT	92293	TTAACACAGGCGUATTCCGUGT
271332733	92294	GCTTCTTTTCAAUGATGCGGCAUA	92295	AAAATTACCTTUTCAGTTAAAAATUAGGCCAAC
271332965	92296	CCTCATAGCAUGGACGCATTCTUA	92297	GCAUTTTTGGCUGCAGAAGAGG
271333904	92298	TGTCCAGACCCCAAUACAGTUAAGA	92299	GTCATCATCAGUGGAACAGGTGUT
271335625	92300	TGTGTGCUGTACAGUCACAGG	92301	CACCGTGUGGGCTGAGTTUA
271339603	92302	CCTATGCAGGGCUACGATUGG	92303	GTTGGGCUCAGCAGGUAACT
271339664	92304	CCAGTCAAAGGUGACACCUGAG	92305	TCACTGUGTGCGTGUCAACA
271346489	92306	TCTGACTATGUGCTCTCAAAACATUCAT	92307	GCCTTACCCUGACATCCTCCUA
271347101	92308	CCATGCCCUCTCTACACUGGA	92309	TCAAGAGACUCGCCACAGAAAATUAC
271348519	92310	TGCACCTACUTCTTCACAUGGG	92311	TGTTCCAUGAGCATGTGGACUAAG
271349198	92312	AGGCAGCUACTGCUAGAAGAGA	92313	CCACGCUCAGCCTGAGUAT
271352298	92314	AGCTGCAAGGACUTAAGTTUCACA	92315	GTTTCTCCUCGCCTTACTCACUC
271353072	92316	AGCAGUGCAGCCAAAATATAUACACA	92317	TTTCTGTTCTCAUAGCCTTGGUGG
271354454	92318	GCACTUCGCACACATAGUGG	92319	CGCTTCUGCTCGACUGCAA
271355820	92320	TCCATCGGUTTGGCACCTUT	92321	ACTTTTCCUCGGGCTGCTTUAG
271355932	92322	GGCGAACAGAUGCACGTUC	92323	AAGCCAUCCGAGGAGCTACUA
271358429	92324	GCAAUCGGCAATAAUCCCGAGA	92325	TGTAAAUGACGCCGCUCGAT
271358747	92326	ACAACTTTGTGUTCTACCTTCUCCC	92327	GCTACAGCUGTCTCCAGUGAAC
271359854	92328	GTGGTCAGGGUTGACTGUCT	92329	TGTGCTUCAGCCACTGGAUG
271360552	92330	CGTACTTGUAGCTGTCGGCUT	92331	AGTGCCACAGGGCUTCTUC
271361547	92332	GTGCAAGGUGTACAGCGAUG	92333	AACCCAAGGUGGGAGAAGAAUG
271362473	92334	GATCAGCACUTTCTUGAGCAACAC	92335	AGGTCCTAAUACACAAAAATGCUGGAAA
271364883	92336	CCCACTCGACUCCCACAUCT	92337	GGTTCCTTACTAAAUGAGCACTATTGUGT
271365023	92338	CAACCACAGCAAUGATAATAACAGGAUT	92339	ACTCTAATTTTATTUAACCTTTCAAGTTCTUGC
271367815	92340	GAAGACAAAAGCACUTCACAAACCUT	92341	TGTCTTGTGUGTGTTGATTTUGCAG
271372163	92342	CCAGAAGUCCCACTCCTCUCA	92343	ACTCCCTUCCAACGTGTCTUC
271372351	92344	GACTTGAAACGGGAUCTCATTUAGGA	92345	GCTCATTCUACCAGAAGUCCACA
271373916	92346	GTCTTTAACCUCTAACTUCCAAGGGAA	92347	GTCTCCACAGAAUTTCCGTCTCTAUC
271374667	92348	ACAGCTUCGGGTGTTAAUGGT	92349	GATCAGTGCUAAACAGGATCTTTTCCUA
271383969	92350	GGATAGTACCUGAGTGTGTCTGGUA	92351	CCTTUCAGGCAGCCGACUAAA
271384077	92352	GTGAGTGAAUGCTGACCCCAUT	92353	CGAGGCUGATGAACTAUACGGAT
271386316	92354	TTCTGAAAACCUGGCAAUCCCA	92355	GCTTGTCUGACAGGAGTGCUT
271388743	92356	TCATTTGTTCAAUAACTGCTTGGCATUT	92357	GCTGGTTTAUCTTCAAATTGTUGAGGAT
271394809	92358	GACGTGGACUTCCACAUCCAA	92359	GAAUAGATGGTUGAGCCCACAAAC
271395109	92360	CAATGTTGAUCCCAGGGATGAUGT	92361	GGGCACAUAGTATTGCAGUCGAG
271398107	92362	CGCTGCCAUTTGGACTAAATUGT	92363	CAGCCAATUACCGTCAAGATTACUGA
271399064	92364	CCATATTCUCCACATCTCTCTTUGGT	92365	ACCACUCCAACAAAGAAGAAATUGAAGAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271399185	92366	GGCATCCUTTTGAACGTUGACA	92367	TGAAAUGGGCCCAAGTUCAGAA
271400719	92368	GTCATCTTTGGUCATTTAGCTGCUT	92369	AGATGCCTUCCAACATGTCTTTUAGAG
271400962	92370	GCCCCAGCGUTTCCGTAUC	92371	CATTTAACCUCCCCTCTCGTTUCA
271406310	92372	GCAGTACACUGAAGAATTCCUGAGAC	92373	TGCATUCGCAGATGCTTUCAAAA
271406385	92374	CCCAACACCACAAGGUGAATUAG	92375	CGGGTCATTTCUACTTGGCATTTCUT
271412312	92376	ACAGGAAACAAAUCAGGCUGCT	92377	GGGACAGGCCCAGUCCUA
271413078	92378	AGATGGCAAAGCCUGACUCC	92379	GACTTGGCAUCCCATTGTCUGA
271417570	92380	GGAAGGAGGGCCCAUTCUC	92381	CCTCCCUCCACCAGCUCAT
271418601	92382	CAATCCTCACCUAGAGATGCGUT	92383	CUCAGGCACCUCCACAAAGT
271419571	92384	GCAGCTGUTGGAGAGAUCAGT	92385	CCTGGAACGCAGUGTACAGAAUC
271420102	92386	CTTAGTGAGAGUAAAGAGATGCGAAUGA	92387	GCATTAAGUGCTCCATAGCUGAGG
271420682	92388	GGGTUCAGAAGTTCUCGGAGT	92389	GCCTGTCAUACTTTGAAAGUGCAAT
271422510	92390	GTAAGTTGGCUTTCCAGUGCAT	92391	CGTCTCCCUTATAACCAUGGCAA
271423764	92392	GGTCTTTCUGCCAACAGUCCAG	92393	CCTGGGCCUGTTAGCATCTUT
271424033	92394	ACCCTGGUGAAGAACATGATCUCT	92395	GGGUCTCTTGTAUGAGAAAGCAAGG
271424978	92396	CACTTCCUACCCGTGGTCAUC	92397	AGTAAGAUGGCTACCACUGCCT
271427204	92398	TGCATACCCAUTAACTGGAUCCAC	92399	GACCAAUGATGGCCAUAGGAAAAC
271429300	92400	CCTGTGTTUGAACCTGGCTTUT	92401	GAAGGGAAGAUTCCAGCATAUAAGGA
271430294	92402	AGAAATTCTGUCCGGTTTCAGATTAUG	92403	CGTGAACTUGCGGTAGGCTAUA
271430708	92404	AAACACCACCACUTATCACUGCT	92405	GGAUTTATTGACTTCAUCGGCCAAGT
271432179	92406	GATGAGACAUTTCACCCTCUAAAAGAGT	92407	CTGGATAATGUAGAGGGCATUGCT
271433293	92408	AATCAGGUGGACAUCACCAGAAG	92409	TCCTGATTGGACAUCTCCCAGUAT
271433400	92410	GAGTTCACCTUCTGCGAGGAUAT	92411	CTTCCACCCACUGTGTCTTCUC
271434621	92412	TGTCACAACAGUACAAATGAGUGGAA	92413	CCAGATGUGAATGTGAAGAUGGGT
271435109	92414	CCAGUAGGATCUCCGCCACT	92415	CCTCTGACUGAGGTTTGTCTTTCUC
271437906	92416	CCTGCCUTGCCTACUGACA	92417	GGACACAGAGGUGACCCUCA
271439294	92418	GCGGGCACCUTATTCTTTATCTUAGG	92419	CATCGCUGTCTTCTTCUGGGT
271442592	92420	CCGACACCAGGAGUACCTCUT	92421	CCCAGGUGGCTCTACUCAC
271442612	92422	GCTACAGGGCCUTGTGUGT	92423	CCUTACTCTCTTCAUCAAAGGGAACAG
271443705	92424	AUGTTACAGAAGAUGAGGAGGAGGA	92425	GCAGGUGCACGCTCTUACA
271445050	92426	GGAAGAUAAUGGAACGGAGGAAGAA	92427	CUAAATACTCTTTTUGCACCCACCAG
271446164	92428	TGGCCAAACUGTTCTTTTGTTTTAUGG	92429	CGGGTATGUGGCTTTCCTTCUAAAG
271446284	92430	CTGTGTCAAGUGGATGGTUCCAT	92431	GAATTUGGCCAAGAAGGACUGAAAG
271446489	92432	ACCATCACUGACCATCTCCUGT	92433	GCCCAGCUGAACTGATTACTTUGAT
271447687	92434	GGTCAGAUGGAGCCCTGUAAT	92435	GCTCTCATGTCUCAATTTTTGCTTTCUT
271447913	92436	AGGUGATGTCTTAUGGAGAGAGACC	92437	GCCACCCAGUTACATTATGTUCCA
271449773	92438	ACCATCAGUATTTGAAAGTCUGCACT	92439	CGATTTGTAACAGGCUTCTTGGTATTUC
271450024	92440	TTCATCAUAAAAGGTGACUAAACCAGCA	92441	TTCCATCCAGGUCAGCAAUCAG
271451531	92442	GCTCCTGCUACATGGGACTUT	92443	GAATCCUGATGTGGUCACCACT
271453120	92444	AGTUACCCAGCAUGCCACAAT	92445	GGAAGGTCGUGGTGCGUT
271458895	92446	TGGTGCTTCUCCCGTAGGUA	92447	GCAGAAGACUCCCAAGTUGGA
271470841	92448	GUAGTACATGGCUCCACCCAAC	92449	GCCTGGAAGCUGCATAGTATUGAT
271498581	92450	TCTGCCTCACUCTCTGTTTCTCUT	92451	ACATAAATCTTCUGAGCTGAGTTCCUG
271498646	92452	ATCAGGTTTGAGUGGTTCACTGUT	92453	TGTCAGGCUTGAGGCTACUGA
271500441	92454	AACTTGAGTTCUGGTTAAAGCTAGTCUG	92455	CCUAATUGGCCGGCAGAAGAT
271500457	92456	AAGTGCCCATUTACAGTGAAGAAUCT	92457	GGAACACTUGCCAATGGGUACA
271504069	92458	GCAAGAGGCACAAAUGTUACCA	92459	CCCTCCTCUAGACTGCATTGAAAUAAT
271504750	92460	AATTGAAGAUGACAGTGAAGUAGCAGAA	92461	ATTAAAAUAGATGTTTCCUGCCCACAGA
271507997	92462	GGAAGAACCUCTCCCTTUCAAACT	92463	TCTTTGTCTCAACUTTATAGGCACCAUT
271509369	92464	CAGUACAGAAGGCGAAUGGCT	92465	TGAGTTGAGACUGAGTGCATTTCATTUA
271511024	92466	GGGTTTTCTTTUGACTTATCACCTCUCA	92467	GAAGCTACUTGCCTTTTUGCCA
271511836	92468	CCTGUCAGCCAGACUCAGGA	92469	GCAATGACATTAAGUGAGAACACACCUA
271511886	92470	GAAATTTACCAUAGCAGGTCTTCTTGUCT	92471	GTGCAGCUAATGAUGGCAAAGG
271513143	92472	AGAACAAAUGAGAATGCAGCAUACCA	92473	ACAACCACTGUCAATTATGTACGUGAT
271515969	92474	GGTTTCTCTCUCTGTGCCAUCT	92475	GCTGATGAAUACATGATCCCCAUAGAAAA
271516398	92476	TGATTGATUAGACACATGUGAGAGCAG	92477	TGAATAACCCCUGTCAACCUCAGA
271518803	92478	CCAGGGACUCCTATCCCCAUA	92479	GGATGTTCCCAUTGGTCTGGUC
271519242	92480	AAGTTTGACAGGCACUGGCTUA	92481	CGGCATCATUCCCAGGAAAAUC
271519793	92482	TGACCTUGAGGGCCACTGUAT	92483	CTGAAAGACGAAUGGTTTGATACUCAC
271520970	92484	GGGCAUCAGGATGUGGGT	92485	ACCACATGCACAAUTAAGAAACATTUGT
271521218	92486	GCCACGAGGGUTAGACAAUGT	92487	AGGAATGTATUGGATTCAGAAUGAGCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271522846	92488	AGAGAAGCUCACAAAAATTTGTCTTUGG	92489	AGCTGTCUGGTGTGCTGUT
271522952	92490	ACTTCTGCTUTTGCTTCTTTUAAGCC	92491	ATTTGCTGTCTUGCCTGTGACUA
271523537	92492	GCUTCTTTUAAGCCAACAGCACA	92493	CCCGCCACAGGAGUCAAUT
271524137	92494	CAACAGCAUCACGGTGUCC	92495	TGTGAGGCCUATGAGCTCCUA
271524350	92496	CTTGCAAUTGCTTTTGUCCGGAT	92497	GTCATTCTTACCUCAGTTTGTCTTTUCC
271527129	92498	ATTGGCUGAGAACAAACUGGGT	92499	GCTCTCGAAAUTTCACCCCAUGA
271529233	92500	ATGATACTTAGGUAAGATACTTACCTCTUGAAA	92501	CTTCATTCAGUGCATTCATCTTUCCAT
271529357	92502	CAATGGAAAGAUGAATGCACTGAAUGA	92503	TGAAAGACUCACTGCCATUCGT
271529589	92504	GGAAAGATGAAUGCACTGAATGAAGUT	92505	TCCTATGAAGAAGAACUGAAAGACUCACT
271534474	92506	CUAAAGCACGAGGGTTUACCAGA	92507	GCAGCATCAGUTGTTTGTGTTTGUAAT
271534610	92508	ACCTGGAATATGUACGGACTCTGUAT	92509	CAAGCUTTTCGACAUAAGGGACAG
271534733	92510	GGAGUCAAAGTUAAGACAAGACAGAGT	92511	CCAAGAACCAGAAAUGTATCCCAGUAA
271535753	92512	CTGGTTUGCAGGTGACATUGG	92513	GACCAGGAGAAGCUCAGTTUGAT
271540092	92514	ACTCCAAGUCACCTTUCAAAACCA	92515	AGTCCAGUAAACACCAAAUCGCT
271540405	92516	GAAATGATTGCATUCAATGTACATATCUAACA	92517	GGAGAATATGATUGTGCTGATGGTUCA
271540817	92518	CAGTCATCTUGCCCATTACATCTUAAGT	92519	CACAAATTTTCTCUCTCTCTCTCCTUCT
271542023	92520	CCCTCTCTGUCCCACCCAUA	92521	CAGGAACUCATCCUCAGGCA
271542150	92522	ACACAGAATTAUCAGCTGGTUGGAAT	92523	ACTGCGGUACAGTGTAACUGG
271543759	92524	GAGAAGCUGGCCCAGATTUGA	92525	CTGAGTCACGGGUATCGTCAUT
271544036	92526	AGCCCUGAGAATGCCTTUGG	92527	GGAATGATUAGCAGGAGUCAGACA
271545350	92528	GATAATGAAGAUACCAGTUGGAGGCT	92529	GAAGTGTGAUGTGCCCCAUCT
271545807	92530	GGCCGGGUTGGGATGATUC	92531	TGCAGGUAGAGGAGTTGUGGT
271546691	92532	TTTTCTCCAGTTCUCCTCTACAAATGUG	92533	CCGTTTTGAAGAUTGTTGAGAAATUGGA
271547975	92534	CCAGATTCCATUCCCTTAGGCAUT	92535	CCAGCUGGCCTUCACCAG
271550480	92536	CCCAACAGTCUGTATTTCAAGTGUAAGA	92537	GCAGATGAAGCAUTTTTCTCTGUGAAT
271550600	92538	GTAAATGATUCAGACTTTCACUGGAGGA	92539	AAACCGGCACAUACATCTGTGUA
271552092	92540	AAACCGGAGCCAACUTTCUCT	92541	GTCCCUCCCCAGCATCTUC
271553763	92542	GCAACGCCUTTTCTGGCAUAC	92543	AACCCGAGGUGAAAAUGAACCA
271557778	92544	TCCTTTTGCCAACAAUCCAACATUAG	92545	CATTTTGCCUACCAGGAAATTTGGUT
271559960	92546	GCAAGGCTAUAAAGTCGCTUGAAA	92547	GACCCTGTUGACAGTACTTUAAGAGAT
271560707	92548	CCTGTACTACAUGGAGTCTGATGAUGA	92549	ACAGGACCTACUTCTCTAATCTCAGUG
271561703	92550	TCATGCAUACGCTCAACCUCAG	92551	CTCTAAUGCCAAGGCAGTCTUGT
271562723	92552	CCCAGGGCUGTCTGTAGAUG	92553	TTCTGGGCGCUGTACAUGAG
271564168	92554	GTTTGTATGGCUCTTACCGTCUGA	92555	GGAGGCUTTTCTCAATUCCGACT
271564224	92556	GGCUGACCAGCTCCGUT	92557	GGAAGGAGCUGGAUCCCAAT
271564759	92558	GCAGTTTGCUCAGCTGUACC	92559	ACUGGAGAAAUGGCACCCAAAA
271566381	92560	CCAGAAAAGAGUACCCTGTGCTTAUG	92561	AATCATCCAGUGCTCTAATTCCAUGAAT
271567273	92562	CGAUTCTGTCTUCAGCCACGA	92563	GCTATCAAGGUCGAGCACUGT
271568793	92564	TUCTCGAAUACACCGACCACAAAA	92565	CAAGGGTATTCAGUTGTCAGTGGTTAUA
271570488	92566	GGGACCGUATTCTGAAGCUCAA	92567	ACCGTGUCTGGAAACAUAGCC
271581805	92568	CUCAAGAATUGGAAGCCAGCAA	92569	ACCAGGGCCCUTTTTAGCUAC
271585946	92570	TTCAGCAGAAAACAAAAGUGTUGAAGT	92571	TUTACCAGTGAGAUAGGAACAAAGCAAA
271587765	92572	CTTCTGCTAATAAUGCACTCTGAGUGA	92573	AGTGTTCATTGATUTGGCCTTTTTGAUT
271588830	92574	GAUTAACTACUCAAAGGCCCCCAT	92575	AGCCTCUCAGCAACAGAACTUAC
271592904	92576	GCUGAACATCCUAGAAGCCAAGA	92577	GTTTGCCAGUGTGACUCCAAC
271598774	92578	CCACAATCCUGTCCACATCUGT	92579	CTTGAAGCTGGUATCTATGAAGTUCCC
271610687	92580	AGTCCACAGAUGTTUCCAAACACA	92581	TGCTAACTTCCCUCCTTTCTTTTUCAG
271619673	92582	CCTTTAGTTTCTUCTGCTTCTAGTCTUCA	92583	GTGCTTGUGCCGATAATCAACTTUT
271629469	92584	GTGCAAGTTGUCCCATTTTCAUCC	92585	TCTGACACATTUGCTTTCTTCCTCUT
271630168	92586	GGACTTGAAUGGCTCAGTGTUCT	92587	TGCTTCAGGAUGCCTCATGUG
271633165	92588	GACCCGAACCAAACCUTGTUT	92589	CAGTAGAAGAAGAUGGCTGUGGAG
271633856	92590	ACTAAAGTGACTUCTTTTCTGGCTCTUT	92591	TCCUCTCCTUCCCCAAGAAACA
271636420	92592	GGAUCTCUGACCAGAGGCCAA	92593	CGTAGACAAGGAGAUGCAGGUA
271637613	92594	CCAUCACCCCAGAAGCACTUAG	92595	TGCTGGATACCAAUGAACATGATUACA
271638675	92596	GGGACACTUGCCATAAGGTTTAUCAG	92597	CTAATATGAUCCCAGCAGCCUGAG
271639407	92598	GCAGGAACAUCAAATGTCAAGTUCA	92599	GGGAGCTTGUAGGTAAATGAAACAUAGG
271640782	92600	GUCAAGTTTCTTTUGGAGAAGGCAAA	92601	GATGCTTTTUAAGCCCAATAACTGTUGA
271645780	92602	CTGCGAUCCGACUCACCAA	92603	CATATCAGAGCUTTGAACAGGTAGUGAA
271650199	92604	CCTTGTCTGACUCTGCTGCUC	92605	GTAGCTGGUGGTGTCCATCUC
271651731	92606	GGGACCCAGGUTTAAGAUGCT	92607	GGGAGTCACUGCCATTTTUGG
271652708	92608	GCAGCUGGTCACCUACGA	92609	CCTCGGUGGCTTCUGCAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271655445	92610	CCCAUCCCGGAAGAGTUCA	92611	CCGGGAGGUGAUCCCCAT
271655774	92612	GTAGCCUGAGAAGGGTTCTUAACAA	92613	AGTGATTUCTTCTGCTUCAGGCAA
271656348	92614	GCCCGGCCUTCCCTCUAT	92615	GGAGCCCUCGTAGCCGUA
271657569	92616	GCAAGATCACCUGTTGCCUGA	92617	GGAATGAAAAUCCAAAGCAATGUACCA
271659821	92618	TCCTTACTTTCUCCACTTTGCTTTUCA	92619	CTTUCAGGAGCCGGUAAAACAAG
271659990	92620	GCTGACCUGGCCTUCCT	92621	CAGCAGGGUCCCACUCAC
271660081	92622	GGGAGGGCAACAUCGAUACC	92623	CCCACAGCCUGGCTTGUC
271661205	92624	GGCTTGUGCAGCCTCUCT	92625	CACCACGCUGACCCUGT
271664562	92626	CCUACGACACGCUGCACAT	92627	GGGUCCGAGCCGUACAG
271666697	92628	CACTGTCTGUCCTGGCTTCTUA	92629	ACAGCAUGCCCGTCAUGAT
271667326	92630	CCCTCAGCGCUTGCTTUACT	92631	GACTGAAUCGGAGAUGGAGACC
271674055	92632	CGTTCTCCAUGAACTCTGUGAGA	92633	TGTGGCAAUCAAGACCCUGAAG
271675952	92634	CCAGGAUGGGTTGCCATUGA	92635	CTTTCTCTCCUACAAGCTTUCCCA
271677659	92636	AACUAATTTTUGGCAACAGCAACCT	92637	GTAGATACTGAUCACTGGAGTCTUCAGA
271679741	92638	GGCCTCGCUCAGAAACUCAC	92639	GATGACCTCUGCGTCCTTGUT
271681153	92640	GGCCUGAAATUCCAGGACAACA	92641	GACGTCCAGGUTATGGCUCA
271682755	92642	GGUGUCCCAGCCAGGAGA	92643	CCUCACCCAGCAGCTUGA
271683660	92644	TGGTTGUGAAGGACCUCCCT	92645	GGAGATCTTCUCACTGGGCUACAT
271684678	92646	GCCTGAACACUGCACATUGAA	92647	TCATAGCGAAUGCTCUCAGCAG
271684748	92648	CCTCGCCAAACUCACCTUCAAA	92649	TCGATGTCTCCUACGTCAAGATUG
271688300	92650	TGACCUCGTAGUCCAGCACA	92651	GGACAGAGCUACCAUGCACAAG
271689328	92652	GGCGAUGGCCCTGGAUT	92653	GAUGCCUGCACCGCAAAG
271689600	92654	GTCACCAATUCAAAAAGCGGTUCA	92655	GUCATAGGAAGGAUGAAAGGAGCAA
271690212	92656	GTTGGUGCGCCCAGGAUA	92657	CCTGAGGCUAATCCTGTCCTTUC
271700839	92658	TGTCCUCCTCGATTUCAGCAAG	92659	CCAACAGAUGAGAACAACGTGUCA
271700920	92660	ATCAGATUCACACAAACAUCAGGAAGA	92661	TGGCTGACGAAGUGTTTTTAUCAAAC
271714114	92662	GTTCCTGCCGAUGTTAGTGUCA	92663	CCAGACACCAUTAAGCCAGUCAC
271717115	92664	CTCTCGGUCACTACAGGAGTUC	92665	AATCTTCAGTAGAUACATAATCCTGTCATTTUC
271722677	92666	CCCTCTCCUCCCTCAGTTUC	92667	GACTCTGTCUCTCTGTCTGTCUCA
271724623	92668	AAGUCAGCAACCCCAGGATUC	92669	TGTCCAGGAGUGTTAGUCACACA
271726671	92670	ACUTTCCTATTAAUGGAACCGAAGCC	92671	GCTGGACAAAGAUGGCCACAUAAA
271727076	92672	CTATTAAUGGAACCGAAGCCUACCT	92673	CACAGTTGGAGAAUCTAATGCUGGA
271729407	92674	CCAGAAAAGGAGAAUAAUAGAACAGGGA	92675	GCTGTCAGTTAUGTGATGGCTACUG
271729435	92676	TCCTCTTATGTGUTCGCTTTCCTUG	92677	AGCUAAAACGGUGAAGCAAAACAAAA
271730159	92678	TCACUACCTUCCGCACAACAG	92679	GCCAAGAAAGTUCAAAAGAATCCTUCA
271730421	92680	TGGCCAUCTTTGUCCAGCA	92681	TTCCAAAATACCUTACTCAGCATUCAGT
271732426	92682	TGGCATGUGCCACCATTGUAA	92683	AGCTTTCAGCAAUAATGTTGCCAAUAA
271754661	92684	CCACTGUGCCCCAGAGUT	92685	GTCTTCCTCUGCCTCTGCUG
271758520	92686	CCACCAGGUGCAGGUGAAG	92687	CCCUGCCGGTCACUACA
271793572	92688	AGCAAGCAAGUAACGUAGAAACCA	92689	GTTGCCUCTTTCATCUGCCAAG
271794522	92690	GGCCCTUGGACTGCCAUAT	92691	GCCTUCACACTCCTUGCAC
271797946	92692	AAAUTATCCACGUAAACCACACCGA	92693	TGATGGCATTCCUCACTGTAAAGAUAAA
271798176	92694	GGACCTGCUCTTCAATGUCGT	92695	ACTAACACUCGGCTCTCAGUCA
271798691	92696	TTTAGGTCTUGGGTCTCCCGUA	92697	GGAGAGCAGCGGUAGTAGGAUAA
271800930	92698	GUCCTCCTUAAGCACCCAACT	92699	GGAACTTUCAGAAGAGGTGCUGAC
271801030	92700	GCAGGGAUGAGGTCCACTUC	92701	TGAGCUCAGACACCCCATUA
271801215	92702	GAGGAGAAGCCGAUGTGUGA	92703	CGGAACUCGTGCACUCAGAAG
271801927	92704	CCACAGUAGAGCAGTTTTTCATCUGA	92705	TTGCCATUGCACAAAAGTATTGACUT
271804530	92706	CATCTTAGAGGUGCAGGCUGT	92707	CCAGGCUGGAGATCAGGAGUAG
271810162	92708	CTGAATCGGUCTTCCAUCAGGT	92709	CGTTTGCATTUGATTTGTCTGATUGCT
271812029	92710	CAGCAAGCACUGTGCTAGUAGA	92711	ACGGTUCAAGAAACTTGCUGACA
271813834	92712	GCCTGCUCCCGAAGGUA	92713	CCGCTGCUGGAGTTGGUC
271815492	92714	ACCCGTCCGUACTGGTGTTATUA	92715	CGCUTGAGGAGAUGGAAGCC
271815793	92716	CCTAGAACUGATGGUACGCAAGT	92717	CTTGTGAAAAUGGAGGAAGATGCAUT
271815911	92718	CCATTCUGGCAGTAGTTGCUACA	92719	AGTUAACTTGTGAAAAUGGAGGAAGAT
271816064	92720	TGCATCTTCCUCCATTTTCACAAGTUAA	92721	GGGTTAATTATTTTAUGGAAACACAAGAUCC
271816086	92722	CCTCTUCGGGCGACAUGAT	92723	CACCCUCACGCCAGACUC
271816452	92724	TCAGATTGUCACAAACTGCCTUGAT	92725	CTGTAUCCAAGCTCGGUGGAAA
271818011	92726	TCAGTCAUCACCTCCACCAUACA	92727	CACCATATGACUCCCTGTTAGTGUT
271818352	92728	ATGAAGGUCAGGACTTGGAAGUG	92729	CTTGGAGATCCUGGTGCTACTAGTAUA
271822232	92730	GGAGAGCCUTTCTGCTCUGA	92731	CCTACCACACCACUGGCTUAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271824929	92732	GGGCAGCUATTGATACCTUGCT	92733	CCCCTUCAGGAGTGGTTCTUAC
271826894	92734	ACCTTCCTTAUCTGTCTCCUAGCC	92735	TGCCAGTTCUCCATTTGGGTTUT
271828833	92736	CAGTCAUCGTCGCCAUCACA	92737	TGGACTGACTGUAGCTAGCATTATTCAUA
271829408	92738	CCCCUCAGACAGGGTCTTUG	92739	ACCTCCUACCCTTGGGUCAT
271833181	92740	GAGGTGGUTGCCGATGUGA	92741	GTAACCCUCCCCCUCCCAA
271834954	92742	GAGCCACUGCCTTCATAGUCA	92743	TGGTTTTGTAAAGUGTAACCCTCTCUT
271837489	92744	CCCAAATAUAAGACCATTAGTGCCUGA	92745	CAATCGGCTUTCAAAACATGGUAAAGAA
271837703	92746	AAAGGTTGUCCTTCCTGUGACC	92747	GCCCTGTAAUGTTTATGCGATCUAC
271837888	92748	GCAACCUCCATCAAATTTUAAAGACACA	92749	GCAACACUGGAAGAAGTGTGATUC
271839566	92750	GGGAAUCTTUGGCCCACCAT	92751	CTTCACUCACAACGAAATTGTCUCAG
271844092	92752	TGCTACAATUAAATCAGCCATUGCC	92753	AGACGAUCAAAACAAGACTGAAUGAAGT
271845993	92754	CAGCCCUAAAGCCATATUCGGAT	92755	CTGAGCAUGCCAAGTTCCTGAUA
271849889	92756	CTGATATTTGTAGGUGGTGATCCAUGAA	92757	CGAACCATUCGAACAGCTUCC
271851227	92758	AGACTCCAGUCACAGGTGGUA	92759	AACTGAAGGACTUATTTGGTGTCCAUAG
271851622	92760	CCCCACCCUTCATGTGAAGUA	92761	CACCUTCTGATTTCUCCCCACAG
271854941	92762	CAAAGACAGUGTTAATTGUGCAAGACA	92763	GTTATTCACAAACCUCGACAUAGGGA
271858911	92764	GGGTCTCTTUGTCTTGGGCAUA	92765	CTTTTACAGUGAAGTTTAGCAACUGCAA
271859326	92766	CCAAGCCCCUATTCCCAUCAAA	92767	TTTTGTTCCTTUCCCATCGGCUA
271872516	92768	TGGACACUGGCCAAGATTTUCT	92769	GCTTTTCTGAUTGGCTTACAAUCCT
271879916	92770	CCACUCUGCCCCGGAAAA	92771	GUCACTCUGGCGGGACAC
271880464	92772	GGGCATAATGUAGAAGTGTCUGGAAAC	92773	GATGATCAACTUCCTTGCAATGTAACUT
271880524	92774	TGGCTTUGGACCAGTCCTUAC	92775	GCCTACTTGATTCAUGTGCTCTGTATTUT
271881208	92776	CCAGAAGUGAAAGGAGCUACCAA	92777	GGGAGUACCACGUCAGAGG
271886243	92778	AGGGCACATGUAAATATCAAGGCTUT	92779	CATATGAAUCCACAAGGGTAUGCCT
271886519	92780	ACACAACGUGGCTTGCATUAAAAA	92781	GCCUTGUCCACAAACACCAGT
271890430	92782	GTAATCAGATCCTUCTACTCCACGGAUA	92783	CCTATUCAACAGCGTCUAGCCA
271895145	92784	CCGGCCAUGGAATGTATTCTCTUT	92785	GCACCTCCUACTCCCTACUCAC
271895412	92786	GAAGATTGGCACUGATAAACCTUGAG	92787	GGGTACACUGCATTCAAACUGT
271895544	92788	AGTUAAGAAGCAACCCCCUCAC	92789	AGTCTGGAGGCUGGCATCUAT
271896899	92790	CGAGGUCCCCAGCTAGGTUA	92791	GAGCCTCAUGAAGCAGAGGUC
271897489	92792	CCACCCTCUGATGCAGTCAUAG	92793	CAGGAGCUGCAAACATTGACATTUT
271898868	92794	GGTTCAGCCUGTCTGTGATUCAT	92795	CTCTGCCCCUGAATCAGCTTUAA
271900511	92796	CTAAUCAGCACAGTGGUCAGAGA	92797	GTCACAGUCCTGGTCAAUGGG
271900720	92798	CUTGGGCACTUACGACAAGGT	92799	GGAACACCUGCAGGAGTCTTUT
271906494	92800	GCTCTGCUGACCACTGAATUAGAC	92801	CCCACCCAUGTACCAGCTCUA
271907684	92802	CCCACACAGGGUGACATTCCTAUA	92803	TGGACTTTGGUATCACATAGGAGUCA
271908017	92804	CATGTTUCAGGGAGGGACCAUT	92805	GAGGTGAAAAUACCACTAGCATCCUA
271910403	92806	TGTUGACACGCACACAGUGA	92807	GCAGUGCGAGACCACCUG
271914870	92808	GGTUGGAAAGGAAGTCCUGGT	92809	GCAATGATGGUGGCCTTGUC
271916095	92810	GCACAGGAAACGUCCGCTUA	92811	GCTGACCUCCTGGTCTGTTUT
271917247	92812	CCCTGACACUCGCTGGTUAG	92813	TGAUTTTGAGTTUGGGAGACCACA
271919485	92814	TGAAGAGCAAUATTTCCAUCCAGAACA	92815	GATCTCCAGUGTGATCGACTUGA
271919810	92816	TCTAGGGTGAAUTTCAGTCATTUAGCC	92817	TGGGTCCUCTGAAGCCUAGAA
271919872	92818	GCCCTTGACUTCTTTCACAGUGAG	92819	CCAATGCCAUTGTTATGCTGTUACA
271920948	92820	CATCTGCTUCTGACGTACTUGGA	92821	CATGUGGGAGGAAGTAACCUCT
271922030	92822	CTGAACCAUCTCCGCAGUCA	92823	AGAGTGTTTTGATUCTGTGAAGCACUAA
271925889	92824	GGGUAAAGGCCTTGTTAUAACCAA	92825	GGACAGAACACCACGUCAGUC
271926688	92826	GGCTAACCUGGCAGAGAAUGG	92827	CATGTGGUGGGACCATACTUACT
271927356	92828	GGACACCATAGCAUGATAGTCCCUAA	92829	CATGCTTCCUCAACTCTTCAUCAAAC
271928459	92830	GTGCTATACAGUGAGCATTTGGUACT	92831	CGAATTATGTCAUGCACAGTCAAUAACA
271931166	92832	GAATTAGGUGCTTTCCTCUCCCA	92833	CCTCTGAAUGGCGTGGATGUC
271932773	92834	TGGAAGAGGUCCGUGCAGA	92835	TCACTCCTTGUGTGCCCTCUA
271934011	92836	AGATTCTTGTGCAUTGTGATTTCGTUT	92837	GATCAAGTTGTUCAGGAGAAAAAUCCC
271936106	92838	GCTGACGGUCCCTTTGCUT	92839	GCAGTGTTUCTGCGGAAAUAGG
271936584	92840	GGCAGGTCUGCTGGTCAATAUA	92841	AGAAATGGGTAUGCTTGTTCTGGUAAT
271936779	92842	TCCCCAGAAGGAUGACTGAGUT	92843	GGTTCTUCGCCCGTGGUC
271937803	92844	TTGGCATGGGAUTTTTCTCCUGA	92845	CACCACAGACTGUTTAATGGGATTTCUA
271938809	92846	CTTCCAGGUGCCATGCTAUGT	92847	CCUCAGCCCCACAAAGATUCAT
271940050	92848	CCATGTTAACUGCAATGATACCCAAUT	92849	GTCGACACAAAUCCATTGAACTCTTTUAT
271940283	92850	CAUCGACGACACCACUGGA	92851	GGCTCATTGTCAUTGATGTCTTGAATUT
271942876	92852	TGTTGTTTGTGGUCTTGTTGCTUT	92853	GCATCGUGTTGTUCACGCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
271943508	92854	GGTGAGCCUGTTAATCUGCGT	92855	CAGCAAAGGAACCUCCTAAGACTTUA
271944066	92856	TGGCUGCCACACTTCCATUAA	92857	CGGTAAUAACCGGUCCGACAG
271945643	92858	GCCCATAUGCCTCTCUCCAAC	92859	GCCATTTCCUCCATACCCTTTACUC
271945806	92860	CGTGAACAACACGAUGCTTUAGAA	92861	ACUTACCTATGUGGGCAGCCT
271946062	92862	GATCTATAACTGGUTCACCAGGATGTUC	92863	GCAGGACUAATGGTTUAGGGAACT
271948043	92864	CCCGAGUCAGAGTTCATCAUCA	92865	AATCAGCGAGUCACCACCTUAC
271948419	92866	AGCCTGCUAGAAGCTACCTAUACC	92867	CTCACCGUCACAGCCUACAC
271948789	92868	GUGAAGCCTTUCCCCACCAA	92869	TCGGTCCUGTGACATTGUGAAC
271948984	92870	CATACCTGGCAAUAAAGGAACGAATUT	92871	AGGGACTAAUGACAGTATGCTGUCT
271949406	92872	TGCTGACATAAUGGAACACTAGCTUT	92873	CCTCCCUCCTGGAGCUGT
271949934	92874	GGCGTCUCCCATCUGCAC	92875	TUGCACCAUCAGGGAACCAA
271953393	92876	CTCCCCUCGCTTCCAAUGAA	92877	GGAGAAGCAGCAUCTTCCAGAAUA
271955264	92878	GCTTCAGAGGGUCAGACATACUGT	92879	CTGTTGGAAUGCATCGGATCTUG
271958187	92880	CGAGCACCAUCTCCTTTGGUT	92881	CCAGAGCATUAGTAGCATGTTTUGAAT
271959196	92882	GCGTCATGUAAGCATCAAUCACC	92883	GCTTCAGTCAUGCTCATGGGTUT
271962815	92884	CAAGCTCCCCUACCATGACUT	92885	CCACACCCTUAAGAGAAGAAAACUCA
271967993	92886	ACCAGAGGGUCUCACCAACAT	92887	GTTTCTCTGGUGACTCCCAGTUC
271970372	92888	AGTCCAUGTAGGTCUCAGACACA	92889	CCTCATTCTGCUGGAACTGATGUC
271971042	92890	GAGTTTGAAACUAGTCCAGACTGTAUGT	92891	TGCAATGUCCCAAGCAATATACCTUAAA
271971583	92892	CGTTTTGTUCACTGTAACCUGCAA	92893	TTGATGATAGUGAGAGGTCTCUCAAA
271973343	92894	AGGATCCATATGUATAACTGAGGTUGGA	92895	CCAGCAAUGCATCAATACAUACGG
271978395	92896	GAAACTCTUCATGTCCCCUCCA	92897	CCTCCTGGUAACGGGATATGUC
271978951	92898	GCAGGTTUGCTTATTGGUGAAGG	92899	CTGGGTGCTUCTACTGCAGAAAUA
271980735	92900	CCUATGGTAATUGAAGCCCAAGGA	92901	GAGAGGAGAAGCCCUATTTTGTUCA
271982450	92902	GCACCTUGTTGTCTGTUGACCAT	92903	CAATGUCAGCCCAGCCAUAC
271984964	92904	CGAGCAAAGAAAGCCAUGTTGUC	92905	CAACUGTCTTTGGUGGAGAAGGAT
271989311	92906	CTGTACAGAGGCACUTGTAAGUC	92907	GCTCATTTTUCTTTTCCCAGUGCAA
271990230	92908	TCAAGAGUCUCAACACGGGAAAC	92909	GTTGCTTCAAGACUTCAATCGTTTTCUT
271990833	92910	CATTTCCCACUGTCCCTUCCAA	92911	CAUAAAAGCAACCGCCTUCCC
271991845	92912	CTTGACTGCAUGGTTCTAGCUGA	92913	ATGACCACATUCTCTTATTGCTUCCA
271996184	92914	GTATTACCTGCAUAAAACTCTGAAUGCC	92915	GACCAGTCCCUGCTGACATTTAUT
271996862	92916	CGTCATCCUTCAGTTGGAAUCCAG	92917	AAATGCUGGGAGACAGAAAGACUT
271997410	92918	GGGCATTAACAUATCCCATTGUGT	92919	CCAGCUTCCTAUGCCCAGAG
272000202	92920	GGUGGAAAGAAAGAGAAGGUGGT	92921	GAGGGACCCAAUAATUGCAAAACAG
272001333	92922	TTTCAAAATUCCAGAAAACAAGCTGCUA	92923	GATGTGTTUGCAACAGTTTGTATTTUCC
272003272	92924	TCCCCGUGCATAGCTTTGUC	92925	TCAAATTGGCCUTCTGTAGTUACAAGT
272005881	92926	CCUACACUCCCCAGCAAACA	92927	TGGACGAAUTTGCACUCCAACT
272007653	92928	TGTGGGCAGGAUGAGGATCUA	92929	TCTCUACCAGGCAGGTGTAUGT
272011244	92930	GTGCACCAGUGTTGAGAACTUC	92931	AGTGGTUCCAAGTCACATUAAAGCA
272012432	92932	TGACCTTGGGAUCTGATTCTUCCT	92933	GCCGACATTCAUTCTGAACATCUG
272012489	92934	CACTGGAGUCTCGTGAUGGA	92935	AACTGAGCCCAAAAUGGGUCA
272022662	92936	CAGCTCCUGCCACTGCTUA	92937	CTCACACCCUCTCCUGGAC
272024217	92938	AAAAGTTGUCTGCCCUCCAAAGA	92939	CTGAAGTUCACATGCUGAGGGT
272025776	92940	GGGACUCACAACAGCGAUGAA	92941	AGGUGGCAGTTAAAAUGAAGCAGT
272026579	92942	CGGUGCCCAGATUGAACAAAGAT	92943	CATGCCGUCTGCAATCTCUC
272031576	92944	CCAAAAGCUGAGTAGUGAGGCT	92945	AGAAGTGTCCGUTCATTGGTGUT
272033016	92946	CAAGGGCCCAAUCTACAAGUACC	92947	TGCTTCCCUCACTCTAGTTCUGT
272033280	92948	ACAGCCUCCTCCUGCAAAAAG	92949	CTCATCCAAAACUTCAATGTGGACTUG
272034430	92950	CAAGAGGCCAAAAGUTCATCTTUGT	92951	CAATAAAGGCTACGUGCCAATTTTTGUA
272038150	92952	AGAAAGTAAGCAAGAUGAGAGAGAUAGGT	92953	CCTGAGTTAATGUGTGTTTCTTTGTGUT
272042474	92954	GGATTTCCCAGUTTGCCAUGGA	92955	TGTCTTACTTTGUCCTTGTTTTCCCAUAA
272043876	92956	CCCACAGGAAAAGAAUCCATTGUG	92957	CCUCCCACCUGAACCAGACT
272045255	92958	GCCTGAGCAAGAUGATTCAGAUGG	92959	CCCAGACCUGGAAAGCUAAGG
272046961	92960	CTCTCCTGATAUCCCTTTCTCCTUCT	92961	CCCCCGUCAGCACTGUC
272051138	92962	GTGAAGTAAAUGAACCAGAGGUAAGGT	92963	GCAATTCCUGCCAACTAAACAAUGG
272052089	92964	GGGAAAGUCAGAGCTGCTCUT	92965	CGTTCUGACAGCCCCTTGUG
272052400	92966	GGGAACUGGGCATCAGUGAG	92967	CCAAGGGCATUTCTCTGTTCTGUT
272055426	92968	TGGTAAACAAAGUTGAGAGCAUCCA	92969	GAAACAGCTGCAUTTAGAAATCAAUAGCA
272057281	92970	GGCTTUGACAGCGAGAAUCC	92971	CCCUGCCACCCGCTUAC
272058794	92972	CACTGTTTCTUACTTTTGACATTCAUCCA	92973	AGCTCTACCACCUCATCCAUCA
272063787	92974	TTCCTTACAAGCAUGTATAACGGCUT	92975	CCACCACACACCUCAGTCTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272067171	92976	GTCTGGUCCACAGTGTGTCUG	92977	TTTTTCTTTTTCTUCCCCCACTAGAUGT
272069646	92978	GCAAGUCCTUCCACAGAACCC	92979	GAGATTTTGUGGAGAAATGGTTGAUGAA
272070863	92980	GGCTCGGGUTGGCTCUAAA	92981	GCTAGUGGGCGCATGUAGG
272071222	92982	CACGTGGUCTCTGCTGTUGA	92983	AGCTGAGGGCUTTCACUGAC
272083197	92984	CAUTGAGGAGGUCACAGAGAACC	92985	ATGGAGTTGUGCAGGAAATTCUCA
272085265	92986	CCAAAUGACTGAUAACAGGAGGGAA	92987	TGAUGAAGAAGGUGGAGGAGAAGAA
272086695	92988	AGGCTGAAUACCGCAAAGTCUT	92989	GCTGCTGACUTACACACTACCUG
272088823	92990	GAGAACGGCCAUATUACCACCAA	92991	CCTGAAGGGCAUTGCTCUGT
272089384	92992	AAGCACTGCUCACCTGGUC	92993	TGTGCTGAUGTTTGTGGTAUGGAT
272090110	92994	CCTCGGGCUGTGCTCTTTUT	92995	CCTTGGAUCTGATGCAGUAGGG
272090476	92996	TCTATGACCUGCTGCUGGAGAT	92997	TGCCTCCCCCGUGATGTAAUA
272093240	92998	ACACCAAAGCAUCTGGGAUGG	92999	CTTGCTGCUGTCCAGGUACA
272094659	93000	CCGUCCGCAGCUCAAGAT	93001	CGTAGACCUGCGCGTUG
272095991	93002	CGCCGCCUACGAGTUCAA	93003	GCGGGUGCAGTAGCAUCAG
272096492	93004	CGTTCTTTAUCCCGGCGTTUC	93005	GCATTTCAGGCCUTCAGTTCATAUAAGT
272097513	93006	CTCAACAGCGUGTCUCCGA	93007	CCUCGCGCACCGTGUAG
272100855	93008	ACTTCAUCGCATTCCTUGCAAAAG	93009	CATGAUGAGGGTAAAAUGCAGCAG
272101653	93010	GCUCCCACCCAGUGAGAAAC	93011	GUCGTCAUGGAAGGACACCA
272105274	93012	AAGACAGUGAGCUCCACCAAG	93013	ATCATCGAGUGGAAGTCTTATTTGGUT
272108412	93014	CUCAGGGACUGCGGAAGAAG	93015	CTGACAACCUCTGGGCUGAT
272108799	93016	CAGGTAGTTCUACAGCTCTAACACAUAC	93017	GTGTTGGTGTTUAGATGAAGAACCTTUT
272109048	93018	CCTGGCUACATCTTCCTUGACT	93019	GAGAGUGCAUCACACAACGAGA
272109858	93020	CTCACCUCCTGCTTUGCCA	93021	CGAGGCUCCAGGGTCUGT
272109932	93022	GGGTGTATGAAGGAUACTCCATCTUC	93023	GGGATTUCCACCGGGAGAUT
272115530	93024	GGCCAGGGUCACAGTATCTTUG	93025	CTCGATGCAGUACTCAGUAAGCAG
272116463	93026	GCCATCAGTGCUAATTTTCCTTATCUCAT	93027	ACCAGAUCAGCACTGCATTUGAA
272120561	93028	TGACGAUGCGGCGAUAGG	93029	CTGCCCCCAGAGAUGATUGAG
272123278	93030	CAAAAATCCACACUGGTGGUCAA	93031	CAGGCCAGAAAGUTTGATGATGUC
272123362	93032	CGUGACGGGCGUCACAT	93033	GTGUACACACGCTGACUGAAC
272123659	93034	TTTCAGAGGACAUTGATTGCCCUT	93035	CCAGAGCATTTACAUATGTCTCTTCCUT
272124432	93036	GGGAGUGGGACATGTGCUAA	93037	CAATGTTCTGGUGGTTCAGCTUC
272126825	93038	GCTTATGTTTCTGCUCAGAGTCACAAUA	93039	GGAAAGAUGGACGCATTGUGAAT
272127989	93040	AGAATAGTCCCCUCTGATCACAGUC	93041	TGGAGTTCTCUTCCCTTAAGUCAGT
272129413	93042	CAGATCCACCUTCTCATTGUGCAT	93043	CAGGGAAAGGAGAGUTCCTATGUC
272130408	93044	CAACAATGTCUGAAAAGAGCAUGGT	93045	AGGCAACTUTAGAAAGAACUCACCAG
272133116	93046	CGUACGCTTGTAUGCGGGAAA	93047	CAGGAAGGAAGGCCUCATCTUG
272136807	93048	GGTTTGAACUGATGCGCATGUG	93049	CAGCTTGTTCUCCTCGCTGUA
272138685	93050	GTGAGGGAGUTTGAGGTCCUG	93051	AAATCTCTGTTAUCATGTGGCCTGAUT
272141861	93052	TTCCGGGAGGUCTCCTTCUAC	93053	GTTCUCGGCCTTGTGUCCT
272141974	93054	CCACTGTCTUCTTTTTCTCTTCTUCCA	93055	GCTACATCTCUCAGACATCCCTAUCC
272143373	93056	ACUGCCCGACAGACACUC	93057	AAGGCCCGCUCGTTCUT
272144118	93058	CTUACGCCCACAUGAACGG	93059	AGGAGGCTTGUGAATGGATTGUT
272152114	93060	GACATCUCGGGTGGCAUCAT	93061	TGATCCATGTUCCAGAATCAAATUCCA
272156608	93062	CACACAUGGAGAGCCCAAAAAUAAAA	93063	TGTGAACCTACUATGTGAAGAGTACUGA
272174775	93064	CACTGTGAGUATATTGTGATGUGGAGA	93065	TCACCCAACATGUTTACAATCAACAAUG
272179541	93066	GATACAGAUTCAGCCUGAGCCA	93067	GAGAAAAAGACTGUGAAGATGGTAGUGA
272180150	93068	CACTGTGATGAUGTCACCAGUCT	93069	CAATTGATGCUGACGATCCCAAUG
272182416	93070	CTTACAAUCAAGCCACTGTTUGCT	93071	TGGCGATCAUCAACAAATTTCTCATATUG
272184623	93072	GATTCTGTACCUCAACATCCCATUGA	93073	GGTCCCUGGAATGAAGGGUAA
272188136	93074	GCCTGGATTAAACUGAGTACTCCAAAUA	93075	GCTAATGACACUGATATCCTGGGTUT
272189078	93076	CTTTCTGGGUGGTTAATCCATAAGUGA	93077	CAATAAGUGGACAGGGCAGAAUG
272189445	93078	TGGTACCATUGCAACCTTTTUCA	93079	TCTGCTTCTCTCUTCCTCATTTCAAAUT
272194184	93080	CTGACCAAAGUATGGCTUCCCT	93081	ACACAGAUACACAACCGCTTTCUC
272200093	93082	CTTCTGGUGGCCACGACUT	93083	GAGGAUGCGGGACGCTAUC
272200687	93084	CGCUGGCGGAGGAGTUG	93085	ACGAUCCCAAACCCAGGUG
272203665	93086	GCACTGGTTTUCTGAATCACACUGA	93087	GTCATGAATACCUTTCCCATCCCUT
272205726	93088	GGGTGAAACCUCCAACUAGCA	93089	CCCACACAGACACAAUGUGAC
272207334	93090	ACAGCUGCACGCCTCUC	93091	GGGTCTUGGCTGTTTTCUACCT
272208089	93092	AGAAATACTGGGAACAUTCTGCCTUT	93093	TGAGTAAGCAAAGUGGCAGCUT
272210196	93094	CGTCACATUGTGTCTGTGUGG	93095	CTTTAGACGCCUCCTTCCTCUT
272210303	93096	TCACUCCCATAUAGAGACACAGCA	93097	GTCTCTGGACUAGTTGAATGAGTTTUGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272215074	93098	TCUATAAGCCUCGACAGCCAGAAT	93099	CCCTTTCAGCUTCTTGTTTGGUC
272215493	93100	CCTGGTGGGUGCAAAAAGAGUA	93101	TTGGTTUCCGGGAAGGAUGAC
272216685	93102	CCTCAGGUCTTTGCUGAGAGAAA	93103	GCTCTCGGUGTGTGTCTTUCA
272221835	93104	GGAGGCUTTCTTCTCTUGGGAAA	93105	CAAGAGCAGUTGCTCAGAUACCA
272227493	93106	GGCGGCACACCCUAUAACAA	93107	GCGCGAUGAGGAACAAACATUC
272232188	93108	CAACCCGACCAAAGCUTGAAUT	93109	CATTTCCTCAUGCAGCAATTTUGGA
272232230	93110	GUGCTTGCUACCGGGACAT	93111	CCACAUGGGCAAAGGATCGUAG
272233055	93112	CATAGCAGCAGCAGCUGATTUT	93113	CCTGGTACTACUGGCATCACAUC
272235319	93114	CTGCATTCAUGGGAAATTGACATGUAT	93115	GATCTGUCCACGACCCATUCC
272238289	93116	TGAATGTGAACCCUTTCATGTCTUGT	93117	CCAGCAGCAUGTCGAAGATCUC
272239352	93118	AGACAGAGACCCAUCCAAGUCT	93119	AATTTAGTTGCTAUTTGTGCCATTGUGT
272240734	93120	CAGCGACUGGATTCCUCCAA	93121	GCAGATTATGGUGTATTCCAGUCCA
272240847	93122	GAAAATGTGUAGAGGGCATGGUG	93123	TCATCCAGCATUGAGTTATCTTGTGUT
272240988	93124	CCACCCUCTUACCCAACAAAGT	93125	GCCAAGTGUCCAACATAAGTAGATGUAA
272244687	93126	TGAATTAACATUTAGGAATGGAUACAGCAGAA	93127	GCTGCCCAGAUATTATCAAGAUCCT
272246685	93128	CCTGCCAGUAAGGACACUCT	93129	GTUCGCGGCATTCUACAAGG
272247687	93130	GATTCAGGCCACAUCTCTCTCUG	93131	ACAGAAAAUAAGACAGCCAUGAACACT
272248515	93132	GTCATCAAAGAAAAAGCUCTGACCTUAC	93133	TGCATCCATTUCATGACAGCUACT
272249595	93134	GAGGUGGGCACCGUCAT	93135	CAGGAAGUGGGCGCACTUA
272249633	93136	GGTACTAAATGCAAUAGAGCAGGAGTUC	93137	GGTATCTGGCUTGCGGAUCAT
272254024	93138	TGUAACGCACACAGAACACUGA	93139	GCTTTATTGTTTTCUTAGGTGAGGTTUCC
272256598	93140	CTGGUGGCTGCATTUGACAAG	93141	TCTCCTCAGUTTTCTTTAGGTTUGCAT
272261323	93142	TGTATGAAAUGGCACTGCCTAGAUAAAA	93143	CTGTGGCCUGTATTCACCUCAG
272262139	93144	GTTGCAGAGAAAUGCTAACTTTGTCUT	93145	CTCGTTTTCAUCTGGGTTTUGAGG
272266382	93146	CTAAGTGACACUTCCTGAAAACTUCCT	93147	CAAACTTGGGUCTGTTGTTCCUG
272267886	93148	CCTGAGGCCACUGATTTGGUT	93149	CCACCAGCUCTTCTTTTGACUG
272274323	93150	CCCTTTACGCACGUCAAAATCUT	93151	GACTTCGGCAAUGCAGTGUG
272277838	93152	CUGGACTGCUGGCAGAAAGA	93153	AGTGAATGCCAGAUAACAAATTGAATGUG
272286291	93154	TGCCAGTUCCATGTAAATGUAGCA	93155	GACAGTTTAGUGCCACATTTATTCTTUGT
272287639	93156	CGGCTTCACUTTGTCCTGAAUG	93157	AGCGTGGAGAUAGAGAACATTACUCT
272293909	93158	CATCTTCUCAGACATCAATCUGAAGCA	93159	GGTCCUCCCAGCTGAUGAC
272298901	93160	GAGUACCUGACGCGGCAT	93161	GTTAGGTCGTUCTTCACGAGGAUA
272306531	93162	TCCTGACAGTACUTACCTACCACAUC	93163	GGTAGCAGUAGAAGATGATGAUGACA
272306952	93164	GAAGGACCCAGGACAUCACTUG	93165	AGCAUTCAGACTAUGAGAGCACAAA
272311041	93166	AGGGACCUCAAGAGCUCCAA	93167	GGGATCTAGCACUAGCTCTAACTUAC
272316150	93168	TGCCAAAAGACCAAUAGTATTGTCUACC	93169	TCAAGTCTTCAUGGCCTTCATCTCTAUA
272339562	93170	ACCACTGGGAGUTGCCATAUC	93171	GCTGATGUCAGAGCGGUCAT
272352854	93172	TGAGCAAATTGTUCACCTGGTGAUAT	93173	CTTTGCACATCACUGACCTCTTTCUA
272356431	93174	GGTGATTATGCUGTACGTCTUCCA	93175	GAAGAACATTTGAUGGGAAAATCAGGUT
272357451	93176	CACTGUGCCATCATCCUGGAA	93177	TCTCAAACTGCUCTGAAGTGTTCUG
272361742	93178	GGGCACCAUTGTTCTCCATUAGA	93179	TGATGGCCACGUAGATTUCCC
272371485	93180	TGAGGTCTAUAAGGCCAAGCUGAA	93181	GTCAGGAACUGGAGTATGTTCUCA
272373012	93182	GUTTGAAACUGCCAGGCAAGA	93183	CCCTCCAGGCGAAUGATGTUAG
272379017	93184	CTCGCUGCTTTTCCUGAGAGA	93185	GCCACAGTUCCGAGACCUT
272379822	93186	CCCAAAAAGUGGGAGCAGUGAA	93187	CTTGUCCCACCACTUGAAGGA
272380095	93188	GCCCGGCUTAGGAGACUT	93189	GCCTCGUCCTCCUCGCT
272380270	93190	ACCGUCGTGGUGGAGGA	93191	ACGUCGGGCGUGAAGAG
272380559	93192	CTCCTCACCUTTCACGAUGGT	93193	GGGTCTCAUCAGCGCUGT
272381493	93194	GCUGCUGGCGGACAAGA	93195	CACGAGUACCCACUGCCA
272381649	93196	CACCUGCTCCAUGAGGCT	93197	CGCCGCCUCATCGTUGT
272382009	93198	GCCCACAGCGCUGAUGA	93199	GGCTTCCAGAAUGGTCTCAACUAC
272382164	93200	CGCCAAAGUCGATGTTGATGUACT	93201	GCCCGGAGGGCUTCTUG
272382473	93202	CCGGUGUCCGAGGACAA	93203	AGGCCTCCUCCCCGTAUC
272382521	93204	TGGGTACUCGTGCATGCUG	93205	AGCCCCCUCACCCTGUAG
272382748	93206	TGGCCUGAGGCUCCAGA	93207	GCTGCTGCUACAGCTCCUT
272382972	93208	CCTCACGUCGAUGGCGAT	93209	CACCUCCCCACGACAGUT
272382984	93210	GCACGTACUGGTCGCUGT	93211	CCCGCCCGACUTCTTCUC
272383262	93212	GCAAGGAGCUGUAGCAGCA	93213	CCAAGCUGTCCAUGGAGCAT
272383311	93214	GGGCUGCGGAGAAGAAGUC	93215	CCCGAGGACAGUGGGUACA
272383486	93216	GGCGAGCUGGCCTTGUA	93217	CGCCCCCAAGCAGAUCTUG
272383532	93218	TCGCCGGGAAUGTCCUG	93219	CGACGACUACATGCCCAUGAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272383555	93220	CCGGCUGCAACTGUCGT	93221	CCGUCCTUCGCCCACAA
272383762	93222	CGGCACGAGCUGCACUT	93223	CGCAGUAAGAGCCAATCGUC
272383908	93224	TGGGCUGCAAGATCTGCUT	93225	GAGAUCGGCUCCCACAGG
272383949	93226	GGTTGACCAGGUGGTGGUG	93227	CCATCCUGGAGGCCAUGAA
272384413	93228	ATGGGCCAGUTCGACCAUC	93229	GCATCCAAGUGCATCAUCAAACC
272384572	93230	CGGAACUCGAAGAGCTCCUT	93231	GCCACUCGGACAGCTUCT
272384768	93232	CCCAGGUTGCTGCUGGAG	93233	CTCTGCCUCGCTGGAUGA
272384882	93234	CACCAGCCCGUAGCUGT	93235	GGAGCAGGAGGGCUGGUA
272385094	93236	GCTGACCAGGUCGGUGAG	93237	CTGCUGCCTGAACAUCAACAAG
272386578	93238	GCCCGCAUCAGGGTGUAT	93239	CACTGUGGCCGCTCCUA
272386942	93240	GAGGGCGAUCAGGTACTTGUG	93241	TCGAGUACUACGAGAGCGAGAA
272387519	93242	GGCCCACCUCGAUGAAGA	93243	GTACCGTCUGTGCCTGTCUG
272387972	93244	GGTCAGGGAGUAGGTCCTCTUG	93245	CGAGUCCAUCGCGGAGA
272388122	93246	GCCTTGCUCCGCCACTUT	93247	CGCAAGUGCGGCUACCT
272388395	93248	TGGTCATGUACCCGTAGAACUCA	93249	CGACCCCGGCUTCATGUC
272389006	93250	TCGCAGUTGAGCTUCACGAA	93251	GACAGCUACGGGCUGGT
272405912	93252	GTGCAAGTTTUGAAAATGGAGGGAUT	93253	AGGAGCAAUGCGAATACCTGUC
272407668	93254	CCACTGGCUGGCATCGUAG	93255	ACAGTGGUATGGCCAAAUCAGT
272408578	93256	GGATAGUAAACAGTCCAUAGGGACCA	93257	TGGACCTCUACAGTGGTUGGA
272408618	93258	ATGAAGGGAGAUGGGCAGACUA	93259	ACCGGAAGTUGTAGGTGGAGTUAT
272416716	93260	CCACAAAACUGAAATGCGTAUGGT	93261	ATGCATTGGAATUATCTCAAAGCCCUA
272417093	93262	CCTCCCTCTTUCCTCTGTGCTAUT	93263	CTCATCCTAGACUTCTTGAACTGTTTGUA
272419258	93264	ACAACTAAUCGATGGGAGUAAGAGGA	93265	GGCAACTGTAUGAGCCACTAGTTAUG
272419976	93266	GTTCCCAACAGUGCCTACACUAA	93267	GTGACGACCGUGTTTATCAGAUG
272421659	93268	GGGATCCCAUCTGAGTTAATACTTUG	93269	CCTGCCTGUGGACTTGAATTTCAUAAT
272422175	93270	TGCTGTTUGGACAAGATGAACTUCA	93271	GGUAGCACCAGUGAAAAGGAAGA
272422709	93272	CTTGTTGTTAGUGAACCAGTGAAUCAG	93273	ATGGAACCCUTTACAGCGUAACAT
272423994	93274	CTGCCGUGGATUAGGAAGAGG	93275	CAUCTGUACCAGGCCAAAAACA
272424557	93276	AACAGACUGGAGGAAGCTUGG	93277	TGCAAGGTTAUAAACGCAAAAGATGTUG
272426933	93278	CAGATTGCCTTUCCGGATAAAAATUACA	93279	CTTAAAACAGGCUTCACGAUCACAAA
272427871	93280	TGAATGAGCUCAACGTACAUGAAGT	93281	TCACATGGCTUAACATGACACCTUAAAT
272432548	93282	GAAATGCTTAGCUGAGAATGCAGTTUAC	93283	AGAAGGATCAAGCUGAAGCACATUA
272443262	93284	GGGATGAACCAGACUTAGATCCTGAUAT	93285	TGCTACTAGTTTUCCTTCTCGACAATUC
272443264	93286	TGTTTGATCACAUGATGAAGCGTAUGT	93287	TGGCTGATGGCAUAATAATCTGAUGAG
272447032	93288	GGAATGAAGTGTUTTGAGCGATTCTUC	93289	ACATCAGACACCAUTTACAGAGTTCCUA
272449599	93290	CATCGTGCAAAUTGTGCTAATUGAAAAT	93291	CATTCTTTGATUGCGTTTCTAGAGCTUT
272451401	93292	AGCUTGCTAUCACCACCAGAC	93293	GGAGGGTTUAAGTAAACGCCATUACAT
272453373	93294	CCACAGAAGAAGAUCATCAGTAGCAUT	93295	CCAGAATTAUTGTCTGTCUGCAGGAT
272454736	93296	CCGAATGCAGUACAGTATGGAGTATTUT	93297	TGAACTTAAACAUGTTGACGCCUACT
272463029	93298	GAAGUCUGCAGAGAGGGAAGAG	93299	CGUGACTTTCTUCACAGACAACAG
272470023	93300	TCTTGTCCGAUGCTGCTTAGUAG	93301	GAGGAGGCCAGGUGTTTUACA
272478632	93302	AGTCTTTCCAUTTGGTCCAUGCT	93303	GCCTTCAATGTCUGACTAAAGTACTTCUG
272479307	93304	AGCTCCCCAUACTCGCUGT	93305	CTAACACCACCUTCCCTGTCTUG
272482804	93306	TGCCTCAGUCCTTACCCUCA	93307	CCAGGAACUGAGUCCAGAGAAG
272486207	93308	CACACCAGCAAUGUAGCAACA	93309	CCACTATTCTTUCATGGACAGGCUT
272490115	93310	GTGUCCCAGCATTGUGCAAAA	93311	CCAAUAGGCACCATCCATUCCC
272493639	93312	CTTTGGATCUCTTTCCCGCUACA	93313	AGGAAUCTTCTCCUCCGAGCA
272495457	93314	CCTTGTTGCUGTAAAACAGGTAAUGT	93315	TACAAACAGGTUGAAATACTGCTGUAA
272498146	93316	GCCCAUCAAACTCTACUGCAAC	93317	GAAGCAGAGGCUCCAAAGCTUA
272501825	93318	GTTATATTAACAGUGGTCACUCACCCA	93319	GGATCTTACUCGTGTGCCAUCA
272503520	93320	GCATCAATCCUTACTGTTGGAGUGG	93321	CTCTTGTAGGUCTTTCGCCCTUA
272505648	93322	TTCAGTGAGCUGGAGCATCUG	93323	CTGCCTCUGTTCTTTGGUGAGA
272506810	93324	GAGGGAAGCUCTTGGTCACTUT	93325	GCTTAACCTACAUTTCCACTTTTGUGT
272507389	93326	GGGCUAAGCCAGTGCTUC	93327	GCTTACCUCGCTTTTGGCTUT
272507692	93328	GCTTGAAUTGCTTGUAGCGACAT	93329	GGTGATCCCATUTGAATATGCTGTTTUT
272509301	93330	GGCAGAUGGGCTGAGAATTUG	93331	CGTAGAGCTUGTACAGTGTCUGG
272509377	93332	CTTTTATCATTTUGAAACCAGGTCGUGA	93333	GGGCCGAAAGAAUTATATATGGAAGTUT
272514078	93334	CCTGACUGGAGGCTTCTCUCA	93335	GGTGAAACAUCGGGCUCAC
272516708	93336	GTGAATTTCTUACCTTTCCTCUGGAGT	93337	GAAUGCCAGTTAAUGAAAACAGAACGA
272518057	93338	GATTATAAATGTGUTTGGCTTTGGUCGT	93339	GAGTTCGCACUGGGTTTTGTTUAA
272522366	93340	TGGGAGGGUCGGAUGCT	93341	ACAGCTTGCUCCCTCTCCAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272524148	93342	CGGCGATGCUGAGAACCAAUA	93343	GAAUAAAGAGGAGCAGGTUGAGGAA
272526015	93344	AAGCAACCUGCTTGATGAUACCA	93345	CCTTAGACUTCCCTGUGGACAGA
272529702	93346	GGCCCCUGGAGAGGTTTUAAT	93347	CAGAAAATCTGCUCTTAGGGCUCA
272531392	93348	CTCTCCCGUCCCTGACCUA	93349	ACAAGGAUGGAAAGGCACTGUC
272535051	93350	CCGTCUGCTGCCCTUACA	93351	CCUAACGGCCCGUGCAG
272535480	93352	CAACTATGGCUGGCAATTGAAUCA	93353	CCTGTGACGUCTTTCCTGTTTTCUT
272535818	93354	TGTGUCTCCTCTTUCCCCAGAT	93355	CAGCAGGCUGTGGGUGT
272537513	93356	CTCTGUCACCTCCTUGAGCA	93357	CCTCCCTCCUCCCAACTGTAUT
272538031	93358	GTGGGAACACACGGUCATUCT	93359	CCAUCCTUAAGCCAGCGGAT
272538217	93360	CAGCAATCUTCAGCTCUCCCT	93361	TGGAGGTCCAUCCTTGTCTGAUT
272540646	93362	CGTCAAGUTCCGCTGUCCA	93363	GGTCTUGGAACCCAGAGACUCA
272541602	93364	GCUAACCCUGCCCAACGG	93365	CCAGCTGCUGATGGCTUCT
272541778	93366	TGCCACACUCAGAACATUGCT	93367	GAGAACCCCAGAAUAAACACGTAATUC
272544189	93368	GCCAGTTTTTCUAACAGCATTGAUCAT	93369	GTTTTAACACCUTCAGUGGGCAAG
272546777	93370	GGCCGUAAGCAGACAAATCCUA	93371	CTTATUGTTCCAGCUGACACCAC
272547623	93372	CATGUCACCACAGGCAAAUCC	93373	GCCTGAGATTTCUTTCCCTTGTGTUA
272548323	93374	ATTCAAGAACCACUGCTAUCAAGGT	93375	GGAAAATATTTGAUTAATGGCACCUGCAA
272552144	93376	GGGCUCGGTCTAUGACGA	93377	CCACUCACCCGACTTCUGAAC
272552201	93378	GCGUAUCGCCAGCACGAT	93379	CGGGCCCGACUGUCAAG
272552769	93380	AAAGCCTCCCUGTAAATAACTGUGT	93381	GAAGAGATAUGCTGTGCCCUCA
272553089	93382	CCACCUAACAGGCTGTCAUCA	93383	CTTTTGTTUCACCAGTACCCAAUCC
272553983	93384	GTTGACCTGUCCCAGATTCAGUC	93385	GCCTCTAUGCCTCTAAUCCAAGGT
272554089	93386	ATTCATGAAGCCCUTGCCAUCT	93387	GGACCTTCATCUAAAGACACAAGCAUAAA
272554310	93388	CCUGAGGGCACAGCATAUCT	93389	GCAATTCGTCCUCAGGTAGGATTAAUAT
272555064	93390	ACACTAAAATUTTCCTGGGUCACAAGA	93391	ACCCTTACCACUATCAGAGAGTUGAG
272556344	93392	AAACTTGCAATAUTCCTACCTGGUGT	93393	GGCCTGATCUTCACAGTCAUCA
272560316	93394	CUCCAGAACGACUCGGGAA	93395	GGCUGCAGGAGACCTUGT
272561181	93396	GCCTCUGAGCTCCTCTUCAC	93397	TCCAGCTCUGGACCCACAUA
272562503	93398	CTGAAGCCUTTTGTCGTUGCC	93399	AGCCAGGAAAUTCTGGTCACUAAAC
272562597	93400	CTGCACACACUAACGCGTUT	93401	TGAAGCCAGATUGAAGTTTCCTAGATUAC
272563016	93402	CTGGTTTTAAGCCAGUGAGTGTCAUA	93403	CACTUCAACCTCCGUCCAGT
272566989	93404	CTTCTGAAATUGAGTGTACCTGCUACT	93405	ACCATTGATUGAAGACTGCATTCTUGA
272569662	93406	ATCCGAATGGCAUGAGAACCTUT	93407	GTGATCCUGGTGAATTTCTTUGCC
272570275	93408	AAAATGTCAGGAUAAAGTGGATCUGCT	93409	AGCCATACTUCCCTTGTCATUGG
272574905	93410	CTCTTTACCUCCCTTTCATAAGCUAGAC	93411	TCAGAAGTTUGAAAGGCCAGTAACUC
272575545	93412	GCAGTTTTCAAUTGCCTTGAGTUCA	93413	CTTTTCCCCUTGCTUCCCAAC
272579288	93414	GCCACCUTGGAGUGACAAAG	93415	TGAUATGTAGCTUACAACCAAGAACACAG
272581653	93416	GGACAGGUGGTTGCCAAGAUA	93417	GAGCATCAUACGTCTUCAGGCT
272582008	93418	GAGACACAAGUCACGTGAUCGT	93419	CATTTCATGTTTGUACTGCTCGTTCUG
272582037	93420	CTCCTCTGGAUACCGTTCTATAATCUGAA	93421	TGCTTTCTTCTTUGGTGTCCTTGAUAG
272582086	93422	CUTCGTGGTGTAUGAGGAAGACAT	93423	CACCCUGCCAGCAAGATUG
272584604	93424	CAGAGGTACAUAATTTCAGAGGCTUACC	93425	GTTAAAGTCUCATGGCGCUCAC
272587052	93426	GGCAGAGAAAGAUTGGCCAGUA	93427	ACAGGACCAGACUCCATAATGGUAG
272588651	93428	TTCAAAATATATCTTAAUTCAAAAGGGCTGCUT	93429	CTGGAGAGAGGCUTGGCTAATTTUA
272590527	93430	GGGCUGGACTGCAACUGAAC	93431	CCUGCGTCTCUGGAAAGGAA
272592175	93432	TCCTTCCTTTUGCAGCATCCAUT	93433	TCTTTCCUGCAGCAGAGTTTTATTUCA
272595776	93434	CCGTGCUCCGATCCTTUG	93435	CACTTGCCCUCCCCGUT
272597081	93436	GTGTGCAAUGACTATGCTUCAGG	93437	TGGCTCTUAGGATCTGCTCAUAGG
272599539	93438	GAGCCAGAGGAGGAUGGAGUA	93439	GCAAGUGCAAGACGAGUGG
272602669	93440	TCGACACTCUCCATTCAATTCGTUT	93441	GGATGTTCUCAAGACTGUCAAGACC
272602707	93442	AGTTTGATGCTUTCCCCACAGUA	93443	TCCAGACUGTCAAAATGTUAAGAACACA
272604259	93444	GAGTACCUACCTTATAACUGACCGGAA	93445	AGGTCTTUGCGACAATAAGGAUGAC
272605102	93446	CTTATCTGGCCAUGCTGTTTATUGG	93447	GCTCUGATAGGGUGGGACAAG
272607132	93448	CCCACTTUGTTTCTGGCUGAG	93449	CTCTTCAGGGCUACCGTCUAAAAT
272613081	93450	CTCAUCTGAACCAUCGCCACA	93451	GGCATGCCCUTTATGTTCCATUT
272617013	93452	TATTTGTCCCAUGCACACGGAUA	93453	AAGAGAAACAGAUGGGAGCUCAC
272623718	93454	TGTCTGTACCAUAGCTGGUCGT	93455	ACCCAGUAACATCGCCTTUGT
272626428	93456	CTGATTGAGAAAGAACUTTATGCCCUCT	93457	CCAATCCTGAAAUGTTGACACCAUCT
272629616	93458	TCGGTAAACACACUCTCCTTTTUGT	93459	GATGUCGAAGGCCUCGGT
272631873	93460	ACATCCAGGGACCAGUAATCTUC	93461	GCTTCTGGCUCTGAAAAUAAAGACAA
272632729	93462	GAGAACAUCGTCCGCUACGA	93463	GCACGTCUGAGGCACGUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272633725	93464	GCUGCCCGAGAUCGAGAG	93465	CCGUCCCCCUCGAACAT
272635116	93466	GTGGGACUGCAGATATAGAUGCC	93467	GTGGATCCCCUGGATTTGTUGAA
272636468	93468	TTCGACTCCCUCCAGACGUAT	93469	GTAGAGCUCGGCCAGCTUC
272636857	93470	GGTAGAGTGGAUGGTCAGTGUCT	93471	CTGCAGGATACUTTTGTGGAACUC
272640997	93472	GGAAAGAACCACUTTATTTUGCACCT	93473	ACAGTGAAATATUGGTTCTGACGTUAGT
272642188	93474	GGGCTAUAGGGTGTATATTUGCAGAAC	93475	ATGTGTACCUGCAGGAAAUCCC
272642351	93476	CCATCTCAAGUCCATAGCACTUACC	93477	TGACACUCACAAAGTGCUCAAGT
272643368	93478	GCCACCTUAAAGTGGGACGUG	93479	CTCATAGATAUCTCGCGTCAUACCAAAA
272645173	93480	ACCAGCUGGACAGAATATTCAATGUAAT	93481	AACAAAGACTCAAGUAAAAGTAGCTUCCA
272646005	93482	GCTATTCATUAGGATCCCTTTCUCGGA	93483	CCAGCAGAACTAUCTCCTACTACTCTUT
272646247	93484	GCAACTUACCCAAGCTATGATUAACAG	93485	TAAAGCTAGTTTUATGATTACTTGAUCAGAAGT
272647003	93486	GCTGCTGCAUTGTTCCCAUA	93487	GTTTTTCACAUCACCAAGGCCAUAG
272648525	93488	ACAGTTGGGAUTTCTGGGTGUC	93489	GGACTGTUGACCCGAAATATACAAATUC
272652098	93490	CAGGUAAGATGAGUGGGAAAAGCA	93491	GTGCATGAUGATGTGCUGGAG
272652304	93492	AGATCAACTTCUAAGACACCACUCACT	93493	GCTGATATCACAAAGUACCATTTCUCCA
272653271	93494	GATACAATCUCGAAGCAGTCCUCAA	93495	CGGACCUCAGAATTAGCAUCAAC
272653591	93496	TCATTTGCTUCTGTAAATTCTUGGAGGA	93497	CCATCCAAUGCCTTGUAGAAACCT
272653826	93498	CATTTTGTTUGTAGCTTGUCGACCA	93499	AAGTAATTATTCUCACACCTGCAGTUCA
272656471	93500	TGCACACTGUTTCGTTGACUGAT	93501	TGGCGTUGAGAATCGCUCT
272658426	93502	CCCCTACAUGATACGUCAGGCT	93503	CCAGCTAGTGAUTTTTGAAACAGGTTUT
272659444	93504	CGCCCTCUCTTCCCTUACAGA	93505	GGCAATGCAGUAAAGGTTCTCAUAC
272660778	93506	GATTGAGCUCGTCCATCUCCAG	93507	TUATATGCTGTUGCCCCAGAAAGA
272663909	93508	GCAAACTTTTUAGACCGTAAGGAGCUA	93509	TGGAAGAAGAUGGUGGAAGAAACAG
272667913	93510	CAGTTCTACUCAGGAAGATGGTUCAA	93511	AAAACAAACAUGGAGGCAUGGG
272674376	93512	AGTAAAAGGCCUGAAGACAGGUG	93513	TCCAGGTCCUCACTGTAGTUGT
272675604	93514	AAGGGAAGGCUCUACAGAAGGT	93515	CAAATGAGAAGCUATGCTCTGATGTTUC
272679257	93516	GCCATATCTUCTGCCTCTTTUACCT	93517	TGACCAGACAGAUGAAATGGCAUC
272682572	93518	GUGCGGAAAGGAUAAGACCAAGT	93519	CTAAGCTUCCGGATGTCATACUCA
272684092	93520	GGCCTGACUCTGCCTGUT	93521	CAGUGCCACACCCCUCA
272684571	93522	CTTCTCUCCCCACCCATCTCTUA	93523	CAGAAACCCAAGCUCTTACTGAATTUT
272686798	93524	GATACAGAGCAGUGCCTTUGAAGA	93525	CAATGACTCCUCTGCACTTCUAGAG
272690724	93526	CCTTCTTGCUGCTGCTTTCTTUA	93527	CACTCAAAGTAGUGCACACATTCUG
272690727	93528	CATGTCTCACUCACAACTUACCACAA	93529	TGATCATCAUAGCCAGAACAUGCC
272694587	93530	GGGAACTCCUGAATTTGTAACUGCAA	93531	TTCCCCAGAGTAUACTTCATAAGCATGUA
272697665	93532	TGACAAGGTGGAAUTTGTAGAACTACUG	93533	ATGCAAGTTGUGGCTTTTGGTATUT
272698141	93534	ACAGCTACAAUTGCCTGGGTUT	93535	CTGAAGGUACTCTCATGCUCCAC
272699167	93536	GAGGAGATUTACGTGTATAUCCAAGCA	93537	CCCTCCCUCCCAGTCAAUCA
272701752	93538	CTTGAGTGCTUAGGACTAAAGTGTGUA	93539	CATCCCCACUAGCTGAAUGACA
272704125	93540	GCATTTAAACTGAUCATCAGGACAGCUA	93541	GGCAATGAAUGACAGACTCTAUGACAT
272705412	93542	CAGAAACACGAUGCCCAGTTUAC	93543	AAGAUGTUCCGAGCAGCGA
272706532	93544	GGGAGGATTCUAATGCCTCTTUC	93545	GCAAGTGAGAGUGGAGGACCUA
272709783	93546	AGTACCTGUCAGACATGGGCUAT	93547	TTGTATAAGCAGCUTCTGGGTCAUC
272713661	93548	GTGTAAGGTTTCUGATTTCGGACTTUC	93549	GACAACACGUTTTGGGTCAUGAT
272723516	93550	GTTCCCTTAGUAGTCTCTCCTCUCAT	93551	CAGAGCTGCCUATTGGCACTTATAUAG
272726522	93552	GCAGATCACAGCAAUCACTCCUT	93553	CTCGACACCUTGTCCTTACUCC
272728231	93554	GCTGTTGTCUGCTGTGCAGUA	93555	GAUGGACGAAGGCAAAGCUG
272729343	93556	CAGGGAGUGAGTGGCTGTUA	93557	GGAAATAGACTUTGCCCCCGUAG
272729953	93558	GGCTGCUGCCATGCAGUA	93559	CTGTGUCCCCAAGGCUGT
272734148	93560	AAGGAAATTAGUGCTGGGCGUAT	93561	CTAGCAGACCCUTTCCCUCAC
272734182	93562	CTGGCCACAUCTATGGTTUCCA	93563	CCTGGGCCUCTCCTCACUAC
272735411	93564	TGATCTAGCCGAUAGCCCTUCT	93565	GCCTGCCTTTCUATTTTATCTGAACUG
272738068	93566	AAAGGACAGTCAUGAGTTGGTAATATTAAUC	93567	TGGAAGGCCGAGAGAUCATTUC
272738338	93568	GCCTTCCACTCUAGCATAGTAATCTUCA	93569	TTCTTATGTATGUTTAATTCTGTACAUGAGCAT
272738457	93570	TGCATCAACACUTGAGTCTUGGA	93571	GCCCTTGUTGCAAGTCUGACA
272740330	93572	CUGAAGCTTCUGAGCCCCAA	93573	CACTGCCCCUCTGCTCAUAG
272743168	93574	CCTCTGATUCCCTCTGCCTUC	93575	ACCAGGUGCGAGUACAGGAT
272751753	93576	CCUCAACAAGAAGGACCUGCT	93577	TGTATGAGCCCCUCTCCCATAUC
272753550	93578	GGUTTTCUCAAGAAGGAGGAGCA	93579	CTGTACTCTCUCTTTGGGACATUCT
272759222	93580	AAAACCCTTAUACACAAAGAGGUACGG	93581	TGGGTTTCUCCTGGCATTUACAG
272761644	93582	GTTTGTGACAUAAGCAGAACGCTUT	93583	CTTCAGAATCUCTTGCGTTTCCUAC
272764071	93584	GCATTTGCUAAAAACATTCAAAUACACAA	93585	CACUACTGCACAGUCAAGGAAGAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272764204	93586	TCATCATTAAATTCUTCAGCCCACTUCT	93587	TGTTCTTACCAGUAAGCAGAGCGATAUA
272765791	93588	TCAACTTGCTTCUTTATGTCACTGUCT	93589	GGCAAGAAGAUGGTGGTGTTAUGAT
272768567	93590	GCTCAGGGAAGGUCTCTCCUC	93591	TGCTCAUCCTCCUACCCCAAT
272768781	93592	ACATTCCTTCCTUGAGCAAGATTTCUAT	93593	CCACAAAAGGTTUCTGAATTAGCAACUG
272769579	93594	CTTCTCTCCUGAGGACGTTUCA	93595	CCAGTGATGCAUATTTCAGTGGGAAUA
272770409	93596	CCTGACAAUCAGCACCTTTAATUGG	93597	AGCAGUGGAACUGAACAAGAAGT
272770967	93598	AGUGGAGAACGGCCTTUCAAA	93599	GTCAGAAGGTCUACCCAGAAAATACUG
272771715	93600	GATGAACTCUCCACTTCTTGTUCAGT	93601	ACCTGCCAACACUTCTGAAGATUT
272778397	93602	AAACCAAAGTGGUATGAGAAAGCUCT	93603	AAGACTCCUGCTGTGTGAUGAC
272779969	93604	CCTTTGAGTCAAUTAGTCAGGTAAGUGA	93605	TGTGGAUGAAACAGGAAACAATCCUT
272780231	93606	ATTCUTAACATCCAGUAGGGCAAAACA	93607	CTGGUCCCCAGACATTUCAGA
272780381	93608	CCCTTGTCAUCTGTTCCAGAAUG	93609	TCGAACAAGCTTUACACCTTCTTCATUA
272783145	93610	ACTGAGAAAAAUGAACTCUGCCCAA	93611	GGCTCCCACGUCTTCTAAAGUC
272786317	93612	AGGCAACATTCAUTAGACTCACTTTCUT	93613	AAAAAGATAGTAGCUCAAGTGGAAGUGG
272788559	93614	ACTTCAACAUCATTGTCACUGCCA	93615	TGCTGATTGACCUCTTATAATTGACGUT
272789065	93616	CCAACTUGGCCTGTTCCAUCT	93617	TTTGGTTATGCUGTCACCAGUGT
272791781	93618	TCACGATGTTCUAAAATGAAGGAAGAGUT	93619	GAGTGTTAAAAUCGCTTTCCTTCTTGUT
272792761	93620	CCCCCTCCUGGTGGCTUT	93621	GGCAGGUAGCCCAAGGUG
272793580	93622	CUGGAACUGAGGAAGGAACAGAC	93623	GCAUCAGAATGTUCCAACAGAGGAA
272797249	93624	CAAGCCUCACCCCAGGTAAUA	93625	TGTCACAGAAUGTTGACTTTUCCCA
272797574	93626	ACGGCATAAATGUAGTCTTTTCCCAUT	93627	ATAGCTATTGTUGCAGAAACATGTUCA
272800257	93628	CCGACGTUGACCGCAUC	93629	GGGCAAAUGAGCCTCUCAGT
272801761	93630	GGCAGGGAGUACTGUAAAGGG	93631	ACAGCTTGTUGACCCATTTGTTTUT
272801828	93632	CACCACCGGUACTTTTATTTGTTCTTUG	93633	ACCTTGTGCTTUGGAAAAGAAGGATAUT
272802093	93634	CTCACAUCAGAAAAGGACCUCGAT	93635	GGGAGCGAGUGATGTACGUG
272803832	93636	GTAAGCACAUCCGATTTTCCAATAUGG	93637	CAGTGCTGAAUGAAGACAAAGATGATUT
272809088	93638	CCCTAACTUGGCGCATGACUT	93639	TGCCTTACCTCUCTTCAGAGTTAUAGAG
272809684	93640	CTGTTTTCTUGAAAGTTTAGCTTCUGACT	93641	CGAUGGATGCTGUAAACAAAGAGAA
272810408	93642	GTCTTCUAGGTTCCCUCCCCAT	93643	GAAGGUGAGAAAAACAGCAACACUT
272810529	93644	TTCTGCTTCTAAAUTCAGGCCCTTUA	93645	GGCTTTATCUGAACTGAAGTCTTGUACT
272812611	93646	CCUACGGGAUCGAGAGACC	93647	AGTCCCGGUGCTCTUGAGA
272816108	93648	CGTGCTTTTGTTUCAAACTTAGCATCUA	93649	GCTTTTAAGTCUGTGTTGGCUGA
272816705	93650	CCCAGCUGGCACTTAACATTUAA	93651	GCTGCAGCUCAGAGTTTTTAUCAAAC
272819653	93652	TCACAACAGAAAAGAUATGCUGGAGAAT	93653	ACTATCATGAGUGCTGTCAGTCTGUA
272820430	93654	GGAATACGGUGTCCCCUGT	93655	GGGTAGUGAGCGTTGUACGA
272828560	93656	ATGTTTGCTGUGCTGTTTTTCUGT	93657	GGAAGATGGAAUTGCACCAAUAGGAA
272831478	93658	AGTGTCATGUCACAAACTCUGCAT	93659	TGACTGGAUCCACTGAAUGGAGAA
272834131	93660	GUACCACCAGGCAAUCCAAAG	93661	ATTCAAAACUGCGGACATATATCCUGT
272836461	93662	CACCTUCACCAGCTGUACAAGT	93663	TUTTACAAGACUGCCACAGACACA
272837313	93664	AATGAGAAAACCUGGACAGAACTUCA	93665	AAAATTTTCAUGCAACTATAGAUGACAGAAAC
272842645	93666	TCAGTCAGUCCCCACCACTUA	93667	CAACUCGGAGTGGTTUGAGAAC
272852885	93668	ACAGCGGUGACAGAGAGAGUA	93669	GCTGTCUGACCAATGCCTGTUT
272853118	93670	TGAAAATTCCTAGGAUGCCATCTTCTUT	93671	CTTATCCACTUCAGGTTTTAGGGCTTUA
272855174	93672	CGACUCAGACGGUGCCT	93673	ACTCCAGUGCATTTCTATCGUAACC
272859192	93674	GCAATGAACAAGACUTAGGAATCCAGUA	93675	GGTACTTUCAGAAAACACACAGAAUGAGT
272861654	93676	GATGTAGUTTTGTTGTTTTUCCAAGCCT	93677	CAGTCTTCTCUTTCCATTCTTCUCCAA
272861795	93678	AGCTTTAGGATCCUTTTCCACTGTATTUG	93679	TCTATTGTTGGCUTAGCTGCATGUAA
272884529	93680	CGTCCTGGGAUTGCAGATUGG	93681	TCACGTTCUCAAAGCAGUGGAT
272887045	93682	GUCGGAGCGGAGGAAGUG	93683	CCCAGGCUTGGCAGGUG
272892115	93684	GACAGTTUCCAGCCUCCAACA	93685	TCCAGATATUGCAGATGAAGAAUCCC
272892384	93686	GCAATACCATUGGTTGTTTTCAUCCAT	93687	TTTCAGGUGGTGUGCGGAA
272894878	93688	TCACCTGGUGTATCGGCTTUG	93689	CCTGTTCUGGGCATCAGATGUA
272899388	93690	GGCGCTTTUAAAACACCGAUCT	93691	CCCCGGUTCTGCTCUCA
272902800	93692	CCUTGTTCGTCTAUCCCCCAGA	93693	CTTCTGCAACCUCTGCCTTTCUA
272907578	93694	CACAAATGGCUATAGGCTATCATUAGGT	93695	GCACTTTCAUCCAGATTACCTGUCT
272908084	93696	AGACCAGGGACUTGCGUAGA	93697	TGTGAAAATCCAUCCTTTCTCTCAAUAA
272909360	93698	CCTATUCCCCAGCCUACACCT	93699	TGGACATTTGGGUTTCTCTGTGUT
272910209	93700	TCACUCAACATTUCACCCACACA	93701	CTGGACGAGGUGAUACACCAG
272911081	93702	AAUGCATAUGAGGCCAAACAAAAACA	93703	CTTAGTTCAUCCTCGGCUCCAA
272911558	93704	TCTACATACCGUGAGTTCCAGATTTUG	93705	GTCAGAAGAUGGAGCTCAGCTUT
272912413	93706	GAAGGAUCCAAGAAACCTGTGTUCA	93707	TGTGCTTATCTTCAUCTAGGAAGCTTUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
272913001	93708	TGAGCTCCATCTUCTGACAGATTATCUA	93709	TCTGCTTCCTUGTCAAAAACCAUGA
272913141	93710	TCTTCTCTCTCAUACTTACAGCTCUGG	93711	TTTTCCGGUGGTCCACTGTUT
272916159	93712	CCACCCACUAGAGGACUGCT	93713	AGACCAAGCACUAGGCCCUAA
272918534	93714	TCTGTTTTUACGAGCACTGGAAGUT	93715	GCAACCCCAGGCUCAAAAATAUG
272921329	93716	GAAGCTGTAAGAUGGTAGAGCAAAUGA	93717	TTACCAACAGCAGGAUAACTTATGUCC
272921861	93718	CTGGAGCCAAUTCGAAUAAAACAAGA	93719	CATAGGAATAGCAUTGCAAGCATTCAUA
272923420	93720	GTGTGUGGCTAGGTGUAGGAT	93721	TTTCTAATTATTTCUGTGTGGGTGTGUGA
272928598	93722	CTGGAUGATAACACTUCCCACAGAA	93723	AATTGCAGAATAUGTATAGAGTGUGGCA
272928668	93724	GTGGTGCCACUGAGAACUAGAC	93725	AAAAGCTTAATGTAUAATCCACAAATGATUCAT
272932646	93726	GGGAGCUCACCCTCATCUC	93727	CTCAAGAATUGCCAAGAAGATGCTTTUA
272932976	93728	CCATGCTUCCCCAACACTCAUT	93729	CATGTGGGAGAGGUCTCTGUC
272934434	93730	TCATCATCTGAAGAUCCATCCTCAUCA	93731	TGGTGTATTUCACCCCCAGATATAUAGT
272942716	93732	TTCAACTAAACUTCTAAGATGUGGCAAGA	93733	TCTUAAAAGCTGTGUGCAAAAGCAA
272946083	93734	CCCACTGUCCCCATTUGCT	93735	CTCUGGCCCCAGGAGTUC
272948297	93736	AGCTTGATCUGGGCGAUCAC	93737	GGAAGGCCUGGATGGGAGUA
272949310	93738	CAATCTTAATACCAGUGTGTCTCGCUT	93739	GGATGAGUATGTCCGUAACACAACAG
272953308	93740	GCCTGGGACUCCCAGAACUAA	93741	CGTCTGGUGAGTGGACTTTGUG
272956066	93742	AAAAGCAAATUCAGAAGCAUGCCA	93743	CCCAGAGCGUCTTGATCCUT
272957761	93744	TCAGGGAAGAGGUTGUGGGT	93745	TGATTCTGCCCUCTTCTCTTTUCAG
272958936	93746	AGTGGGAAAGAAUTACCATCUGCAA	93747	GAUCCATTTGCUGAGCACAGAC
272959310	93748	AGGCUACAACAGCAAAAGCTCUA	93749	ACCAACTCATGACUGTCCTTTCTTUG
272960133	93750	CCCGGTCUGCAATCTTUGGA	93751	ACATTTGTGCTTTAUGGTGTTCTGATTUT
272963226	93752	TGTACAACATGUGTTCACCAGUGAT	93753	TGGAACTTGGGUGTTCAATGAGTUT
272964489	93754	GCATCGCCCAUTTGCCATUC	93755	GGTAAGGCACACUTTTGTCAGTUAC
272966064	93756	GCATATTCCAUAAAACACAGCAUCAACA	93757	GTATGCGAACTGUAAAAAGGGAAACUT
272969485	93758	CCTCCCGTUGGCAACTCTUAA	93759	GCACACCTUGCATTGGTAUGGT
272971131	93760	GGTACAACAAUCTTCCCCGCUAA	93761	CAGAAGCCCCUAGCTCCUCT
272971139	93762	GGCUCACCCAACCAGATATUAACT	93763	AATGGAATTGCAUCTAATGTACACCUGA
272971441	93764	CTGATGCACUAGCTGCGGUA	93765	ACACTCGUAACCACACUGAAAAAGAA
272972218	93766	CCCAGCTCTGUTTCCCTCTTCUA	93767	GACCTAGAUATGCTGTTTUCCCAAAAG
272976878	93768	CTTGACGGTGUCTTTCTCTGTUC	93769	GTAAGTGUGGAGGTGGGTTUCC
272978391	93770	CCGAACTACUGCTTCCTCUGG	93771	ACCGCUAACAGCATCAUCGT
272981640	93772	TUCTCACCTTGAAUAAAGAAGGGAACAG	93773	CAUCAAGGCAGCCCCACUAA
272982782	93774	TGTTTCCAAGGUTGCATGUACAA	93775	TTTAGCATGUGCAATGAATTCUCACAG
272983143	93776	ATGTATGGUGTGTACTTGUGCAA	93777	ACAAACTTGAUGACTTAGTTCGUCCAT
272983732	93778	GCTGCTTCAUCTTCGTCATCAUCAT	93779	AATGTGTGAGGUGAAGGGAUGG
272985784	93780	TCACGTACAGCAAUGAACACTUCA	93781	CTGTGGAGGCCUCAAAGGUT
272987754	93782	TCCACTGCAUACAGGAACTCCUA	93783	ACCTTCACACAUATATTGCTCTTUCCAA
272988802	93784	AGGATAGGGUCCACGCUGAT	93785	CCGCAGUGCCTCAUCCAG
272989313	93786	GGAGAACAAACCUTATGCACATAUGGA	93787	GGAGCTGGTCCUTTGTTTAATCAGAUT
272990306	93788	GGAGCGTCUGGAAAGCAUCA	93789	CTTACTTCAAAGAAAAGCUGTCAAACUCA
272991963	93790	GCGACUCCATTCUGGAGAGAA	93791	CAGGTGAACCUTGAGGCUACAG
272992621	93792	CGTGGAGGUAAAGTGCCUGAAT	93793	TTTTGCAGGTUAGACTCTTTTCUCCAA
272993305	93794	TGGAAAGAGCAAUATATGTGTGAAGGUT	93795	TTTTCAGGUAGCCCAAAAGUGACA
272997140	93796	TGUAGGAGACAUCAGCAGAGGAA	93797	AAAGAAACCACACCUATTACTCTGCUC
272999418	93798	CACTGAAATAUGCATCACTGGTUAAAAA	93799	TGGATGAAUGAATTTGAGAAGUGGCA
272999734	93800	CATCTTTTAATCCCUCTTGCCACTUCT	93801	GGTGACAATCUGTTTTCTTATAGGUGGT
273000365	93802	GGGAGACAGUGCACAUCCAAA	93803	TTCTTTGTCAUGGTTTCTTTATGTUGCC
273002351	93804	GAGCCTTACUCTGTTCCCCUT	93805	GCTCCTTTUCATGTCCCUGAAGA
273002949	93806	TGAAAUCCAGTTTGUCACACAAAAGAAC	93807	TGGAAATTCUGGCCGTTTATTGTTUA
273003474	93808	CTTTTTGUCCCTTCAACAUCAACCA	93809	GATGCCGTTUCGAGAATTTTATTCACUT
273003937	93810	TCTGGTUGCCAGTGTUGAAGAG	93811	CCATTAATTACCACAAAUCCCAGTGAUT
273007098	93812	ACTCAGGTCTTTUAGAAAGCCTAGAUGT	93813	AATGUCAATCAGAGTUCACGACCAT
273007400	93814	ATGACTATCCAUCCCTCCATAGUAGG	93815	ACGAAGAGAAGCAAUCTACAATGAUGT
273008565	93816	CAGTTGAGTTCUGTTAAGTCATTGATUCC	93817	GTAUGCAGCCACCACCATUAC
273008867	93818	ACGTCAGAATTCUTACCATCTGTTGTUT	93819	AGTGGAAGGAGAACAUGAATCTCUCA
273008982	93820	GTGCCACAAGAACUACATCCAUCT	93821	ACTGATGTCAAACUTCTCGATTTCTUCA
273009973	93822	CTGTAGCUGAGATTTCACAUCCAACT	93823	AAAGGCCUCGCAGTGGTAATAUAC
273010461	93824	CATTTTGTCUAGTTCAGGACUGAGGAT	93825	CCTTACTCTTGUAGATATTGGTCCTGUCA
273012109	93826	CTCTGUAGGCCGACUGCT	93827	TCCAUGGGAGACAGGAUGCT
273016031	93828	CGAGCTCUCGACGTCUCC	93829	GCCTGCGGUCGTAGCAUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273019483	93830	CAGTACGUCAGTGCCAUCAAGA	93831	CCTUCCCGAAGGGUCCCA
273020157	93832	AGACTTCACUGTCAGCACUCAAG	93833	CTGCCCUAGAGAGAGGTAAACTTUG
273022342	93834	GCAUGAACTCAGAUGGAGGGAA	93835	TCTCTGATCCUGTCCGTCTTGUAG
273023377	93836	CTGTACAGCAUACTAACTGGTTUGGA	93837	AGAAGATGGUGAATGGCGUCAC
273024683	93838	CATTUGCCGCCAGUGGA	93839	GTCUCAGGGCTCUGCAACT
273026586	93840	CTTGGAAGAUCTGACCCGAAUCAA	93841	ACACTTUCAGGCCAGTTTCTUCT
273033088	93842	GCUCCCCCAGCTCTUCAGAT	93843	TCTCCCTAUGCCATCTUGCAC
273034737	93844	CCCACCUGCTGGTTGUAGAG	93845	GGGAAUCAGCCTCACAGUCAT
273037727	93846	CCCTCTTCCUCCTCCTCTTGTUA	93847	GAGCAGGCAUGGTCTCTTCUAC
273039038	93848	ACAGGATACCTTCAUATTCTTCAGCTCUT	93849	GGTGTTCAGUTTATGTGGGATUGCT
273039257	93850	GAGCTGAUGCCGGAGGUC	93851	AGGAAGCCCUGGATCCUGAA
273039409	93852	TUCACAGACUCACAGCAGCAAT	93853	TTTTAATGCTGTTTCUTAGAAGTTTTGGTTAUG
273046282	93854	GGCCGUGGUCAGAAAAGAGAA	93855	AGGTACCAGAGGUAGTGGGTUG
273048706	93856	GGUCCCGGCUGACAAGT	93857	GAATCCGCCUAAAGTAGTGACTCUG
273049182	93858	TTCACTGCUGCATTCCCTUACAT	93859	CCCTGAGGUAGTTTCTTTUCGAGAA
273049324	93860	GGGAAGGAGCUGGATCTUCAC	93861	GGGUCAAAGGAGACTTTTUGGA
273050992	93862	GAGUAAGTAGCACUGCACAGCAT	93863	AGCACTCGCUATGCCAAUAGG
273051341	93864	ACAATTATGTCCAAUGAGACAGTTCUACC	93865	GGAUGAAACACCAGCTAGUCAGAT
273054234	93866	CTTGGCUGCCCTTUAGACAGA	93867	GGTAAGCTACAUCGTGCATTAAAACTUT
273056345	93868	TTGUGCCAGGACCAGAAAUGT	93869	TCUTTCTUGGCACCAACAGGT
273056357	93870	TGTGCCAAUTGGTGTCTTUCCA	93871	AGATTCTATTGGUGAAACACCGACUC
273061413	93872	CATCCCACCGUGATTTTCTTTTACUG	93873	TCTTTTTAAAGAUACTCCTGGGCAUGG
273064258	93874	GAGACGCCUCCATUGAAGGAA	93875	AAGCTTUGCCCCTGGAUACC
273065601	93876	TGTTTACCUGGAAATGACCAUCAAAGT	93877	AAATGCATGACAUGCTCCAATTGUT
273067549	93878	GGAGGCAAGCUTGGTTATGUCA	93879	ATGTTCUGGGCTCUGAACGAG
273069004	93880	TTAUTCAAATGCAAAACUGAAAAAGAACAAC	93881	TCAGTGCAAGCUCTATCAGTACTACTUA
273069038	93882	TCATTCTCACAGCUAACACATATUCGT	93883	AAGCAATGAGAACUTGTAGTTCATUCCT
273070820	93884	ACATCACACTUGCAAAAGAAGTATGUA	93885	CACTACUAGGCCAACAAAAUAGAAAACA
273074756	93886	AGGAAGTGGCUGGACTCTCUA	93887	GCTCCATTGTTUTACTGTGCATTTTUAC
273076612	93888	GTTACAGCUGTTCCAGAAUAACAGAGT	93889	CATCCTTATCUCCCTTGCTUGGA
273080770	93890	AGAGCCACCUCCAUCCAAAAC	93891	GCCCCATUCTGGCACUGAC
273080859	93892	GTUCCCCAGGCUCAGACA	93893	CUGAAAAGCCCCCUGAGGAG
273083855	93894	GGAAATGUCCGTCUCCACAGA	93895	CCAUCGTTACTGUCAGAAGAACCC
273084092	93896	TCAGGUGCAGGGCATUGG	93897	CCCCAACCUGAGGAAUCACA
273084527	93898	GACAGGTGUGATTCCTCAGGUT	93899	GCUGAGGGACCACATCUGT
273084658	93900	TCTCCTCAAUGGAGCACAGGUA	93901	CAATTGGUCAGCTGCTUCCAC
273084857	93902	CAGGUGCAATTCCUCAGGCT	93903	CCUGAGGAGCCACACCTAUCT
273088245	93904	GGAGAATGTUCCCTTGACATACCUG	93905	ACGAUGAGGAGAGTGAUGAGGAA
273088370	93906	TTCCACAACCCAGAUGCTGUT	93907	CTGAACTUCCCAGTCTTCCUCA
273089728	93908	ACATACCTGCUGCTGCTTCUT	93909	CUGAGACAGAUGACGAAGACGA
273091519	93910	GGGTAATCCCAAUCCCTCTUCC	93911	ACCCTTUAGCAGCCTCTCUCAT
273092002	93912	TGGCGTAGTGUAAAGGGAAATAAUAAGG	93913	AGTGAGCAGGUATCCAGATCUGT
273092150	93914	GACAGAGGAGACUCTTCAAAUGGT	93915	CACCUGAGGAATUGCCCACT
273095802	93916	GTGGAGACAUGGGTGACTCUT	93917	CTGTCCCCACCAUTTGAAGAAUCT
273098681	93918	GGCAGCAGUGGCATCUC	93919	TGUGCATUGCCCCAGACC
273098904	93920	GGGAAGUGGGCAATTCCUCAG	93921	CCUTGTCUCCACCGGAAGA
273099170	93922	GAATGGAAUGCTTGCATCUGCT	93923	TTGCAGTCTUCAGGAGGGTCUA
273099345	93924	GGGAUAGAGGCGTCUCAAGT	93925	GGAAUCGCCCCTCTCUCC
273100131	93926	GTTCTCCATTGCUTTCAGCATCTAUG	93927	AAGAGCCCCAUGTCCTCACUA
273103793	93928	TTCCTCATCACUCTCCTCAUCGT	93929	GGCAAGGGATUCCTTAGAGAAACUT
273104619	93930	CCAGTGGAGAAAAAGGUGATGATUCA	93931	AGGAATUGCCCGCAUCCC
273105339	93932	GAGGCTCCUCCTTGACCAAUG	93933	GCAGACTTTGAUGTGTGTGTTTATGTUT
273105630	93934	GGTGCAAUGCCUCAGGAAGT	93935	CCCCUAAACGAGGAGAUGCC
273116363	93936	GCACCUCATCACGCUGAACA	93937	ATTTCGATGCACCAACAUTTATCACTUC
273117672	93938	TCCAGGTTCTTUTCATTGGAGATCUG	93939	CCTAGTGTCCUCTCAGCAGTATTTUT
273120186	93940	CCCAGUGGCAUAAGACACAAG	93941	CACTTATCTTCUGTGCTTTGGUGGA
273120194	93942	AGAAAGCCUCCTTCCTCATUCAAC	93943	CTCTGAGGUGACTACGTGAAUGAC
273122844	93944	TTCCTGATGCAAAAGUCCCAAAGUA	93945	ATCTCTAGACTTTUAGGATCCCACTUGAA
273123962	93946	TGAATGTATGGUTTCCCCCUCCT	93947	CATGTTGAACACUGGCAAAAGAAATCUA
273129202	93948	AUTGTGCTTTAAUGGCGCAAGT	93949	TGGUCCACGGAGGTCTAUGAG
273130214	93950	CCUCAGGCACAGCGCAUA	93951	TGAGGAGCCGCAACUCUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273130362	93952	CTGTCCAUGCAGGCAACAUAAAC	93953	GCCTGTGCUATAGAACCATGTUACAAT
273132694	93954	AGCCUGCGGAGATAGGUGT	93955	ACCGGAGGACUCGCUCAT
273133804	93956	CGCACAGCUGGTGCAATUC	93957	GAGCACUGGAAAGGGAGAGTUC
273134267	93958	GGGAAGCAGGUGAGUCCT	93959	CCCTGCCUGTGGTGUCA
273135891	93960	GGGAUAGGCGCGAUACCT	93961	CACCTGAGGAGUCTCCCCUT
273136495	93962	ACAUAGGCGAGTCCUCAGGT	93963	CGGAGGCAUCTCGTCTGTUC
273138387	93964	AAAATGCCATGUTTGGTCGTTUGT	93965	AAATGATATTACUATGCAGAGCTUGCCA
273138417	93966	AGTAAAATTTCCTUAGTCCACGTTGGUT	93967	GTGGAGCGUCATTTTACTATGAAUGAG
273139449	93968	CAAGTGGUCACACTGAAUCAGGAA	93969	CCTGUGGCATGTGUGAGAAAAA
273139484	93970	TGGATCCAAUAGTTGCCCUCCT	93971	TGGAGAAGTGAUGCCATTTATTGAUGAA
273140702	93972	AGAACACGTCUTGTTAAATCCCAUGA	93973	GGGTACAUGATTGGUGCACAA
273141468	93974	AGACGCATCTUCATTTACAGTTTCAUCA	93975	GGGTATTGUTCCAGTTGUCAGAAACAT
273144105	93976	TGAGCATAUGGGTCAGTGUAGGA	93977	CAUCTCAGGUAGAGCCCCAGA
273147101	93978	GGTCATCTAAUAAGTCTGGCUCAAAAGT	93979	TCTTTTUACAAAGGGAACCAUGGAAGAT
273147161	93980	TGCTTAGTTACTUGCCGATCATAAAUCT	93981	ACCATAAAGTTTUACCATTTCATATUAACCAGT
273147400	93982	TCAAGTGTTCTUGTACTGTTTGATCUGT	93983	TTGTGTGTGGUTTTCCTTATUAGGGT
273147446	93984	TTGAGGCTGAAGAUCACAAATAATAGUGT	93985	CCAGGATATGGCUTGTGATACTTUCAT
273148752	93986	CCTGAACCUGAACGAAAUGCCT	93987	CCAUGATGGAGUCCAGGACAAAA
273149596	93988	TUGGAGGAGAAGGUGCCAAAG	93989	CTGGGUGGCCTGGAGTUAAA
273149876	93990	GGGCTTUGAAGACATCAGGUG	93991	CCTAGAGGUGAAGAAGGAAGAGCUT
273150923	93992	CAATATTGCAACAUTCTACATGGUCCAA	93993	GATTTGGTTGUGAAGATTCGCUGAA
273150942	93994	GGGAAAAGCUGGAGCATTUCAGA	93995	CTTGTGAGTGGUTATTCTTCATTTUGCT
273151624	93996	TGAGUCAACAAAGCCCAGGTUT	93997	GATAACTUGGCTGTGCCUGAGA
273153844	93998	TUCCGGGACUCCCCAAAAG	93999	ACACUACCCCACCUGGCA
273154335	94000	TTTCAAGAATUAAGGCTATCCUGCAGAA	94001	GGGACATAUAACAGCTGAAATACCUCAA
273155130	94002	TGTGGAGGGCUGGTGUCT	94003	GCACCGCCCACCUAUCC
273155983	94004	CCCCGUAGGACTAGGAUAGGG	94005	CCTGGUGAGCTCTTCCUCAAG
273156222	94006	CCCACAUCCAGAGTAGCACAUA	94007	CATCCCCUGAGAGCATCTUGG
273157452	94008	CAATGTGCATUCAAAAACAGCAUCAAAT	94009	CCCCTCTGUTGGATGCAGTUC
273157706	94010	AACATCAGCUCTGGAUCAGCAA	94011	GATCTGGUGGCAGAGCAGTTUA
273158396	94012	GGGCCATACAUAGTTCAACAAGUGA	94013	TTTTTCCCUTCCGTTGUAGAGACC
273159061	94014	ACTGCCTTATGUTTTTCCCCGUT	94015	CTATCCCAUGGGCAGTCACTUAC
273159693	94016	GCCAUGTUAGCGGCCAAGA	94017	GCGGAGGCACUTACGGUT
273160371	94018	GAAGCCCUCUAGAACAACCCA	94019	CTCCTGCTGCUGCTTCAAGAUA
273161949	94020	GCTGGGACATTUCTCTGATAATCAAUGA	94021	TGCTACATCUCATAGACAGGAAUAACCT
273161997	94022	GGGTGGAGGGUACAAATUGGAG	94023	TCAAGGAAGAGAAAAAGUTGUAGAAGCA
273162458	94024	CUGAGCCCAGAUGAGGGAAAC	94025	TGCAGGGCUGUAGCAACAAA
273165502	94026	CTAGCCGUCTGTCTGTGUACAA	94027	CCGGTGAATAUTTCCTGTAAAACUAAGAC
273165897	94028	GCTCACCGCAUCCATCAGUG	94029	CAGTTCCAUCATTACAGCCTUCCT
273166522	94030	CTTTAGGGAAGGCUCCCCUACT	94031	CATGCCAAGGUCCCAAGUG
273167520	94032	TCACTGCTGUCACACTGTTUGT	94033	GGCAAATGGAAGGAUTCCCTATACTTUA
273168323	94034	AACCUGAGAACAGAUGAAGCCAAA	94035	CCACTGUCACCCAGTUCAACAG
273169371	94036	ACAAAUGCACCCGUCCCA	94037	GCCCCCUGAAGTTGCCTTUAA
273169715	94038	CACAGAGGAGGAUTGCCAAAAGUA	94039	CATGGGAACAGUATTGGACCCUT
273173188	94040	CAGCGAAGUGTGGGCUAGAG	94041	CTTTTTGCCCAUCACCCGTUA
273173484	94042	TCTCUGCAACCACAGGUGAAG	94043	AGCCAGCUGTGGGACUAGAA
273174131	94044	CCACTGTCUGGTCCAATATGTUCT	94045	TGCGGCACAAAUTGACTGUG
273175090	94046	TGAUGACACAGTUGGCCACA	94047	GGCAGGACCAGGUGACATTUAG
273176949	94048	TCTTCTCCAGAUTCTCCGUCACT	94049	GGCATTTTAAAGGCUGAAGAAGGTTTUA
273178971	94050	GGACCCUTTACAGGUGGGAAGA	94051	GGTTTCCCUGAGGGCCTUAC
273179178	94052	GTGAGGGUGGGCGAGAAUAAG	94053	CGACCCTTUCTCCCGAGUG
273183948	94054	TGGACTGGGACUGAGGACUG	94055	CTCCAAGUCACCCAGACATCTUT
273184333	94056	CAUCCACCUGGAGAACAGAGAC	94057	GCCCTATCTGUCATGCTCCTUAC
273184812	94058	TCUACUGAAAGAGCGGGAAAGA	94059	CGTGCTCACAUTCTCTATGAGAUGT
273185038	94060	CATATTTGTACCUGAACACATCCAGCUA	94061	ACTTGGATCCAUTAAGGAGTUCAGGA
273185319	94062	TCCTGAACUCCTTAATGGAUCCAAGT	94063	TGCATGTGTTTTUGACATGAGCATUT
273186269	94064	AAAAGGCACTTUTAAGAGTTATTAGUAGGCA	94065	TCAGTTTGTTTCUCTGCACCTTTCUT
273188069	94066	ACCTCCATAAGAGUTTCCCTGAGATTUAA	94067	CGTACTCAAAUGGAAAAGATGAUGAACA
273188169	94068	TUCTCCTAGGUGGGCAGGT	94069	GGAGCUACGGCGCTTUG
273190949	94070	GTGCAGAGAAACAAACUGAGATTTUGAA	94071	AATGCGAACTGAUCGTCCCTTTUA
273192425	94072	CCATTTCACAAUACACAACUGGCA	94073	GGCCAAUGGTTTUGCAACAACT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273192649	94074	ATGTTCAGTGGAAUCTCATGTGATUT	94075	CTCTCTTCTTATUAGAGGGCCCTTUAC
273193763	94076	ACACCAATAGUAAAGGGCCCUCT	94077	CCACAAGCUCCTCCTUGAGAAAC
273194684	94078	GGGCCAAUCAAAUGGCAACT	94079	GTGGTACTGAUGCTTGTGTGUC
273195987	94080	AGGCTUCGAAGAGCAAGGUT	94081	CGGAGGUCTTCGCCUGAC
273197769	94082	GCACTGGATTAGUAGGTCCTCTTCUAC	94083	GCTCTGTTTUCCTGCTCCTAUCA
273198237	94084	CAACTTTGTTUCCCTCTCTGTAAUACAC	94085	TCGCTTUGGACAAACUAAGCCT
273198390	94086	AGGCTTAGTTUGTCCAAAGCGAUAAA	94087	CTAAAGCAGGATCUCTAGGAATTAATCUGG
273198417	94088	ATGGATUCCAAGAAGCGUCGAA	94089	GCATTTATTCUATATTTTCATTTUCAGAGGACG
273199204	94090	GCTGTCCAGGUAGTGCCAUA	94091	CACTCAGCUGTGCUGGCT
273201154	94092	GACTCUGGGAAGGGCUGAG	94093	TCTCCGACCCUCCCATGTUA
273201603	94094	CATAAAAGTGGUCACATCTACCCCUAA	94095	TCATTGTGTTUTGATTTGCAGUGCT
273201713	94096	GCCCGGCUCAACCTGUT	94097	GCGGGCAGCAUGAGGUAG
273202791	94098	GCCTGCACUCTTTCUGCCA	94099	CGGCCGGUTCTCACCUT
273204257	94100	ACAAGCAACUGAGAATTTCTUGGAGAA	94101	AGGCCTGCCUCTCTTTACCUA
273208434	94102	TTAAAAGTAGCTUTTAACTTGCAAAAUCAGAAT	94103	TGGCTGGCCAUGATCTATATTAGTAUCT
273208773	94104	GCCAGACAGCAGGGUTTGUAA	94105	CCCGTTCUGAACCTAAAATGAGUG
273210112	94106	CGGCTTTUCCAGCAAGTTCTUC	94107	TCATTGCATATUCGCTCAGTAGCAUA
273211066	94108	GACTGTTCAAGUACTATTATGCUGGACA	94109	AAGAAGCCCACUTTACCUGCAA
273213163	94110	GGGAAGAAGUAAGAATTTGAUGCAAAAG	94111	CAAACCATACTUGCCTCAGATCUGT
273216623	94112	AGCTGCCUCACACCCAAAUAT	94113	AGATGAAGAUGAAGAAACCAAAGAACCUT
273217867	94114	ACCTGCACUAAAGGTTCTTTGGUT	94115	CCATTGCTTGAAUGATTTCTTTGAGCUT
273218346	94116	CCCAUTTTCUCCACGGGAACT	94117	CGATCAGAGCCUAAAATCCUCACA
273220086	94118	GGCTATTTATCUTGGTTGCAAUCCGA	94119	CCAGTUCCAGATTGGCTUGAAAAAT
273223261	94120	GGGAACUATUCACAAAGAAGCCT	94121	AACTGGAGGAUGAGAATACCTAUCACA
273225209	94122	CTTAACACAAACCUCTTGACAUGGG	94123	TTGTGTCTGCUTTGCTTCTTTUCAG
273225455	94124	GACAATGTCUCTCTGAAGGCUGT	94125	GGATGAGGUCATCTCCAAATAUGCAAT
273228059	94126	TGTTATTUAAACGCCACAAAACTGUACC	94127	GTATTTCAACUGTGCAGTCAUAAACCAA
273229747	94128	GCACAGAGAAAAGCAAUGAGAACAUT	94129	AGTCTTTTCTTGAUGGTTGACAAAUCCA
273229750	94130	CTGTTTTTGTATATUTACTGGGCGCUT	94131	GATCACAGTGAAAUTGGATGGTGTUG
273230023	94132	TCCAATGGAUTTGTCAACCAUCAAGA	94133	TTTTCACACUGCTGTTCCTUCCT
273232951	94134	ACATACAGCAAUCGCAAAAATGTCTUT	94135	TCCCTCAGAAAGUCTTGACACAGAUA
273233547	94136	ACATACTGCUTACCAGCAAUAAGAAGAC	94137	GAGGGAACAGUGTTACAGAAATTTUGAC
273234329	94138	CCACAATAAACGCAACAUACAATAATAUCA	94139	GCAATTGCACAAUCCTCTTAUCCT
273234654	94140	ATAGAAAAUAAGGCTTGTACCUGGCAT	94141	GCCTCTCAUGAATGGCCTTATUGG
273234980	94142	CACAAGCUCACCGTTTGTAGUG	94143	CAGGCTAAGGUGAGTATGAACTGUG
273238145	94144	GATGCAUCCCCAGUGACCAA	94145	TTTTACAGACAAAUGCCACTGAGAAAUG
273239626	94146	GGTTTTUGGCCAGGACTCCUT	94147	CAUGCUAGAGCGGCCCAT
273240676	94148	GGCUCCAGGGCUAGAAAAGT	94149	CAGCAGAUGGGCCTTTUAAACC
273241257	94150	ATGACAGATTUCATTCTGCCTUCCA	94151	GGTCATTGAGUACATCGGGACTAUC
273242886	94152	GAAGCGCCAUCTTUGCGA	94153	TCCATGTGTCTUTCCTGGTGACUA
273246947	94154	CCTCCUCACTTTTGTCTUGCAAC	94155	GCTGAGTGCTCUGACTTTATGTCTUC
273248173	94156	CTGCUGAAGCTGCTGUAAAGAG	94157	CTTAUGGGACACAGGCUGGT
273250529	94158	GTGACAUCAGACTCTGCUGAAGAT	94159	CAGGTGCTUATGACCCAGUCC
273251335	94160	GAGGTTGUGGCCCTGTATTATTTUG	94161	CTAGGCAGUGGATCATCTTCUGA
273253708	94162	CCTGTTGGCUACTTCGTTUCGAAT	94163	CCGAGGGUGAAACCTTTGTAUGAA
273254086	94164	TGACCAGCCUGTGTCCCAUA	94165	GCAGCACCCUGGAGCTUT
273254136	94166	ATGTGGGAGAUGAGGACUGGAT	94167	GCTTTACTTCAACUCCTTGTTACTTGUGA
273255079	94168	CAAATGCUACATGCAGTGUACAAACA	94169	GGGAAAACUGCAGUGGAAGA
273256005	94170	GCUGATCCCCUAAGGAAACAGA	94171	CUGAGGCTUCCAGGACAACA
273256305	94172	CCATCCAUGCTGTCCTCAUCT	94173	TGTATACCTTCAAAUTGTGCCTTATGTUGA
273256516	94174	CTGGGTCAUAAGCACCTGUCT	94175	AGGGCCUTATGCCUCCCA
273257548	94176	CUGGACCAGGAGGCCTUG	94177	CCTTCUAGGACAGGUGGCAAT
273259318	94178	CTGTGUGGAGCAGGCTAACUT	94179	GAGGTAAAGCCCUCACTCTCUG
273259620	94180	TCTAGAAGCUGTGTTCAGGAUCCA	94181	AGGAGATCAACAUCAGCTTCGUC
273259799	94182	GAGCTTGGUTTGTCTGTACUCCA	94183	CTGAUTCAAGGCTTTUACAGGAAAGG
273260789	94184	CACCTTCTTTUCCTGGCCAUCA	94185	CCAAGTCCUGTGACCAGCUC
273261878	94186	GGACAAGCAGGAGUTGUGAGT	94187	CGUAGACCCAGCCGTTTCUT
273262578	94188	TCCCCGCUGCTGAGGUA	94189	GGGTTGGGAUGTGTCCTUG
273262849	94190	CTTCTGCAGCUCCTTCTTCUCAT	94191	GGATCCUCCCTGCUGGAAAAG
273263268	94192	CATTACUATTTCATGTCUGCCACAGAGT	94193	CTGGCTATAGCAUGAGAATGAGTAGUC
273263426	94194	GGGCCAGCUGCATACGUT	94195	CAGCAACAGCAACAUTCTGGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273264587	94196	CCTCGACUATCATCCATTUCACCA	94197	AGAAGAAAACGGUCAAAACCAAAATUGA
273265942	94198	CGGCCCUCCCTGATGTGUA	94199	GCCAGCAAAGCCUCTUCAAC
273266397	94200	CCCCACUCTCGAGCUCAAA	94201	TUTTCTAGCAGUGGGCACACA
273266842	94202	CCCACCCTTGUTTCAAGTCTCTUA	94203	TCACACAUGGCCTTGGAUGAAG
273268091	94204	CCATTTCACCAUCCCTTGAAUGCT	94205	GGTGTGTGUTTGACTGAAUCAGG
273268324	94206	GGCAGGCACUCCTGGTTTTUA	94207	GCCTTATCTAAAUCAGTGCCTGUCA
273268855	94208	CCCAAAGGAGGCCUTCUCA	94209	ACCTGCUGCCAATTCCCUT
273270976	94210	TGACTATGCAUGAACACTTTUCAAAACAG	94211	CCAGCATTGGCUACTTCTGAAUCA
273271271	94212	CTCCACAGCCUGATUCAGAAGT	94213	GGGCTGUACAAAGTCATCATCUG
273275824	94214	ATCATGCTCUGTCCTGGCTTUAG	94215	TCTGTGCUCCCTGAGGUGAA
273275901	94216	TCCCATGTCAAGUTCTGGATCTGUA	94217	ATGGCAAGGTAGUTGAATTGGATACUT
273276259	94218	TGTCGTCATCAUCATCATCCACUG	94219	CCAGAGTTUAGACCCCACTTAGTTUG
273276935	94220	GACTTGGAAGAUGCAGAACUGGAT	94221	ACCATUAAAACCACCATCCCUCAC
273279233	94222	TCCACCCUCCTCCACCUT	94223	CCTGAGGCUGGTAGAAUCGG
273279806	94224	CAAACCAGAAUTCAGGAATGAAUCAGAA	94225	ACAAGCUAGTGGTGCUGCAT
273279966	94226	GCCTCTGUCACATACTCAACAUCAT	94227	GCTGCTCTGUGATGACTGTGATATUAG
273282012	94228	CCAGGTTGGGAUCATTAGTTTCCAAAUT	94229	CTTGATTCTGAUGACCCTTCTGUGA
273288034	94230	GCCGCCACUCCACCTUG	94231	CTCTTTCCTTCUTTGCCCTTCUGA
273290509	94232	GTCCAGGCAGUATGTGTGGUAG	94233	CACCCTGAGAAGUTCCCATCUT
273291202	94234	CTCCCGTUCAGCCTTCTCATUAG	94235	CCAAUGACCCCCACTUGGAT
273299217	94236	CTCAAGGTCTUTAACATCCAGTUCCT	94237	AGAAGCTCCUTTGTCAACATCUGT
273301515	94238	AGCAAAAUATTACTTGTAAAUAGGCAGGGA	94239	GTGAGCAGTUACCAGATACTTTAGTUGA
273303014	94240	GCAGGGAAAGUTTCTTCAAGCTTAUT	94241	TTTATAAATGUGACTGTTGTTUCAGGCT
273317968	94242	CCAACATTTAAAGUCGAAACTGCTUACT	94243	GAATAACGCCUGGATTTATCTUGCC
273318054	94244	ACAAUGTTCAGTGUGCCAGGT	94245	CTTTCCATAACUCTCTGCCCAUCAG
273324919	94246	CTCGUCTCCATUGAGCAGGT	94247	AGGAUCCCGAGCTGGAUGA
273327612	94248	ATTATCAGACGUTGTTUCAGACGGT	94249	CCTGUGCACCCAGATTUGGAA
273332112	94250	CTTCTTGTUAGAAGGTTGGTTTCUCCAT	94251	AGCTACTTTTCUCCTTCTCTGACTUACA
273334035	94252	CCUTTTTCUCCCCCAGACCT	94253	GGCTCTGAUCCACTCCTTTCUG
273336836	94254	CCCGATGGCCUAATGTCTGAATUAT	94255	GAAAAGAACCAAUCGAGAAACTGCUG
273343431	94256	AGGGCAGAAUCAGGGUACACT	94257	GAGAGGACACUGTAATGTTCCAUGT
273344246	94258	GGCCTUGTGGGCAUCAAAAT	94259	TCUTCAUCCAACACCCCACAC
273348830	94260	GAGTGGATGCCUGAATGACATTUG	94261	CTGCTCACUCAGACCTAAATGAUGG
273353908	94262	GATTTCATGAAUGTCTAGAUGCCCAGT	94263	CCAAAATGGUGGCCCTTAAAGGTAUAA
273355766	94264	CCAGATTGTTTUGTGCCATCACTTUA	94265	ATATTTGAATTACTUCTTAGTGTACGTUGAACT
273356036	94266	CCTCTGCUCGCTTCTCTCTUG	94267	AGCACAGCGAAUCTGGAAAACUAT
273357097	94268	CCAGTUGGCAGGGUAGGAC	94269	AGAGACCCCGUTTTTACCCTGUA
273357212	94270	AACTGCATTAUTCAGACCAUGCCT	94271	GCCACAGUCAACACATTTGGUT
273357997	94272	CTTGTTGAGAUGGTGGCACTUG	94273	CAGCGTTGUAGAGGCATCTTCUAA
273358689	94274	TCACAAGGAUGCAAAGAAGTCTTTUCT	94275	GGTGGAAUCCAAATGTGAAACUGAAAAA
273359285	94276	CTGTCTCCCUTGCCCUCAT	94277	GGGCGACGGACUCTCCUA
273362205	94278	CCTAUGAGGAGGCAGAGTTGUG	94279	GATGUGGAGCCUGGCAAAGA
273363028	94280	TGAGCAAGGAGUGTCAACATTATCTTUA	94281	GGTTCTCUCTGATAAACATUCACCACAG
273363644	94282	GCTGAAGACUCCGCTGGTUA	94283	GCUTCTTUAGCCCGGAACCC
273364186	94284	GAGTCCGUCGCCCUCAC	94285	GCGCCCUGTGACTCUCT
273365629	94286	AGTACTTCCGUTTTTACCTCATUGGT	94287	GAGGAACTAGACCUTCCAATTGAUGAT
273367532	94288	GAACCAGAGTTTUGTTTTCTTGTTCCUT	94289	GGTCAGGAGAGUTTGATATCATTGCAUA
273368146	94290	CACCCAAUGGCCTTTGCAAUAT	94291	GGGAGCUGAATATGTATCUGCAAG
273369319	94292	CTCAAAGCAAAUCCTCATCCACUCT	94293	TGAGTTAATCATGUTTTTAGAACTGAATTUGCA
273372027	94294	CGATATGGTTUACGCTTGCGTTTUT	94295	ACAAGGTUAAAAGGGCCTATAGTTCUG
273374406	94296	CTGCATAGGCAAUCTCAGAGGUC	94297	TGACTCAAAATGACAUTAGCACCTGUAA
273374911	94298	CCTAAATCCTUGCCTTTCACTUCCT	94299	AAAGAATGTTCAAAUGTCATACGTGTTUAA
273375148	94300	TTTAAAGCTGUGTTCTGTATUCAAGGGA	94301	TCCAGATAACAGUGAAAGCACCAATTUA
273378128	94302	CCATGGACTTTAAUTCGCCAAATGATUA	94303	GACGTGCTUGCTTTCATTTGAUAGG
273380946	94304	GGACTTTGCTAUTAACGTATGCACUCT	94305	ATTCAGCTTAAAACUTACTGTCGUCAAAC
273382346	94306	GCTACTGAAUGCTCACCACAAUCT	94307	CCACACAAUCACCCTCTTTATTAGTUGA
273383375	94308	CTGCTCTAAAUGACTCACCCUCA	94309	AGAUGGAGGAAGUGAAACCAAGAAAC
273386619	94310	AGTTAGGAUAGAGCATGTGGTGUGA	94311	TTGGGCCAGUTTACTCTGUGG
273389154	94312	GGAUTAAAGAUGCCAGGGACAGAC	94313	GCAAGTTGAAGTUTATTGCGTTGACAUT
273392299	94314	CTGAACAACAUGGCAGAUGCAA	94315	ACAGTTTTCUGACATGGUGGCT
273395823	94316	TGAGTCCGUTTGCTUCGCT	94317	GCACTGCATGAACUAAAAACCAAATAUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273398885	94318	AGAGATTTACCAUGCATGAATUCGAACA	94319	AGGAUTATGUGAACAGAAAAGAGGCAA
273399183	94320	CTTTGCCTCTTUTCTGTTCACATAAUCC	94321	GGACGAAAAACGAUTTCTTGTTACTGUT
273405354	94322	CCCTCCTCAUTCACCCTCUG	94323	CGGACTTUCCCTGCCUCAAG
273406105	94324	TGACCCTTTAUCCTCAGTGAUCCT	94325	CCCAGATCAGGUCTTATATCTGUAGCAA
273407536	94326	GCACUGGCTTUAGCAGCAAAA	94327	CCAAGAAGTCAUCAATGGAAGTAATGUC
273412275	94328	GCATGTUGAGCTGCACGUA	94329	CAGGCCTCUGACTCTGCUG
273414242	94330	TCCATTGTTCTUGCTTTTGCTTTGUT	94331	GAGATGTTCATUTTCCCCAAACUCAC
273414536	94332	GTGTTCUCACAGATGCTGUCGAT	94333	CAGTGTTTGCCCAUTAATACAACTUAGA
273415698	94334	ACCTAGCCTGUGTGTGACTATTTCUAA	94335	CCATGAGACTTGUTTCTGTCAGAAAUG
273416843	94336	CGTTGATGAUAATGAAGTTCGUGACCT	94337	TCCATTCTCCUGATGTACCTTCUACAAT
273417522	94338	ACCTTCCCAAGAACUTCACTATUCC	94339	ATTTTAGCCTCUTTGCCCCCUT
273420212	94340	GCAGCTGUAGGATGCAGAGUAA	94341	GTTCAGAAUCAAGAAGGAATGACAUCAAA
273420976	94342	CAAAATATAAAGUGCCTGGCUCAGT	94343	CCCTTTACACUACGCCAATTTACTAAUGT
273424020	94344	AACCCAACAACUCTGTTACACUGT	94345	GATTTCAGCCAAAAACUGGATAUCAACT
273425275	94346	CAUTGACUGGGCAGCCACT	94347	GUGCAAGACAGCGAUGCAA
273426398	94348	AAGGCCTTUCCTTTCTCTUCCA	94349	TGGTCGTUCACAATGTATGUACACT
273426769	94350	TCCATGGTAUAAGCAATTCACCACATUA	94351	ACCAAAACTTGAUAGGCAGCTUCA
273442304	94352	GACAGAGGCUGAGTTUGAAGAGA	94353	TCTTCTTGTCAAUAAACCAGAGGCTUAC
273446829	94354	GTATCATGUACGCATAGCUCGAGA	94355	CCCTCTGAUGAGCTCTGAUACAC
273447121	94356	CCTTCCCAUGGAGCTCUGAC	94357	TTCCAGTUGCCGGATCATCUC
273449324	94358	ACAATGAATGAAUGGAACAGAGAGGUAAC	94359	GGAAGAAAAUCAGCGGAGCTAUAAACA
273452724	94360	AACCTTAATACGUCGCCTTTTCTTTTUC	94361	GGAATGCAUACAGAGGTAGAACAGTTUT
273456006	94362	GAAGCAGGTUTGACAAGTGGUAAG	94363	CCTTCCUCAGACTGCTGUGA
273456083	94364	GTTTGACUTAAGGCAGUAGAAGAGAAGT	94365	GCTTAATGTAUACAAGTGCCTCAGUGAA
273456673	94366	GGTATTCATTGTGUTAATGGGTTCAATAUCC	94367	ACTATTCCUGGAGGUGGAGCAA
273456802	94368	TTCTTTAGCTUCCAGAGCAGTTGUAG	94369	CTTTGCUTTACTCCUCCCAAGGAT
273457021	94370	TCTAATTCATACCUATCCCTTGCAUACCT	94371	GACAGAGAAGCUTCACAATCAAGUG
273457035	94372	GCGACAUCCAGTTTGUGCAG	94373	CTTCTAGCCAACCUCTTTTCGAUGA
273457358	94374	ATTTTTCCATGACCACUCTGTACCAUT	94375	TGCTCATTATTUGCATTTGAAACCAUGT
273457724	94376	TTGCCAUCCACACCAAAGCUA	94377	CACTCCAAAAAUTGGCATGGGUAA
273458756	94378	TCAAGCACATAUAAACTGTGAGATAAUCAA	94379	CACUTCUGGCAGCACAGGAT
273458782	94380	CTTACCTGTCGGUAATTTCTTCTAUCCA	94381	GGTAAAACAGUGTTGUGGGACAGAT
273459104	94382	CTGTGCUGCCAGAAGTGTTUAAAA	94383	TCACGTAATCAGCAAUGAGTATTCTCTUC
273460280	94384	AATACCACATAUGGTGCTCTTTCTUGT	94385	ATTAGCATGGCUCTGAGAAAGTGTUAT
273461017	94386	TCUTTCACAACCATUAAAACAGGAGACA	94387	GTACTCTTTTTCCUGTTGCTGTTCTTUT
273461041	94388	AATAGCTGGUTTACCCAUGCCAA	94389	CAGACTUGCCTTCGCAUGAC
273461244	94390	CCATTAGCTTGGAUAGCTGCAGAAAUAT	94391	TCAAGCAGCUTGGTAGCATTTUG
273462333	94392	GTGTTGAAUGGCTCUGCAAGAC	94393	TCAAAACAAGUCAAUACAGGAAGGAAGA
273464031	94394	TGCCAATTTTUGGAGTGACUGAGAT	94395	AGTCAUCATTTTCATCAUCAGCAGACA
273465242	94396	CTTTGCAGGCUCTCACATTTGTTUT	94397	CCCAGCCGUGGATAATTCTTATAUGAT
273465317	94398	CTGTGTCTGGUCTATTGCTAGUGAG	94399	CCCUGGGAATAGCTUCAGGAA
273465835	94400	AGCAATTTAACATATUACTGATCATAGTTCCUT	94401	CTAGTGGACAGAUAACCCAAGTCAAAUC
273466031	94402	TGCTTAGATTTGACUTGGGTTATCTGUC	94403	AGATACUGAAACAAGAAUGGCCCAAA
273469372	94404	CCTACTTGCUCCAACAATATCACUGAT	94405	GTGATTTATCCTUACTCCTGCCTTTAUCC
273470034	94406	TCTTCTCTTTGTCUCCCATTGTTTCUG	94407	TCTCGACAUGTCAGTTTGUCACAT
273471824	94408	TGCCTCCTTGGUATGAAACATCTUT	94409	GTGTCCCCACAUGAGGAAAGUAT
273476603	94410	AGCTGAAGCUGTACTGUGAGAC	94411	GCAGCAGTCCUTTAGTCCTCUAA
273477760	94412	GTGCAGUGGAGGGCUCAT	94413	TGGUGCCAGCCTUCCAG
273480691	94414	GCGTTTGCAUCGCTGTCTUG	94415	TUGGTGAGCUCCCGAAAGAAG
273481492	94416	GCTAACAAAAACCUCCCAACTCCUA	94417	CCTGAAGTATUGGGCAGCATUC
273482808	94418	GTCTAAGTTTATTCUGCTTCCAATAGAUGCT	94419	CAGGTGCAAAGCUTTTCCAAGAUT
273483827	94420	TGUAGTCTAGCUGCAAACACCAAG	94421	TCTTTTGAUCAGGTGUGGGCAAT
273484011	94422	AATGGCCUTCAGTGCUCCAA	94423	GCATCAAATUCTTACTTCTUCCCCAAAT
273484429	94424	GAAGTGATGGGUTCCTGGGUT	94425	CAGCTTGCAACAGGUAATGTTTTGAAUA
273484614	94426	CTGTUTCAGCTGTTUCAGCAAGG	94427	CCTTCAATGGGCUTATTTGGCTUA
273488966	94428	CCAACTGTTCCUCAGGACATAAUGAA	94429	CCAGAUCACTGUGCAGCAAGAA
273491642	94430	ACAGGAAGAUGGTGACGUAGGA	94431	CTGACTGTCUGTCCCTCCUCT
273496401	94432	GAACGAGACTUTTCTCAGATGTUGGA	94433	GTTTCTACUGCGACATUAGCCAAAAA
273496925	94434	CCTCTGCCAUTCACTTCATCTAUCAA	94435	TTGCCAACACAACACUTTTUAAGCA
273498592	94436	CCCATAGCACUGAAAGAGGAGAUT	94437	AGAGCUGGTATUGGAGGCAAAG
273500221	94438	TTGAGAGCTTTUACACTACAGCAAUCAT	94439	GTGAACGUGGACAAAGCTGTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273500770	94440	ACTTACTTCUGTGCTCCCUGAGA	94441	TGCTCATTTGCUCCTTTTCATTTTUCC
273504119	94442	CGCCCTCUGGTCTTCTGACTUA	94443	CTTTTCCCUGATGGTCCAUCCC
273508156	94444	TGAGTCATACUGGTTCATACAUAAGCA	94445	GGAATCCTCCACUCTCTTCACTGUA
273508667	94446	TCCATCCCTUCCTCAGTCAUCT	94447	TTTGACTCTTUGTCTCTCACTUCCC
273510104	94448	TGTACTTUACAGAACGGTCTTUCCAAAT	94449	CATCTGAAUGGGAAGTGGTAUAGCC
273511083	94450	AGCTCTTTGUGCTTCTGAUCACA	94451	TGATGTCATUGCCACTGUCGT
273512363	94452	CTACTACCCCUCCACCUCAGA	94453	GGACACAGCAGAUGTCTTUGAGT
273515136	94454	TTTAAGGTGUGAAGTAGCTGUGCAT	94455	TTTACAACTCCAUCTACATTGGTUCCC
273515705	94456	GCTGGAUGCTGAAGTGUCCAAAT	94457	GGGAAGAAAGUAGCCCCUGT
273520201	94458	CATATTCATGUGGTAGGAGUAAAACGGA	94459	GCAGGUGAAGGAGCAGGAGAUA
273521490	94460	ACATACATGTGUCCAGAAGCAATCUAA	94461	GTGGTTCTGGAAGUAACTCTGATATGAUG
273521664	94462	GGCUCAGCTCCUACGAAAGA	94463	GTCTGTGUGTTCGAGUGGACAA
273522366	94464	TCCTTACCTCTUCCTTGCTGTTTUC	94465	GGGTTTGTGGAGUTATAGGTATTGATGUT
273523154	94466	GTTCGTGTTGAUTCTGTTCCTGAUG	94467	AGAAAATGCTACUGGAGACACAAAAGTUA
273523428	94468	CTGTGCCCAUTTCGAACTUACAAA	94469	CTGGAGCAAUGAGCTGAGTUG
273529969	94470	AAAGCAAUAAGCTCCATUAGAGCAA	94471	CTUCCAAGGAACCAGUGCGA
273530063	94472	GTACTTCAACTTUGCCCCCTTCUA	94473	CAAAGGAGGCAACGUTGAAGTUT
273532346	94474	CGGACCUAACAUGGGAGGGT	94475	AGCTGATGCUGAGAAGCUCAAG
273533565	94476	TCTTTATTTTCCUACCTTCGCACUGG	94477	CTGTCCATTTGUGAATCCTGAGAGUT
273534040	94478	CCGACCAGGAACAUTCTACGUT	94479	AATCCTGGAAAUCCAGTUAACAACCA
273538790	94480	CAGCTGCTAUTCCACACCUGA	94481	CCATGAGGGTAGUGTTGACAAAGATUAA
273543052	94482	TGCTCTGGAUTTGTTTTTCAGUCT	94483	GGAGGTCGGUACCACAAAGTAAUG
273545827	94484	AGAGATGTGTCUGACCTGTGAUCT	94485	CCACGGAGCGCUTCCTUAC
273546003	94486	TCTTGCTCUGCTGCTCTGUAAC	94487	ACCCAGCAGCUCCUACAGAT
273547169	94488	TCCAAGGCACAUTTGGTCTCUC	94489	ATGTCCACGGCUTTACCACUT
273551757	94490	CCCACUGGTGCCCUCAC	94491	TCCACAACTCUGCCTCCTCAUA
273556611	94492	GCAACTGTGAGUCAGGGAAAUG	94493	GGGAGTAGCAGUAGTACATGAUGA
273557530	94494	AGUCGCCCTUACACAAACAAAGT	94495	ACAGAGAAAACAAAGUACAAGUCAACAGT
273558187	94496	CCTAACCTGUGTTGTGCCUAAGAC	94497	GTGTGACCUGTTCTTCTGUACCA
273559054	94498	GGGTUAGGCCAAAGTTCUCAGT	94499	TGACATGCUGCGACTCTUCC
273561533	94500	TCTGCTCCUCTAGCACCTUCA	94501	GGGAGTGGUTTGGGTCATAUGG
273564146	94502	AGTTTATTTCTGCUAGTATCACTTACCAAUAG	94503	CATGCAAACUGAAGATCGAACTAUGAAA
273565067	94504	ATTTCCAGAUGGCTGGTCATUAACA	94505	ACTTCCTCCUCCAGCTGGTUAT
273566340	94506	CAGUGTTTTCATGGAUAGGAAGGAAC	94507	GGCTGACACUGAGGCTCTTUT
273567045	94508	CGAGCUGGAGTTCGAAUAGGAA	94509	GATGTTGTCUCCAAGCAAAUAAAAACC
273569839	94510	TCCTCGCCCUTCAGATACUCA	94511	TGGAGGUCAGUGAGCAGAAGT
273572061	94512	CAAGCAUCTCCTGCUGGACAA	94513	GGTGTTTGUGGCTCCUCGT
273572534	94514	TCTACCUCCTTCAAACUCAGGGAA	94515	CATTAACTAGCGGUTTTCTCAAAUCACT
273573158	94516	CCGUGATAGTGAUGCCCACAG	94517	TGGAGTGCCUGTTTTGTGUACAG
273577360	94518	GATGAGAGGTGAGUTTTCACTGAAGUAT	94519	GTAGGAATCCUGATCCACATATUCACAA
273578432	94520	AGAACUCAGAACAAATAGACAUGCAAGA	94521	TCACCATTTCCUACATGATTGGAAGTUT
273580586	94522	TTTGCAAAGCAGAAGAUAATGGTGTTUT	94523	GTATAGCACCUCGAGTGTTGAGATUAC
273581285	94524	TGGTGTCTCUCTCTGATGTUGGAA	94525	AGTGGTGTTGUCATTGTAAAGUGGT
273581612	94526	GGAGAUGGTTCTCATTUAAGCAAAAACA	94527	CTTTCTAGTTGAUCACCTTTGGCAGUA
273581620	94528	TCTCCUGAAGATTCCTTUGAAGCA	94529	GCTATTUAAGAGCAGGGAGGUGAG
273581895	94530	TCATCTCACTTUACCTGATGTGCUG	94531	TCCAGTCTTACCUATGCTCTTTTCUACT
273582289	94532	AGTCAUGGAGAACCCGUCCT	94533	TGAGCACTGATUAGTCTCACTTTGAAUT
273583443	94534	TGGGAGAUGTTGCTUGCACAA	94535	ATAAATTGAGGGTTTUGTACAGTACCATATUA
273584216	94536	TCCAATAGAAATAUCAAGACCAAAGGGTUAC	94537	TGATCAGAAAAGAUTCCTCAGGCTCUA
273584325	94538	CAAGGCTGCUCTTGTCCUAGAA	94539	TGCCTTUGAGCAGCTGAGUC
273585600	94540	CCCCATGUACTCTCCCACUGT	94541	GGTAGATGUGACGCCCUCA
273586077	94542	TGCAAGGUAACTGCUCGGAAAT	94543	GTGTACTGTGGAAAUGTAGGGAGAAATUA
273586380	94544	ATTCTCAGGGAAAGUGTAGGTACUT	94545	TTTAGGGTGTUGAAATACCTACCATUGT
273586664	94546	AGGGACTTUAGATATCACUCAGCAAGA	94547	CCGCATTUGAAGCCTCCTGUA
273588213	94548	CCUACCTGTGUCCCAGCAAAG	94549	TGATUCGGCAGCAGAUCCAG
273588361	94550	CTGTTCCCAUCCCCTAATGGAUT	94551	TGCCAGGCGAUAGTGGGUA
273588870	94552	CCGCACACCACUTCCAAGAAUA	94553	CACCTTGTGTCAUCAGTCAGTTTTAAUT
273592739	94554	TGCAGCTGTUTCCTTCTCCUG	94555	CCCCCTATAUCGCTCCTGUCT
273592866	94556	AGTUGGACCACGACCTTGTUT	94557	CCTTTGCTCUCATTTCCTTCATAUACAAC
273593056	94558	CACCCTCCAGAUATATCCCCGUAT	94559	CAUGCCCATGUAAGAAACAAAAAGGAA
273593196	94560	CTACAGGCCAAUTATCCAAGAAGCAUA	94561	GGATCCAACCAUTCAGACTTUCCAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273594826	94562	TGAGGAAGAAGAGAAAGUGATACUGGA	94563	CAGCCACGCCUTCCTCTAUG
273599358	94564	GGTGGTTCAUCTGTGAGCAGUA	94565	GACAACTACACUTGGGCGTUG
273599646	94566	CCTCACCGGCUGTTCACAUC	94567	CCACCTTCATCUACCTTGTCTCTTCUA
273600893	94568	GCTGCTCTCUGAATAAAATAAATGGTUACCT	94569	TCTCCUCCACGACTTGCAAUG
273602316	94570	ACACGCCCUCCCCTTCTUA	94571	CTTCCCCCUTGGCTTCCUT
273602546	94572	AGATTCTTCUGATGAGTGUGCAAGG	94573	TGGCTATATTTTCAGUTTGCTAGAGCUT
273610266	94574	GGAUTCAGACCUCAAAACCACAGT	94575	CGTTGCTTTCUGGAAGTCAACAUT
273611626	94576	GACTUCACCAGGACAATTCCUCAA	94577	GGAGTTCCCCUCCGTTTUGAC
273612098	94578	AAGCCCCACAUAAAGAAACCTCTUAAT	94579	CCTGAGAAGGGCGUCACCUA
273613242	94580	GTCAGGTTCCUCGCTGTCUC	94581	GGTCGACATUGATGACTTACUGACT
273614818	94582	CGTGGAGGAAUCAGCAACUGG	94583	TCCCGTACCCCUCCACATATUT
273618289	94584	CCTTTTCGUAACCAGGCATTATGAUCT	94585	GGGAGAGGAAGGUCTGUGAGT
273618551	94586	CAUATTATCCATTUCAAGGGCCCACT	94587	CAATCGTCGCUGCTGCTAUC
273619831	94588	AGCTTGTTGAUAGCCTTTGTTCTUCT	94589	CTTTCCATCATAUCCTGCTGCACUA
273620428	94590	TGTCTCCUGGGAGGAACAUCAA	94591	GCCCTTCATTATAUGTTGTTGGTATCUG
273621515	94592	AATGAGGACUGGTGTGCAGTUT	94593	AAGAATGUGGGAAGGGAAGTACTAUCT
273621770	94594	GGAACAGAGGACACGUCACUT	94595	GAAAGACAGATUCCTCCAAAAACUCAC
273625083	94596	GCCAAATGAUTCCAGTATUCAAGACAAAT	94597	CCTTAAGGUGTAACAAGUGAAAAGCA
273625285	94598	CATCCAGGUAAACTGGGCATUCT	94599	CCTAATTCCAGGUGCCACUCC
273627933	94600	GCCCGTTGUTCTCACCAAUAGAA	94601	GTUCCACGCCAUCGGACA
273629636	94602	GTTACCTCTCUCAATTTTTCTCGCUCA	94603	AAAGGCAGAAAGAAAAUTCGGAAGATUC
273630597	94604	CCTUCCAGCCCCACGATUAC	94605	CCAACAGTTTUCAACAGAGGCTAGTAUA
273630704	94606	GCTCCCTCUCAGCAATACGTTUT	94607	CAAGUCTCCUGGAAAAGGCAGA
273632887	94608	CACCAUGGGAAAGGTGGGUT	94609	GATTCGUAAACAACAGAAAGAACAUGCT
273635667	94610	CTATGAAAGUCAGCCATCTGGUGA	94611	AGCTGAGCUCTTTTGCTGTCUT
273643059	94612	GAAGTTCGUGACCTCATTTCUGACA	94613	GAGGTGGAUGAAATAAAGACUCCCAA
273645219	94614	TGCTGTTTGAUCCGATAATCTTCAAUCA	94615	GCCAAACUGCCCTCTGTGUA
273647102	94616	TGTAGAAGGUACATCAGGAGAAUGGAT	94617	GTACGATTAGCUGCCAAGAGCTUAA
273647981	94618	CCTCGUCCCGCTCAATGUA	94619	CATGCGTUGCCCCAATGUC
273648404	94620	TGAGAUAAAGCAGAAATGUGCAAGGA	94621	AGGATGAUGAAGAAAACTCTAUGCACAA
273653487	94622	GGGCTTCACAUACAATAATCCTTGUT	94623	ACCTGGCAAGUCTGTCACTUAC
273655585	94624	CAUGAGTTTGCUGGGAAACAGA	94625	TTGATACTTGUGTACCCTGTTTUGACA
273657147	94626	CGGAUGGCACAAGCAAAAUGG	94627	GGUCCACGGAGGTGTAUGAG
273659227	94628	TCTTTCCTTUGAGGAGGGCAAUG	94629	AACTAGTTTAAGGUACAGTCACATGCUT
273663154	94630	TGATCTGTGGCAGAGUTCTATTTTTCUG	94631	AGAACTGGUCCATTGGGTTUGG
273663821	94632	CCTGCUGACCAGGGTATCUACT	94633	AGGCGGGAAGCAUCGAUAAAC
273666313	94634	CCACGTTTGAUAAACTTTCAGAAUCACA	94635	TGTUGAGCCAAGAAAGCCAUCT
273670519	94636	CUCAGCCAAGGGTUCGGT	94637	CACTCAGCACAGCUATACCUACA
273672522	94638	GCAAUAAAGCCAAACCCCCUAC	94639	TCTTGGCTCTTUATAACCTGTTGCTUAA
273674748	94640	CCAGCCCAUGGATGAGAAUGA	94641	GAAAGAAGCTGTUAAGACGTCTGAAAUG
273674754	94642	AGTCTGACACUTTGGGACCUCT	94643	AGGCTCATTUCATGGCAGUAAAGAAA
273678059	94644	CTTAGAAGTGUGAGCGCCTACTTTUA	94645	CAGAAAAGCAUTCCACTGTGUAAACAT
273678567	94646	CGCACAUCCAGATUGGAGACAT	94647	GGAGGGAGCUAGTTAGAUGAGGAG
273679425	94648	GTTGGCAGGGUGGTCATAGUT	94649	TGGGATGATUCACAATGGCCTTUT
273684389	94650	CACAGAAGTCACUCGTTACACATUG	94651	AGAGGGUAGAGAAGGACATTGTCUT
273688298	94652	TCCTTCCACUCCCTTAGTTTCAUCAT	94653	CAACAACCCTACUTTTTATTCCCCAUT
273690484	94654	CGCTTGTGCAGUTGATGAATAAAGAAUAA	94655	TTGACUTGTTGAGATUCCCACACA
273692250	94656	GGTGTTAAGCCUGCTCTCTCTUC	94657	CUAATGCTUACCCCAGAGACAACAA
273693989	94658	AGGTATTGCACAUGTGAAAATGTUGG	94659	TCTGGGTGAAAUGGCAACTGUT
273695315	94660	ACAAGCUCAACTCCUAGAGCAC	94661	AGATAAGGGTTUCAAGGCATGCUT
273698951	94662	GCTTACCAGGGAAUTCTTCCTTTAAGUT	94663	GAAGGAGAAAAUGACACAATGTCGAAUG
273700480	94664	CAACTCUGGAAGAAGCATAGCUCA	94665	CTTCAGTGAAAACUCACCTCTCAUCT
273702065	94666	CTCCCACTUAAGCGTGCTUCT	94667	TTCCCAGGGAUAAAAATTCAGCCUT
273702334	94668	GAACATCUGCAGCAAGGUCAAG	94669	GCAGGTGUTTATGCGGAUAGGA
273702375	94670	TGTTAGGATCACUTGCCATTGGATUAA	94671	GGCTTTTGCTATAAAUATGTTACTTTTAACUGT
273705807	94672	CGACAGCGGUTTTCTTTTATUACC	94673	CTGCAAGUAGGGCATCCTTUGA
273707150	94674	GUGAAAAAGTCCUGGGAGGGAT	94675	ATCGGUGAGGAGCTGAUCAAC
273707403	94676	ATGACCAAAUAAATCACATCTTUAGGAAGGA	94677	CTTCGAAUGGCAGAGGAAATUGG
273707434	94678	GCACTTACACUTTATCCCCAATTUCC	94679	GCTCCAGACUGGTACAAAGATTTTGUT
273709097	94680	GCAGGGAGAUGGAGTAGATGACUC	94681	AGTCTGUGCCCTATCUGGGAAA
273712950	94682	AAAATTCTGTUAGAACCATGAAACATAUCCA	94683	GGATGCAGAATAUGCCAACTACTAUACT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273713635	94684	TCCTCAUCAGGAGACTGGAATUCT	94685	AGGGTTTGGCUGCTTTCTUGA
273714387	94686	AAACCTCAGCAUCAGCATCUGT	94687	TCTCTTGCTCUCTTTCCATTTCTTTUCT
273715183	94688	GCTTCCAGAATUAAGAGGCAGTCAUT	94689	AGATGATCAAGCUGGTAAACTGUGG
273715941	94690	CTCTTCCUCAAAAAGGATAAGCACUGT	94691	CGTTTCATTTTCUTGTGTTTTGCCUAGT
273718435	94692	GCCCAACCAGACUGAGTTCAUC	94693	TTTTCTGCTTGTTUTCACTTTCACAGUT
273723726	94694	CCAGGCUCTGGCTGUGAA	94695	CACCAGUCCTCTCCCTUCC
273724365	94696	ACCTCUGACAGTGGGCUAACT	94697	TCACUGCCAGAGACTGAUGACT
273724891	94698	GGGTCAGUGCAGTTAGCTUCT	94699	CTCCACTCUCACCCATCAUCAC
273729070	94700	GGGUACTCTAACUCCCCCAAA	94701	GGGATGTTAGUACTCTGTTATTCUGGA
273733346	94702	GCAGGAAAGGUCCCCCAUT	94703	CCTCCCCGUTGAGTCCCAUA
273738559	94704	TGTCCCAGCAUCGCACAAUA	94705	GCTCCCTGUCCATGGAGTUG
273741341	94706	CTACCGTAAGCUTCATTAGATTTAAGUGT	94707	AAAGAATCUGAAACGTGGTCCAUGA
273741383	94708	AATTTAATCATTAGCUCCGCAAAGCUG	94709	CTTGGGCATACUCCTTAACTTCTTUCT
273750309	94710	ATCTGAGACCCCCACUACCUT	94711	GCTTCUCCCATCCTGAUGGA
273752064	94712	GCACGTTTTAAUGGAGTAACCGCUA	94713	AGCGAAGGAAGAUGCAAACUGT
273756816	94714	AACCAGGGAAUGCUGAAGGAG	94715	CCATCCUGGAGACACCCAUCA
273757086	94716	CTGGACUAACATCCGUAGAGACC	94717	ACTCTCATCAAAUCCGACATCGUT
273760220	94718	TGATTGAAGCUGCAAAGAATGGAAAUG	94719	CAAGTTGCCUACAAGTCAATGAAACUG
273769864	94720	CCTGUACCCCACCCTTGTUC	94721	CACCCTCACCUGACTTTTCTTCUC
273770211	94722	CCTGGCTCAGAUTAGAGATCTCGUT	94723	TGTGACCCCUATGGAGGTCUAC
273779730	94724	GCTGTCUGCTTGCATUCGG	94725	CCCCTCTGGAUGGGATTGAUG
273786510	94726	GCCCATATAAAGAGUGCTCCAATTUCT	94727	CCTTATAGGCUGCGACAUCAGG
273787572	94728	GGATTTCTAUGGGAACTCAGACATUCA	94729	CTTGGUCAGAAGAAGCCAGGAUAT
273787680	94730	TGGGTTGCUTTCATGTGAGUGT	94731	CGUATGATGTGGUGGGACCAT
273789607	94732	AAAGATCACCUGTTCTGTTGACUGT	94733	GGTTTTCAUTGCAGGAUGACGA
273792248	94734	AGAAGAACGTUCCGATCCTCTAUACT	94735	CCTGGGCUGCATTGGAAAUG
273792447	94736	CAAATAAGAACTUGCAATGAAGGGUGT	94737	ATGTGTGAATAAUAGCCACTCCTTTCUC
273792945	94738	ATGTACTTTAGUAATTTAGATTTATGUCGCCT	94739	GCAACTCCTTAUGGTATCGAATCTTTUG
273793030	94740	AACTACAAGTACAUTTCCTAAAATGTATTUCCA	94741	GAGAAGTTGUGAGAGAATTCAUGAAGGA
273794115	94742	GCCCTUCACCTATGCAAUCCC	94743	TTCTCTTTACCUCTTCCCACCTGUAA
273796572	94744	CAAAGUCACTAAUGAACAACACACCAA	94745	CAAGAAAGCUGGGCGUGAAT
273797805	94746	CCCTTCCAUAAAGGCTTUAACACAGAAT	94747	GGCATAGTUAAAACCTGTGTTTGGUT
273797969	94748	CAACAGGGACCUGATAUACAAGCA	94749	GAAATTUCCACCCAAGCATAACTUAC
273804615	94750	CTTGACCTUCACTCCCTUGGT	94751	CATCCCTGAUCACCCCTCUG
273808856	94752	GTTGTTCTGCAUCTTCCTCUGGAA	94753	CGTAAGCAGUATGAAGAGUGGCT
273812908	94754	TCAGTTTGAUGAAATGAACAGCTUCCT	94755	GTTCTCTGGUGTCTCCCAACTUC
273813570	94756	GATTTGGCAUGAGGACTGGUCT	94757	CATATGCUCATCCTCCUGGAACA
273817847	94758	CATTUGAAGCAGCTGTUGGGT	94759	ATTATGTGGTCAUGGTGAAACTACTUC
273819567	94760	GCAGGCCUTTCATAAGGGUCA	94761	GACTCATAUGCACGACCCTUGT
273822238	94762	TTACUCCTGAAGTUGGCACAGG	94763	CTCAGTCUGACTCTTTUGGAACAAGT
273825037	94764	CATTGTTAGTTGTAUTACTACTTGACAGUCC	94765	GTGCCCTTTGGUATGTATTCTTTACUCA
273825722	94766	CCTGTTTAGGUTATTGGAGTGAUGAGT	94767	CCAAAAATATTTCCUGTTGGCGTTCTUA
273827029	94768	GGGCTTGAACUGGTGTACCUA	94769	AGGATGGCAGTAUAACACATCAGATTUC
273828274	94770	CCACTCTGGUCCATAAGTGCUT	94771	GTCCUCAAGAAGCGGACCUT
273828717	94772	AATAATGCAAAGACCUCCCTTCUCAAA	94773	GCTCTCGTATTGAUTCGGAGCTTTTUAA
273829964	94774	TGAAATCTACACCAAUGACACAGTUCC	94775	GTGAGCCACCCAGCUCTTTUA
273830178	94776	GGUCGTGAGTUAGAGGACCCA	94777	AGTACCCCUACGTCTACATCTUCAG
273830269	94778	CCAGATUAAACCAGATGGCUGCAA	94779	AGATTTGCTGGAUACGTGACAUCA
273834567	94780	CTGTTCATGTTCUGATTCTCTTTGCTTUA	94781	GCCAGAGAUAACAGAGCTGCUT
273835307	94782	AAGGGACAGAAAUTCCAGGTCTUG	94783	CCCCGGCCUACTACTGTUG
273838101	94784	CATCTUCAAGTTCAGTUGCAGCAAT	94785	CACAGAUTCGAGAAATUCAAGGCAAG
273838365	94786	TTTCAGTTTCUGACCCATGUCACA	94787	GCAGTGGCCAUTTCATCUGGA
273844133	94788	CAGCTCCUAAGCCAGAAGAAAGUT	94789	GTAAGGCCCUTTTTGCAGTUGG
273844314	94790	AGCAACATCAUGGGCAGTTUG	94791	CCTGATACATGTUCCCAGACACCUA
273845717	94792	CTATCAAGAGGUGCAGGTGUCA	94793	AGAACAAACUGCAAAAGGCCCUA
273848468	94794	AGCTTCAUCAAGAGCTGCCUT	94795	AAAGAAATGCATUGTGTTGGGAGTUC
273849478	94796	GGGCTGCUGACTATAUGGGT	94797	CTCCACGACCUGTTGTAGATTCTTAUT
273850796	94798	CATCATACACCUCTCGCUCACA	94799	AGGTCCUGCTGAUGACCCA
273852533	94800	ACTTCAGAAATAUCAGCTAATGGGTCAUC	94801	TGCCTCACUCAGTATCTGCTGUA
273856047	94802	CCTCCATCUCCCTTGGCTTTUG	94803	GCAGGGCAUGAAGAAAACTGTUT
273856957	94804	ACTTTTGTTTCCUCTCGCCAGTAUC	94805	CCATCATCTCUGGGAGGTTACTUAC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
273860266	94806	GCTTGTGGCUTTACAAACACAUCAT	94807	GGATACAGAGUCCCTUGACACC
273864900	94808	CGGCUAAATGTGTCUGAAAGACCA	94809	AGGGTTTTACUAGGTCCTCAAUGACA
273864922	94810	CTGCTCTCCUGTGACCAAUCC	94811	AGAAAAGCACACAAUGGTTAUCGAGT
273865504	94812	CCTAGCTGUTCCTGAAGATUGGG	94813	CCCACAUCCAGCAGTGAAUGAA
273871689	94814	CTACCCAGCAGCUGGTACUC	94815	GCTTATTTCCUCCAGTCTCTGTTCUC
273872082	94816	GATCACTGGUTCCAGCTGCUA	94817	TTCCACGACAAAUAATGACCCCTAUG
273874657	94818	ACATATTTCCAUTGCCAGGCUGA	94819	AGCUAAAATUGAAGCCACACAGAAAC
273882982	94820	TCCGAATGAUGGTGCCAAUGT	94821	CCCUACAGCAAGCAGTTTGUG
273883185	94822	CCCUTGAAGGAUGGGCAAAAGA	94823	GGCAUCAAGGCGATTGTCUGT
273885182	94824	GGTCTAGCUGCGTGAAGCUG	94825	ATGGUGCAGCGCATGUG
273885232	94826	TGAAGCUGUGCAGCACCA	94827	CGCUGCGAGCCTUCCAT
273886790	94828	TCATTTGAAGGCAUGGTCATUCAGA	94829	TCAGGAAUCAGGAGTTAGUGAAGAAGT
273888046	94830	CGCTGTTCATCUTCGGATTCACUA	94831	TCTGTTTTAATGUCGAGTCAGTGGUAAA
273891216	94832	TGCATTCUAGAAAAATTTGCTUGACAACT	94833	GGAGCAGCAGAUATTGATCATAAACTUG
273893468	94834	GCTGCTCATUTTTCACCTGTUCAA	94835	CCATGATGGUAGTTTTCTTCCTUAACCT
273894474	94836	CTCTGTAGTCTGUTCTTGGAAAGCAUAA	94837	CCAGGATTGUGGATGATCUGAAAGA
273895867	94838	CCTAGGTGTGUCTGGAGGTTTUG	94839	AGAAGAAAUTCTGCUGCACCAGT
273897311	94840	CATTTTTCTGUACTGTTCGGCTUCA	94841	CCTTGGAAAAGCAGUCTAAAAGGTTUT
273899463	94842	GCCCAGACACUCTTCUCACAT	94843	CTTCCTCTAACCUGATGATTGTCACTUAC
273903439	94844	CCGGTACUGAGATGACTUGGAGT	94845	TGAGGGAGAGCUGTCTTGUCA
273906826	94846	CCTATCTCATCGUCTTATATTGGCTUCA	94847	TCTCTGGGUTGGAGTGGAUGT
273914282	94848	ACCGATGAUAAAGGTGTACAGTTTUCC	94849	CCTCACCGCAAGUGTTTUCAC
273916896	94850	CCTCCCGCCAGCUTTCAUC	94851	GAGGCCAAAGUTGTTGAUGCC
273920439	94852	CGCTGUGAGCAGCAUGAAT	94853	CCTCCGGGCUCCATCUGA
273923662	94854	CATGCUCAACCCCACTTCUCT	94855	GCTACAGGCCUTGTCCTUCAT
273926165	94856	CAAAGCUACCUCAGCAGCGA	94857	TCGTACTTGAUCTTGCCGTTCUG
273926655	94858	CTCAAAUGGCACAGCTGCTUA	94859	GCTTCCTUCAAAGACTCCTCUGG
273927941	94860	CCACAGUGCCTTCTCCTTUACC	94861	AGATTCAUGGCTTCGUCGCT
273936388	94862	CUACTUCCCAGCAGCAGGAC	94863	GGGTTTTCAUCAGCTGACUCAAGA
273937210	94864	CTTCCCUACCCGCUGAAGAAG	94865	AAAGCAAGCUAAAUACAAACACAAGCAT
273941488	94866	GGGTTGAAGACUGGGCTUGT	94867	CAGACAGUGATGAACCUCAGGA
273943268	94868	CTGACATGCAGAAUATATTGGCAGTUC	94869	TGAGATTCAUGACCGGTCTGTTUAC
273946986	94870	AAUGAAGAAAGAGTUCCCCAGCA	94871	GTACAUGGACAGGCAGACAGAUAC
273949165	94872	AAAGCTGAUGGTGATGATGUACAGA	94873	TCAACCAGTUATGAAATCAGUACCAACC
273949224	94874	CCTCTCAGUTCCCACGCUAAT	94875	AGTCTTCTCTGACUCACTCTCTCUG
273949545	94876	GGCAGUCAAGGAGAAACAGTTUT	94877	GAGCAGAGCUTAGCUGAAGGG
273949908	94878	TCAATTAGGTTATUTTGAAGTGGTGTUCCT	94879	TGTTGTTTGTGAUGAAGGCCATATTCUA
273950509	94880	GCTTTAGAAACAGCAGAUGCTTCATTUT	94881	CCTGTAAGAUCAGCACTTTAAAGGGAUT
273954148	94882	ACCCTTTGUCACACGTAUCACAC	94883	GTGCAGTUCCCAGGACTGAUT
273955008	94884	GGATATGCUGAACTAAGTUGCCACA	94885	CCAGAGCAGGGUTGAGCTUAC
273959429	94886	CGCTGTTGCUTCTTCTTCTCAUC	94887	ACAAAGTGUCACCCTGCAAGUT
273961901	94888	GTGCTTCTUACCACCCCTGUC	94889	TGGTATTTGGUAGAGGCGACGUA
273970301	94890	GTACAACTGAUGATTCCACTUGGAAA	94891	CAGTTGCUGCATGGUAGAAAACC
273971325	94892	GTGGTTUCAGACACCCUCACA	94893	GTGTACCUGCAAGTGGGTAAUAAAAGA
273974839	94894	CAAGAACTTGAUGAATGCTGUGGT	94895	TCTCTTCACCAAUGGCTTTTTCUCT
273975205	94896	CTGTGACCUTGGAGACUGACA	94897	TCAUAAAGGCATTUGGCAAGGGT
273975316	94898	AAAGAAATTACCUCTGCCTGAUCCC	94899	GCAGAAAAAGCUAAAGCTGGAGAACUA
273977618	94900	AGTGCTAGCCAUTAGTAACAUGGAAG	94901	CAGTATGTGAAAUGTGGCTGACTTUG
273979995	94902	CTTTUCAGCGACAGCGGTUT	94903	CUTATCCTTTTUGAGGAAGAGGAAGCA
273982179	94904	TGCTGCTCCAUTGACGACTUT	94905	GTGATTGCGCUAATGGTAGAAAAAUACA
273989940	94906	CTAAGTAGTAACCCUAAATTTGATTAGCTUCA	94907	TGTCTTCACAUACTGGATTTUGCCAAT
273989997	94908	TTGCATACCUGAAGATUGGCAAA	94909	CTGACATTACAUCCTCATCTTCTTCUGA
273990205	94910	AGTATCAGATGAUGAACAATCTTGTCUC	94911	AGGGAAAGGAGAUAGTTGTGACTCUT
273991601	94912	ATTGGCAGGCAAAUGAAUAAAAGAACAT	94913	CAATTCTCATTGUTTCCCAGCATUCC
273992254	94914	GAAGTAAAACUCTGCTCTTUCCCAGAA	94915	TGAUGATGCUGAAAGAAAACAAGAGAGA
273992345	94916	TTCTTCTCTCUACCATATGCTCCATUCT	94917	TGGAACAACUGAUGGAGAAAAGAAAAGT
273996984	94918	CCTGCTGTGUCATGGAAGAUGAA	94919	GGCAGACTUAGATGCTGTCCAUA
273999563	94920	CCTGTTGACTTCUCAGCATAATCAGAUA	94921	CTTCATCTGAUGGCACTGAAAAGTUAC
273999827	94922	GGAAAATGACAAAUTTCTTCTCGCUCA	94923	AGAGCGAUGAAACTTCTGAAGAUGAT
274000677	94924	CGCCTGAGTCUTTAAATCATACAAAGUC	94925	AGATTCTGAUGAAATGCTAGCAAUCCT
274001249	94926	CTCTTAATTCCAUGATGGTCGTGTCUT	94927	CUCTTCTGAAGAUGAGAAACACAGCA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
274001506	94928	GACTCATCCUGCTCACCTCTUT	94929	AGGATAAGCGTAAUTCTTCTGACAGUG
274002624	94930	GTTTAAACTGUGTAGGTGGAAUAGCAA	94931	TCUAGCACAACAAAGACACUGAAACAT
274005442	94932	CTATAGCACUGTCAGAAGAATUACGCT	94933	AGATCCCCACGUGTAAAGACUACA
274006160	94934	CAGTTCCCTTTUTGCTCTGCTTTUT	94935	GCAAGCATCUCAAAACCAAAACATGUA
274007285	94936	GCTTCCCTCACCUATAGAATTCTGAUCAT	94937	AAAGAAGGCAGUCATTGUCAAGGA
274009500	94938	TTCTGTCGGUCGCCUCAAG	94939	TTGTGGTCUGAACCCCAAGUT
274009735	94940	GCCCUCAGCGAGTUCAAAG	94941	ACTGGTTCAGUCTGCCCATUT
274012212	94942	GCTTGTTCTUAGGGAGTTTCTCTTTTUC	94943	AAGGAAATACAAAGUGGCTCATCAUCA
274013208	94944	AGCTCTTAGCUGATTTGCCCUT	94945	GATGAGTCACAGUTCTTCTTCAGAUACT
274014805	94946	GCAATATCAGAUAAGCCATCCTGTACUT	94947	GCTTCCACUGATGGTGTCGAUA
274015843	94948	GATGATGAUGAGCCACTTTGTATTUCC	94949	GGAAGAGACAAGAUTGTTCATCATCUGA
274016450	94950	CCTGTCCAAGUCCACATTTCUCT	94951	TCACTCCTGTUTCCCTTTCTAATUCC
274016571	94952	ATGATGAGCCACUTTGTATTTCCTUAGT	94953	CUTGGAAAGAGTUCAAGGAAGAGACA
274019585	94954	TTCCAATGCAAGAUGAGCCTTCTTAAUA	94955	AGCCAACAUGAACTCCAGTTAUGT
274021766	94956	CAAATTTGAGAACUGTAGGGTCATTGUG	94957	TGTGCACCGCUTACTAGGATCUA
274022240	94958	CTCGACCUCGCCGATTCUT	94959	GGGCGTACUCACCTTCTUCC
274022360	94960	GATTTCTGAATTAUCTGTTGCCTGCUT	94961	GAAATTAGATGATUCCTGTTCTGGCUCT
274023876	94962	AGTGCGGAAUAAGAGTAGGTUACAGA	94963	CAGTTGUTGCAGCAAAAUAAGAAGAAGAT
274024423	94964	GAGCCAGAACAGGAAUCATCTAATTUCT	94965	GAGAATTUAGAACAGTTGTUGCAGCAAA
274024513	94966	TCTTCTTCTTATTTUGCTGCAACAACUG	94967	GGTCGAAAGGAGUTGTCCACAAUA
274024613	94968	GACTAUACGCCAGCATGTUACC	94969	GCTGAAGCAGCCUAATGTACCAUT
274025845	94970	CGGCAGGGUCTGGGUAAGA	94971	CGCTTGTCCUCCTCCGAGUA
274027307	94972	ATGGTGTTUAAAAGAAGTAACCCTUCCA	94973	GGAAAGAUCGCCTUCAACCAGAG
274027526	94974	AGAGCACGUTCAUCAAGCAGAT	94975	GCTCACCTUGTTCTGCTCGUA
274028676	94976	TGGCTTATCTTUGATACGTCGTTCUAAAA	94977	TGTGAGTGUAAGCCAATAUGAAGAACAA
274029194	94978	CGCCAUGCAGGCCAUGAT	94979	CACCAUGCUCACCACCAAG
274029522	94980	TGCTTTAGTUGCATCATTGUCAGAGT	94981	TCAGGCCAAUTAATTTTATGGTUCCCT
274031429	94982	TCACCAUTGCTTGTUGGAGGA	94983	CAGATGTCCCAUCCATGGGTUT
274031774	94984	CCUCACATTCTUCCACCAGAGAAG	94985	CUGGGATAAAAGTUGCAGCAAGG
274035281	94986	GCAACCATUCCTGAAGGCUGA	94987	GGCCCCCGAUAGAGTTTUCC
274036060	94988	TGGCCAAATTUGAAAATTGATACTGCUT	94989	CCCCCATCTUAAAGAACAGACAUGA
274036071	94990	GAGTUGAACCCAGCCGUGA	94991	TGTTTCAGGCCCAUCAGTGTUT
274038201	94992	GCAAUACGACCAACAAGATCAAUACAAT	94993	AGGAAAGUGAACAAAAGTTGCAATUCAA
274041543	94994	CCATTCCAGCCCUGAGTCTUA	94995	ACTTGGTTCUCCCCTCUCCAG
274042172	94996	GATTTATUGGACCACATGCUGACAC	94997	TCGUCUAAGGCCCAGGGAAA
274045627	94998	TCTTCACAGCAUTTGATAGUGGCT	94999	GCAGGTTCAAUTTGTTTTACTTGUGAT
274046587	95000	GGAGCUCCUACAGAGGCAT	95001	GTGCCGGAUCCTCAAGAACUT
274051097	95002	TGATAGAGTTGUGAGACTGGGTAGUT	95003	TGAAUTAGCTAGUAGGGAGAAGACAGAAG
274051863	95004	GAGGAUGGCATACAGUGACGAG	95005	CCTGGGTGUCTGTCTCATUAGGA
274052304	95006	CCCCGUCCAAACAGGACTUAT	95007	GTAACUGCTGGACUCCCCAAG
274052411	95008	GCTTTGTCACUCAGTCAGGAUACT	95009	GCCTGACAUCCCTGACTCUGT
274052725	95010	GGTTGATTCUGTGGCTACUGACC	95011	TCTGGGTGAAUAATACAGCATTUGCAT
274053221	95012	GCCCAACUCAGTCTTCTGCTUAT	95013	GAAAGGAATCUTTCAGGACACUGAAGT
274054673	95014	CGACACAGAAATAUTTGTAGCTCACCTUT	95015	TTGTTTUCAGCCAGTCCCUCAT
274070974	95016	GGACCTTCUCAGGCTCTCUGA	95017	GTACCACAGAAUTGCTGCTUCC
274078084	95018	GTCCTGGATTUTTGCTTCTCATUGG	95019	CCCCCAAATTUGATCATGAATCCTUCT
274078500	95020	TTCTTAGAUTGTTCACGTUCAGACAACT	95021	CACCGCAAGUAATACTGTTTUAAAGCAA
274083392	95022	AGAAGTTGUTCTAACGCUGCCT	95023	GAACTGTTTGGUGTGCAAGGTUT
274087077	95024	TCCTCTCATATCAAUCTGCTGGTAGUT	95025	GCTCCAGCAGCAGUACAAUCAG
274093861	95026	TGATAAGTCATTUGTTGCTGTTGCUG	95027	TTTTGAGACAGGUCATGCACTTGUA
274094385	95028	GCGGCGCUTCUCGGAAA	95029	GGGAGGAUGUGGAGGAGACC
274095346	95030	CGCUGAGGCUCCAGGAC	95031	TGUCCGCACGTUCAAGAACA
274100283	95032	GCTGCUCTCAACAUGCGAGT	95033	TCCGCTTGUGTCTCCAGTUG
274104082	95034	TCTACCCCUCATGAAGTUGCCT	95035	GGATTATGUACAAGCCACTTCCUACA
274104583	95036	GGAGATGGACUTTGAGTACTUGGAGAT	95037	CCCAGCTUGGTAAGCAGCUC
274104685	95038	CTTTCTCATCUGTACCCCACGUC	95039	GACTCCAATCCUAACGAAAATGAUCCA
274152802	95040	ATTTATUAAGGCACCAGCCUGAGT	95041	GGAAATGTUGCTTTTGTCAUGAAGAAG
274158370	95042	CTTAUCCAGACAAATUCCAGGGACT	95043	TGCCTGUCACAACTUGGGAAA
274158694	95044	GAAAAGAATATATGUGGCTATCCGGUGA	95045	CTTGTACAUGCAACCTUGGAAACA
274160800	95046	GGAATCCAGUTCAGAAATCUGAGCAA	95047	ACTGTGTCAGTUTGTAATGGTAAGUGT
274166332	95048	TGGTCCATCUGTCAATCCAUCAC	95049	GAAGTGGAGCAUTCATATTGTAAUCCCT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
274173378	95050	TGACACCUCACTTCCTTUGCC	95051	GCGGCCAAGUGTTACACAAAUT
274182987	95052	ACAAGGTGGTUTAAATGTCCCCUT	95053	CAGATGAGCUGAAGGUGACAGT
274185591	95054	GTCCUGCGAAGGCACTUG	95055	TTTTCATUGGCAGCCCCACUA
274185630	95056	CTTAGCUCCAGGGTGTCAACUT	95057	CUCCTGUCGAAAAGCGAGAAGA
274188037	95058	CGUCCGCAGAGGUAGACAA	95059	AGCCCGUAAGACUGACCGA
274188775	95060	GGGAAUGCGGAGATGUAGGG	95061	CTAGTGGGUGGCCTCTCTUG
274194055	95062	TCGCCAAAGAGCUACCCATUC	95063	GGGAGAGCUATGGGCTGUC
274196119	95064	TTTGGCTTTTCTUCCTCCTTCATTTTUC	95065	AGGAGTTTUCGGAGCTCTTCUC
274197231	95066	CTTAGCCGAGGCUTCAGCUT	95067	TCAGUACAGCAACAACATCUCCAC
274200063	95068	ACCTCTGUGGGACATCCCTUA	95069	CTTGTATGUAGCGAACGCACTTTUT
274203322	95070	CGACGGAGGGCGUAGUG	95071	CCTUGGGCAAGCCUCAAAG
274205736	95072	CGAACUGATTTCCTUCAAAGACGAG	95073	CGGAGGAGCUGTTTTGATTCGUT
274207048	95074	ACTTCCCTTGUCTGTGGTTAGAUAAGT	95075	AACCATGCCAAAAGUTGTACCUAGAA
274209126	95076	GTCAAATCGTCUCTAGTCAATGAAUCAGA	95077	CGATTUCTCCCCTTUCAGCAACAT
274209251	95078	CCTGTGGCUACTGTGTAGTTUGT	95079	CCATGCGTTUCACTTTCCCUCA
274212392	95080	GATAACTCTCUCCCCTGTTTCUAGGA	95081	GTCTGCTCAGUCTGTGACTUGG
274215023	95082	CCCUCCCCGAACCTGCUA	95083	CCTTGUGGGTGGCCUCA
274221897	95084	GCTGUCGCTCGUCACCA	95085	AATGTAGCCACAUGGCACAAAATUAAG
274227048	95086	CAATTCTAGGUACAACTTTTGGCAUGG	95087	TGACUCAGGTCTGTUAGGGAACT
274229552	95088	AGGCACCGUGGCUAGAGA	95089	CCTGTCCUCTACCCUGGCA
274230722	95090	GGTTGGCCCCUGAGGTTUG	95091	CCTTATCUACAGGACCAGTCCTUG
274231820	95092	CTCTACCTGCUCCACTCTACUCA	95093	AGAAGCUACUCCGGGCAAAG
274231927	95094	GATGGUGGAGGTGUGGGAT	95095	GGGCUGCCAACCUCAACT
274231949	95096	GGACATUGAAAAAGAACAAAGUCACAGT	95097	CTGCACAUTCTTGGCUGCAAA
274232217	95098	TTTCCCAGTUGGAGTCATTCGUT	95099	GGCAGGCAAAAGGUTCAAGAUG
274233230	95100	CUGTCTGTGGUCCAGGGAAG	95101	CAGCUACAGGCACTCCUCAT
274234535	95102	CAAATGCTAATACUAAAAATGAGATACCTUCCT	95103	GACAAGAGUCGACACAATTTUGGAAT
274234778	95104	CAGATTTUAAAACCACCACTTGCTUACT	95105	GCAAAGAATGGCUCAAGAAGTACUG
274235326	95106	GGCGTACUGCCTGACUCT	95107	TGGGUCAGCTUCGAGCAC
274235752	95108	GCCCAGCUCTCCCCAAUA	95109	GUGGGAGUGGGAAGGAAGG
274236587	95110	CCCAGUGCTGAGTUGCACAT	95111	GAGCCCAGUCAGUGAAGAGG
274239083	95112	GCATCAGGAUGCTCCTTTAAATGUGT	95113	GAATTTGTGCCUTGCTCAGTAGTTUT
274241245	95114	ACCCTTTTCTTCUTCATTGCTCTTUCA	95115	GAACAUGATTCTCTTTUGGACCACAAAG
274243448	95116	GCAACACCUCTTTTCCCAUCCT	95117	GATCAGGGATGGAUCGAACTTTAATCUC
274244696	95118	CCCCTATUGGCTCCCCATUG	95119	CTGGACCAGGUGAAUGGACAG
274245997	95120	GCTGCTTTTCUTTCTTCTTCAGUCAA	95121	TTGTCTCTTATTUCAACCCCTCUAAACAG
274246902	95122	GGAGAATGUGATATTTCTGCAUAGGGAA	95123	GAGCCCTGUCAGCAATGAGUA
274248347	95124	GAGGTTCCUGCTTGATGCUGA	95125	GGGAUCCCCCAGACAACCUA
274250697	95126	CAACTCACCUCCAGCTGTUGAT	95127	GGGACUGACCATGCGTTUCAA
274252120	95128	AAGCATATCGCAUGCCACTCUAAT	95129	GCCTCTACTTCUACAGGATCTTTUGG
274252586	95130	CTGCTCTGGCUTCTGGGTUT	95131	TCCCUCCCACCCAUCCAG
274254359	95132	GGGTAAATTGGUCCCAGTTGGTAUG	95133	CCTGGATCTGAGAAUGTGGATTCTTUT
274254905	95134	GGGAATGAAGUTTCCATGTCUCAGA	95135	ACTGGGCCAAGCAUATATTGAACUG
274256503	95136	CTUCAGGAGCCAGUCGGT	95137	CTGGTCCUGCCCAGTTCAUT
274258653	95138	TTCTTGGCAAUTTTGAAGTTCUGCAA	95139	AATTCTGTUCCACGACAGGATUC
274260207	95140	ACTCUGCCGCTCCCUAAGAT	95141	GCAGGATUGGAGGGTTCUGAG
274260245	95142	AGCCAGCCACAAAUGCCUAA	95143	AGCCATTACCUGTTGCTGCAUA
274260440	95144	TCCAACCGGCAGCAAUGUAT	95145	GAACAAAAACTCUACCACCATTCCTUAC
274263725	95146	TCCCAGTCCUTTCTGTACATTGUG	95147	CCATGUCAGCTCGCTTUCCAT
274267917	95148	CACCCTGAGUAACTTGGCTAUGT	95149	CAGUGCTAUCACAGAAGCCCAT
274268865	95150	CCGUCAGGAGCCCTATGUCT	95151	TCCACAGCUAAGAAGATCAGTATCTGUA
274274633	95152	CCAAGTTCAGGUCCAGGAGUT	95153	GTAGGAGGCUCCCAAGCTTUC
274275690	95154	CTGCTGTTCUTGCCTTTCTUGAT	95155	GGCCUCAAACAAGTCAGTCUGG
274279238	95156	CCUTCTTGTCAUCAGGGCCAA	95157	GTGTGTGGCUGACAGAAACUG
274280525	95158	TGACTCACCUGGCTCTTUCAC	95159	TGGTAAAGCCUGTGGGTGAGUA
274285742	95160	ACATGGAAGGUGGCAUGGT	95161	CCAGCUCATGCCCUCCAG
274290336	95162	TGGUCAGGTUACGCAGCAAG	95163	TGTCTCAGCUAAGGACATAGGTUGA
274290898	95164	GGGTCCAGACAUGCTACTGGUA	95165	CAGTAGTCTCUAGGGTAAACCATGTTUT
274294288	95166	TGTGAGTTATTUAAAGGCCTAGGCATAUC	95167	GATTTGGATTUCCAGGAGGTAGUCAT
274294675	95168	GCTCTTGACUCGGCATGGUA	95169	ATTTGGCAACATUTTGTATGTACAGTUT
274295628	95170	GGAUGGAGCCAGGCGUT	95171	CCUGCCCAGGCCATGUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
274298971	95172	TTTGAGTTCATTCUTGCTGAGTTTGTTUT	95173	CAAAAUCAGCAACCGGGUAACAG
274299635	95174	AAGAGCCCUCATGUGGCAAA	95175	GCTCATUGAGGACCTGTUGGAG
274301341	95176	AGGATAGGGUGCTCGCTGAUA	95177	TCTATCCTTCCUCACTGCCCUAAG
274304312	95178	CGAGGCAACAUGGTUCGG	95179	ACTAAGGAAGGCCAGUAGCAAUCT
274310649	95180	GTTTACCUGCACACCCUGAGAA	95181	TCCCCAUCCAATCATGTGUCAAG
274311050	95182	CATCCGCCUCATACCUGACAT	95183	AGGATGCCUTCCGAGATGUG
274312505	95184	AGATTGCTAGACUCCACCCUGT	95185	TGAACGCACCUTATAGTAAACAGTTUGT
274314469	95186	GAGACUGAGAGGCAGTGTTTUCA	95187	GCCAAGCTCUATGTCTACATCAAUGAG
274314509	95188	CGGUGCTAUGAAAGGAGGCAAA	95189	CTCCAGTTCTCUCAAGTTTACTTGCUAA
274324061	95190	GGCAAAACTTGCUTGTGTGTGTAUA	95191	CAGCTGUACTTAGTCCUGCGA
274326728	95192	CGCTCCUGTAACCTGAUGCC	95193	GCATUGAGCGGCTCAUCAAC
274328061	95194	GGCCTUGAGAACAGUGCAGA	95195	GTGCCCACUCTCTGTTTTUGG
274328501	95196	GCAATGGAGUTGGCTGAGUGT	95197	CAGGACCCTACUAGTCTTTTAATCTTGUT
274336215	95198	GTACTGCGAUGACTTGGAGUGA	95199	ACTCAGAGGTATCUTCAGTTTTCCTTGUA
274336321	95200	CCCUAGAGAGGATGTUGCAGAAC	95201	TTCCCCUGAACCTTCTAGTUCCT
274339719	95202	CCCCATAGUCAGGGAAGGTAUCAG	95203	CCTCTTUGGGCGACTATGUGAG
274349754	95204	TGCTGTCTGCAUCTTACAAAGTUCA	95205	GATGGCUGACTGGTTCUCCT
274351964	95206	GATACCACTGTUTCAGGTTCCTCUAA	95207	AGACCTGAAAAUGTCTTCTGAAGUGAAG
274355724	95208	GGTCAGUGAAGAGCAGTCTTUCA	95209	GCUGCAGGAAAAGGAGTUGGAT
274357394	95210	GCCCGGCCTUCATTTTCTTAAATAACUA	95211	TCAAACUTGUCCACACAGCGT
274358298	95212	GUTGTCCTCGTTAUGGAGAAAGAAGA	95213	TGTGGCAATATTUACCTGTGTCTTUGT
274362058	95214	ATGCTATTCCUAAAGACATTAUGCCACAT	95215	CAGCCUCCCUCCCAACAC
274362413	95216	CTTCCTGATTGTUATGAGGTGGTGUT	95217	GCTTTTCCAGUTACCAAAACTCUAGGA
274364891	95218	CACATTCAGATUGTTAGAAAAGCAUAGG	95219	CCTCAGATTCUGATGAAACCUCCA
274365520	95220	ATTTTATGCTCUCCCAATAAGCUCCAA	95221	GCATGCUACAAAAGAGCUCAACAAT
274368103	95222	AGCTTAAACTCAUGGAGGTTTCAUCA	95223	CTCAGCTCGUGCCAATTAACTTATUC
274369973	95224	AGGGCAGCUGAAATGGTTUAGG	95225	CCAGTTGUGTATTGTGAAAUGGCAAT
274371701	95226	GTCTGGGUCATCCAATTCUGAGAG	95227	TCTCCTUGGACCCCACAAAUG
274377363	95228	GCTCTTCTGGACUAAGTGTTGATUCAT	95229	TGATAAACTATUGGTAAGTGATACUAGCAGAAA
274385132	95230	ACTGTAGTCCAUTCATTTAAAACUGGCT	95231	GAAGCCUGACAGGTGAGATACUG
274393388	95232	CACCAGAAUCACTCCCCUCAA	95233	GAGCATGAAGAUCCCCAACUCC
274394971	95234	CGACAAAUACCCACATGCTGTTUT	95235	GCTGAUGAAGAGAAACATAAACGUCAAAT
274397103	95236	CCAGTUCACGCAGTCGTCAUT	95237	CAAAAATACAGGUGAACCCTUGGAC
274398698	95238	ATTUGGGCAAAGCCAAUGCAA	95239	GCCCACTTTCUGATGAGGAATUAGA
274403011	95240	ACCTTATATCCUTCTGGGAACAUAGCA	95241	GCTTTTCTTGGUAGGTCACATAAUGAGT
274403466	95242	GCCAAGCCUGAAGCTGTUC	95243	AGCAAATAATAGGATUGATCTTAACTGTCTTUT
274407104	95244	CCAATCCAGCUGCATTCATTCUC	95245	GCAGAAAUCAAAGAACAATCUGCAGAA
274407115	95246	TCTCUGGGAACAGCACCTCAUA	95247	ACTTGGCTGAUATGTTTCTTCCAUCC
274409819	95248	GGCCCACGAGUCCCTUG	95249	CGGUGGCACACGUGAAGT
274413113	95250	GACAGCGACAAGAUCATCTACUCA	95251	CGTGTCUCCATCCCGUCT
274413847	95252	GCAGCAAAGAUGGAUGGAAAGGA	95253	GGGCAGATTTTUCCAATTTTACACUT
274416260	95254	GGATGAATTUCAGGGACCCUCAA	95255	CGAUACCCCCACUGACGAG
274418510	95256	TTCCTACTTGGGAUTTTCAGTCATTUCAT	95257	CACCTTGUACAGGAAAAGACATTTGUG
274422532	95258	CAGGTTTGGAGUCTAAAAAGTUACCCA	95259	TTTAACAAGATGCUTCTCGGAGTUCT
274423175	95260	CTTGGCAUGCAACGUACAGAG	95261	CCAGTGTGCUCTCTAGGATTTGUT
274426231	95262	TGGTGATACAAUGGCACAACATUACA	95263	CTCAGCUCAAAGAAGAGTATATCUGCAT
274428095	95264	CTTCAGAUACAGGGAAAGTAAAGTUGGA	95265	TGATGTTTCTGUCTCCTTTGGAGUAAC
274432685	95266	CAAGTTTGAATUCAGATGTGCCUCAG	95267	CATTTGUAGACCGAACGTCAGAUGA
274434358	95268	GCTGGUCAGACAGTTCAGCUAA	95269	TGACTGACAGUAGGAGGTGGUC
274435304	95270	CAACCAATCTUCAAATCTGACUGCAA	95271	ACTTCACAAGGAAUTGGAGCTTUACT
274438115	95272	TCAGCTCCCAGGUGTTTACAAUAC	95273	TCAGCAATGCCTUCTCTTTACCTAGAUA
274438194	95274	GAACATACCAGCAUGTACTTCUACAGT	95275	TGAGACAATATTGGAUGCAGAAGTTGUT
274447625	95276	GTCTUCCAGAGCAAGGGCAUAT	95277	GATTTTGATTUCACGAATGGCTGUGA
274451720	95278	AAGTATCCCATUCTCCTGCCCUA	95279	GGGTCACTGATUGTAACAATTCTAACUC
274457301	95280	TCCTCUACCCCTCAAUCACAGG	95281	TGCATTCGACUGTTGAGGTUGA
274459612	95282	AATGCTCCAGUGACTGTCATUCAA	95283	CAGGTTGUGGCCCTGTACTAUG
274467186	95284	CAAUGAGAAAGAGGGCTUCCCAA	95285	CCAGTCTACCCUGTAAAAATGTGATUCT
274467277	95286	CAGTCGCAGGAAUTCCAAATAAAGUAG	95287	GTTGGTGGAUGCTGTTGCTTUT
274471475	95288	GCTCAAUTACGGCUCCAGCA	95289	GGACAGGCCUGCTTCCAAATTUA
274471919	95290	GCTAAAGTAGCAAUAGAAAGTGCTGTUC	95291	AGATGAGACAUGGAAAACAGUGCAT
274473703	95292	TCAUAGCACCCCCACAGTAUGT	95293	CCCTACCCUTGAGGCTTGUG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
274473710	95294	CCCCAACAAGUACAGAUGCAAGT	95295	GCTTACCACCUGGTGTUGAAGG
274478288	95296	GGAAAGGGAAAUAGUGAAGAGAGGAA	95297	CTGGGAGCAUCACAATCATATUCAAC
274480689	95298	CTGCCGAGACUTATCUAAACCAGAA	95299	GGTACCACAGUACAATATTGCACUACAA
274484547	95300	CTCCACAGAGUTCTGTTGTUCAGAAT	95301	GTCCTGGUACCACTGTGTGTAAUG
274487647	95302	TTCTGCTUCCGAAACGUGGT	95303	AATAGCTGCUGAGCTGGAGTUT
274491275	95304	TTACTATTGCUGGTGTCCCAAGUC	95305	TGTTGAGCUGGCTGGCTUAC
274491731	95306	CCATCTGTAATUCCACAGCAGTCUC	95307	GGTGATTAACUGTTGACCCTGUGAA
274506632	95308	AGUAACCAAGCCGCAGGTUT	95309	TGAGATCAGUGGACCTGGCAAUA
274518607	95310	CAACCCAACAAAGCGUAGTGAUT	95311	GAAGATGGAGUTATGTTAGGTTGUCCAG
274521144	95312	CAGTTGCTGGUACTAATCTGCTGUAA	95313	GGCAGTATTTGTUCAGAAGATGACTGUA
274528239	95314	CTGGGTTCTGCUTCTCAACTAGTTTATUA	95315	CTGCUGCCAAAGGAGACUCA
274529213	95316	GCTGCCAUATTGGGAGUGGAT	95317	TCAGAUATAACUGCCCCACCGA
274530885	95318	CAACAAGTGTTUCAGAAGTTCATUCCC	95319	GCCTAAATUGGAGGAACAGAAUGGT
274538891	95320	GGTAGTTTCUGAGATGCCUGGAG	95321	CCAATCGCTCAUTCAGTTGTATTCUGAT
274542821	95322	CTACAGCGTTUCCTTCTACCTUACT	95323	CAAATCAACAGACGUATGCAAATUCAGA
274547317	95324	TGGTGGATTCUGCATCATCATCUC	95325	AGTAGCTAAUAGCAGTCTCCCAUGT
274550060	95326	CCTTCGCTCAUTAGTCTGCAUGA	95327	CCTTCTACAGTUCCGACTTACCTUG
274558184	95328	GTGTCCATGGGUTATAGTAGAATCTUGG	95329	TUTTCTTCTGUGAAGCAGGGACAT
274561382	95330	ACCCTTATCTGUAAAAGTCTGAGUCCT	95331	CAUATTACTCACCUGCGACCACAT
274563218	95332	GTTTCCAUGGAGAGCTTGTCUACT	95333	CAAGAGTCGGUGGAACCAGUC
274564223	95334	CATTGCCUCCACATGGCTTUAG	95335	GCTAATTTACUGCAAGTCGAGAGGUAT
274565212	95336	TGTTTCUCGAGCAGAAATGTATTCUGA	95337	AAGAGATGTTGUAAGTGACGTAAAUGGA
274566705	95338	AGTGACTGCAUCTTGGCTTTUACT	95339	GTATTCUCAGAGCAGGCAGCUA
274567805	95340	GGGTCCUAGAGGTTGCATAAAAUCA	95341	AGGTAGAUAGACAAAGAGCTTUGCAG
274569972	95342	AGCTGGUCCCAGAAAGATTUCC	95343	AATTAATTCACCCUCCACCCAAACUT
274570497	95344	CATCTTTATTAGCUGCCTGCTCUGA	95345	GTGATGATTUGCCCTTACTCAUACAAAA
274583113	95346	GCTGCTCCAUTTCCATCCTCUG	95347	ACCACCACCUCGGGTAGAAUT
274584780	95348	GTACCGGCUGTGTTTATTCUGAGA	95349	GGAGAGTGUGCTGGATUCACA
274588668	95350	GACTTGAGGCAUTGTTATTUCAGCAT	95351	CAGAAAAGUGCACCAAACCAGATUC
274590562	95352	GGAUGGGAGGAAUAGGAGGCAT	95353	GTCATTGTCCCCUTCTTTCACUCA
274592046	95354	GACCATGACTUAATGGGACTGCUA	95355	CCGATGCAGGAAAUTCTTTTTGUGA
274592761	95356	GTCCCATGUCCCATGAATCUAAGG	95357	ACTTTCUGACGGCCATUGGG
274594084	95358	ACAGCTAAUGGAAGGATTGGAATACUG	95359	ACUAAAAAGGUCAGAGGAGAAGAGGAA
274599636	95360	AGAAAAGCAACUGGATGCGCUA	95361	TGCAAAGUCCCGACAAUACCA
274601735	95362	GGGTTGCUTTTTGGAGUGCT	95363	GTGACGCUCTCTGCTGTUAGA
274604614	95364	AGGGCAACCUCCACATTCAUC	95365	GTTTCTGTCAUGAGGAGGGUGAC
274605373	95366	ACTTTCACUAAAGGGATTGTTGTCAUCA	95367	CTCCTAGAATUCAGCCCCCAAUT
274609702	95368	TGGAGGAGCUTCTGGAACTTUG	95369	GGTCACCAACCCCAUGTCTUT
274610484	95370	GGTCAGUCCCCCTUACAAGGA	95371	CGAUCGCCCGCTGUAAGAG
274610951	95372	CAGGUCCAGGTUCAGCAGAC	95373	GGCAGAGTTUATGGAGCAGCUT
274611718	95374	GCTGGTGUACAAGTTTTTATTGGUAACT	95375	TCTGGCCAUACTAGCCCTGUT
274614174	95376	GCCAACCAGGAACUTCTTGUG	95377	CAGAACCGACAUTACTGGCATTTUT
274617857	95378	GTCTCGCGGUACCTTGUCA	95379	GTGAAGATUCCCGTCCTCCUC
274618569	95380	CCGCUGAGCUAGCAAGGAAT	95381	CTTTCTTACCCUGTGTCTTUGCC
274618756	95382	CCCATTCTTACUTCCCTGGGAUCA	95383	GAGACTAGGAACUCTAGACTTCCCTTUT
274621561	95384	CCGGGACUTACTAAAAGCUAAACAGA	95385	TTGCTGCUGCTTTTGGCUAC
274622039	95386	CGTCCAGCUACGAAAGAAGUGG	95387	CCTAAAUGAGGAAGGACTGTUAGACAAA
274623280	95388	CGGCATAAGUCCAAACACUCC	95389	TCGTTCTCCCUTCGGTCUAGT
274627094	95390	GTGTCTCTCUGGTGCCATCTUAA	95391	ATTCTTCTAGTTGCUGAGGAAACGTAUC
274630055	95392	GCACTCCUTTCCATTTCTUGAGG	95393	CTACTGAGCCCUTGGTTGAACUT
274635715	95394	CTCCGAUGACATGGCCTUCA	95395	TGCTGGAGACUTCTTGGCTTUT
274638263	95396	AGGAGACUGATGACTAUGGGAAGG	95397	CCACTGTTTTGUAACTTTTGGGTGUT
274642953	95398	AGATGAAGUGGAAGGTTTTCUGCAA	95399	AGGCATGUGAGGGATGAATCUC
274644740	95400	CGGAGUAAAAGTCAUCGAAAAAGGGA	95401	AGATCGTGAGGGACUAAGGTCAUAA
274648232	95402	GGGAGCUTCTTAUGGCCAAGA	95403	CUGGACTGGUAGGCCGAAG
274651102	95404	TCATCACUCCAGAAAGCTTUGGAA	95405	CCAAGGCUAAGCAGGAGGUC
274656543	95406	AATGGGCCUCATGTGUACCAG	95407	ACATGGTGACATAUGCTTCTTCTTGAUT
277835991	95408	GGGAGAGAAAAGUGAGUGAAAGG	95409	CTGACTACTTCUTTCTTCCTCTUCCAG
277842284	95410	GAAATGTGTTGGUGGCTGTTGUT	95411	ACTGCACAAGGCCUGCTAUG
277875628	95412	CTCTTGCTCTUAGCTCCTCCUACT	95413	GTGCGTUACTCACCTGUGAAAAAT
277883385	95414	CCCAAAGAUAAAAAGACAAUGGCAACA	95415	GGCAUAAGGTUCGGGAAGAGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
277889550	95416	TGACAACTCUGCAACATCTTCCUC	95417	GAGTCTUCCTTCTTGTUCGAAACCA
277895199	95418	AGAGTUGCCCACGGUAACAA	95419	GCTTTGGAUGTACCGATAATUGCAG
277903609	95420	GACCTAAAGTCUCCAATCATTTCTGUGA	95421	GUCAGGGAGAAAAUGGCCAGAT
277921410	95422	CCAAGACATGUGCAGCTCAUC	95423	ACGTCCCAGUTCACCTACUGT
277925179	95424	TUCTGCTTTCUCCAGCCCAAA	95425	GACAACAGTCTUCTCATCCTCATUCA
277938767	95426	GTGGAAGAGGUGGTGAGCTUAA	95427	CAGUGCACAGAGGUGGAAAG
277963588	95428	CCTCCCGAAGGUTCATGCAUT	95429	CAGAAUGGAAGCATTTTTCUAAAAGCAAAG
277968558	95430	GAAGGGAAGCCCCCUAGTAUCT	95431	CAGCCAAGCAGCACUATTUGA
277976185	95432	CAGGCAAGUATCGAGAGUGCT	95433	CCAAGCCAUGCTCTCTTCATUCA
277994181	95434	GGTATGGTGTAUACTTGCCCTCUGA	95435	AGAGCTTTGTGUCAGCTTTGACUT
278004977	95436	GCAGGUCCGCAGTCAGAAUC	95437	GGACCAAGTUGATGACACCUCA
278007644	95438	TTCAAGTGACUCCTGCTTCATUCA	95439	TTTTCGGUCGTGGATGGUGAT
278014888	95440	TCUGCUCCAGCGAACAACAAT	95441	CAGGTACATGTGUGCTACATAGTGTUAA
278022257	95442	GGAATCTGCUCCTTGGGUCAGAA	95443	GTCACCUGGAGGACAACTUGT
278025557	95444	CGAATTCGTUGCTCCTCTUGT	95445	CCTTCTTCUCAGGAGGAAAUCGG
278026270	95446	CCTGCTCATCUGGAAACTCCUC	95447	GCTGCTTCCACUTAAGAGTCUCA
278026999	95448	CGAAAUGGAAGCCGTCAUCAGT	95449	AGCTCTGCAUCGTCTCCUCT
278029449	95450	GAAGAGGAUGTCAUCCGGCAAA	95451	TGGCTTTCUCCCTCTTCCCUA
278045847	95452	GTTGGCUCAAAAGCUGGGAAAAA	95453	ATCTCACATTUCCAAGTACATTCUCAGG
278049465	95454	TGGGATACUCACAGGTCUCCA	95455	GCTCAAGUGGTCCTGUCGAA
278059076	95456	CCCTGTTCUCCCTGATUGGAA	95457	CUGAGACCGUCACCAAGACC
278061167	95458	GGCCGAGAUGCAGATGATTCTUA	95459	CCGAUGTUCAGGACAACAGCAT
278061579	95460	CTGATTGCAUACAAGTCAATGGCATUT	95461	GGCACTGACUACAAGATCTACCTGUA
278066288	95462	CCGAGCATUGTCATTCAAGGUG	95463	AGAAAAATUGCAGGCTAGCTUGAGA
278075537	95464	GAAGGCAGCCACUTGACACUA	95465	CTTGTCCAAUCTTGTCUCCAAGGA
278076711	95466	GTCCCAACTGUATCCAAATCTGCTUA	95467	TGGAGTAAGACAGGUCCATCAAGUAG
278085044	95468	GGAGGATTACCCUGTGGACATCUA	95469	GACACAGGCUTGTCCACAAAUG
278095106	95470	AGTAACCUGCGGATTGGCUT	95471	GAGCTAGAAAUAGGAACCAGGACTUG
278131676	95472	GTATTCUGGAGCCACTAGACCUCT	95473	CCTGGACCCACACUTTGAATATATUGA
278136247	95474	ACAACCCACAAGGGCUTCAUC	95475	AACCACAATTACACUGATTGCACTUC
278141231	95476	GTGUCACGAAGGCGTTTUCAG	95477	CGGAAGCGACUAAACGUCCA
278155206	95478	CATGTTGTCUCTTCTGCCCUCA	95479	CGGTAATCTTTUCCTTCTTTGTTGTGUA
278217652	95480	TTGTGAUGCCAAAGACTCUGCT	95481	GCCCCACTAGUTTCTCTTCTGTAATUAT
278237463	95482	CTTUCCAACCTGGUGCCAAAC	95483	GTCAAGTGACUATGACAGCTCTUCC
278251277	95484	TCCTCACTCUTTTTGCCTTUGCT	95485	GTACCTCTCCUTTCTCCTTCCTTUC
278279830	95486	GCAGTGAAUGGCTGAGGCTUT	95487	AAATCAGTTTCUGAATCTCTTGCTCUGT
278282065	95488	GGGCTTGTUGTCACTTACCUT	95489	AGCCGGTUGTTATGACAAUGGA
278293774	95490	AGAAGCCACAGUTCTCCAGATCAUA	95491	GAGAAACTUTCAGCTCAUGAGGGA
278296948	95492	CATACCCTCUGTTCTTTGGTCUAGG	95493	ACTTTAAAAGGAGCUGTAAGGCCTAUG
278308084	95494	GAAAATGGAAGAAAACCUGACTAGCUG	95495	CCACAGTGTGUACCCAATAACTUAAAGA
278324282	95496	ACTGCTAGCAUTGGGAAUCAAGG	95497	CAATTGGCUGAGCAAGATTTTCTAUCT
278361614	95498	CTCCCCTGUGCCATTCTCAUAA	95499	TCTACACCAUCCAAGTCCUGAGAG
278365715	95500	ACACCAATTTCAAGGUTTTTGGTTGTUT	95501	CCAAGAAAGUGATGTAGTAGCUGCAT
278367295	95502	GAAACGTGUAAAAGGATGCAAATCUAGT	95503	AAGGAACCAAAGUCATTCTCACTUAG
278373837	95504	GCGCATCUCTTTCCTGUCCAT	95505	GGTGTTTACTTUGCATTCCTTCCTCUA
278381703	95506	GGAGACCACCAGCUTCCTTUG	95507	GACTATUCCCAGCACAAGACACUT
278387712	95508	AGGTGTGGCCAUTGTAAAAACUCA	95509	TGACAACTGAUCGAAGGAACGUAAC
278397493	95510	CTATATCCCAAUGGATGATGACTUCCA	95511	GGTAGTGGUGGCATTAGCAGUA
278401592	95512	GTGCCCCUCCTGGAAGAAUAT	95513	AGUACGGCCACCAAGAAGUG
278402695	95514	CACCUCACCUGCCGACA	95515	AGGTTCTUCCCCAGTGUGAGT
278404854	95516	AGAUGCCGCACUCCAAGAA	95517	GUGAAGGUCACGGCCACA
278406504	95518	GACAAACGACUGCTCCUGGAT	95519	TCCUCCCCACGCUGAAC
278414054	95520	TCCAGCAGACUCAAAUACAAGAACC	95521	GTGATGATGUGGCACTAGTAGTTTCTUT
278417321	95522	GGUGGTGAAGUCAAAGCGAGT	95523	CCGTUGGAAGGAAGCUACCAT
278419194	95524	TTGACTGTUGACTTCACTTUAAGCAGA	95525	GTAACCAGUGGAGTGGCTUGAG
278421494	95526	GCAGGUCACGCTGCCUT	95527	AGCCACCUGCGGTCTUC
278427324	95528	GTAGGAGTTUAAGTGGCCUGGT	95529	TGCCTAAGTCCUGCTTAAGTCATTUT
278430502	95530	ATCTCCATCUCCTACCCACAUACAT	95531	ACTCAAAGCGACAGAUAACACGTUAG
278432780	95532	CGUGACGUCAGAGCAGGAA	95533	TCACCUGUCGGCAGGGA
278434184	95534	GACAGAAAAAUCTCAUCCAAGAAGCC	95535	GCGTTAGGGCAUATATATCAGAAAGTUT
278446241	95536	TGTGACTGCACCUAACAAGATTCAUAT	95537	GTATTCGTGUAATGCCGCTGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
278463573	95538	CTACTTGCCAGAUTTGGCTUGG	95539	CAGGTGGCAUTGAAGGAUAGAGA
278480890	95540	CGTGACCUCCCTGAAGAGTUG	95541	CCACAGAUGCUCCAGGACAAAG
278490458	95542	GTGGTTATTCTTUGACAATTGCTTGUGT	95543	CAGCCGGUTGCAATCTUCC
278491863	95544	TCACTAUCCCCCAGCCATCTUA	95545	AGCUGAACGAACUGCAAGGT
278494027	95546	CACAGCAUCCAGACCCUGAA	95547	TGTTGCTCAUAACGGTTGCTUCT
278503690	95548	CCTGTGUGGCAGGACTUCAG	95549	TCTTGTCCAGGCUAAGAACTTTCAAUT
278508199	95550	GGCACTTAATTUTCAGCTTACGUGT	95551	ACAATGTGGGUCCCTCTGUCT
278519750	95552	CAGATTCCUCAGTGGGTACTUGG	95553	CCACTAACCUCCAGTTTGTCAAUGAAA
278526579	95554	CATCUCACCAGGACAGTAGAAUCAG	95555	CAACCTUGAGGAGAGAAAACTUAGACAT
278551515	95556	AGAGGTUGAGGGACGGAGAUT	95557	CTTCAGGTTTTGAGUTTCCTAGACCUT
278556741	95558	CCAATGTCGGAGUTTGGAAAACAAAUT	95559	AGTTCAGCCCCUATAACUAGGAACA
278577058	95560	CACCTGGUGGTGCAATUAACC	95561	GAGCTATUCCCTGCACCUGAT
278595982	95562	GCTCTGCAGUGTCTTCTUCACC	95563	GCATTCACTGAUGTGGATGTCGAUT
278598235	95564	CCTGACGGCCUTGTCTUCAC	95565	ACACUCACAAGCCCCTGTUT
278603657	95566	CAAGTGAGGGUGGAGAATTUGG	95567	CCAUCAGCAGGAACACCTTUG
278604434	95568	GGCTTUCCCAAGCAATTTTGAUGG	95569	ATGCTTATTUCACAACTTGCTTTUCACA
278613126	95570	ACAGCCCGGUGACTTCUG	95571	GACCTGCAGUTTGTGGAAGUG
278625785	95572	GATGGTGACCUTCACGTCUGT	95573	GCCTAACATAUCCAAGAAACTGGCUT
278633561	95574	CACCTACATUCGGCGGGUA	95575	CTGGGTAUGACACTGGAAAUGGT
278644364	95576	GGGTCTGCUCTCATCGGTTUT	95577	TCCTCCTUGGCAGTACUCCAT
278648093	95578	GAACTUGGCGCCCAAUGAC	95579	GCTTCCTGAUGATGACAGAAGUGAA
278648189	95580	CAGAAGUGCCAGGAAGCUGAAT	95581	GGCTCTAACCUCTCTCGGCUA
278705665	95582	CTGGCCTUGGCATACCACUA	95583	TGGTCAGUTAGCGUCAGCAC
278723481	95584	GCACAGGGTUTCCTGTCACAUA	95585	CGACACAGTCAUCCTCATTCTTAUAGG
278730008	95586	TGAATCTTUGGCCAATTGCUGACT	95587	GAGAGTGCCCCUACTACACUG
278737289	95588	CTTGCCCAUGTTTGGCUACAAA	95589	GCACTCCAAGUCCTCCAAACUC
278742323	95590	TGGCAAGGAUGCAGTGAATTGUA	95591	CCTAACATGGUTCTCCCTCUCC
278747148	95592	CAGGAGGUAGAGAGTCGCCAUA	95593	CTAGTACUCGGGCCTCACUCA
278752590	95594	TTCAAAATUCACCCGTTTGTTGUGT	95595	CAGGAGAAGGUATCCCTATTTTUGAAGA
278761968	95596	GCCCCAGAAUCCATCGAGTUC	95597	GTCTCUCCCCGCAAAGAGUC
278776869	95598	TAGTATCCUACTGAGGAGUCCACAAAA	95599	AACTCACTGACCUAAGCTTTGTTGAUAT
278780757	95600	CTTTAGTGAAGAACUGGTGGCUGA	95601	TTGCCAUAGAAAGAAAGGACAUGGAAT
278810810	95602	CATGCGGCAUTTATCTTTUGCAG	95603	CCGATGGAUGATTCTGTTTTCAUGAAG
278817606	95604	CTCAGCCTCUGCGCTTAGAUAC	95605	GCAGAGTGUGCTCCTTTCCUC
278852243	95606	GTATTTTCTTUAAAAGCGCTCACUGGAT	95607	CTCTGAGCATUCTGCAAAGCTAGUA
278852788	95608	GTTCCUGAGGAAGAACTAAAUCCAAAGA	95609	CACATTAGCUAGAAAAGCAAAACCUACT
278880619	95610	CCCCACCCAAUGGAUGCT	95611	AACUGAGCAGGACCTCCUCT
278926834	95612	TGTCACTCUCAGGATAGCAGCUT	95613	CTGATCAGAGCUCCTGCACUT
278929044	95614	CCACCTCUGGACTTGCCTTUC	95615	GCCGAGGGAAUGGGCTUAC
278934621	95616	GCCGGGACUCAGGTTAUCAA	95617	CCTCTGTGCAAUAACTTCCCTTTUCT
278970516	95618	ACAGCCCAAGCAAGAUAAGTUCT	95619	CAGTCACTGCAAAGAUCAAATTGATGUT
278973197	95620	TGATGACUGAGAAGCTAUCCCAGAAA	95621	GUATCCAATGCUAGCACAGGCT
278977111	95622	GCTCAAAGGUCAGAGTCATGAUCAA	95623	CCCCTGAUGGTTTCTCTTTUCACAG
279018110	95624	GCCCCAUGAGAAGUGAAGAGAA	95625	GCCTCUACAGGACAAGAAGCUC
279020701	95626	GGGAAAGCUGTGGAACTTCUT	95627	GAGTCTCATAGGUGATTTTACTGTTGUCA
279021273	95628	CCGCACCTUTGGAACTCCUT	95629	GACACTAGCCUTACCTGGAACUC
279022258	95630	CATCTTTCTATGAAUCTGCTCCGUGAT	95631	TCGCAGAGAUTGTGGGTTCUC
279022950	95632	TCTTGAAATGUTCCTGTCCAUAAAGCA	95633	ACACAUTCTGTTTGTUGAAGGGAGA
279032446	95634	AGTGGTATTATUCAGCACGACTTGATUT	95635	CCAGCAAAGUTAAAGCAUCAGGT
279032462	95636	GCAGGACUTCTTGCCTTUCACA	95637	GACAGCUCCACTGGAAUCCAT
279036646	95638	CATTGGACATGGAUCTTGTTTTTCTCUT	95639	GCCTTGTCCCACAUATTATAACGGATUA
279036829	95640	ACCAACTGGGUAGGAAAGTCTUCT	95641	GGAATTCCAUCACCCUCACCAAC
279042260	95642	GTAGCCTCUTTGACAAACTUAAGAAGGA	95643	GCTTGUAGCAACAGACACAATTUAGG
279051441	95644	ACATACTCTGUGCCTGGAGUGA	95645	TCTTTTACTGUGCACTGGATUGCT
279064943	95646	GATCCTGUAGCCAGTGATGGUG	95647	CACTTCCTAAACUGGTGGTGUCT
279074864	95648	ACAUTCAGGGUAGGGAAGGACT	95649	AGGCTGATAAUGATCTGAGGAUGACT
279095618	95650	CTGGAUAGTCATACUGCCAACACC	95651	GTTTCTCATGCTUTTGAGCAGAGTTTUA
279150282	95652	TGCATCAAACCUCCACGAUGA	95653	GCTACTUCACTGCCAUCCAGAAC
279155326	95654	GGCAAACAGUCAGGAAGTGCUA	95655	CCTGGCCGAAAAUACATTGTAAATGUC
279157869	95656	ACAAAACAACCCUCCTUCAGGAA	95657	AGAAAATCAAGAAAGUACACCTGTTGUCA
279159679	95658	GGGCTCACUCACTTTTCCUCAA	95659	CAGAAAGAUCTGCTGTUCAAGGAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
279161507	95660	CTCTGCTCCCCAUCCTCAGAUAT	95661	AGCTGTAGAGUCATTTGAGGGACUA
279161711	95662	GTGCCAGUGGTTTCTTGTUGAA	95663	CAGCACAGAACUCAACCTUCC
279166018	95664	CCUCGAAAACCCAAUGGCAGA	95665	CCTCCCTATTUACCATTGACACCAUAAT
279174197	95666	GTGACGGAGUTTGCAGTTUCA	95667	TGTCTCAAAGAAAACAGUGCATCTUACT
279175606	95668	GAACTATGCUACCCTCCCTCUCT	95669	CATCTCCCAGUCCTTCCUCCA
279179721	95670	GTGTCUGCGAGAAAACTTTGUAAAAACA	95671	CCATAACAAAACCAUCCAAGGCTTUC
279181511	95672	GACAUGAAAGCACAGATGAATUGCT	95673	AGAGCTCTTAAUATGTGTGCATTTUACC
279206785	95674	CCAGGACCCCUCAGTGUG	95675	CAGCCCAGAGGUGACUGT
279210544	95676	GACAUTGATCUGCACGCCAT	95677	CCCCAAGAGUAACCGCTCUCT
279229108	95678	GTAGTAAGAAGGAAAAUGACAGCAUGGA	95679	AATTCCTTGCUGGTATCAUGGCA
279241863	95680	TTGATGATGUAGCCGGTAATCCUG	95681	TCGGGAGAAAAGUGTGGGAGUA
279255889	95682	CCCTTTCTGUACCTTTTGCCAUCT	95683	TCAGTGGGAUAAGCAGCAUGAC
279265333	95684	GCACCUCATCATGUGACCCAT	95685	CTGGTGATCATUTATCAAGTGCATTUCT
279298323	95686	GTGCCCUCTAGGAUGAAGCC	95687	GTGCCGAAGCUCCAGTAGUC
279302681	95688	GCAGAAGUACACAGUGACCGT	95689	AAACAGGGUACGUGAAGAGAAAGG
279306495	95690	CCACTCGUTGAATGGUCCAGAA	95691	CCCGGCAAGCUGATAUACGG
279309689	95692	GATGGTGUCACACTCGCAGUA	95693	CAGGAGCUGGAAGGAAGCUG
279313588	95694	TGAGCAGATGAUGGAGTTGTTGUC	95695	TGTCCCTUGTCCCACAUCAC
279318659	95696	CCTUGGGAGAACATUGCAAAACA	95697	GCCTTAAACCUGGAGTTGATTAUACCA
279328640	95698	ATTATCATGGCAGUGAAGGAUCAAACT	95699	CGGCCGUGAGATGAGTGUC
279333659	95700	CCAGTGACAGCAUACACAGUGA	95701	CCTCACACTCUGAACTAACCCTTTUT
279334346	95702	CATGCTGAGACUTAATTGAACGGGUA	95703	AGCTTCGCUGTGTGTTTTGTUC
279340960	95704	CTGGGCCCAACUGTGTCUAA	95705	GGCAGGCACAGUCACAAUCA
279350737	95706	TCATTAGGCCTUGTGAAAAAGGGUAAA	95707	CTTACCTTCCAUGTTGCAGACTTTAUG
279354186	95708	CCTAACUAGCCGAGGAAGAACTAUGAA	95709	GGAACTGUAAACCTTCCCUCACAAT
279357238	95710	CTGATCGUCCAGGTCACCUT	95711	GGAAGGGCGAUAGTCCUCCT
279362090	95712	ACATGGCATCTUCTAATCCTTCTGUG	95713	CTGGCTGCAUCTCGAGACTUT
279365051	95714	GATCCCAGUGTGAGTGCUCAG	95715	TCGTCACACUCGCAGTACTUG
279367698	95716	GTAGGATAAGUTCTGAACGUCGAAAAGA	95717	AATAGCTGAUGGTAAGCCTCAUCAC
279374287	95718	CACAGCAGUGACTTUGGCAAG	95719	CCTTCACCTAUGTTTCCAGTGGUT
279377701	95720	GTTCGCATCUTGATAAGGCCUCT	95721	AAAACATUGCGACCACCTTCUAAAAAT
279386876	95722	CCTGAGCUAGGGTGGTGACUT	95723	CACCAUCCCGAACUGGAAGAG
279393263	95724	TUCTCAACAUCAACCCCAACAAGA	95725	ACAAAAAGAUGTGGUGGAGACACA
279410685	95726	GGTCCCCACUGTGCTGTUT	95727	CTCCAGCUTTCCCTUGGGT
279438743	95728	GGTGCAGAGGUGCTCACUG	95729	CCTCACCCUGTGGCAAGUA
279439320	95730	CTCCGCCUGCACUCACAT	95731	GUGCGAGAGGACCACUGAG
279441199	95732	GCCACGACCACUACACUCAA	95733	AGGAGCTUAGCCGTGCUG
279450306	95734	GATAATGCAUACCTGTCTCTUGGCA	95735	TCCTCCCUATGGCCACUGT
279463595	95736	AGAGUAGACCACACCACTGUCT	95737	GCAGAAAGTAGUGAATTGTCTTCTCUCA
279463868	95738	GGGUCAGAAGAGGAAUAAACAGACA	95739	GCATCTCACGUACCCCUACAAAG
279464888	95740	CACAAAACTUCAGCCCCAACTUT	95741	CAGGCUCAGCAAATGGTUCA
279468539	95742	CUTGCTTTGACUGACAGCCA	95743	TCUCCCCCACCGTCUCAA
279479868	95744	TGATCTGTCCUGGAGACCTCUG	95745	ACAGAAAGGCAUCCUGGAAAAGG
279496552	95746	AGGTGGGACUGGCTTAATAUAAGGA	95747	GGCTAGACTTTTCUCCTAAAGCCTTAUT
279512947	95748	CCCACTGGCCUTTGTTTTGTAUC	95749	AACTACAGCUCCCCCATUGAC
279526366	95750	GCATGCGCCUACCACAUCA	95751	CCCCCAGCCAGUACUCAC
279529079	95752	GGGATGCUAGCTAGGGTCUAC	95753	GTCTGAAACCAAAAACCUTCTGTUCAA
279533294	95754	GAGGGTGUAAACTTCTGCCAUGAT	95755	ATTTAATGTCUGAGTGGUGGAAGCA
279543782	95756	GCCAGACACUCAGTGTTGUCA	95757	GCTACTCACUGTCTGCCCTTUT
279571291	95758	CCCAAACAGAUCCCAACACAGUT	95759	GAAGCCUATGGCAAGUGCAAG
279574945	95760	CCUATCAGTTAACTUGGGAGGAGAAA	95761	TCATAAATUGAGCGGCCTAAAAGTUCT
279575836	95762	CGAATUGATGGGATAUGAGCCAGA	95763	TGTACAGAGGTUGCAACAGTTAAGUAAT
279593714	95764	GCACCTTGUCGTCACCAAATUC	95765	CCAGGCCTCUGTCTCTGTTGUA
279617495	95766	CCTATCTTTCUCCTTGTTACCUGCAA	95767	GCCCATTGACAUAATGTGATGGTTCUAT
279650790	95768	GTATTACCCTUCTCTCTAGGAAUCCAGA	95769	CTACCAAGGCUGGATGAUGGT
279656826	95770	CTTCUCCCAGGCAAGTACAAUCT	95771	GGAGCTTGCACAAUTCAAAATAACCTUT
279722960	95772	GAGTTGTUGGTCCTCUGGGT	95773	GGAGUGCACGAAGTUCAAGGT
279726858	95774	ACACACTAUGCTCCTCUCCACA	95775	GCTAACTUGGCTCCACACUCA
279726929	95776	GCCCCGACUCGATGCATUC	95777	TCCTCTGACCUTCCTGCTCUAC
279730978	95778	GGCTTGCTCCUTCTTTGCCTUA	95779	TGCAACTCTAAGAUGTGCTGAACTUAC
279758838	95780	CAGCAGGAGGUCGCAUAGT	95781	GGAAGGCTCUGATCCACCUGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
279764590	95782	CCTTCUCAAAGCGCCTGTACUC	95783	GGTGTGCUGCTTCTTCCCUA
279807173	95784	CTCCCAUGACCCAGAGGGAAUA	95785	GCTGGAGATCUGCTCTGTCTTUG
279832077	95786	TCTCCGTCTUCCCTGGAATUGA	95787	AAGTGCCCUGGTGTTTCCUAC
279836018	95788	TTTTTACAGTUCCTGCCACTUCCT	95789	TGATGTCTGGCUTGTCTTTATTCTTUCA
279836374	95790	GCCATATTUGACCTCAAGTCUAGACA	95791	CCAUAAATGAGAUAAGGAGAAGCCCAAG
279837730	95792	TCCAAUGAACAACGGTCATGUCT	95793	ACCACCCAAUGTTCAGCUCAC
279840143	95794	CATGGGUCCCAGCTGAGUG	95795	CGTGCCATGUCTGGTCTTCUT
279847159	95796	CACCCGCACUCGATAUCCA	95797	CCTCTAACCAAUGACAATCUCGACAG
279849043	95798	ACUTGGCCACUGACGAGAAG	95799	ATAAAGGACAGUTCCCCAACCUG
279857566	95800	GCACATTTGUTTTCCCCTGUCC	95801	TCACACTCTGUGGTCCACTUCT
279878940	95802	TCTCTACCAGUGACATGGCUGAA	95803	TGGCAUCAGTGGUAAACACCAG
279892369	95804	CTGAACCUGTCTUGAGCGACAT	95805	GGCCACTUCTGAATCTGUGACC
279893800	95806	AAATATTTCTUGACCTGCTUCCCCAT	95807	AGACACCUGGAGCAAGAAGGAUA
279902802	95808	GGAGGAATGAUGCATCCCACTUG	95809	ACCAUAGGTGGUGCCAGAGAT
279912750	95810	CTGGAGCAGGUTTCCUCGAT	95811	CTCGACCTGAUGTATGTATGTGCUT
279917202	95812	CACAAAGCTACUGGCTGTGATTUC	95813	ATGACUGAAGGCTGACTTUCCC
279935289	95814	GACCTAGGCAAAUAGATGGGCAUT	95815	TCCTGTTGGAUTCTGGCCTUC
279941344	95816	GAATCCTCGUAGAAGGACATTGUGT	95817	CAGGCAAGGCCCACUTCTUA
279943274	95818	AGGATGAGAGUCTGCAGAGCUT	95819	GGAUGGTGTGUACGAAGCCA
279944514	95820	TTTTATCAAAGCUTACTGGCCAUGT	95821	ACTGAGGTTGGUTACTGTTGGTAUC
279947219	95822	CTTTCAGGTTAUCCACAACAGAATCUGA	95823	CGAGGGACCUGGAAGTTGUT
279953221	95824	GCACAGGCCACAUTCACGTAUAT	95825	TCATAUCCAGGCTGTGUCGACT
279960948	95826	TCCTTTAGAUAGCAAGACTTTCCUCAGT	95827	CGCTGAATCTTUGCTATGGTGAAUAT
279961952	95828	GTTTTCACTGGAAUTCAGGTCTAUGA	95829	GAGTGTGTGUGTCTTGGTAAUGGA
279970946	95830	CCTGUGCAAACTCATCUAGGGAAA	95831	GACATCACUTACAATGUGAACGACAC
279972545	95832	ATGGGCTGGUAAGAGACATGUG	95833	CTGAATTCCGGGACUGGGATTUA
279976137	95834	CCTCTTCAUGACGCTTGUGGAAT	95835	AGTGGAAGUAGTTGTATGCTTUGAGAAG
279976555	95836	GCTTGCAGGUCCATTCTCCTUT	95837	CCCTCTCCTAACAUTTTCGTTGTATCTUC
279984182	95838	GCGGCGACCUGCAUCAT	95839	TTCAGGCACGUGCUGAAG
279987408	95840	TTCTCTTAGUGAAAAGTTAACATTTGUGACT	95841	GGTTUGGCCCGAGAAAUACGA
279987498	95842	TTTGAUCGTATTTCUCGGGCCAA	95843	TTTGGATTTCTTCUCCTCTACTGTCUCT
279988150	95844	TGAAACTGGUTGGAGTTGTUGGT	95845	CCUTCGUGGACAAGACCGT
279989777	95846	GUGCGTGTUCACGAACGG	95847	CCCUGCUAGGAGAGAGGAAACA
279995709	95848	TGAACCCCACUGATTTACCATTCTUT	95849	GCTCTUAAGGACACTTUGACAAGCA
279995917	95850	GGCAGGCAAGUACCTUCACT	95851	CAAGGTCTGGUATCTGCTCCTUAC
279997548	95852	GTTCCCCCAGUCTTAAUCCACA	95853	CTGTGACCCUTGATGGTGGUT
279997833	95854	GACAACTCCCUGAGCTGGUC	95855	GCTGTAGTGAAACUCCTTGGGTUT
280010060	95856	CAGGCCUGCCTCGTATAUGA	95857	CTTTTTGAGGUCCTGAAGUCCCA
280030316	95858	CCCATGAGAUGGTTGTCUGAGAGA	95859	CAUAAGGCAUAGGCCAAGACCA
280065059	95860	CAAGACTGTGGAAUCTATAACTGACAUCA	95861	CCAAGGGUCAGCGTCCUA
280118997	95862	GTAGGTGAAGCUGAGGGTTATGUG	95863	GTTCATCAUGGTGGUGGCAAT
280124403	95864	GGCAGGUAGCATGTGAUGAACA	95865	CCAGCUGGAGTTCTTTAUGCC
280124478	95866	CCCCAAAAGCCCAGUGTCUAC	95867	GCTTCCACAUGAAGACCUGGA
280130525	95868	CGGCCAAAUTGAAAAGGUAAACAGT	95869	ATGUACAACGGGTCGUGCT
280135277	95870	AGATGGTGUCCCCCUCGAT	95871	GGTGAGUGCTAACGCUCAGA
280136303	95872	CTTGAAGGAGCAAAAUAAGATGAUGCC	95873	GGTCATCCUGGGAACAGTGTAUCT
280143383	95874	GCAGAGAUGGTTCUCCAGCAAA	95875	TCGTGTTCCUTACGGTGGUG
280145337	95876	CGACCCCTUAGCACGAGTUA	95877	ATTTCGAACCUCGGUCGCA
280151388	95878	GGTGGACCACUTTGAAATACCUGT	95879	CCTTTTCGGACAGACUATTACCUCAGA
280166064	95880	CTATTTGCCACACUGATGCAACUC	95881	GTATTATTTTUCAAGCCCCTCCTTUCC
280182409	95882	CTGCAGATTTUGAGCTTGTTGTAGAAUT	95883	CTAGACTCUATTTCCTCUGGACGGT
280208780	95884	TGATGACCAAACUGTACCTCTCTTTAAUG	95885	AGAAGCTCAACCAUGCCAATGUA
280209396	95886	CTGTACCTCTCUTTAATGAGCTGGUAAA	95887	TGTTTTGTTTTGUGTTTATTCCTUGCCT
280221803	95888	ATGGATAACAGAAAAUGACAGTGAUGGT	95889	CACTTATGAGCGUCCTAAAGACUCC
280230433	95890	TGCAGGUACAGTCCCAGAUCAT	95891	GGCTCACAUGGACTTTCCTTTUC
280290434	95892	TTGCTTATTTCUGTTTCAGTTTTGUGGT	95893	CCGAAACCCAAAAUGAGTCTCCUA
280291358	95894	ACAACACUGGAGGTGAGAUCCT	95895	GGATGGACCGCUACCTCAUCT
280292693	95896	ACCTCGGCUCTCAUCCACAT	95897	CUGCAGCTGUCGAACAACC
280295251	95898	GCAGGUCCTGCCCTUCAC	95899	TGGCACCGAUGCUCACA
280343608	95900	CCACAGACACAGAAACUGAUGACC	95901	GTTTCAGCGGUGGGTAAUGGA
280350475	95902	GCCAGCCAGUTGTCTCCUAAG	95903	CTGGCTAAGUCGAGAGGCAUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
280351319	95904	CCUCACCCAACGAAAAATUACAGAAT	95905	CCAGTGACTCUGGATTTGGTTCUAA
280356584	95906	TGCACTCAAUCAAGAAGTTGCATUAAAA	95907	ACCTACCUCAGGTGAACTTTGUCT
280374446	95908	GTCAGUGGAAGCCCGGAUAG	95909	TGCCCTTGAUGGTCACACTUG
280383576	95910	AGATTCAGTCUGTTTACAAATGUGAGCA	95911	GTCTTATTTCCAGGUCAACAAAGGATUC
280395024	95912	CTCUGGGCGACTGUGCT	95913	GGCTCCAAGUCCGCAACUT
280395776	95914	CATCCAAGUCAGCCCAATCAUCT	95915	TTCTGTTAAUGCCAAGTATTGCTTUCC
280412270	95916	GGGATTAACUCAGGTAAAAUGCACACA	95917	CTCATTTCCUCATGGTCACAUGGAT
280412479	95918	GTAUGAGGGAACACACTTGUGCT	95919	TGACTTCATGCCUCTACTCTCUCA
280413127	95920	CTGGACACAGUGTGTTTGATTTTACUC	95921	GCCTTGGGTAAGUACAATAGCAAAGTUT
280422354	95922	CTGGCAAAUAAAACTAGGGCAUGA	95923	CUACTCCUGCACCACAGAAGG
280424627	95924	GGGAAGGGUCTGGAAUAGGT	95925	GTGTCCTGGGUACATGTCTTUGT
280435079	95926	GAAAGAAAGAAGAACUCTAAGCUGGGT	95927	CAATTGAGTGCTUCATGCCTTTAGAUG
280439481	95928	CACCAAAGAUGTCCGTCCUGT	95929	GCATCTCTGTTUACTGACACTCTTTUG
280442508	95930	GGGAATCTTCUCTGTCAGCCTGUA	95931	CCTATCTATAAGCAGCUGTCATGAGUC
280465168	95932	TCACCUAACAUGAGCCCACAC	95933	GCAAACGGAAGCCUGUGACT
280485800	95934	CAAGAUGGCAGCTTCUAGCCT	95935	CGTGGATGAUGCCACCTTCUT
280496861	95936	ACCCGGACACAUGCCTUCT	95937	GAAGCAGCUGUCCCCACA
280498520	95938	CGCAGGUAAAGCGTCACTTUT	95939	GGATCCUGACTCCATUCGCT
280502282	95940	AUGTCGUCAGCCGCACA	95941	AGTCCTCCAUGGCCAGUCA
280534854	95942	CTTCCTGGGCUGTGTGTTTUC	95943	ACAGCTGCCACAUTCACACUT
280546358	95944	GTACTGACACCUGCATGUCCA	95945	CTCTCTCCAGACUCCACACUCA
280554192	95946	CTTTTTCCATTUCTCTCTCCCTUCCA	95947	AAAAUGCTTCCAAUGGCAAAGGAA
280568621	95948	GGGCCACGCACUTTTCTCAUA	95949	TCAGTGGTTGAAUCCTTACTCCTUG
280575152	95950	GGGATGUGGAAGAAACTGTGUT	95951	GCATTCTCCCUTTCACTCACTTTUC
280590363	95952	ACAGGTCACAUCTGGCTCCTUA	95953	GAGAAUAAGTGCGUGCCCAAC
280594190	95954	CTGAGUGCGAGGAGTTGUGT	95955	GCTTGATGACCUCAGGAATGUCA
280604259	95956	AGGTCGCCACCUAGCTUCT	95957	TGTGGCTCCUTTTGTTCTGUCC
280610934	95958	GCCGTAGUATCTCTCGTUGCT	95959	GACTCAGGUTTGAAGAGCUGACT
280611711	95960	GCCTGGCACAUCCAGTCTUA	95961	GCGTGCATCUGTCTTGTGTCTAUAT
280699501	95962	AUGCATGGAACTUGAGGAGACAA	95963	CAGTTTCCCAUTATGCCGTUGG
280702370	95964	AACATGACCUTTGACCUGCCA	95965	CTCGTGAAATUGAGAGTGAGTGTAUGT
280711609	95966	CAGACATTCGUTCCCACTCAUCT	95967	AGTCATTCGATUTTCTTCTTATGGUCCAA
280714748	95968	CTCGUGATTGCTTTUGGAAGAGG	95969	TCATAATCGGCCCAUTTTGGTTCTUA
280723064	95970	AGTCAGCUGAGGGAAAGTAUCCT	95971	CATTCTUCCACACCCAGCCUA
280726094	95972	GGTAUCAACCCAGGAGTGCTUC	95973	GCTTACATUGGCCCCATAUCAGT
280785881	95974	GCAAAGTATAUGGAAGCTTCTUCAGGAA	95975	GCUTCTGTGTCTUCAGCAAAAAGT
280785989	95976	CTTTTTACAGCCUAATAGTCCCAGUGA	95977	CCTGAGTAGAAAAUGGGTTCTTTGCUT
280786127	95978	GGTAGAAAAACUTTTTGCUGAAGACACA	95979	GAGTTTTTACAAUGGCCACACCUT
280790829	95980	AAGCCCGTTUACATTGTGGGUAT	95981	GACTGAGACGAUCACTGGCTUC
280795457	95982	AGAGCATTAATAAUCACTGCCCTGUT	95983	GAGAAGTATGUGCATGGTGUCAGA
280812582	95984	GCCATAGCAGUAGCACTGGUA	95985	AGGCTGTTTAUCTTTTCCTTCCAUGT
280817280	95986	GCTGGAACGGCAUCAACTUG	95987	CAGGCACTAAUCTCTAGCTAUGCT
280831534	95988	TCAAGACATAAACUAACCAACAAGTUCA	95989	CTCTGGTUCAGACTGCAGUAACC
280838585	95990	AAACCAAGCAGUGGTTACGUACT	95991	GTGGATGTUGCATTTGCTTTUCAC
280848182	95992	TTTCCAAAACAAUGATGAACATUCAGCA	95993	ACCTCTTTUGGCAAGCAUCCT
280849998	95994	GACAAGUCACCACAGGACAGUA	95995	TTACTTACCUCACAACGTAATUCACACA
280851197	95996	TCTCAACCACAGUGCATTGTAUGT	95997	TTGGTAGCGATGUAAAAGAATTAAAATTTAGUT
280855226	95998	GGGCAATCAAUGGATGAAAGUGG	95999	CAGTTAACTTGAUCCAAAGCTCTGAGUA
280859434	96000	GAAACCTACUGCAGGGUGAAGAAT	96001	GCAGTATTGUAGCCAGGCTTCUAAAA
280861146	96002	CTTACTGTAACUGCTGATGGTTAUGAGA	96003	TCACGUTGTACTTGUCCACAGAG
280866059	96004	CCUCACCCGUGCCCAAG	96005	CCCAGCCCUACCGTGUT
280870270	96006	ACCUCACCTAUGAGAGGAAGGAC	96007	TTAACAGCAUGACGUGCAGAGA
280896801	96008	CTGACACCAUCCGTCTGTCUT	96009	AGATAGTCUGGTAGCCUGCGT
280897554	96010	TCTCCAUCCCTTTGAGCUCCAT	96011	ACATTTCCAAAUCCCCCTGUCC
280903287	96012	CCTCATCGUCCTCATCGCCUA	96013	CCCCTUCGACAGGACCCUAA
280907855	96014	CCTTCCTGCAUCCAGGGAATUT	96015	CTCTCGAAUCCAGGCAAGGAAUT
280911485	96016	GGGAAAUGAAAGAGCGCCTUG	96017	CCCAGCAGGAUCAGAGAAAGUG
280912370	96018	AGAACTAGACCAUGGATTAGGTGGAAUA	96019	AGAGTTTTTGACAAAUTGAGTTCTGCAUT
280939198	96020	GTGACCTUCTCGTCACUGGAA	96021	GATCGGAAGUTGCTTTGTTTUGCT
281118981	96022	GCUCAGGGCTGTAUCACAGAGA	96023	CTGGGAGCUCTATTCCACCTUAC
281120020	96024	GGAGGACCGUGGGTGAAGAUA	96025	TTACTCUGCCCAGACAACACUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
281125072	96026	GTCTCAGUCACCTCGGTGUT	96027	GCTTGGTTAAACUGAGGTTCTCCAUA
281125773	96028	CCAGCCCAUCTTTCTTCTATTCUGA	96029	TTGTCACCAGGUCTCCTAUGGA
281140222	96030	CTTTGAACTTGUCCACTGGCTUC	96031	GGGAACTAUAGCTCGAGGTUACT
281160122	96032	GGTTGUCACAGCCAATCATCUC	96033	GACACTTTCUCTTCCTCTUGGCAT
281248390	96034	GGGTTTTGTTAUTGTACAGGAAAUGG	96035	ACATGGAAGCCAUGGAATTCTUCA
281256717	96036	ACTTGATAACAACAUTTCACTGCTCTUCA	96037	AACTTTGTTTTCCUCTGCCTCAUACA
281261580	96038	ACAACAGCUGCCTCUCCAAAA	96039	CTCATTGCAAAGUGCACACUCA
281287631	96040	GGGTTCATCTUCAAGGGTGGUT	96041	GCTTCTCTGCUGAGTCCCATUC
281288089	96042	AGATGAGGUTCTAGTATTUCCCGAACA	96043	GCTTCACTGUGGACTTACAAATGUAAAA
281290144	96044	CTGTGTGACCAUCTCGTGTGAUT	96045	TGCCUAGCCGAAGCTGAUG
281299447	96046	CCCUCACCUCGCAAGCAT	96047	TCCCUCCCCAACCCTTCTUA
281319925	96048	CCAGTGCUCAGTAACGTGCUC	96049	AGTGCCCAUGATATGCAGGAAUC
281323794	96050	CAGGTATGUCAAGGAAGATACAGTUGT	96051	GACCGTCATGGUGAAAATATTCTCTTUG
281325934	96052	TCACAAATAAGATUCACGTAGATTTTGUGAAA	96053	GGCCTATATUGCAGGGTTTGATGAUA
281326039	96054	AGTCATATAAAACUGAAGTTTACCATATCAUCA	96055	GAAATCCTCATUCCTCTACAATCAGUCA
281326836	96056	TGTACGCAUTCACCAGUCAAAGAAT	96057	AGGCATTGTGUTTCTTTTAGGUACAGT
281327176	96058	GGAACGGCAGUAAGCTGATCUA	96059	CCAAGAATATAATACGUTGTTATGGTTGAAUG
281330379	96060	GGTACCCAGAAUTGATGGAAGTGUAG	96061	TCCACATTAAGCAUGAGCACTCATTTUA
281332426	96062	GCTTCTTCUACCAGCTTTTTAAGCATUT	96063	ACAGACTGCUGAACCTTTGTAAUCA
281371173	96064	AACAAAAACUGCTGTGGCGUT	96065	CTGCATCTGGGUAATTCTTTCACCUA
281378196	96066	AGTAGTGUGAGAAACCTTTTGTUGAGG	96067	CAGCATTCUCCAGGTGACAGUT
281383356	96068	AGCTACCCAGTUTAGAGAATCTTCTUGA	96069	AACATTTTAACAUAGGCTCTATCTATCTUCAG
281384591	96070	GCCAGGTTAUCAGCTGGATGUG	96071	TCCCATTTCTUAGTGTGCACAGAUG
281384992	96072	CTTACCTCTGCAUCTACCTCAATUCC	96073	GCTAAAAGCAGCUTTGTGCCATTUA
281394192	96074	CCAGCUGGCACAAATTUAAGGAAA	96075	ATTTAAATATGCUGCTGGAAAAACTCUG
281397300	96076	CACACCGUCTTCAAACAUGACA	96077	CCTTGTAGAAAUGGATACTGACCAATUGA
281400409	96078	CATATTGGACAUGGAAATCUCGGGAA	96079	CATGACTACUGGTCTCCCAATUCA
281401671	96080	CAGCTTTGATAAUGGCTCTTCAUAGAGT	96081	CAGAACTTTTUCAGCTTGGAGGACUA
281404698	96082	AAGTGCUAGCTGGTTGUGCT	96083	TCTTACTTTGGCAGAUAGGTTGTGTUC
281405650	96084	CTTCCCCCTUCTAAATGTTCATAUGACT	96085	GCTATTTGCAUACAGATACCAGCTUGT
281410162	96086	ACTCCCACCCAACUATAGGAAAUACA	96087	CTACACATGUGCACGTAACUCAC
281411909	96088	CCCATGAACCUGGGTATUGGT	96089	ATTTCCCUGGCGCAGATAGUC
281416215	96090	GGTAGATGACUGACATTGACCAUGAAA	96091	ACTTCTUCGCCCGTTCCTUC
281419625	96092	GCGUGGAGAACAGCGAGATTUAT	96093	GGGTTTGGAAUGAATTCTGGGTUG
281428145	96094	AGTGAUAACAGGGCAGCAAUGT	96095	GAGGAATAUGACCCTTAACCAAUGACAAT
281435992	96096	GGTTCCTAAGCUAACTCTTCCCAUCT	96097	ATCCCGAAGCCAAUGTACCUC
281442216	96098	GTGTCAGCUCCAGGTUCAGG	96099	ACCACTATCCAGUCATCCTGTUCAT
281445291	96100	CTTCGGGAUGGACAGAUCCT	96101	GCTTTCUGCCCTCTGTGUGAC
281457107	96102	AAUCCAAGTTCATUACAGGAAACCCA	96103	GAATACAGTGGCCUAAAGAATCCTGTUA
281465474	96104	ACAACAGCAATUCCTTCTAACATCUCAA	96105	GAATTAAACAUGTGGACAUGAACCAAAAGA
281557168	96106	AGTCAUGCAGGAGGGAAGAGUA	96107	GCAACAAACUCAGAATGACCTUGAT
281560886	96108	ATGGTGGGAAGGGUGAACAUC	96109	GCUGATAAACTUGGAAGGAAAAGAGGAC
281573775	96110	GCTGAGAUGGTGCTTGCUCAA	96111	CCAGTTCACCUCTTTCCACUGT
281576991	96112	CCCCAGAGAAGUGTTUGAACCA	96113	GCCAGATTCUCTACAGCCTTUAGAT
281583697	96114	TCCCACACCUAGAAAGTCTTATUCAGA	96115	CCATCGACTUCGGCCTATAGTUT
281596219	96116	GCACCACAGGGCAUTCTUGAT	96117	CCCTGGCTAAAGUTAATGACATTTTCUT
281669088	96118	CCTAAAGUTGCTATCTUGGGAAACAGT	96119	GGTTCTGTCTTTUTCCCAATTAGCAUT
281673029	96120	GTAGATCAGAAACUCAGGAGTGTCTUT	96121	ACCTTGTTUCACTATTTCAAUGGAACCA
281676225	96122	GCATTGTTTTGCUACCTGGAAGAAUAT	96123	ATGCACTGAUCTTTCCCCTTUCAA
281752141	96124	GTGAAATCTCUAGCAACCATTTTGTUGA	96125	ACCGCTTTATUACCAACTGTTCTCAUAA
281752450	96126	CAAGAACCAUGTCGCCATTGUG	96127	ACGAGAACCAUTTTTCTTCUGAACAGA
281752762	96128	AGTTGGTAAUAAAGCGGTCTCAAGTTUA	96129	GGAACGGTUCTTGAGACAUACAGA
281755492	96130	AACTCAATAAAGAUGGCTTACTGAUCCC	96131	GCACACAGCCACUTTCCTAGUT
281766210	96132	GGGTCAATAGAGUTAATGCAGGUGA	96133	GGAAACGTAUGGTGTAGATACTUGCAAT
281766357	96134	GCTTAGATAAUAGCTTGGCUGCACA	96135	GCATGAACUACCATCAGCCAATUGA
281771074	96136	GGAGGATTTUATAGAACAGAUGGCAAGT	96137	CTCCGTGAUGTTGCTTGATTUCA
281776362	96138	GGGAGGATTUCATGATATGCUGGA	96139	CCACAGUCTGGTTTCTUAACAAAAGGA
281788185	96140	GTGTGTGCUAGGCATTCAGAUAGA	96141	TTGGTCTGGAGUAAAGAAGCCAATUT
281788759	96142	GGGTGTGATGUATAGCTACGTAAUGT	96143	TGCAATGAAUCAAACACAGCAAAAAGUA
281790449	96144	CACCCACUTCCUGGGAACAG	96145	CUCTTGCCAAUGCACGAAGG
281791083	96146	GGGATGAGAGCUATCTTGTTCTTTUT	96147	CAGGCATUGAAGCAAAGCATACTUAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
281793725	96148	TTTGATTTTACTGCUCTGCTTTTGTUGT	96149	GTGTGCATGACCUTGTTCTTGTUC
281794666	96150	GAACATTAGTGCUACGCGGAAUG	96151	CCAAGCCACUCCACUCCAAT
281796022	96152	ACCATTCTGCAAAGUTACTACCCAAUT	96153	AGTCAACTGAAGGAGUTGCTGTAATUT
281806662	96154	TUTACATGTGGUCGAGGCCAAA	96155	CATAACCAAAUGCAGAATAGGCUCAC
281812746	96156	TGACAGATAAACGCUCCATATTGTTUCA	96157	AGCAAGGAAAUACCATUCCAACCAT
281813764	96158	AACCTCAAUAGGACAGAGAACTCTTTUG	96159	TCAAGCTCGGUTGCTCTGUG
281816797	96160	GCCCCCAATUCCCCTAAACATUC	96161	GCAACAGACAGUGAAACAGUAGAAC
281817538	96162	CCTTUCAAAAGCACTGUCACCAA	96163	AAGCTTCCTAGCUCAGGAAAACAUAC
281825518	96164	CCCGAGAGUGAAGGCTUAACAG	96165	CACACUGTCAGATUGGACACAGA
281834804	96166	CATAGGGCUAAGGCAAGAGGUG	96167	TTGGGCAUGGCTTTGGACTUA
281835645	96168	GAATTUCAGGCATTCTGUGCAAAGAT	96169	GGTACCATAUGTGATCCTTUACAAAGCT
281835796	96170	GCAGCTTTGUAAAGGATCACATAUGGT	96171	GCCAATTCTGCAUTCTTTTCTAAGTAAUAA
281897799	96172	GGAAUCAGCGGAGGAGGAUG	96173	CGTUGGCGTGGTUGACT
281923114	96174	CCUGAAAGGGAAACUCACAACCT	96175	CACAGUTCATUCCAAGAGACCACAT
281929773	96176	GGTTCACTATCAGACUTTCTTAAGGCUA	96177	GGCAGGTUTGTGGCCAUCT
281933393	96178	ACATGAGGATAUACCTGGCCUAAAAGA	96179	CTGTCTTGUAAAGCATGATTGCAUAACA
281977331	96180	TGGCAGTTTUCGAACAAAATAAAGGAAUT	96181	CTTCAGAACTTCCUGGATCACGATAUG
281977947	96182	CCAAACGCAAGCUCACACUG	96183	AATCATACTGGAAUGCATCCATGTGUA
282012566	96184	AGGCTATAATTUACTCACCCTCTTUCCT	96185	TCTCATTTGGUCTGTTCTTGTUCCAA
282013144	96186	TTCAGATAAUGAAGGGCACGTTCTAAUT	96187	CUGATCTTGCUGCCAAAGCA
282014738	96188	TTCCUAAAGTTCGAAUGAGAGCAGAAG	96189	TCACCCAGACAAAUGTACTTTTUGGT
282036821	96190	CAGGAGUGACAGGGCUACC	96191	TGAATGATUAAACGCCCCTUACCA
282039668	96192	GTGTTGATGGAAUAATTTGCCCCUAC	96193	GGTGGCTTAGGUGTAACTGGAUT
282050328	96194	CCCTTTUCCACAGCCACTUCA	96195	CCATCTTGUGATGCCTGUACAC
282056971	96196	GGGATTGTCAUTTGTGCATTTUGG	96197	TGGGTTUCACCACAGTAATATTTCUCAA
282062707	96198	TGTTGGAAUGCATAAGAACATAUGCT	96199	GGAACTGAAACUCATGACATCTGUGT
282062920	96200	GTTTACTTACCAUACACTGGCCTUGA	96201	GCACAAAGGAUCGTTGTAAACTCTATUG
282068065	96202	AGAAATAATTGGUTCCAGCAACCUGA	96203	TGGCAGTAAGTAAAUTATGCTGGTTCUT
282077769	96204	AAGATTATGATAGUACCGGTTTATUGCACAA	96205	TGAACAGAUGCAAGGAAATCCUCAAT
282078140	96206	TGCACAATTCUAGAAGCTTATCTGTUAGG	96207	TCATCTTAUCCCATGCGTGUGAA
282093342	96208	CCTAGTGGUGAGTCAGGCAUCT	96209	GTAGGUCCACGGGCTCUG
282095462	96210	CAACACCCCCUTCAACCUGA	96211	CUATTCGGAGCUGACCCACAT
282112938	96212	TGGTGTGTGUCATGTTCTGCTUAT	96213	ACATATTCGTUAAGCAACTGGGCUT
282119945	96214	GGGAAGATTUGGTTGTGTCUGGA	96215	GGCTTCTGTTUTGAGACTATTTCUGAGT
282127298	96216	ACGATCCTTUGTGCCAACTGUAA	96217	AATGTGAGGUGGCTTCCAAGAUAC
282128968	96218	AACCAGCAUAATTTACTTACUGCCACT	96219	GAUTCATGUCCAAAAGGCACACAA
282132617	96220	AGCACTGCTUCTCTCGAAAGUC	96221	GCACAAATAATGTUGTACTGATGTGCUT
282148423	96222	CCTTGCCGCAUGAAAGGCUA	96223	CAGCTGUGCGAGGTUCAAAG
282157061	96224	CCAGGAACAUATGCAGAATTUGCC	96225	GGCTCACCTCUAAAGAACTCATTGAUA
282164552	96226	CTATCAAGAAGUGAAACTGGAUCAACGA	96227	CCCACACCAGUGTCACAUCAAT
282178889	96228	CCCCACUTAGCCGCUGA	96229	GGGUCCCCAGGGUGGAA
282184631	96230	TGGCTAAATACAAACUGAATGAAGGUCA	96231	GAAAACCUCAGCAGTAATAGTGAUGGAA
282195023	96232	ACGACGCCUTTTGGGTGAUA	96233	AGTACTTGTUGGGCCCACTUT
282196815	96234	CCATACTTTCCAUTTTCAAAGCUGCAT	96235	CCTAACATCTAAUACATTCTTGCUGCCT
282242303	96236	CAGAGATUAACAATCCCCUGAAGAACA	96237	GUCAAAACCCAACAGAAUGAAGCC
282256911	96238	CAAGTTAGTGCUACTGGAAAAUGCAAAA	96239	GGTGAAGATGAUGACCACACUGAG
282259218	96240	ACTGCATTTTUGCACTTTTTCTUCCT	96241	TCATTTTGAGAAGAGCAUGAAACGGUAT
282265071	96242	ATCCTTGAAUCGAAGGCCAGUT	96243	GCTTTACTCUGAAGCACTACTTAACUCT
282267948	96244	GCAACTCTGAAAUAAAAGCAATCTGGUT	96245	ATCATGATGTGUAAGCCAAAAGAUGA
282268085	96246	TCCATTAGTCUACAATCCTTTCUCAGGT	96247	TTTAGGTGGAAAUTCTTGCTTCTCTUCA
282268377	96248	GTCTACAATCCTTUCTCAGGTCATCTUT	96249	CATCATCTTTTAGGUGGAAATTCTTGCUT
282275217	96250	CCACAGGAAGCUGAACACUGAT	96251	TTTTACCCCUTGTGGAGAGUGG
282278952	96252	GAATACTUACGGGTGACCAAUCCC	96253	AGAGGTACUCAAGCCCGCUAT
282285486	96254	TCAAGAGCAUCACGACAGCTUAC	96255	GTGAGUAACAGCTATGUAAAAGGGACAT
282316828	96256	GCCCTGAAGUATATTTTTGTTGCUGT	96257	CAATCTACAGTUGAGCAAACCTACGUAT
282319604	96258	ACAGCAAGCAAAUAAAAATGGAGAAUGG	96259	AGCATATACACAUGCCCAAATAUCAAGA
282320404	96260	CCCTGTTGTAAGAAUCAAGGTATCCUT	96261	CATTTGAGTTTACGUCAACCTAGCTCUA
282426334	96262	CAGGGTCAAUCTCTCCCGUT	96263	AAATGAACCAAGUTTGGGAGTCUCA
282467247	96264	AAACCAAGCCAAAUTCCATUGCAT	96265	TGAATCTCTGAGUCCATGTGAACTUC
282478237	96266	CTACTUGCCAGGAAGCACATGUAT	96267	GUTACATGTGGUAAAGGAACAAAGCAG
282483637	96268	ACATTCAGCUGACACCATACCUG	96269	ATTGCATCAGTUTAAGGCATTTGUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
282525511	96270	CACTTTGTTTUGTGGAGTGUGAAACT	96271	GTTTGTCCAGUGACTTATGTTUAAACCA
282527970	96272	ACCTGAGACCAUTCTGAATAAUGCC	96273	TCCATTCAUGAAGGACAGACTGTUC
282529330	96274	CATAACATTTCTTTUGAGCACCTGGTUT	96275	TCTTTTCACAGUGCTCAGTGACUT
282533077	96276	ACTTGTCTCTUCATTATCCCAATUCCAC	96277	TCCAGAAAUACCTGGTCUAAGAAAAGGA
282539053	96278	CACCACAGUAGTGGTCAUCAACT	96279	CAAGGUGGCATGTTATUGGCAAA
282542800	96280	ACCACATUGGGATGAACATUCACT	96281	TGGTGGTTTGTCUATCAACTTTTAGGAUT
282550522	96282	TGACATGTUAACAGACAAGAGTGCTAUC	96283	GTAATATGUCAATTTCCCAAUGGCCAAA
282553462	96284	AGGGTTCUCCAAGTACATGUCT	96285	CACATTAGAAAGGAUGGTGACTATUACCT
282553706	96286	TTCTCCAAGUACATGTCUGCACAA	96287	AAAACCACATUAGAAAGGATGGUGACT
282554656	96288	AGTCACCATCCUTTCTAATGTGGTTTUT	96289	CAAAGTGTCAGAUATTCAGAGTGUAGCA
282556394	96290	GTGGCTTGTTUACAATTTCACAGTUG	96291	AAACCACAGTTTTGAAUTTTCCTATTCTTGUT
282576160	96292	CAGATGAAUGCCATCAGTTUGCAC	96293	GATGAGATGAUAGACAGGCAGAAGTUAA
282577341	96294	ACTTTTCTCTCUCTGGCTAGGUACAT	96295	ACCTTATTATGUGTCTGAGTCTGUCCA
282577439	96296	CAATATCCUCATACTGGTUGGACAGA	96297	TGTCAGAAGTTCUCCATTTTAGAATGAAUGT
282578321	96298	ATACCCATAUTATATAACTTAGUACCCACACT	96299	TGGGATTAUTGAATGGGUGAACAACA
282578325	96300	GTTTGGUCAGAATAGGTCUCAAACCA	96301	GAAAAGAUGCAGAGTCTCGUAGAAGAG
282579012	96302	GTCTCAAACCAGCAGUGTTGTUC	96303	ACAGTGCUTAAGAAAAGAUGCAGAGT
282579870	96304	AGTTCTCTTCUACGAGACTCUGCAT	96305	GCCTTCAATGACAUTCTTTGGTTAUGAA
282583961	96306	ACACTACTGACAUTCAAGTCCCTTUG	96307	TTGGGTGGGUCATCCTACTGUA
282602113	96308	GCUAGCAGCCAGAAAAUGACCAA	96309	CCATAUCAGGGCCCGAGAGAUA
282607198	96310	TCCTTACCATCAGUTCAGGTGATAUGA	96311	AGCCTGTUGAGACAAGATTUCCAA
282615988	96312	ACGCAGCAAUAATTCATTATGCAAUCC	96313	GAGCTCCTGAUGTACTAATAGCATGUT
282681423	96314	GTTGTTTGTAUCACACGTTAGTGGTCUA	96315	GUTGATTTTGATGTTUACCAGGACAACA
282681634	96316	GAAGGAGGACUACTCTATGCTTTTGUG	96317	TTGCCACTCTAATUGAAAGAAAGTAGTCUT
282687788	96318	ATTTTCCAAUCCTGTCAGGUGACAT	96319	CTGAAACTAGUGAGAGCAGAACAAATUG
282691778	96320	AAGCTTGCAGCUGAAAGAGGUA	96321	CGTGACATTTCTUGACTCTTCATTTGUT
282725734	96322	GAACTGAUAAAGGGAAGAGCTAATUGGT	96323	TCAGGCACUGAAAGCUGAGAAAT
282729136	96324	TTTCTGTTTGAUTTGCTGTGUGGAC	96325	GATCAGCAUACCATAAAUACCCAAGACA
282735525	96326	TGAGTUGACACAGATCAGAUGCAA	96327	TGCCTTAGAATGGUTAGCTTTAGATGUC
282747174	96328	ATAGCUCAGAAGTATTUCAAACAGGCT	96329	ATTAATTTGUCAGGAACTGGGAUGAAGA
282752384	96330	GCACUTAGGCTUCAGGCAAAAA	96331	CTGTTCAGAAACUGGACCUGGA
282752754	96332	GCCACTTTGCUGTGCTGGAUA	96333	CCCTTGCAATUGAGAAGACTTATTUGT
282754619	96334	CACCACCUTATCAATGGTUGCC	96335	AAGGACTGUCAACATAAAUCCAAGAAGA
282754712	96336	AGTCAACAGAGUTAACTGAAACUGCAT	96337	GAGGGTAAGAACAUGTTAATCCAUGGT
282758133	96338	CATAAATCGGCCCACUAGTAGCAUAG	96339	TGATGTUCACCAGGCACTAATUGT
282759508	96340	GACATCCAAGTTAUCACTACAGAAGGUT	96341	CGTACTCACAAUTTCTTTTGGCTTUACT
282761434	96342	ATATTTGATAATGTUAAGCACTTAACCAGUAGT	96343	GAATACAGTGGAUCAAATAACGCAGTUG
282761708	96344	ACTGATGACUGAGAATTTACCUGCAAAA	96345	AATCAATGUGCAAGGAACAAGAACUG
282762575	96346	CAACTGCGTTATUTGATCCACTGTATUC	96347	ATTATCTGACGCUGAAGGGAATTTUCT
282776170	96348	GCCAGAAUGCACAGTCAGTCUT	96349	GTGTGGGTAATTUATACAACCCTGAUGT
282779880	96350	ACTCCTCTCTUCCAAAGGGATATUGA	96351	AAACTACTGGTUAAGTGCTTAACATTAUCAAAT
282846816	96352	GCATACCAUCATCTGCCCUCA	96353	CCTCCTTGCAAUTACATTGTGGUAAC
282863158	96354	ACCTTACCUGTGATGAGTCUGCT	96355	GAGAGAAAAGATUCACATCAACGAAUGG
282869649	96356	TGTCTGATTUGGTTATCTGUGCACT	96357	GGCTGAATGUGAGTATCGACATGUAAAT
282880470	96358	CUAGGCTUGCACAGAGGGAT	96359	TCCCGGTGTAUGAATCTCTTGGUA
282886729	96360	CCAGTGGCAUGGAGTATCUGAG	96361	TCTAGCCCUGCTTCCATCCUAA
282896541	96362	CCGGTCAATGAAUTGACACAGAATUT	96363	AACATTGACACUGAACACATTTGAUGAG
282905757	96364	CAGACUGGACACCCTCTTUCC	96365	GGUCTGATGUCCCAGAAACACC
282925364	96366	CACGGGACAGUACCAGTGTUT	96367	CTAUGAGCGCCACATGUCCT
282960851	96368	CTGCTCCAUGACTCTGUCCAC	96369	GAAGTTCAGAAGGAUGTGTGTAUGCT
282984326	96370	TGAACAGAUACAACCACAGATTCAUACC	96371	GCATTACCTTAUACAGGAAGCTACUGAT
282986707	96372	CAACCAAGATACAUCTGGCATAGUAAGT	96373	TTCTTTTUAGGCCAAGACCCAUGT
282986965	96374	GTAGTCGCUGCTCAATGUCAAGA	96375	GGGTATTGGUCAGTAAAATGGTATUAACA
283004468	96376	AAAATACTGAATUGCAAACCTCAAGUGAA	96377	CTCACCAGAGAGAAAUGGCTTTAAAUAC
283007813	96378	GAAAACGUTGGCAATTUCAGACAAC	96379	GCTCTAGTTTTUGGTAGAATCCCTUCA
283057285	96380	CTGTTACACCUTCTTTACAGACUCCAT	96381	GGACAACTCTUCATGCAAGACAAUAAC
283058118	96382	CCATAAUGAGAACTGTUGAAGACACCT	96383	TGTCTUGAAGGCAGCTGGUT
283060597	96384	AAATATTACCTGUTAGCATGCACUCCA	96385	GGTCCCCAAGCUATTATTGAAGTGAUAA
283071903	96386	GAGACGCCCUGGAACTTGUA	96387	GCCAAAGTATTUCTAGCCTATCCUCAAC
283073007	96388	TGTGAGAAATGTCUACACACAAGCTUT	96389	CTTGTTCCUGAGGGACCCTUT
283075626	96390	GCGACCUCGATCTGTTCAUGAAA	96391	GCAAAAGATTAUGAAAACATGCAGUGGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
283079514	96392	AGCTGTCATCAUCCACATTGCUT	96393	CTGCTTTTUCACAATTGATCTCUCGAAT
283083996	96394	CAACAAAAACTUCATCGTGAGAAUGACA	96395	GCCGCUCCGATCGTGUA
283085596	96396	TCATTCCTCAUTTGTACACGAUCGG	96397	CTTGGGCAUGGGAATAACATACTTUAA
283121544	96398	AAAAAGCTAAACAGAAAUTGAACCACCUT	96399	CTGCTTTAAGTTTUCACATGAGTCCUT
283121653	96400	GCTCCAAGGACUCATGTGAAAACTUAA	96401	AGGATCTATTACTAAUATCGTAAGCATCTTTUG
283124538	96402	CCCTGGCTACAACAUATACCAACATAUT	96403	ACTGTGAAUGTGACAAUGGACACT
283127011	96404	CTGAAAACAGTGUATCCAGCAGCUA	96405	GGCCTCGTAACUGCATCTAATACUAAAA
283144502	96406	AACAAAACAAUAAACTTGTACUGCCAA	96407	GGCAATGTCTACAUCCTTTTCAAAGUCT
283165738	96408	CTAGGAAAUTAGACTGUCCAGCCAAA	96409	CAGTTCATAUATCAGTCAAUGCCACGA
283168724	96410	GCCATAGAGTUAACATTCGTGGCAUT	96411	TGAAAACGGTAUGTGGTAGTTTGAAUCT
283219268	96412	CGTATTUAAAAGCTAACTUGAAGCAGCA	96413	AAACTACUCCACACTUGGCACAT
283220045	96414	TCATAGCGGUTTGACGCUCAA	96415	GCATTTTCUCACATGCACTGUAAAAGAT
283281688	96416	CAGGGACCUGATTCCCTUCAAT	96417	TCAAAATCCACCAAUTGCAGCTUAC
283296944	96418	GCUGGGAGCCCAACAACUT	96419	AGGAGCCCCCAUCACUCA
283306387	96420	TCTTGCATGTCAUAATGTCAGTTTGGUA	96421	CGACCCTUGACCACAAGUAACC
283313013	96422	CCTGTTCCUTTCCCCAAUCCAAA	96423	AGACTCTCAAUGGCAATCCACTUG
283314925	96424	GTCCCAGUGGAGCACATGUT	96425	ATCCACAGUTGTAGTTGCUGCT
283323898	96426	TGTACAGGAATUACAGTAGACGACUCT	96427	AGTTTTACAUCCCTGGGUGGAC
283332949	96428	CGTAUCGCCAAGAUGCCAGT	96429	CCAGGCAUAGTGTGTGAUGGT
283342781	96430	GAACGAGTCUTTGGGAACGUG	96431	AGCCGTGTTTUCCCTTTGTTACTUA
283360114	96432	AAGGCTTCAUCCATGACCTGUT	96433	TCTTUCGCCGGUGGACAAG
283363328	96434	ACATACACGUGTTTAAGGCAUACA	96435	ACACAGAATGCCAUGAAGCTAGUC
283368852	96436	TGATTCTTTTTACCUGTCTGTCACUGG	96437	TCUTCTTTCAGUGCACAACCACAT
283375389	96438	GTGTCCTCAUCTTGGCTCTCTUC	96439	ATTCTGATTCTUAGTCATCACTCCUCCT
283386731	96440	CAACATAAACAUAAAAGACUGGCCACA	96441	CGAGCTGTAAUGCACTTTGAATCATTUA
283388314	96442	ACCTGTAAAAAUCCAAGATGTTCCUGAA	96443	GACTATCAGAGUGTAACCCGTTTUCT
283395824	96444	AGTGAAATCAGATTAUTGAACAGTATAAGAUGC	96445	GTGGUCCAGGGCCTUGT
283397837	96446	TTACTTCTCCCCAAUTTCCGTAGTUC	96447	TGTGGTCUGCCAGGAUGAAAAT
283403090	96448	AGCTAGGTTGACGUAAACTCAAATGUT	96449	TGGAAGAUCCAGACAAAGATGTUAGAGT
283403251	96450	GCTTGATATTUCCACTAAAAGCCACUCT	96451	GGTATTGTATACTCUTGTCCTTCAGCUT
283405313	96452	TCGCAGTAACUAGCACTTTGUCC	96453	GGAATCCGCAGUTTGTGCATATTUT
283476185	96454	TGUGAAGGAAATATGTAUAAAACAAGCAGGA	96455	CCTCAAAGUCAAGGTCTGAATAUCGT
283476215	96456	GAGAAGAAAATCACGAUATTCAGACCTUGA	96457	ACCCTTACAUGGCTGCATAGAGUA
283485642	96458	ATGACTCTCTTUCCCTCTCTTCUCAA	96459	GACACTTCUCCCACTCTGCUG
283488456	96460	CGGACTGACCUCCAGTTTUAGAA	96461	CATGGGAACCUTACAGTTCTTGTUCA
283497024	96462	GATTCCGCCUCCACATGTUCT	96463	GAGACACACATCAUTTCTTTTTGTGCUT
283503083	96464	GCAAAGGAUGCTTTGGAACUGA	96465	AAATGTCAGGCUTCCCAAGTCUT
283542865	96466	ACTGCAAGAUTTACCTTGAUCAACACT	96467	CCCTTCCGUCCTTTCATUGGAA
283545243	96468	GCCTCTGTUCTAACAGACAUCAACT	96469	CCTTTTGAUGACACCGGAGUGA
283559913	96470	TTCUTTCTTTTTGACTCUAGGACAAACAGT	96471	TCAACACTGGUGCCTCGTTUT
283570491	96472	TGAAGCAUGAGAACATATTACAGTUCAT	96473	CTCTGAGGGAUTTATAGCCAGCAUT
283587600	96474	TAATTACATTGGAGAAAGUAAGTTTCACATGUT	96475	CAAAGTGACCAUCTATCTTCTUCCACAT
283588639	96476	CTTCTCTCUGTTCTTTGUGACACAC	96477	GTACTAAAGCUGGCTTTGCACCUA
283590722	96478	CAACCCAGUAAGACAUACACCAGAA	96479	TGTGAAAGTGUGTTACTGTCUACACAT
283594981	96480	TCAUCAGCCACCAACUCGAAA	96481	CAGGTCAACUCACAGGAGGATUAC
283598048	96482	TTCCAGAGTTCCUATTCAGGGCUAT	96483	CATGAAAGCCUTGGCTTGCUG
283598411	96484	CATAAGCUGACGACGGCCUT	96485	CCGCCGAUGCATCCTTUCT
283603108	96486	CCAAGTGCACCUCGGTGUA	96487	AGAAGUGTTCCCUCAGAGCCA
283604607	96488	ATAACAAGCAGUGGCAUCCCT	96489	CAAAGAAATTGTAUGCTGCTATGCAUGA
283605102	96490	CTCCATCAGGUTCATGCAUAGCA	96491	AATTGCTGTTTCAAUATAAACAGGTGGTTUT
283617205	96492	CGTTTCUGCCGGCUGAAGT	96493	TGGAAGAAGTTUAGAGTTGGACAAUGAG
283662325	96494	ACCACAAGAUAAGAAATCTTCCATTCUG	96495	ATCTGTCACTUACGTTTTGGAGUCAT
283662385	96496	GGGTACTTTGAAUCCCTATTGTGTATUGT	96497	CTGTTAACUAGCAGGCAGCUGAA
283677332	96498	CCCTGGTAAUAGACCACATTTGGUT	96499	CCCTCUAATACCTCUGGAGCCAT
283678518	96500	AGGTTGGUACCCGGAGGUA	96501	GCGAGAAGCCAGUTCCCAUAG
283679808	96502	CACATGATGTUGAACACTAGAAAUGCAA	96503	CACCCGACCUTGTTCUCAGA
283680890	96504	AGGATAGATATGUATGCCATGGGATUAGT	96505	CCTTGGAGTGUATCATCCCTTTUCA
283686814	96506	ACACAGTCCUGACTCCAACAUC	96507	GCTAATTGTTCAAAUCAACTGGACUCCT
283686868	96508	AAGTATCACTCUGAGGGCTAGAAGUT	96509	GATTTATTGUGCAGACATGTACTUGGAG
283700663	96510	ATCATATACCUCATTCCAGCTATUGGC	96511	AAGTGTTTTGCAUTGACCAATUCCA
283707673	96512	TGTGAGTTGGAGGUTTCTGTACTUG	96513	TCTTTTCTAGTGCUCAGCTTCTTGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
283710748	96514	TTTTGAGTGAUAGGTTAGCTTTGCUGA	96515	ACCACTGCCUACTATTAGGGUAACT
283714100	96516	GGAATCCTCUGGCACACCTUC	96517	ACTAAGCATTGCAUTTCAGGTCTAUCAA
283727830	96518	AAGTGACAGTTUCCACATTACCAUCA	96519	ACCTCTTAUACACATCCAGCCUAAAGA
283730043	96520	GGTAGTGGAAGAUAGCTGCAGUT	96521	CACATAGAGCUTGGGACUGCT
283765127	96522	TTGCTAGGGAUTTAATTTTTGGACUACCA	96523	AGCTCCTTUGCAGTTGATGAGUAT
283770404	96524	TGATGACATTUCCCTGGCCAUT	96525	GCUAGAAAGGCTGGUCACCAC
283776005	96526	GCCAAAGTAAGAGUTCTTGCCTTCUAAA	96527	TGGTCAUGAGCCGATTTTTAAGUCAAT
283777611	96528	GGAGCTGATTGUAAATATCCCATGTGUT	96529	ACTTTTTGAAGACUTGGTTTACCUCCAT
283784323	96530	AGCATGACCCAUCACATTTCTUCT	96531	ACACAAGAAAATCUGTGAAGTCATCUGT
283788728	96532	GTACCCCAAAAAUAGCAGGACTCUT	96533	TCATAACGAGACUTCTGCGGATUG
283788846	96534	GGAGAGCATUGTAGGCTGTCUG	96535	CTCTCACCAAUGTGTTGTTACTUCCT
283788910	96536	TGTAACAAAUGACAGGAGGGAGTUG	96537	AGTCAATCGUCAAGGATTTAGCAAAUGA
283836053	96538	GCAAAUTCGATCCAUGAGCAGAAAC	96539	TGAAAGAAAGAGTUTTAGGACACACAUCA
283839618	96540	GCATCAGCTGUAACCATAATTTCAAUGT	96541	CAGTTTACCCUTTCATACCUACAGCA
283864245	96542	TATCTTTGCCUAAGGAAGTACUGGAA	96543	AGTTTTTGUATAGGACUGCGCCAA
283864949	96544	TCUGTATTTGTTCTUGGCGCAGT	96545	CCCTTCATATUACCACAGCTTGTTUGA
283875548	96546	GTGTACATATUCCCCCTTTTCUGCT	96547	GCCAACCCAAAGUCAGCAAUG
283877707	96548	CTGTTGAAAAACAACCUGACAGCUT	96549	ACTAATTCAGTCCUGACATGCCAUT
283892392	96550	CTCCTCCUCACGACCTTTCUC	96551	GGCTTGUAGACCCCTTGAAUCT
283904448	96552	GCAGATGATGAGUAATAATTGCATGUC	96553	TGCCACTTCCAUCATTTGTTACUCAA
283911093	96554	CCTTAGTUCACAGTCTGTATUGCAACT	96555	TCATTTGACTTUGGCCAAGGUCT
283914250	96556	TGTATGCAAGTUATGTTTCTTCGCUGA	96557	CTGGCTCCTTUAAGCTATTAGCAGAAUT
283926830	96558	GCTAAATATGAAUGCGTGACATUGCT	96559	CCAACCAAGACUCTTTGATGATTTGTUA
283958763	96560	TCTTTGAATGTUTGTAGCTAGAUGCAGAA	96561	CATGCAGTTACUGAGCTCTAGUGT
283975281	96562	TGCAAACAUGCAGTTCTCATACUCA	96563	GCATTTTTACCTUGCCAAGTACTAUGAC
283984885	96564	TCTGTGACCAUGGGCATCAATUT	96565	GGGATTTCCTUAGGTAGGTATCCTAUGT
284006355	96566	GTAGAGATGAGGACUACAGCCCAUA	96567	TCTACATGATCCUCTTGTGGAAUGGA
284008048	96568	GGAATGCCCUTTCACTGGTTUACT	96569	GTATTACCATTAGCUTCTCATCCTTCACUT
284018566	96570	CCACATACUGGCTGTTGTTUACGA	96571	GCCATCTGCUTTTTGTGAAATTUAACAT
284094978	96572	CATCCCAAAAUGTATTGAGCAGUAGGA	96573	GTTGTTTTGGGUTCAGGCCTTATUG
284096998	96574	GTCATTAATTCCAAAAUCATCGTGGUCA	96575	TGGTGTTATCAGUTGAAAGAATGACUGT
284114386	96576	CGAGTATTTCCAACUAATTTCCCAGGAUT	96577	CACATGATTCTGUTCTCCCATTTTCUG
284117222	96578	AGCTGGCTGUAATATTGAAAGGAGUT	96579	CAAACAUAACCAGGAGATAGGUGGAAAAT
284125592	96580	ACTTGGTUGGAGAGCTGCTUAAAAT	96581	CCCTCTGUCTGCTCATUCAGG
284129794	96582	GGCTGTTCGUAACCTGCTGATTTAUAT	96583	CCAAGTGCAGUTTGTAAAGTTTTUAGGA
284139668	96584	AGGGAGTCATTTAUGGATCGTATTCTGUA	96585	AAACTGAUAAGCCAGGAGUGAAAAGT
284140582	96586	CCAAAAAGGACCUTAGCTGCTCUA	96587	CATTCTTGGAATUGCAGAGTTGCATUAT
284140973	96588	CGCTGATTTTGTUAAATAACGTGGTGUT	96589	CTTCCCCTCUCTTTGGCACTUA
284142331	96590	ACTCCTGGCTTAUCAGTTTGATCATTUT	96591	GGGAAATTAGTUGGAAATACTCGACGUA
284145573	96592	CCAAGAATGCUTTCGTTTTTCUACAGT	96593	GCTGACCTTGTUCAATACCAAAAACUC
284176671	96594	TGTATTGGAACTUGGGAACAATTCUGT	96595	CAACTAACTATUAGGGATGCTGUGCAA
284234024	96596	TGAAGATTCTGAUGTTTGCTCTGTUCT	96597	CAGAAGATCGCCUGCATAGAAATTTUT
284237796	96598	CGCACCCAUCCTAAAACTGCTUAT	96599	CAGATGAATUAAACACGTACAGAGUGGA
284238766	96600	CACCAAATCCCACUGTGACAATUT	96601	CCAATGAAAAATCUCTGAATGTCACCUT
284250516	96602	AUCTTTAATGTTTAGUAGAAAGCGAGACA	96603	CTGCUCGGCAAGGACCAAUA
284250590	96604	TGGUCCTUGCCGAGCAG	96605	CTGGATGATGACUTTGGAAATGACAUT
284252379	96606	CAAGACACTGUTGGATTTAACUCAGAGA	96607	CCTTCACGAACUTGTCTCCCTUAC
284258261	96608	GCTAAGCTATUCAACATTGCCUGGA	96609	CCCCTCTCAAAUTATCATCCGTACAUA
284270179	96610	ACTTATGTTTCTUGCAATATTCTGGTUAAAAA	96611	GGAGATTGCUACAGTGCTTUCAGA
284270209	96612	ACAAATATGAAAUACCTGTGGGCAUCT	96613	TGCATTATTGUCTCCATGCUAAAGAGT
284270557	96614	TGAATUGCGGAGAACTGTGUACT	96615	TCATTGAAGGCUGGTTATTUACAGAACT
284276577	96616	GAAAGTGACUATATTGTGAUGCCCAGA	96617	TGAATTCAGGGUTTACTTTGTAGUGCAA
284346107	96618	ACTCTTAAAAAGUACTGCTGTUGCCT	96619	CATCTGTCTCUGGAGCAGCAUAC
284365870	96620	GCTGCAACCAGAGCUCTAATTUCT	96621	TGUTGTTTTTAATTTUAGGGCCGCAA
284374831	96622	AGTGCAAATGGUACCAAATCTCCUT	96623	CCGTTTGTTTCUGGGATATTGGAGAUA
284379455	96624	CACACACATTCUTGTGAGCACUT	96625	GCTCTCACTUCCATGGATTTATUCCC
284380659	96626	GTCAACTTUAAACAGCCATCAUCAGAAT	96627	TTAATGACTTATTTUGTGCTTCTGTAGUAAACA
284428752	96628	TGTACCUAAAAGAAACACAAUGCCT	96629	TCCTCCTATTTTUCATGAGTGGTTTCUG
284429991	96630	CATGATGTAGGAUCAGGGAATGTUCT	96631	GCCAGTGTAUGCTACCAAAGUCA
284434129	96632	GAUGCCUGGGCAGGAGAAAT	96633	GATATCACUCTTCCTUGCAGGAGT
284454677	96634	AAAGTCTTAGATUACAAAGCTTTACUAACACAA	96635	AGTGACGAGAGAGAAUTGCAAUGAAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
284455842	96636	GTTTAATGTACCUCGCTCCATTCACUA	96637	GTATGAATAACTTUGGCCATCGTCTUG
284456269	96638	CCCAACUGGGACAGGAAAATTCAUT	96639	CAGTGTUCCAGGAGTTGUGGAG
284456717	96640	ACCTTUCCCCTCCUCCACAA	96641	AAGTTGCCCCTUTCTTTCTAATTACGUAT
284463504	96642	TCTTCATACAAGACUCACCCTUCAAGA	96643	CTTGCCUGCCTTTTGTTACUCA
284488710	96644	CCCCTCATTUTGCTGCCCUA	96645	CCACCCUCATCCATGTUGACA
284496531	96646	AGGAGCCUGACGAAATCCTCUA	96647	ACATAGCGUCCAGCAGGAUG
284499726	96648	CGTAGTCAACCCAAAUGGGTGTUA	96649	GTTCTGAAATAACCCUAACCTTACCUGT
284503176	96650	GATTCCTGUAGCTGCCUCACT	96651	TTGGATCCUGAGAGGGAGUACC
284547951	96652	CATAGCATGUAAACAGTTGGGAAUAGGT	96653	AGAGATGGAUGCTGGCCAATUT
284548790	96654	GAGTTCTATTUCACAGTTTACCUGACACA	96655	GAAGGCAGAUGGGAATGAATAUGAAGAT
284552138	96656	TGTATATAAGATGUGGCTTGTTGUGACC	96657	TTTTCTTCTUGGCGACTGTUAGGAA
284552408	96658	GATGAATACAUGTTGCCATTUGAGGAG	96659	AAGCTAACTGGAUAACTTACAGCATGUT
284556658	96660	GGCCTGTTUTAAGAGATTATUGGCAGA	96661	ATCACCTUCCAGAAAATACTUGCAGAA
284564354	96662	CATGTAACTUCCTGTAATTTTUCAAGGCT	96663	GCAAGCCATUCCTTTTCCTACUGAA
284567672	96664	CTCACCAAGTTTUACTGGACTAGGTAUT	96665	CTCUGAACACGGACATGUGGA
284574029	96666	GGCUTTCAAGTTCCUACAGAAGAGG	96667	CCCCAGAGAUAAAGTCAAAGATGATUCT
284577335	96668	CAGACAAGTUGACCAAGTAUAGAAGCAA	96669	GGCTTTGTTTUACCAGTACTTTTGUCC
284675777	96670	ACTATATCCACUCTTACCTGAAUGGCA	96671	GTAGAAGATUCAAGCTTTGCCTAUGGA
284679529	96672	GGTAAGCTCTTGUTAGCTCCATCAAUAA	96673	CATGGAAAAAGCAGUACACCUAAGAAAA
284744507	96674	ATCAGGAAAUCCAGGAAAATGTCTTUCT	96675	GCCGACACCCUTTACAGTCAAATUAA
284746756	96676	CCCAGTATGUTTTGGTGCUGGAT	96677	ACTGTGAUGGTTCGTGTUGGAG
284753434	96678	CGGTTGATTTUACACCAGGAGGUT	96679	GCACCUACCUGAAGAACAGGAGA
284756111	96680	GGGCCAATAAUTATATTCGAGGTUACT	96681	GTCTTTTUCGAAGAGCATGTGAAGUT
284758652	96682	AATGGGCCAUACCAAATTATTCUCCT	96683	CCAGAGAGAAUAGAAAGCAGCTCAAAUA
284762169	96684	TCACGCAUCAGCCTCATUGT	96685	AGAAACCTTTGAAGUTCCAGAAATTGUG
284763569	96686	TCATCAAGUGCCATCCAUCCAC	96687	GCAAATTGCACAUCATCCTGTAGTTUA
284765480	96688	ACCATATTATGAGUCAGGCGAAAUGG	96689	TGCTAAAAGAATCUGGACATGAAGTUCT
284765703	96690	GGCCAUGAAAAUCAAAACCACAACT	96691	TCTTAGCAATUGGTTTGGATTCCUGT
284766325	96692	GAUCCATCACUCCGAAAAGCCA	96693	CCUCTATATCTATGAUGGACCAGACAGT
284766478	96694	TGGCGTTUGCCGTCTTTCTUA	96695	GGACTCUCCGACUCAACACC
284766633	96696	GGGCTATTACTGUCTGGTCCATCAUA	96697	TGGTTAACAGCCUAATAATAATTATCCTACTUC
284768236	96698	GAGUTTGTGGTUCAGGACAGGAA	96699	GTTTGATGAGACACUGATATTCAATTTUAGCA
284768320	96700	CAGCACGCUTTTTGACATCTUCT	96701	AGAUGAACAAAACUGGGCCACA
284774584	96702	GGATACTAACCUGTTGTCAATCUGCAC	96703	GTTGCAGAAAGCUAAAGCCAUCA
284785802	96704	CTGCTTTTTCUTTGTGCCAGUCAA	96705	TGAAAAGAGACAGGUATTCCAUGCC
284803520	96706	CCCAGGGCUCAATTCCAGUAAC	96707	GACCCTGAGAUACTGAAAAGCTGTUT
284835791	96708	GATCTGAATTCACCUTTTCCTCTACGUT	96709	TGTGACAGGGUGAACTTGCUG
284839729	96710	CTCCTGATCCUGAAAGTTCTUGCT	96711	CCATGCTGUAGGCATCCTCUC
284843518	96712	GGCTTGTAAUTTTCAACTTCUCAGCAA	96713	GCAGAGCAGCUACTTCTAGAAAAUCA
284846222	96714	CTCAATAGTUAACCGGGCUGGA	96715	TGCATACTAGGGUTGCATTTTAGGTTUA
284851999	96716	CGGAGCUCCTGACCUACAC	96717	GGCATTTTCUCATGTCAATGUACACA
284866094	96718	CAUCCAUCACAGGACCACAGAG	96719	TTTTGGCAUCAGTGCTCTCUCA
284874763	96720	CAATAACAATAGUCCTGACTTACCAUACAGT	96721	CCATTTATTCTCCUGGGTATCCTGAUGA
284878493	96722	GGTACTCTUACAAGCCAAAAACAATCUT	96723	TGCCTTTTTCUCCACAGTCAGUT
284891501	96724	AGAGTTCCATAAUCTCTACGTATTGUCACT	96725	AGGTTGCAACAAUCTACAAAGAUCCA
284896146	96726	GTGACTTCATTTGCUGTTAACTGTATCUC	96727	GAAATGGCCUCTTCCAGAAAACUC
284949116	96728	AAAAGUAGGGCAAACAGAAUGAGGAA	96729	TGCCCCAGUTTCTATTTAGUAGCAG
284949709	96730	TGAAGGAAGCCCUGATTGATCTUG	96731	CCGAGAAGCUCTGCTAGTCUG
284964077	96732	GGAACGACTGUTGTCTGTTGTAAAUAGA	96733	TCAGACTGAACUGAATTATGATGTTCUGG
284964094	96734	AGAAGATTUGGCCCATCATGAACUT	96735	GCAGTCCAAAGCAUTATTTCCATATATAGUGT
285025396	96736	CGTGTUACAGCAGCATTTTUGGAA	96737	ACGTCCTCGUATAAGGCTTTTTGUC
285043149	96738	CATGTTTTGAAGUGTCGCCTTTCUA	96739	AATCCTUGCGGAAAGGAGCUT
285058216	96740	AGGACAGAGAAAGAAUAAGTAGCACUCT	96741	GAGTGCAGUTTCAGAAUGAAGCA
285067867	96742	GTTCTCACAUTCAAGTATAUACCCAGCAA	96743	CCCAAGUAGGCTTCTGTUCCA
285080116	96744	AAACAAGGGAACCAAUATACATGAUCACT	96745	ATTTCAGGCUGACCACTCAAUGT
285081564	96746	AGTGATGTUAAAGCCACGTCCUG	96747	TCCCAGTTTGAUTTCCTTGCTGTUAA
285112533	96748	TGCTUCAACAACATCAAUGCAAGG	96749	CTGATTGCACUTGGACCATTGUAG
285118642	96750	GGGATTCUGGAGAGTCACCAUCT	96751	TCCTGATUACCCAGAAGGGTAUGG
285129480	96752	GAAATTGTGUCCCCAGGCUCT	96753	AAGATGCTTGUGGAGGAACAAUGA
285134453	96754	TGGATATGAUGCCACTGGAUCCT	96755	GCACTTGGTAUCACATTTGAACTGUT
285144333	96756	GTCUTCCATAGGUGCACCCA	96757	TGCAATGAUGCAGTGGTUACAGAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
285145171	96758	ATCAGAGATTATCGUCCAGATGCAATUT	96759	TGTATTTCATAATCTUCCTGTTTCACCAGUT
285149030	96760	AGAACTGTTGGTUTGATATGTCAGCUT	96761	CAAAATGACAGAUTGAGCCACCAUAC
285174978	96762	GCCATTTTGTUGCAGTTTTGTTCAUT	96763	TCTTGGCCUCTTACUCAAGGACA
285176915	96764	CCAGAACACGGUATTCTAAAAUGCCT	96765	CCCCAGCCCUTGAATATGAAACUC
285177034	96766	TGTAGTGAAAAAUAAAGCATGTCTGGAUGA	96767	GCACTGTTCUATCACCAAACTAUCCAAA
285177464	96768	GAGTCGAATCTUACTTACCAAACTCCUT	96769	TTTCCUAGCGCCCTGUGG
285179532	96770	GTACTGATCUGTTTTTGCTCAUGCAA	96771	GGACTGTTGAUGTAACCCAUGGA
285180096	96772	GAGGCAAATUACCTTTTCCAUGGG	96773	TGCTGATCACAUGGATCTGTTTCTUT
285182434	96774	GTTCTTCCUGCTGCTGCCTUA	96775	GGTTAACCAATUCTGGGAAACATAUGAA
285187700	96776	AGAGTTTAGTGTUCAGTTCCGCTATUT	96777	TCCAAATGTCCUGAAAATGTGTCAGUAT
285188270	96778	GACTCCUGGAAAACAATGGAGAUCA	96779	GACAAGGCAGGUAGCTAAGTGUAAA
285191869	96780	CTCAACTUGAAATCGCTTUGCACA	96781	CGATATCAUGCACAATTCAUACAACCAT
285200215	96782	TGTCAGCCAUGGCCAAAGUT	96783	CCTGACCAGTUAAACATTTCATCCTUT
285230068	96784	ACGCTCCTCAUGGTTAAAATAGAATATAUG	96785	AGCCUGGAGGAGAGAATCAUCAA
285230145	96786	AGTCTTGGTATTUACCTGTCTGTTGAUG	96787	CAAGCAGAGCTUTTGCTAAAGAAAGUAA
285237447	96788	CATTAATGGGTCUTGAACAGTGTGTUT	96789	AGCAATTTAAGUCTGAGGCCTAUCAAC
285245790	96790	TGCTTGATGATUCAGTCTTTCCATTTCUA	96791	GTCACCUCCCCTCAGTAAGUAGT
285261665	96792	CTAATTAGGCAUTGAAGGAAGCTUAACA	96793	GGGAATGGUACCTGGAGUGGT
285265290	96794	ACGTAAGCACUGCGGTACTUC	96795	GGAAGGCUGGAAGGAACAAATTUC
285282790	96796	CCAGTCTUGTCCTCTCUGAGCA	96797	TGCAATGAGUATGCATGGUGACA
285286225	96798	GATGTAGCTAATACUAAAGCCCCAGUC	96799	GCTCAGGATAUTTCAACAGCTGUGT
285302550	96800	CCACAAATAUGATTCATGGUCACCACA	96801	GGAGCATGACCUGGATGATGUC
285316519	96802	GAGAGTCTUCCACCGTGCAUT	96803	TTGCAAGGUAAACAGCAAGATGUAAAC
285329817	96804	CTGAATAAGGCCUTGACCUAACCA	96805	ACAACCTGATGCCUAAAGAAATGCTUA
285361767	96806	CAGCTCAGTUCACCTATGTCTCTUG	96807	CCTGCUGAGAAAGGCATGAAGUAG
285378603	96808	GTGACTGACTUAGCATCTTACATCTTTUG	96809	TCAGGCCTCUCATTGAATAAGGAGUA
285388456	96810	TCACTTTCTGGAUGAAGGTGGAAATTUT	96811	AGAAGGCACAUGTAAGTUCCAACT
285480821	96812	GGCATGTTTCUCAGGAGTGTGUA	96813	CATTGTGGCACCAAUATTGACUCAC
285501519	96814	ACACTCTCTTTTUACTAGACAGGTGGUA	96815	AATGGAGTAGUGAACATTTAGCCAACUT
285548535	96816	GCAAATAGTTCUGCCAGCAGTAUG	96817	CTGCACAGAAAAGGAAUAAACACTTUGT
285572889	96818	GGTCTCUGCGGCCCTAATTUC	96819	GGTGTGGUAAGAAACTGGGTCTUAA
285577072	96820	GCAGCAGAAGGUTGCCUAC	96821	GCACCCACUCCUGACACT
285673634	96822	CCUCAGAGCTGATUGCCAAGA	96823	GATTTGAGCAUGCCCATUAGGAAAC
285683794	96824	CCATCAATGCAGAUTCTTCGAGTUC	96825	ACTGAAGCCAAAGUCAATCAAAAUGAAAA
285699181	96826	TTCACATCCAAUGACAAGGCCTUAT	96827	GGGAGAGAAAGUGGAGATGCTUAC
285702008	96828	TCCATGCTATTTUGGTCTTGAATGCUA	96829	ACGCUGGCAAAATGTTTUGGAAA
285702179	96830	CAACAAUAAACACAACCCTGCAUACA	96831	CGGGCTAGTTGUGTTAGTGGATTTUT
285709961	96832	CTGCTGCTUCCTTTGTTCTGTUT	96833	GATGTATUAGCCCATCAGUCCACAG
285716837	96834	TTCCTGCTTUATTAACGGCTUCCA	96835	TTUGAGGATGTTTCAUAACCAGAAAGGA
285719579	96836	TCTGATATUGGACCCTTCCCUCAT	96837	CCACCUCCCAACTCTGUCAC
285720114	96838	ACAAGAATTCTGCUGCTGCAATAAGAUA	96839	CCACAGGCACAAUCACGAUG
285744066	96840	TGTCATCTTTTCUTTAAGCCTCCAAUCT	96841	GCCATTCAACAUGAAAATGTCGAUGT
285747265	96842	TTCAAGCTTGUAAGAGCATGAAUACGA	96843	GGCCTTTGGAAAUGGTTGTTAAAAUAGT
285767745	96844	CAAAATAGGCAAUCTCCTTTCUAAGCAAA	96845	TCACAAGGUCCTGTTGGTAUGG
285779038	96846	CTCCTGAGTAGUAAGGGAGGCAUA	96847	GAGGAGCUAAAAACCAAAGTAGAACUGT
285780764	96848	AGCTGCTGATUAATTGTCTCCGTUT	96849	GUTACUGGACCGAGCCCAAG
285834532	96850	GGAGCTTTTCUGAGAGGTTCUCAA	96851	CACUGCAAGCCAAAAUGAAAGACT
285840722	96852	CCTTCAACCUGCTCTTCTCUGG	96853	CAATGCCAAUAAAACCTGCAAGAUGAT
285846611	96854	GCUTCUGAAAACCGAGCAGACA	96855	TGTTGGAACAGGAUATTGCAGGUC
285849174	96856	GCUCTACTCAGAAAUAAGGCCAAGT	96857	GAAAGAAAAAUGGGAATCGGUGGAA
285860264	96858	TTCATTCATGGCAUTTATACTGCTCUGA	96859	CACAGGTTGUGCAAGCTTAUGT
285867622	96860	CACATACTTTCCUTTCATTGAGTTUGGT	96861	CTGCCTTTGAAGCUAAAGAAGAAACAUA
285871715	96862	GGAGAGGTTUCTTCTGTGGCUAAC	96863	GATGATGAACUGGATAGCAUGGCT
285873003	96864	CCCCCAAAACUAGCTCAACATTUT	96865	GAAGGTCATTAGUCCTACTGGGAAUG
285881099	96866	GGCCTTTCUGCATCAGACTCTUA	96867	GCTTGGGACUGATGACCUAGAAAAAT
285886847	96868	ACACAGAUGGGACCAUAGCCT	96869	GTGACCTCATUGAGTTATTCTGCTCTUT
285904863	96870	TTTCTGCATCUCTCCCCACUG	96871	ACTAAGUCAGCAGGTTGAUGAAAAGT
285905566	96872	GGGTAGATTTATUGTCCATGTGCAAUC	96873	GGATTTCTGTUATTTTGCAGCUCAGT
285910178	96874	GAAGUCTGACAUAGCACCACCA	96875	ACTCAGAGCCUTGAAAACGUGAA
285912767	96876	GTGCAUCCAGCTCACTGUGAT	96877	ATTAGGTGTGUGAGCAGGUGAC
285917060	96878	GCCTGGACAUGACAGATACTTUGA	96879	GAGTTCTCTGUGGCTGCCAATAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
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285930418	96882	AAATCCGAATGUATTGTTCTGAGAUCCA	96883	GAUCCTTTGUACCAAACCCCAGAT
285954553	96884	GGGTGUCCCAGCAAAGTUCAT	96885	GGUGACCACCUCGACCAC
285962936	96886	GGAUGTAGGATCAUGAGCAGGAG	96887	CCCCGTTCUGTCCCGAGUAT
285965281	96888	TGCCTTUGAACCTCACAAUCGT	96889	GGACAAACGAGACCGUGCTUA
286027699	96890	GGTGGTGCCAAUATGTAGACAUCAAT	96891	CAGCATGGGATUCTCTAAATAAAGCTUG
286036580	96892	CAAGTTTGTCAAUCCGGTCTTUCC	96893	ACTGGCTTACTUATCAGAATGGCTTUT
286055295	96894	AAGGGAACCUAGTTGATACTAUGAAGA	96895	ACTGGGCACUTTCTAGCGTUG
286059899	96896	CTTTTTCTTTUGCAGCTGTCGUGA	96897	ACTUCTTCCTGCUCCGAAACC
286070103	96898	CAACACUCTCAGUGGACCGA	96899	CTAAGGGATAAGGUCAGAATGCAACAUA
286090884	96900	GCCATTCTGAUAAGTAAGCCAGTUGT	96901	ACAGGAGGAGCUGGATATAGTTATUAACC
286092481	96902	ACATGCCGCAAUGAGTUCAGA	96903	GTGGTTTTGCTUAAAATTCTAAGGCUGT
286096063	96904	TCTTTCAGCGGCUTCCTTCUC	96905	GTAGAGGAAGAACUTCCGAAGGUC
286102619	96906	GAGTTGGAACUACCACATTGCTTTATUG	96907	ATGGTGTCUTTGCTTTCCUGGT
286111400	96908	ATTCATTTTCUGCAGCCUCCCT	96909	ACAGTGCTUGAGAATAGCAAACTUACA
286119614	96910	GCGATTATUGTGCTTTATTUGGAAGACT	96911	GGGCUCCCCAATGACTUCAC
286122015	96912	ACCATTCTTTCCAACUCACTTATCTTUCC	96913	ACAGAACAGGCUTGACACTTUCA
286128378	96914	AAACTTGTTGCUGTTGTCTTUCCC	96915	GTTTCTTTATCTUGCATAAGTCCAUGCT
286131790	96916	GGAGACACAGUGCTACUCAAGT	96917	AAATTCCAATGUCCCCCGGUT
286142091	96918	CCTCTGGAGCAUTGCAGAUCA	96919	AGGCAACAAAGAGCAUTGCAAUAC
286144600	96920	TGTCAUGTTCTTGCUGGAGACC	96921	AGGUAGCAGAGAAACAGTUGAAAGAAA
286151315	96922	GGACUGAGTTTCCUGGGCAAT	96923	TCACCACCUGCTGCTGAAUG
286154531	96924	TTCTTGCTUCCAATTCAATTTTCUGCT	96925	AGAAAGAGAGACAAUGAGGAAGAACUCT
286158915	96926	CCAGGUGGTUCAGCAGAAACT	96927	GGTGTCUTTAGCCUGACAGCA
286160963	96928	GTCTTTTTCCATCUGCTTTATCAGCUT	96929	CAATCAGTUGGAGGAAAACACCUT
286163401	96930	GCCCAAGUTACAGAUGAGGGT	96931	TGCTGAAUCTCTTGCGUGACA
286166607	96932	TGATCTTCCAGUGTTCGTCTGGUA	96933	AGGGAACTUGAAACCATTGUGAGA
286169645	96934	GAGCTTGTTGUAGCTGAACTTTCUG	96935	CCTGGCGAAAAGUCAAAATTUGGT
286175635	96936	ACATTGGTCUCAGTAAGTCAAATUGCT	96937	TGTGGAAAAAGAACUTATGGTCAGTGUT
286184025	96938	TGAAACGCAAUACAAAAGCATGACUAAC	96939	ACTGUGGGAGGTUCCAGGAT
286187363	96940	GCTGCCTTTGUGTGTTTAGCAUAT	96941	ACAACAAAAACUGGAAGAATCCUCCAA
286188371	96942	GGAACTGGGTUAGATTATTGGAGGATUC	96943	ATCATACCATACAGUCCTCATAGACATAGUC
286188511	96944	TCATGGCCUCTCCTCTTGTTUC	96945	GACTUCACCACCCCAAGTAUCC
286188723	96946	GTTGGTCACACUTTTGCTTAAATUCACT	96947	GCACTGAAAAUTCAGGCAGAUGG
286192273	96948	CTCCTCAGUGTCCACCAUCC	96949	GTGCTCAGAUTGCATTATTTTGUGAAAC
286196692	96950	GAGCAAAGGAAAGCAAUAGUGCAA	96951	CCTGGCTTCUTCTTAGCAGGUG
286204365	96952	GTGCTGCGUAGCTGATCTTUAAAA	96953	AGCTTACUAGGCAGAATAAUGAAACCAAA
286206233	96954	CCCUAGGGAGGAAGCAACTUAC	96955	CCAAAGCAAGGUTCCCATTGUC
286208090	96956	TCGGATCTACACACUCTATGTTCTGUT	96957	CTCTTTTCTTAATAUAGCCCACAGCTGUA
286212555	96958	ATTCTGCCTGAAUTCTCTGCATCATUA	96959	CCAAAGGCUCAATGAAGAATUGGA
286215694	96960	AGCATCTCUGCACACTCATTACTTUT	96961	ACAAATCUGCCAGAGAAAATCAGAUCAT
286218273	96962	GATGTCTGGGAUAATAACAGAAGTUCGT	96963	GCCTGATGGAGCUACTTATGTATTUCAA
286218676	96964	GCTCATGGCTTTUCTCAAATTGTTCTTUT	96965	ACAAAGAGAAGUAGACAGAAUCACAAG
286218972	96966	CCAAATTGTCCAUAATCTTTGCCTUGAA	96967	CTGGGAAAAUATAGCTAUGGCCAGT
286226436	96968	TCATTATGACUGAGTAGATTGCGUGAAG	96969	TCTTCUGAAAGGGATTCAUGCCAAG
286228770	96970	GCTGTCTCACUGTCTATACTUCAGG	96971	CACTGAACTTAGAUGACACTGGAAUGAA
286244707	96972	CCTTCTCAGCCUGGCTTCUG	96973	TGGGCAACCUGCUGCAT
286249533	96974	TGGAAGUCCACAUGCAGCAG	96975	ATTTGGTAGUGAGGCAGGTAUGG
286249837	96976	TGGTGGGUAGCGUGCAG	96977	CCATTTGGTAGUGAGGCAGGUA
286252927	96978	ACATAGATTUCCAGAGCCAUGCAA	96979	AGTGAATCTCUGAAACAGCUACAAGAAT
286254843	96980	CTACCTTTACATCUCCTGAGGTTTGUG	96981	CTTGAGGACGACUTGCATTAGTCUT
286255182	96982	TCGATATAAAGUGTTAGTTCTAUGAGGACAGA	96983	GGACTATCCTCUGCCTTCCTGUAT
286255377	96984	CCUACCAAUACAGGAAGGCAGAG	96985	CCACUTTGCTGGUAGCACCAT
286255776	96986	GCCTAATACAGCCUGTGATAAAAGUACA	96987	GATGGGAAAAAGUGGTUCAACGG
286256827	96988	AGACAGGGAUCCCCATGCTTUA	96989	GAAGATAGCCAGGAAUCCCAAGUC
286262269	96990	GTGTAGCCUGGATTGCATCCAUAA	96991	TTTGTCCCAGGUTTTGAACTCUCA
286262556	96992	GGAAUGCCAGGATCTUCACAGT	96993	ATGGTAAGGGCAAUATGACTAAGAAUAAG
286263175	96994	CCAGTTGTGTUATATCTGAGCCUGAAAA	96995	AATGAATTACAUGGGTCTTTGGTCTUCT
286264620	96996	ATCCAAAGATCUTCCTCTCTCUACCAA	96997	AATGAAGTAAAUTCTCATCGUGAGCAGA
286269397	96998	GGTTCCAGTTTUGTCCAGCTCTATUA	96999	CAGGTTTAUGACACCAGAAGCATTTUT
286283103	97000	TGCCATGCATTUAACTCATTGTGAUG	97001	AGAGATCUGGGACCGAGGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
286290648	97002	CCCAGTTGATTATUATCCTTTGCTTGAUG	97003	CGCACCUCAGACGTCTTTUG
286293208	97004	AGCCCTATGCUTATTCTCAAGTTTUCAA	97005	TGTCAAAGAAAUTCAAGGAAAUGGAGGA
286294374	97006	GGACCAAAGCCUTATCACTTGGUA	97007	GAATGCCAUTTGAAGATCUAGCAACA
286299183	97008	AGAAATUGGAAGCCTTTCAGUAAGACT	97009	ATGTGGACTUCTTGCTGGACUC
286301720	97010	GCAGACAACUCTGTCCCUAAGAA	97011	TCCAGGAGAGGUTTAAAACAATGTGTUA
286304307	97012	GATAAGTGTTUGCTCGCTGUGG	97013	ATCTCCTACCCCUTTTCTCTTTTGATUG
286306942	97014	CAGAACGTCUGTAATTCCCAUCCT	97015	CAAGCGTGGUGAGCCTTTUT
286310192	97016	GCTTGCUGTCTGAGAAUGAGGAT	97017	GCCTGAGAAGCUGGAAATGUG
286321229	97018	CCCUGGAAAAACCAUCACACCT	97019	GCCCTGGAUCTGTGGAACTUG
286325784	97020	AGACGACGACGACCUCUCA	97021	AGACGCACACGUTCAUGGT
286328580	97022	GGAACTGATUCAAACAATTCGAUAACCAA	97023	GCCTCCATCGAAUGTCTTCCTAAUG
286329954	97024	GGTCTTTCATTTCUCCAACTCCAAGUA	97025	GGAACATGGAAGAUGGCGAATUG
286335906	97026	ATGATAAACATTCCUATGGTTTCCAUGACA	97027	TGGTATTCTATGACUGCAATCCTGGAUA
286336627	97028	GTTTTGTATTCAUAATGGGAGCCATUCA	97029	GGTCAGUGGAGATGTAAAGAAUGGAAT
286337436	97030	ACATTCTGGUAAAGGTTTGTCCCAUT	97031	AACATGGAAATTTUACTTACGGCACUG
286339231	97032	CCAGGATUGCAGTCATAGAAUACCA	97033	TTTGTCATTTGTTUAGTGGTCAACTGTUC
286339402	97034	GGAATTCCAGGAUCAGAACAGTUG	97035	ATTGGAATCTGGTUGTTTGAATAAATTTACUT
286363980	97036	TTCAAATACACUGGCTGATAACAACUCT	97037	GATCCGCUACAGCTGTGUAACT
286371633	97038	GGGTGGCCAUCAAGGATGUAT	97039	AATTGCAGAGUAGCTCTTGUGGAA
286373934	97040	CUTTGGGUGGAACACCAGGAT	97041	CCTTTCAGUGACTCTTCUCCAAAGAAA
286385670	97042	TGACAUAGCAATAGUGCACCACAT	97043	GAAGAUAAGGCTTTGATUGAACAGAAACT
286390498	97044	ACCCTTGGUTACCATCAUACACCT	97045	GATATCCTGACAGUTACCCAAATCTUCA
286392707	97046	AGCTGTTCACACUTTATCTTAGCTUCAT	97047	CAAGGAAGUGCACAGGCAUT
286393781	97048	TCTGTGTTUTTCACTACTUCAGCCA	97049	ACTCTCTCTGTACUCACTCTGTCTTUT
286396598	97050	CTGAAATGCUCCATGCACACAUT	97051	TGAGGCTCUAAAAGACTGGCATTATUT
286403466	97052	GGATGAUGAGGCGCTCTUGAT	97053	GAGGTAATGGAAGUTCAAGAACATCUCT
286411892	97054	TGACAGTCCUGGTAGGATAATGUGT	97055	GGATGGAAAAGUAATGTGGAGUGGA
286414130	97056	ACACTTACCUCCACATTTTGGAAUCAG	97057	CAATCAAUGCACGGCGGTUT
286416149	97058	TGAGCACAATCTTUCCTTAAAGATTATATUACA	97059	TTGCTGCUTGGAGTGAUCACA
286416802	97060	TGTAATTGTTTCUGTTCCCTGGGUT	97061	GAATGCCCUGATCCTGGAAUACC
286417430	97062	ACUCCAAGCAGCAAAAACTUCAG	97063	CCAGCAGAAGUGAAGCCTAGTTATTAUG
286418467	97064	CCUAATTGAAAGTTGUCCCCAAACC	97065	AGAAGGATCTCUCTCTGGCTAATGUT
286419140	97066	TGAACAATATACAAGUATGTCTGAGTUCACC	97067	TCCACTCAACUATGAAAACAACCAUGAA
286420935	97068	GGGTGCTGATTUTATCACAGATGATUCT	97069	GGCATUCAACACCAGTGACUGA
286423964	97070	TCTGGCTGAAAUATTGATTCCCTTUCC	97071	GCATCTGCAACGAAUAATGAAGGAATUT
286426780	97072	TCATGGTTGTTUTCATAGTTGAGUGGAT	97073	TGCATAACACTUCCATACATGATATUGCT
286427116	97074	GTCCCACGGAAAUCTGTCUCT	97075	CCGGTGGUCGTGCUCAAT
286427537	97076	AUCTGGGTGAUGGGCACAG	97077	TGACCCUCCCTCTGCAGUT
286429364	97078	GGGTTGGUTAGGCACTUCAG	97079	CCTGGCTAUCCTTTTCCATAUGACAA
286429620	97080	TGTCACTTUCACTTTGTATTTCUGAGGT	97081	CCACCCCUGCAAAGGCAAUA
286431505	97082	ACTGTTGTTTACUTTCTGAATCTCUGGT	97083	CCCTCACAAAUCAGGGTCTACAATTAUT
286433787	97084	TCCACAUGCAACGCAGGTUA	97085	TGAAAAGATTGGCAUTAAATTGTGGCUT
286439285	97086	CATACCTCTACAAGUTGGCATTACUCC	97087	TGGAGATGAUTATGTGGTUGGACAAAA
286440423	97088	CCCGAAGGUGTTGGCUGAAA	97089	AAGAGCCACTUACCGGTTACTUG
286447630	97090	TCTTCGGAGCUTCCTTGTUCAG	97091	CAAGCGCCAAAUCTCTTGCUA
286450143	97092	TGGCUGGCACATGUAAGAAACA	97093	CCATCTGCTCUTCTAATCCAATACUGAC
286456495	97094	GCATUCAAAGCACAGCAATUGAC	97095	GGTGATUGAAGCTGAACCUGGA
286457207	97096	TGATAGAGTGUCCAGGTTCAGCUT	97097	ATTTAATTTTUCAGCCCCATGTGGUG
286458248	97098	GGCCATCCUGGTGAGAGAAUC	97099	AACTATTTAATAAGGAUATGCAGAGACTTGUT
286477428	97100	GAAAAAGATUCCTGCAAGTUAGCCAAA	97101	ATCTTACAGCUCTGCCAGTGUG
286485654	97102	TGGTGTTCUGCCGTGCUAC	97103	TCAAGGGAGGAGUCCAACUCAT
286488097	97104	GTTCTCCTTUATGTGCTGCUCCA	97105	GCCTTATTTCUCCCCAGTCAGTUAT
286489720	97106	TCTGCAGAATTUTAAACTCGCCUCT	97107	AGGAAAUCACCUGCCAGCAAA
286499106	97108	CACTATCTCTUTGAGGACTTGUCCAA	97109	TTGACATTUCAGAAATCCAGUCCGT
286504551	97110	GACAGTTUCCACATCUGAGCAC	97111	TGAGCTGTCUCTACCTTCTTUCCT
286509190	97112	GCCCCAGACUAACTGCATCAUC	97113	ATCACAGATACUCACCTAACCTCUCAAT
286521196	97114	GACAGCAAGCAGCGAUATTATUCC	97115	GAAACCATCAUACCAGGGAACAGUT
286526587	97116	CTGAATTTCTCUGGACTCTCCCAUT	97117	TGACUCCCGGUGAGGAGAC
286528968	97118	GAAGCCUCCGGTGGUGT	97119	CCTGUGAAACCAGGCUCAAG
286559822	97120	GTGCACTGUTTTGTGTGUCGAT	97121	CTTTTGAAAAUCCCATGTAUGACACCA
286570546	97122	CCAATUGGACGGTGAGUAAACC	97123	AGCCGTTGUATGAAACTCTUAAACAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
286571384	97124	TCTCTTTTTGUGCACATACTCCTTUGA	97125	TTCCACTTTGUCTATGCGTCCUAC
286577285	97126	CCCTUCCACTGACTTUGCGT	97127	CTGTAGTCUGCTGTTTCUGGAAGAA
286577714	97128	CCAGATCTAGCAAUCATTTCCTCUCC	97129	TCTGCAGAGGUTGAGAAGAUCAA
286586248	97130	GCTTTTCCATGUCTACTGACACATUCT	97131	TTGTTTTGCCCCUAGTTCCAUGA
286587073	97132	CAGGCTCUCAAGGATCTGATCTAUCT	97133	TAAAGAGGCTAAGAUTTATTCTTAATTCUGACA
286638933	97134	TTCATAGGCAUTCATCTAAGUAACGCA	97135	GTTAGTCGTTUGAGGCAGAACUGA
286644168	97136	AACTCCTGTACUTTGTTTACATTCUGCT	97137	ACCCACCACAACAUTTAACAGTAGATUT
286645813	97138	AGTACCCGAUAGGCUAAGGCAA	97139	AGGTGCATGTTUCTGTTTACTGCUA
286677984	97140	GCCAAAUATAGAUAAGGGAAACAGAAGGT	97141	CAGATTCCTGACUGGAGTGTCTTUT
286691724	97142	TTTGCTTTUAAGGGAATTCATAGGUAAGA	97143	CCAGGAUGAAAGTGGGAUCACA
286698250	97144	CAATGTGATCUGCTCCATTATTTUCCAG	97145	TGUAAGTGGTTTCUCAGGAAGCAAA
286701320	97146	TGAGGAGTAACUTCTCCCTATGTTUGT	97147	GCAAATCCATUGACAACAGGAGUT
286704751	97148	GATUGACCCAAAGGACCTUGACA	97149	ATCACAGAUAGTGAAATTUGGACCAGAG
286706277	97150	CTGUTTTATTTCATAGTUGCAGGCAGAA	97151	CUAATGGCAGTUGGACCGGAA
286707314	97152	TGCTTGAGATUACCTTTGCACUCT	97153	GCTCUAGACAGGAAAGCAATTUCAGAA
286719198	97154	AGGATGTAACCAGUATCACAAGCAUAAC	97155	GAATTGGTTAACUTGAACTGTACUGCAT
286731775	97156	GTAAAAUCACCAATUGCCCCCAA	97157	CCTTCCTCATUACAATCCCATATUCCA
286733791	97158	CTGCTCGUCCCTTAUCCAAGAC	97159	TCATTTCTTTCATUTCAGACCTTCAUGGA
286734136	97160	GCTGTTTTCUGGTCATTTCCUCCAT	97161	ACATGGTTCTTTUATCCTTCTGCTTTUAGT
286748733	97162	TGTCAGUCAAAACCACTTGCUAAACT	97163	CCTTATGACAACAAUCTGAATTGTGUGT
286748836	97164	TGCATTGCUAGTACGACACTUGT	97165	AGATGAUGGAAGACCTGGAUGGA
286753007	97166	CCTCTGGCACUGTGATCTUCC	97167	ACTCCCTCTCUTGGACTGCTTUAT
286756890	97168	ATGACAACTUGGCAAGGCTCUAT	97169	GGCACCAGACTUGGAATGGATTATAAAUT
286768488	97170	TGAAGAACAUAACCAGCATCACAGUAAT	97171	GTTTUACAGCAAAACUGCGAGAGT
286768824	97172	TUTATCCAUCAAAGAGGCACACACA	97173	ATUGAAAGGAGAAGCAAACAUGAGAGA
286774778	97174	CCTTTTGTGGUCCTTGTGCUCT	97175	ACTTACATTGGUTAAGGATTTGCUGACA
286776765	97176	TCCCAGTGAUTGGAAATATCCUACAGAT	97177	ATCTCTTGTAACAUTGTACCTCUAGGGA
286778448	97178	GTTCACCUCACTACTCTUGCACAT	97179	CGAAAGGTGUACATGGCTTCUGG
286782031	97180	GAGGAAAAGTCUTCATCCTGAGUCT	97181	GGGTAUGGCTGCTTUCCGA
286790941	97182	ACTUGGAGAAGAGACUGACCACAT	97183	CAGCATAGGUGGTTGTUGGG
286793761	97184	GCTCACTGUGGGAAACCUGAAG	97185	GGCCCGTUCCTTTTCATACUCA
286793941	97186	TGATGAUGGCCGGGATCTUC	97187	AACGATUGAGCGCCTCTTCUT
286808758	97188	GCAGTGAGUGAAGGACCAACUA	97189	ACTCATTGGUGGAGGUAGCAAAG
286809608	97190	CAGGTGUTTAAGTATTTCUCAGGAAGGA	97191	GTGTCCUCCCAGATGAUGAGG
286812883	97192	TGCATGTCAAAUGAGTTATTACCAUCACA	97193	TCCATTGGCTCUACTGTTTCATTTAGUT
286812957	97194	TCACACTTACGTUTGGGTTACTTCTUT	97195	GGGTCGTCTTUCTGTGTCGAATTTUA
286818393	97196	TCAAUGAGAGUCCGGAGAGCAT	97197	GGTGTGTGTGUGTGTGAACTCTUA
286823090	97198	CATGACTCAACCUGTATCCTGAAUCA	97199	CCACCAAGCTUACTCTTTATTTTCTUCC
286828429	97200	CACTCCGCAGCUTTGCTAAUC	97201	TCATGCACTTAAAUAGAGGCACCAAUAA
286831282	97202	GAACACAAAATGGAUTTATTACCGGCUA	97203	CAAGACTACACCAUGTGAACACUGA
286845967	97204	ACTGGTCTGUTTCTAGGAGTUACAAGT	97205	AGAAGAACUTCTGCAGUACAAAAGCA
286847949	97206	CGTGGAAUCGCATGGTGTUAG	97207	CCAGCATCAUCCATGGGAGAAUAA
286860432	97208	CCAUCCAGGAGCTGTTUGAAGT	97209	AACTCTTCAGCCAGAUTCAATGTATUCT
286887004	97210	AATGGTTTACATUTCCTGTACACUCAGAA	97211	CCAGCCUGTTCAUGGAGACAT
286887046	97212	TCGATCAGATTCAUCACCAAATCAAUGT	97213	TGGAGGAAGCCCUGTTATTTTCUG
286887226	97214	GGCUGGGCUGCCAGAAG	97215	TCTGTUGCCACTGCGUGT
286889530	97216	CCTGTAGGGCAUCTGTGAATTGUC	97217	GCTCTUCCCCTTGAGUACCACT
286889655	97218	CCCCATTUCGAGTCCCATUCA	97219	ACACAGGGATATAUGAAATTGATTTTGGTAGUT
286933824	97220	AAGCAAAACCAACAGUCTGAATUCAC	97221	TCTGTGATCAUACCTGTGACCUCT
286940249	97222	AACCCTGAGAUATGCTCTCCTUCT	97223	GCUGCGGGCACAGAAATTUA
286944371	97224	ACAAGCACAUTTTATAGAGTUGGAGCA	97225	GGTGACAUCAGGCTUGAGCAA
286947879	97226	GAAGCUGAGCAGAAGTCUGGT	97227	CGGGAACGUGCTGACCTAATUAT
286957052	97228	CACCTCTGTTTUGCTGAAAGCTTTUA	97229	TGAGGAAAUAUCAACCAAGAAGGAACAA
286959885	97230	GCTGTATAGTTUGAAGTGCTTCCGAUAA	97231	ACTTGGGTCTUGACTAAAGCTTGATUAA
286963775	97232	TCATCTTTGTUCAGGTAAAAGCUCCAA	97233	CUACCGATTAGUGAGCGACACC
286969677	97234	CCCACUACCAGUCCACAGACA	97235	CCATGGAGATTTUGAGACACAAGGATAUT
286971747	97236	ATCTCCUCCACCTTCTGAGUGAT	97237	GAAGTGAGCAGUGCTTTGCUG
286972332	97238	TGCCCAGATUTAACAAGGTCAUCAAT	97239	GACCCCTCTAGUGTAACGTGATATTTUT
286979686	97240	GCCCTCCAUGGTACCAGTUC	97241	GAAAAGTCTGTUGAAGCTCTTAAGTGUT
286986693	97242	CCTUGGGAACGAACTGUGCT	97243	AGCTGCTTCUACTCCTTCUCACA
286987007	97244	CCCAGAGCAGUGTTTTAAACUCAGT	97245	GGCATACAGGUTGGAAGGATGATUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
286988319	97246	AGTAACTGAUGCATGGCAGTUCT	97247	GCTTCTCCGGGUTCCTGTUG
286991964	97248	TTTTTACCUGCATCTCAUCAACCCA	97249	GAGUAGAGCCAAATTCATUGCAAACT
286992019	97250	TTACCAACCUGGAAATAGAATUGAACGA	97251	GTGATGGCAAGUCAGCAATUGG
286997961	97252	GCAGTUCCGCCATGGTTTUT	97253	TCACTAGGAAUGACCACATCUCCA
287000072	97254	CAGGTTACCATUAACTTCATCCTCTUCT	97255	CCTTTTGGACUGGTTGTCAAATGTUG
287001473	97256	GGGTTTUCGGATCTGCAUCAACT	97257	GCCTGACUCCATCTGTCACUC
287013749	97258	CCTGCCCTUTCTGAGTCTTUGT	97259	GAATTCCTCCUGTGAACTTTCCCUT
287016724	97260	TCCTGAUGGGAAACCAGGTGTAUAA	97261	GTTTAAACUCAGGATTUGCACAGAC
287023544	97262	GGAAGTGCCAUTGAATAGAGGTUCT	97263	AGTGCCAGAUGGCTTTTCAATATTTTUC
287025945	97264	GATGGAAAACAGACUAGCAGAGCUT	97265	GAGAAACGCCGGAUCTCCUT
287040549	97266	CUGGGTGTTUGGAAGCAGAAC	97267	GCCTATCACCACUGATTGTTUCCAT
287042962	97268	GAATCGUTTTCAGCAAUGGAAAGAGAT	97269	GTATGTUCACCCACCCTTGGUT
287046095	97270	CCTGAGGUCAGACTAGGGTGUAAG	97271	CAGGGTUGCAAAACUGCGT
287046438	97272	TTTGGATCCAUCATGAAGAAAUGGAGAT	97273	GCTTCCCAGUTGGGTTTCUGA
287049349	97274	AAGAACATCCCAAUTGATGACTGGAUT	97275	TGAAGAGGAUAGGATCAGAGAGUGG
287053482	97276	CAAAGTUGCCAAGACCUCACAC	97277	GGGAAGACATTUCCATAAAAGGAGUGAA
287057746	97278	AAGCACGAAAUTCAAAAGGAGUGG	97279	TGCAGCCAUGTTGCTAAUAGAGAT
287058234	97280	GCCTTGUGGAGGAGTUGAGAAA	97281	ACAACCAGGACUCCAAATAAAAGATCUG
287062457	97282	AACATTGTGCUAGGTAAACTGTGUCA	97283	AAAGAUGCAGAGAAGGCUGGAAA
287067777	97284	CCUTTTGCTUAGAGAAGGGAGGT	97285	TTTCTTACCGCUCACAACTGUCA
287072844	97286	CCTCAGATUCCCACCCAGUGA	97287	GCATAGATCUGGCTCGUACGGA
287080425	97288	GCAGAGUAAAAACAACCGTCCUC	97289	GAACATAAAAUGAGCACUCAGGAAACAT
287115071	97290	GGTCTCATTTUCCCATGGCCAUA	97291	CGACTCCAUCACTACCATUAAGCAC
287116268	97292	TGTGTTTCUAGACTACAGGGUCACT	97293	TGTTTTGTTGAGUAGGAGAATCACTUCC
287117354	97294	CCTGAACTCAGUGGAAGTGATUCT	97295	GAACATAGATTGACAUTTTCAAATGACAGUGT
287143223	97296	CGCCCGGAUGATTGTTAUCCA	97297	GCCAATGCCAACAGUTAATTGAAGUC
287144219	97298	GCATCACCCCUTGCACAGUT	97299	CCCUCAGACAAAAAGAAAGTUGACAT
287150916	97300	GATAACAATGATUCACCTTAGTGTCTUCCA	97301	GTCAAGAACAGUTGGATGCTTUCC
287150997	97302	ACAGAATGAAACTTUAAAATCTGATGAAGCTUA	97303	ACATGTAUGCCAGGACCTGUAAGA
287151024	97304	CATCTTCTTACAGGUCCTGGCAUA	97305	AAAATAAAGCCATGUACTTAAGCTTGTTTUT
287151388	97306	TTUCCTAAATCCTCUGCACCAAAAGA	97307	AAGCTGUAACTTCTTGUCAAGAACAGT
287153345	97308	GATTTAACAAGAACUTGGAAAGCAUCCA	97309	TGGTTTCTTAACAUTGTGTGACAUGAGA
287155042	97310	TGTGTGGAAAUCAAAATCAGCTTTTUCT	97311	CAATAGAAGAGGCUCTCCAAGTAGGUAT
287161929	97312	AGTTTTGTGGCAAUGAGGACATCUAT	97313	TGGTGGAAGCUGTGAATGCAAATATUA
287166234	97314	AGTTACTGCTCAUCTCTAGCTCCTUT	97315	AGTTCATGGACCUAAGGACTCGAUA
287169659	97316	TGAGAGUGACCAGGGCAGUA	97317	GCTGTCTGAAGGCCUAGTTAATGTAAUT
287173840	97318	CAAACATCGGATUCCCATTTCCTTAUT	97319	GCCGAAGCUTTGCAUAGAGG
287181011	97320	TGGGCAAACCCCUCAUCAAC	97321	TCTGTACUAAAAGCCTCCCGUAGAA
287182336	97322	CAGGGUCTTCATGUAAAAAGCAAAACA	97323	CCAAGTGTUGAAAGCCATTTAGAAAAUC
287183000	97324	GAACATATTTCCCUGTGCTCTCTUGT	97325	CCATCTTTCTUCCACTTGATCACUG
287183045	97326	CCTCACTGAUTTTAGCTTCTTUGAGACT	97327	GTACAACUGGACCGCACUGA
287183806	97328	GCTTTCAACACUTGGCAAATCUGAG	97329	TGTTCAGGATCUTTTGAATTGGGTUGAT
287187111	97330	GTCCAGTTGUACCTTCAGACAGUAAA	97331	ATGAAATTTGTUCAGGATCTTTTGAATUGG
287190402	97332	TTCATCTTGCCUAACAAAAACTAGAATTATUCC	97333	TCTTCAGUGAGGATATGUCAACAGGAT
287197072	97334	GAGCUGACCAGACCAATTGUG	97335	TCAGCGGGUCATTGTGGAAUT
287200216	97336	GAGUCCGACCGAGGAGTUC	97337	TGGTGTCTGGAAUGAAGTATGTTTUGT
287205821	97338	CTTGACCATUCACAATCAGTTCUGG	97339	CTTTAAAGGTUTGCTCATGTUCCACAT
287207216	97340	ACTCCUCGGTCTCUCGCT	97341	CCCCAACGGUCTCTUGGA
287216686	97342	AACTTTCAAAUGGGTCTCTGCUGAT	97343	GGAAGAAUCCACCTACCTGCUAC
287223135	97344	AGTAAGTGTTCTTUCTTTTATGCCCCUT	97345	GGGCCAUGGTAGATUCACAACA
287224892	97346	TCGGCGTTUCACTGGAGATTUT	97347	TGAAACTCTAGUACTTTGCTTCAATUCAT
287228163	97348	CCTGGATTATUGGCAACATCTUGGA	97349	ACTGGTUAAAGAAGAGTACTUGAAAGCA
287231080	97350	GATGCTTGCUAATAGGTTGGCUCT	97351	CGGACAAAUCGGCUGGAAAC
287233376	97352	CCACACTCATATUCAGTAAATGTCTCUT	97353	GCCTTTAAACUCTACTGCTCTUCAGG
287233657	97354	CTGAAGAGCAGUAGAGTTUAAAGGCA	97355	TGTCCAAGTCUGTTAATGAACGAAAUGA
287234185	97356	TGAAATCCTGUGAACTTGGCGUT	97357	GGTCTCAAGCUCAGGTGCTUAC
287234862	97358	GATGCCTTCTAGUTGCCTACTAAGUT	97359	GCTAUGAACCAACAGTUGGAAACAG
287241417	97360	ACAGGTGGCUGTGTGAATGUC	97361	GGCATGCUCGTCCCAGUAAC
287244225	97362	CGGGTCAAGGUTATCTGGAGTTUT	97363	CCTTCATGTGTUTTTGAAAAGGGAUAGG
287249694	97364	CAGAGATGTGGUCCCTGTCTUG	97365	AGCTGAATTTUATTGGTAGCAUCACCT
287268958	97366	GCCUCTTCAUGCAGCAAGAC	97367	GCTGCTGAAGUGGAGATTUCCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
287269078	97368	CCTGCTGTATCUCCTGCTTCATTTUT	97369	TGACCAAGCCAUTGTUAAAAGCAC
287277983	97370	AGAUACCGCGGAAACTCAUGG	97371	AGCCTTTCTTTUCACCACGCAUA
287296769	97372	CTTCTCAGCAGGCUTTGATACUGT	97373	AAGACCCTTCUTTACGTGGGATUG
287311681	97374	AGCTGCCAGUTGCTCTTUCA	97375	GCGTTTGTTUACCCTTGTTACCTUAG
287317606	97376	GGGAGACAGCAUGGGAAAGAUT	97377	CCTGTTGAACUAATTGTGTCTTTCTUCC
287325674	97378	GACGAGCTGUCATTCTTTTATTTGTUCA	97379	CCAATATGCCAUTGAGATTCTTCCUGT
287326855	97380	TTAAAACUGCAAGGGAGTCTUCGAT	97381	GTGGGCGAAUGTGTCTTUCAG
287331434	97382	GGACTGGCUGGCCAAACTUT	97383	TGGCCTATAGGUAAGTCCTAGCAAAUA
287332829	97384	CCAACACATAUTGTCCAATTTUCCAAGT	97385	AGTCCTGTCUGGCGAGAAGTAUA
287339526	97386	TGTTACAATTTUGCTGAAGCTTTUGGA	97387	GTACCATTGACUGTCATGGCUGA
287340985	97388	CAGGAAUAGTGAACAGUAGACCCAAAAG	97389	TGCTGGTAUAGGTTGTTCGAUAGGA
287349982	97390	GGAAGTCAGUACAGTTTCCAGGUG	97391	ACCTTTUGAAGCTGAGAUAACAAGAAGA
287382813	97392	AAAAGCCUGGTGTCUGAAAAGAGA	97393	CAGGCUGAACAGACCCTAAATGUAG
287382957	97394	CTCACCTCACACUAGACTGGCUA	97395	CATGAAAGUGTGTTCAGAAUCACAGAAC
287393325	97396	CCCAACATATTTAUAGCTCTCACCUCCT	97397	TCGAAACATUAGACTTCGGTUAGAGAAC
287394214	97398	AAGAUGAGACTUGGCCGAGAAG	97399	AGGCCCTUAAACATCACATACUAAACAA
287394696	97400	CTGTCTAAUCAGCCGATCTUCACA	97401	GAAGCUTCTAAGAGAUAGAAAACAAGGT
287410691	97402	CTGGTGGUGACAAAACATGCUT	97403	GCAGCUGCTGGAAGUACGG
287414439	97404	CACAGAAUGAGGATCTUGAGGCA	97405	CCCCCAACUGCCGCAUA
287417544	97406	AAAAGGGACTUTAATCCTCAGAUGACC	97407	GCAAGCTTCGACUTCCAGGATATUT
287421386	97408	GCTTTGGGCUGGGTGTUC	97409	AGAATAAAAUGGACAGTGCAUCACACT
287425402	97410	TGTTAGATTACATUAAGGGCAGTGGTUT	97411	GGTTAACAGGAUTCCATCUGCCA
287427733	97412	GAGTGGAAGCCUTTCCCUGAT	97413	GTCAGTGGAAUATCATGGUACAGGAG
287435934	97414	AATGTATAGCATTGUTTCCAGTTAAACATUT	97415	GAACGACUGCAGATGGAUGGA
287436207	97416	ACCATTGAAUACCTTGACAAACUGGA	97417	GTTGCTTATAUGAAACCTCCCCTCUT
287462660	97418	GTAGATTCUAGGTAAAGCCCUGCAA	97419	GGGCTUAGGCACACTGUGAC
287472400	97420	GTAAAAGAACACCAAGAAUCGAUGGAC	97421	GTCAAUGAATCACAAAUACGCAAGCA
287482402	97422	CCAGAAGCUTAGCTUCCACCAA	97423	GCATCUGGTGGACUCAAGAAAGG
287488869	97424	CTGGTTCUAAGCCCTTCTUAAGGAAAT	97425	CCTGUTACAGATAGCUAAGAACAAGCA
287489042	97426	CCATTCUTCAGCACUGGGAACT	97427	TGTTTGGATUGAGAATGGATAAAGUGACA
287495943	97428	GTACAGCAATTCAUCGAAATCATCAUAAACA	97429	GGCTAUGGAAGCAGCAGUCT
287496006	97430	AATACCCGAAGUTCAGACTGCUG	97431	AGCAGGCCTTAUGTAATGCTAAGATUT
287501588	97432	AGCTGCCACACUTGGGAAUC	97433	GCAAGCUGGCAGCGTUC
287505349	97434	CAGAGUCAGCAGCAGTAUGACC	97435	TGTCTGGGCCUCTACCACUT
287508294	97436	TCCTCUGCGCTGCAGTUT	97437	CAGGTGUGGGAACGUGGA
287512495	97438	ATCAGTUCAACTTCATCTUCCCCAA	97439	TTGAGCUCCAGGGAGGAUAAAGA
287516435	97440	AGCAGCCAACUCCCCAUC	97441	ACACAGGUAGCCAGCAAAUCC
287522598	97442	GAGAGAAGUCTAATTTACTCUGCACCAT	97443	GCTTAGGCCUTAGAAGATGACAUCA
287522692	97444	GCCTGGTGTAAAUGTTTATTGTGATUGA	97445	GCAAACTAAATCCAUTTAACATGTCAUGCT
287528613	97446	GACACATAUGAAAAGGCAUGCACAT	97447	TGGCATGAGUCTCACATAAACAUGAA
287533358	97448	GATGAGATAAUGCCAGGATACTACACUC	97449	GCAGTGTGTTUTCAGAGGGAGUAAAA
287538480	97450	ACAGGTUCACACTGGACCUACA	97451	GGAAATCGCAAAUGATCCAGACAAAAUA
287542466	97452	ACCTTATGTTGUGCAAGTTGTGTTUT	97453	CTAGTTCCAUGAAGCTTGGAGUAAACT
287542684	97454	TTTCTGACTCTTCUAGCCACTCCAUA	97455	CTGTCTTAAAACUGTGCTAGATCUCAAGT
287542937	97456	AUTATTTAATATACAUGCAGCACCCCAGT	97457	CGGACTGACACUTAGTAGTACTUCAAAT
287544880	97458	CTGTGGGCGCUCAGGTAUT	97459	AGGGACGAGGUAGAAGAGGUG
287545749	97460	AGCCTTCATCUGTCCCTTCAGUAT	97461	AGATAAAACGACUCATCTACTAGGUGCT
287547429	97462	AGTAAAAGCACCUAGTAGATGAGUCGT	97463	GCCCTTTGGAAAUGTACTGATCTGAUT
287549443	97464	CCTCTGCTGUTTGGGAGTAGAUT	97465	GTGTTTGGTTUGAGGCCTGTUG
287553807	97466	CCTTACAGAUGGTAGCAUCGACAA	97467	GCCTTATUGGTGGCUGAGGAA
287554957	97468	CAGAAGACACAACAUCTCTAAGTUACACA	97469	GGTCCAAAGUAGACATTTCCUCACA
287558469	97470	TCTCCTTTCCUGGACAAGCUACA	97471	GCCAGGAAGCUCGCCUA
287562697	97472	TGCGTAACATUAGGCGAGCUT	97473	CCTTGACTTGCCCUTGTTTTATTTCUT
287565568	97474	ACAGGAAGCAAGGACAUGAATATCTUAC	97475	CAGGTTGCUGTAGAGAAACUGAAGAA
287566653	97476	CTCGATCCUCTCCAGTAAAUAGACC	97477	GAGTTATTTGTUCTGTCAGCGTAUCCT
287568532	97478	AAGTAAAGAUCCCCTGGCATCUAAAAG	97479	CCTGCTGAGTAUAATTGAAAAGCGTUT
287582163	97480	ACTTGTTCTUAACCTTTTTGAAUGGCAC	97481	AGGAACAACAAUACCCCATCTTTUGAAT
287583814	97482	GCAGCAGAAACACUGATGTCUGA	97483	ACTTATTATGTGGUCATTGTCTTGCCUT
287585042	97484	CCTCGUCCCAAGACAGTTCUC	97485	CGCCATCACAUTCTTGACAATUAAAACT
287588762	97486	GTGCAUGATATCGUGGCAGAAC	97487	AGAGATGGCGAUGGATATATTGACUACT
287590652	97488	GGCUGTAACTAAAUGGGCACAAGT	97489	CAGCAGAUACACAAAGUACCAGGAG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
287602592	97490	CTATCTGTTCAGCAUGTCTTGGTCUT	97491	CCAGTGTUACAGCTGUCACCA
287605867	97492	GGTGAAGGGCUGCTACAAATUCAT	97493	TGCAATUGAGAATGTCTUGAGAAAGAAC
287622293	97494	CTGTTCCUCGGAAAGTCTAUGGA	97495	TCTAGTGCUACTGTGUCCCACA
287626344	97496	TTCAATATAACTACTGUTTGCCTCTAAGATTUT	97497	GGAACAGCCACAAAUACUGAGGAAT
287626514	97498	CCTCAGTATUTGTGGCTGTUCCT	97499	GGGTTTGATTTAAUGCCATCTACTGTUA
287630566	97500	AAGATGATAGUGAGATCTGTCCUGAAGT	97501	TCCAGTGCTUATTTCCCTCAGUG
287631286	97502	GATGAATAAUCCCCACUGAGGGAAA	97503	GATTGGTGGUGAAGCAATTTAACCAUAT
287638090	97504	ACAAAACCACACAAUAAAAACUGAACCT	97505	GAAAAGAGGCUGGTGAATTGUGAAC
287652183	97506	AAGTTTAGATGCUTGGGTTCCTAUGG	97507	TCCCTAAATGACCUTTTGGCACAUT
287663353	97508	AAGTCATGAAGGUATATTTCGCUGCT	97509	CCCATGACCTUAACAGTTACTAGTTUCA
287664314	97510	GCGTTAACUCTCCCAGUGGAA	97511	CACAGTTCCUGATGATGTATTUGCC
287665422	97512	CCCTTCTUACCGTGGTTCUCCT	97513	CACUGAGAACUCGGCAGGAA
287668873	97514	ACCTGAUGAAGCTGUACGAAGG	97515	TCTTTGTAAGTACUCCGGCTTCUG
287677940	97516	GAGGAAUGAGGGCAAATGACAAUG	97517	ACAGACACAAAUTGAAACCAAAAAUCCT
287681705	97518	AATGTAGCAUGTGTTCUGCAAAACT	97519	TCAAACGGACGAAAGUGTUGGAT
287683597	97520	CCTUTGTAGTTAACCTUGAAACCAACAG	97521	CTCTCCCTTCTTUGTCCATCTCTTTTUA
287700691	97522	TTTGTTACTAACTCUTGGCTCTCATTCUC	97523	GGAAAATTCACCUCATCCATUCAGAAAT
287708908	97524	ATTTGCUCACCAGTAAGTTUACCCT	97525	GAAACUGCCATCCUAACCGAAGT
287732541	97526	CCTAAAATCAAUGCCAATCTCCTGGAUA	97527	GAUCTTGCTTTUCCAGCCAACC
287741458	97528	CATGTGAAAACAGCCUCCCTUG	97529	TCTGTCCCTTGAUGAAGCATGAATTTUA
287749970	97530	TCATGCCACCAAAUGGGAATATACTUAG	97531	TGGTAACATTCTCAUGCAATATTGGGUA
287757594	97532	CTTTGTUGGCCCTTGCAUAAGA	97533	TTTCTGTGTTUCCTTCCCTGUCC
287769724	97534	AAGCCCAGAACAUTAGGAACTTUGT	97535	TGATCACAAGCAGGUTGCTGUT
287770886	97536	AGTTTACCACUCTCTCTTUCCAGA	97537	GGTTCCTTTGCUGGAAACCTGUA
287776993	97538	TCCATTTCTCTCCUTTTCCATCAGTUC	97539	GGGATGAGGUCGATGTATCUCT
287778555	97540	GCAAGTUCCAGGGCCAGUA	97541	AGTGTGGUCCATTCCTUCACC
287781817	97542	GAGGCTGUCTGTCGGUCAAG	97543	CATCUTCCAGATCAUCCGGGAAAG
287783105	97544	CTTCTCAGUGGCCCTCACTUC	97545	GCAGCTTUGAACTGATCCAUGAT
287793603	97546	GCCACAUGCCCUACACAGAT	97547	GAGGAAUAAAAGAACATGGAGTUGCAG
287797189	97548	GGCAGTGUCACTCCUCAGAAG	97549	TCTTGGGAACCAGCUGTTACCUA
287801609	97550	TGGTTCTCAUCGACTCGCTTTUC	97551	ACTTGAAAGCUTAGCGCCUCA
287816156	97552	CACCCAGCUCTCATTTACAUGGT	97553	CAGCCCGAGAACUCAUAGAAGG
287822869	97554	AGGAGGAGUCATCCCGACUG	97555	AGTATGTGTTGCUGTTTTGGTTTTGUAA
287825454	97556	CACCAUCCCCCATGTATCAUCT	97557	GCAAAGTCUGTGGCCAUCCA
287829890	97558	GGACTATCTGCUGGAGGAGAUG	97559	CCACCACUTACACCACUGCAA
287832487	97560	TGCTTCCGAAUATTTCCATTCUCAGAAA	97561	GTGCTGTGUGCAGAAAGTCTUC
287833854	97562	GCATCCCAUGCATGATACCCAUAG	97563	CCAGAATCCCCACCUCATGGATAUA
287838183	97564	GCCCACCUGTCTGACTGAUAA	97565	AGCACTAGUCGCTGTATAGGUGT
287842150	97566	TGTTTTGAGGAAAAUGTTTGCCTUGAG	97567	CTCCTTCUCCGGCATTGTUAAAAG
287842482	97568	CTCCAGAGTCAAGUTCCCATTATGUAAT	97569	ACTTTGTCAGAGGAAGAUTAACAATTUCACT
287851706	97570	TTCTTGTAAUGGCCTTCAGTGAUCAA	97571	CTAGCCGUGCCGACGUA
287891289	97572	AGCCACTCUCACCTTCUCCA	97573	AAGGTCCUACGCTUCCAAAAGG
287893219	97574	CCTGGACCAAUGGGCAUCT	97575	AGAGAACGUGGCGAUGGG
287897749	97576	GCTCAGTUAGCAGCTCAUCCA	97577	GCCUGAGACTTGUCCAGGT
287902080	97578	GCCTCUGCTGCUCCACA	97579	CGCGAGAAGAAAGUGCCAUGA
287906348	97580	TGTTTTGAGAAGUACAGCAGUGAAAGAA	97581	GAUAAAGAAGTCAUCCCCCAGGAG
287911951	97582	AATGAGTGCUTTCACCTCTUCGAT	97583	CCUGGGCAAAGCAACAUCAG
287915445	97584	GCCAGAGCACUTGCTAATCUCT	97585	CAGAAGCATTAUGGGTCTAGCUCA
287926571	97586	ACCTAAAAUGCAACCCTAGTAUGCAA	97587	GTGCGACTAAUGAACTTATTTGGTUGAA
287930540	97588	CTCTCACTCCAGUCATAAGCAACUT	97589	AGAATACAUCCAGGAAUCAAGAACGG
287931186	97590	CTGCTGTCTUGGTTTCCCATUC	97591	AGCCCTGGAGAUGACAAAGAUAGT
287933693	97592	GCACGACTUACAAAATTATGGAGTGUAT	97593	AGTCAGTATGCAAAACUCTTGGTAAGUT
287937230	97594	ACTACCAAGTAAGAGUTGTAGATAGCTCTUT	97595	GCTTTGCTACAGAACAUAATTGGGATUC
287938976	97596	TCTCCCCCAUCATAAAAGUCCAGA	97597	GGGATTGGTGGACUATAGTTATGTGUAT
287943066	97598	CCTTGGTATACAAUATGAAACCCTTGTTUG	97599	ACTGTTATUGGCCGGCTTAGUG
287945714	97600	GGTGCTGAAUAAGGAAGATGGTATTUGA	97601	CTTCAGGTGTACAUCTCCAGTTTGUAAA
287949252	97602	GAGGATCCACTUCGTACTTCCAAAUAA	97603	AGTACATTGATGUGATTGTGTGTGUGT
287961753	97604	CTAAGAGGCCUCGCCTUGAA	97605	GGTTTCUGGAACCGCAGUGT
288038277	97606	GAATTAGTGGGAAAUATCAAGAGUGCCA	97607	AGATCAAGCAGCAUTCACAAGCUA
288040426	97608	ACCATTGATTCCUGAACAAGGTCTUC	97609	ACTTTAACTTCCAGGUTTCATCTTTCCUT
288070076	97610	TCTTGTCAGCTAUAACTGCTTCTTCTUC	97611	AACATTTAACCAUAGGTGGCTATTGTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
288076698	97612	GAGATGCCUCTTTTCAAGGGUGA	97613	GGGCTCTGCUGTAAGGGAAUG
288078950	97614	CACUCCAAAGACCUGAGGAAAGG	97615	ACACCTCCAAAUGGAAATAAGATUGGAA
288082703	97616	GCTGTTGAGCCAUATGAAGTTUGAG	97617	CAGTTTTGTUACAAGTGCAGCTUGA
288115832	97618	GCTGTGTTGTUCAGTAATTCTACCAUAC	97619	GTAGAGACTCUCTGGCCATGGAUA
288122432	97620	TCCAGGTTGUTTTGGCATTTGUC	97621	GCAGCCTTACAGUTACAGCTTAAUACAAT
288123915	97622	CUCCGGAGAUGGCACAGA	97623	GGGCATAATGTTUCTTCTTGAAAGCUAA
288124928	97624	AGTGTCTTTTCAGUGCTGTTAAGUGT	97625	CAGGCCCUGGACCTCUG
288126393	97626	TCTTCTCTCCAGCUATTTTTCACTGTTUT	97627	GGGCTCAATUGCGTTTCATTUCA
288126519	97628	TGAAACGCAAUTGAGCCCUGA	97629	TGGAAGACCAUCATGACTACTTACUGA
288129777	97630	CCCAGAACGUCCAGCAUCAG	97631	CTCCTATTCAUCAGCTGCTGTATTUGAT
288131384	97632	CCTGAAGCUTGGTTTCUAAGAAAGAAC	97633	GCTAAAAGACTUGCACAGGACCUT
288132265	97634	CACCCCAGUCTCCCAGUT	97635	CAGTGTGAUCTGCTGGTTUCC
288133625	97636	ACCTGCTTATUAAATGTATCCCAATUGGT	97637	CTTTGACCGCUCAGTCTCATATGUAT
288134928	97638	GGGTAAAACUGCCATTCTCTGUGA	97639	ACTCTCTGTGTTTUACTGATCTACCTGUA
288137494	97640	ACACTTTCAAGGGAACAUGATGGATUT	97641	CTTACCTCGTCAUTGATAACCTCAGAUT
288138334	97642	CGTGAACAUCACCCUGCAGA	97643	GGGACGUGACCTGAATGTAUG
288142149	97644	AGATTTTCACCTUCTGCAATGGTTTUT	97645	GGCUGGAUACAAAGAAAGAAGAGCA
288151934	97646	GATGAGGTCCUCTGTTTGCCTUT	97647	ACAGAAGUGACCGCUCGAAC
288154313	97648	GTTTGGCAGATAUTGGATGAGATTTGUT	97649	TCUAGAGAATCATGUCCAGCACCT
288154806	97650	TUGCACAGGCCGACUGAA	97651	AGTCAATGCUAAAAGCCCTUGCT
288155355	97652	CAUGGCAACGACUCAGGGT	97653	GCAGACGUGUGGCAGAGAAA
288155528	97654	TGAGTCUGAGGCCTCUACCAC	97655	TGUGCAAAGGAGCAGCUAGAT
288168338	97656	GGAUCCCAGCGAATCAUGGAT	97657	GGTGGACAUGGTCACUGAACA
288171458	97658	GUAACACAAGTTUACCAGACCCACA	97659	GAGAATTGAUAAAGACCAGGAUGGGAAA
288172829	97660	CCCAGGAAATATUTTCTCTCCAGTCUT	97661	CACAUGGGTAATAAUAGCAGAAGAACGA
288174682	97662	CATCAATAAATUCCTGCCGCGTUAT	97663	TCCTTTTAGCUGAGGGAATTUGCT
288175566	97664	GTTTGTAGGAUGAGGATGTCCAUCAT	97665	CACTAUAGAAAGCCCTGGTTTUCCA
288175942	97666	CCATGTGCAGUTTGCACCATUT	97667	GTCTGTTTAUTGTCTTTTGTUGCAGGAT
288176354	97668	GGCTTTCTATAGUGCCATTAAGTCCUT	97669	TTGTTAACTTTGGUCTTGGAAATGCAAUAG
288176885	97670	TTTTGCGCCAGAUATCAAAATCAAAGUT	97671	TGAAATGGGAAGGAUATGTGTACUACCT
288177953	97672	GTAUCGCCAGGGCCCAUAT	97673	CATCTAAACCGCUGGGAGGUT
288179385	97674	CTCCAGACAGAAUTTCTTACTGUGAAGT	97675	CAGAAGGAAAUGGACCAACACTTUG
288192409	97676	CTCCTTGGCUGTTTCCGGUA	97677	CCCAACTTAAAACUGCCTATTACTUCAG
288193957	97678	TCAAATGTTGGUTAGTGGATTGTAUAAGGAA	97679	ACTGTTTCTCTCCUTTTCTTGCTCAAUA
288215387	97680	AGTGTCTTAATUTGAGCTTTGGUGGA	97681	CATCATCTGUCACATTGGAGAUAAGCA
288222684	97682	AAGTAUTCTTTATTGGGUGGAAGCAACT	97683	CAATATAAACTCAUCTCCAGCCACUAACT
288227046	97684	ATGCTGACCACAUGATGATTTGATTUG	97685	CCCACATAAAAAUGGTACCTGTGTTUT
288227869	97686	GGGUTGGUGAAGACAGGAACT	97687	CGCTCGTTGACUAAATAAATCTGAUCCA
288230441	97688	GAGGAAAAGACCAGACUCTUGAAAGA	97689	CACTGTACCCUTCCATGGCUA
288238542	97690	GGCAGAGACUTGCTAAGGATTUGT	97691	GCAGAGACUCUCCACACCGA
288244301	97692	GTGAGCTGAUGTTGACGCTTUG	97693	AGAAGCCGAUGGGAGTAAGATGUA
288254810	97694	ATTAGGTAGCUGATAAGGTCUCAGAACA	97695	AGAAGAUAAGAGACCAAGCCCUGA
288255489	97696	CTGAATATTCTTCUCAGCTACAGCAUGT	97697	TGAATCAAACCACAGGUAAAGCUGAA
288256383	97698	AGGTTTTCAACCUCACGCTUCT	97699	CCAAGAAAAUGCTAAGCTTTGUGAAACA
288263135	97700	AGAGGTCUACAGAGTAACCAAACUGT	97701	GACTGGACGUTCTCUGAAGGAG
288267742	97702	TGATACCTAACAGGUGGTCTAGAATUGT	97703	GGGCUCCACUCGAGAAAGAGA
288268313	97704	ATCACTAGCTUCTTGCATGGCUT	97705	CCTTAAGUTGGAGCUGGAAAGGA
288272097	97706	GTCAUCAGCCAGGGAGGTTUT	97707	CCTCTTACCUGTTTATTAGUCCCAAGA
288273391	97708	CTGTTGAAGCTGUCTTTCAAGTTCTUT	97709	ATGGAGUCCAAAGTCATCACUGAAAAT
288281106	97710	ACAAAGTCAAGCCUAATGCCTGAAAUAT	97711	CCAUAGAGGAGCAGAUGACCCA
288282014	97712	CTCAGAGTAACACUGCTGGCTUT	97713	ATCCCCUCTGTTGAGAUGGACT
288289691	97714	GAATACCCTUTCTCCGCCUGAT	97715	TGAACAAGACAUGAGAGAGCUGAC
288291244	97716	ATTCTTCCUGAAACAGAACCATCTTUCT	97717	GCGGAACUGAATGCTUCCAAA
288303413	97718	TCTTCCAAUGGCTGTGGTTCUT	97719	CACAGCCAAAGACUGTACCTUC
288316383	97720	CAAGCTGGAGGGCAUTAAGTTCAUAT	97721	GCTACATCAUGCAGGGCAGUAAC
288316871	97722	GCGGTGTCAAAUTACTGTCCCTUT	97723	GCTCCAGGAAGGUATTGUGCAG
288319928	97724	CCTTCACTGTCAUCTCAAAATCTGGTUT	97725	AAACTTGAGGAUGAGCTGAUAGCC
288328104	97726	CAACGTCUGCTTCTGAUCGACT	97727	CCCTGTGTAACCUTATGACCACUT
288329905	97728	CACCCACCGGAGUGGUT	97729	TGTTCCUGGCGCGCUAT
288330494	97730	CAAGTUGCGCAAGGUGGA	97731	GTTGGAGUGGGTGGUGGAT
288334654	97732	TGAAGAGAGCCAGGAUTACTACCAUA	97733	TCTTTCCAAAAAUGCTGCTGUAACAC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
288335376	97734	CACTGAGTGAAAUGACTTGCAUGG	97735	TGUCCGAAATAGAAAUGAAACAGAGCAA
288339648	97736	CTGCATATTTTUGACACTCGTCCAUT	97737	GCTGTACTGUGAAGTGATGTAGATAUGT
288390205	97738	CATATATTUAGGGAGTGGUGCAACGA	97739	GUCAACTCCTTGUAAAGCAGCAG
288395643	97740	CAGCTTCCUGTGAGTUCCACAT	97741	GGATGGGAGUGGCTTCAUACA
288401724	97742	CGACTCGGUCATGTGTCUCA	97743	TGGCTGACAUGCAGGGATUC
288403406	97744	CACGGGAAAGUCUGAGCACT	97745	CCTTTTCATTTGAUTTGCCATTGTUCCA
288426005	97746	ACACAAUCCCACACCAATGATUCA	97747	CGTAGCAGTGAUTCTGTGTTTAGUAACA
288442599	97748	GACTGGTUCGAGTGCTGGUAG	97749	CACCGTTAGAAGUAGAGCTTTTUCCA
288469338	97750	ATCACAGATCAUACAAATTTATATACUCACCAA	97751	GCAGTCGGUTCATCGGTUCT
288474451	97752	ACTGTTTCACACCUAATTGCTAUGGAT	97753	ACAGCTGTTCCUAGAACAAGTTCUAC
288474492	97754	TCAGGCACAGAACUGCATUGT	97755	ATTCAAGTTCTGAUAAAAAGTGATGATTTCUCA
288489431	97756	CGTCTTGGGTAUGCCTTGCTTCUA	97757	TGGCACAGTUGAGTTAAAGAAATAUCAGT
288491911	97758	GAAAACCAAATTCUACCTCTTGCTUGG	97759	AGGGATATGUGATCTTCTUACCCAAACT
288493129	97760	CCTAGAAAAUCTGCTCCUGCCT	97761	CAAGGATGCUCAGGACGTUGA
288496689	97762	GGTGACCAAUTAGGCGGTTTUC	97763	GCGATTTTGUGACCACCATACATTUAA
288503751	97764	CTUGAAGAGCGGGCACTTUG	97765	TCTCCAGUGCCTTCAGGATUAGA
288509870	97766	CTGGAGTAUCCGTCCGCAUC	97767	GCTGGTUGAGAACCCATTUCCAA
288555471	97768	ATCAAAAGAGGCAAAGGUATTCCAUAAGT	97769	CCACCACCAAUTAUCAGCAACAAAA
288560080	97770	ACAAAAUGCAGTCUGAGCCAGT	97771	CAATTTTGUGAAAACGTTTACTGCUGAA
288567490	97772	TGTAAGTGGAAGACAUAGAATAGACTUGGT	97773	GAACGACTUAAAGATGATTUGGGAACAA
288580845	97774	GCTTGACTGAAAAACUCCTCACACTUAT	97775	ATCACAGGUGATGGCCTGAUAC
288582514	97776	AGTGATGAAAUTCCCTUGACACACA	97777	GAACGCGAGTUACCTATTTTTGTAAUGA
288588300	97778	CAAGTGGUGTTGCCTCUCAGT	97779	TGAAUGTTTAATAAGGUAGCAACAGCCT
288591171	97780	CTGTAGTGAGTUCTTTGGATGACAAUC	97781	ACGATTTTGCTUGTGTGTATGTTTTUCT
288628510	97782	AGGTTTCCCAACAUTTTCCAAGAAUACT	97783	GTCAUAAAACACGACGGTGUCC
288634708	97784	ACAGTTACTGUGCATAATCAGCCTTUA	97785	GGCAAAAGCUTTATATACCAGUCAGAGG
288635591	97786	CCGTACCACAGGUATAAACCTTGUA	97787	GTCTTTGCATCUCCTGATCCTAUCC
288645827	97788	TGAAAGGAAAAUTGCAGCTGAAUGAAA	97789	CCAAACTGTGTACUCTGCTGTATACUAAA
288650843	97790	GTGGAGAGUATTACGAAGAAUCAACCA	97791	AGTGTCATCTGUGAAGACAAACUGAT
288659801	97792	ACUGAAGAGCATTUCCAGCAAGA	97793	TGGTGAGCUCTTTGACTUCAAAGG
288674113	97794	CTATCUGGAAGCAAAGCATTUGGT	97795	GCGATGGATTTUCTAATCGTGATGTTUT
288682907	97796	CCCAAACUGGCATTCAAACCUT	97797	GGTATCATAUGCCTGCAACCCUT
288686174	97798	CCAAGAAATCTGAUGACACTAGAAAUGGA	97799	CTAAGUGAGCAGAAACCTGTUGGA
288691869	97800	TTGTACTGACAUTGTGACATGCUCT	97801	CCCCAGACACUCTTGAATTAACCATTUA
288694773	97802	CAATTTCAATGGCUTTAGGGTCUCC	97803	GCATAAACUGGAGGGTGCTCUAT
288699047	97804	GTTGGAACUGACCCAAGGCUA	97805	GGCTTCACUGGATACGTTTAUGGA
288712389	97806	CAGTTTGATGCCACUAAGACTTCAUC	97807	GCTTCCAATTUATGCCCAGAUCCA
288713001	97808	CTGGGCATAAAUTGGAAGCTGTTUT	97809	AATGCTTAAAUGACAGTGATTATAGUGACA
288723163	97810	GCAUGCTATUGGAAGAGGAAGACA	97811	GGAGTCAGTCGUAATTGGAATCAUCC
288727667	97812	GCATACCUTCACACCTUGGAAGT	97813	CCACGCCCGUTTCGAAAUG
288728137	97814	TCATATGATACUGTGTTTTCCCCUCAT	97815	GAUAGCCAGAAACACAACATUCCAG
288733490	97816	CAAAGACCATCCAAUGTAGTAGCCAUT	97817	AATGTGAAATACCUGAGTTGGATGACUT
288739686	97818	GTTTGACCCACAGUAAAATCATUACCAA	97819	AGTTGCAAAAUTGCTGTAGUACCCT
288741447	97820	TGATTTGTGGCUTATAACATGACACUGA	97821	CATGAGAUGTGGAACUCACAGGAA
288743561	97822	TGGAGTGTGUGGCTGTGAUG	97823	CGCCUGAGACACGGTCUG
288747331	97824	CCTGGCCCUGTGGUGAT	97825	ACUCGCCTTAGAUGGAAGAGAAAGA
288756103	97826	CAGTAGCAAAUGAAATAGGAACTCUCAGA	97827	TCACCTCAGAUCGGTCAGTUCA
288759366	97828	AGAACCTCUAACAGCTTUGCACAA	97829	GCAGTTUCGCAGGAUGGG
288760522	97830	CUCCAGCACAGCCGCUA	97831	GGAGCACCAGCCUCUGA
288761472	97832	GCCCATCCUGCGAAACUG	97833	GGAAAGGUGAGGCCACTUACT
288761879	97834	CCTCAGAGGCUGGTGCUC	97835	GGACAGCAAGGCUCCTCCUA
288763888	97836	CTGTAGACTGATUCCAAAGCGGTAUT	97837	CGGTTCAAAACUACTTCCACAATCAAUC
288777734	97838	GCTCATUAGAAGGCTGGAGUGT	97839	GCCTTCCAGTTUATAAGATAGTCCAUCAA
288785574	97840	ACAGTTTTGGUGTTTTATGTCUCCAGA	97841	CCGTCAGAAAGUGTAACCACTGUT
288786430	97842	CCGGGCGUCTCTACTGATGAUAT	97843	TTAGTCAGGAAGCCUTGAAAAUGGAA
288791019	97844	TTCATGTTCTTTUGCAGTTTCTCTTTUT	97845	CCCCGTTACUGCTTGAAGATTAUGAT
288796354	97846	TTTTTCCAGCAUGACATAGAGUACAACA	97847	GTCTGCTCUGCTCTTCCTTCTUC
288798199	97848	GTTTCTUGCCTCTTGTUCCAAAACT	97849	CGGTGGCAAGGUTGATACTTCUG
288804924	97850	CAGGTGTCUGCTTTGGTATTTAAUGG	97851	TCTGCAGTUTCTGCTTCUGCAT
288808126	97852	AGAAGCAGCUCCGUGAAGAAAG	97853	CAGCTCCGACAGACUGATTCTUA
288808606	97854	CTGCACTTCUCTGTGGGTUG	97855	ACCAAATUGAAGAGGCAGAAGAGTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
288811151	97856	TGCTTGTATTTUAGGAACACCTCAUCAA	97857	CGTGACCGUCGTGAGCUG
288811789	97858	CAACAGCCCAAGUGCAAGUG	97859	AUGCTGCTTTUGGAAAACAAACAGA
288826965	97860	CAGUTTTGUAGACAGAGGCCACT	97861	AGCCCGCAGAUAAAGTGAAGATTUT
288833731	97862	ACCTTTGTGAGAAAUAACGTCTTCUGA	97863	GCAGGAAGAAUTAGAAAAGTTTGAUGCT
288837825	97864	GCTATCCAAGAGACUGAGCTGTTUC	97865	GTTTTGTCUCAAGCTTCUCCAGAGAT
288839234	97866	CCGTAGATUTTCGGTCAUCCAACA	97867	TCAGATCCTTTCAUATGTGCATACAUAC
288855621	97868	CCAGTGCUCAAACTCGGTAUAGT	97869	AGGGTCAGUATCTCTCTCCUGAAG
288870147	97870	ACATCACCTUCCTATTTTGCATUGAAGA	97871	CTGAAGGAATTCAUAGCACCCTCAAUAT
288871443	97872	CCGTGTCAAACUGGATGGTUACT	97873	CATCACATGATAUACTCCGAGTCUGG
288873798	97874	GGTGCTATGAAUTCCTTCAGGAAUAAGA	97875	TTCTCCCACAGCUTGCAGUT
288891043	97876	GTACAAATGCUAAAGCAAAATGGCCUAA	97877	TGTGACTGGACUATCACCGUCA
288892329	97878	CAGATTAUAAAGAACGAAGGGTGUAACCA	97879	GGGTTATCGACUGGAAGGAACAUC
288895357	97880	GCCAAGGAGAUAACATAGTCUGCAT	97881	TGTGGAGGCAAUTTAACAGGATCTUC
288898222	97882	GGAAGTTUGGTGAAAGAAUAAAGCCT	97883	GTCTGTACAAAGCCUCATAAGCTCUT
288909724	97884	CACCACCAAGACAGAUGATCUCT	97885	ACCTTGTGAAGAUCCTGGCATUC
288912015	97886	GAACCCGATUCGACTACCATATUGA	97887	AACCACTATCATUTTCTTTGTCCTTUCCT
288919719	97888	AGGCAGGAACCAUTAAAACAUCA	97889	GTTCACGAUCACATTTCCACUCAC
288934392	97890	CCATTTCTCCUGGCGCTGUT	97891	CCAGGUGAAGCGCAACUCA
288953720	97892	GATTACCTTTAUGGAGAGTGGGUGA	97893	GGCATCCUCCTCCAGATACUCAA
288957366	97894	GCCAGCCUCTCTCCATCUACA	97895	CCGCCUAGACTTCATCCUGAT
288958612	97896	ATGCATATAAATTCTUACCCATGATAGCAUT	97897	TGCTATAGGUAGGAAGTGTTGTACAGUT
288964890	97898	TTTCCTCAGGCCCUCAAGAGUA	97899	CCCAAACCUGCTCCAUGAAGT
288968248	97900	CCCTTGGAGAAGGUGTCCTTTUT	97901	TCTTCCAACTTUACCATACGGAATTUCA
288970582	97902	GAGGTTCCAAAACGUAAATCCACTTTUA	97903	CAGGAATUAGGAGCUCGCGAA
288970731	97904	CATCCCAATUAGAGGAGCTAGCUG	97905	CAAGTTCCTUATACAATCCACUAACCAA
289024169	97906	CTGGTTTACUCTCTTGCUGAAGACT	97907	GAATATTCTTCUTCTGCTCCTUGCC
289030728	97908	GCAACACCAGGACUTCTGAAAATUC	97909	AGTCCUCACTGAUGAGCCACT
289035237	97910	GAAAGGCAGUACAAACAGTUAAAACCT	97911	CAGUGCACAGCCAAUGGAAC
289036643	97912	GCUGAGCCTGGUCAAGACAAC	97913	GUCTTCCCTCTUGCCAAAGACT
289036770	97914	TGTACAGUTAGGTAAAGTUCCAGACCAT	97915	CGAATTGAUGGCACAACATTTTCTAGUT
289041610	97916	TCCAGAAAGGAUGTATCCCUCCAT	97917	AACACTTTGTTTTAUAGCTGTGCAGUG
289045998	97918	ATTGGAAAUGTTCCTCUCCCCAAA	97919	GTTTTTACAUGAGCCAUCCAGCAA
289052018	97920	GGGCAGUAATCCGAUCAACCAAAT	97921	CATCACACTUACAGAACTTGCTGATUC
289053354	97922	GCTTGTTATTGGGAUTAGGGAAAACUCT	97923	GTAAACATATCTUGGAAGCCCAGATUG
289055422	97924	GGGAATATUGCGCCAAAATCCUACT	97925	AGCAATGCACAAUGTGTCUGG
289056233	97926	TTCTGTAGAGGUGAGTCAGTUGGA	97927	GCCTGCUGCTTCAGCTUCA
289062154	97928	GCAGGACAGACCGUGGUG	97929	CTTGGCAUAGACCCAGAAGUGA
289063264	97930	CCTTATTTGTATUCACTGCTGTGAUGAC	97931	TCTTTTAGTGAAAACGUGTGGCTCUA
289064462	97932	CTAATCCAAAAUGCAGAAATCAGAGCUT	97933	CUGCACUCCACACACGAAGA
289066247	97934	CCTCUCACAGGGTCAAUGACAC	97935	GAAUTAGGCTTCTUGAGGCAGAGA
289067982	97936	GGACUAACCGGCUCAGCAAA	97937	GCATTCTTCTCAUATGCTGACTGAUACT
289072448	97938	ACTTTGUCCAGCCAGGUACAC	97939	GAAGCCATUAAAGCAAGGUACAAAGA
289076789	97940	CCACATCAGUGCTCAGTTTAGTAAUG	97941	CCATAATATCUGAAGAAACCCTCUCCCT
289076840	97942	GAATAAGAATAUCCCACAGCUGCCT	97943	ACAAAATGGUGGCTTTGGCAUT
289083142	97944	TGTTCCCTGCTCUATAGCCTCATTAAUA	97945	GCTTUCCAGAGAAACCTGATUGAGAAA
289086730	97946	TGTTGCAGCCUGAGCTTCUAAA	97947	TTTCUGACGAAAGCCACCUCAA
289088345	97948	GCTGCCCUGAAAGTTCAAGATATAUACT	97949	AGTCCCAAUGCTTTCTGTTUCCA
289104357	97950	ACTTGTCTGTCUTAAAACTTGCCUGT	97951	CACAUTTTCCCACUCAAGCAGAAG
289120065	97952	ACAUAGGAAAGGAAGAUGAGGAGCAT	97953	GCAGGTTGAAACUACTCAGAGAAAGATUC
289125118	97954	AAGCCCTGUACTTCGATGUCAC	97955	GCCGUGUCCAACAGGAGAT
289128153	97956	ATGAATCACGGCAGUGGTGUA	97957	GGAGGCAAGAAGGAGUGUCAG
289134880	97958	GGTTTTACTATTTUCAGGCTGATTTUCCT	97959	CGCTGGACACCGUGACTATUC
289153538	97960	CCTAACATTUACCCAAGGAATCUGGAT	97961	GAAGATCCTGGAAUTGATCCTTCAGUAG
289157212	97962	GTCCUCAAGGTGATTTUGAAAGACAG	97963	CATCAAUGACCAGGCACTUCCA
289162138	97964	CTGCTGCTTCUTGCTGTTGTTTUA	97965	GGGAAGCCAAACUACTGGATGUG
289169798	97966	CACGTCCUACACTCAGTTCTUCC	97967	ACACTCAAUGACAAGCGCGUAA
289175087	97968	CCAGAACTTUTCTGCTAGCUCCAT	97969	GCCTTGTGGAUATTGTTTTGCTTCAUAG
289199472	97970	GCCTGCTTUGGTCAGTACUGT	97971	AGTCCAAAGAACUTCTGCATCTUCT
289225820	97972	TGTTTGTGCUGAAGGACACACUAA	97973	TGATCTGGTTCUTGTCCCACTUG
289244495	97974	AACTACAACUTCTTCCCUCGCAA	97975	AGCCTUCACAAAAGACACCUCAT
289280089	97976	GAGAAGGCAGAUTTGTGGUCACT	97977	GTGTGACATCTAAUCTCCCCCATAAUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
289294658	97978	ACAGTTTGGTTAGUGATGAGTTGTAUCC	97979	CCAGTUCAGGCCCCTGUAAC
289297575	97980	AGGAAGGCCUGACCCTGTUA	97981	GGCTTTCUTTTGCTCCUCCAG
289299495	97982	TGTCATGGUAGAAGTTTGCUCAACAA	97983	ACCTTGAGGUGTCGGTTCUG
289301233	97984	CAGGAAGTAUAGACGGCTTTTATGTUGA	97985	CTGATATGAUCTGGTGTUGACCCA
289319185	97986	CTGGCAAGGAAGAAGAUTGAAAUACAAG	97987	CCCGUGGUAGAAACCACAACA
289327400	97988	ATTTTCCCUGTGTTGCUCCCT	97989	CCACATATAAUGCAACAGCTAGCTUAC
289332169	97990	GACTGAGAAGACGCUGTACCUG	97991	CGACACGAGGUAGTCAAACACUT
289334147	97992	AAACCGAAACAGCUCCTCTUGT	97993	AGATCAGAAGAGAGAGUCCATUACCC
289336659	97994	GCAGGAGAAGUGTTTGACUACCT	97995	CCAUGCCCAGCTCUCAGAC
289391194	97996	CGTGGTGAUGCCAGCTCUA	97997	AGCCCUCGACUCCCACT
289391907	97998	CCUCCAGCCCCATGGUC	97999	GCAGGGCCUGAGGAAUGT
289432624	98000	AGCGCTUCGGGTGAATTCAUA	98001	CTCCTTAACAAGCUTCCCCUCAG
289514853	98002	GATCGCTGACTUAAGGTATCACTGUAA	98003	GGGTCTTTATUCCAGATGAGATCTUCAC
289521631	98004	CCATAAGGAACUTCTGCAGCUCT	98005	CATGAAGGTCUACTAACTGTAGGUGAGT
289533285	98006	AAGCAGACAGUGTAAGGGCAUT	98007	GAACAGAUGCCGUCCAAGGA
289545078	98008	CATGAAGTGCUCAATGGCAUCC	98009	ACATGTGTATCUGACACCCTCCUT
289554230	98010	TCAGTTTTGTCUCTAATGGGCTTUCA	98011	AATGCCCAAAGUATAGTTGCACAGUA
289581629	98012	CCAGCCCACCCUTGTCTUT	98013	GATUCCAAGGCAGCCTGUG
289584606	98014	GGACACACTCUCAGAAATAAAGACGUT	98015	GGGAAAAACATGCUCAAAAGGACAATUA
289592872	98016	CATTAAGGUCAGCGTCATGTCATUG	98017	CGCTGGUGCAGCTCTCAUAT
289593479	98018	CCTGGACUCACATGGGTUCAC	98019	CCCCACTTATCUTTGTATATCCCTGUT
289604994	98020	TCTGGAGCUGCAGAGAGTCUAA	98021	GATGCCATCAAAUACAATGTCCUGT
289612943	98022	CTGTCACUCCTGAGATCUGCAA	98023	CGAAGAGUGAGGGAAAAGAATAAUGGT
289617289	98024	GTTCTGATUGACCACACATAATGUAGAGT	98025	GGGACAGCACUTCTTACCATGTTUAAAT
289620690	98026	CCUTCACTTTCCUGGGCAACAA	98027	TGTCCAGGGUCTCTGUCCAAT
289630689	98028	GACTCTCTGAUTCTAATAGGGUCAAAGG	98029	CTCAGGCAGCCAUGCUAACT
289633834	98030	GAGTGCAGUGTTTGUGCAAACT	98031	AGAGTGCTGTTGUTTAAGTCACTACUG
289638280	98032	GGGCTTCCAUCTCAGATUCCT	98033	GGATGAAAGGGCAAAUCAACCUT
289645278	98034	AGTGGAAACTUGTGTCAGAGGUC	98035	AGAACCCGUGTGTTGCTUCA
289666258	98036	AATGTGAAGCUCTGCATTATTACUCCAT	98037	CCCATTGCAAAAGUAGGTGTATTCUG
289669704	98038	GGGTTCTCUAGGTCTCGGTGAUT	98039	AGTAAACAGAGAACACUGCCCTUAC
289729590	98040	GTGGTTUGGGAAAGATACCTGAUCT	98041	CCATAGGCCUGAACAAAATGACTUG
289734803	98042	CTAATAGCTCUACCCACAAATTGTGUCA	98043	GCTATAATCGGCUGCCCCUT
289747898	98044	GCTACAGGAGCUGTGCAGUAAAC	98045	GGTGCTTGUGAAAGCGACUACT
289750628	98046	GGGAGGGUCTGGAAGATGTUA	98047	CCAGCCCAAGCAGAUATGUAAGG
289763646	98048	AGTTGGCCUTGTCTTTCUGGT	98049	TGTGGAGGAGCUGTTTTCTTTTUGA
289786277	98050	TGCCCCAACCCAAAUGGAAUA	98051	GCTGUCAAACAGAGGTGGAUGAG
289851209	98052	TACCATACTGGGCUTCTAAATTTGAUAC	98053	TCATATCACCAUCAAGGAGAAGGTTTUC
289852400	98054	TTTCCTCTTAGGCUGAAAACCTTCUC	98055	ACTTCAGGCCCAUCATACTTCTTUC
289865538	98056	TGCUCCCGAGCTTTUCCAAG	98057	TGATACCTTTAAAUTCTGGCCAUCGAAA
289877403	98058	CTCTATACATTAGUCAGTGGCTCCTUG	98059	CGTAAAACTCGCUCTCGCAGUT
289879498	98060	GGCCAAAUAAAACTAGGTAUGAGAGCA	98061	TGAGAATGAAGGUGGATGATTGCUAAG
289884780	98062	ACTGTGTTTTCAUTCCAGTGTCTUACA	98063	CTTCAGTTGTTUTCTTGAGATTTCUGCT
289908301	98064	CAGCGUCAGCATUGACAACC	98065	ACATCAAAGAAAGGCUTCCAGUCA
289915453	98066	CAACACACCCUTTGCTUCCAC	98067	GTCTCCAGCAAAGAUGTATGTCTTCUT
289931679	98068	CCGCCUTTAACUGGAGCAAAAAC	98069	AGCCCACCAACCUCUGAAC
289933703	98070	GCAGAAGCUGGTGGACUACAT	98071	AGAAAGGAAGGACUTACTGCACUAAC
289948189	98072	TCAGCACGCCUGACTUCAAT	98073	CTATCATGCCCUGTCTCTGTCTUG
289989503	98074	CATCTGAGGGUGGTCUGCAAA	98075	TCTCTTTCTTTUGGTTCCCCTGAUG
290001558	98076	CCCTACAGCTUAAACTATGTAACACGUA	98077	TTATCTTCAAGCUGCAGTCTTUGGA
290010324	98078	CTTTGCCCTCUTGTTCCAGAAGUA	98079	CAGTTATTTGCAUCTAACACTTTUCGGA
290018871	98080	CAGTGATTCUGAGGTACAAAGCCUA	98081	GAGCCACACUCTCACCAUCAG
290033920	98082	TGGACCCUAATGACATGAUGAGAGAAA	98083	CCATTAAGUGACAGTCGUGGCAA
290042554	98084	TGGGAGAUGGAAGTCUGCAAG	98085	TGTATCTTCCCUGAACCTGTAAATTUGG
290050469	98086	CCGGAGAGCCCCUGUGA	98087	GGAGGGUCCACGTTGUGA
290055503	98088	CATUCGAACAGCCCCUAGGAG	98089	CCATGCCUGTGAACGTGAUGT
290060530	98090	GCCAGGUTTTTCUCCCAACAGAT	98091	AGCTGGTCTUCAAGAGCGAUG
290062379	98092	GGTCCUGGAAGCACTCGUT	98093	CCAGCTUCGGGACTTCTGTUC
290073841	98094	TCCATUAACACATGGGTUGGCT	98095	AGAGUGAGCACTGGGUAACCT
290080751	98096	GACGTCCCCAGUGCAGTAAUAG	98097	GCATTTGCCCUCTGACATGUT
290086475	98098	GACAGACACUAAGTTGTGCUGAGT	98099	GCATTACTUACCATGCTTCAUCCCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
290125061	98100	TGGAATTCCUCCCTACCATGTATUCT	98101	TGGGAGCUTGCGGTTCUG
290130224	98102	GCGGGAUCGGAATGTUGGA	98103	CCGUAGGTTTTCUGCAGGCAT
290133183	98104	CACTCCGTAUCTTCCTCGCATUAT	98105	CTTGGUCCGTAGACTUGGCT
290134531	98106	GGCTCCGGCAAUGAGAAUAGG	98107	GCACGGACGGUGUCAGT
290139697	98108	CACAAGCATACCCUCCTTAGTTCUT	98109	CTAGCCCUGGAGGCTACUACT
290140384	98110	CAGTGAGTGAAAUGTGCTCTAAUGT	98111	CACACTCTGATTUTTGTGTCTGTTTCUG
290141860	98112	TCTTTTGCUCTTTTCCCUAGGCAA	98113	CATACAAGTTGUGTTCCTCCATUCC
290148217	98114	ACACAGTAGUCAGTGCTGGTTUG	98115	CCCCCACCUGTTTCCTUCAG
290149158	98116	ACCCTAATAUCCTAACCATUGGGACT	98117	GGGACAAATTUGAGCCATGACTUG
290156214	98118	TGTTTCATTTGGAUCCTTCTTTGACUCA	98119	GCAUTTTACTAAGACUGAAAGCAGAACAA
290225645	98120	ACTCCUGCAAGGCACACUC	98121	GCACCCAGGGCUTCCAUT
290230726	98122	TGTCAAGGTGUCAGAACACTGAUG	98123	ATTGGCAUGCCTCTTUGCAAG
290252269	98124	CCTCTTTCUAGAGAAGGCTAUGCAG	98125	CCAGGACAACCUATCAUGCAAAAGT
290252723	98126	TCTTGCCTAGGUTTTCTTTCATACTUACC	98127	GTTCCUGGACCCACCATTAUGAT
290255112	98128	CTTACCAGAUGACCCCTCAAUCC	98129	ACGGTTACUCAGGAATACATTTUCCC
290273258	98130	CTTCGTTCAGAGUTTAAAGCAUGCAA	98131	CTGTTAGCCUGAGGTCTTTTGGUAT
290278382	98132	GTGGCACAGCUAGACGCUAA	98133	CTCCCAAGGUCCATAGCTCAUC
290283794	98134	TTTCCATGGTCUTCTCAACTGCUT	98135	GCAGTGTGACUTTAATAGGAUGACCAG
290284526	98136	CATCCATTCCUCCTGCTGTAUCAT	98137	TTTCCTCUCTGGCCCUACAAGA
290299138	98138	GGGAGACUCCCATTTTGAUGAC	98139	TCACCCAGAUGTGTGACTTUCC
290300089	98140	CACCAGAAGUCCATGTCCACUT	98141	GTGATGGTGACUATCATGTATTTUCACA
290302624	98142	ACUAGCAGAAAATTGUGGGCCAA	98143	TCTTCCAUGGGCAACTAAGTAAUCAAAT
290306010	98144	CTGCTTTACCTUTCTGATTCAGGUGA	98145	GTACATCGCUACAATTAUCAGCAAAACA
290354563	98146	CTGTCCCTTUGCTTGGACTCUA	98147	AGATGTTGUCGTGCUCCACAG
290363468	98148	AATGCUCAGGAGCAGAAGUCC	98149	GCAGCTACUGACTTCCTTCTTUGA
290383347	98150	CCTGUGGAGAGCACGTCTUC	98151	GGAAUCGCCCCAGGGATUA
290394493	98152	AAAAATGTTCAGCCACUTAGAGATCUCA	98153	CTGATGTTCCUATAATCCGGCCUT
290395517	98154	GGACGGCUGCAAGGTAGUC	98155	TCTCAAATCGCUTTTACACCCUGAT
290402346	98156	GGGCACAAGAAACUCTAAAGCTCAUA	98157	CATCTTAGACACAUGGAACAATGGAAUT
290409297	98158	GGUTCCGUGGACAACAACCT	98159	GCAGAGCCUGTTGAAGTTGUG
290417349	98160	GGCTTCTUCATCCCAAAGUCGT	98161	CTGCTCCCUCAGTCTTGCAUT
290420800	98162	AGCCCCUGACTTCCCTCUT	98163	GUAAAGGAAGCCAACAUCCGAGT
290427059	98164	AACTCCUGAAGGCTCTTGGUG	98165	AATTUGAACAGAGGAGGUGGAAAAGAT
290434199	98166	GCTTCCTTTACTUCCTCCATCTTCTTAUT	98167	GAAGCAAAGGAGAGCUGTGAAUG
290440703	98168	CCTCACTCTCCUCTGTCTTCCUT	98169	TTTGCAAGTGUTCCAGTTGGUG
290445150	98170	CACGGAAGGUGGGATUGGAT	98171	GACAGGAGGCGAUGGAGTUC
290448455	98172	CTCACTGGGUGCCCGUT	98173	CCACCCUGTGCCCAUACT
290451239	98174	TCCATTGCCUGTTGCUAGCAT	98175	GGCTTCTACUCCGCTTCCTUG
290455147	98176	CCACUGCAGCCAUCGCA	98177	GGGACCAAUACAGAGGTCTCUGA
290485882	98178	CCCACGTCCAUGAAAGGCTUT	98179	CAGAACGUGTCCAGCTUCGAT
290504337	98180	CTGAATTACTTUGAACTTCGGATGCTUT	98181	GACAAGTUGGAAAGACCTCCACTUAT
290505083	98182	CTTTGGCTUCAGCAACGAGUT	98183	GCUGACGAGGGTGUACAGG
290507409	98184	GGAAACAUTACCUGGAGCCAGA	98185	GCAGGGCTAAGAGUTCTTCTACCAUA
290511608	98186	TCTGGAGCCUGGGAGUCAT	98187	CCAGUCCCACCACUGAGG
290529254	98188	CTTTCGAUGGCCAGAATTUAAAGGT	98189	ACAGTCUGTGGACATAUAGAAGGGAAT
290532421	98190	GAGTTTUACGAGGGAAGUACCGT	98191	AATGCTCTTCGGUTCCTGGAATATUT
290542980	98192	GTGTGGGTATUGTTGCATTGTTTCUT	98193	TGCTGTGUAGCATATAGUAACAGAAACC
290552761	98194	GTTACATGCCUTGAAGTGAUGAGGA	98195	GGTAAAATCCACUGTAACGGCTCUAAC
290555788	98196	TTCTGCTGAACAAAUGAGTCACTUCT	98197	CACACACAAUGCGTATGACTUGG
290560703	98198	GAAGAAGGGATTCUTACATCGATGACUT	98199	TCCTGGGTCUCTTTTGTGCTAAUC
290583791	98200	GGGTGTTAUGGTTGGCACAUT	98201	AGCACTUGCGTACTCCAUCAC
290589068	98202	GTCCCCTUCGGAGCTTTCUAT	98203	CGGAAUCCGGGAACCGUA
290599412	98204	CTGGUGATGGAGUACGCAAGT	98205	GAGCTTCCUTCTCCTTCAUGC
290616155	98206	CTTCTATGTCAUGAACCCCTTUCCC	98207	ACCTTTTTAGGAAUTGCTCGGATTUCA
290647478	98208	TCATTTGACGAUACCCGATUGCT	98209	TGCAAGGGAGCGAUGAAGUC
290661675	98210	TGGTTUCACAGTCCACUGAGG	98211	ACCTTCAGGUCCCTGTGUACAA
290663779	98212	TTGCTCATCTAUGGCTATCTTGCAUT	98213	AGCAAAAATCTGUTTCTACCACTUACCT
290666500	98214	GGAGCCATACUACTGCCTCUCA	98215	CCATGATGCUGCTGTAGTCGUC
290668296	98216	AGACAGGACCAUTATGAGTCTCUCAA	98217	GCCTTTTACACUCCTCAAAACCATTTUA
290668320	98218	CTGTGCACTATUGTCACCAGAAAAAUA	98219	GGAGAAAAGGGCUGGAGGAATUT
290675718	98220	CAAGGCCUATGAGGATGAUGGT	98221	GTTCTAAGGGCUGATCAGTCTUCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
290681866	98222	GGACAGGUACAAGAAGCUGACA	98223	TGAUGTGGAAAGTAUGAAGAAAGCCA
290702459	98224	GGATTGGTTUGACCCATATGTGUAGT	98225	CAGCCTGUACATACTCCCTUCC
290704438	98226	AAATGCATTAGUAGAGAACAGCAATCUGA	98227	TCCAGGAGGCUCTATCTTGAAGUT
290708959	98228	GGAUAACCACAAAGAGAGGATUGCT	98229	CATAGGATGAAGUGCGAGCUCA
290712597	98230	CGCAAUAACCTCATACUCCACCA	98231	TGGGTCTCTUAGCAATGTGCTTUT
290717217	98232	GTGTTTGTTTUTGCAAGTAGUCACCAT	98233	GCGUTTCATCATAGUCACCAAAGGT
290718519	98234	AATTATCCTTUCTCAGGTCTUCCCAAC	98235	GGATTTCTUCAGGGAAAATTCTCCTUCT
290723749	98236	GTCTACUGCCACAACAGAGGUT	98237	GAGTTAACAATGCUGAGGTTAAGGUACT
290765366	98238	CTCGCCCCAUTCCCTGUA	98239	CGAUTCUCCCGGCCAACC
290767711	98240	GGTTGGCUCCAGCCUCAA	98241	GCATGGTUGGGATGTCCUGA
290771444	98242	CCTCCAUCCAGCAGAGGTUC	98243	GTGTCCTTTAGAUTGACCCATTACUCT
290802552	98244	TCATGGATGUGGCTTAAACAACUCA	98245	GCTGATCCAUGACCCTGUCA
290899997	98246	GUAGGGCCAAAAGAAGUAGCCA	98247	CGGTCTGGAGUCGCAGTACUAA
290906713	98248	GCTCAAACTTUAAAAGGATGTAGUGCA	98249	GGCTGGATGUGTGGTTCAGTAUA
290907513	98250	TTTTTCTTAGCAUACATCTGTGGAUGGA	98251	CAATGTGAGGCUGTTCATCTGTUG
290907869	98252	CTTCCCCAUCTGCTCACAGUA	98253	CACCCGTUTCATGGGAUGGT
290909291	98254	GCATTCCTAGUGGGTTCAGGACUA	98255	CCCGTTGUGAGGCTGAUCAC
290919521	98256	CTTATAAUGGGCCACCTGCTUC	98257	GAATCAAAACACGACAGUACATUGGT
290926352	98258	GCUGGGAGAGGCACTCAUT	98259	TGGACUCCCAGCTCTTCUCT
290934405	98260	CGGTGTAGAAACUCCATTACGUCAG	98261	CCAGGCAGATAUTAAAAGGCATTGUG
290941878	98262	CTCTGTGGAGGUAAGGCAGUT	98263	TTTTGGTTTAACCUGGCTTCCUCA
290944030	98264	AGGAUACUGAGGAAGCCAGGT	98265	GCAACTGTGAAAAUTTCTCCCCATAUT
290949272	98266	TGTGCUCACACAGCATACUCAA	98267	CATGTCACTTGUGACTTCTGTTTTUCAG
290957729	98268	CCAGCACAGGGUGTATATGGUT	98269	TGTGTGACGUGGGTUGGAC
290961692	98270	TATTCTGAATTAATGGAUACAATGTTTCCTCUT	98271	CTGCAATCAGGAAUACCAGGTCTTUAT
290965893	98272	CCTAGCTCUGCCTCACACUCT	98273	CCAGAAUCUCAGGGCCAAAAGAA
290978553	98274	CTTCTCTCTCAUCTCTCTTCCTGUCT	98275	ACGGAAGTTCUTGGTGTAGGUG
290988450	98276	GCCCTGAUGGCACCCATTUA	98277	CTCCAUCCCAGGCTACAUGAC
290997370	98278	CCACATGAGCCCCUGACTTATUC	98279	GTTCTGUGCAAACGTAGGTGUT
291015748	98280	CUAGCATGAUGACCCGCAGA	98281	AAGGGAGGUCCTGTTCACCUA
291071884	98282	TTTTGUGGGAAGCCCTCUGT	98283	GGGTAACAACCUCCCACGUC
291088900	98284	CTTACGTTGAGCUAGCACCCUAA	98285	CCAAGUCCAACAGAAGTACGUG
291101263	98286	CTTTTCTATCTTCUCCATACACCCCTUG	98287	AGATGAGCATUGCTGTCTGTTUGAT
291132545	98288	GGTCTTUGGGCCCUGCT	98289	CCCTCACAGCCUCCTCUCT
291133822	98290	GGTGGGUTCCCTATGUCCAGAT	98291	GTAAGTGUCGGGAGGTGCUG
291144055	98292	AGTTTATTCCUGCATGAATTCCAUGGT	98293	GGCCTTCCCAAAUATGGATCATCTUC
291145028	98294	GTTTTAAUACACAGCTTCAGAAUGGCA	98295	GCTAACTTACUAATGTTGCCTTUGCAT
291189570	98296	CTCTATAGCAUACATCACCCCTUCCT	98297	GTAGCAGACAAACUGCAGUGGA
291205814	98298	CCAGCAUCAAGGGTGTGGUC	98299	ACTCGAGUTGGCAGUCCAA
291221756	98300	GAGCCTGGGUTTCTCCTCATUC	98301	TCTTCTCGUCCTCCAGCUCAT
291225154	98302	GGCCGUCGAGUGAAACCA	98303	CUGCCAACCAGCTUCCCT
291232913	98304	AAAATGCCTGTTUGTAAGCAGTCAUC	98305	GGCCAGGGUTTTCATTGCTTCUA
291237029	98306	AAGCAAAGAGGUTGGAGTUGAAAAAC	98307	GGTTTGGCACUAGTAAAGCTGACTTTUA
291243141	98308	TGGCCAGAGAGGCAUCTGUA	98309	CUGAGCCACAGCCCUCAT
291247110	98310	GGGAGGAAAGUCACACATCUGG	98311	TGTTGTACUCCTTGCCATUGAACA
291265557	98312	GAGTACTGCAAGUTCCCCTUCT	98313	GGGACTAGAGUGGATGCUCA
291285690	98314	GGCTGUAGCAACAGCTTUGGA	98315	GTTUCGAGAGCCCAGTGUGAA
291323964	98316	CCTAAACAACCCUGCCTUGCT	98317	GTTGAAAGAGGUGAGGTCCTAACTUAC
291340274	98318	CCAGGTCUCACCCCCUAAGT	98319	CGAAATCCCCUGTCTCCUCAG
291393059	98320	TCCAUTATTTATTGUGCGGAGGAAAAGA	98321	CAAAGGAACCACGUGUGCAAAA
291411553	98322	TCACATGCGUGTCCCACTUAA	98323	GCCACTGGGUCTTGTCCAUAG
291413278	98324	ATCTAGTTAGGAAUGAAACAGAAATUGGAT	98325	TTGTAGACTGGUAGGATTTAGCUGAGT
291428262	98326	CGCATGGGUGGAGACTAUCT	98327	CACTCTCUGGCCAATGCCUT
291436248	98328	CAGGCAGACACUGGCAGUAG	98329	ACCAUGGAACCTGTACUCCCA
291449323	98330	GATTGCUGGGAAGGGTAAGGAAUT	98331	CCATCTAGCAUGCCATCAUCCAT
291452387	98332	CACAGTGGAAUCCTCCAGGUT	98333	TGGTTCCCTGUCTAATCCTCTTUGT
291481334	98334	CCCAGGUGTTGGATGUCAAC	98335	GAGACAAGTAAAUCCCCCTGAUAAACAT
291484886	98336	GGACAUGGGTCACUCAGGCA	98337	CTGCAAGTGUCTCCCAGGUAA
291492922	98338	CTCACATGCAGUTCTACCACCUC	98339	GATCATGATGUCTGCCTCUCCAT
291494900	98340	CTGUCCCCCACAGTGUGT	98341	TCCTCUCCCCACCCACTUC
291504549	98342	GGGTGTCCUCATGGTTCTAATUCA	98343	CTGCTCACUGCCACAGUAGG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
291511143	98344	CCAUGAAAGAGTUCGCCGAGAA	98345	CTCGATGTCUGCGAGTCUCC
291516963	98346	CACCGAGAAGCUCACCAUGT	98347	CCCTAAGUGCCAGTATGCTGAUAAG
291518494	98348	ACTGCGGUTTTCTCGAAUCCAT	98349	TGTCCTATCUAAGCCGCCCUT
291533322	98350	AAGGGCAAAAGAACCUTCCACUAA	98351	ACCGCCAGAUCACCATCTUAC
291562146	98352	TGTTATTTGTTGUTTTTCCCCTGUGAAC	98353	TCACACCTCTUGAGATCAGAGAUCA
291569246	98354	GCCTUCCCGGACACAGTUAA	98355	CGAGUCGAGUACGCCAAGAG
291570020	98356	GATGCTCUCGCTGCATTTCTUG	98357	CAGCGTGTUTCTAGGTCGUG
291586253	98358	ACUGGGACUCGAACACAAGAAC	98359	GCCTGGAUCACTTCAATTGCTUC
291595161	98360	CCTGAGACAAAUGGGCUACACC	98361	AGCTGGAAAATAUCTCCACTGTCTTUT
291599879	98362	TCTAAAGCUCCTCCCUCACACAT	98363	CATCCAGCACCAUAATCCTCTTCUG
291609872	98364	GGGATGAGAUCAATGCCATTCUG	98365	GGCCTGGCAUGATCTTTAAATUCCT
291617219	98366	AACGAAGAACACUTCCGAGGUC	98367	ACATGGGAACCUGGGAATACTTUAC
291640055	98368	CTGATGTGCUGGGTGTGATTTATTUT	98369	ACCCCAGCCUTGTCTGTTTUT
291657011	98370	GTTTCTCAGGCUCCAGTTCTATCTUC	98371	CCTCCCUCCTTCTGTUCCAAAA
291664931	98372	GAGGCCUGGATGUGGCA	98373	CCCAGCUCTCCCTCUCCAT
291668852	98374	GCACAAGAAGCUGGGTGUCA	98375	CCTGGCUTCCTGGGUGAG
291670311	98376	GAACATCUTCCTAAACTUCAACCCAGA	98377	TCCATAAAGCAGGUAAGTTTTCACUGAA
291673984	98378	TGTGGTTTTGAUTCTCAGATGGTUGT	98379	TCTCTGCAACCUTCCACTGUC
291685287	98380	CGTTGGTUACCTTGGCUCAGT	98381	CACCCCUCAGACTCTGAUGGA
291693774	98382	CAGGGCTUCTGGGCACAUAA	98383	GGCCATUCAGGAGAAGGTTTTUGA
291719875	98384	GCATCTCCCUGGCTTACUGAC	98385	GGAUAAAGAAGCCCUGAAGAAGCA
291721642	98386	ACTGAATGTUCAAATGCAGAGAUGGAT	98387	GCTCCAAAATTUCCATCTGGGUGT
291729352	98388	TCCACTUAGAGAGAAACUCCAAGAACA	98389	CTCAGTGGTTGAGUACAATACTGGAAUT
291737171	98390	CACCCACCCUTCACTCTUGAC	98391	CATGATUGACCGCTGGUACCAT
291756906	98392	CCUGTTCTUGACAAAGCAGCCT	98393	GCTGCCCGUATCATGTUCAC
291760028	98394	GCUCAAAGTTCTTTAUGGAGACACCT	98395	CAGCTTCAUAACCGAAGATUGCT
291763535	98396	CCAGCAAAGUTGGTGGUCCT	98397	TGTCTTTCAGUCAACCAGAGUAACAAA
291780361	98398	CAAAGAGAGACCCUTGACGGAUA	98399	TGCTGTGAACUCCTCTGCTUC
291784752	98400	GTCCCAAAUGCTGTACCUGCT	98401	GGAATTCCGAGAAAUCTCTTACCUCAA
291787835	98402	GGAGGCGCUGGTTTCUGG	98403	TCAAGGGAGAGCUGGCTUCT
291788766	98404	TGCAGCAAACUTGTCTCTUACCT	98405	GTGTTTTTGUCATCACTTTTGUCACAAC
291801994	98406	ACACTGAATCUAAAAAGGACCCUGAAG	98407	CTTCTTTTGTTCCUGTTGCATACGUT
291812909	98408	TGGGAATGGUGAGGTCACUCT	98409	AGATATCTTTCUGCACCTAGGACUGA
291835844	98410	CTGCTGGTUCACTGTGTCUGT	98411	CCUAGAAAGCGGAGACAGUCCT
291838754	98412	TGATGGTAGTUGAATAAAAGTGCTTUGA	98413	GCUGCACCCAAAGCACAAUT
291838975	98414	AGCATTGGATUAAATTGTGCTTUGGG	98415	TCTCTTACCTCAUCTATGCCATGTCUT
291848207	98416	TCCTATCTGCUCAGATGGGCUAT	98417	AAGTTGGTGUACGGTCCAAUCC
291859500	98418	TCCTTTTAAGGUCTAGAGCCCTUCA	98419	CUAGCCAAAGACAUGGGCAGAT
291892586	98420	AGCATTGTTUGATGGTTATTTTUGGCA	98421	TCTTTTGACUAATCAGTGTGTUCAGCAT
291896426	98422	GGUCTACGATGAUGCCCACAAT	98423	CCTCTGCGUACAGGTGAATGUC
291910267	98424	GCCAGCACAGAGUAUCCAAGAC	98425	GCTGGCTGUCAGTACACCTUC
291945238	98426	GGGCAAGAGUTGUCCACAGAAT	98427	GTCAGAGACUCGGTAAAGCUGAG
291962472	98428	GTGGAGACAUCCTUCCGCAAA	98429	CACGGTGUGGGAAATTGUCAG
291996038	98430	AGAGTTGTAUAGGAACTGTCAGUGCT	98431	TGGAATAAAATGUAAGGTCACCCACUT
292025909	98432	CCATGCUGCCCCAGTATGUA	98433	ACTTCTCCUGCTTCUGGAAGGT
292040994	98434	CCCATCCACCUCAACGUCAG	98435	CAAGGTCAAGGUCTAGTGGGTCUA
292065172	98436	GUCCGCACCCCTTUCCT	98437	GGGAGGCUCCGGTTACUCA
292091297	98438	GCATTGUCCCTGTUGCACAAA	98439	TCCCGGAACAAGGAUGAAGUG
292104380	98440	CCGAGTTTCUCAATCATGGCCUT	98441	GCTGGCCTUGCTGAATGATUCT
292108769	98442	AGACCCCCUCCTCCAGUAAC	98443	TCACCTCGAGAGUACAGCGTTUA
292115598	98444	GGAGATTUTTGGTGCUGAACCCA	98445	AGGAGAGGAAAAGUGTGUCAAGAAG
292167848	98446	TTGGACATGTTTUCACAGTAGTTGUAGA	98447	TCTUTCTCTAGTCCAUAGCCAAACAGA
292225273	98448	TGTCTATGGCAUGTTAGAACAAGUGT	98449	AAGGCATTATTAAGUATCCCCAGACCUA
292225639	98450	CAAACTTAATTGGCUTAACGTTCACCUT	98451	CAAATAGAAGGAGAGCUACCACAAACUT
292234822	98452	GGCUACTCUGGCGCAGAAAT	98453	GCCAGAGATGUTAACAGAGTAAAGUCAA
292290112	98454	GCTGGCAGUCCTGTTTGCTUA	98455	CCTTCTACCTUCCCCTTACTTTTTAGUT
292306550	98456	CCACCCUGACTTGTCTGUCT	98457	GACCUGGCCACCAUGGAA
292309940	98458	TUCCACCAUCCGCAGCA	98459	GGTCAGCTUGGTGAAGAGGUT
292312757	98460	CCCACACUGGCCCAUGAG	98461	GAGCAGAGUGGAAGACAGGUT
292323364	98462	AGCAATCTGCCCUTTTCTGTCUT	98463	CTCACAGGCUCCACACTCUG
292328108	98464	CGAAUAGCCAGGCUGACACA	98465	GAGGACTGCUAGGAGCTUCAA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
292343085	98466	ACTGCUGACCAGTGAATCUCC	98467	GCAGCUAGGUGCAAAACAGAGT
292354879	98468	CTTCTGGACCGCUTGGGUA	98469	ACACCAATGATGUGTGATTGTCTCUT
292372050	98470	AGCTTGACAACCUTTTAGTGAUCCAT	98471	ATGTTGTCTUGCACATACTTTGCUG
292380461	98472	TTCTCAAGAGAUGCTCCTGTUGG	98473	CUACCCGACTUAGGCACGAT
292388317	98474	CCTCCUAAGGGAGCUGGGT	98475	AGGGUCCCTGCCUGAAGA
292495736	98476	CCTGGGCAUGAATGGACUGT	98477	AGTGCTAUCCGGAAGAAAAGCUG
292505619	98478	GCCCAUGGAAGCATGTCTCAUT	98479	GTCATAGGAUGTGCCCUGGAAG
292512802	98480	AAGGACAGCCCUGCAAGTUT	98481	CAGGGCAGAAGCCAUACTTCUT
292514635	98482	CGTGGUGCGGCTCATGTTUA	98483	GCCCCCUGTTGGAAGUGAAG
292519688	98484	ACAAGUGAAGCCAGATTCCCUAGA	98485	CCCTTAUACACGCCTCTGUCAT
292520061	98486	GCACCACUGAGGACUACGAC	98487	AGATGTCTUAGCACCCCTGUCT
292526173	98488	GAATGTGUCCCGAATUGGGAAGA	98489	GGTTUCCGTTTGAUCCCAAGG
292530636	98490	CTCGCCUCAGTTGCCATCUA	98491	CAGGAACGGCUGUGGCT
292531531	98492	CCCTCCUGAGGCCCUGAT	98493	GCTGGCAGACCUCCACTUC
292531829	98494	GAGCCCCUGTCCCACUT	98495	GGACCGUGGTGGCUCAG
292532939	98496	CACCCGCAUCUCCAACGA	98497	GGACAAUCTTUGCCCCCAAAT
292540608	98498	AGUATTTGAAACACUGGAAGCACGA	98499	CAAGGCCAGGAAAAUGATGCTUAC
292541895	98500	GGTTCCTTCUGACACCTGTCUT	98501	CAGGATGGCUCTCCCUGAC
292643503	98502	GGGCACGCUTACUGACAC	98503	GACGTCGCUCACCAACGUA
292645477	98504	GTCAGCAGAUCCCAGUGGT	98505	GGCCCUGGCTCTTCTGUA
292658032	98506	AAUCCAGACAGCAGAATGUCGAA	98507	TCTCTCATATCCUGTGTCTCCTUCAG
292668983	98508	TCAGTGAAGGUTGATTTGCCCUT	98509	TCTACCCACCCAUTCCTTUCCA
292787724	98510	TCAGUCCCAGAGCCAGGTTUA	98511	CTCCCTTTUCCGACCTUCCAG
292818304	98512	TCCCTTCGAUGTATAACGATTTCUGG	98513	CTCCCTTTAAAUGACAGTGTGGAGAUAA
292883975	98514	GGAGATTGCCUCAAGCTGCUA	98515	ATTTTCCCAAGAGUCATCCAGGUC
292888944	98516	CAAAGAUGGCAAACTUGCCCAT	98517	GGCATCATTUATTTCATCTCGUGCAA
292890365	98518	ACATTATGGUCACCATGGGCTUT	98519	AGGTGAAAAACTUACTTCAGGTGGTUT
292890812	98520	GCACGAGATGAAAUAAATGATGCCTUAA	98521	TATTAGCTCAAGAAAUAATTCACAGTAATCUGA
292892127	98522	TCTGTGGATTTTUCTCAAAGTCAGCUT	98523	GGTCCTTTCACAGACAUATGTATTCCUT
292893765	98524	GGTGGGAAGCCUGGCTUAG	98525	CUTGAUGGAGAGCGGGAAGA
292895216	98526	ATTCTGGAGGUAGCAUGGCAAG	98527	TUCAGCAAGGGCACUAACACA
292901226	98528	CGTCCTTCCUCCTCCTCUCA	98529	CTCGGTGCUGGCTTCTCUT
292908914	98530	GTCACACUGTGGGUGGCA	98531	GGGUGUGAGGGCAGAAGT
292912887	98532	CAUCGCAGGCCCCAUCT	98533	CCTCCCUCCCCATGCCTAUAC
292919812	98534	GTCTCUGAGCAGCTGCCAUT	98535	CAUCACUGCCACCACGGA
292922358	98536	GTGGAGAACTUTGAGCCTCTCUAT	98537	ATTCCTGAACCUCTGACUCCCT
292989818	98538	CCAGGGAGCGCUACGAUG	98539	CTGCCAACUCTTTGTCCGTTUT
292994096	98540	CCGTCGCCCAUCATCAAGUT	98541	GAGAGACACCCCCAUCCTTUG
293003093	98542	TCCTGATACCCUCTACCCCCAUA	98543	GGTAGCTTUCACTGCGTGUGT
293009296	98544	CCCATACCTTCAAAUATTAGAGCAACCUA	98545	GCTGTTACATAAUTTGTCAGGTTGTUGA
293009476	98546	CCAGGTTCUCCTCACAGCTUG	98547	CTGGGACUGCTCCGAAGAUG
293013878	98548	TGGGCCUAACGGGTTUCAC	98549	CCTGGUGGACATCGTUAAAGGAA
293015876	98550	CCTGGGTCUCACACTCAUCCA	98551	GCCACAUCCAUGACACCCAT
293033067	98552	CTGCAGCTUGTAGTAGGAGTUGG	98553	CCCTTCTCCGUGAGAGTGCUA
293165293	98554	CUTCCCTAUGCCAGGCAGAAA	98555	CAGGTAAUAGGCACCCTUGAAGAAG
293177385	98556	TTTCTCTAUCCCAGGTCACAGCUA	98557	GTGTAUCGAAGGCAGUGGAGAG
293179009	98558	AAAGAGCAAAGGAAGUCAGTGUGT	98559	GGAAAGAGUCCGCCCACTTTUA
293182415	98560	CAGATTUCAGGGACGATCGTUGA	98561	CCAUCAGAAAAGGTUCCCCAAAAA
293196050	98562	CCTGTGGCCUCTGTGTGATTUT	98563	GACTAATGCTATUGACAATGCACTUCC
293210964	98564	GCTGCAGGGUGACTGAAGAUG	98565	GGCCTCGUATACCGCAUCAA
293218313	98566	CCUGAGCUCCCGGAAAAGA	98567	GCATAGGAACUGTGGTTUGAGAGG
293219929	98568	CTGGGTUAAAGTGCUGCCAAG	98569	CAAUGGATUAGGCCAAAAGAAACCA
293283547	98570	CCATGTTGCUGGAGAGUCAGA	98571	TGGGCAUGCAGGTGGATATTTUT
293300191	98572	GTTATTGTTCAGUTGGTCACAAAUGGA	98573	CCACAGCATCAUATACCCCTACTUAC
293337729	98574	GGGUGCAGAAGAGCCUCA	98575	GGCGGUGGTAGGUGGAA
293363369	98576	AGTGGTCTTUCTGTGGCTAGUG	98577	CGAAACTAUCCGAAAAATUGGGCAT
293368255	98578	GCAGAGGAAACGUCAGAAGCUC	98579	TTGTACCUGGACCTGTACTUCCA
293372605	98580	GGAAAUGAATACTGAGUAGCCAGGAA	98581	ACTTGAAAAACUGGATCTGCUGAAGT
293373573	98582	GCGGAGGCAUGTTTGGUAGT	98583	AATATACTCAATAATAUCATAGCCACTCAACUC
293390275	98584	AAGGAGGAAAGCCAAGUATCTGUG	98585	CATCCTGACAAUATTACTGTGCUGAGAA
293469713	98586	GCAAGGTACUTAATGTTTCTUGGCAAA	98587	CCACAGATATGTUCTTCCTCAATGCAUA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
293474182	98588	TTCTCATCTUTTGCAGGTUGAGGAT	98589	CCCTAGGTTGUATTTCCTTGAGGAUCA
293520808	98590	TCUGTCTCCTGUACCCCAACA	98591	GCGGTTAGAGUTCTGCCGUT
293530175	98592	GGGTTACCCUCGATCCCTCUA	98593	ACACACAGGUCAGACAUGCAG
293543761	98594	AGCATAAGGAAUGTGTTTAATGAGUAGCA	98595	TCCUCCGAAGCUGGACAAAC
293545975	98596	GCCATTGTCTUCAAAACTCCAAAGUAT	98597	AACAACTGACUTACCTTTGATTUCAGGA
293566702	98598	GGGCTTGUGGCACCTUGA	98599	AGGAAGGGUCAGGUGGGT
293585649	98600	CAGACTGTCATUATCCTGTTCTGUGT	98601	CTTATCTCCTCUTGTCCTCTGCTUG
293589786	98602	TTTCCTCCCUCTGCCCTCTUAA	98603	GCTGAAGAAAAGCUAGGAGGAACUC
293598118	98604	GGCTGCUCTCTCCTGAUAGGT	98605	CCCUAGACCAGCAGCTGTTUG
293603325	98606	AGCCCUCAGAAAGCATTTUAGGT	98607	AACCTCAGAATCCUTTCTTCCTGAAUC
293606970	98608	CTACCCUCAGAGUCAGGGACA	98609	TGUGAGAAAGGCUGCAACACT
293610572	98610	ATCTTCAGGCCUGCAGUCAC	98611	TCTAGGGUGAAGAAAAGAGTCAGGUT
293615623	98612	TCTTAAAGCATAUTCAATCTGTGCUAACAGT	98613	CAAAGAGAACTUTTCAATCACCCUCAT
293615996	98614	CAAGTCGAGCUTCTGAGATUCGAT	98615	GGGUAAACCAGGAATATUCAGAGAGG
293617632	98616	TTCCTTTTTCTTUCATCTTCCTCACUGT	98617	CCATTTCCTUGGCAACAAAAATCATTUC
293621578	98618	ACTCATCACUCCTTCCCUGGAT	98619	TTTGAAGUGAGGACAAAGCTCATUAGT
293630941	98620	CGGUACCCCCACTCUCACAA	98621	GCCCAAAGCAAACAUCCATGATUA
293650732	98622	GATGGAAGTTAAAGUTTCTGGGAGUCT	98623	TTCGTTGTACUTCTGGCTGGUC
293657085	98624	CACGGGAAGAAAUCAAAGAGTCCUT	98625	CGAGAGGAUGACAGAUGAGGCT
293703468	98626	AATGTCTTCAAGTUGTCTACAATAAAGTTTUT	98627	TGAGACTCAAUGATGGCAUACCAAAG
293703679	98628	AGCTACATAAACUACACACACACATCUG	98629	CTTAATTTCUTAACAGCTUCGGCAGT
293704544	98630	GCAGGGUCCCGCGAATUAG	98631	CCCAGGUCCTCAACTTUGAAGAG
293704592	98632	TTTTCTTAGAUTGCTGCUGGACACT	98633	GCATCTGAUAGAGAAGGTAGGACATUCT
293704792	98634	GCTTAGGTAUGTTTCTCAAUGAGCACT	98635	CATTTCGGCCAUTTTGCTTTAAGGUAT
293709361	98636	ACCTCGATCUCCTTGTAGUCGAT	98637	GGGTCUCACCCGGATUGT
293709989	98638	TGCCTTCTGCUTATCTTTTTCCTCUT	98639	TCCCTCUCCACGACATCCUT
293710649	98640	ACTGACTCCCUTACAGTTCUCCA	98641	CTAGTGGCGAGCUGGATTCUAAAT
293713309	98642	TGCCCTTUGGGCTTCTCTAUACT	98643	GCACCTGTCTAAAUTAATCTTGGGTTUC
293713660	98644	GCAGTCAGUGCAGTGCAAGUA	98645	TGAAGACACAUCATUGACAGACGAC
293713986	98646	CACTTCCUGCTGAGAUGGCAA	98647	CCAGCGCAAGCUTAAAGACAUC
293714743	98648	CGCAAAGUTGTAAAAGCUCAGCA	98649	GCTGGTGTACUCCACTATTTCUGT
293715656	98650	GCACTAUCCAGCTGTCUGCAA	98651	CTAATATUCCCGGCCAAAAAGAAAUGAA
293717503	98652	TGGTGTGGAAUGTCTAGTATTCUCACA	98653	GCTTCTCCTTAUTTAGAGTGAACUGGAT
293719256	98654	CCAAGTGATUCAGATGGAGCUAGAT	98655	GACGATAGTTTCTUCTACTAACCCGAUG
293720467	98656	TCCACCUCAGACGGAAATTGUG	98657	CTCTGGCTTAATAUCTCTGTGAATCACUT
293724426	98658	GTGCTGGUTGTCTCATUACGG	98659	AAATCACACGCACCUTCCTUCT
293724669	98660	CTCTGGTTUCAGTGTCATGTGUCT	98661	GAAGTGGUGCAGCCACUCT
293728308	98662	CAAGACCAGCGGCUAAUCCA	98663	GATCCACACAUCAGACATTCATCTCUA
293729148	98664	CCATCAAAUGCAGCAACCTGUG	98665	CTTACAACTAUGCAAACTCCCTUCACT
293729618	98666	CAGCCAGGAACAUGAGCTCTUA	98667	TCTCACTACUGCAAAACCTTTCTCTUT
293731390	98668	CCATGGATUGAGGCCTCUGG	98669	CAAAACAAGAGCACAGUTGAAACAUCT
293736615	98670	GGCTCTCAGCAUCCATCATCAUC	98671	GACTAACCGACUCCCCAUCC
293738975	98672	CTGACCUACTGCCAUGACAAGA	98673	GTACTCAGAACUCACCCUACCAC
293739482	98674	CCAGUACAAGGACTCTTTCUGCAT	98675	TCCTCACAUCCCTGATCTCAUCC
293740973	98676	CCATGGUGTGCTCTTUGGAGAA	98677	CCCACTAUACCTATCTATGCUCAAGAAGT
293747925	98678	CTCTGCCCUTCACUCAACAAAGA	98679	GTGCTTTGCUGAATTTTGGCAAUT
293749338	98680	TCCCTGATUCAACGACATAGAGUACA	98681	ATTCTTGGCAACUTAAAATTUCACGCT
293753214	98682	AATAGCACAGACUGAAGCATCTTUAGAG	98683	ATTTGGTTAGCTUTCATCCCCATCUT
293759193	98684	GATATTTCCCCCAAGUGACACAGUA	98685	GCATCTGAUGGCTCCATACCUG
293760490	98686	GCTGACUGGGCTGUACCAAAA	98687	ATGGTCACTUGTACTGTTTAUGCCAT
293762842	98688	CUGAGGTUCAGCCAGCAAAGA	98689	TGTCCTTUCAATGGCCUCCAC
293766834	98690	GAUTGUGAAAGACGCCACGAC	98691	AGCCAUTAGACUGGGAAAAAGCA
293769976	98692	CCAGUGGGCAAAAGGAAAUCCA	98693	GGCTGATGGTUGTTTTGCTATGTTTUAAT
293770196	98694	GCTCCCCCUCTTCTGGUGAA	98695	CTGTTTCCGUGCAGCAUGAG
293773427	98696	ATTTCCTCTUGGAAGGGATUCAACA	98697	CCUGCACCCAGACTACAUCC
293773695	98698	ATGTACATTUTCCCCATUCCCCAT	98699	GTCAAGCAAACCUGGAACACAATUAC
293776398	98700	TCTCTGGGACACCUCTCGTTTUA	98701	CCCCACAUCATCATTGACTAUGGAG
293778112	98702	CTTACCACAUCCACCUGGACAAG	98703	TCTTGAAGAGACUGAGACCTCUCAA
293780301	98704	AATACUGGAGCGGAUGGCAAAT	98705	ACAGCATGUTTGGGAAAAUAACAACC
293781512	98706	ACAAAGTCAGGUAATTCTTGUAAACCCA	98707	ACCTTGCAGAAUGACTACTTUGCT
293782019	98708	TTCCCTUAACCAAGACAATTUGGAAA	98709	GATGACAATUGCATTGCTAGCAUAGAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
293783932	98710	GACAAGGUCACTGGTTCTUGAGT	98711	GGAGCCUGAGGAUGAAGGAG
293786210	98712	GGGTGACGACUTCTTGTTUGAT	98713	CCCAGCTTCAUCACAGAGTCCUA
293788128	98714	CTGGAATCACCUTGCTGTCCUT	98715	CAGTCTCUGGCCTCCCCUA
293789702	98716	TGGATCTAGUGTCCGCUGCT	98717	CAGCGCCCAAGUTCATTAGUC
293796462	98718	TGATGGGAUGGAGCGTCUGA	98719	CTCCTCTCTTUACTTGCAAACCCUT
293797228	98720	CATGCCAAGUCCUAGGAAGACC	98721	GATCGTGACCUTTGTCCGCUAT
293799071	98722	GTGAUCACCAGCTGAGAUGCT	98723	CAGATACAAUCATATGCTCCTUCCGA
293799534	98724	GCCCCAUCAAGCACATCUCA	98725	CTCCCTGGAUGAGGATAGAAAAATGAUT
293802393	98726	AAATATTACCUAGTCCACAUGCCAAAAGT	98727	AGCGTGGGUAAATACGATGGTTUT
293802587	98728	ACATAACCUCCACCTCTCTCUGT	98729	CTGAAAGGTGUAGACTTCCAGAAGUT
293805218	98730	TCCAGTTCTCAAUTGTCCTTTAAAGUCA	98731	AGGACATGTGCAUGTTTACACCTUAA
293809138	98732	GGCACTAGAAACUGGAAAAACUAAACC	98733	TGTTTTCAGAGAAAGUTTCATTGUGCAA
293810449	98734	CAGCGAGGCCAUGAAGTUAGAT	98735	CCTAGGCCAAAAUCATTTTTCAGATGUT
293810657	98736	GAUTCACUGCGCAAAGCACA	98737	GTTTAATCAAACUGAATGCCGTGAAGUT
293813543	98738	CCCTCACGAUAGGTGTGTCAUT	98739	TGCCAGCTUATCCCCATCAUC
293814570	98740	AGGTAGAAACTUCTCATCCAGGUAACA	98741	ACAGGCAGCUTCAAAAGAUGGT
293815620	98742	AGGCTTCUCATAGAACAGUCCAGAA	98743	GCAATGTGCCCUGGGAATTUG
293816315	98744	ATGAAGTATATUCCAACAGAAGATGTTUCA	98745	GTTCTTCCAGUGACAGACCTAAUAACAA
293816419	98746	CCAACAGAAGAUGTTTCAGGUAAAACAAA	98747	CGTTCTTCTUGCAACCTCCUCAAT
293816619	98748	CTCCTTCCCUTTGGCTCTGTUT	98749	GGGAGCAGGUGTTATTGATTGATAUGAT
293816706	98750	GTTATTAGGUCTGTCACUGGAAGAACA	98751	GATTATACCCCUGCAAAUAGGGCAT
293819156	98752	AGGGCTGCUCCATTCAUACAG	98753	TGGATCTTCATCUGATCTCTTTCCUCA
293820708	98754	CCCTGAGCGUCTGGGAAUC	98755	GTGCATCAGCUCCTTGGUCT
293821663	98756	GGAATGUGCCCCTTCTCUAAGAAA	98757	CTTTAGATGGCUTCAAGTGTUCAACAAT
293821678	98758	CCCAGCACAUAGTCGGGAATUAC	98759	TGTGGTTAUCAAGGGTCATCCCUA
293823138	98760	GGGUGGTGAGAGUGAGAGAGAA	98761	TTTACAGTGTUCCCAAGGAGUGG
293823222	98762	GTCAAGCUGAGCTCUCAGAAGA	98763	GTGGGAGGAACCCUTGUGG
293825407	98764	GGGAAGCCTUTGGCACAGATTUA	98765	GCAAGACACUTCCCAGUAAGCC
293827129	98766	CAGAGTTAAAATACUCCCAGCATACUGA	98767	GTTTTCCCTCUAAGAATCTGACGAAUGT
293828094	98768	AGGGAGAAUGCCACTCCAATUT	98769	TGTGAAGGTUACAACTACCAGGUG
293829085	98770	GGGTTGCAUGCTGTGAAGAUAAG	98771	GCTTGCATTCACAUTGTGTCTTTTGTUA
293832025	98772	CAAAGTUCACAGGACAGCTCAUC	98773	CATGCAGUGGGCTCAUAGAGAA
293833673	98774	GCUGGTAAGTGUAGAGGCAGACT	98775	GCCTTTTCCTUTTTATAGGCTCUGGAT
293834090	98776	TCACAGAGTATCUTAAGTGCAGAACUACA	98777	AAGAGGAGCCUTTGGAGTTGTUT
293834652	98778	GTGAGCCUTGCTTTCTCUGAAG	98779	CTTTCTGGAUCTCAATGGCTUCCA
293837270	98780	CATCTTTTGCTCUCCACTTAGCTTUG	98781	ATTGGGCTGATCUATTTGATTCCGAUT
293838190	98782	CAGACGCCGGGUGAGTAUG	98783	ATTACAAACCCGUGGCTAGGATUAG
293838914	98784	CCACTCTGCCUGGGTATCTTCUA	98785	TGGCCTTUGTCCACGAAUGAG
293842240	98786	GGCUCCAGGCAGGAAACUAAC	98787	GCCCATGAACUTGATTATGGCUACC
293844588	98788	CAAGTAGCTCTTUCCCATCAATGGUA	98789	GAATTGCUCGGGATTCATCTTAUGAAC
293845481	98790	GAGTGGCTGUGCTACATGTTUG	98791	ACAGATTCTUCCCCAGCGTUT
293849179	98792	TCAATTACAAATUGGACCTTTCCTUCCT	98793	TCGTGTCTCAUTAAGTGTTCCUCAAAT
293850788	98794	GAAGTCCGGGUTCGAGGUC	98795	GCTACACCAACCUCTCGUACA
293850803	98796	CGCCGATGUACGAGAGGUT	98797	CCGAGCGUCGAGCUCAG
293853138	98798	CACCCCGCAAUCTUGGACA	98799	GAACGCUGATGACAGCUACGA
293853803	98800	GCGUAGTACCCUGCAAAAGACT	98801	AAGCACAGGAUGTTTTTCUCCAAAC
293858398	98802	CCTGGTTUCCTGCTCTACUGGA	98803	GCTGAGCACAGUGTCUGCAT
293859426	98804	TGCTCTCUGAAAATGGTTUCCAGAAT	98805	GAACAAAGGTUGCCACACAGUAG
293861257	98806	CTTTACAGACAUGTAAGTGGTGCUAACT	98807	CGTCTTGGACAUTACTAAAATTGTGUGA
293862648	98808	CAGCAGUGGAGAGATTTGTTTATUCCT	98809	TTCTGCACTAAAUAAACTCACCTGTCUC
293863398	98810	TGGTTGCTGCUTTGAGAATCATCUT	98811	AGAAAGCCUCGAGCTCAUCAG
293863977	98812	GGGTCTCAGGUTGTGTTTATTUGG	98813	CCCCTCGCUTTCACCTTUCAG
293865122	98814	AGGTACUGGAGGAAAGTTTAUGGAAAAC	98815	AGTGTACTUCCCTTTGCTGUAAACAA
293865602	98816	TGACATTGTTUACAGCAAAGGGAAGUA	98817	AGGAAAAUGTGATATUCAGAGAGAGCAA
293866752	98818	GCTACCUCCCACCCATUCACT	98819	TCCCCCUACCTTACCCTUCAC
293867760	98820	TGTGGTUACCCCAGCAUGAG	98821	AACGAGUGGCGAATGAUCACA
293867989	98822	TCACAGACTGTUCTTGCATATGAGUT	98823	ACAGATTATUGAAAAGGCAGCTGAGAUT
293874503	98824	CTGACACATUAGCACTATCACTGCUT	98825	AGCATAGCAAUGCCAGATCTTAUGT
293876579	98826	CCGCTTCGGAUGGTGTTCAUT	98827	TCCTCAATCGUCTCCTTTAUGCC
293878958	98828	GTCAAAATACUGCATTGGCUGAACA	98829	GAACTTUGGGAGCCCCTAUCAT
293881328	98830	TTGTTCTTUGCACCTCTCTCUCC	98831	GGCTCTCAAAUACAGTCAGAGGGUAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
293884057	98832	CCTCCCTUGCTAGAGCUCACT	98833	AAGTTCGACAUGGAATTGGAUGACT
293886550	98834	CCTACAGAUAAGAGAGCACTUGGAGAT	98835	TGGAATTATGUTTCGACACUGGCT
293887128	98836	CGAGAGGCAUGAGAAGGTTCUT	98837	GTCAAUGGAGGAGAAAGTGUGAACT
293889780	98838	GCGGTTUGTCCCGUCAAAG	98839	TGGCCATTGUCCCCATTTTTCTUA
293890506	98840	AGTTCTTUGAGCTTTTCCTUAGGCA	98841	TGAGCAGTGGUCATTTTATGAAUCAGT
293894756	98842	AACCTTGCCTUTGTGTAGAGCUT	98843	TGTAATCAUGCCAACATCCUGACC
293895601	98844	CGGCGAAGATTUAAAGAGATTGCCTUA	98845	ACAGACAAACAUGTTCATTTCUCACCT
293896609	98846	ACTUGCTTGAAGUGCGAGGT	98847	CGTAGGTTGTGCAUCAGTAAGCTATTUT
293897225	98848	GAAGGTTCTUGGATCGGGCUT	98849	AGCCTTGGAAUCCTTTCTCTAGAACUAT
293900375	98850	AGTTGGGAGACCAUGCAGUAAAG	98851	GGATTAAAGCUCAGGTCCAGGUT
293900474	98852	AAAATTTTACCAUGAGGCTTGTGUGAAA	98853	GCAUCUGAACCCACAGCAAG
293902855	98854	CTCTCACCAUAGTTCCCCUCAGA	98855	CAGAGCTAAGUGATAACACCAGGUAT
293909043	98856	GCAGCCUCACCCCACUAA	98857	AGTTCAGCAUCCGCUACCAG
293909498	98858	CAACCUCCCCTTCUCAACCAAG	98859	CTTGTGCAGTAUGTAAAAGTGGATUCAT
293909646	98860	GAGCATACAGTAUTTGTTTGGCTGUT	98861	ACCTCTGAAACAAUTGCTGACATUCA
293914173	98862	AGCAGCCACAUTGCTACTGUT	98863	TTTTTCCTTCCAGGAUGTTGCCTUA
293914297	98864	CGGAACCACUCGAGAGAAAAAGUC	98865	ATCATTCTUCAAGATTCGTCAUGGGT
293915262	98866	CCAGCCCUGCTUCAACCAA	98867	CAGCAGCUCCAGGTCCUC
293915654	98868	CCAGUACCGCGCTCUGT	98869	GCAUCCAGCCCACGCUC
293917641	98870	CCAACCAAGUACCAUACACCCAAA	98871	CUGCCGAGAGATTTUCCCACA
293918415	98872	CAGTAAGGCUGCCAGCAGAUA	98873	CCTGTACCCUTGCCTTTGAUCC
293919516	98874	TGACAGCAGUAATTTTGGCAGUGAT	98875	CTGTAUTGAAAGAAATCTUGGACAGGGA
293920779	98876	AUTTTCACACAGTUGAGACAAGGGA	98877	TGAAAGTTCGCUGTGGTGTTUG
293921749	98878	AAGGAGGCCAACUAAAAGGATAAAUT	98879	CCCAATGGCUTATCTTACACUGGAT
293923134	98880	GAAAGTACTCCTTUACCTGTAGTTGGUG	98881	ATTCATGCTTTCUTGCTGTTCGTTUAT
293923272	98882	TCCACTTAAACCAUACATGCGTUGT	98883	GCCCCCGTAUAACTCCATTCTUG
293924695	98884	GATTATCCTTACUTGGAAAGCTGUCGT	98885	TTCTGGATTTTGUGGGTAGAGCTAAAUT
293925353	98886	GGAAGUTATGGACTUGGAGGAGAGA	98887	TTTGTAAATAUGGGAAGAACUGCAGGT
293927180	98888	CCGCTCCUGAAGAAAUGCAC	98889	GCCGACTCUCACCATCAUCAA
293927735	98890	GGGAAAAGCUCCAGATCGACTUT	98891	GTCCCCTUCCCCCTGTTACUA
293928765	98892	CTTTTAGAGGACAUGCTCATCCTUCA	98893	CTCTGACATTUATTTCCACATTCUGCT
293930921	98894	TGCAUTCAAUAAGGGCAGGGA	98895	CCTCTCCAGCUGAAACCAAATATUACAA
293933059	98896	AGACAUTCATTUGAAAGCGGGAGA	98897	CCCCAGATGUCAAGCTACAAAAUACAT
293934686	98898	CACGACCAAUGGGAACCUGA	98899	CTACCUGGACCAGUCCAACAC
293935877	98900	GTCCTTTTTGAUTTTTAGTGGUCCAGAT	98901	AGTTCCACAUGAGGGCGATUT
293936253	98902	GGGAATATGUGACTGCTTCCTUACA	98903	CGCAGATCAUCACCATGTTTAAAGAUAA
293936336	98904	GGTTTTAGTUGCACCATCCUGAAA	98905	GATAACTTGTUAAATGGAAATCTUCACGCT
293937775	98906	TGTCTCATTUGGTACAGAATGTUGCT	98907	CATCUGCCAGACCTTGUACCC
293937895	98908	CAGGAGGUGTCTUGCGGAAT	98909	GTGTGCCATAUGAAACTTCCAATUAAGT
293941029	98910	AGGCTATGCAUCTCCCCUCAT	98911	TCCGTGTGTACUCTTCATAAAGCUG
293941175	98912	CAGCCCTAUCAAATGAAACAATUGGAA	98913	CAGTAGGAGAAAGCAUGTTTTTGAUGT
293942004	98914	CCTGTAGGCCUCGAAGGUGA	98915	CCGCCUGGTTCUAACACACAT
293943973	98916	CTGGAACTCACAUAACTCTTGTGUACT	98917	ACATGGAGACAUCCAAGTGATACCUA
293944473	98918	GCCAUCGCCCCATTGGAAUT	98919	GCTTCCAGAGCACCAUAATAAATAGTTUC
293947596	98920	TCUGGTAACATTCUCCCCACCA	98921	TTTCCAGACUGCTGACAAATTGUACT
293947636	98922	CAGGGACCAAUCCCAGGUG	98923	CCTGGCTTCUAGGTTTCTAATTCTGAUT
293954419	98924	ACAAGAGCCGCGAGUAUGAC	98925	GCAACTGGATAUTCATCCTCAAGUCC
293954686	98926	GGGTCTTTTCCUAGTTTGCTATTAUCA	98927	TCTTTGTTCCTUCCCTATCTGTTCATUAC
293956644	98928	GGGCCGUGGAGGCTTUT	98929	TGTGGGCUAGCGTGAUGG
293957501	98930	CCGTACCAUCTTGAAGCCTTUGA	98931	GUTCAGCAACAUCCCGGAGA
293958259	98932	CCAUCACGCUAGCCCACAG	98933	CGGGUGAGGUACCAGGAA
293960108	98934	CAGTAGATTUGACTAGTTTCAUCCCAGA	98935	CAAAAGCUACGAGGCTCTTCUCAA
293960858	98936	TCTACAGCAAATUTCCAAGAGAGCUT	98937	CCAGGACACUCATTUGGACACA
293963463	98938	GCCCAGTTACUGAATAAGCAGATCTUT	98939	CACAGGCAAAAACAAUTCCATCCATAUA
293964537	98940	GCCCCAGAAAGAGCUTGGAUAT	98941	GGTCTAAAAGUAGACTGAAGGGTCAUCT
293964855	98942	GAGTCTAATTTTUCCCCTGGGUCA	98943	ATGTGTGAAUCAGACTGCTGTATAUGAG
293967181	98944	CCTTTCCTTTTUAGGACTGGTCTTUGA	98945	TTGGACCCCUGAAAUAAGAGAAACC
293967518	98946	GTGTCTUCCCAAAGGGTCUGA	98947	GCAGATGUCCCACTATTAACUCCAAG
293973398	98948	GGCCTACTUCCCTCTCTCUGA	98949	CUCCCCACAGGCGUACA
293975493	98950	ACAGAGTCTUCGTGTTTCATCTUCAA	98951	GTTATGGAAGCAAGUTCACAATUACCC
293975925	98952	CACCCUGAGCCCCAUCAA	98953	CGGUGAGGAGAAGCUCACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
293976103	98954	TCTCCACCAUTAATGTAGTCUAGGACAA	98955	ACATGCCACUAAATCTGAATCGUCAT
293978595	98956	AATGCTTGAGACAUCATTTCTTTGCUG	98957	CTTGCCTTCTUACAGCCCATTUG
293979537	98958	TTTTGGCTTCTTUACTATCCTGGTCTUC	98959	CATGTGGTTTUAGAAGTACCCCTCTTUT
293984448	98960	CCCCUGTAGCAGUCAGAGGA	98961	GGTTACAAGAGCAUGTAGTATGTGUCT
293988127	98962	TGGAACCUAACCCTUCCCACT	98963	GCATCCCCUCACCTTCCTUCT
293991877	98964	GGCGTCAGGAAUTTCAGCCAAUA	98965	GCTTCCAAUCCTGCTCGUC
293991912	98966	CTCAGAUCACTGAUGGGCAGT	98967	GCTTGCCUGCCTGACATCUAT
293992602	98968	CAATGACAGGUTATTGGUCAACACAAG	98969	TTACCTTAACUTCCACATGUGCCA
293993809	98970	TCCAGTGAAACUGCATCATCUCAA	98971	CCTGTGAUCGAAAGTCTGCUG
294994032	98972	CUTACCAUCCACGGCAAGGA	98973	CATGCTGGAUGTTTGCCTCUAC
293996898	98974	GTTTGATCTGUGCAATGCCTCUT	98975	AATTAGAGTTAAGUAGGGACCAUCCCAT
293998182	98976	CACACCCCUAAGTGAGTGATCTUT	98977	GGCGAGGACUACUCCAAAGG
293999246	98978	AATTAGTGCUAACTAGTTTCAGUGAACA	98979	GCCTGCTCTUTAGTGGAAACTAUGAA
294000233	98980	CTGTGAAAGCGAACAAUATCTCCATTUT	98981	GTGTTTTCCAGAUTATTGCTCAGTUGT
294000388	98982	AGTTAGTTTTACAUTTGTCTGGUCCACA	98983	GGAAGAATAAGGUTTGGTGTTTUGAAGT
294002756	98984	GGUCCACTGCTUCAGGAGAAC	98985	GGCTCACUGATGCUGACAAGAA
294003858	98986	GGGTUAACAAGGAGCCTGGTUT	98987	CCGAAGAGCUCACTTCUCCAAG
294004934	98988	CACACCCCCUCCTCCUCA	98989	GGGCAUGAAGGACUCCAAGT
294006760	98990	GGAACACCGACCUCACAGTTTUT	98991	TGGGCAAGTCUTTGATTTTGATACUGA
294008013	98992	GCAGAAUCGGCAAACUCAGG	98993	CUCCACCAGACCAGGGUACT
294008465	98994	CCTTCCACUCCAGAGGACUGA	98995	GCCATGGUAAGGATGGATGCUT
294008875	98996	TCACCTCCGAGUGGCAGTAAUAT	98997	CAGCACUCCCTTGAGGGUAAG
294011102	98998	CCTGCGCCGUGGAGAAUAC	98999	GGGUGGCAGTAATTGUCCAGA
294013987	99000	GAGTGAATTTTUGCGGTCTCATGUT	99001	GTCCTCATTTATCUTAACAGCTTCCUCT
294016796	99002	AGACGATGAGGUGGAAGAGGUA	99003	CCTGACCTGCUCCCTTTCTTTTAUAG
294019663	99004	TGTGGAAUGTGTGGCTUGAGT	99005	GAGAAGCUGAACTTTGCCCTUG
294020044	99006	GAGAACTCAATGUCCATCTCCATUCT	99007	AGGGTTAAGUGGATCAGTGGCUA
294020310	99008	CCTCCCCAAAUGCGAUGCT	99009	AGCUCTACCGAAUCAGGACCA
294022088	99010	GGCAGUGAGCGTGGAGTUAA	99011	GCUCCCACAGGAAGAGGUG
294023878	99012	TCACAGAAGCAGUGAGGATGAUG	99013	CAGAAGUGAGGGAAAGTUCAGAGG
294023907	99014	CCGAGGGCAGGUCUCCA	99015	CTCTGCCUGGCTGTUCCA
294024687	99016	CATGGAACAUCTGATCACUGGGT	99017	CTGGGAGGAGGAGUACGAUGAA
294026393	99018	GTATCCTTTCTCCUCATCTCTAGCAUCT	99019	AGCAACAAAACAAUATGCCTUGGG
294026880	99020	GAGCCCTGAGUCCTAATACCUG	99021	CCCCTGUCCAGCTGTUGA
294028623	99022	CTGACCTCTUCACCATTTTTCTTTCUG	99023	TTCGGAAAAGCUCUGGCCAT
294028836	99024	GGTGCTCAGGAUGCATTTGTUT	99025	CAGCAACCUACCTTGAAATGUCC
294029495	99026	CGGACTTAGACUTGAGCAGGUG	99027	CCCCAACCUCCTTACAAGACTTUG
294029711	99028	ATGTTGGCCAAGAUGAAATTTAGCTTUT	99029	GTTTTCTGGGCUCTTGGAATATCTTAUCA
294030465	99030	TGGAATCAUGGCCAGAGCTUT	99031	CCTTTGGAATGUAATATAGGTGTTCTUCACA
294031686	99032	GGCATTGUCCTCATCCUCGT	99033	CCCUGACCAGGGTATCTTUCC
294032303	99034	GCAGGATGCUGAGTGGTACUG	99035	CCCTGUGGGAACAUCCAACAT
294032471	99036	CAAGCAATUGGAGGCGAUCA	99037	GTCCCCATTTCACUGAACTAAATAGCUT
294034002	99038	AGAGTCCCCCAGUTCTGAGUC	99039	TTGGTCTTCUCCCTTCCCAGAUAT
294035378	99040	CATAGTGCTTAUAGCATCCTCTTGACUT	99041	CACAGGTCTUGGATCAAAGTUCAGT
294036621	99042	TCACATTUGAACAGTCATTCTUGAGGA	99043	CAAGGAAGTGUCCAGTATGAATAAGUGA
294038881	99044	CCACAGAAACGUGCAGAUGGA	99045	GGGCACCTUCAAGGACTATGUG
294039509	99046	CTCCTGCATCUCTCTACTTGAAGUG	99047	TCCUGCUAAAACCCAGGAACAAT
294042653	99048	GAGTTTTGGCCUCTTCATTTTGCTUAAT	99049	GGGATCCAAACAAUGAATATAAATUAGCC
294042767	99050	TGTCCCAUACCCAGTCCTUGA	99051	AGTTTUACTTCTTGATCUGGGAAACACA
294044289	99052	ATTCATTGTTTGGAUCCCCTGGAAUA	99053	CAAGGAGAGAUAGAAGTTGGGCTUT
294044396	99054	GAGGCACUAGCTCTGCCAUT	99055	AGACCUCTCUCAGCACCACT
294044403	99056	TGAGAATGUTTACCGCUGGCA	99057	CGTTTCTTTATTUCTCCTCCTTCAUCCA
294044688	99058	CTTGTATTCAAGGUCTGGCTGGTTUA	99059	TGCTAATCGGAAUTCTTCAATGGUCAA
294046785	99060	CCUTATTGAGGUCAGCACGGT	99061	GCAGCCAGUCATCTTUCAACAG
294046833	99062	GCTGATATTCAUGCTTTAAACGTTGUCT	99063	CACATTCCUGCTGTCTCAGUACAA
294048929	99064	GTGGGCGUGGCAGAUGA	99065	TGGGCUGACTCTGCUCCT
294050980	99066	AGTATGCUTCAAGGAUGACACCAAA	99067	ACACAATGACCTUGCCATCATAAGTTUA
294052358	99068	CTCUAGAGGGCCTGUGCAAT	99069	TTTACCCTTUCAATAGTCACACUCACC
294055743	99070	TGTTTCTTCAUTTTCCCTGGUGAGT	99071	TTCCCACCUTTGTTGGAAGUGAA
294058203	99072	CCTUAAGCACCCAAAAGCATAUCCT	99073	GAGCUGCATTGTUAACCCAACA
294059848	99074	TGUCAUAGGAGGGAACACGCT	99075	GTCCTCTTCCUACCTCCTCCTTUA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294064195	99076	GGGTCAUCCACAGAGGACAGUAAT	99077	GCAGGTTAGACCUTGACAGTGAAAAAUA
294065610	99078	TGAAACTCAAATCUCTCAAAAGGCTUACT	99079	GCTGGTTGUCCCAAAATCACTUT
294072504	99080	TCTGGGAUCAAAGTGCTTUGGA	99081	CCATTGAUAACACCAACATCCCCUA
294072966	99082	CAACGAAAAATCUGTCTGATGCAUGT	99083	TTCATACCAAUGCCATGGTTATCGTUA
294076807	99084	CTTGAGTTTCAAAGGUTGCTGTTCUC	99085	GAATGCTGGAAAUCCAGATGTTCUAGT
294077423	99086	CCAGGAACTUGGATCAAAGGGTTUA	99087	GCAAACCTUCACTTTCCAAGUGT
294078714	99088	TGAGCTGGAGAAUTTGGATTGUGT	99089	CAGAACAUGCCTCAAGUGCAT
294079109	99090	ATTGTCTACTTUTGTTCCTACCUGCAA	99091	AATGGAACTCUCTGTACTTTUGCCA
294083636	99092	GGGTAGGUCCTTCUGCCAAC	99093	GACUGGCUGCAGAAACACAAC
294085884	99094	CCTGCGAACACAUTGCTGUAG	99095	TCCAATCAUAAGGGACAGTAACTGGUAT
294087847	99096	TCTTCACTTTGCUGTTGAGATTCTTUGA	99097	AGATACACTGGGUCAAGTCTACAAAAGUA
294089965	99098	TCATTTGGTGTGGUTTTCTGTTCTACAUA	99099	CACCCAGAUCAAACAAAACACTTAGAUT
294092006	99100	CCAGGUATCTCTCUGCCCACT	99101	CACAACCCTCUCCTGCTTTCUC
294092717	99102	GATCAAACTCCAAUACAGCAAACCATUT	99103	AAGAGAGGGACCAAAGUTGGTTAAAUT
294093373	99104	AAAGCTGTAGTCUTTTCTAAGCAGUCA	99105	TGCATGCAATAAUCTGGTTTTTCAUC
294093970	99106	CCCTACCTTCUCATACTCGTCCUC	99107	GGAACGUGACCCCCATTUCT
294094253	99108	CTGGGUGGCATTTATTTGTUACAAGAAT	99109	GATTTTAAAACACUGGCAGAGUCCAG
294094470	99110	GGGCCUATGGCAUGAAGAGA	99111	CATGAGTGAGGAGGUACCACAAUG
294095425	99112	GCTCTGAATTTTUCTTCTGCTGCTTUT	99113	CTCACTATTUGTGCGAGAUGGGA
294098980	99114	CCGTTTTCCTCUATCCACCATCTTATUT	99115	AGCGTTGGCAAGACAUTTCTACATUA
294099299	99116	GGAGUCAGGGCCGAGAGAUA	99117	ACCCAUTATTTACCTUAAAGCCGAAGT
294099307	99118	GGCUGACCACCAGCATGUAAT	99119	ACACTTGTGCCUTCTGCTTCUC
294102499	99120	CCTGAATTCUGCTATTATCTAUGACCGA	99121	GGTCCAUCTCAACUCCAAACAACT
294103183	99122	GAGCATTGCCAAAGUCCTTCTTUT	99123	GGTTTTCCCCAUTTATTGAAGCATUACA
294106689	99124	GTGCCTUTACCCCUCACGA	99125	CCTTGCTGCAUTTCTCTTGAGUCT
294106837	99126	GTGCCTAAATUGTTTGTAGGGTUGG	99127	CAGGAUAGGAAGCACACATGUCAAT
294107291	99128	CTTCAACTGCTUCATTTCCTTCATCTUT	99129	GTTCTTCGAUACTGGTAUGGGAAAAAGT
294107756	99130	ACAAGATAGCTCAUTTTTAGGCAACUCA	99131	CUCTCTCTTTATTAAUGCCCAGGAAACT
294107928	99132	TATGCAUCAGTGTTGTTUGGCAAT	99133	GCCCCCAUATCUAAGCAAAGGA
294109366	99134	AAGAACAGAAUGGCTCTCTTUCAACA	99135	CCGCAGCAUTTCCTTUAACCAAAAT
294113623	99136	GGACTTUTTCCTCCTUCCACACAT	99137	GGGCAATAUAAACATATGCATCGUACAA
294113796	99138	GGCCTTCAAUGAGACTATCAAGATCTUT	99139	TGTACUGCACCAGAUCAGGGT
294116556	99140	ACAAGCGAGAGAACUGATTGAUACC	99141	CATCTGGCCAGUCCTAAGAATTTCUAA
294118155	99142	ACTCCACCAGUTTTAATACCUACCAGT	99143	CTCTTTCTTTAGGUTCCAGCAACAAAUT
294118650	99144	GACAATTGUACCACCCTTAAGTTGATUC	99145	AGGATAAAATAGTUACATGGATTTGCUGCT
294118651	99146	AGCATTTTCCAAGUAGTCTAGCTTTCUT	99147	ATGCCCTGCUTATCTGAAGGUG
294119837	99148	GGTACTGAGAUCAAATTCTUGGAGGA	99149	AATACCCATCACUCCCGCTTTUT
294120449	99150	CCAAGAAAGAAAUATGCAATTGGTUGCT	99151	GCCAGAAAAUCAACAACTAGAUCAACAT
294121214	99152	GGGCACATUCTTGGGAATUACAAA	99153	GGCGAUGAAGGAGGTGACTUAC
294123642	99154	CTTGACAUCCTCTTCTGUGGCT	99155	CATCCATAGACCUGACATGTGTAUCAT
294124173	99156	CTTGAGCATACUCTTTCATTTGTUCAGA	99157	CCTCCAGATUAGTAAAGCCAGTUGAAAA
294127269	99158	GGCAGCAUTTGAGAGCUGACT	99159	ACACGTCCAACUCATGTGTACUG
294127306	99160	ACCGCGUGAAGAAGCTCAUC	99161	GGUCGCACAAGGAGUCAAACT
294127471	99162	TCAGAAGAGAAGUAGAAGTUCCACCA	99163	AAATGAATGUGAGGGTACACTGTUAGAG
294130274	99164	GAAGAAGCTCAUCAACTCACAGAUCA	99165	CGAAAGTCGUTCACTTCUGGGT
294131241	99166	CAAGACTTCUCGAAGCTGATCTTTUAGT	99167	AATGCACTGUCAAAATCCAGUCAAAA
294131938	99168	CCGCAGGCAGACUCTGUAAAT	99169	CCCTTCUACCTCCGGCUGA
294133164	99170	GAAGTTGAACGAAUGGAATGUGCAA	99171	ACTTAUAGACCAGAACTGCUACAACAGA
294133690	99172	CTTCTGCCACUTCTAAGTTGACCUA	99173	ATTCCTTGUGGCAGAGUGGAG
294134941	99174	GCTGTAGACUAAAATCCAACTTGUAACGA	99175	CGTCTGCAAUGAGTACAACTGCUAA
294135762	99176	AGTCTTCCTCTTUTGATGCCTTGAAUT	99177	TCTATTGGTTTAUCGACTGTCCTTCUGA
294135873	99178	CCTCCACGAGUTTGACTCCUT	99179	GGGAAACUGTACUGCAGCCA
294138303	99180	CTGGAAGGGUCGGCUGAA	99181	GTGACCTGUCCCCTCCUCT
294139721	99182	TGUGCCAATTCUGCGAGGAG	99183	CCTCGCUGCCCTCAAACTUAA
294140466	99184	CAGAGCAGTCAUGATATCTTCTTCCTUT	99185	GAAATTTCAAGCCAAUGTATTTCTGCUT
294142967	99186	CGGGCCCUTCTGGUCAAC	99187	GACACCUGGCAAACACCAUC
294143104	99188	GAGCTCAACUTTTAGTGACTUAGAACCT	99189	GCTCCUAAAGACCAAACTGTGTCUC
294145451	99190	GGTTGAGAUGACAAAAAGGGTUGAGA	99191	GGCCACCAUGGGAGAGUG
294145530	99192	TGCCATTGATCUCTTCAAGGCTUA	99193	CTACCAGGAUCTCAAAGGAAUGGAAAAT
294146122	99194	TCCTCCUCTCTTTCAGUGGCT	99195	ACACACCCAGUCTGTTCTTCAUC
294149872	99196	TGGGTGCACACAAAUACACAGUAT	99197	AAGAGGGAAGTUTTTGGTGGTATTUCT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294149955	99198	CCTGCCCCUGATGGAACUT	99199	ACCTTGTAGUCTTCCCUGGCA
294150435	99200	GGTCCTCAGUGTGCTTGTAGUA	99201	GCTCATTCCTUACCCAGTCCUCA
294152247	99202	GCTTTGAAGTTTCUCTACGTTCCTTUT	99203	CACATGGACCAGCUATTCAAAUAGAAGA
294153785	99204	CGCTGAGUGCAGCCGUT	99205	AGGAGUGAGGGCTCTGGUT
294158643	99206	GCAGAGGACUGACCUCCCT	99207	ACCTGCAGCGUGTAGTCTUC
294159274	99208	AGACCCACCUGAGGACATUCA	99209	CTCACCUCCGAGCUGGAC
294161405	99210	AATGACCTTTTGCUTTGCTTTTCCUT	99211	GTTCATCGCCUAACTAATTAACTGCUG
294163015	99212	GGAAGAAGGCCACAGUGTUC	99213	AGAGUGCAGAGGGCCUCA
294164548	99214	GCTGTTTUCCGCAATTCTTTGAAUAGT	99215	GGAAATTTTGACUGAACAAGACGUGA
294164839	99216	CCCCAACAGAGCAUCCTAGUT	99217	CTGCTTGTCTTCCUATTGATGATGTATUG
294165497	99218	GAGGCTCACAUGGTGGTGUAA	99219	GTCGTATGTGUGTTCTGATGUGACA
294166190	99220	CTTACGGCTUACTGCAATGCATUC	99221	GCCCGUGTTGCAGAUCC
294166813	99222	CAACGAGAUGCTGUGCAAGA	99223	TTCTCGAUCACGGCGUACAG
294168910	99224	GCAAGCGACAGACACUTCUAAAA	99225	GGGAAAGCUCATCGTAGCUGT
294169804	99226	ACTGCCAATTTUAAGGAGCTGAATUCT	99227	AGTTCTCTGATGCUTATCTGACTCCUAA
294169854	99228	CCUTTGTTATCTACUCAAGCCAGGA	99229	CTTTCGGCTTUTATGGAAACCTUCA
294170580	99230	TTTTAACCACTUCAAGACTGCUCCAT	99231	CATATAGGUATCAGAAUGGCAAAGCA
294170586	99232	TTTTTGCATUCCAGGTTGCTGTUT	99233	TCAAGTTUCGGACAACGACTTUAGT
294170750	99234	GAACCCTGUGTGATCATGGUCT	99235	CAGAAAGTATCUGCCACTTAGTAGCAUT
294171402	99236	TGGCCCGUCTCTGCTTUG	99237	CGGGAGGAGAGUGGUGAGT
294172724	99238	AGGCTCAGUAGAACAGAAAAAGUACAAG	99239	ACAAAGGTTCAAAGUCCTTGAGCUA
294172970	99240	TCCTACCUGGCAGTTTTCAAAAUGA	99241	TGGAUGGACTGGCUAAAACAAACAT
294173018	99242	GTTATTTCTTACCCAUCTGACTGTGTUCT	99243	ACAGTTUGGAACAACAGCAGAGAUA
294174098	99244	CAAAATCCTGTTCUTCTCGATAGGCAUA	99245	CTGTATTTATTGCUTTGCCTACTTUGCAT
294175231	99246	CAGTGCUGATTCGCUCAGG	99247	CCTCTCTTCTTCUTTCTGCTCCTTCUA
294175255	99248	GATGGTTCAUGCTCTGGUGGAT	99249	GTGTTTAGGTCUGCATGAATTTGATUCC
294177180	99250	GGAAAATACUCACAGCAAATGACATTUAGG	99251	CACCACTAUGTGCCATTTUGAAACAA
294179051	99252	TTCAGGATCCTUCAAGGAATCAAATUCA	99253	CCAAGCAUCCAACATCCAAGTUAGT
294180913	99254	CGGAUGCGGTATTGTUGAGGA	99255	ATTTGGTUCAGGAGGATGCAUGT
294181567	99256	GCCACTTGAAUAAAACAGGCAGCUA	99257	GGCATGGGAAUCTCTTCAUCACT
294183039	99258	CCCTCACUGGGAGTCACUGT	99259	TGTUCCCCAGAGCAGCATUG
294185961	99260	ATTATTCCGGTUCCACAGCTATUAGAC	99261	GTTTGTGGTTGTUTGCATGTATACTGUA
294186460	99262	CATTGGACUGTATTTTUGCCCAAGA	99263	AGTGTUACGACCCAGAUACAGACA
294187859	99264	GTGAAATAGCACUTCATGTTGGUCAAT	99265	GCTTCTGGATUCGAGATGTAATTTTGUC
294190524	99266	CGCCAAGAACGAGUCATGTUT	99267	CCAGGGAUAAGAGACAAAUGGAAAGA
294191255	99268	CATTGCUGCCAACATCAUCCA	99269	CUCCACCTTCUGCAGGACAAT
294191398	99270	GCACCGCGUACAGGUGAA	99271	AGGAAGCTCUTAATGCCGUCAG
294192709	99272	ACCATGGATGUGAAGTCATTCUAAGAAAAA	99273	GGAGAAGAACAGUTGCTGAGATCUG
294192972	99274	GACGUGGATCAGUGGGACA	99275	CCCUCCCACCCGCUACA
294193562	99276	TTGCTCCUGATGGAATTUGGGAT	99277	TTCCAACAGCUATCAUCAACAACAGA
294197818	99278	CAGUCAACAUCAGCGCAAAGAG	99279	TCTAACACTGUGCTCATGTGGTUT
294198437	99280	ACTCUGAGAGCCCCAAACCUA	99281	TGTACTCCUCCCCTTCTTUCCAG
294198660	99282	AGGCUAACTAAAACATUCGGAAACACA	99283	CCCAACTCCAUTGGCAAGUC
294198794	99284	GCATGTTUCAGGAAGAAAATUCAGGAT	99285	AAGCGCTUAGAATCAAAATTGTUGAAAA
294199341	99286	CAAACCTGTUGCTTTGCCUGAT	99287	CAGCCATTAGTCAUAAATGTTTCTGCUT
294202560	99288	GUTGGTGTTUCCAGGGAGGAAT	99289	GCCCAUCACCUCGACCAC
294205160	99290	CGATGTCAUTCGGGUCACCT	99291	TCACAGCTGCAUCTCTCTCTTUC
294208716	99292	CGCAUAGGAAAAGCCUAGGAAAG	99293	TGTTTTTCCCUTCCCGUCACA
294209663	99294	CGAACAATUAACATGAATGTTTUGCAAGG	99295	AGTCAAGAATCUTCAAAGTGCAAUCAGA
294209889	99296	TCTGATTGCACUTTGAAGATTCTUGACT	99297	GTGTGCUGACCGTTTTCCTUG
294209953	99298	ACCAGGAUGCCATCCACUACA	99299	TGCCACAUCCGCCTCAAUT
294211985	99300	GTCATCCTUGGCATGGGCUA	99301	ACACATTTAACUCAACGTACTTCTGCUT
294214787	99302	GCTTCCUCAGGCTUGCAGT	99303	AGAGTCTCCAAGGUTCAGTTCUCA
294215904	99304	CAGTUACTGAAACACUGACACAGGA	99305	GCCTGUGACAGCAAGTUCCA
294219723	99306	ACATGCCCAUCATAATGCAUGGT	99307	GATCTCGUGGACCTCCUGAAG
294226207	99308	ACAAGGTCAAAUGCTTCTGTTGUG	99309	TTGGAGACGUATTCTTAGAGGUGGA
294238331	99310	TCTGGTTUCAGCTAGTCUGGGA	99311	ACTGCTCTAGAAUTAAGAGGGTTUGGA
294247179	99312	AGTGGTTCTUACTCCAGCCTTUC	99313	CTTGCCAAUTCTGATGGUGACAAAA
294256807	99314	TGCTTTGGGAGACAUGATGTTUCT	99315	GCTCTTCCTTUCCTGTGTTCTTCTTUAA
294257169	99316	CCAAAGCCCCUCAAAAGAAGGAUT	99317	GCCCATUGAGAGCCTGAUGAC
294260986	99318	GGTGGTCAUGAGCAGACGUA	99319	CCCUGCAGAGCCUGGAAG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294262511	99320	CTTACCTACCATAUGTGGCCATTAACUT	99321	ACATAGCATCAUCCTTTGGTUCCC
294263207	99322	GCUCCACGGAGCCGATCUA	99323	AAGUCGGTGCUGAGGAAGAC
294263913	99324	GGAAGGAUCTTUAGACCAACAACGA	99325	GGAAATACGUACAAAGAGTTTGCAUCAT
294265105	99326	GCTGCCACGUCCACUCAC	99327	GGCUGGCCAGAGAAGACTUAC
294266209	99328	GCCTTGGCATTUAGACATCTTTGAAUT	99329	TGCTATTACCAACAAGUACCTATCTCUCA
294266430	99330	GCTGAAGUGCCACTGTCCUC	99331	TGUCCCATGUACCCCAACCT
294266574	99332	CTGGCCAUCAGGGTUACCAT	99333	CACAGUGCCAGAGGCUGA
294267858	99334	CCAGCATGUCGCTCAGCUT	99335	CGGGCCUACAUCACGGT
294268403	99336	CTTCAGCCUCTGGCACUGT	99337	CGACCTCTUCCGGGCCUA
294269056	99338	AGACTAGUCCCTGTTTCUGAAGGA	99339	AAGACTAUGCCCCCUCAGGT
294271893	99340	AAAACUGGAGGGAGGACCAAUC	99341	GCCTCAACTUGCAGCTAGGUT
294272777	99342	CTGTGGUGGGAAGCTCAGUAA	99343	TCAGATTTGAAAUGCTAAACCUCAGAGT
294274209	99344	TCGCATTCTTUCGGTTGCCAUA	99345	CGACCTATGAUGCGGAGATGTUG
294277265	99346	TTTAGGAGAGAUCAGAGTGGCCUT	99347	GAACTCTTTGTTUATTGCTGCCGUAAT
294280675	99348	CCAGAGGTGUCTTTGCTGAAGUC	99349	GGGTCTGUGGACTATGATGGUA
294284051	99350	TCATTCTGTTATTGUCAATTCCCCTGUT	99351	GAACAACCAAGCUAATATGCCATTTUCT
294285102	99352	AGGGAGAUGGAAGGAAAUGGGT	99353	AGUCAACAAAACGGACAGUCAGA
294288824	99354	TGAAGTAATTTCUAATTTTTCTGTCTCUCGACT	99355	GCTAAAGTGUCCAGCAGCAATCUAA
294290318	99356	CCATTCCTTACUCCAAATGTGGUCA	99357	AGTCTTGCUGGCCTTTCTTCUT
294291738	99358	AGTTGAGCCUAGTAATTGCATCATUGA	99359	TTTCTCTTTGGUCGAACAATUGCC
294294702	99360	AAAATTCACACCUACCACAGGTUAAAGA	99361	GGAAGCATTAUCTTGACCAGCUGA
294295348	99362	TCTAAACAACAGTAUAATGCCTGCCTUT	99363	CATGGACCCCUGATGATUCCAC
294297094	99364	GGATCCGAUGCTCTAGCAGTUT	99365	CCGAGCTUCTATCTGGGAUACC
294298181	99366	GGTGUGCAAGGGTATUCGGAA	99367	ACACUCCGAAUCAAAGCCACAA
294300955	99368	GTAUGAAGAAACAGACTGGUCACCT	99369	TGTTTCTCCTGUGACTTCTTCCTGUA
294301094	99370	ACCTGTGUTCATTCACAUGAGG	99371	AGAGCTTGTUCTGGCCGTUT
294303058	99372	GGGAACCTUACCCAAAATGUGGT	99373	CTGTAACACCAGAUACCATTTTCAGUCT
294303645	99374	ACCCCUTTCUGGGAGGCA	99375	GGCTCCCUGTCTGGAGACUAT
294303689	99376	GAGACACAAUCACUGACAAAACGG	99377	CCTTCCCCUTTCACACTCUCA
294304450	99378	GCGCCCUCACCGTGAUG	99379	GCGCCGUGGTTGTTCUG
294304577	99380	TTGCCGTUCTCTGCCGUAT	99381	ATGGCTGUCTCTGAAAUGCCA
294304679	99382	AACATGTTTTUGGGTATTTCTGGUGT	99383	GACCUCAAGCCTUCCAACCT
294308696	99384	GTAGTUCAGAGGAGTUGGCAGT	99385	GCCCTGTTUCTGATTCTGTUCCA
294310102	99386	TTGAGAUCACAGGTGGTGTUGAG	99387	TCATGGAAACAGAUCTTTACAAGCTCUT
294315442	99388	TGCACCACCUACCUCCAGA	99389	CATCACCUGCCCCTTGTAGUT
294315773	99390	TGATTTGTGUGAAAATTCACTGCAUCAT	99391	CGCTGAACTGTTUATGTCTCCAGTAAUA
294316318	99392	TTCTGTGTTTAAUCTGCTGTCTTAAUGGA	99393	CATCACAACAGAGACAUTCAACAACUT
294316532	99394	CCTGCCUGGCATTUCAGAGA	99395	CACCATCACCUGCCCCUT
294318125	99396	CGGCATUCCCACCAACUACAA	99397	TAGAAAACAAUACAGTACTTTCTUGAAGGAAAC
294321965	99398	CGAAAGCAGUCAGAGTCTTCCUT	99399	AGGTTCAGAAGTUGCAAATAAAGCAAUG
294322908	99400	GCAAGCCCACAGAUGAGAAUCC	99401	CACCCTTUGCCATCTGTCTUGA
294327369	99402	CATTGCTGAGGUGTTGTGTCTUC	99403	TTTTCAATGCUTTGCTAAATGUGACCA
294331135	99404	ACCCCTTUCAGGACCCUGT	99405	CTTCCCUGCGTCCTTTCUCT
294331153	99406	CCTGAAGAGCUCTCAGGCTUA	99407	TTTGCAACCCAGAAUGACTTTGTUC
294333337	99408	ATTATTATCGCTGUCTCTGAGGAGUCT	99409	GCGTCCAGUAATAATCTTUAGACCCAAA
294333828	99410	CCAGUACCCAGAGACCAAGAUCA	99411	CAGTGAACCGUAATTTCUCAAAAGCA
294338759	99412	CATTAACACCAUTATGTTUGCAGCCA	99413	GCTUCAGAAGGATCAUACCAGACAT
294339044	99414	AGCCTGTUGCAATGGTCCUC	99415	GCTAACATGAATCCUTGTCTCCTTACUC
294340048	99416	TTGTTCCTTGTAUAAGAAATGGTGCUGA	99417	ACAGGAGGUACACTCAGTGAAATTUG
294340986	99418	GCCAGATCUCACAGGAATTACACUAT	99419	CCTCACACGTTATUTAATAGGACTGTACUT
294343234	99420	CTCUCCAACACCCGTACAUCA	99421	CTCCTCCAAACCUAACTGTCATTCUAAC
294344119	99422	GAGATTGGAGAAUTCCCTGTGTTTTUC	99423	GTCTCACTCUCTATCTGAATATCUCCGT
294344662	99424	TCACCCCUACTCCCAACUGA	99425	GTCACTTTCUCCCTCCAUCCA
294345021	99426	CAGTGTCGTATUGTTGATCTGATAUGGT	99427	TCAATCCTAAUAGGCAGAGAAGAGCUA
294345660	99428	TGGCATAGUGGAACATGTGATUGA	99429	GCTTGGUAACACATGCTGTATUAAACC
294347028	99430	CAGGTCAUGGGTTATAGGUGCAA	99431	CCCTGTAGAGAAUTGAAAATGGUGAAGA
294349993	99432	GCCTTTCUGAGGCAGGGTTUA	99433	CAGGUAGAAAGUGCGAGGCT
294354433	99434	AGCACAGTCAUCATGGCCTAUC	99435	GCTTTGCTATCAUGAAATGTATGCCAUT
294356489	99436	AGCAGAGAACCUACCAGAAACUCA	99437	ACACCAAGGGACGAUGUGG
294358109	99438	GCGAATATCTTGACUCCTTTAAGGTGUT	99439	CCTTTCCAAACUTGAGGCTCUGT
294358911	99440	ACCCCTUCCAGGAGTTTTCUCT	99441	CAGTCUTTTATCAGCUGGACAGGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294361022	99442	GGAAAAAGUCAGGAUCCCAGCAA	99443	CCUCCCGAACACACACTCUC
294363585	99444	GAAGATTTAUCAGCGTGCATTUGGT	99445	GCGGCCTUACCCTTCCATAUA
294366601	99446	CTGATUCGGCCAGAGCTCUT	99447	TCCTCTTTTCUTATCCTCCUGCCA
294368728	99448	GAAGGGCGCAGGCUGUA	99449	CCCACACCUCCAGCCUCT
294368868	99450	GGACTGGCCACUCGCTATUG	99451	CCACGCTGCUGTTCTCTGUT
294369059	99452	GGGTTCACUAGAGACCTCTGUCAT	99453	CACAAAAGCACUTTCCUCCACAG
294369853	99454	GCATGATTGUACATCTCTCTCTUGGA	99455	AAUATTTTGCTAGATUCACAGGGACACA
294373144	99456	AGAGUCCGAAGTCAGUAAGGACAA	99457	CAGTGAACCUAAAATGCCTCTAAUACCT
294377010	99458	CAGAAAGTTTGAAUTCCCAGCCAUC	99459	GGTGTAATGATUCACAATGGCTUGT
294377806	99460	GCAGTCCACAAAAGAUGGGCUA	99461	GAGCGCUACGATGUGGAAAC
294388462	99462	GCTACGAAAGUCCACGTCUCT	99463	CTTCTCTGCAUGGTGCCCTTUA
294388921	99464	CGGCCACCAUGTTGCTTCAUA	99465	ACCTTCTGAAUAACAAAGGCCACTUAC
294394252	99466	CCCTCCCACCUGATGTGTTCUA	99467	GTTTGACATUGACATTCGGCUACAG
294394686	99468	CAGCCCCUGGATTCGTACUC	99469	ATGACCTCUCCTGTGGTTTTUCC
294397342	99470	ATGAATCATGTGCCUAGGAAAAGTAGUT	99471	CTGACATGCUTGCAGCTTCTUC
294400710	99472	CCCCGCAUCTCCTTGTCCUA	99473	CCTTCCCUTTCAGGCUCCAG
294401589	99474	GGAAAUGGGCATTGTUCAAGCA	99475	CTCCTGAGGAUTCTGCCATTTCUC
294404714	99476	CATCCTCACUCCCCAGATCUCA	99477	GGACTGAGTAGUGTATATGTTTGUGCAG
294405965	99478	CACAACCTUCTGCTCCAUCAG	99479	CCCAGGAUGCTAATGGTCTUGT
294408656	99480	CGCAACTTAUGGCTTTTTCATTGUGT	99481	GGATGGTGTUACGGTCACTCUG
294411379	99482	GCAAUATTGUAGGGAGCAGGCA	99483	CTGTTTCCCUGGTCTGTTTTUCAG
294413684	99484	GCATTGCUGCAGAGTCTTUGG	99485	TCTGCAGAGCUACACAGTTUGG
294418399	99486	CAAAGAAGGAACAGGUATACTTUCAGGT	99487	CCCTGGTUGATAAAACATCGUGGA
294419032	99488	AAAGCGAACACAUGTAATTTTCCTTUGT	99489	TGGACAGCGAAGCUCTATAGGAUAG
294419390	99490	GAGCTCCCUCCTGTCCUGA	99491	TCAGCTCGCAGUCCAGGUA
294421359	99492	GAAGAGUGCATTCCCAUGAAGAGAA	99493	TGGAGACTGUGGTCTTCTUCCT
294422256	99494	GAACUAUCAGAAGCCCCAGGAA	99495	TCATGGAGGUACCAGTUACGGT
294422316	99496	ACATCAGAGUTACTTTCUGGCAAGAC	99497	AGCCTTCAUACCAAACTTCAATCAAUGA
294422981	99498	TUCCAAGGCCAAGAAGCUGT	99499	TGCTGTGUGCCACTCTCTAUG
294423471	99500	GCAGGTGCUCAAGTACGAGUC	99501	GGCUGGGATUCCCACAGAAC
294425130	99502	CTGGCCTTCUGTTCCCAATATUAAGA	99503	GATCAACCAAGCCAAAUTCCUCAAC
294429227	99504	CCGAGAUAAAACCCTGAGGTCUCT	99505	TGTCGATCUCTCTGTTGUCCGA
294430352	99506	CTGATTTGCATCUTCACATTTTGCTTUT	99507	CTTCACTGGUATCAATGTAGGTUGCT
294431628	99508	CTGCTTATUGGCCTCUGAGGA	99509	GTGGCCCCUCCTAATTTGACUT
294432287	99510	CCGCATUGCCGAGAUCCA	99511	GAAGTAUGGAGCCGCCACUT
294433156	99512	TTTACCUGAAGCTGTTCCUGGAG	99513	TTTCCCTGAGUGTGAATTTTCCUCAA
294434028	99514	CCCAGAAGAGGAGUAGGGTCUC	99515	GATGTTCCTCAAAUTCTGAAACTTGCUA
294436151	99516	CGCAGAGAGCUATCCTGUGAGA	99517	GCATCUGGCAGATAACAUCGG
294437722	99518	CTTGGTAUGGCTGCTTCTAUGGAT	99519	TCTTCAGGUGCTTTAGGTCUCCA
294438408	99520	TGACCCTGCUCAGATGGAGAAUAT	99521	ACATGTAACACAGAUTGATGTUGAAGGT
294438704	99522	AATCCCACCCCAUTCTTTAACTCTUAC	99523	ACTGAGTCGTCUGCTCTTCTCTUAA
294442204	99524	GCTTCGTUGTACTTACTUGGCAGA	99525	CAGCATCATCAGUGTAAACAAAAAGUCA
294442325	99526	CTTTTTGTCAUGGCCACAUGCT	99527	TCACAGTGGAGUTCCGCATUAC
294444129	99528	GTTAGAGTTGCAUTCCATTTGGUGAAA	99529	GTCGGACUCAAACAAATGTTCACUC
294445074	99530	GTCCTGGACUACTAAAAGGAGTAUACCA	99531	ACTCAGTCAGGGUATCAGTTCUGT
294445583	99532	TGTGTGTGGCAUATACAGGTAUAGGT	99533	GCATGTAATCACAUTGGAGGTTATCUGT
294449085	99534	AGATTTATTATAUGCCCTGGACUCCCT	99535	GTGCGCUCTTTGTUGAAGAACA
294451535	99536	TTTGTGCTTAACTUACCACTGACTCUT	99537	ACAAAAGCUGATTCTGTCAUCACCA
294452298	99538	CCTCCCAAGCUGAGGCTTTUT	99539	CTATCTGCGACUTGAAGAGAACCUT
294455648	99540	TUCAGGTGCTUAAGGCGACAA	99541	CCCTCCCATACAGUCAACTATGAATGUA
294456422	99542	GCTTGTGUCCCAGCTCUGAAC	99543	ATGCUGAAGACCACTGGUCAC
294461496	99544	GCTCAAGGAAAGCCAUTTCATUGT	99545	CTGGGCUCAGACGUCAAAGAT
294462278	99546	TCATCCGCCUCCTTCATCTCUA	99547	GGATGCUGCCTTCTCCUCAC
294465760	99548	CCCTCACCACACUCCCCUT	99549	CGGGAAGAAAUGACAGCAAUACAG
294474736	99550	CAGGATTTGTAGUGTATGATGGAGCUT	99551	CTATGTCAGAUTTGCCUCCCCAT
294476455	99552	CGGCCAAAAUCAATGUGGAACAT	99553	CTTTATGTCCTCUCCTCCCATCUG
294478446	99554	GTCTACCUCCTGGAAAGAUACCCT	99555	CACUGGCGACAGCUGGAA
294478924	99556	CCCGGTUCTTCCAGCUGT	99557	GCAAGAACAUGTCGGAGTUCCT
294479424	99558	GCTGUCGCCAGTGTUGGT	99559	CCTGACCACCCUTCCCUGA
294480260	99560	GGAGAACAAAGUGGCUGGAACT	99561	GGGCAAAAUCCAACAGCAUCA
294481931	99562	AGAAGGACAAAGGAAUTCAGAAGATUCA	99563	CGATTTCGCTUCTTCAGTGGTUT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294482420	99564	CTGGGTACAUAAGAAGGTGAACAGTUT	99565	TGCCCTCUTGTTCCCAUCAAC
294490632	99566	AACCCGAGGUTTTCACTUCACT	99567	CAAACTGGTATAGAUCCTTACCCCCUAA
294493434	99568	CUGCCGAGGGCUCACAA	99569	CGGCCCCUCAGACCUAC
294495323	99570	CAATTACCATGAUACCTCCCCTUACC	99571	GCAGTAUCCCATGTTCCTUCGAT
294496317	99572	ATCACATTTCCATUGTCCTTCAACTCUA	99573	CTCGAAUGAACTGTGGTTUCCAG
294497195	99574	CACAAATCUGACCCTACAUACAGAAGAA	99575	GGTGTTTGCAUTGCTCAGUCA
294499863	99576	CCTCAGGCUTACTUCAGGCAAA	99577	TGAATUCCCCACGGUGGAAA
294509130	99578	AGAGGCTGUGAGATGGCATATUC	99579	GAACUCACAGGGCCUCAGAT
294514999	99580	AAGGTCTTTGCUGGTGATAATUGGA	99581	GGCTAAACAACAGAGAUTTTCCTCCUAA
294526156	99582	AGCGTGAAATTTUAAGTTGCCAAGAAUT	99583	CTGGACTGGGCUATCTCACTUC
294529830	99584	TUTGGGACTCUGACGGCAAAT	99585	TCTTGTGAUGGAATATGCUGAAGGG
294535709	99586	GATAAAGACAGGUCTAATGACACUCACC	99587	GCCCTAAGAUGATGGAGCTUCT
294535797	99588	ATTGGTCACTTTUTGTTTTGGTTCTUGA	99589	ATCTCGATTACUTGGACTTGTUGGG
294538206	99590	AACAAAUACATUAGGAGCGAAGGCT	99591	GAAGAAGCACUCAAACAGTTUAAGCAAA
294538491	99592	CTCACCAGAUAGGAGGUCCAGAT	99593	AACAAACTCUAGGTCCUGGCAAG
294538662	99594	CCAAGTCCTGUTCCTGACTCCUA	99595	GAGGGAGGAGCUAAACGGTUAC
294542636	99596	GCGUGGATCAAGUGCCAGAT	99597	CATTTTCTTUCCCCATCTTCACCUC
294546189	99598	GGCACGGCCAUGAUCAC	99599	CAUCACATGCTUACAAGACACACA
294551632	99600	AGCCATGCUGCACGACTTUA	99601	GAGAACACAGAAAAUAUAGCCACCGT
294552564	99602	CCCTGAGCGCCUCATCAAAUT	99603	GCAGACTTTGAUATTTGCACATCTCUAC
294555409	99604	CTGAATCUGGGCTGAGCCAUA	99605	CCUGCAGTCATUGCAGAACCA
294562536	99606	CCGGATCUCAGTGTCTUGGGA	99607	TGAGCGUGCCCCGUAAC
294562663	99608	CCTGAACAUCGAGATGCCUGAC	99609	AAGTACTGUAAAGCGAACACATGUGA
294562706	99610	GUGGGAATAAAAAUGCGACACACT	99611	ACCTGAGCAGCUCTTCAATCUC
294563749	99612	TGTGTTACTAGAUATGATTGCTATTTTUAAGGG	99613	TCCCAAATAGACUCCATGATTCGUAGAA
294563847	99614	CTGUGTTTCGAUGCCCAGA	99615	TTTTCAAACGAGCUGAGAGGTCTAUT
294564161	99616	GCATAGATGUGGCCATCGAUGA	99617	GTGGGCGGGCUGTTGUA
294564652	99618	CAATTCAAAAUTCAGAGUCCAACCAACA	99619	GCTTTGTGUGTGACCUGCAGA
294565194	99620	GTCGGGCGAGUTGTUCCT	99621	GCTACTUCCGACAGUCGCT
294565410	99622	GGGTTGUAAGCCTCCAGGUA	99623	ACUCCCGCUGCAAGGAC
294568934	99624	TCCTCGAAGAUCTTGACCAGGUA	99625	CATCAACUGGGTCAAGUACGACT
294569290	99626	CCATCACTCGUCGGCATCUG	99627	CCGTGGCCUACGCTACUAT
294570093	99628	CUTAACAAGGCUCAAAGAAGAGGGA	99629	TCTCUCCAAGGGCTGGTAUCT
294573284	99630	TGTCTTGTGGAUGATGTTTTTGTCGUA	99631	CTTGTAGATTTTUGCCTACTCCTCCTUT
294573609	99632	GGGACTTGATUTCCAGGCTTCUC	99633	AGCUCCCUGAACACACACAAA
294573897	99634	CACCCAGAUGCTTCAGGUGAG	99635	CCAAGCAGAGGACAUCAGCAUAAT
294581633	99636	CATACCTGGAACUGAATTAGTGGAUGA	99637	AATTGGCAAUCCAAAAACGTTTGACUA
294583170	99638	CCATAGGCUCATTTTTCAGGCUAGT	99639	GAACTATTUGCTTTCTCTUCCACACAAA
294584322	99640	GCTAACTTCAUCTTCCTTCCCAUGA	99641	CCATCTCCCUCCCCCTUCAG
294585035	99642	CCAUAGTGTTCUAAGAACGGAAGCAT	99643	CAGAACACUCGCGGTUCAC
294588030	99644	GCCTGTTCCAUGGCACCTTAUT	99645	TGTGTAGTCATTUACCTTGGTCCTGAUA
294589882	99646	GCTCTTGACCAUCGGAAACUCT	99647	AAGAGGAGCUTCAAGGCTGUG
294593009	99648	CAGAAGGAGAAGUGAGCAAAGGAAAUA	99649	AGAGGCTGCCAUAAATCGAAATUCA
294593201	99650	TTGCCTTUGAGTTCAGAUCCAACT	99651	GCATTTTCTCUGGATTGGCUCAGA
294593642	99652	GGCTCUCCAGCCTCCCUA	99653	GTGCCCCGCUGACUGAT
294594349	99654	AAAAATTTCCACUTTGCGTCTCCUG	99655	TTGAGCGCUAACGTCTTTCUGT
294597046	99656	GAGCCAAUCCAGAGAAAAUGCC	99657	TGACCTACTGAGUGTATACAACTUCCT
294598488	99658	GAAGACUCCGAGCUGCGA	99659	CACCCGGGAAGUAAGATCTTUCA
294598745	99660	TGGTGGTAAUGGAAGAGGAAGATUAGA	99661	CCTTCCCCTTUCTTGCCCCTAUA
294601567	99662	GGGACCTTGAUGGTTTCTTCUCA	99663	AGGGCUAGATAAGCCTUAACACAGA
294602226	99664	GGATCAGTTUGCTTTGCATGGUG	99665	CAACAACACTUACTGTCTCCAUGAGT
294606386	99666	GCCCAGAGAUACTGAAGCACTUAA	99667	GCAGAGAAGCUGGAACAATTTUAGAAAA
294607418	99668	CCCUTTATUCCAGCCGACAAG	99669	TTTCAGCUTAATTTCUGGAGAGCCA
294608980	99670	AGCATTTTCUTCTTCTTTAUCCAGGACA	99671	CCCGGATATATUCAATGTCTTCTTUGCT
294611653	99672	GCATATAGCUCATCTCCTTUACCAGAAT	99673	TCATCAUGACAGCATCTTCUGAAGAAC
294612486	99674	GACATGCTCTUTCCTGCAGTTUC	99675	AATTGAAGGACTUTTCTGATCCCTTUCA
294612858	99676	TTCATTTTGGACCUGGAGAAAGTTCUT	99677	GTTTTATAGTTCUCTCCAGTTGUCAGGAT
294614326	99678	TTTAGTCTCTGCGAUATGATACCAGCUA	99679	TCCUACCCTGUGGCAACAAC
294624815	99680	CAUCGCAUAAGAGCAAAGAACACT	99681	CAAGGCCUGTGTCUAAACCGT
294625539	99682	ACCTGGUGGGCTCAAAGUAAAAT	99683	GGTGCAAGTGTUAAAATATGAGCCTTUT
294631932	99684	GACAGGAAUGCCCCAGTUAACA	99685	CAATTAAACUGCACAGTCCATCCTUT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294632404	99686	TTTTCCTACTATACAUCACCTTCAGAGATCUT	99687	ACCAGGACACCAUTTCCATCTUG
294633037	99688	CCTGGUGAAACAAACAGTTCAAAGUAA	99689	GCAGGUGACTAACAUCCCCAA
294636034	99690	CAGATTTTGUAGCCGATGGATGUG	99691	ACTACTCTACTCUCTTATGGCAGGTAUG
294636526	99692	ACCTGGCCAUGATGGTTTTCTUAA	99693	GCTGTTUCAGCAGCCAAAGTAUC
294636781	99694	CAAGATGGAAAUGGTGTCCUGGT	99695	AGTGCCAATATUCAGAGGCATAAGTUT
294637354	99696	CCCCTAACACUACCCCTAUCAAAAA	99697	TGTTCCTTCUCGCCTTGTTTUCT
294637665	99698	GGAATCUAGAGAGGGCACAAUCAAG	99699	GGCACAGGUTGTTTGGTTACUCA
294638268	99700	TGATCAGAUCGAAGTTUGCAGAGAC	99701	TCCAAGTTCGAUGATTGCTATGCTAAUT
294639707	99702	ACAAGGTUACCAAGCAGUGGAAT	99703	AGAGAACCCUGAGGGAGATAAAAATCUT
294645661	99704	GCTGTGTUCACCATAGCUGGAA	99705	CGTTGTGTTTUAACAAAGCTCATCUCT
294646266	99706	TCATTUTTCTATCCTCAUCCAGGGAGA	99707	GCTAAACCATCUGACTTTCACTTCTUGA
294652721	99708	GGGTCACCACAGUGGAACUA	99709	TTTTACTTTTUCACCCCAGACTUACCA
294653147	99710	CTCACCUGCCCTGTCCTUC	99711	ATCTCUGGGACCCUCACACT
294653180	99712	ACCTCCCAUCCCGTATCCTUT	99713	GACCTTTGAGGAGUTCCAGGAATUAC
294653237	99714	TUCTCATGTCUGAAGCGCAGT	99715	GCTGTTTTTAAUGCCATCTCTCTCUCT
294654436	99716	AAACTGCCCUTTCCGATCACUT	99717	AGATGTCTTCCTUTGAAGCAATGGTAUT
294660223	99718	TTTTGCTAUGGGAAGACATTAGACUGAAA	99719	GACAGGATATGUTGACACTCCAAAUG
294661112	99720	CAAACCAGCTTCUTTCCAGAGTAAAUC	99721	AGUTACAGGGCAUAAAAGGAAAAGCA
294661286	99722	AGAGCAGCCGCAACUTATUGT	99723	GTACACCCTAAGAUCTGGACCTTUG
294663017	99724	GGCAAAUAGCCCATGTCCUCAT	99725	GACACCAGUCUGCCGACA
294663219	99726	ATTATTCCGTTAUATAAAACAATCCUCAGAAGT	99727	TGTTTTGCTGUTTATGCAGTTTUGGAT
294667806	99728	TTTCCTGAUGGTCTGATATTUAGAGGGA	99729	TGATCATATTUGGAATGAACCACUGGAA
294669874	99730	CTTGTTCCCAUCTCCCTCACUC	99731	GTAGAGTCUGCGCAGTUGGT
294671485	99732	GACGTAGAACCGUCGCTGUT	99733	GGAGTTCUTCAACCTGUCCCA
294673757	99734	TGTTTTGTTGCAUCTTGCAGCUT	99735	GACTGTGAATGUAGAATCTCCAATCUCT
294674959	99736	CGAGCCATTCTUGGTAAGTCACAAAUAT	99737	TGTTTTTGTTTTUGTCTGCTTCGTUACA
294676361	99738	GGGAAAGTGUCTGAAGCAAUGG	99739	TGCTGAAATCAUCAGGAATCAUCAACAT
294676979	99740	GCTGATGAGGGUCACCAGTUG	99741	CGGTCCUGCTTGGUGAGG
294678301	99742	GCAAGCGUGACAACAATTTTTATAGUGT	99743	CGAGAGGAGAAAAGGUAGCAGTTAAUGA
294679080	99744	CTCAACCTACTUTTTCTGACGTCUCAT	99745	TCAATTGCTGCAUCAATGTCTTCTTUG
294679145	99746	CUGACTGTCAAUAAGAACCAAAGGACT	99747	AGGAGUGGAGCTCAAATTUAACACAAA
294680182	99748	GTGTGTGTTCUATGGCTTGTUGG	99749	CCGCTGGCAAUGCTGTAACUAT
294680304	99750	CTTAGCTACTTGAUATTAGATATTGATCAGUGG	99751	TTTAGGTCTGTTTUCAACGTAAGTCCUT
294680587	99752	GGCAGGGAUGGGAGGUGA	99753	GCTGCCCUGTATCCTGTTAUCC
294682136	99754	ACCATGUCCTGAATTCAUGAAGAAACT	99755	GTGTTCUGAGTCAGCUGGGAAAA
294682509	99756	GCAAAAUGGCAACAAATGAAAAATUCT	99757	TTTGTGGCUGGTATACAAUAACAAGGT
294682834	99758	CACTCCAACUGAATCCUCACCAAAT	99759	ACTGAAGTTGACUAATTTTCCCCACUT
294684130	99760	TGATGAGAGTAUCTGTTGGGAUCCA	99761	GCGTATTTCCCUACTCAAAACACCUA
294684548	99762	GTTGAAAACAGACCUAAATATGCUGGAT	99763	ACACACACUACACACCCCAAAUG
294684623	99764	CCATTTGCCCGUCCCTCTUC	99765	GCCATGTTGCUCTTGTTGAGUT
294687841	99766	CCACTGAAUGGTAACCAUGGCA	99767	GCTCATGGUTGTTCAGGUAAGAAG
294689387	99768	AGCUAGGAAGCAUCACAAAGAAG	99769	CACCAGUTCCAUCGGGAAGG
294689592	99770	TUCAGACACCAUCGCCAACAT	99771	CCACUCCACACCTCTUGGAAAG
294689974	99772	TCTCAAGTAAAAGAAGUGTGGGATTGUT	99773	CTCTCATGAAACATUTTTAAGGACAAATTCTUC
294691111	99774	CAGGGATUGAGGGTCAGGUG	99775	CGTGGCGGUAGTGATTGAUGAG
294693664	99776	GGATTCTCTCCUGTCTGACACCUT	99777	GTAGGUGAGGATGAAUGGGACAC
294695050	99778	TCTCCAGUCACCCCAUAGAGAC	99779	GCCTAGGTTUGGCATGCTTUT
294696370	99780	GGCUGACCGGTGACUGT	99781	TCTTGCUGCTCCGCUGT
294700374	99782	TCACCTTCUGCTCCGTTGUG	99783	CAGCCAGGUGCUACCCT
294702434	99784	CCCACCATCUTAGTGCTGAUCT	99785	CCTTTTGTGUATGCCGAGGUG
294703590	99786	TGTGTUCACCTGCAUCAACCA	99787	TGAGGAGGCUGATCTGTGAGUT
294704489	99788	TGGTGAUGCCGAAGATGTTTACUAC	99789	GTCCCAUCTTTGTTUGGAGGAACT
294705199	99790	AATTTCAAGACCAAGUTTGGAAUCAACC	99791	GGGCUCAGGCACTCUCA
294705339	99792	GTGTCCUGGCCTCGCUA	99793	CAGTAGGCCUCCAGGAUGAG
294706844	99794	GGGTCCUGGGAATCCUGGT	99795	CGAGGAUGGAGGAGGAAUGGA
294707158	99796	TCACCUTCCAGCUCCGAGAT	99797	GGATUCCCAGACGCUCAGG
294708383	99798	CCAAATGACTUCATCGGCGUT	99799	CCCCCATAUCAGTAGCCTGTUG
294709692	99800	AGAATCACAAAAGAAUCTGGCUGAGT	99801	CTTCTTATGTCCUTGGGATTGGUGA
294710065	99802	CTGAAGGAACUCACTTCCAACTATAUCC	99803	GTGGTUAAACGAGGTGGCAUC
294710384	99804	TGACCCCUCACCUGACCAT	99805	CGGAAGGCGCCAUCUCAC
294711329	99806	CTGAGCCCUTTTCTTTCTTAUGAGACA	99807	TCCAGACCAGUACGTUCGAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294712737	99808	GGGAGAAGAUTGTGUGGGCAAA	99809	AACGCCUTCTCUCACACAGG
294713882	99810	TTTTTGCCTTAGUGTCTTTGTGTUGAG	99811	CAATGCACATTGCUTTAGAGTGTCAUAA
294714880	99812	GCGGCAGCAGUGATGGATTUAT	99813	TGTTGGTTCCAAUTTCTGTGTCAUCT
294717574	99814	GGGAGGUGGTAGTGGAAUACA	99815	AGCTTGAGGCUGAAAAGTAGCUT
294717847	99816	GGAGCTUGAAAGGTAGTTACCUGT	99817	GCTCGCTCUCCTGTGTTTCUC
294718913	99818	AGGGAAGGGCUAAAGCCUCA	99819	TTCCCACTCUCCCTCCTTCTUAG
294720984	99820	CTGTGAACAAGCAAUGTAGGTGUT	99821	GTACTCCGGUTTCTTCTTCCUGAC
294721639	99822	CCAGGCCCACAUTGGGTAAUA	99823	CCCTCCACUACTCTTAACTGCUCA
294721820	99824	TGCTAATGTTGGUGTTCTTGTCTTTAUGT	99825	GGTTCAUGGGACCACACTGAUAA
294723476	99826	TCGUGAAATTAAGCTUCAGAGGGAAG	99827	CATAGCCUGGGTGTGCCUAA
294723502	99828	TGACCATGATGUTGTCACTATGTCUG	99829	CGCTTGGAGGCUGAAAACCUT
294723591	99830	GCAGGCAGCCUACAGCAUAT	99831	CCCCCATTATTTCUGAACCAGTTTCAUT
294724879	99832	GTGAGAGGUGGGAACAGTGUC	99833	GGAGGTCCAUGCTGGTCCUAA
294730514	99834	TGAGGAGTATGTGUATACATGTGAGCUT	99835	AGCTCCTUGCCCGACTUG
294735320	99836	GAAGATGAUGCCATTGTCCUGGAT	99837	CCTTCTGGUATAATGGTGUGGCT
294736816	99838	GGAGUACCACCCCGUCAGT	99839	ATGATTTCUCGGGCTUCCACA
294737461	99840	GAAAGAUGACAGCATUGAAGGCAT	99841	TTGCTTTTAGACTUGAATCCCCCTTUAA
294738847	99842	CACTTCCUCTGTCCCCUACCT	99843	TCCUGCCCGGCACAUAC
294742730	99844	GGGAGGCUCCAGACAGATATCUT	99845	ACTCAAGGTGTCUTTTGTATGTGCTUAG
294743909	99846	GAGGATAGCGUATTTCCCTTUCCA	99847	CCTTTTGTCUCATGGTTGTTATTUCCAG
294748792	99848	GCCCUACCCCACCATTTUCC	99849	GACCCCTATGUGAAAATTTACCTCCUT
294753723	99850	AGUATACUCCACCGAGAACCAC	99851	TCGGCAUGCTGGTAUAGAGAGA
294754558	99852	CTCTTTTCACUATGACTGGAGUCAGT	99853	AAGTGGGCAGUGCAGAUGAT
294756414	99854	CAAAUCCCAGCTCUCGAAGAGA	99855	GCAACACAACAGUTTTAACTTAGTGCUT
294758238	99856	GGAACACAACTUGTTCAATGTGCUT	99857	GGCTGGCAGCUGTGATTCAUA
294759137	99858	CAAATCCTTUGAGGCATCUGCAAAA	99859	GTAGCAGGGAGGCUTATUCCAG
294760272	99860	CCTGACAGTAUCCCTCTCTTCCTUT	99861	GGTGGUCCAGTCCGUCAAG
294763766	99862	CTTAGTGGTUTTCTGAGGGUCAGG	99863	AATGGTGGUGAAGAGACAGATGTUAAAA
294763999	99864	GGCCACAAGAUGAGGUGGAAAT	99865	GTCAACCUGAAGGTGACTGTGUT
294765259	99866	GCTCAGUGATCGCCUCCAA	99867	GATATGTGGCUCCTGGGAGUG
294767362	99868	CTGGTUGAGAGCACTGGUGAT	99869	GGTUGGAGACCAAGAGCAUGAG
294769870	99870	ATATTTCAAAAUGTAACGGUCCCAGAGA	99871	TCGCCTGGUACAGGAACAUAAAAAG
294771437	99872	TGGGTATACUCTGGCAGAAAUACAAGA	99873	TCAAACAUGCCTGGGUGAACA
294771469	99874	TGTTGGATTTTUACCTAGCACUGCAA	99875	GAGGGUCAAGUCACAGACAAGAAG
294772032	99876	CCCCAAAGGAAACUACTCTCGAUT	99877	AGGGUCCCCAGAGCTTGUA
294772722	99878	TGGCAGTTGACUAGTATCCCAUGT	99879	CCAGGAACAUCCAGGUGAAGG
294773538	99880	TGGAGGUAGAGCCCAGTTAUGG	99881	CCCTTCCTGTACUTAAATTGCCTTGAUAT
294774274	99882	CAACTCTGCUTAGGACTCUGGAT	99883	TGCATGAGACACUTACTGTGTAUAAGG
294781783	99884	GGAAACACUGGTGACUGCACA	99885	GGTTCTTCUCAGCTGATGTUGCT
294782855	99886	GCTGGTAGTAAGUAGAAAGGCTTTTGUT	99887	TGAATTTTTCCATCAUGTGTAATATTATGUGGT
294784561	99888	CTGCCCTGTUACATTTCTTCTTCTUG	99889	CTGACACAGCCACAAUGAGUG
294786444	99890	GCCTCTUGAAGCCTGUCACAC	99891	TCTAAAGGCACAGUGAGGGTTTUT
294787101	99892	CATATGAATUCACAAGGAGUGAGGGA	99893	TGACATUCAGACACACAUGACCAA
294787386	99894	GGCCTAUCAGATTCAAGTUGCAAG	99895	CGTGTTCTCCAUGTTGATTCTTTGTTUT
294787677	99896	CTTTTCCTTTCUTTTGACTTCAGAUGCAA	99897	ACACATTCATACUGCACTTCAAGGUA
294788699	99898	TTTTATCTGGUCGGCTATGGGAUG	99899	ACCTTTGCTUCCAAGAAAGUCCAA
294789044	99900	ACCCGTGUCCAGGAACCTAUAAA	99901	TGUCAATGCAUGCAAAACACAGT
294789478	99902	CAGUCCGCUCAGCAGGAA	99903	CCGGTCGCUCTCGTCUG
294790341	99904	CAAGCAGCACUCCCCTTGTUA	99905	TGTTGGCCTTGUAACTTTTGATGTTTUT
294791334	99906	GAGAACCCCUCTTUGGAAAGCA	99907	TGGAUCAAGAGCCCAATGGUC
294791500	99908	CCGCCCUCCTTCCTGGUA	99909	GTCACACCAUCCCCTGAUCC
294795751	99910	TTCAATCATTTCAUGCATAGAGGTCCUT	99911	AATCCAATGGGAACUGTTCAAACAAAUC
294796312	99912	TGCAAAGCTGTUGCATTTTCAGTATAUG	99913	TCTAAGGUGATTTTCAUGGGAGGAGAT
294798402	99914	ACACGTGTCUACCTCCCACUT	99915	GAAGCTTCATATUCTCTTTCTCCCTTUCT
294800194	99916	CCCCCAGAUGCTCTACCUG	99917	AGCUGCCCTCUGGAGAAGT
294800605	99918	GAATGTTGTCTUACCTGACCAGGUT	99919	CACGCTTTTTGUCTGTTTGACTAGATUT
294801120	99920	GACTCUGATGCTTGUCCACACT	99921	TTCTCCTTTCAUGAGCTCCCAUC
294805639	99922	CCCUTTCCUGAGACCAGCAA	99923	GAGAGTCCAUGTCACCCUCAC
294810772	99924	GCATCCCUCCTGGAGAGCUA	99925	CCAGUATCAAAUAACCAACAAAAGCACA
294811908	99926	CTTCAACACUGACCACUGCAAT	99927	CTTCAGCTUTTTCACCCUCAAGAAG
294812877	99928	AGAAAUCCTCUGCGGCAAGAC	99929	GATTTTGTUGACCTTTGCUGCCA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294813189	99930	CTCAGAGCCACCAUTAAGGTGUT	99931	GGTAACUGAACCAGAGUGCAGA
294815286	99932	AGTGGCCGAUGACTTTGTACUC	99933	CCCAGTGGGCUATCTTACTAAAACUT
294816247	99934	ACTACCAUGGCCAAAAAGGCTUA	99935	GGAGCAGTGUGGAGAGCTUG
294822323	99936	CTCTTGCCCUCAGAGGTUGG	99937	CCCATTTGCCAUCTTCCTCCTTTUA
294822700	99938	TTGCGAAUGAGGTTGUAGGCT	99939	CCATGTTGACCUTCTACCTGTATGTUC
294826414	99940	TCTGAATTAAATUCCGCACCATACUGA	99941	AGGTGCTGATAUGGAAGAATTTCAUGG
294832211	99942	GTGTCCTAGGGUCTCCACAUC	99943	CCTTTTCATCAUATGTTCTCCCCUCAA
294833769	99944	CATCTGAUGGGATCCCUGCAC	99945	GCCCCTCTCUGAATAGGTCACUT
294837322	99946	CGTCATCGUGCAAAGTCCUG	99947	TTGCTCTTTAGTCUGTTGAGCTTACAUT
294839781	99948	GGTCTTCTGGAUACACAGGTAGUGA	99949	GGGUAACCCGACACTTUGGAC
294843971	99950	CTAATTCTAAAAACUACGTTTTCATUGCACCT	99951	GGCAGTGTTUGAACAGCATTGUAAAAT
294843999	99952	CTGTTTGAACTUTCATATATTCTTGUGCCA	99953	CTCTGTCTTGACUCTCATCTTAGCUAGA
294847780	99954	TGGGUCAAGCCAGTACAGAUA	99955	CCCAGACAAUCGAGGTTGUAGT
294848776	99956	ACTTACAGAATCCAUGAGATAGGCTUCT	99957	GGAATAGCAGACUCATATGGTTTGAUCT
294852581	99958	AAATACAACGTUGGTGATTTGGTGUG	99959	AAGCCTGGAGAUGAGAAAGATTAAGUG
294853263	99960	CACUCCCGACUACAGGGAAC	99961	AGCCTCCUTTGCGGGUAAAC
294855254	99962	ACTACTUGCCGCCAGAAAUGA	99963	TGAAUGCCCAAAGGTGACUGT
294855667	99964	AUGCTTTTTAATCTUCCCCACCCA	99965	TGCCCACUCTCTCGGAUCAT
294856790	99966	TGCTCAGGGCAAUCTTGCAAUA	99967	GTACTAUGACCGAAAUGCCGAGA
294856943	99968	GCCGCAGCUCGTTCAUGAT	99969	GCAGTCACAGUGCCCUGAG
294858107	99970	TGCUGGGCATUGGCGAT	99971	GCCACAGAGCUGTGTGCUA
294861159	99972	CAGGGACGGAGCUGACTTTUA	99973	AGUGCAAAAUGCCAACACAGAG
294862001	99974	GGGAGACAAGCUGCACTTUGA	99975	CTCUCCCACCTAUCCCAGGAG
294865610	99976	CCTGGUCCTTCTCCUGACACT	99977	CATCGGCAUCGCCAACTUC
294866475	99978	CTCAGUGGAGGCGTACAUCAC	99979	CAGAGGTGGUGGTGTTGCTUA
294866890	99980	GCATCCGGCUCATGCAUACA	99981	GCGUCAGCCAAAGAAGGACUC
294869337	99982	TCCCAGAACAACUCATGTGTTAUAGAGA	99983	AAGACAGCCUGATTCAGGTTUCA
294869532	99984	TGAAACCTGAAUCAGGCTGTCTUG	99985	TTTAGCAAAGACAAUACACCCATATUCT
294870462	99986	GCAACUCCACACAGCCAAUCT	99987	CCAUGGGCGAGAAGTGTGUC
294871817	99988	GTCTCGUTTCTGAGTUGACAGCA	99989	CCTGAAATGAACUCAGCGATTCTCTAUA
294874537	99990	CACCGTUCATGACGUGGAG	99991	CTCAUCCAGCCCTGTCTUCAA
294883767	99992	GCAGCCCGUTGGUGAACAT	99993	TCAUACCAAGCAGGCCTTUGG
294885571	99994	GTTTTTCTTTCCUTTCTTGGCCTUGT	99995	ATTCAGACAUCAGATGGGTTTUAGGG
294896033	99996	CAGGCCUGCCUCACACT	99997	CGTAUCCAGAGGGUGCCA
294896998	99998	TCAGCTAAGAAAUGCTGGUCCAC	99999	GAGCGAGUGCCTTTTATTCTUACCT
294897620	100000	ACAGTGACTUAAAGTAGCTGCTTUCC	100001	GATCTGAGCAGUGGAAGCTGUA
294899373	100002	CGAGGGUGGGTGCTGUC	100003	TTCTTTGCCCUTCCTGGATCUC
294907170	100004	CAAGGACAUAGCCAAGCUGGT	100005	CTCAGTGTAGCAGUTCTATATGGTTGUT
294910146	100006	CCUAAGACCCCCAGACUCCAG	100007	TCCCCATGCAUGTCTCTCCUA
294912226	100008	GTTGGGAGUTGCTUGGAGGT	100009	GCTCACGACCCUCGCTATUG
294912284	100010	GGAAGCUCAGACTGTCCUCAGA	100011	CCUGAACAAGAGCCTGTAUCACT
294916433	100012	CCTTGTTGAAUGACATGGATGAAAUCAT	100013	GAACCCACCAGAAAAAUGAAGGAAATUA
294919863	100014	GTTTACTTATUGCCCCGAUGCC	100015	TCTCCCTGUAAGGCTGGTUGT
294924087	100016	CAGTCTTUGGCCGGGTTCTTUA	100017	GCCATCCCCAAAAGUCTGTTAGUG
294933106	100018	CTGGTTTTTAUTATGTGGGUAAGAAGCA	100019	GCCACCAUCACAACAAAAGCATUT
294933611	100020	CTGAAGGUCGCAATGATGATGUC	100021	GCCTACTTCTTTUAAGCACAGAGTTTUT
294938610	100022	TGTGTTCATTUGACCTGACAGTUGT	100023	GAGGUGGCAAAATGAAGUCGAAG
294949645	100024	GAGATCTCUGAAGTTCCUGGAGT	100025	TCTTTTTGCCCUTTTCCTCTGAUGA
294949939	100026	ATTGUGACGTGTGUGGCAAAC	100027	GTCTTGGUGCTTCUGACCGAT
294951237	100028	AACATTTCCTCAGAGUAGACTCCTGUA	100029	ACCCACTTACTUCTTACACTTTACUCACT
294955758	100030	GACGGCTUCCCTTGTGGUA	100031	CUTCTGGCCUCCGGGAAAG
294958418	100032	CUGCGGAGCTTUCCACCT	100033	CAGCUCAGGGCAGGACUT
294958761	100034	CCTACTGCTGUGAGCATGACTUA	100035	CCCUGGAUCCGGCCAAG
294962290	100036	GCAAACAUGATCGTUGAAAGAAAGCA	100037	TTGTCTGTUCAGCCAGCTCUC
294964045	100038	GCGACGUGCTGGTAGUGAG	100039	CCCCAGGAACUCCACAUAGGT
294964282	100040	CGGCAGCGAGGUGACUT	100041	CCCTGCUTGCTGCUCAC
294965234	100042	GAAACAGCUGCCAACATTGCUA	100043	AAACUCCGGGCAGCACTAUC
294967549	100044	CTCTAGACCUCGACGACCCUT	100045	GCAGAACUTGCGGUCACACA
294969432	100046	CAGUCAGAGGACGAGTGCUT	100047	AUCAGGAGCCUGCCACAC
294970276	100048	GAACTUGACCCCAGGUGGAAAA	100049	AAGGAGGAAAATUAAGCAGTGAAGUCT
294971180	100050	CGCTCCCAGGUCGCAUA	100051	CATTTGCGCUGGCTGGUG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
294971293	100052	AGGAGUCCCAAGCCTUCCA	100053	GGTGCAUGGCGTAGAGCUT
294972858	100054	GAGATGGGTGACUACAAAACATACTTUCT	100055	GATATGCTCCGGCUAGTTACAATUCT
294974068	100056	CTCATCCCCAUCGAGTUCGT	100057	CAGCCGGUGGTAGAAGUCC
294975421	100058	GGCAACGUGGAGCAGAUGAA	100059	CAGUCCAGAGTCUGCACCAC
294975555	100060	GCTTTGGGAUAGTCTGTGCUCA	100061	GCTTTATCACCUAACAGCACGATGUAT
294976400	100062	CGACGAUGAGCTGGAGTUCAC	100063	GAATGACGAUGAAGATGCAGTTGUT
294978723	100064	GTACGAGAUCTACGACAAGUACCAG	100065	TCAGTGACGUCATAGCCAAUCAG
294980827	100066	AGTACCTGUGGAAGAAGATUGCC	100067	TCGCTTTGGCUTTCGGGAAUAT
294980917	100068	GGGACAGGAGUAGTCTUCCAA	100069	AUAACGCGUCGGAAACCCT
294983156	100070	CTGGGCCACCAAUCTCAUCAA	100071	CCATTGTTTCUGTAAGTCATGUGGAAAA
294983490	100072	GCCACCUTCTGATTUGGGAAGT	100073	GAGCTACTGCAUTTTGACTGAGATTTUT
294985593	100074	GAGUGTGAGGGUCCCAGAGA	100075	CUCGGGCAGGCAGAUGAG
294985763	100076	ATGATAGGCCUCAGGGAGAAAUCT	100077	GCTCACCCCUTGGAGCAUAT
294987700	100078	GCAGUAACCCCAACACGGAUAG	100079	TCUGAAGAGCUCCAGGAGCA
294989499	100080	GAGACTGACUCCCATCTCAGCUA	100081	TGGUGAGCCGCAUCGAC
294991368	100082	TGGCCAAGAAGAAAUCTCTGAUGG	100083	CGTGTCCAGUACCACGUGAA
294993383	100084	CTGCTTUCCACCACCTCGUA	100085	GTCATGACCCUGGACCUGAAG
294994210	100086	CCGGGTGUACCTGATTCUGGA	100087	CAGCCCACAGUAAACUCAGAGA
294995667	100088	GGCUGGCAGGTGAGUGAC	100089	GCTTGCCACUCAGCATCUC
294997101	100090	TGGTACGUGGGCAAGAUCAAC	100091	GCATTCAAUGAGAGCTCUGGGA
294997269	100092	ACUGCCUCAAGAACGGAGAAG	100093	CACGGUGAACACACTCUCGT
294997324	100094	CAGTATTTCUGAGATGCCAUAAGAGCA	100095	CTGGACAGTTAUTCGTGTCTCTUACAAT
295031204	100096	CCCTUCACAAGGAGGAGTCUCA	100097	GAACAUCCGCCUGCGAGA
295039807	100098	GTCTTCTCCUGAGCCAGGUC	100099	ACTTCCCUCACCCATCTCTAUGT
295041637	100100	GCTCAAAAGCUCTCTGTTCTTUGG	100101	CTTCTGCAGTACUCTATTCAAACAGCUA
295047038	100102	ATCACCAGAGGUTTTTCATATCGAAUGT	100103	GAGAACAGGUAACCAGTTTAATCACCUA
295047540	100104	TTGATGTCUTTGCCTAUGCACA	100105	GCTCTGATAUGCCCCATCTTCAAUT
295050590	100106	TTTTCGTAATGUCCTTAGAGCTGGUC	100107	TTCCACAGUTCTCTGAAUGCCAAT
295051388	100108	CTTCGAATGGTUTTAAATGTGATGGUGT	100109	TCTTGAAACCAACAGUAAGTCATCUGT
295051597	100110	GTATTCCUGACGGTTCATUGCC	100111	GCACATTCUCTGGGAACUAAGGA
295052989	100112	GTGAGTAGGAGUGTGTGCATATCUT	100113	ATTCACTCTTTGAUTGCAGAGTTCUCA
295054327	100114	GTCCCATCUCGCACAAATAGUGA	100115	TCTGACAGATUTGTTATTGAAGUGGACAT
295056881	100116	AGGTGATAGCUTTTCTTCAATTCTUCCA	100117	TGGGCACCTACUCTACAATTCTGAUA
295057289	100118	ATTGGCATUCAGAGAACTGUGGAA	100119	ACAAGTATTTUGAAGACCATCAAGUCCA
295061082	100120	TTTATTCCTGUAGGTGTGAAAUCCAGAC	100121	GCCACCAGCUTCTGTAAACTTGAUA
295061193	100122	TCAGCACAGCACAUCTGAATTUCT	100123	GCAGATTCTTCUAAACCAACAAGUACCA
295066797	100124	CCCACATTCGAUGACCTCTGTTUT	100125	GATACCACCATUTCACTATCACAGUGT
295066826	100126	AGTTCAAACTUCTTGGGCTUAGAACA	100127	ATTGAAGATGCCAUTGAAAGCAACUC
295068814	100128	CTCGAATGCACUTCTTTGCTUGT	100129	TUGGAGUCAAAGACAAACCCCAT
295070142	100130	CCTGGGAGCCUTTTCUGGAC	100131	GATTGTGAGCCACAUTAAGTTCTTUCAA
295075583	100132	CAGCCTGGATGAUGATACAGATGAAUAAT	100133	CTATCGAGGUGGCAAAGTGUCA
295077533	100134	AAGCCTTCTTGUTTCCAATTCCUAAGA	100135	CGGAATATCCUGAAAGGGCAGAAUA
295079833	100136	GAGCTTTGCUTCCTTGGUGAAAA	100137	CAAAGAACAGAGAGCUTTTGAGCTUAA
295083065	100138	CAGGATATUCCGGACCACATTTTCUAT	100139	TGCCGTAAUACAGCAACTCTCUC
295083633	100140	CCTTGACAUTTCTCATACUCACACCA	100141	GAGGTCCAGGAAGGUCAAGTTUC
295084127	100142	TTCCCCAUTGGACATCUCAAAACT	100143	CGCAAGTCTGUGCAATAAATACTTUGAA
295085960	100144	GCAGTCGTGCUGGTATCATCUT	100145	CATCCAGCAGGGCUTTTCUGA
295087643	100146	GTGACTTTGAUGCCAACAATTTUCC	100147	GAATTCAAAGCCUTCACAAAUACAGCA
295092326	100148	TUGGACCTTUCCAGCAACAAGA	100149	GCACCTGGTUGGATAAAGTTCAUAGG
295101783	100150	TCTCTCTTUAGACCTGTCCCUGAAC	100151	CCAGAACCAAACGAUGGACTUC
295102367	100152	GGCACAUCTTCUGGAGACGAC	100153	GCAAGAAATGCCUCAGGAGGTUT
295102835	100154	CCTTCCAGATAUCTTCACAGAGCUGA	100155	GGAGTTCAGACACUTATAAGGAAACGUA
295122172	100156	GCCACAACAACUTCTTTTCATUGGA	100157	AAGTACAAGCAAAGUCATTCTGAGUAAGA
295127668	100158	GGCCTUGGCTGCAACUC	100159	TGAAACCAGCUATGTGAAAGTCCUT
295133034	100160	AGCAGGCCAUCAUAGGAGAGA	100161	ACAAGCACTGTUTTCCTGAGATCUT
295139298	100162	CTCTTGCACUGACCTTGATCACAUA	100163	GGAAGCTGCUCACCCAAGATUT
295141266	100164	CAGTACTGUCACCTACTCAUGCAC	100165	GTTTGTTGCTGUTTGTCCAATCUGA
295144058	100166	CTGCAAGGACUCAGAGGCTUT	100167	TCCTTGTUCCGAGCAGTAAUCAC
295144845	100168	TGCCGGUACTCCAGGUACT	100169	GATAATTGTCCUGGTCATGATTGCAAUG
295145414	100170	GGTCCCTCGTAUCAAAACATTAAGAGUA	100171	AGACUCCTTTCUGAGACAGGCA
295146914	100172	TCCTGTGAACUCTACAGAATGTCUACA	100173	CCTAGTTTCCAGUTATCCAGCAUCAG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
295153438	100174	CAUGACAAAGGCCTGUGAAGGA	100175	CAAATCCAACUTGACTGGTGUGG
295157023	100176	CCAACCAAAUCAGCCACCTUCT	100177	CTTTCCCACUACCATCAACTUCACT
295159371	100178	GGCCUGGGAGGACGATTUAT	100179	GCTCCTTTAATGACUGGTTCCTCATTUT
295159697	100180	ACTGGUAACAGCTTTTGUGGGA	100181	ATTGTGATAGAAAUGTCACTGAGTGUGT
295159952	100182	TTCCCAACUGTCCATTTTUGGAAA	100183	CAAGCTGCUCAGGCUGAAC
295163631	100184	CAGAUTTCCTCCUCAGGAGCAT	100185	CCTATGTCCTUGTCACCTGCCUA
295164599	100186	TGTACTGGCCAUCTAGTGTUCCA	100187	TCATCATUGCGACCTUCAGGAAAA
295167779	100188	CTCACTGGGUTGCCTCUGT	100189	CCTCCTCCUCTCCTCTGGUC
295172446	100190	GGATCTGTUGACCCAGCAGUG	100191	ATGTCTCTUGAGCAGAGGAGUCT
295185831	100192	CAAUGTCACACAAUGCCACACAT	100193	CUTCACTGTCTAUGCCACCCA
295192467	100194	TCACCTGGUAGCCCAGAUGAT	100195	GGTGGAGCUGTACUGCAACA
295193116	100196	CCCATCUGAACCATCAAAAATGUAGAG	100197	CTGTTACGCGGUCTCTCUGG
295195362	100198	AGTGAGTTGTAGUTAAGGGTAGGAUCAG	100199	CCCTCTCUCATCAGCUGGGAT
295197735	100200	TTGGCAAGAGUTCGGCTUCT	100201	TGGCTTTCTCTCAUTTGTTATGTGTTTUG
295198314	100202	GTCTGGAAGUCTGCGTTGAAUG	100203	CTTGTGGAGGCCUCATGACTUT
295198786	100204	CCATACAAGGUGGCTGGGUA	100205	CTGTCUCAAGAGAAGACCAATGTUCAT
295200186	100206	CUGTAAAAGTCUACCCCAGGCT	100207	GCAUCAGCCGCAAAGAGCUA
295204772	100208	CCTTCTGGTATTUCTGCCACCATTUAT	100209	CTTCCCGAAUGTGTGTUGCC
295206131	100210	TCTAATTGAACUGCAGACATGGTUGAA	100211	GTTTTGAGTTAGUCAATCTTAGAAATGAAUACC
295208552	100212	CATACTCCATCUGCAGGGCTUC	100213	GAACTGACGTUGGCAGGAAGUA
295212341	100214	ACAATGGUCAGAAAGACAATGCCTTUA	100215	TGAAGTGTGCUAATGGAGAUCCAC
295219107	100216	CGACUCCCCCTCTCGUCT	100217	GTGAGCGCGUCGTTGUG
295229718	100218	CTTGTCGGGCUTGGTGAAAAUG	100219	CGTGCTCUAGGGACACCTAUG
295246033	100220	CTCCTTTCACUCTGTGTCCUCAAA	100221	TCAAGCATGAAUTCAGTCCUGACAA
295248843	100222	ACGAATGTUAGAGACTGCUCCAAAG	100223	TGGAGGCCAUGCTTTAUGCAAT
295256038	100224	TCAGGGTCCUTGTTAATCTGGUCA	100225	CCAGGAGTAUGCCCATTCCAUA
295257036	100226	TCGAGGUGGAGACCCATGUT	100227	AGACCTGUGTGTCTGATUAGAGAGG
295267449	100228	GUGGAACCAGAGCCCUCA	100229	GGGAAGTGCUCCTGGACUT
295267816	100230	CAGCCGAACUCCGACACAUA	100231	CCTCCCUCTTCTTTTUCCCAACAG
295268787	100232	GAACTACCAAUCATCAAUCCAGGCT	100233	TGACTAGTUGAAGGGCCTUGAC
295272242	100234	GAGAAGGACCUGGTGUGGAA	100235	GTAGCCAGAGGCUGTGGUC
295272457	100236	CCTTCUGCAAAGGCUCAGACT	100237	GAGGCCUCCTACAUCAGGAAAC
295275519	100238	CAAAGAACCUCACAGGGCCUT	100239	CAGTTATTGGCCAUTACACTCUGAAAAT
295279322	100240	CCCCAAAAUAATGTCCCCAUCCA	100241	GGATTGCAAUACCACCTGUGGAG
295279645	100242	CCCCTACUCACGTTGATGAUCAC	100243	GCCTCGUGAATGACCCAUCC
295289765	100244	GGUCAGGAAAAGAAGCUCAAACAG	100245	CGTGGTUGGAATGCTTCAUCA
295296277	100246	TCTGTTCCATTUGTGACATTGTAUGACT	100247	TTTCTAGCTCAGUGGTAAGCTTAGGUA
295303273	100248	TTCCCAGCGGGUAAGUCAC	100249	AATGTCUGGAGCGCTTCTGAUT
295307439	100250	AGAGGCAATAATTUCCAAAGCAGATCUT	100251	CTTAACGCGAUCTGCTCTGTUG
295308640	100252	AGCTGAGGTAACUCATTTTGCCAUT	100253	ACCACAACGCUCTGATTCUCC
295309321	100254	CATCTTCAGTGUCTGGGATCGUG	100255	ATTTCTTAGGTAUGCCTGGACTGTUG
295311625	100256	GAGAGAGTUGGAGTCAATGGUGA	100257	CCCCTGGAATCAUATACCATACAGGUT
295313710	100258	GCTTGCACAGAUCTTACACUGG	100259	CCTCTAAAGTCTGUCTTCATGATAGGUT
295315984	100260	GGCAGTCCCAAUGTTGGATGUT	100261	GTGACCCCCGGUTATCCTUG
295318702	100262	AATTGAACCCUTACACCCUACGG	100263	AGTAGCCTCATUGTCATCATCCTCAUAT
295326112	100264	CCAUGGAATTCUGGACCAAGGA	100265	CAAGGTCUGAGGACCGGAUG
295334985	100266	CCAAGACGACAUAGCCAGGAGUA	100267	TCAAGGAGAUCAAAGGCUACAAGG
295338993	100268	CAGCCACAGUGACGAAGAUGT	100269	TCACAGGCUGTTTCTGACTTUCA
295340564	100270	TGGAATTCTGTAUGTGGTCAAATCUGT	100271	ACAGCTGCAAUGTACTGGTAUGAAT
295343366	100272	TGGACACCGCUGTGATTUGT	100273	CAGTTCACTTUGGTTTTCCAGCUC
295347043	100274	GTTTGGTGGAUGTACCCTTTCCUA	100275	CAAAGAGUACCACAAAAGGTTGAACUT
295349603	100276	GTTTAACGAAGCCCUCCGUGA	100277	CAGCCCCUTTAGGACCAAUGT
295355970	100278	CGCCATUAACCGCCAGATUT	100279	AAGAAGGGCCAGUTCTTGAATGUAG
295357206	100280	CUCAAGGACCACCGCAUCT	100281	GTCACAGUGGCCTCGCUA
295366735	100282	CTCAGUCAGAAGAAAAUGGACAAAAACC	100283	ATGACCCCTUACACAACGTCUC
295371486	100284	GCACTGTGAAACUCATTCAGGUAGA	100285	GCTCGUGGACAAGATTGTGUG
295372071	100286	CACTGTCACTCAUTTTTATTTTATACTGCUT	100287	TGAUGCACCCAACUGACCAAAT
295372078	100288	GTCATTGCATUTTGTTTTCAGTUGACA	100289	TGACCAAACTGAAGUGCTATCATACAUT
295374367	100290	GCTGAGUGCCCTCTGTCAUT	100291	TCCAGTACTTTCAAUTCATGGAGCAUAC
295375594	100292	CATGGCAGCUAGTCATTTGUGG	100293	TTCACTTACTTUGCAATCTTCTCCTUGA
295379979	100294	CTCCTUACCAGGGTCCCGUA	100295	GATGGATGTGUACTGCTTCCTCTUC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
295386119	100296	GUCACCAACAGCAGAUCCGT	100297	GGUGGGAGGAGTGTTUGACAAAAA
295388887	100298	CTGAAGUCTGGUGAGCCCAA	100299	GCCTCCUCGTTGCTGUACAT
295389686	100300	GATACTGAATGGUAAGGTCAGATCUGG	100301	TTGCTTCAGGUCATCAGGAATTUCT
295393510	100302	TGGAAGGGAUCCAGTTACTTGUCT	100303	GGCTTAGCTTCUTGATTGCAACAUT
295395052	100304	CAAGAUGAAGCCCCTGUGGAT	100305	GTCTTCUCCACCCCCACTCUA
295397769	100306	GGAGTGGACUGCCGCTTUAAT	100307	CCAAGGGTTAATUCTTCAAACTGCTUC
295398054	100308	AGACTGTGGUGGTTACCCATAUGA	100309	GTGAAGCTGUCCATCTCCUACAAA
295398339	100310	CAGCTTATGAUGCCATTCTUGAAAGA	100311	ATGTTCACTTACATUTTTGTGATTAACACAUT
295398349	100312	CCGACCATTUCAGAATCAGACUCAT	100313	AAATCTTGATTUCATCTATACTUAGGAAACCA
295399556	100314	TGGGTTTTCCUTCTTTAGAGCAUACC	100315	TTTGCCAUAGTTAGGCUCAGCA
295406268	100316	GCATCACCATGAUGAAGAGTTTATTGUT	100317	CTTGACCCTTCAUGGTTTCATTTGUC
295410181	100318	GTTGCGCTUTCCTTTCTGUCAA	100319	ACAGGGTTUGAGCAGTTCTTATUCC
295410224	100320	GTCCACCAGGCUTGAGTAAAGUA	100321	CGTCACTAUCTTTTCACCAUGGCA
295413041	100322	CAAAGCCAAUCTTTGAACAUCCACAT	100323	CCAAAATATCUCAAGCTGGCAATUAAGT
295414203	100324	CCCACTCACUACTCTGCACUC	100325	ACTGACTUGGGCCTTCCCUAA
295421755	100326	TCAAAAAUTCCGCUGCAAGAAGAC	100327	GATTGUACCCGGACAGGATUCT
295438680	100328	ACGTGTUGAGCAGTTTTCUCCAT	100329	TGCTGTCCTTUAATTGCAGCAAAUC
295507117	100330	CAGCACAAGGGACCUCCTUA	100331	GTGGAAGGUGACATCAAGTTCAUAACT
295529635	100332	GCTCTAUCACCCACCACCCUAT	100333	TCAAAGTGGUCCGACGACUG
295534270	100334	AAACAAGCUGGCTCTCAUGGT	100335	ACGGAGGTCUACGGAGACATUAAA
295540805	100336	CATACTGCTCCUGCCACTTCUC	100337	GAACAGCCCUAACAGCCTCUC
295546596	100338	GCTCTGTTUCAATCAGGGUGAC	100339	GATGAGACAGCUGCUCACACT
295653627	100340	CTCTAGAGCCCUGCTGACTUA	100341	TCCCCUGAAAAGCTACAGCAUC
295669960	100342	CTTTGCTGAGUGCCTGGAAGUA	100343	TCCAGCCUCGATTCTCUACACT
295697883	100344	GCUTCAACUCAGCAGCAAAGT	100345	ACCATCTGUGTCTCCTCTTUCCT
295750193	100346	CTCTTTTCCCCUGCATCCUCAA	100347	CTCTAACCACTCUGTCCTTGCTTTTUA
295755375	100348	GTCCATAUCAGGCAAGCAUCCAT	100349	CAATGATGAAGGCUTCTCTTCTAGTUCT
295765836	100350	ACTGAATCCGUTGACGTCCUG	100351	CCCTUGCACATGUCCCAAAG
295948974	100352	CTTTCTTGTTTUGAGTTACTGTUGCCT	100353	ATTGGCATCUCATTTTTGTTGTUCACA
295979824	100354	CCCCCAUGATTCACGGUAAAAAC	100355	TTCACCUGGGAGCAGATUAACAC
295999350	100356	TCCAGCAUTGGTTTCUCCCAT	100357	CACGGGAATGTAUTTACCCATATCTCUT
296091087	100358	TTCCGTGGCAGAAAUTCTAAAGTUACT	100359	AACAACTCTATAUTGCTGGAACAUGGAA
296098056	100360	TGGTGAATGATUCAACAAACTGGGUAA	100361	CTATCACTGGCAUCCCCTTCUG
296102124	100362	GGTCATGAAUTTGAAAGGTGUCAGG	100363	TGAGTGGCTAUCACTTCAAACUGAAAT
296109707	100364	TGTTTGTTGAAAAGUAGTTCTGGGUCAA	100365	CTTGAAAGCTTGUGATCAGATGCAAUAA
296201281	100366	GGTTGGAGUAACAGATAUAGGAGGAGAG	100367	CACAGTGCTUTTCTCCTGTTAUCCA
296221928	100368	AGAGAAGAAAAACUGCAGACUCCAA	100369	CCTGCACTCUCTGTTTCCTGUC
296264999	100370	GAGGUCAGAGCGGAAACUCT	100371	CCUCAGACAGCAAAGCCUACC
296386012	100372	CGAGAGUGCATCUCCAGCAT	100373	CTCACTGUCTTCTCTGTUGGCA
296481638	100374	GAGAAGCACAGUAAACACGAGUGA	100375	TCAGCACTTUCTGGCCACAUT
296495732	100376	CCATGGTAAAAUGCCATACCTGAUAGA	100377	CGTCTACGUGAAGGTGAATGGUG
296507169	100378	CATTCCACACAGGGUTCCCUT	100379	CCAACCCUGAAGGAGAAUGACA
296522444	100380	GAAGTAGTAAUGGAAGTCGAUGCAGT	100381	TGTCTCTACTUCCCACCTGCUT
296524226	100382	AGTGAAAATGAGAAACUAACAGACACUT	100383	TCCTTCATCTGACUGCCCATCAATAUA
296644032	100384	CCGCAACAGGAGUACUGACT	100385	CCACAGTACUACTAAAAGAACGTUCGAC
296644538	100386	CTTCTACAGTUCAGTCGAACGTUCT	100387	CCTTTACTTCATUCAGTGTTCCAGAUCC
296658907	100388	TTGATGGTGACUGTTTTAATGAGCUCT	100389	GGTGGAGAAGUGGGTTTTCAAAUCA
296696534	100390	GAGACTGAATUGAGGCAGTGTUGA	100391	GCCATCTTTGGUGAAACCATGGUA
296720285	100392	AGGAGAATGGUGCTCCAACTUC	100393	TTGTATCTCTGUCTTCATCGCCTUC
296754499	100394	AGGTGAAGGACCUTTGACTUACCT	100395	GCTCCGCCUCTTCCACTUC
296757366	100396	GGGAACGCCGUGGUCAG	100397	TGCGGGAGGUTCCUCAGT
296834898	100398	AGGCTAAAAACCUTAGAAAGACACTUGT	100399	CAGTGCACTACAUACTTACCCACUT
296838561	100400	TTATTCACAACGUTCCAAAATCCCTUG	100401	CCCTCCCTTUCTTCGTCTTCTUG
296934176	100402	CTACAGGUGGCCAACTGTCUT	100403	GCTTCAUTGCCATUGACACCA
296943217	100404	ATTCUCGGCCATGUCAAGCA	100405	GGATAGGGCUGAATGCUAGGG
296968373	100406	ACTCACUAGGGACTGGAUCGT	100407	CACTCGGATUGCCACCAAAAUT
296979899	100408	TCCTTTTTCCTUTCTAGCAGAGAUACCT	100409	GGAAAGUGTTCAAGCUCCGGAA
296997750	100410	ACAAAGAGGUGGTGGGTTUCA	100411	CTTCCTGAGUGAGGCATTTATTTGTUT
297053607	100412	GAATATTTGCCCUAGAATGCCAGCUA	100413	CCCGGAACCAUGATAAGAAUCGAA
297065964	100414	AGAGGCAGCACGUCCAUAC	100415	GCAGGGCCUATCTATTCACCTUT
297077428	100416	GUGCAUACCAAGGGCACAGAAT	100417	GCGTAACAACAAAUCCAACATGGUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
297088026	100418	AGTTCTTCAAATGAUTCATAGGGCTUCA	100419	GTUCCACCCGCAGUACAGAAA
297104433	100420	TGGTCAAUGGAAGCCTGTGAUAC	100421	CTAAGGCAAGCUGAATACAAACAGUAAA
297115407	100422	TGGGATACUCACCAGGGTCUC	100423	GCTCACCTCTUTGCTCTGTGTTUA
297151302	100424	GGUAAACCACAGATCTUGAGCCT	100425	TCCCCTTGAUTTCTGCTCTCUCT
297195318	100426	AATAAAAGCCUCATAACTGACUGCCA	100427	TGCGACTCUTGCTGTCUAACC
297203310	100428	CAGCTCCUCGCTCTCCATUC	100429	CTACAACCUCACCGTGCAGUA
297212183	100430	CTGCTGGTUGAACACATACUGG	100431	CTTGTTTCTUGCCTGCATGTTTUG
297245557	100432	CCCCACAGGCUGGTCTCTUA	100433	ACGATCCAGACUCATCCCUACC
297258830	100434	GGUAGCTCATCUCCACAGGGT	100435	GACAAAGGGCAAAGCUTCTAUAGGT
297411701	100436	CTGAGTGUGGGCAACTCUCC	100437	TCATGTGTGTTTCUTTCTCTCCTTCUC
297471359	100438	GGCGGUGCCAAGACCUC	100439	GCUGCCCAGCACGUAGT
297473348	100440	CAAGAAAUGCGGCAAGCUCAA	100441	AACACGCACUTGACCGUCT
297473986	100442	CGGGCGACGACUACGUG	100443	CGTCCGGCUCCTGTTUGAT
297476094	100444	TGCCGAGGACUTTGCAACUT	100445	CTCTCCGCUTCCAAGCTCUC
297476478	100446	CGUGTTTCTGGAUGAGGACGAC	100447	GGCACTTUGGCGACGUT
297477134	100448	GCAGCTGCUGAGACGCUAC	100449	GTGCTGCTUGGTGATGTTCUT
297477698	100450	CCUGCAGCGGATCAUGGT	100451	AGTCTGGGUCGCTCUCGT
297479520	100452	GAGGGCGAAUTCATGGCTUG	100453	CCATGATCUTCCTGCGTUCGAT
297481480	100454	GCCGCCUCTACTACAGCUT	100455	CAGGTCGAACAUCAGGTCGUC
297483440	100456	CGCGTTCAUGGTATGGUCCAA	100457	GGATCTTCUCGCTGTCCTUCAG
297485609	100458	AGCUTCAAGAACAUCACCAAGCA	100459	AGAAATUCAAGCTCAGGUCGAACA
297486312	100460	GGGCAAGCGCUGGAAAAUG	100461	TCTTCTCUGGGCTCUGGCT
297488074	100462	ACGCCGACGACCUGAUG	100463	CCCTCGCUGAACGAAUCCAAAT
297490392	100464	CCGACUACCCCGACTACAAGUA	100465	GCATTTCTTGCUGGAGCCCUT
297497526	100466	CCTGTCGCUGGTGGAUAAGG	100467	GAACACCAGGUCGGAGAAGUT
297503942	100468	ACTTCGAGTUCCCCGACUACT	100469	CACCACUACAACTTCCUCCCAA
297542383	100470	GTGTGAGTTTTCAUTTACCACATCTUGT	100471	GGTGAUGAGCAGTTGTUCCAG
297542779	100472	GTTTACCTATCAGUATTAGCCTGCTUGT	100473	CCTGGTCUGATGATGTAUGCCA
297549214	100474	TGTUCCCGCAGCCAGAUT	100475	GATGGAGAGAUGTATCCUCCCACA
297550913	100476	TCTCTGCCUGAGTATCTTTGACUGT	100477	CAGGTATGCTUCCTTTGACTATUAAGACT
297684986	100478	GGCAAUAGCACAGCCTCTCAUA	100479	AACTATAAGCUGTGGCATCUGGAC
297693200	100480	CTCGGGUCAGCAGAGTCTUG	100481	CACCCAGAAUTCTAACACTGUGGAG
297693489	100482	CTCGGATCUCATACTCAACAUCGG	100483	CCCCAUCATCCUGAAGGAAGT
297699282	100484	CCTGTGGUGGTGCGATATUCC	100485	TGACAGTCCTTTUTGATTGCTTGTCTUA
297705057	100486	AGCAAUGCAGCCCGTCTTAUA	100487	CAACTTACAATGCUGACTATGGCUACA
297709835	100488	GTGTTGUCCACCTGCTTCUCT	100489	AGGAAGCTGTUGTCATTATGATGATUGT
297715645	100490	GTTAGAGAAGGCUTCCCAGCTUT	100491	AGGTGCCACTTUCCACATTTTACAAUA
297837128	100492	CATGGAUCAAGGCTGTGTUGG	100493	CTGCAACTGUTTCTGTGAAATUGACT
297844653	100494	GGGAGGAUCAGCAGAUGAGAAA	100495	CGGAGCGUCAGCAAGUACC
297857896	100496	CCAUCAGAGCGGAUCACACAG	100497	CTATGATTCCTCCUCTCCCTCTCUT
297880136	100498	AAGGGATCUCCCTCCAGGTUT	100499	TTCGATTACAACUGCTCCTCTGUG
297893405	100500	AGTGTCCATCUCATTCAGCAUCAC	100501	AAGCCTGTGUCATTCCTTTGUCA
297918708	100502	CGAGCCUGGGATTTGCTCAUA	100503	GTGTTTGUGCACGAUGCCAT
297938522	100504	AGUAGAGAGAACGGAACUCACACA	100505	CCACAACACTAAAUGTGGACAGCUA
298168761	100506	AGAGCTCCUGAGCCCAGTUA	100507	CGCCTCUCAGGAACAGTATAAATTUGT
298205781	100508	AATGGCGGCCGUGTACTUA	100509	CTTCTGTGACCUCTTTCCTTATCUCAG
298326130	100510	CTCCTTTAATGTUAGCCCTTGACTAUGA	100511	CACTTCACGCAUCAGTTTTUCAAGA
298328660	100512	TGGCCCUCGCTTATGATCUG	100513	CTTCCTGATUCAAATGAGATTGUGGAAA
298339473	100514	AGGGATGAACUTTCTTCTUAGAAGCAAT	100515	TCTTGGTAGATUGACAGTCACCAUCT
298654226	100516	TCTGAGCAGAGGCUTCTCUCAT	100517	ATTCTCTTGTGTUCTTTGGTTTCTCUCT
298904286	100518	TTGTTATTTTTCTTUAGGGATAAGAGAAGAUCC	100519	GCATTTGTAGCUCACCGAACTGTATUAT
298905366	100520	CCCCCAAUCTCCCCUAAGGA	100521	CCATGCCAUCTGGCACAUCA
298906482	100522	GCAUGAGGTAGCUCCACCCT	100523	GAGGCCUGGCGTATTTUCAC
298906497	100524	GCCCUGCAACAATTAGTUGGAA	100525	CCATCAGTCGGAUACACACATATTCAUC
298907602	100526	CCUGAAAAAGAGGACGUGGACA	100527	CGTGGUGGTGGTCTUGCT
298909430	100528	CTTGGGCUTCTCCAGCUCAAT	100529	CCTGCATACCUGTGGGCTAUG
298910341	100530	AAGUCAAGCAGCUCGAGCA	100531	AGGAGCCGAAGGAAUGAGUCT
298915050	100532	CCTGGUAGCCAGAATCATUACAGG	100533	AGCTTGCTAAGUAATTCAGTGGCTATUT
298916335	100534	CATTCTTCTCUCCCAGCTUACCT	100535	GGCUGUGACAAAAGGAAAAGCA
298916908	100536	CTCACCGAUGCACCCAUGAT	100537	CTTGTUAACGAGCCTTTCTUCCAC
298919420	100538	GTGCTUCCCTCCTGUCCAC	100539	GCGAGUGGCGCTGAUACC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
298920356	100540	CCUCCTTTUCAAGAGGCCCAAA	100541	GACTCTGCUGAAAGTGGTCTUCA
298925596	100542	CGGAAGCACCACUAUGGAGAAAC	100543	TCAGTGTGCUAACCATTGATTATTCUGA
298926721	100544	TTCTCCCAUGCCATGUGGAC	100545	TTATCAACGGUGAAAGCCTATTGGUAT
298926789	100546	GCAGTGGUGGGACACACTUA	100547	TGGAGGATGAUGTATGTAGGUCGT
298928334	100548	AGCUGUACCGGGAGCGT	100549	ACAGGGAGUAGGGAGACACAUC
298936414	100550	CAGTAAAGTAGGCAUACTTATATAGTUGGCA	100551	CGCAAGAAAAUCAUAGCAGAAAACAAGA
298938594	100552	GGGATAAAACAGUTTCTCTTAAGTGGUG	100553	ATTTTTCTCTTCUCTGAGCTAACAUGCT
298942092	100554	AGATATTTGTGCAUGGTGATGGTAGUG	100555	TGATCTTTGTGUAGGTGGATGCAATUT
298942621	100556	CTCGATTCUGCTCGGTTCUCA	100557	CCCCGGAAACGGUCGUA
298944377	100558	GGTCCCTCUTCAGTGGCAUAT	100559	ATTTTGCAGAACTAUTATGGAGCTGCUA
298945880	100560	CCAAGTGGGTUGTCAGAAAATATCAUCT	100561	AAGAAATAATGTTTGUCGTAATTTGGCTGUT
298949956	100562	GGACUCGGAGGUAAGGAAGCA	100563	GUCCCAGCGGGCACAUA
298952269	100564	GGAATGUGCAGCTGAGGUCAAT	100565	GAGCTGAUGAAGAGAGUGGGT
298955234	100566	TGTAGGUGCCCTCATACUGGAA	100567	TUTATGGCAGGUGAGGAAAGGG
298955681	100568	TGCAAGAGGUGACCCAAGUG	100569	CGACCAGUCCACCAGATUGAG
298959678	100570	GAGCUGCAGGACGACTTCUAC	100571	GTACATUGAGGTCTGCUGGGA
298963808	100572	GGACACGCUCATAGAGTGGUG	100573	CCCCCGACCGUCUACGA
298969749	100574	GGACTCGUGAATGTTCTTGGUGA	100575	TTTGCCCGCAACUCCTAUGT
298970381	100576	AGAGAAAGUTTTGGUGAGGGCAA	100577	TGTAGAAAUGGCCGGATUGAAGT
298974348	100578	GGAGGCUGCATCATCGUACT	100579	GGGCTGACAUCTGTCTGTGUG
298978017	100580	CGCUAGCAAGACCAAAAGGATUT	100581	CAGTCACAAUATGGAGCTUCCGT
298979697	100582	GGTAGUTCAGGCTUGGCAGAA	100583	TCGGATGCUGTGTTGAAGUGAT
298986546	100584	GCAAGAAGUGGGCAACACCUA	100585	GCATGAAAATGUTGATGTGTCTUGCAT
298990026	100586	CCTGGCACTUACTTGATTCCATAAAUAAC	100587	AGTCAGCGGAUGCATGUGAT
298992986	100588	GTCTAATAAAGUTCCTGTCGTUCAGCA	100589	CCTGAGUGGCAGACGACTUA
298994600	100590	CUCCCCCAAGAUAGGGAAGAGT	100591	AACATCGCCUGCGTTAUCCT
298994759	100592	TTGGTCCCTTUCTTTGCACTGUA	100593	GACCCAUCGCCTTTGATGAUGA
298998844	100594	CCAAAGGGCUCCTUGAAGGT	100595	CCUCCAGAACUCAGACAAGGG
299006727	100596	CCTCACCUCGCCTUGGT	100597	CGCUCCUCCGGGAGACA
299006781	100598	CGCCUCACTGTGCTUGGT	100599	CCGCAGGCUTACCGUGAA
299007962	100600	CCCGUACCTCUCCAACGG	100601	TUGGGAUCGGCGCAGAA
299008308	100602	ACCAGGUTATCATCUAAAAACGACAGG	100603	CTGAGACAACGUACGACAAAATATUGAA
299014461	100604	CACCAGCCTTCUATTTCTGGATAAGTUT	100605	GGGTTGTGTCUTAACTGCAATACAUT
299017958	100606	CAATATTTACAAUAGCGGGCAACUGAT	100607	TGAACAGGAUCCAGAGCUGGT
299019388	100608	ACCCTCCACACUGCTCCUT	100609	TGGTGAUCCGCGUGCAG
299019950	100610	CAAGCUGTATTCTGUACCCACAGAT	100611	CTAGATGCCUGAAATGTGCAGAUG
299020163	100612	ATTAGTUGGACAGCTCTTCUGACAC	100613	TTACTAGACACGGACUCTGAATGAGUAT
299020477	100614	CCAGACCCAAGUCAGTGACATTUA	100615	CCAGATAAACAAAUGGCAGTGCUT
299021195	100616	GCGAACGACGAGCUGAUCC	100617	GCCGCGGUGCTTCCTUA
299021676	100618	GUAGGCCACACAGCCAUCA	100619	CCUTCGCGCUGAGCAGT
299022024	100620	GGAGGGAACGGUTCTUACAGT	100621	GAAGTTAUGGGATGTCGUGGCT
299022120	100622	AGAATATTAAACCAGUTTTATTTTTCAGCAUGT	100623	GACTCCACCATUTTCTTCCTCTTCAUAA
299023057	100624	CCUCGGGAGGCCTCTUAC	100625	CCCAGGCUTAACGTGCATUC
299024987	100626	GGTGUACACGGCCTCGUT	100627	GCCCTTUCCGCCACGUA
299026699	100628	CCGATTCCGCUCTCTTCUAGG	100629	TGTCTCATGUGCCATTTTCTCTTTUCT
299031333	100630	TTGTGUGACACCTGACAUGCT	100631	GGCCCTCAUCTCCTTCATAUACAAC
299037641	100632	TGTGGAGUGAGGTAATTTUCAGCAT	100633	TGCTGTCTTUAGAGTATCCUGGCT
299038461	100634	GGAGTACAACUCCATATTTTCTGAUGGT	100635	CTGGAGACACUGCCTTUGACT
299040700	100636	AAGAAGCCUCTGAATGCCTUCAT	100637	AGGGAGAGGGCAGGUCTUAC
299040875	100638	CCTGUGAGGACCGGCCUA	100639	CCAGGTGCUCCGTGTACUG
299042105	100640	TCTGGAATCACUCGAGCCUGA	100641	GGTTGTCCUGTCAGCGTGUT
299042374	100642	CAACGUAGAGCAGATGTUGCAC	100643	GAGCTGTCAUGCAGAAATGGTUT
299042838	100644	GACCGCUGTATCCGCTUCT	100645	CACATCCUGAGGCCUGGT
299045348	100646	GCUCUAGGGCCGGGAACA	100647	GATGGGCUGGGACCCUAAC
299054807	100648	GATCTGAAAUAGAAACCAAGGCUGAGT	100649	GAACTACAAGACUGGGAUGGACAG
299058466	100650	TTGAGCTAGAGCAGUAGAAATAACAUGAAAA	100651	GTAGTTCTGUAGCCATTGCTATTCTUGT
299065839	100652	CAGGGATUGCAGAGGCGTAUT	100653	GGGCGCUCTGAATCACTUCC
299066175	100654	CTGCTAGACUCATGTAGATUGGCT	100655	CGCGGTUGGTCCTGCUA
299067593	100656	GTACGCAGUCGCGGUACA	100657	CTCCGGAAGUGGAAGCTTCAUA
299068952	100658	GGTGACUCACAGTAGCUGGACT	100659	TTGGTTGACUGCTCTGTCTTTUCT
299072574	100660	GCUGGUAGAGAGGGCAGAAC	100661	GGCCUTCUGCCCGAAAACA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
299074230	100662	ACCCCAUAGCCCACAGGUAT	100663	CAAGACACUCTCTCCCUCACAG
299075599	100664	GGCAUAGCCCACGAUGAAGG	100665	ACCCCACCAUCTGGTAAGUGT
299076224	100666	GCGAGGGAACAGUCTGACAUAT	100667	AGAGAGGCUGTGGGTTCCTUA
299077514	100668	GGCCUCGAAGGCAUCACC	100669	TGTGGTCCUGGGCCAGUA
299079254	100670	CGTCCAGGUACCCTTTGGUG	100671	CATTCTCTCCCUTGGCTTTCUCT
299080185	100672	GCATCCCUAGCACATTTTGUAGGT	100673	GCAGAGGTATUACAATGCCTTGAUCT
299080416	100674	ACATTCACCAACUTATGCCAATTCTCUT	100675	TCCTTTCTGAATAUTGAGCTCATCAGUG
299080712	100676	CCTCUACCCCAAGAGTCTCUCT	100677	CGACTATGGCUACAACCTGGUG
299081217	100678	AAATCTCAUTTCAGCATTUCAGAAGCC	100679	TGAGCTUCCAAACCCTGUCAAAA
299082503	100680	GACACCAATAUGCAGCCGTTUT	100681	CATCAGGACATUGTGACAAATGTTUCC
299083221	100682	GCCTCACCAAUAGCCACGUT	100683	CCTCUGAGCAACCCUGGAC
299085019	100684	GGTGAGGCUCCTGAGUACCA	100685	GCTGUCCAACCACATCTCCUC
299086156	100686	GGCAAAGCUCACACUGACC	100687	ACTGUCAAGAGCCCCAUCAGA
299086528	100688	GGTCCCAUGGCTGGUGA	100689	GGATGUCCCTCUGCAGGAT
299086650	100690	TGGAATGCUGAGCAGCTGUC	100691	GAGGAGCUGGTGGTCUGT
299087102	100692	AGGTGUGCGGGCUCAAG	100693	CTCTUCCGTTCCUGCCAGT
299087229	100694	AGAUCTGGTCCUCACGGAACA	100695	GATGCAGCUCTGATCCUCACT
299087524	100696	GCUCAGCGCATCUGCCAT	100697	GGAAGGCAGAGUCCAUGCAA
299092715	100698	GCCCCCAGGGUTCGATTUT	100699	CGTGAAGCCUCATGCUGGT
299096824	100700	GGATGTAGAGCUCCACCTUCCT	100701	CGTGGCCUCGTTTCTCAAUG
299102593	100702	GGUAGCGGCAGAGCAUCAC	100703	CAAACCTCCTUCATCTGCTCCTUT
299103977	100704	TGTTATACCTGCUTTACTGCCTTUGG	100705	CCCCTCCTCCUGCTAATGATATTTUAT
299111828	100706	CCTGCAUTGATGGCUCCGT	100707	CTGCCCAGAGUGTGCACTUA
299118497	100708	CTCAGUGCCTCGUCACAGAT	100709	ACCTACTGCAGAUGCTGTGUC
299121238	100710	GACGTCAUCTGAGTTGGUGGA	100711	GCCCTUGAACCAGGUGAACAG
299125255	100712	CCTCGTUGCCCCUCACC	100713	AGTGCCUGGCGTGAACUC
299128474	100714	GCCTCATCUCACCAACAGCUT	100715	GGTGCTTTAAGGUGAAACAGACTUAC
299131980	100716	CCATTACCUCAGACTTCTUGGCA	100717	TTTGTGTACAACUGGATAACTACTTGAACUT
299143228	100718	CTCCTCCCACCUCTTAAAGTTAUGA	100719	CACGGAGGAUTAAAACTTUCAAGACAA
299155916	100720	AGAACUGAACCAAAGGCACUGA	100721	CTGUCCCCACGGAAGGTTAUAG
299157917	100722	GCATAGCAACAAUTCTCCCACCTTTUA	100723	ATTTTCAAGTTTCTUCTCTGTTCTGTTTUGT
299166900	100724	GCAATGAACUCATTTGTUCCCCAA	100725	GCAGAATTGUGAGAAGCTGGAGAAUAAT
299168048	100726	AAGAGTCGUGTGCTTGATGUCAT	100727	ACATTTTTGCATAACUGCATAGATACAATTTUT
299170618	100728	CTCUCGGTGCUGAGAGCAA	100729	CCTCACGUTAATCCTGUGGAAGT
299171939	100730	ACTCCTTTCUTTTTGAGCAGUACACA	100731	CTGATGCCTGUTTTTCTTTCTCCTUT
299172421	100732	CTACCACGCUACTACCATAUGCC	100733	GGAGTUCACCAGGCCACATUT
299172709	100734	GAGCCAACUGGAGCGUGA	100735	CGAGGAGCCCGCUTGUT
299174492	100736	TUTGGAAAGAGCUGAACACAAGGA	100737	CTGCAUCAAAATGGTTUCCAGGAC
299175013	100738	AAGTTTATTCTUTCACAGGTAUCACGGT	100739	AACCAGCCTAAAUTTCAAATACCTCCUT
299193777	100740	CTGCCCUGAGCTTTCCCAAUA	100741	GCUAAGACAAACAUGCGGACAG
299199908	100742	GCCTCTCTTUGGTTCATAAGGTGUT	100743	CAGTGACATCAAUACCCTCTATTTCUGT
299201595	100744	CTGAAGGCAGUCATTCTTCTGGAUAT	100745	GATAATTTGCGGUAAAAGCCTTUCAGT
299202090	100746	CACUGAAAGGCTTTUACCGCAA	100747	TGGAATCTCAUAGAATTTTTGGCUGACT
299210923	100748	CUACCCGCAGAGCACUCC	100749	ACTGGCAGACUCGAGACTGUA
299226761	100750	GGGAGTTGGCAUGACCCTCUA	100751	CCTCCTTAGGUGTCCCTCAAUG
299226830	100752	CTCTGCCCAUGCCTUCCA	100753	GCCUCAGGGAGCUCACCA
299232433	100754	GGAAAACUGUGGACCAGAACCAT	100755	TTCCCAAAGGUGAAATGGATGUGA
299235064	100756	AGTGGAAATGAUGGCAAATGCCUA	100757	CAGAAACTAUGCAAACTAGUGAAGCAT
299237732	100758	TGTTTTGCUCCATCATTTCUGACACT	100759	CCTGCAAGTAUAAGTTGTGCTTCCUT
299241622	100760	CTGCCCCACUCACCTCUC	100761	GGCATCGUGTTCTCATTCUGGAT
299242970	100762	CCTGCTUCGCCAGAUCGT	100763	GGACACCUGAGGCUGCT
299243469	100764	ACATCACCACCUGCAAAUACCC	100765	GGAATTGTCTGTUGACTAGTGATTGUCT
299244123	100766	GAGUACCCCAAUCGAGCCAAA	100767	CATGACAATUGATTTCCCCGUAGG
299254899	100768	GGACATGCCUGTGCCCTUAA	100769	CCACCAUGUGAGGAGAGAACC
299255022	100770	TGACTCCAAAUAGGAGACGUCAGA	100771	TGGAAGCAGGUCTTTTATTTGGGUAA
299255290	100772	CGCCAAAAUCATCCCTGTGUCT	100773	GCAGGTACUGAACACAUGGCT
299260155	100774	CUGGCCUCCAAGAGCAAGA	100775	GGCTTGCUCCGAAUGGGT
299260804	100776	CACAGCCUGGTCTCCAGUC	100777	GAATCCAGGCUGCCGCTUA
299262405	100778	CCACTCCCUCTGCAGCTUT	100779	CAUCUGCCCAGAGGAGGAG
299263215	100780	CAGCTGGCUCTCCACUCT	100781	AGAGCTGUGGGCAUGGAC
299264572	100782	CCAGCCUCCCCTCCUGT	100783	GGAGCTTAGUGGGCAGACTUG

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
299265006	100784	GGGCAGACUCGCUCCAA	100785	AGAGCTGUGTGCCTCAAUGG
299266795	100786	CAGCCTCUTTCCCTGGUCAC	100787	TGCTGTTGTUACCAGCCACTTUA
299281162	100788	GAACTGGGAGUCAGGTGGTUG	100789	CCGGTTTCCCUGCTGATTTUG
299281965	100790	GGACGCAGUGGCTGTGTAUC	100791	GCCCATGUCCACCGTAUCAT
299283776	100792	GATCCCTTTTCUGCTGCTGTGUA	100793	CTCAGCACUGACAUCCAGACC
299283946	100794	AUTCTTTTACCUCAAAACCACCCAAT	100795	GTATTCAUGGAAGATGTUGGAGCAGA
299284128	100796	TGCTATTCTCCUTACTCCAAATGTUGAC	100797	TCAGCAGACAACAUTGGAUACACC
299295816	100798	GAAACACAAUGAAGAGAAAAUGGAAGCA	100799	GTTTGTCCUTTCCCTUGAGCAG
299301887	100800	GCGTATAUCACACAAAGTAUGACCCAAT	100801	GUGAAAGUAACCACAGCAACCAAG
299304410	100802	TGCACAAAAUACATACTGAUCCAGGT	100803	CACCCCTUCCCTTAAACTTCTUACA
299304443	100804	AATGGATACCTTUTGCGTTCTAGTUGA	100805	TGTCTCTAATGCGGUCTCATAATGAUG
299304626	100806	AGCTTTTTGAUCTGGAGCUCGAT	100807	GAGUTGAGGAUGAAGCAGAACCT
299325664	100808	GTTAAACTGCUGCCACTTCUGG	100809	CTGCCAACCUATGTTTAAAGCATTUCAT
299338747	100810	CAAAACUGGAAGAACATCAGAAUGCT	100811	TTCCTTTCTGUTCTTATAGACGUGCC
299340592	100812	TTCTGCGCCCACUAGCATUAT	100813	CTGTTTTAAACCAUAGTGAGTTTGUGCT
299344663	100814	GGGAAACTGTUCTCTTCCATTCUC	100815	GAGGAUAAACCTGTUGCCACCA
299349059	100816	GCCTGCAGCUCCTGTATGTUAC	100817	TTTCAAAGGAAGCUGTGGTACAATAUGA
299354001	100818	CCTGGGTUGAGTTCCAACTUGA	100819	TCAAAGCUGUACAAGAAAGCAGGAT
299367199	100820	TTTTGTAGGTTCUGCAGCATATCTUGA	100821	CACCCACACACAUAGTGAUACCA
299382653	100822	AGCTAGAGAGAGGUAGGAAACACTUT	100823	CCUCGTUAAAAGCAGGGAACAG
299401901	100824	CAACATCGCUCTCCTCCTTCUC	100825	AGTGGAGCCACUTTGGTATCATUAC
299438638	100826	AAUTGATAAGCUAACCAGAGCCAGAC	100827	TCCTUGGTCAGAAUGAGAGGAA
299452569	100828	GGGCTGTATCUAACTAAAGTGTTTUGA	100829	ATCAGAAGGAAGCAAUGCACAUACT
299454121	100830	TCCAGCAGUGAAAATGGCUACA	100831	CTGGAAATTGGGUACGATACTGTATCUT
299468427	100832	TTCTGCTTTTCCUGTAGCAAGAUCA	100833	ACAAGTGUGGCCAGAGAAGTTAAAAUAT
299488471	100834	TTTAAGATATGAUGGCACCCACATACUG	100835	TCTCCTTCUAGCAAGTGAGGATUCT
299494310	100836	CCTCATCCACUCTTGCTCUCA	100837	AGACAAGAGGUTTTAGAGAGTAGUCAAGT
299567575	100838	GCACAAGAAUCCTAUGAAAAGGCA	100839	GATTCAUGCACACGUCAAGCA
299641367	100840	GCCTUGGCCTTGCUCCAT	100841	GCTGGTGGTUTCCCATTCTCUA
299668735	100842	CCCCTAGUGAGCTACGCUGT	100843	CTAACTGGGAUCGCTAUGGCAAT
299681189	100844	GCTTGCAGACUAGCCACUGT	100845	GAAGAAGCTGAGAAUGTGATGAAATUCA
299688548	100846	ACTGAGCGGUGGTTTCATUCA	100847	TGATGGATACTAUTGCACACCAAUGT
299702761	100848	GTTCATTCCTAGUGCTGGGTGUA	100849	GAAGATGTTCGTUGGTTGGTATTCTAUGA
299705079	100850	CCACCCGCACUAGCCTTATUAA	100851	GCTGGCTAAGUAACACCAATAAAATGUCT
299708217	100852	TGCGGAAGCUCGTACTTGAAAUAAT	100853	AAAGTTTTACAUACGGCTAUACGACAAGA
299708733	100854	TGAGUAAAGCCACCTTCTGUACCT	100855	GAACTCTGUGAGTGGTTGACUCAA
299710819	100856	ATTGTTTCCAGUCTGTGAAGTTCCUT	100857	AGCCTTAATGAAUACCAGCCCAAATUAT
299713684	100858	CAGAAGTCGTTUCCCATCATCTAAUACT	100859	AGGTAATGGGAACAUTGTAGGUACCA
299720388	100860	TCCATTCUGAGAAACTTTGCTTUCCAT	100861	GGTCTTCTCUCTGATAATCATTTUGCCT
299741860	100862	TGGAAGAGATACAAUGATGCACAATUCT	100863	CCCCUTTGAATGTATUGGAACAGG
299782144	100864	AGGGCTGUGTTTGTCAGTUGT	100865	CAAACGTGCUCACCAACTTCUT
299795551	100866	CCCCCACACUCTCAATTTTGUG	100867	CGTGAACUGGCCTTTCAGCUT
299799222	100868	CCACTGCCCUGAGAATCTTTTUC	100869	GTGTTGGTTUGTTTGGAATCTUCACA
299805726	100870	GATGTACCCCUGCAGCUGAAT	100871	GGCTGAAGAUGGACTCAAAGAATTUG
299808646	100872	TGCACAAGACCCUGTCTTUCAG	100873	AAGGATCCAAUCAGCTTCAACACUAA
299810576	100874	GGGTGTGGUGAAGGATTCTCCUA	100875	ACTACATTCCAAGUCCTCCACUCA
299812034	100876	GCCTCTTTAAUTCAATGATTCCUGCAT	100877	AUGTTTTACAUGGAGAGGAGGAACAC
299822840	100878	TTTTGGAAAAGUAGCATGTCTUGACAC	100879	GCGTGAGCCUTGAGGAGACUA
299825413	100880	AGTGATCTTTTUCCTGTTTGACACUT	100881	GGCAGAUGGCCAGGTAUCC
299829519	100882	GGCCTGGAAGGUGAACATGUA	100883	GCACGCACCUGUAGGAGAG
299830397	100884	GTGTTGCTTUCACTCTGTTTTUCGT	100885	GCAUAAAGACGGAGAUCAGCCT
299830736	100886	CGTCTCTTCCCUGTTTTAGGTTTTUCA	100887	CCCCTCCUCCACAATGATCUT
299830836	100888	GTGTGTTTTUAAGCCGGATUCAGAT	100889	CCCAUACAGAGGCACATGATCUT
299830842	100890	GTAGTGUCCCACGUGCACA	100891	GACAAGCAGAAGGAGUTTCATCUCT
299835976	100892	CAGATGCUGACCCACUGGAC	100893	GTAAAGGTUCAAAGTGAATGCCUGAA
299841625	100894	GCAACAACCCCAGCUACAUAGA	100895	TGTUCAACAGAGTCUGAGGAAAGG
299861569	100896	ATTTTGGUGACCCAUGGGAGAAT	100897	GCTCGATUTGTGCCGUCAGT
299879931	100898	CCTTUGCAAGCACAGGTTGTUAG	100899	CCGTGAACACCAUAATAGAAAAGGUGAA
299883195	100900	CAACCCAAUCCCACACGACTUA	100901	CAGCGAUCAUCGAGGAGGA
299884941	100902	GGCGATTCCUCCTTCTTTGTTAACTUA	100903	AGGTCTTATGTCUGTGTTGCTCTCTAUAT
299892714	100904	GTGCTCTATTTUAAGTATGCAGCTGAUCT	100905	AGTUGGCCACACGGATGTAUG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
299895996	100906	TGAAGGGACCAAAUGCCAACUT	100907	TCATCGATGUCTGGCACACUG
299896526	100908	ACCGUCGGAGCTCATCUAGT	100909	GCAACAACAAUAGCAAAATCACAUGAGA
299902356	100910	TCCAGAUAGCAGGAAAUGGACAGA	100911	TCTCCACCATAUAAGGGACCGUAG
299910055	100912	TCCAAACTACGGUCCCTTATAUGGT	100913	GCTATAAGCACAUCCTTGGCTACATUAT
299913316	100914	CGAGUGGTCCUGAGGACAGA	100915	GCGGCUCCGAGAUGACC
299914498	100916	CCTGCAAAGAUGATTTTGACCAUGA	100917	TTACCCUGATGGCGUACAACC
299915521	100918	CAGGCGGGUGACGTUGA	100919	CCACAACCCUTGTCCCUGAG
299929083	100920	GGACATCCCAAAAUGACCCTAACUG	100921	CCATGTATGCAUCAGTCTCTTAGGAUCT
299936193	100922	AATAAGGCTGTGAUATAAATAGTGTGUAAAGT	100923	CAGGAAAGGAGCUTACAGAAATTUGG
299937233	100924	GGTGGGTGACACUCTTTTAATAATUGGT	100925	AGATCCTGTTATGUCATCTATGGGTCUT
299938571	100926	GTTGATCTTAATUGTTGCCTGTGGUT	100927	TTACAUCACCAACGCAGTCCUT
299950708	100928	GTGTGTGTAUCTGAGTGCCUGA	100929	AGAUGGACGGATTCAUGGAAAGAAAAT
299955405	100930	AAACGTAGUCGTCTCUGCAACAA	100931	GCTGACUGCAGCATTCAGUAAAA
299961287	100932	CATAAGACAAUCGCTAAGGTTACUGGT	100933	CATCCGCAUCCCAGGAGTUC
299973096	100934	TCGAGACACGGUTCCCTAATTAUCT	100935	GCCTCTCTUGGAAGTTCTCACUC
299979189	100936	TTGCGACGUGTGUGGGT	100937	GGCUGAGCTTTUGGGACAGA
299979246	100938	GGCTCCAAUCCCGGTTCAUA	100939	TCAATACTGUGCTTTGCACUCACA
299986029	100940	GCCTGCCCCGUTTCTCUT	100941	CCGGTCATAGUAACGGGAGAUG
299993106	100942	GGCAUCGAGCAUGACAACC	100943	TCATCTCCUAAACACCCCTGUCT
299995896	100944	AACCCTTTUACGGAGTCTTTCATCUC	100945	AGAAGGGUGAAGCTCTTTUGGAAC
300006074	100946	TTTAAAGUGACGTCCUGCACCA	100947	GTAUGTATTCATCTTGUCCACGGAGAT
300029390	100948	AAAGACTTTTCUCATTAATGTAATTUGAAGCA	100949	AGATTUGACAAGAGCACAGAUGGT
300035759	100950	CTATCUCAAACACGCAUGCCT	100951	ACAATTCCATGTUCTCCAGAAGCATUAA
300042335	100952	GGCTCTAGGAAUTTGAAGCCUACA	100953	ATTTUGCCCAAAGCAUCAGCAAT
300053468	100954	AAATUCCAGAGAAGAAAGCTAUGGCA	100955	GAGAATTAATCUGGAAGCTGGAAGUCT
300057107	100956	CTGATCCTTUGGTGGCACUGA	100957	CTGCTGAAGCUTGTGTCTUGG
300060992	100958	GCATCGCCCUGCTTTCATTCUA	100959	CACGATCTCUTCGGCTCTCUC
300077631	100960	GUGCGCAACGCCTTUAAAAGA	100961	CTGCTTCCUCACAGTGGAGTUT
300080283	100962	GGTTCGAGAAGUCACCTCUCC	100963	TTGAAATTACCUTGGTTCTGGUGACA
300081778	100964	GCCTGAUCCCAAGUCGAACA	100965	GAGTGGAAAUCCTCACTGTCCUC
300094567	100966	TCCACCUGUCAGAGGACGAG	100967	TGAACCACCUAGGCUGGAGAA
300100284	100968	GTTCCTCCCUCTGAATCUGCAA	100969	CCACCCCUCTGTGGUCAT
300106693	100970	TTTGCCTTACTGUTTAGGAATGACCUT	100971	GTCATCATCTUCACAAGCAAAAUGGAC
300108595	100972	GGACCCACUGGATCCTUACC	100973	GCTTCTTUGAATTCCAAGUGCAAGAT
300111057	100974	ACACCUACACUCCGGGAGAA	100975	GGGAGCACATUAAGGACCAATATAUG
300122718	100976	GTGCTTGGCUTTCATCGUCAG	100977	CTGCAGGAAGAUGAACGCTACUA
300123039	100978	ACCTTTACCTCUAGTGACAAATCTCTUGA	100979	ATTCCATTCUGCCTGATAAGCAUGT
300128035	100980	ATGCUGCAGACGAACTGTUCT	100981	CGUTTTCAGAUACAGCAAACCGAAA
300141127	100982	TGGGAGTTTUGCTGCGAATGAUAT	100983	TGTCCAGTAAAGAUTCTTATGGTUGCC
300151336	100984	CTGGTTGAACUCATGGACCUGA	100985	AAAGGATCAACUCACGTGTATUCACA
300169265	100986	GGAAACAATTUGACAAGTATGAUCACACA	100987	CTGCACTTATUCCTCTTTGCTTTUACAG
300172750	100988	CAGCTGTCUGCATGAGACCUA	100989	CUGAAAGUAAGCAGGAGCCAGT
300196634	100990	CTGACATTAAGUGTTCTACGAGAUCCAT	100991	CATCAGCUGGAGCTCGAGATUC
300206062	100992	GATCCCGUCCTGTCCGAAUAA	100993	CTCCAATATTUAGAAGCCGCUGGA
300211626	100994	GCAGCACAGUCTAACUCAAGGG	100995	ATGAAAGCAGCAAUCGCCTCUA
300222427	100996	CTCCTCTTUGCTGGCAGAUCA	100997	CCTGGACACUATCTAAAACCTUGCAG
300232246	100998	TTCACAGCAAAGAAGAGUACTUGAAA	100999	AGCAAAGUGGCACAATUCGG
300233954	101000	AGGCAATGAGUGAAACAGUCCAG	101001	TCATTCTGTCTUTCGTTTCTCCUCAAG
300262504	101002	GCGATAATCAUGTCCCCAAUGGA	101003	TGTTCCTUCCCAGGTTGGTUG
300280832	101004	GAGAAGUCCAGATGCCCUGAAT	101005	GCTAUCGGCCAGGTTGAUGAC
300283861	101006	TTAACTTTAGTTCACAUCAGCACTGCUA	101007	CAGTGGTTGGUTAATGCAAAAAUCAC
300287654	101008	GTACTGCUAAAGAAGCAGCTTUGG	101009	CGGATTTGTUAACATGCTCCCAAUT
300291622	101010	GCACAAAUCAACGCAGGCTUA	101011	CCCTGGUAATGATGCUGCCT
300291835	101012	GCTCCCGUCCAUCACCAAC	101013	GCCTCACCUCCTCTTUGGA
300292186	101014	GAGGTATAUCAAAACACTTGGCGGUA	101015	CCATTAAATTTTUGCGTCACCTTTUCAG
300316983	101016	CTTTCCAUACAGCTAGCCTGUGA	101017	CAGATGCCATGUTTTCTGAAGACATUAG
300319950	101018	TTCTGTTTUCCCAAGCCTGUCA	101019	CCAGCTAGAACUCCAGGATCUACAG
300325928	101020	CGACGAAAAGAAGGGUAACCAAAAUAG	101021	GCTGCAGTGAUGTTTGTTTCTGTTTAUA
300328794	101022	CTCTTGGATGGCUCTGTATCGTUC	101023	TGCATGAAUGGCCACTTTATTTTTCUT
300332825	101024	GAACAAGCCAAGAGCUATTTTCTTUCAA	101025	TUCGGUGAAAACCACAGCAAAAG
300336630	101026	CCGTTTGCUCTGTTTGTTGAAUGT	101027	TTTCACTCTGAUAACTGCCTTTUCCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
300339261	101028	TCTTCCTATAACGAAAGUGTCTGCTTTUT	101029	GCAACCCAACUGTTCTAAAGTCTTUT
300345575	101030	TGTGGAAUAAAGTTGCUAGAACAAAAAG	101031	ATTCTGAGTGUGGAAATGGCTUCA
300345607	101032	TGCACTCACACAUATAGAAACCATGAUT	101033	AATCTAGAGUGTATCCAAAAUGCCAACA
300346018	101034	GGATGCCTTACUTTTTCTTTTTGGAUGA	101035	ACAAATATACACCUGGACGUAGAGAAGA
300347106	101036	GCCATTUCCACACTCAGAAUAACAAAA	101037	TCTACTAGGTACACUAGTGAAAGAACUCC
300352930	101038	GTACTTACTTGUGTGGGTGCCUT	101039	GGCTGTACACAGAGUAAAAGTCACAUT
300375462	101040	CTATATCCCCAAGUAAAACTGACUCCAA	101041	CAGAAGTUAGCTAAAGACCUCACAACT
300376389	101042	CCCTCTCCUGGCTCATCCTUA	101043	TGTTTTAATAGGUTGATCGGGAUCGAG
300379443	101044	TGTCTTCGCUTTCAGCTTAGTUAGAAT	101045	GGCTTGTTTTGCUGTTCTTACTGATTUT
300393881	101046	GATGCAGCAUTCCCACATGTUT	101047	CCAGCTGCUCACAGCTCTUAC
300407095	101048	GGGTTTCUCTTCCTTGTUGCAGT	101049	CCATCTTCAGAUTCTGCCTGUGT
300410761	101050	GGGAAAACAAGGUAGCTCCUGAA	101051	ATACAAGGACTACUCCAAACAGTGUG
300412769	101052	CTACAAACAAAAGUGCCACTGUGA	101053	GCAAAAACUGGCAAATGTGTTUGA
300418453	101054	AGCTTGGUATTTCTTTCUCAGCAGT	101055	CCCTGTCTUGTCCGAATGAUCAAG
300419782	101056	TTTGTTCTGCUACGGGCUGT	101057	TGAGTTTUCCCGTTGCTTUCCT
300426621	101058	GAACAACCTTTTUCGTGCTCCAAUT	101059	CGTATTGGCCCUTTTGGAGTUAGG
300429944	101060	AGAUGGGACCUCAGGAAGCA	101061	TGCAATCUGAGCATTCUCCACAG
300440327	101062	CTGCTGCUGAACTGUCGAAG	101063	TGCTCATGAGUGTTGGTTATTATTUCCA
300441386	101064	CAGTGTCCCUTGTTTGAAGTUCCT	101065	GGCCCCAACAUACCCTTTCUG
300453352	101066	ACAGCCTCUCCCCATAATTCCUT	101067	GCCAAUGUGCAGACCACCT
300455164	101068	ACAAGGAACUGGTGUCAAAGCA	101069	GGGATTCCTAAAGUTGGTGTCTTAAUGG
300460465	101070	TCGATACAGCAGCAGUATGTCAAUAT	101071	TCCAGCAGCUGTGAAATTGACTUA
300461320	101072	TGTTGGTGUCACACAGCCTAUT	101073	TGATGGATGCCCAAUACAAGATAATUACA
300462231	101074	AGCTGTCATUCATATTCCAAACUGACT	101075	TTGATGGTGGUTTTCTTTTGTTUGCT
300464263	101076	TGCACGTTTTGUTTAAGTTTCGCUT	101077	TGGTTTCACTUTTGCAGGCAAUG
300464541	101078	TCATACCTGTAAGUTTACTGCATCTUGG	101079	AACGCCAGCAGUTACCUAACA
300471160	101080	GGTTAACCCAUCTGACGTUCAA	101081	TCTCTGCCTAUATCAGTGCTGAUGAT
300475835	101082	TTTGGTAATGAGGUGTGCTGTCUT	101083	CGGAAGTTAAGAGGAAAUGTGTCATGUAT
300477595	101084	CAAATTAGCATUCAGCAGTTGUCAGT	101085	CTGCAAAGCAUGTGGTTCUGG
300478975	101086	CCTGGCUAAACTGCTUGCAGA	101087	GCTCATTGUGGTTGTCCTTTTUCC
300479646	101088	CATTCAGACUGAGAGCACUCACA	101089	GACTCTCCAUGGTTTCTCUCAGG
300485344	101090	GUGTGTTAGAACUGGCCCAGAT	101091	CCTCCAAGATTUTGATCCACTTTTUCAA
300487434	101092	CTCTACGCGUTCATTAAGAAUGGAGAT	101093	GTCCGTGGGUATTCAAGTTTGTTTUT
300487785	101094	AGCCTGCCUAGAGTCUCAGAA	101095	GTTGGTCTUCAAAAATTTACCTCTUGCT
300491615	101096	AGCGTUCCAGGATCCAUGAAG	101097	TCTGUGCCGAGAAATTGCUCA
300491726	101098	TCTGTCCUGAATGGCCTUCAC	101099	GCCACCAGAACCUACTTAGAAUGAC
300497277	101100	GCAGCUCCGGAGTTTCTCTUT	101101	AGAGAGTCTCUTGATAAGCTTUCCCA
300497635	101102	CATAGAGGAAAAGUGCCGGTUCT	101103	CCGTGGGTUAGTTCCACCUG
300499196	101104	CTTTTGCCUGCAACCATATTTCTTUAGT	101105	CATGTTCTCAAUGTTCTTTCCCATTUCT
300507683	101106	CGTGGCCUTCTTCACUCAGAA	101107	GCTATGAGCCUGTGTCTGGTUA
300512286	101108	GGGTTTUCATGTAAATCUGGACAGT	101109	CGTGCTACAAAUCAGCAGUCAG
300514290	101110	GCTCAGCUGAAGATAGTGACTTUGA	101111	TCTGUGAAGCCAAGATCCUCAC
300519042	101112	TCTTATCACTACGCUTACTTTCCACAUC	101113	CCAACTCCUGGAAAACTAAUGAGACAT
300521072	101114	TGAGCGAAATAGUTACAGTGACTTUCC	101115	GCTGUTCGAAAGCUCCACAAAC
300528953	101116	TCUGCAGTTUGAGGGACAAGAC	101117	AAATAGCAAUTGCATCAAUGAGAACCAA
300530438	101118	CCCGGCAAAUTGTCCTTAACTUT	101119	ACGCCACTUGGTCATCATCAUC
300535651	101120	CTGTCCTGACUCACCTTCCAUT	101121	CCCACTTUCCCCTTCCATGUC
300544785	101122	GGTCCCAUGCCTCUGCT	101123	AGCCTCACCUGCCTCATUG
300547902	101124	GAGGCGCAGGUCCTUCT	101125	CCCGGCUGCCTUCAAACA
300550073	101126	TTGGTTTTGTTAGUGATCTGTGCAAUG	101127	CTCCTGGCATUTAACCAACCAGAUAT
300555003	101128	GGCUCGAAAGGAATGGAUCCT	101129	AGACACTCCUCAACCCTTCCTUA
300555819	101130	AGAAAGCTAUCAACCCCTTGCUG	101131	TTTTCCUTTCCCCUGCACGAT
300568670	101132	TGATGGGTAAAGAGAAUGAGGAGACUT	101133	AAATGGTGGAGACUCAGATCAATTCUG
300573111	101134	TCGTTTCCUGAACCCAACATTUCA	101135	TCCTTTCACTUCACTTCTGTTTTAUCCC
300577608	101136	GCAGACCAGAUATAGGTCAACCUAAG	101137	ACCCCCUGTTCATUGCAAACA
300586938	101138	TGTCTCTTCACAUTTCGCAATCATUAGA	101139	GUAAACGGAAGGUGACCACCA
300593355	101140	GCCTTCTTAGCAUTTCCTTGGAUCT	101141	TGCTGGCUGTTAACUCACAAACA
300596884	101142	AGCCCUGAAGAAAGGACUCAGAT	101143	GAAGTGGTTTTUGTGGAAGATGUCAAG
300603061	101144	CAAACCTUGCCAACAGGAACAUT	101145	TGGTACTTACCAUTTTGTTGTTGTCUAAGA
300604967	101146	CTTGAAGCCTUTGACCTTTTGGUT	101147	GAAACTTGUCGTGCCTGTUGG
300615331	101148	GAAACCAGCUGCACATGCUAA	101149	CCTGATTTAGGCUTTGAACTGUCCAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
300623133	101150	CCGGCTGUAACTCGGAUGAA	101151	CAUCAGCAGCTTGUCGAACC
300624330	101152	CACTAGTGTUGGGTCTCAUGCT	101153	CAAGCCTUCGAGGAGGTTUCA
300628403	101154	CCTTCGGTGUTCCACCAGTUT	101155	CCTGCAGGATTGUAGGTTACTTAGAAUT
300630684	101156	CAAGTAGCACAAAUTTGCTTTTGGCUAA	101157	AGAATACUGAGGAGATGACGUGACA
300630768	101158	GGATTTTTGUACGAGAACAUGAGCAA	101159	GAAGCUCAUGGAAGACCCAGAC
300631294	101160	TTTTGCACAATUAGAATGTCACGTCAUC	101161	GCACCCTTGTCUTCTCATGTTATTTUT
300636997	101162	CTCACGGAGUCAGTTCCAATATUCA	101163	CTAACTGUCAGAACAGCTCTGGUC
300637911	101164	CCCAAGUCCGAACTCAAGCUG	101165	CATAAGGGUCAGAGTGAUCCACAA
300640549	101166	GGAGAGAAGAAGGGUCAGCAUCT	101167	GAATTTGCCTAUACTTCCAGGTGCUA
300640675	101168	CAACATAGGCACCAUCTACTTTUAGCA	101169	TGATCATTGAAGAAACAUACAAAGAATUGG
300642948	101170	TGATAACACAGCCUTACCUGGGA	101171	GCTGCCTUTGTTTGCCUACAG
300645540	101172	CCTGCTAGTGUAGTCCTTCCACUT	101173	AAAGGUTACAGCTCAUCGAGGAAC
300659642	101174	AGGACTGGCUGTTTTTCGGTUA	101175	CTCCTCACGACAACAUTCTGTTTUG
300662235	101176	GCACUGGGAGTTUCACACAGA	101177	GTGGCTTCUCACAGGGATTAUAAAAAC
300698363	101178	CTGAAGGTCUGGCGGTGUT	101179	GCCAAATATAGCAUGTCAGTGTTTTUGA
300729851	101180	CUGAGGCAAAGCTCUGGGT	101181	GCCCCUGTCCCCUCAAG
300730689	101182	GGAGCUGCCAGGTGGUA	101183	CCACACGUCCAGCTGTCUC
300730821	101184	GGTGTCCUCGAGCCTUGA	101185	CCTCCUCGGGTACCCAUCC
300731148	101186	GGAGACAGCUGGACGUGT	101187	GAGATCTUCCAGGCGCUACAG
300732179	101188	CAGTTGCCUCATGCACUCCT	101189	CAGACCAACUACGCCTTTGUG
300735775	101190	GCGGGAGGAACAGGUTGUC	101191	AGAUCTGCTCCAUCAACAGCAC
300737129	101192	TCAGGCACAAAGGCGUAGUT	101193	CGCCCGCCUAUGACGAC
300777167	101194	GTAAAGTGCTAUGGTCATATTGTGUAGGA	101195	AATUGGCCAGGAUGGAGAGAAC
300780414	101196	TTTACTGCCAUACATCTCCTTTCCUG	101197	TCTGAGCUGACTGGTTCCUCAT
300787345	101198	CTGTCTTCTUCTTTTGACCCUCCA	101199	AAGAACAGGGCACGUTTCUGA
300800048	101200	AGGAAGAGAUTCCCAAAAATUACAGCAT	101201	CAAAGUTCCCUAGAAAACCAGACCAA
300802274	101202	CAUCTTCATGUGGAGGCAGCA	101203	CTGTCATTCCCUACCCCAAAAUAGAA
300812073	101204	GGGCTCCGAGUTTCTGGATCUA	101205	GTGTTCUCACACCGGUGCT
300813580	101206	GCTATTTTGGCUGGCGAAGUT	101207	GGAAGUGGGAGCTAGAGCUCA
300817556	101208	GCAUACACGCAACCCCTCUA	101209	CGTTGTTGUCAAGGGUGAGGAG
300825118	101210	TGGCTCTCGUCCAGTATCUCC	101211	TGGCTTATTCGAAUGGCTAAGATUGAAT
300826738	101212	CCTGCTUCAACCACAAUGGAG	101213	TCTGGTTTACTCGUCTAGTTGACTGUA
300832859	101214	GCTTAAGUCAGCTATTUCCCACGAA	101215	TGGAAATCAGCUCCTTCGACUAAAAA
300847123	101216	TTTCTTGCCAGCUACCAGUGT	101217	TGGACAGCUCAUCACAGGAGAT
300851420	101218	CTATCAAUGCGCGACAGCUC	101219	ACCCTAATTUGAACATCGCTACTUGT
300862091	101220	ACAAAGGACUTGCAAGCCAUCT	101221	GCGATAAACCUTCCAGGGTUCA
300890987	101222	ACATATTAUGCACATGGTTUGAGGCT	101223	TCCCACATCAUCTCTGTCATAGUCAT
300891121	101224	ACTGTGTCUCAAGACTGCATUCAA	101225	CATGTAGCCUCAAACAGATGGTUC
300896048	101226	GTGTCTTUACTGTCTTGTUAACCCCAA	101227	CATCUCCCGCACUCGGAAAT
300900046	101228	TCCUCCCCATCCUCAGGAA	101229	GGTAAACTTTTCUTCACATTGCAAGUCA
300901713	101230	CATACACAAGCAUTCACCGATAAATUCC	101231	GAGCACACUGCTCAGACTUACT
300912867	101232	CTATCCGCUCTCCTTGAAGTUCAG	101233	CACAATCCTTTUGAAAAGATGGCTUGAT
300917802	101234	CCATCTCUGGTTGCCTUCGT	101235	CTGATATGCTTCUCTGTGGCCTUAG
300918409	101236	CATTCCATUACAACCCAGCUCAGT	101237	CTCTGAUCAGGCAGCACCTUA
300936034	101238	CTGGGACUCAGATTUGAACACACT	101239	GAGTTCTTGAUTATGAAACCTTUGCCAA
300936102	101240	TCTCTCCTCGGUTCCTTAATCTCUG	101241	AGGGAAGGATAAUCTTTAGCTGTCAUGT
300942470	101242	AGGCCUCCAAAGCTTCTAAACUC	101243	CCACTTGCCCTUTTACCAGACTTTATUA
300942983	101244	CCTTGTTGUGAAGTGCTTUGAAAGA	101245	TGAUGCAUGAACCCCAAGCAT
300958522	101246	ATTAGGCTTTTGUCATTAGAAAAGUAGAGCT	101247	CAGCATTGGTTUATGATCAGTCTTUCAA
300958678	101248	CATGAUCCCAGTTCAAAUAACGCT	101249	AATCTTCUGGAAGCAAUCCACGAT
300975360	101250	CGGATTCATACUATTCCAACTGTUCCT	101251	CCTGGCCUCATTCTTCAAGUGT
300977858	101252	TCTUCACAAAAGAGCCACAAAUCCT	101253	TCTGGUCTGGCUCACAGAGAT
300986139	101254	TGTTCAATATTAGUGAGCTGCAGAUCC	101255	AATTCGCTGUGCCATCTCCAUAT
300998200	101256	AGTTCACAACUGGAAATGAGTCCUT	101257	CAGCTTGCUGTTGCGGTUC
301003750	101258	CCACCACAUCCAUGACAACAACA	101259	GTGTATGGCGAAUTTGGCGAUAAT
301003795	101260	CCUCAGACAGAGGCAGUAGAAC	101261	GGTAAATTGTCACUTGACCAAGCAUT
301008324	101262	AGTACAGCGGACACUTGCUC	101263	GCCAAGUGCACCATGUGAGAT
301011774	101264	GTCACTCTAUCCCAAGATTGTTTUACC	101265	GCCATACTGUTGCTGTTTTUCCT
301016851	101266	TUTGGCTGAUGAAAGGCAGACT	101267	CAAAGCATCTGAGAUTGAATACAAGCUG
301031167	101268	ACCGGTCGUTGACCTTUCC	101269	GCTTTCTGACCUCTGTGATTGCTATTUA
301047275	101270	CTCTGCATGCAUCTGTCAATGAGUA	101271	AATTCTCAGATAAAUGCAAAGCACUGAC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
301059023	101272	TCCTGGTATTCUGCTATCCACUGT	101273	CAGAGAGGTUAAGAAAGGAGATTCAUGAT
301072386	101274	AGTTCCTTCAACUGCTCCATGUG	101275	TTTGCTCCTACUCACTCTCTTTTUCAG
301083336	101276	GCAATGAGAAGTUTAAGAAGATGCACUT	101277	TCCCTTTGTTUTTCATGTCAGUCCAT
301083808	101278	GTACTAACCGGUGATCCTCTGUG	101279	CAGGTTCTAAACUGACTACCTACCTCUT
301095747	101280	CAGTATUTGGCCTGTUGAAGAAGAAT	101281	CCCAGGCAGAGCUGCTUC
301097724	101282	TGTTCUGACGGAGGATAUGGGAAA	101283	CTTTTTCAGAGGUGGGCGAUG
301107212	101284	CAGAACTUGGAGCCGUGGAA	101285	TCTCCUTGCTTCUCGAAGGGA
301108315	101286	GUGGAAGCAGCTCUGCCT	101287	GTCCTTTTCUCCTTGCTTCUCGAA
301108376	101288	CCATCAAACUCCGGCAGTUC	101289	ACCAGAATTCAATUATACCTTGGCCUT
301108934	101290	CCGTGCCUCCCTUCGAG	101291	TGTTAUGCCCCACGTGATUGT
301114842	101292	ACCTTGGUGTGTGGTGUCAAG	101293	AACUGAGCTTCUGGAAAAGAGAAAGT
301123512	101294	ACTGGAUACTTGTCTGUAGGAAAGGT	101295	CGACTCTTCTUCAGAGATGATTCCTUCT
301132412	101296	CTCCCCCUCCAAGGAGAGUA	101297	TCTTCUAAACACCAAGCCCCTTUT
301137320	101298	TGGATGGATTACUTTAGTCCTGAGAUGT	101299	TTGAATCCUCCGCCGTTCTUT
301158138	101300	CCCATGTUCCGGCGUGAT	101301	CTTGAUGACGACTUCAGACAGGT
301161627	101302	CAACAUCGGGAAGAGAUGCGA	101303	CCGUTAGCTGTAAUCACACCACAT
301168999	101304	CAGUGTCACCAUCGAGCAGAG	101305	ACAGGCGCUTGGTTTTACUGA
301173223	101306	CTGAAGTCGUCATCAAGUGGGA	101307	CTCCACUGGAATTTGGGUCCAT
301181163	101308	GGGTCUGCAGGGACTCUGT	101309	CAATCTGCUGTTGGCUACCC
301188197	101310	GUGGGCCCAAGAGCCAUAA	101311	GCATTGGUGGCCTTCUCGT
301188352	101312	CCCAAAGUCCCCGATCTUGA	101313	CCGGCUACGUAAGCACCAG
301194496	101314	CATCTAUGAAGGGCUCACCAACT	101315	CUCAAAGCTCUGCCCAACAAC
301194778	101316	GCGUAGCGGCUCAGAGT	101317	CAGGGTCCUCCAGCTCAUT
301209189	101318	TCTGTAAATGAAAUGCAACCCTGCUA	101319	GGTTTGCUTCTTATGCUGGAGAACA
301223483	101320	GGGACAATTTCAUTTTTCCTTCTGUCAA	101321	TGGTGGCAGUTGAAAGACATTUAAGT
301224072	101322	GCCTAAATGACAUGTGCTTTGGUT	101323	GUACTUCAGGACGCAGGGT
301231155	101324	GCTTTGUGGAAGCCATGUCC	101325	GTTGTTTGCTUCGGCTTAATCUGA
301236900	101326	GGCTTTUGAAAAGGGTCTGAGUCT	101327	CAGGGAAGAGGUAATTAACAAACUGAGG
301340101	101328	TGTTGCGATUCTCCCTGCTUT	101329	GTTCAAGCCAAUACACCAAAGAAUCAC
301346189	101330	AATACTAAGTTTUCAGACTTGCCUGCT	101331	TGAUGAGCCATUAGAAAGAACCACAA
301353734	101332	CACCATTGGCAUGGGAGCUAT	101333	AAAATTTUAGGAGCAAGCAGTGTUCC
301379015	101334	CCCTTCTGTAGUTATCAGGTGAGUAGT	101335	CAGTTGGAUGAGAGATGGAGAGAUT
301379783	101336	ACCAACCTTTTGUTAATGATCTGTGGUA	101337	AGCAAACTTTUGCAATTGAAGGAAUCA
301380499	101338	TCTCTTTAACTGAAUTGCTCTGCAUGA	101339	GCATCUCGAGACATACUGAGGGA
301393202	101340	CCTCCTGAUTTGTATGAUACCAACACA	101341	CACTTGCAGGCACAAUAACAATCTUA
301393443	101342	CATCTTUGGAGGCTACUGAGAACAA	101343	CCTGTTAGGAUGAGATCCGTAATGUCT
301402785	101344	GCCTCACUCAGAACTGTCTGTTUA	101345	CUGAGAAUGAAGCCCAAAAGCAG
301411748	101346	TGGATAATTTUGCCAGCTCATCUCC	101347	ACTGTGTTCAUCAAAAGTGTTCTCUCAT
301435956	101348	GTGCGGUGGAAATGCCUAAG	101349	GGAGAUGGCAGAAAAGCTUCGT
301455509	101350	GGTAGGACACUTCAACCAACCATUT	101351	CAACCTGAAATUGACACTCCTCAGUAAT
301466556	101352	GTGAGTTTGATUAGCTTAAAACGGCTUT	101353	AGCAGGGUGATGAACCTGTUG
301467557	101354	CAGACCTCUGCGGGATGUG	101355	CTACCTUGATGGCCUGGAACT
301468309	101356	CCAACCCCAACAGGUTCAUCA	101357	GGAACCGUGTCTCGATUAAACCC
301474480	101358	CGAATCACUCCCTGCCATUG	101359	GTATACATTGGCUGATTGCGTAACUG
301474962	101360	AAGTTCAGUGGGTAACCAGUCC	101361	GCCAAUTTTCTCUGAACCAGACCAT
301486880	101362	TGGAAGGCAUCGTCGAUCAG	101363	GCAACUAAAGCUCAAGGGAAGAGA
301514509	101364	TGATGGAAAGUGTGTGUGCAGAA	101365	GTGTGAUCGGTGGCCUGA
301519383	101366	CAGTUCAGGCCACCGAUCA	101367	GAAAACAGTATGUGTTCAGCCAACTUT
301575485	101368	AAAGGUAGGCGCCTCTGTUAAA	101369	CAGGTCTGUTAACGGGATUCCAG
301579164	101370	GTCCTCTAAUTGATCAGGUGGCA	101371	GCTTCTUAGCCCTCTGUGAAACAT
301589434	101372	CATATCAGGCUGCCGCCUA	101373	TGTACACGTGGUTTGTTAATGTTTTGUT
301605301	101374	AGGATGTCUAGGAACATGAUGGAGAA	101375	GGUAGCCAAAGACAAAUCCAGCA
301624430	101376	CACCGAAAGGGACGAUGACUA	101377	TGTGGTGGAGUTTACAACTTUCACA
301632637	101378	AAAAGTCTCTUGCTTGAGGGCUT	101379	GGTGGCACACCAAUGCAGUA
301640193	101380	CAGGGATACUCGGGCCTTUC	101381	TGTTCCAGGGCUTTGCTTCTUA
301646621	101382	GCAGAUGCCGUCGACAAG	101383	TGTTTUGTGCACGUGAACAAGG
301654997	101384	ACTCCCTTUAAAGACCTTGCTATAGTUCT	101385	GCCACAGATGUGATGGAAATCGAAAUAT
301657951	101386	GCAAACTGAUACACAAGCAUGCAAA	101387	GCCTGTCGACAAUATCTAATGAATCTUGA
301660074	101388	ATGAATGTCUGCAGCATCTGTAGAUT	101389	TTTTCCCCUAATTTGTCUGAGCACA
301677427	101390	CACAGAATGCUTCCATGTGGTUG	101391	ACCCUGCUGACCAAAGAGAAAG
301681571	101392	GTCCATCGUCTTGCCTGUCT	101393	CATGGAGTUGTCAAAAACCUCGAAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
301682789	101394	CAGCTGUAACTTTGGCCUGGAT	101395	GGAGTTTTTGUCAGAAAGTGAAAAUGGA
301700401	101396	GCCACTCAUCAGGGCAAAGUT	101397	GATGTGAGCCGAGUCTTCCUAC
301709078	101398	CAACCATTACAAACUTAAAAGGCCAUCA	101399	AGCTUCTGCAGTUCAAGCGT
301709388	101400	GTGAGGAGGCCACUTTACAGUT	101401	CTGGTAUCCGAGTCTTGUGAGG
301718257	101402	CCTGGAAAUACTTCTGCGUGCT	101403	GATCACACCAUCACCACATGUCA
301726971	101404	AGTGAGCGUGGACUGCAAG	101405	AATGAATACAUGAGTGTGATUCCACAGT
301735206	101406	GTCCCCGUGGTCATCTTGUT	101407	GCAGCGGACCUCACACTUAC
301753883	101408	ATCTTCCUAAAGGAGAACGGAAACTUG	101409	TCATCAGCAAAGGUCGCATAUGT
301767193	101410	TGAGGCCCCACUACAGTUCA	101411	TGATGGGCAACGUCTTCUAGAAC
301767580	101412	ACCATAGAAGUCGATCAAAUCCACAC	101413	AATGCATTTGGCUTACCATCAUCT
301778378	101414	CCTACCTGTCAUCAACTTGACCUT	101415	TGGAAAGTTAUCAGAGAACCGATCACUA
301781847	101416	CTAATAGUGTGTCCCUGGAACCAA	101417	CACCTGUGGCTAATACAGAUGCT
301804586	101418	GGTGTTTTGTGAAUTAAAATGCCCAGUA	101419	GGATCTTCCACCUATTAGTAGTCTUGGA
301805355	101420	TGGGAGGUACCTGGTUAACAGA	101421	TGGGCUACATTTTACGUGGCA
301806449	101422	GCCATGATGAUAACAGCAGCTTUCT	101423	GTACCAUCTACCCAAUGGCCAA
301808273	101424	TGGTACCATTUCCATCTCGAAGAAUA	101425	TTAGCACATTTGAAUACTAGGTTTCTTATUACT
301865505	101426	GTTTCTGCCTUACACGATTTGGATUT	101427	CAGCAGUACAGAAATTCTUGGAACAG
301878712	101428	GGCTTACCCAGUTGGCCAUT	101429	GATCTCGGGAAACCUGGAGAAAUT
301891979	101430	TGGAATATAGGAUATGCCAGCUGAAGA	101431	CTTTTGTGTCAUGCAGGTTGUCA
301918910	101432	GTGGCUAGGCCTGTUACAGT	101433	CAGACTUAAGCACCCACCAGUT
301935249	101434	GTCTTTUCCAGGGATGGACUCA	101435	TGGTGTCUAAGAGGAAGGTGTUCA
301940968	101436	CTACTGCUGGCACTAAGACTUGA	101437	GTTCTACAGGACUGGAATGCCUT
301943150	101438	ACAAUGGGAGGAAGTAGUACAACGA	101439	CGAACUCGCTGAAAUCCAAGAGA
301948281	101440	GCATGCTGGCUGATTTCCAUT	101441	AAGGCAGCUACATCCTGACUG
301949562	101442	CTGCGACCCAAACAUAATCATAGATTUC	101443	GACACTTGUGGGAAGCAATATGTTTUAT
301949789	101444	TGCAAAGCACCUGGTGGUAAT	101445	GTCTCTTTGGGUTGTAACTGCTUG
301955516	101446	GAGAGAAGGAGUTGCTUGCCA	101447	CCTTAUGGGAAGGAAACGAUGAAAGA
301961251	101448	CCAGAAGCUCAGTTCATUCCCAA	101449	CCCACCACTAUGACCTCTAATACUAAGA
301962183	101450	GCTCTAAATCAUGATCTGGCATATCUGA	101451	ACCTCGAAUCAGGGAAGAUCG
301969926	101452	CAAGCUTAACTCTTGAUGACCCAGAA	101453	GCTTTCTTCATUTTCCATGTCCAUCCT
301990526	101454	TGAACTGGAUGCTACGCACUC	101455	GGGCCGGUTGTTTATGTCUAAA
301994373	101456	GCCTAGCCTUGCCAACATAGUT	101457	GCCGGGATCAGAUGAAAAAGGTTTAUA
301999504	101458	CCCCTAACTUCCGGCTCCUA	101459	GAGAGAUGUGCAGCAGCAGAT
302004365	101460	CGCAUGCTUCAGGAGAACACA	101461	CTGTAGCATGUTGCTGTCGATUAC
302005074	101462	CAGGAAAUGAAGATTTGCUCAGCAAT	101463	CAGCCTTCAGUATGGCCCTUA
302005814	101464	CTCGUGGCCTCGGUCAG	101465	TGTTGATGTCCCUACTTAGCTGTTUAGA
302016854	101466	TTTCTTTACGTUCTGCTCTTTTUGCC	101467	ACATCCAAUCCGCCCAACAUAC
302021927	101468	GCACTTACCTCACUTAGTAATATATTTAAUGCT	101469	GTGGAAAAGTTUCTGGCTTGATUAAAGA
302023451	101470	ACCAATAAGGTUCATGCTCACCAATUAT	101471	TGAACAGGAGAUACTGGATGCTTUG
302029871	101472	CTCTGTTCUAGGCTCTGCTTTTUG	101473	TTCATTGAATCUACCATGTTGGTTCUT
302032757	101474	ACTGCAGUCTACGTUGCAACA	101475	GCTATCTTCUAACCATTCCTCCTTTUCT
302041350	101476	CCTTTCATGACCUGCTCTTTTTGUT	101477	TTTGGGUAGACATGAAGCUGGAG
302042720	101478	TTATGUAGAACCGCTACTTUGAGAACC	101479	GGTAGAAATAACUCAGCGAAACACTUAC
302044698	101480	CCTGGTGGUCACTGGAUGAAG	101481	TGTGTAGATATGGUAGTGAGCTCTGATUT
302049127	101482	CCAAAGCTGAAAACUGTAAGTCTAGUGA	101483	CAACCCTGATGACUCTCCTTTATATGTUT
302054590	101484	GTCCATGTAAAACUGCAAGTGTCATUAC	101485	GTCCTTTCCUGAAAGATGAACTGCUA
302083778	101486	TGAGTGGUGCCTCCTCCUT	101487	TGCTCCACCACGUTAAGGUC
302084272	101488	CAATGUGGCGGCTTGUAACA	101489	TCATGTTGTGUTTCTAGACGUGGT
302096772	101490	CAGCCCAGGCUCTUCACAAT	101491	CTGACCAGUCTTCGCGUACA
302107421	101492	CTGCTGGUCCTCAUCCAGAT	101493	GCCCAACGCAAACAUCTCTGAUA
302119660	101494	CATGTACACCACCUGAGTGCTUA	101495	CATGCAGGGCAGUGAAGAATTATUT
302137715	101496	TGGTGGTAGUGGTTCCACUGA	101497	CAACGTAGCAGAGUCACTGATUG
302141775	101498	GACTGTCTCUCTCTCCTTGTCUCA	101499	GAGCCCCAUCAGTTCCUCAC
302142779	101500	GCAAUCCCCATTCUGACAGGAA	101501	TCUAGCAACTTTATUCCACAGCCAA
302143481	101502	GGAATACACGCUTGCATTTUCCAA	101503	CATCCAAAAAGAAAAAGUAAGGCAUCCT
302156155	101504	GCTGTTTUCCCATCTGACTTUGAGT	101505	TCCTGGATCUGCTCTTCCUGT
302165899	101506	AAGAAGCACCGUGAGCUGAT	101507	CCTTAATCTCAGGUCTCTATTTTGCCUA
302169660	101508	GGGATTGCACUTAATGTGTAUCAACT	101509	TGAGACAACAUTGCGTGATCTUCA
302178770	101510	TGCTGGGACAAGUTGTCCTTAAUAAAT	101511	GCCAAATGCUAGAAAGGAGGATCUT
302181318	101512	TTGTTTTAGGAUAAAGGAGGCCTUACC	101513	GTATCAGAGAGACCUAAAGGCATTUGAA
302184737	101514	ATGAAGAAUAAAGACCCTGACTUGGAC	101515	GCCACATCUGTTGCAGGUGAA

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
302190707	101516	CUTGTTCTUGCCCCAACCAAAC	101517	AGTGAATTACAGCACACUGATGCTTUAT
302194718	101518	TTTCTGTGATGCUTTAAGTTGAGGGTUA	101519	GAGTTTGCAGGAUTGGTTTTUCAGT
302195640	101520	GGGAAGGGATUAATTTTTCACATGUGT	101521	GCTTGAGGUACAGGTUGGAGAG
302196986	101522	CCAATTCCAAUCTGTCTGGCUGT	101523	GGGCACAGAAUCTCTTTGTTGAAUAAAT
302204466	101524	CAGAAATGGGCUCCAACGUG	101525	AAAAACCCUGAACAGAAGCACUACT
302217250	101526	GGTAGCCCCUCAGCTUGAAC	101527	GACTGUCCCCAGGACATCUAC
302222337	101528	AATGACTCAUAGGACTTACTGCCUAGA	101529	CTTCAGTGCAUAAAATTCGGCUGT
302223380	101530	AGCACUGGACCATGACGUT	101531	GGGCGCUCTGTTTGUCGT
302225794	101532	ACTCCTCCAAGUTGGTGACUGA	101533	AGCATCTGAATTUAGATGACAAGGAGUT
302225843	101534	TCACAAAAGAGAUGACAGCCGAAUT	101535	AGCTTCACATTGGCUTCAGGTTATAAAUA
302235143	101536	TTGCTCTAAATGACUCGTCTGTTCUT	101537	CTGATGCAGAGAGUACAGCTGUC
302251740	101538	TGAAGAATTTCAUACCGTCTGCCTUC	101539	AGCTCAATUACGTTATGGTTCUGCAT
302253771	101540	GGGCCCAGGUATCTGGCUAT	101541	GCTGCTUCTCTCCCUGACC
302254754	101542	CAGGCGCUGGUAAGCAGAT	101543	GGCCCUGCACTTCUGGAG
302265511	101544	CAGGAUCACCAGCAGATGCUA	101545	CTGCTGTATCGAAUTTAGCTCTATTUGGA
302275121	101546	GCCATCUCAGCCTGTTGTCTUT	101547	TGTCTGUCAGAGAGGATCTUCCAC
302284694	101548	GGTCCAGCUTTTCCCCAGAUT	101549	ACTTGTTCGAGACUGTGTTCTTTTAUGA
302294946	101550	ACCTCCUGCCCAAAGCTCUA	101551	CTGAGTUCACCCAGGCUGAC
302297080	101552	GCCCAUTCATCUGCGACAAG	101553	TTTTGTTCTTUTCAGGAGCUCCAGA
302298317	101554	TGATGGAGAGGAUGATGGCTTUG	101555	CCATCCTGTUAAGGCCAGTTTAAAUT
302308380	101556	ACAATGTGACUTGACACGGCUAT	101557	CTGAAGATTGATGUGGAGAAGAATAGGUT
302318531	101558	TTCTGCATTCTUCTACAGAGGCUAAG	101559	TGCCACTTCAAUTGGGAATGTACAUAAT
302331361	101560	AGCTGAGUCACTGTCATUGCAT	101561	CCTATGTAGCCCAGUTTCTGAAACATUA
302334585	101562	CCCCGCUCTGCATTCUACAA	101563	CTGATTCCCTAUGTGCCCTAAAAAUAGA
302335621	101564	GCTTGCAUTGTGGATGUCAGGA	101565	GGTGTGATAGCUAGATACCAAACTUGT
302365729	101566	TTUGACTGGATTAUGGCCCCAA	101567	CCCTGGAGAAACUACGAACTTUCAA
302372548	101568	TTCTGGUCAACAATAUGCCACCA	101569	CGUTCCACAGAUGGCAGAAAAC
302377295	101570	GGAGAGACUGCGAAAGCTTCTUT	101571	CCCCAGTTTCCUACATCAAAAACATCUA
302386216	101572	GGTGGTTAUCCAGGTTGCUGAT	101573	CCATGGCTTCUGTTTCTCTCCUA
302426491	101574	CTGTAGCTTUGACAAAGATCAGGAAUCT	101575	CAAAUTGAGGCTAAUGGAGCAAAAGT
302431663	101576	GCCTCUGACCTTAGGAUGGAGA	101577	CUCGCUCGACCACCGAAA
302436617	101578	CCCCGUAGAGGCGGAUGA	101579	AGTCCTGAGUCCTTGCAAAUCC
302441696	101580	TGTTTTGAGCCAUTCATCTACTUGCT	101581	TGATCCCAUCAGGTAUCCCACA
302449744	101582	CGTGTTGTGGUTTGTTCATTTUCCT	101583	GTTCUGGAGAACCCAAGUGAGA
302460437	101584	CTCTAAAGCCCGGUCCTCUG	101585	ACATGCUAACCCATGCAAGUGT
302468535	101586	GTGTGGTGTCUATTAAGTTTCTCAUGGA	101587	TUCAGGAAACCACCATTUCAAAAACAG
302470016	101588	ACGCTGUACTGAACAAUAAAAACAAAGG	101589	CGTGCUGCCAGAAGAAACUGA
302475390	101590	CGAGGTGUTGGGCTUCCT	101591	TGCCACAAAGUGCUGGAGA
302476427	101592	CTCCAGGUTCCAGUCGAACA	101593	CCCTCTUCCCCACCCTAGUC
302476702	101594	AGATGGCCCUGGTTTTGAACUC	101595	GGTTCTUCCAACAAAAATGTCTTAUGCT
302478055	101596	GTTCATTACAUTTTTCAGATUGGCAGCA	101597	CCAUTGAAGCUCCAGAAAGGGAAA
302491233	101598	CCACCAGUGGAATGCACCUA	101599	CCTUCCCAGAAACAAACAAGUCACT
302521900	101600	ACTCCAACUACCAGCTGGCUA	101601	ACGTTTTGAAGAUTGGCTGAAGUCT
302524649	101602	GGAAAAGCAGCUGTCCTTTCUGA	101603	AGCGAAAACAGUCTCCAATAATCUGAAT
302524675	101604	TTACCACACAUTAAGACACAAAUAGCCT	101605	CAGTCACUCCACAGAATGTATAUGAGT
302527710	101606	ACCAACATTCTGUGTTCTGCGTAUT	101607	TGACAAAATTGCCUTTAAATAGCACUGG
302541298	101608	GCCAGGAGGACAGAUATUCCAT	101609	CAGAGCUGGCCAAGCCAAUA
302541733	101610	TGACTTUCCTTTAAGCUGGCAAACT	101611	CCTGGAGUGGGAUCACGAC
302553248	101612	TCTTCCGAGTUACAGGAATCGUAGA	101613	CTCTCGCUGAAGUGGGACAT
302561541	101614	CAGGTCCCGACUGAGGTCAUA	101615	TGCAGACAGCCUGCTTTCUC
302563128	101616	CGTGACACAUACACGTTACUGGA	101617	GTATTTCTTCAAUGCCGAACAUCACT
302564151	101618	GAGAGATUGGAGGAAGGCUGT	101619	TGACAGGGUTGCCTTGACUT
302571677	101620	GGTTTCTTGUCCTCACTCUGCAT	101621	GAGAAAGGCAGUCAAAGTGTUCAAAA
302572142	101622	CCATCACTUACCTGGGUACCAAC	101623	GGCTGTTTTACUGCTTATTTGACCAAUT
302574579	101624	GGTTUGAGAGCATGCTTUCCAAT	101625	CCCTACAAGAUCTGGCUGACC
302580064	101626	CACGTUGCTCAAGGUCACAAAC	101627	TCTTTCTTTCTCTCUCACTCTGTCTTGUA
302592688	101628	TCTTCTCCUGACCAGTTTCUAGCA	101629	GAGTCTTGTGGUCTCTGCTTCTUAG
302616103	101630	CCAGTTAAGAGGUAACTAAGUACACAGT	101631	GAAGACAGCTTUCCATCGACACUA
302621685	101632	TCCCTUCAGAGGCTGGTCUAAA	101633	ACTGAACAACCTAUATGCTCTGGTTTUC
302624184	101634	AAGAAGCCCAUGATTCAUCAGCA	101635	GATCCCCGAGGAUGTGGUT
302628740	101636	AGAGCAGCAUGACAGAGAGGUA	101637	GAAATTGCATTTUCAGCATTTGTTGUCT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
302640770	101638	GAUCACAUCAACACAAAACAGGCAA	101639	CACCUGAAGTUGACAGGGAGAT
302641739	101640	GCTGTCGGAUTACAGTGACACUT	101641	CCCGUAGCAGCAAGAAGTAGTUG
302647920	101642	CAGGTGACCUCTAAGCGGTUT	101643	AGAAGATGAAUTGAATTCUCACGAGCA
302648489	101644	CCAACATAGUTCATGCTCGUGAGA	101645	GCTGTCTAAAUGAGTGCTTTAUGGACT
302649094	101646	CAGACUGCCAAGGAACCCUA	101647	ACAAGACUAAAAGGCAACCAAAGUCA
302661673	101648	CCAAAUACCTTAUCAGGCCACCA	101649	GGCTTGAUGGAGCCTCATTTGAUAAT
302679131	101650	CCTTGCTGGUAGAACCCCTTUC	101651	GGTGUGACCCAATTGCAUACC
302690987	101652	CGCCAGAGCAGGUTGTAACUA	101653	CCGUTCAACAGGUCCACGAG
302698996	101654	GCATTAAAAGGAUAAAGAAGTGTUGGCA	101655	CTGCCTTTCTCUCATTCTAACTGTCTUA
302702495	101656	CCGTTGTATCGUGTTTGCTGTTUC	101657	GCTCTTTGACUGGCATATACAGCUT
302704072	101658	TGAAGAACTTTGUATGTTTCTGTAGCUGA	101659	GTCTTGCTATGTAUCTTTCCCACTGTUA
302709889	101660	CTCTCUCAAGCCAGTGGTUGT	101661	CAAGCTGAGAAGAUCTTGGATACUGAAA
302715945	101662	AGTAACUGCTGTGCTUCAAACAGAT	101663	AGGTTGAAAAGAUGCTAAGCAATTTUGG
302716872	101664	AACCAGUCACAACAGTGCCTUA	101665	CCCTCCAGUCCATCTCUACGAAG
302737551	101666	TTTCAGCUCAATGGCCUCCAT	101667	GCATTTGGTAATAUCCCTTTTCTGGUGT
302762039	101668	AGTAAAAGCTAAGCUAAGCTAAATCTUCACAT	101669	CGAAAGGCGAAUGCTCATTTTATATUGA
302766250	101670	GGAGAACCACACUGTCACATAACAAUT	101671	GTGTCTTCTUCATTGTTGTTTTGUACCA
302776730	101672	CTCAGAGAAGAAAGUTTAGGACTTGUCA	101673	GTCCAGGCUGAGAACCTTGUAA
302780121	101674	AGCGGTATCUCTGAAGCTUCCT	101675	TGCACTTTATTUGAGGGCAGAGAUAA
302790818	101676	TCAAAAGTACUCAAGAAGGAAUGAAGCA	101677	GAACTUCACCGGTGGUCAGAT
302795534	101678	GTGGCUGATGAATCUCCAGACAT	101679	ACCACTGTTAAGGUAGTCTTTTCTTUGT
302795636	101680	GCAAACGCATAUAGTAGTCTCAAGCUA	101681	AAGAACAGGAUGATATTGTTUCAGCAGA
302795749	101682	CTGTAAGCAACACCCUGGTCUT	101683	TCACAGTUCTTGAGCGUGAGG
302796177	101684	ACCACAATUAAAATCACCTCTUCCACA	101685	CCCACTCAUAAGCTTCTGATTCTTUACA
302805685	101686	TTGTTTAAAAAGGGCACUCGATTGUG	101687	CAGCAGCTGUTGATTCCGTUG
302812515	101688	AGGGTACACGUAATCCCATTTTTGUC	101689	GGATAGTAUGGAAGCCAACCUGAAT
302814351	101690	GACGTCATCUGCTTTTCTAATTCCUC	101691	GGCACTTAATGGUCTTTCATGGAATTUT
302814485	101692	CCAAACCCTAUAAACAGGCCTUAAGA	101693	GCGGUGAAGTCAATGUGCAAA
302819106	101694	TCATTGAAAGAGGUAAAACTGAUCAGCA	101695	AAAGGTCTACUAGATGTGCTUCCAAAAA
302822257	101696	GCCTAAAATCTTCUGCCGTTAAATCTUCT	101697	GGCTGCTAAAAUTATGTCTTGTGCUT
302833975	101698	AAAACATAAGTAUGCCCACACCTUCT	101699	CCACTTTTUACAGCCTTGUGAACAA
302836932	101700	CGCATGCUGCCTTTCTGATUC	101701	GACTCCTAAGGAUTCTCAATGTGGATUT
302837380	101702	CACAGCATGGAUTCGCTTCAUC	101703	GAAAGTGAACAAUGTTGGTTGCUT
302848298	101704	AGGAGACACUCCATTCUGACAAGT	101705	CGTCATATCAAGGAACUGGAGAAGTUAT
302850992	101706	GGCTTGTCCUTTGAAATCCCUGAA	101707	AGAACGAGCCUGTTCTGTUGAC
302865849	101708	CTGCTGACTACUTGACACGTCUA	101709	GCCAACTACUGGTGAATGCUGA
302867481	101710	GAUTGATGTGGUGCGCACAAT	101711	ACTAAAACGACCCACUTGTTCTGUAG
302874292	101712	AGAGGAATGUCAGCGCATCTUT	101713	GTCAAACTTTTAGGUGACCTCCTCUT
302875798	101714	TTTGGCTTCUAAACAGTCTGTUCCT	101715	GCACTTTTGGAGCUTTTGCCAATUAT
302877341	101716	CTGATGCTUGTTTTGCCGTUCA	101717	GCUAGTAAAAAGACUGACAAAGCAGGA
302883186	101718	GAGTGGCCUGTGTTGUCCAT	101719	GTCAUGCAGGCGGCAATUC
302894553	101720	TGTGTTGCUAAATCCATGGCUCAT	101721	AATTAAAGTACCGUCTGCTCTCACUG
302895148	101722	AATGAGCACUAGTCGAGGTCUCT	101723	GACATGGUCTGGATGCUGCT
302901641	101724	CATCCTCAGUAGCTTCAAACCUCT	101725	CCACCGUCCACTTUGAAAGAAAA
302902285	101726	AGAACAUCGACGATGAGUCCCT	101727	TGCAGGAUGGATGATACTCUCAGA
302914469	101728	AGCUTTGACTCUGCAAGAACCA	101729	ACAGGTTAAGUAAGCATCAGTTCTGUT
302920015	101730	GGAATTGGCUCTGGCAACTGTUA	101731	GTTTTCGCGGAGUGTTTGUAGG
302940836	101732	AAATCATCACUCGGCCAAUGGA	101733	TGCAATCACGGAACAUTTGATTCTUAC
302966788	101734	AAAUGGCCCAAAACTCUGACCT	101735	GCTCAAUGGCACGATUACCAGAA
302968032	101736	GTGCTTCATGAUGTTGACATATTCCTUT	101737	CTTGAGUACCAAGGCCACTCUG
302972689	101738	GTGGACUCAGCGCAGUGT	101739	GGAGAAGTUGAATGATCAGCUGGA
302977205	101740	ATCAATTCAAUAACCTCTTCCCTUGCT	101741	ACACCAGAGCUTCGTGTAGAAAUAC
303051272	101742	GTGGTGGCUTCTGGTCTCTUAT	101743	GGCTGTTGUACAGTTCCTTCCUC
303068272	101744	GGAGCAACCAAGACAUCTCTUGT	101745	AGCAGCAUGGCTCCAGATTUAG
303069847	101746	GGAGATGGUGATCTTGCAGAUGAA	101747	AGAAGCAATGGUTGAGGCCUAC
303077854	101748	ACCTATAUCCAAGCTCATTUAGACGGT	101749	AGAAATTCACUGCGCACTTUGAAA
303106616	101750	GAAATGGGUGAGTGGAGGACUT	101751	CGAAGGTCUGCATCTGTTCCUG
303123813	101752	CAGCCAGUGAAGAAGACAGUGA	101753	TTCCAACTCTAUACAAAGCCCCTAGUAT
303129296	101754	TTTCTCAAATAACCUGCATACCGTCUT	101755	GGATTTAGGUTGAGGTGGUGGAG
303130176	101756	CCCGTGTTCUTCCTGTTCAUCAT	101757	CAAATTCTCTAUAGTTAGTGGTCTUCGCA
303163413	101758	GCCATGACAAGGAAUTCTTTTTCUGT	101759	CAGCTATTCAAUCGGATCAACTCTCTUT

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
303176134	101760	CTTCTTCUCAAGACAAGGACTGGUA	101761	CGTCGTTCAUGACGAGGTAUGG
303178379	101762	AGGGCACACAAGUGTTGACUC	101763	GAGTGGGCATAUTTTCACCTCTTCUA
303186548	101764	GGGACACAAUGGCAAGATCUAC	101765	CCTCTTGGUGGTCTCCTTUCT
303192736	101766	GCUGAACCCCTGTTUGGAGAAG	101767	ACCCUCAAAGGCTAACGUGAG
303205548	101768	ACAGTTTCTUCAGAAATCCTGCTTUCAT	101769	TGTTTTTAGGGAAAAUGGAGCTGAUAGT
303208424	101770	AGATCCAGGATACUATCAGCTCCATUT	101771	CAGGTGCATUGGATATTTATTGACUCC
303220266	101772	TAAGGCTUGAGACACTTTGTATTTAUGT	101773	GTCTGCAAAUAGCATAAGAGCAACUG
303222067	101774	TGCAGACAGGAGGACUATCTTTUCA	101775	GCCTTACAGAAAUGCCCAGGTATTTUAT
303242735	101776	CTCTGTTTUGAGCTTCCGGUAGA	101777	GCAGTGAUGGTAGCTGCUGT
303249749	101778	TCTGTGUAACAGCAGCAUGGT	101779	GATGCCATUGCCAGCGUAG
303251635	101780	CACCAATTCATGUACACGACAGGUA	101781	AAGTAAUGGCCCAGGTAAUCGG
303256754	101782	CACATTACCTUCGGCTACTTGAUGAT	101783	AGCGTTCUGAAAGAAATACATTUGCAG
303257213	101784	ACTGTTGTTTTAUTTCCGGTCTAUGGG	101785	CCAUTGATGTUGCCGAAAAGGAA
303257458	101786	CCACTAUAGCGACCCCAUGT	101787	CACACAAAGGACCUGGCTCUA
303258340	101788	CCUCAACAGCAGAAAGCCTUT	101789	TAGAGATTAGTGTTUAGTGGACTATACATACUC
303260558	101790	GAGGCGGCCCAUTTTCTTUAG	101791	GCACCTCCUTCCTCTGCTUAG
303327969	101792	CCCTCUAAAGAACAGCTTGTCCUA	101793	TTGUTGAGGCTAUCGCAGGAG
303351631	101794	CTGTGGCAAUGGAATUCAGCA	101795	GACAACAAGGACAGGUCAGTUCT
303385073	101796	GGUCCCUGAGAGCCAGAGT	101797	GCCCTAGUGGTGCUGACA
303392503	101798	ATGCUAAGGCCCCUCAGAAC	101799	TCAATAGCTTGUGCCGCAAGUA
303400275	101800	GCATCUGGGATAACTACUCCCCAT	101801	ACAGCAGCAAUACGAGGACAUC
303402572	101802	GTTTCTTTAUCAGACCAGTCATUGCAC	101803	AAAGAACUTCAAAGUCAACAAAGCAACA
303406398	101804	TCTCTCCTUCGCCCTCCTUAG	101805	TGCATTCTTCUCGCACTCTTCUT
303410005	101806	CTTCCTGAGUAGCCGATGAGUT	101807	GCTCTCTUGACCCAGCTCUCT
303419578	101808	GTGGAUGGAGACGGGAAATTTUG	101809	GATGCGATUCACATGCTGGAUT
303421953	101810	ACTGATTGTGGGUTAAGATGGTATTUGAA	101811	TCTCTTGGUGTTGGCTUCGT
303427728	101812	GGATGTCGGGUGGCAGTAUG	101813	CAGCTCGAAAACCAUTTCTGTCATUT
303445556	101814	AACGTTTGGAAAUCTTTTCTACCUACCT	101815	TCTTCATCUCGAAACGTGCGAUAAAT
303458813	101816	CCACUGGACGCTGTCUCAAG	101817	AAGGAAGTGGUAAATCAAACTCACAUGA
303472489	101818	ATTCTTGGTCUTAATGGCGAGUAACAA	101819	CCUCAATCACAAUAAGACCACCAGA
303480444	101820	GTATTTGCAGUAGGAAGATGTTGGUCA	101821	GGCTTTGTGTATAUACTGCCAGAGTUAA
303481725	101822	GGAGCTGUGTTTCAACCTTUCC	101823	TGTGACTGUAAGTGAAAGTGAAUCAGT
303497222	101824	GGGTAUGACAGCATTAACTUCCAT	101825	ATTCCTCUAAACAGATTCUCAAACAGAAA
303515953	101826	CGTGGATGATGUAATGAAGGATTCTTUG	101827	GGCTGUCAGCAGUAAAGGAGAA
303516246	101828	GACAGCCAGAAGUTCAGAAUACAGA	101829	TGATGAAGTGATUAAAGTGACAGTGTUCA
303543103	101830	AGTTTTGAUCCGAACCTCGUGAA	101831	GACTCCTUCAGCATCTTCCUGT
303557509	101832	CGGTAAGTTUGGCGGCAGUA	101833	GAAACGACATUGTCACAGAGCUT
303583139	101834	TGTGGAAGATUGCTGTGTTCTGTUAT	101835	CGTAAAGGUACGAGUGACGGAA
303594928	101836	CAAAGCUGCCCTGTTAUAAAAGCC	101837	TTTTCTATAGACCUCCTGTGGUCAGT
303749660	101838	TCTTUATCCAGAGCUCAGCAGAGA	101839	GTAGCGTUCCCGCTGTTCUAT
303756423	101840	ACCCTGUACCTGACCCUGAAA	101841	GATUGGCCACGGCTAUGAGT
303761911	101842	GACGAGGAAAAGAUTGGCUCAGA	101843	ATCAGAUCGCACCGGUGAC
303769400	101844	TGAATATTGGGUACCAAGGAGCCAUA	101845	CACATTAAGAAAAUGGGAGCGATTUGAA
303772478	101846	TTCATGACUGGAACCTGTTUGAAAAAG	101847	TGAAAGUTGACAGTTTUGCAAACGA
303775477	101848	GGAGCTTTGCUTCTAGAACTTUGCT	101849	CCATTCAATGTTUTGGATTTGCTTCUGAT
303818800	101850	GCCTGACTTCUTTTCTACTGGTGUA	101851	ACTCAGCAAUCTGTGACAGUCC
303820640	101852	ACTCAGGGAAAAAUGAATTTACGTGCUA	101853	ACUCAGGAGCCAGAGGAUGAG
303822219	101854	GAAATACCTCUGCAAGAGAUCCACT	101855	ACCCUGGACCCACTCAUCAA
303822861	101856	GGACCATTUCCAGCTCTTGUG	101857	AGGTGAGTAGAAGAUAGGGATGAAATGUT
303829326	101858	GTTCTAGGTCUTCTTTGCCGGUT	101859	TGUTACAGCUGGCAGGCAAT
303837026	101860	TCTGCGCUCTCCACGTCUA	101861	GGAGAGTTGAUTATGTTTGCAATUGCT
303845083	101862	GATCCTCCUTTCTAGCATTUGGCT	101863	TTTGAAGUGCCTCTGGCUGAA
303848648	101864	CCTGCAACAGAUGTGGCUGAT	101865	GAAACUGGCCAAAACCATCCAUT
303850764	101866	CATGGAGUCTGAACGUCGGAAA	101867	GTTAAAGGTCUGTTACCCTAAUCCAGT
303857764	101868	AGGAAGTTUGCAGCACAGAAGAUA	101869	AGCUTTGCAGUCCAAAAGGAAAC
303882817	101870	CCATCAGCUCTGTATGGAACUGG	101871	AGTTGCTGACUTCTTTCTTCCUGAA
303953345	101872	CTCCCAUGGGCCAACUGAAA	101873	TGGGACATGGAGUTGTTAAAAGAAUCT
303962554	101874	TTGCAACTCUCAAGGCCTAUAAACAT	101875	CGAATTGGAGAUCAGGCTTCTGTUC
303970879	101876	ACCTGACAGTCUTTCAGTGCATTUT	101877	TGTGTTTGTUCAGATCCAGCUGT
303971042	101878	TCAGGAAATTCUCCCTGCTCUACT	101879	CACCCAGCAUATCATACCACAGUC
303975722	101880	GACCAAGATUCCAATAAGCCTUCCA	101881	TTCTTAATTUGGAGAAAATACTGGCUAGAAT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
303984230	101882	TGGCTGAGUGGCGTTAUGG	101883	ATTCCTTTCTUACATACCAGTGTUGCT
303995073	101884	CCGACCUGTGCCCTUCAA	101885	ACGACCTUCCTCTTCCUCCAG
303998678	101886	AGUCTTGTCCUGGGACCGAA	101887	CATCTGCCAUGGACATGCAAAUC
304001624	101888	AGCAGGUCACCTTAATTUGGCT	101889	TGGGATCATTTUGGCAGTAATTTUGAGA
304003029	101890	AAAACCACUTTACCTTAUGCCGAGT	101891	GATTAATTTTCTUCAGTCTGTGGTUGCT
304004750	101892	GGCAUGATTTTAATTCUCCCACACA	101893	CAGACAGAACAAAAGUTAGCAGUAGAGA
304005966	101894	CAGCTCATCAAAUTGCTGGTGTUC	101895	TGCCCTTGGGUAAGCTTAATUCC
304006421	101896	AATGTGATGAUTCTTCGGTAUGCCA	101897	GUGTTCATGAUCAAGGGCACAA
304006583	101898	TCUCAGTTAUCCAGACGGACAGAG	101899	TGGTGATTUCAAGGAAAATGTGTTGTUG
304012324	101900	CATCCACAAUGTTGTTGCUGAGT	101901	TTTTACTTGGAAUCCAGGCACUGT
304013814	101902	CCAAAAGGTGCUGATAATTTCCUGAAA	101903	CATTGTTCCTUGCCCTTTGTUCT
304013849	101904	CTTTGCCTUAATAAACCCGUGCT	101905	GACCTGAAGCAGCAAUTACTGTUG
304016435	101906	CACCCAGCGUACATACATTTUAAAACA	101907	ATTTTATACUCCAAGGCCUGGCAA
304017398	101908	GTTCTTTTACCUGCCAATGTTTCUGAAA	101909	CAGATGATGGUGATGACAAUGCC
304018953	101910	AGACATACTTGCUTGACTTCCAUAAACA	101911	CGAAATTTACCUCATTGGATUCAGCAG
304020444	101912	CAGCATCGTUCATGGCAGTAUG	101913	TCCTACTTTAGUCACTTTCATATCAGUCACT
304022779	101914	TCCTCTTTUCCCAGGTTGGUAAAAC	101915	GGGCTTACTCUCTGATATTCTCTGTUA
304091090	101916	ACATGGTAAGAGGUAAAGGACCUGT	101917	GGAAGAAAGGTUCAATACGGAAAACTUG
304098327	101918	CTCAGGAATGUGCTGTTTACTCUCT	101919	ACAAGCATGUAAGAATTTCTCUAAGGCA
304166021	101920	GGAGTTTUCACCCCAACCCUT	101921	GCCCCGGUGAGTTCAAAGAUG
304170277	101922	CAGCTGUACATCGACTGUGAAAAG	101923	CAGAUGAUCCCACGGAGCAG
304176184	101924	CGGAGACAACAGCGUGTTUGA	101925	TGGAACUTGTCAUCAGGCACAG
304181343	101926	CAGCUTTCCGCAUCGAGGAT	101927	GAGTGGUCTTTCCGCUCCAG
304193632	101928	AGTGAGTGAGAUGGGAGTGUCA	101929	GGATGGUGAACATCTUCCGGAAC
304194449	101930	CCCUGAGGCAGAUGAAGAAGAC	101931	GAGAGCUTCTUCCACAGACACC
304204634	101932	GCCUGACCGUCCAAGGAAAG	101933	CGTCCAACUCAGCATTCUCCAT
304210428	101934	AATGCCACGGACUACUGGAC	101935	ATCTGGCTGTUCAAAGCAGGTUA
304232467	101936	ACCATACACGUTTTGGTTTTCTGUCT	101937	TGCCGCUCCTUCACAAAGAT
304240388	101938	GGGCGACUACCUGGAGAAC	101939	GCCTCTGGUCAAAGCTCGTUT
304288819	101940	AACAGTGTTGAGUTTAGGAGGCAUT	101941	TCTCCAGAAGUTGGACGTCUCA
304300912	101942	GAGAGAGCUGCTCCTUGAGAC	101943	TTATTCTTCCCCUATGGCTTTGAACUT
304307934	101944	CTGCAATTTACCCUCCATTTACATCUCT	101945	CCATCTTUGTCATGGUCAGCCT
304331779	101946	CTATGUGCCCAAUGCCAACC	101947	GTCTTAGAAAGUGGCTCCCAUGA
304374767	101948	CTTTTAGTAATAGCUTCCCCAGTGCUT	101949	GGGAGAATCTGUCCTTCAGAATACTUCT
304383326	101950	TGAATAGTGGGAAUGCCTTCUGG	101951	TGACAAAGGACUTCTGTATGTGTTTUCA
304388306	101952	ACGGCGAGAUTCGACCUG	101953	CAAACGCAAGUCGTGGAUGA
304390514	101954	CCACCUTACTCAUCCACGACT	101955	CAGGCAGCAGCCUCUCT
304392555	101956	GTCTAAGGATUGACAGACACUCAGG	101957	CATTGCACAGAACAUGGTTUCACA
304413905	101958	GAGGAAGCATTCUGATTTCACATTTCUC	101959	GCCTTGACAUCCCTACTATAGATAUCCA
304416803	101960	GGGCAAATTAAUTCCCACCTUAACT	101961	GGAAGAGAUCAAGCACCTGAAGUC
304425230	101962	CTTGCAGGUAAATCCAGAGCUCA	101963	GCTGGAAAGTUCCATCTCTGATTCATUA
304430848	101964	GGACAGAAGAGAAUCTATCCAAACUGAA	101965	GGGAUGCAAGAGGGAUGACC
304430875	101966	CGGCCACTUACAGCTGACAUAA	101967	TTGTTTTATCAUGAACATTTATAAUCAGGAAGG
304433322	101968	GGCUGGGTGCUCACCAT	101969	CCCAGGCUGCCTUGGAC
304436111	101970	TTGGTGGAGAAGUTGGCCUT	101971	CGCUACCAGCGCTUCCT
304436290	101972	CGCAGGAAGCGCUGGUA	101973	CUTTGCCUCAGACCCCAAGT
304438287	101974	AAGTAATAGUGGGTGCTGCUGAC	101975	TCTCAAGCUCACCUGGGAAGA
304440057	101976	CAGATCTCAAAGUCATCCTCAUCCT	101977	GCCAUGGACGCCTGCUC
304440530	101978	GGGCUCCUCACCGAAGT	101979	CUGUGAGCGAGGACCAAGA
304442518	101980	CCTCTUGAAGTCGCUGGACAA	101981	GACACTUGGCTTTCTCUCCCA
304455941	101982	TGAACAGTGGAUACTCTGGGUGA	101983	ACTGATGCCGAGUGTGACTCUA
304473740	101984	GGTTTCTCGUAGCCTGCTGUA	101985	GTTGAATAAAGCCUGTTACGTUCCC
304569401	101986	AAATTTTACAUCACAGCCCTCTAAGUGT	101987	CTAAAGTCTTGGCUCATGGAACTATUG
304573280	101988	AGCTTTCCUCCAAGGTTGTTUGT	101989	CUCGAGCAGAGTUGGAGAAGG
304575889	101990	AGCTGGCUTGCAGAATUCCAT	101991	AGCTCAAGAAACUGAGGAGTTTACATUT
304582756	101992	CTCCTGAGCAAUCCGCAGUA	101993	GAGAAAGCAGCAUCACATTATGATTGUT
304590642	101994	TTCTTTACCUGACCTUGGCAACA	101995	ATGAGTCTTUCAAGGACACAGCUC
304596938	101996	GGGCTATTTUAAATGCCACAAUGGT	101997	CCCAAGAGACTAAUGAGCAATACACAUA
304602434	101998	TCATTAAACTGTGUTTTCAGCTCCTCUT	101999	CTCCAGUCCATCCTGTCUGAG
304604328	102000	CATCCTTGAAUAACGCTTTGUCCAAA	102001	GUGAAAACAGACAUGGAGAGCAC
304606183	102002	CAGGTGATTATCUTACATCCAGCCAUT	102003	TGCCAAGAACAAAAUGAATUACAAACAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
304609638	102004	GATAACAAGTGTTUTCCTTTGCTGGUAA	102005	ATGGTTTTAAACUCATGACTTATCACUGACT
304614255	102006	TGTAACTGCUGACATCCUCCCT	102007	CATGCGCUTTGCATTGUCCAT
304614594	102008	AGGGCTCUCGTGTGATCTUCT	102009	CCAATGGAAUGACTATGUAGAGAGGAA
304616799	102010	GGCCAGGUCAGCAUCCA	102011	CTGUCGGCCCAGGACAUC
304620750	102012	CTGTGTGGAUGAAGCTGTTCUG	102013	GTTCACCGUGCCATCTCUGT
304630651	102014	GATGCCCTUGTTTGGTGAUCAG	102015	ATGCCAUGACCAAAGTATTCTTCUGT
304636065	102016	ATCCACTGCUCCAACTGGTUT	102017	CTTTGTGATTGGTUTTCAGTAGAGATGUC
304648248	102018	GCTGAAGTUCCTAAAGTGTCUCCT	102019	CGATGGUGGTCAGAAACUCAGAAA
304651168	102020	AGCAUAACCACCAAUAGAAAACAGGAA	102021	GGAACAGTUCAGTGCCCTTCUG
304659463	102022	TUTCGACUCACGCCCAACA	102023	GAUAGGACGACGUGGAGACC
304661152	102024	GTTAACTGCUGAGCCCAGGUT	102025	AGACAGUGTATUCCAAACGCAGAG
304671880	102026	GCUGACCAGGTTCUCCAAACAG	102027	CTGGCUCCCGAAGUGAAACA
304684577	102028	ACCCACUGGCAGTTGTGTUC	102029	CTCTTCAGTUACCATGGTGATATUCCA
304701890	102030	ACATCAGUATCACACUCACACACAG	102031	CTACGAGCCUCAGCUCAACAG
304723723	102032	TGCACTUACCCACAAATACAATGUGA	102033	CATGCACAGUGTCUGGAAGGAA
304729426	102034	TGCTGAGATAAAUGTCCCAGGATUG	102035	TCAGTTTGTUACCACTGGAGAATCUG
304731908	102036	AGCTGCUGAGCTTTCTCTTUCAG	102037	ATTTCCAUGTTCTCUGGGCCAA
304735387	102038	GCCCAUGGACAGTGGAAACUA	102039	GAGAAAACCGGAAAUGAUGCCA
304740983	102040	TTTGTGTCAACUTGGCTTTAATUCGAG	102041	CTCAGCCTACAUTGTCATTTTTCTTGUT
304748200	102042	CCTGTTCCCCUCTCACTCTCUT	102043	TCACTGAAGAAUAGCTATGCCATTUGAG
304752189	102044	GGTGGTCAUTGACCTGCUCA	102045	GATCTCTCCCUTGTCTCCTCTCUT
304766493	102046	CTGGCAGAAAGCAGCUTTGAUG	102047	CACGUAGGAGAATGGGTUGGG
304767668	102048	GAACCUCUGGCAGGAGCAAA	102049	CAAGCATGCUCAGCCAGUG
304778792	102050	GGAATTGTCTUGATTTCTCTCCCUGAA	102051	CACCTTTCTCAUACAGGCTTCUCC
304779296	102052	GAAGATACTGUTGATCCCAGUGGAT	102053	GAATGGCACAGGGUACGUCT
304784711	102054	CTGGAAUTTGAGGCUACCCAGT	102055	GGAAUAAACCACGUCGCACAGA
304785317	102056	TCCACCAAUAGTGAGCUCCAAGA	102057	GCATAAAGCCTUTTAGGCATACACUGT
304787258	102058	AGCCTACTTACCUCTGACGTGUT	102059	CTTTTCCAACUCCTCCTCCTGTUC
304789820	102060	AGACGGAGCAUTTTACACCTUGA	102061	AGACAAAAGCAUAGCAGAGTCCTUT
304810906	102062	GCTCATTGCCUTTTCACAGAACUT	102063	AAGUCACTTCUAAACAGCCAGACAG
304814428	102064	GCAGAUGTGCUAAGAGAGGAGGA	102065	GCTGTCAACTUAGACTGTGCTTTUT
304814675	102066	AGCGTGUGATCAAAACAUACAAGAAAAT	102067	GAAAGGGUCCGTCAGCAUGA
304821234	102068	AACCCUGTTGCCAUGACAGAA	102069	CACTTCCTGCCUGGTATCTCTUAC
304833090	102070	CAGGACCUATTGAGCTCUGCAT	102071	TGTAAAAGUCCCACTCCAAUACACAC
304840623	102072	GGGCUTGGTGTTUAGAAGAACA	102073	CCCTGTTGCTUGGGATAATAATACUCAT
304844842	102074	TGAAAGATCCAUGGAATCTCTCCAAUG	102075	CCCAUATCCTCCGUCAGAACAAAG
304873343	102076	CTCTGTTACTATTUCCTCCTTGCACUT	102077	CTGAGCAUCCCAAATGATATTGUCC
304901761	102078	TCTGGTATAUGGACGCUGGGA	102079	GTTGACATUAACAGCAAGTTTUCAAAGG
304971504	102080	GGAATUCCAGGTACACUCCCT	102081	GCATCACCAAUTCCATCCTTGUCA
304981287	102082	CCAACUCAGGGCAGGAAGACUA	102083	GCTGAACUGAAAAGAUGAAAAAGGGAT
304984106	102084	ACTGTAGTTTCTUTGTGTCTTGGTUGT	102085	GTTGTCCUCCAGGCTCAUCAT
304997576	102086	CGTGGGAAGUGATCAAATGCTUC	102087	TGCAGCCCCAAUTCCUAAAACA
305007169	102088	TGCTTAUGACCCGATCCUCCT	102089	GCTTGCCUGCCTTGUACCAAT
305017555	102090	CACAGCTGUAGTCTTCCTCUGA	102091	CAGGUCCACAAAAGGUGGCT
305022289	102092	GCUCAGAAAGGGAGGAAUCGG	102093	CCCUTTAGCTUCCAGGAAGGT
305030597	102094	CCTTCCUCACACTTCCTUGAACT	102095	TGTTTCTGCTCUCTGCTTCCTUT
305048918	102096	CGACTCGUGCTGTCCCTTTUT	102097	CCUACUCCCCACAACCCAGA
305053853	102098	TGCAAAAGAUGGGAAACCUGGA	102099	GCGGATGCCUTTCCATTGATTTTAUT
305110972	102100	GGAAACCUTGACCAGUGACCAAT	102101	TGTTTGACAUCCTCCCCAUCC
305134203	102102	CAGCTGCATUGGGAGGATGAUAT	102103	GCUAGACACAGCUGGCACAG
305169528	102104	ACTGGUGAAGCCAUCCCAAAG	102105	GAAGACUACAACAGTGAGCUCCAA
305179455	102106	AGCAGCCACUTTTCGACCUC	102107	GTGAGTTGCACUGGGTTTTTGTAAUA
305185762	102108	TTTCAGGAGTTUACTACCTGCTTAAUGG	102109	TGTCTCAGAUGTACCAGAGTTUGGA
305189078	102110	GGCTGACGUGCTTCTGAAGUT	102111	GGGAAAATCCAUTTAGATGTACUGGT
305196559	102112	ATTGCACAGUTATAATCCCUCAGCA	102113	GTACCAAGCAGAAACUACTACAGAAUGT
305198456	102114	CTTGCTCTUGTTCCTGTUCCAGA	102115	CCTGATGTGTUATCCCAGGAGTUG
305199938	102116	AAGTAGATUAGCAGATTTTCTGUGCACT	102117	CCTCTGACTTTUGCTCCTGTTCATATUA
305203765	102118	GATGATTTCUCCCCTTCCAUCCC	102119	GCCAGGUCTGGUACACACAAT
305212205	102120	GGGCAGTTCUTTTGTGTGTTUCA	102121	GGTCCTTCAUGTGCTGCTUGT
305216725	102122	CCCTAGGGCUGAACATGCUT	102123	CCTTGGCUGACCAATGTCUGAG
305231466	102124	CTTGGTGTCUGCACTCAAUGG	102125	CAGCCAGCUAACAACCUCACT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
305236647	102126	AATAAACTTGCUGATCTTTCCTCUCACA	102127	CTGTGTTGTUACCCTGTCUGCT
305252685	102128	TCTTATGGGCUTCCGTUGCAAA	102129	GCTTTCACGAUGTTCCCTCCUC
305253150	102130	CAAGTGGCCGUGACAGTTUC	102131	GATGCTCUGGCAGTGTUGAAAAA
305256527	102132	GGAAGCAGUCCTCAGCCTTUC	102133	GAATCAATAACUCTCTCTTCCCTUCCA
305262984	102134	TCTCTAAGCCUTTAAAAACACACTUGGT	102135	CCAATGAAGAGUTTCAAGCATTTCUGAA
305269294	102136	AGCCTGCTTAUCTTTAAGGCATUGT	102137	AGAGCAAACUTGATGCAGUGACT
305273589	102138	CCTCTTTCUGGTCTTGGAAUGCT	102139	CCATCTGAAAAUCGGGAGCTCUG
305278422	102140	AATGTGCATACAAAGUTTGTCCTTCTUG	102141	ACTTCAGCUCACAATTGTAATGCAUAGT
305288088	102142	CTCTGCAGGAAGUCCTTUGCT	102143	CCTCAATGATGCUCTTCAAAATGCUAA
305288711	102144	GAGACCCGUGGGTTTGTUCT	102145	GAGGATTTTGGCAUCTGGTGATUT
305300367	102146	ACGGCAGCAGAUTCTAAUGCT	102147	GCAGAAUTCCUCCAGAGCCAT
305304782	102148	CATCCTGACAUCCCTCAUCGAA	102149	GGGAGAUCACAUGGCACACC
305309899	102150	CCTCAGCUGGCGGAGAAUG	102151	CTGAGGACCUCCACCUCCT
305315326	102152	CTCCCTGCCUAGCTGATCUCT	102153	CCTAAAGGUGCCACACAAACUCA
305338851	102154	CCCATCAAAATGUCAAGTGCTTTGUAA	102155	TGGAGTCUCAGCCACCTCUAC
305349186	102156	GTTCTUCAACGTCAUCCAACCAA	102157	CCCATCCTGATAUTTTTCCTGGATTTUC
305363493	102158	AGCTGGCTTUCTGTGAGCAAUAT	102159	GGACUTGCTTTGATUCAGAACAAGAA
305367500	102160	CATGACAATGCUAGAGACGTCTUCT	102161	CACCCCAGAGUTCCATAAUAGAACAA
305390854	102162	ACCTGTTTACAAAUAAGCAGAGUGGAAA	102163	AAGGAGCUGATTTCUGCGGAT
305395790	102164	GAAGCAUATTCCTUCCGAGCAAG	102165	CAGACCATATUACCATCGCTGAAUGA
305396438	102166	ACTTCCUGCCAGGGAGTGAUA	102167	AGAGGGUTAGCTTATUAGAAGACACCA
305399730	102168	CTCAGCGAGGCUGTGTTCUAA	102169	ACATCCAAGAGGAAAUCAGAAAAAUCCA
305400176	102170	TCAGCGUAAAGCAGGUACACA	102171	GAGAGCCCUGCATGAUAAGCA
305400709	102172	GCTGGCTUGTGCACTCTUACAT	102173	CAAAGCCUTGUCCGAGAAAACC
305403909	102174	TCACTGAGGUAGGAATGAUCGACT	102175	CCTAATGAAUGAGAGTTCTGAGCTUCA
305414115	102176	GAATGTTTTGGTAUTTAGCCAGTTGUGT	102177	CGGTTACAAGAACUAGAGAAGAATTUGGT
305417542	102178	TCGTGTTCTUGGTAAGCACUGG	102179	CGGUGGATGAACUGAACCAGAAA
305418697	102180	GAACCCUCACCTGCATGTUGA	102181	TGGCTTTAUCAGAACTGTCAGUCC
305421301	102182	CAGCTTTCUGGCCTCCAAUAGA	102183	TGCUTTCACTAUCGCCGAAACA
305424981	102184	CCAGTGGCAAGCUTTATCAAAAUCT	102185	GCAGGAAAAGAGUGAAGTGCUG
305425390	102186	GGAACACUGCCATGAGAAACUG	102187	TUGGTCTCAAUGAGCGACAGG
305426153	102188	GGCAATATTUCAGGATGATGTCUCCA	102189	GCTCCTUAGAAGCTGUGCAAGT
305429443	102190	CTTACCTGAAGAUTGTCCACCUGA	102191	TGCTGAAAUCAGTGCTUGACCAA
305430502	102192	CAGTCTTGGGAUCCCCAGTUC	102193	GCCTTTCATUCAGTTATTCAUGCCA
305432639	102194	CCAGCAGCAGGUTCTCATUGT	102195	CTGUGGGAAACAGTCTTUGCAG
305433045	102196	GACTGGACCUCTTCCTGATGAAUT	102197	CGAATGGUGCAGAGTATAGACTUCC
305435223	102198	GGCCACTUTGTGACTACUCCA	102199	CTGAAACCCTGAUGAAGTTCTTAGAUGT
305438622	102200	TCTGCAATUCCTGAAGCTUCCC	102201	AGATGATGUGAGCAAACAAGUCAAAAC
305442465	102202	GTCCACCAAUTCCGGUCGAA	102203	TGCTTGTATCTATUCAGAATGTGACAUCA
305443079	102204	TGTTTGGGTCUGTGTGGAAAUCA	102205	GCAGCAAUGAAGTCAGCAUACAAC
305443255	102206	CTGTGCUGCGAAAACCTTCTUT	102207	GTGAACTUGAAGCCCAATTCTUGAG
305447106	102208	AGGCAACAUAAGCTTUACAACAAGGA	102209	ACCTGACATAAAAGUCAATGACCTUACC
305447579	102210	ATCAGAGAGAGCCUTCTGGAUGA	102211	GCAGAGCCCUCCTCCAGAUA
305450852	102212	TCGGTGGGAACUTTGCTCAUC	102213	ACAAGTTCTATAAAGUCCAGGAAGCAAUT
305453226	102214	GGGAGCGACUCATCTCAGUCT	102215	CACCTUGACCCCTTGGCTUAT
305465942	102216	GTGTGCTGGUGATTGAGCTTUT	102217	TCCTTCAUGGCAGTCCAGTUG
305472088	102218	CCAUGAGAAGGTTCUGAGCCA	102219	AGGACCTCAUTAAAAGGAAAAUCCAAGT
305476986	102220	CACAUCAACCCCTACCUCGT	102221	CCAAAATGCTTGUTCTAAGGGAAAUCT
305480200	102222	TGGATCTGAUGCCTGGCTTUC	102223	CCUGCAGAGGAGAAGCUCAAAAT
305527336	102224	GCCACCAUGATCTCCCTCUGA	102225	TCAACATTAACUCCACCGATATAGCUG
305528362	102226	CCATCAGCTAUATCGGTGGAGUT	102227	TTACTCCCAUGTACTATTACAUAGGCA
305536618	102228	TGCUTAATTACTUCAGGCACCGA	102229	AATACCACGACACGUTCGTUCT
305537880	102230	GCUCTCCCCUGCAAAACAGAAT	102231	TTGATCTACTTUATCGCCTGCUCAC
305540868	102232	CCCAAGGCCGACUGCUG	102233	AGGTTAAAAAGGCCACUGAAATGATUG
305547036	102234	CCAGGTAACTUATCTTGCAGCUGAT	102235	GTGGCTTTTAUGGGAGTTACCCTAUT
305551647	102236	TGGCAGAGUAACCAGATTAGUAGCA	102237	CUCAAACGGACAUCACCAACAG
305556322	102238	ACATTTCUCCCAACAATCACAGUAGG	102239	TCTCTGGTTTCAGUGAGTTATACCTUCA
305583982	102240	GTAACCCAACAAAGGUGGTGAAAUT	102241	CACCTTACGTAUGGTCTCTAAATCCAUT
305593567	102242	AAGGAAGCTUAAGGCGGTUGT	102243	GGAGGCAUCAACTTGCAAUCAAT
305596595	102244	GCCATTTCAUCACCCAGTTAAUAAGAAA	102245	TGATGAAAAGAAUCAGGCACUCAGA
305599079	102246	AGATGACTAUGATGCTGATTGUGAAGAC	102247	GCTCCTCAGACAAAAGUAGACAATCUC

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
305615618	102248	TTTCTTAACACTCUCCTATCCCTGUAACT	102249	AGTCTCTGCUGGACAATTTGAAAGUA
305621970	102250	TGTACACACACGUTCATCTCTTTUCA	102251	GCATTTGCAAUTGACCTGTGUAAAGAAG
305624700	102252	TCACACAAGAGGACUGACCCUAT	102253	AAGAACAGAAGGAGAAGUACTTAGGUCT
305630293	102254	AAGGGAGAGTUCAGAAGGTAATATGGUAT	102255	GCCTTGTCTAUAACAGTCCCCTUAG
305633496	102256	GCTTTACCTGUCCTCCACCUT	102257	TTTTTAGGTCAAUTGGCATGATTTUGCT
305640540	102258	GATGGUGAAAGGAATGCUCCAGT	102259	GACAAGACAGGCUGGACGUA
305647661	102260	GGAGCACAUCGGGAAAGATGAAAAUA	102261	GTGGCCGAUCTTTACTTTUCCAGA
305651691	102262	TTCCTCTAGCAAAUAATGACCCUGAAC	102263	TCAGATTCTCUGAGTTCTCATCTUGGAT
305651721	102264	TGAGAAAAACAUGACGGTGAUCCA	102265	ACAAGGCAAAUCCAGAAGTGTCATTAUT
305653145	102266	TGATCCCCTTUAATTGTGTCTCATTUGT	102267	ACTTAATTGTTAAATUTCCATGAGTGAATUCAA
305661436	102268	GGCAGGTTTTUATTTACCGCCTUT	102269	AGACAAAUAACTAGUCACAACAGACGAC
305665606	102270	TCACATCAAGATTUGTTCTCTGAAGTUCT	102271	CACATCCTGUCCTAGAAAGCUGAT
305674229	102272	CCCAGCTCUTATTTGTCCCTUGT	102273	TCTGAAAGGAGUCCATCCACCUA
305675697	102274	GCGATTCTCUTCCTGCCUGAA	102275	AGGGCACTUGGATCCCGUA
305697237	102276	AAGCAAAGAACAGUCTCCTUGAGAT	102277	CAACCGGUACTGGUCAAGGAC
305703288	102278	CCTGGAATAGUGGAGGTGCTUG	102279	TTAAGGCCAGTUAAGAGAACATGTUAGG
305719241	102280	AGGATTGTTCAUACCACAGGTGTUC	102281	GCCCTTGUGCCTCAUCACAAA
305731430	102282	GCCGTGUTCTGGGUGGAG	102283	CGGTAGCCAUAAGCACAACATTUAAAG
305745974	102284	GCTGACAGUGGCCTTCAUCAC	102285	TGGAAATGACUAGGGAATGGTTCAAAAUT
305755393	102286	GGGACACACUGCTGAUGACAG	102287	CTTAGGACCTCCAUCTTTACCACCUA
305768974	102288	TGGGUAACUGAGAGCAGAGGT	102289	CACAAAAGUGGAAGAATCGTTGAUGAA
305770045	102290	AGCTTGGUGAACGGAAAGGUT	102291	CCTATTCTGATUGGTATGGCTCTACUCAT
305778514	102292	CACAAGUCTCATTTUGGGCACAG	102293	CTGAAGUAGCAAAAGGAACCCUGAA
305787949	102294	GTGTACTTUGAGCCGTGAAAUCC	102295	ACGTGAACAGAAUTTCTACTGAAUGAGT
305788085	102296	CTTGGTAGCCACAUTCTTGAAGTTTUT	102297	GCCTTTACTUCACCATTCAATTTTCUCT
305797489	102298	GGGACACTAATGAUATTCTCTCCCAUT	102299	TGGCTGGUGAAGGTCCCTUA
305807650	102300	TGCAAGCAGGGAAUGGAATUCA	102301	CCAGCGACACCUGGATGTUC
305815511	102302	TGAACATTUCCCACAGTGUCACC	102303	GGTGTTUGAGAGGGCTTCTCUT
305816919	102304	CCAAAUGATTTCAAAUGACAGCACAGT	102305	CCACATATCUTCCTCTTGUAACAGGGA
305827655	102306	GATTCCCTUGCGGAGCTTUAC	102307	GACCUCTCATUACACACCCAAGAC
305859235	102308	GCCCAGGCUCTGTACCTUC	102309	TGTCCGCAUGGCCTTTCUT
305878183	102310	TTTTGGTGTGUTTGTCTCAGATUGAAC	102311	TCCTGAGGUGTGCGCAUAAAAA
305892028	102312	CTTCAGGUGGTGGAGAGAUGT	102313	CAGAGACTCACCCGUTTATAATAGTTCUT
305896794	102314	GTTGGCAUGGCAACCAAGAUA	102315	GCAGTTTGTCUCACTACAGCTAUGT
305913690	102316	TTCATGAATTGCCUTGTAACCTAUGG	102317	ATTTTAACACTUGGGACTGGTTCUCT
305916191	102318	CAGTATCATTGAUTCGCAACAGUGAC	102319	GAACTTTCACAAAAUGGATCAACTCUCA
305919165	102320	GTAGTTUCCTTTACCTUGGCCAGA	102321	TTCACGATTCCUTCCAGATTTGUGT
305934920	102322	CCAGATCTACUAAAGCAGAAUACCAACAT	102323	CTTAGAAAAUGCCAGCAGTGTGATUG
305937676	102324	CTCCTGATCTTTUATGGTAGTTCTGGUT	102325	AGGGTCAGUGCTGTGGACTUA
305944841	102326	GCTGATTTCAGGUTCTGATATTCTCUCA	102327	AGTCCAATUGCAGGCAACUCT
305958208	102328	GGAGACCUCAGTACTGCUCCAT	102329	AGAGGGTGATUCAGACTCAGTUAGAG
305959282	102330	AGAAUAACATCACAGUCAAGAAACCACA	102331	AGGAGTUGCGACAGATGAUCAAAAT
305966286	102332	GAAAAACAACAACCAGGUCTGUAACA	102333	TGCTAGACUCAGTAGTGAAUCAACGA
305967513	102334	CAGCCCACACUTCTTUAAGGGT	102335	GCCTACTGATGAGUATTCTTTCTTCCUT
305970013	102336	ATTTGAAAAGAAGUCCTAGTGGAGTCAUC	102337	AGGGCCTGCUCAAAAGTCTUC
305972948	102338	ATCTUGGAGGTTCUGCAAACGA	102339	TGGAAGCAAUGACTGAGAAATUACAGT
305975318	102340	GCTGAAGTCTUTCTTTCATCTGAUGACA	102341	CCAAGCTTTUCCAGAGAATGGTGAUAAT
305978709	102342	AAGGAUAACCUGCCCAAAAGACAA	102343	ACTGAAAAATGCCCUTTTATCACCTCUA
305984521	102344	AGGCCAAAGACGGGUTTCATUA	102345	GAGTCAGCCAUGATTTTCTUCCCT
305987171	102346	CAUCGCUACAAAGCCCAGGA	102347	CGACUGCCACCATCGTAUAGT
305989530	102348	TGTACAGUACACGCTAGUGAGGT	102349	CCTGCCCGUCAATGTCATGAAUAT
305993159	102350	CTTTGUCGCCAGCTTGAUCC	102351	GAAAATCAAUCAGCCAAACTCAGCUT
305998645	102352	CCTGTGGGCUGTTCTTGGTUAA	102353	GCTGGCTGUCCATGTTCTCUG
305998873	102354	CCTGCAGAGUGGTGATGTAUGA	102355	TGTACATTCAUGGTGATGTTGCUCT
306010580	102356	GGACACGTCCUCTCCTCTCUC	102357	AGGGTGTUCACCTTGCTTUCC
306012731	102358	CACAACCUCGCCCAGTUC	102359	CGGAGCGCCCUTCACAUT
306013774	102360	GACCCGCCAGCCCUAUT	102361	GCGGCUGTGGGTTTUGG
312164499	102362	ATTCAGTUACACGAACACTAAUCAAAGA	102363	AACCUAAUCAAGGAAGCGGGAAA
312165990	102364	AAGTAGCUTGAGAAAGTUGGAAGGAAA	102365	TCAGTTTGCTAAUGGGTTGCTCTTAUAT
312166422	102366	AGGTCCATTTTUCTCTGGTTTGUCA	102367	CCAUCACAGCTACAUGAACGCT
312166453	102368	AACCTATCCCGUCCACCUGA	102369	CTACGGCGGAUGGACUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
312166891	102370	TGGTTCATGUAGGCAGGGTTACUA	102371	GTTCAGCGUGGCAUGAACAT
312167073	102372	TGACCCACCAUATTCTGGTACUGA	102373	CTCACTTAGTUTTCTTTTGCTTUGGCA
312168705	102374	CAGAAUGAGCTCTGCUCCCT	102375	AGCCGAGGGUGTGGAGUA
312170638	102376	GTGTCAGCGCUCAGATTUCAC	102377	GAACCCGGUTCUAGAAGCCA
312172362	102378	GGAATGAUGCGGAGGGTAACUG	102379	CTGTGGCAAGCUGAAAGUAGGA
312176088	102380	CACAATCCUCTTGGGTCUGACA	102381	TGAGTUGGGCAAGUGGAAAGA
312176746	102382	CTCATGTAAGGUCCGTTGAGUGA	102383	GCCTAUACCCAGCAGCCTAUG
312177014	102384	GCTTGUCGCAGCAGAAGUC	102385	CACTGGAAUAGGCGTUGAGGAT
312183495	102386	CGGGAGUAGGCATCAGATUAACC	102387	CATTTCCAUCCGCTCCAAGUCT
312183949	102388	GGCCTGTGUACATCATGTUCCC	102389	AGCCCATGAUGAACAGCAGUT
312186287	102390	CAGGUCCATUGAGGGCAACAT	102391	CUAAGCAGUCGACCCCGAAG
312186942	102392	GTGTUCCAGAACCAGTTGTUGAG	102393	CUCCAGCAGACCAUAAGGGAT
312190343	102394	AATTTAAGTACATTTTUCTCATTGGCATATUCT	102395	ACCTCACAGCCAGAUACTTGGAUAA
312190773	102396	GTCTTTAGCCCAAAGAUACTAGCATUGT	102397	CGACTTGGAUAAATTTTGCTGAUGAGT
312191961	102398	GATGGGCUACGGCCAUACAG	102399	CTCACATCTCCUCTGCTTCAGUG
312193992	102400	TCTTCATCCUGTGGACCCAUCA	102401	CCACTTTTCTTCUTCCCTCTTCCUC
312195371	102402	GGTAACGCCACUGTTGAUCAC	102403	GGCCACTGGCUGTTGCTATAUAAA
312195965	102404	GCTCAAGCUGCTTCTTCCGUT	102405	CATTTTGCUGGTGGGAUGAACT
312196064	102406	GAACATCCATTUACTGCCAAGAUCC	102407	TTCCCTTTGCUATATTCCCACGUAAC
312201018	102408	GTAAAACACAUTTAGTGAAGUGAAGCCA	102409	CCTCCCCUCCTTGTTGCATTUT
312207041	102410	CAAAGGCACCAUTCCCAUCAAG	102411	CACTGCAUGTCTTGCATUCGAT
312212885	102412	GAAACACCCAUATUAGAAGGCAGAGA	102413	TGTTCUCCCTCGTATUAGGCCAT
312213134	102414	CCTAACATAAATGGUCAGCAGAAGCTUA	102415	TGGATAGACTGAUACTGCTTTGTTUCC
312216531	102416	CATTTTGCATATCAUTGTAGGACTTGGUT	102417	CATGCAAATGUGTCTCTCCAUCAC
312218001	102418	GGCCAGACCCAAACUTTGAUG	102419	CTGTTCAUGGCCTGTATCTUCAGT
312218273	102420	CCATCCTGTTUGAAATTTTGTCCUGAAT	102421	ACACCTUAACACTGGAAATUAGCGA
312221077	102422	CAATGTTGGUGGCAGACATGUT	102423	TGCAACCAGUGTTTCTCTGUCC
312222574	102424	ACAGCAUGGCGGTAAAGGUT	102425	CCCTGTGTTGAUGTGGTATGTCTATTTUA
312225467	102426	GCCAGUGAGAAGCAGTAUACCA	102427	CCACCACTUGCCACTCAGTUAG
312225628	102428	CCAGGAUCAACAAGCACAATAAUCA	102429	GTATTCAGAAAAACAGCUACCCTCUCT
312231292	102430	CTCATGAGCTCUTATGTGTTATGTTUGGA	102431	GCCTCTCTUCATCTGAGTTGUCA
312234934	102432	CCAAUCACAACCCUCACCCAT	102433	CTCGGAAACGUCAGGTUGGA
312237680	102434	GCCUTCCCUCCACCCACT	102435	GCTGAAACCACCCUTTCTGATCUT
312238708	102436	CAGCTGAGCCAGUCCTGTAUT	102437	GGCAGCTACUCTCAACCAUCAG
312242703	102438	CCTTCCUGACCTCACCACUCT	102439	CACCCAACCACUGACCCATAUT
312245072	102440	GACAGAAGTACUGAATGAGCCCUT	102441	TGTCTTTTCTUCCCAGGCTGAUG
312246490	102442	ACCTAGGTAUCTCATGTTGUGAAGT	102443	GCTAACCCAUCATGGCCCAUC
312255016	102444	AATGTGCTTTCACUAACATCCTCCUT	102445	GATTCATGUGACCGAGGTTTUCAC
312256589	102446	GGCGGAUCACAACACUCCAT	102447	TCATGATCGUAACATGTTTCTGCTUCA
312256721	102448	TTATTGTGGTTUGTGCAGTTTTCAUAAT	102449	AGGCTCATTUGTGCTCCTTUGT
312258709	102450	CCCAUGGAACTTTATUACGCACCT	102451	TCTGGCUCAGAAAGAAAATUGAACAAC
312261652	102452	TGTCAUAGCCCCGTGCUG	102453	CAACTTACCACUACTGCCACAAUCT
312262188	102454	CCTATCCTTTTCUCCCCTCACCUT	102455	TGGATATGTCAAAUATGTCGACCUAGGA
312263003	102456	CCAGTCCUGAGAAAAGCATUCCAG	102457	ACCCAGTCAGAUACAGACATTCUCAA
312263150	102458	TTTATCTGTGCUGCCTTCTTTTGUAGA	102459	AACCTTTCAGUGTATTTATGTCTGUCACA
312263466	102460	ATCCCATTCCAAUATGTAGCTTCTGTUT	102461	AGCATGAAGCTAUGATAATGGGAAGUC
312269277	102462	ACTTGGGAGUTACGAGATUCCACT	102463	CCCTTGTGCCUCCTGTTATUCC
312269727	102464	GACAUCACGGCTACAUGAACAC	102465	TCAAAGGTATTUGTGCAGATCAAUCCA
312273490	102466	GGATTGCTUGGAGGGTGGTUT	102467	GCCCTTGGTTTAUTGCCTTGAGTATTAUT
312276454	102468	ACACAGAGAAGGUCCACUGGAA	102469	CTTGACUTGTGTTTTCUCCACCAG
312289608	102470	GGCTCTGACAUACTTGATCTGTTUCT	102471	ATCAGCTTCCUGGATCATGAAAGUAAAT
312290346	102472	TGGAGGAGUGCAAACUAAAGAAACA	102473	TCATTCCUGCTATTCCTTUGGAGAAG
312296361	102474	CCCTCCCUCCGCTTCUC	102475	AGTAUAGCAGACAACCCAAUGAACAC
312296554	102476	GTTCAGCAUACAGGCATCCTUGA	102477	GCTTTCTCAUGAAGTAGTTTTCTUCCCT
312299006	102478	CAUCTTGTTGTGUCCCCGAGT	102479	TCTATTACGATGUGGAGCCATTTCTTUT
312301746	102480	CGAAGTCCCAUTCCAGGTGUG	102481	TCCAGTUACCCACCCGAUCT
312304035	102482	GGATGTGGAUTTGCCAAGTCUG	102483	TCTCAACCUACAACAATCGTUGCT
312305787	102484	ACCCATUGGACGACCGAAAAAUAAA	102485	ACCCCTAAAGGAAUCTGAGAGAAUAACA
312308632	102486	CCCTTGACATCAUTCTGTGTTAGTACAUA	102487	GAGACCCTCUACTGACTGTTTTGUT
312308822	102488	ACAAGAUGAAUGAAAACGGAGAGACA	102489	ATGTACATTAAGCUTTGCAAAATTGUGA
312314033	102490	CCCCATGUGGTGATGATTTGUGA	102491	TGCTCTCGUTTATTTTCCUGGCA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
312316549	102492	CACCTCAGGCUCCTTGGTUT	102493	AUGCCCCUACCCGAGGA
312316809	102494	GATGTCAGGCUGTACTTAACACAAAUG	102495	TGCTCTTCTUGCCCTAAATGTTCTUT
312323690	102496	ACTCCTGACUCTGCCCACUA	102497	CCTTTCAGGCUACTGCTGCUT
312326580	102498	GACTTCTCCAUTTTCAGTAUAGGCCAT	102499	ATTACCACCTGUGAATAGTAGCATCAUC
312326593	102500	AGTGACTCTTTUACAGGAGGCAAUAAC	102501	GTGATGAUGCAGTCUGCACAAA
312326784	102502	ACTTCACUGCTGGCUGCAT	102503	TCGTTTCCAUTCCTAAAGCUGGAC
312328294	102504	CAUCTGCTGAGUGACCACACA	102505	GCACCACUGAAAACTAUGAGAACCC
312330096	102506	GGCAUCCCCAGCACUGA	102507	TGCCTGTTUCCTACTTCUCCCA
312331201	102508	GAACAAAACAACCCUACTTACCUCCT	102509	GUGCCGAGGCCUGAAAGAA
312336682	102510	CCCATCGUGGAGTCGUAACT	102511	CCCCATGAUGGATGTGCCTUC
312343363	102512	ATGACTACAAAGGAGUGTTTACATCGUT	102513	CCTGGAAAGCACUTTCGTGGUA
312343653	102514	CTTCTGAGAAGGGUCCGTGAUG	102515	TCTCTCTCUCACCTCTTCACAUGAT
312345929	102516	CTGAAGACAAUAAACCACAGTAAGUGAGT	102517	TCGTTTGTCUTCGCAGGAUGT
312347560	102518	GGTCATCTGGAUCAAAAGGCAAUG	102519	CCCACACUCTTGCCTTCUACAG
312347822	102520	CAAAACAGAAGGUCAAGGGTCUCT	102521	ATCCACAAGUCCGCTGUCC
312349897	102522	GAGGAGTACCAGGUGTGAATTTCAUA	102523	TCTTTGTTATCUCAGTGTGTCTAATTUAGC
312350980	102524	ACCTGCUGAGAGTGGTCUGAT	102525	CTGCCCTUGAGAGTGGCUAC
312351544	102526	GGTGGCCCUACTTATGAAAUGGA	102527	GCACATGAAGAAAUGTGGTTGGUT
312352120	102528	TTAGAAGAGGACUGACACCUGAGT	102529	GCCAAGATUAGAACCCACGTTUG
312352559	102530	GAUTGGAGTCUCACCACACAGA	102531	CTTTGGCTUCACGGTGGTUG
312353734	102532	GGTATACAAAAAGAUGTGATACTCACUGGT	102533	TGACAAGCAGAUCAGCATTAAGAAGUT
312354081	102534	CUGTAAATCTCATUGGCAGGAGGAT	102535	ATCGTTUACAGGCUGCCCAA
312355592	102536	CACTCTCCUGGATCTTGGGTTUAC	102537	CTGGAAGAAAAGACCUGGUCGAA
312355686	102538	CCTGCACGTUCTTCTTATTAACTUCCA	102539	GGCCAAUGGGCTTTGGTTTUAC
312357096	102540	GGCTACGACUCTTTAAAATTUGCACAT	102541	CUCGGTGCCUAAACAAGCAG
312359002	102542	TGCTAGCATAUGTCCGTATGUGA	102543	CAAGTTCAUTGGCTCUGGAACAG
312359759	102544	GGCTCUTTCCACTUGCCCAA	102545	CTGCCAGGUAACAGAAGACUGT
312361590	102546	TCTTCCTCCUCTTCTTCATCGAUCT	102547	CACAATAGCAGTGUAGTCACAGAAACUA
312364906	102548	GTTCATCTAACACUTCAGTGGTCUCA	102549	GAAAAGATAGTGTUCATAACTGTAAATACTUGC
312365709	102550	CCGGCTAUACTTTCAAAACUCAGG	102551	ACCACATTGACCUATGGTGTTAATTCUT
312366887	102552	CACACTCTUCCAGTGGCTUCT	102553	AGTGTGTAAUTCCGTCATUGGG
312367415	102554	GATCCTTGTUCTGGGCTGAUCT	102555	CGAGGACCCUCAGATGUCCAT
312370322	102556	CCGUTCACACTUGCAGAACAG	102557	CCGTGATCUCGTCCCUACCA
312371398	102558	GCAGATTCCAGUCAACTTGCUT	102559	TCTCCAGAGAAACCGUTATCTGAUCT
312372501	102560	AGCCACAUGGAAAAGCUGAAAAC	102561	AGACAATCATTACCUCTTTCTCAGCTUC
312373278	102562	CCUGGCAACCAATCUAGGGT	102563	CATACAGACCUGCTCCCTTTUCC
312373333	102564	CACCAGGACUGTCTGCGAUA	102565	GTTCTCATGGTUATCCTAATGACACUGT
312375193	102566	GATCTGGAGAAACUCATCAGGTUCA	102567	AGTGGUGACATTCCTTAUGCGT
312377486	102568	CCCGACTCAACUTAAATCCTGGUT	102569	GAAAACGTGAUGTGAAGAATTCUCCT
312377733	102570	GGACCTGCUCCAGCTCCUAT	102571	CCACACCUGCCTTTCCCAUC
312378979	102572	CAAUATGCCATGUAGGAAAGACGAC	102573	GAGTTGCTGACCUAGTTCTGATTUGA
312381093	102574	GGTGTGGAUGTATCTGGCUCAAG	102575	TGCTAGTCTUGGAAGAAGGAACUAGA
312381179	102576	GCTTGCCTUCGTAACACATTTUAGA	102577	GTGTTTTTCTUCACAGCCGGUT
312383656	102578	GCTCATTCCAGCAUCTGCTTCUT	102579	CCACCCCAUTTGCCTCUACAG
312387756	102580	ATACTCTTUCAGAACTGTAAGCUAAAACG	102581	CTCGCCACCAAUTCUCACAAAG
312389295	102582	TCCGAGAUGGCTGGCTATTUG	102583	GGTGGGAAAGUCTGTGTCUCAT
312390434	102584	GACGCAUGACAGTCTUCAACC	102585	GTACAGGCAGUGCAGTCTTUGA
312390829	102586	GCCATAACTTCUGGTTTCTTTTCACTUT	102587	TTCTCTCAATACUTAAAAGGTCAGAAUAGGT
312390836	102588	ACCATATAGAAGAAACAAUTTTATATGGUGCA	102589	CCAGGAAGAGCUTGGCUAACAA
312392053	102590	GAAATGCGTUACCTTTCGCTUCA	102591	AGATUAACAGAAGGAAGUGAGAGGCT
312392429	102592	CTGATACTATTCUCTAAATTTCTGCCUAGGT	102593	CAGATGAAGGUGTGGUACAGACT
312393379	102594	GCTAGGTTGAUGGGAATATGAGCAAAAUT	102595	CAACCAGAUGACAGCCCTTTUC
312395471	102596	TGAGGTCUGAGTCAGCTTUCACT	102597	GGCTTCGUCATCGTGTCCUC
312396222	102598	ACAGATTACCAAAGCUTTACCTGUGT	102599	CGCTTACCTCAAAUACTGAAAGGTCUT
312396246	102600	CTCAAGAGAACCAUCATGGCUCAT	102601	GAUACCCAGGACGAGUGGAC
312397125	102602	GGCUAUGGAGGAAGCCAAAGAA	102603	TCACCAGCUAGCCACAGTAGUAA
312398407	102604	GTAACCAGTGAUGAAGGATCCAUGAAT	102605	GGGTCTGUAACAGCCAATCUG
312398603	102606	TGTATTATGATGUCGAGCCATTCCTTUT	102607	CCCTGTUCAAAGAATTGGGCUCT
312398870	102608	TCCAGCAAAUGAAATTUACCGAAGGA	102609	ACCTTCTAAACACAAAUCAGCACAUAGT
312400070	102610	CGUTCAGCACUCACCAAAGG	102611	TCAGCACCGUGGUGCAG
312401463	102612	CCAGUTCACAAAAGUCCAGCAC	102613	GAGACTGTCCCUGAGTGGTAUAGA

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
312402491	102614	CCGGATCUCCACGTCGUA	102615	GCCUCGCUGACAGAAGAGAAG
312405699	102616	ACCAAUACGGGAGAAGUCAGGA	102617	CTGAGACCAAGUCTGCUGCAA
312405832	102618	TCACCGTGUTCAGCGAGTUC	102619	TGATGTACGCGUGCATCTCUC
312406126	102620	CATGCTCACUGCTTTCTTCTUGAG	102621	CCGTGGTGUCAGAGCAGAUG
312406640	102622	CATCUGGGAAGGACUCAAGCAG	102623	CAATGAGCCCUTTGGTTTTCTTGTUAA
312406888	102624	GGGAGGATUGCAGCAGACTUG	102625	CTGACCUTGTGTTTTUACGGGAAG
312408211	102626	CAUGCAUGGGACAGGCAGA	102627	CCTAACCCTAUGCTCGCCTUT
312408288	102628	TGTCACCCUCACTGUAGCGA	102629	GGAAACCUGACCTUCCCAAGAG
312412678	102630	ACCUGCACAGGACTGCTUG	102631	CCCGACGGCACCAUCUT
312413777	102632	CATGCCATUGACTTTGCCTGUT	102633	CCTTGAACTCUGCCGAGGTTAUC
312417932	102634	TAATTAGTGTTAUCCCGAATAATACATGUACAG	102635	TGGACTACTCUGAGCAATATCGAAUCA
312418056	102636	TCAACCCCCUCACTGAGTCUT	102637	AGAGACGTCUTCAGCTCCUCA
312425979	102638	ACCTACATTTCUGCCTCTACACTUAAAG	102639	TTGGACGATAGUGCTTTGAAAAGTCUA
312427143	102640	GCACTCTTTGAUGGGCTTTCTCAUA	102641	CTTTTGCCAAAGAAGUGGGCUT
312428072	102642	CAAGGTGGGCUTCAAGGUAGG	102643	TCAGGACACCAGGUAGCCAUA
312428143	102644	TGATTTCCTGTUGCCCCTCTTUC	102645	GUCTCCTTGAAGTUCAACAAGAAAACC
312438611	102646	GTCGCAGAUCACGAGGTGAAATUA	102647	GTGGAGGTTUTAGCTTTTGTGUGG
312439095	102648	ACTGAATTATCTUCCACGGCAAAATCUA	102649	CATCCTGTGCUTTTTAAGGAAAGTUGT
312439552	102650	GTAAGGCCAUCAATGAGCCCUT	102651	AGCCAATCAGCAUCATCATCAUCA
312443102	102652	GCAATUGCTCACTUCAAGCGA	102653	GTTGGAGCTTUGACCTTTTGCTUAC
312443105	102654	GATTTCTCCCCACAUTCTCCATATTGUT	102655	AGTCCTTCCTCAUGATAGTCTTCCUG
312446293	102656	CCATCTATCCGCUCTAAATATCCTTCTUC	102657	TTTAGAUCAAAAGGTCCCTUCAGCAA
312448965	102658	AGAGACTATTCAUGCCCTTACACUGA	102659	GCTGAATTUGCGACCTGTAGAUG
312450988	102660	CTTCTCATGTGUTGGCTACAGGUA	102661	GCACTGGCUGGAAGAACTCUG
312461369	102662	CCAGCGCAAACAUTCTGGATCUA	102663	GGGTCTCATCUCCACATTCATTTTTAUG
312463282	102664	ATGCTAATTUGGTGCCATTTUGGT	102665	TCAGTAACGACAUCCTTGTTUCCAAT
312465149	102666	TTACTGCTUAACCCACAATGTAATTAAUCT	102667	GCCAGGAAATCAUGACTGAGAAAGAUAT
312466648	102668	ACCTACCCCAGACUCCTCUCT	102669	CAAGGGATTUGGCTTTAGCCTUC
312466883	102670	GGCTCTGGCUCCTCTCAAGUA	102671	GACTATAACUTTCTGACTGUGAAGGAGT
312468743	102672	TCAAACAAGAAAGUGCAGATGTAAATGUG	102673	CTTGCTACUACAATGTGGGAUCCT
312469012	102674	CATGTTATACTCUCGGCCTCCUC	102675	GCCTTTTUGCCAAGAATGTTUAGGAA
312471458	102676	CTAAAGTTCAGUAGCAAACATGCTUCA	102677	ACCATTTTCAAUCTGTTGTTTCTUGCC
312472013	102678	AGTGCTTGTTCTUGGATATCACGAAAUA	102679	GGGACAGTUAACATGTGAGCTCUT
312472905	102680	GTCACTGUCGCCAATTTGCUT	102681	GAGAAAAGAGACUGGATTTGGATTUAGGA
312473688	102682	AAAGAATTTTUGGCCTTTTACAGTUGGT	102683	ACCTTTTGGCAUTCTGGAAAGUG
312474645	102684	ACTCTGCUCGAGGUCCAAGA	102685	TGATGGTTTGTUGTGCCTTTGTATTUT
312476582	102686	AGCACAGAAACACCUAGTATTGATUGAG	102687	TCTCTGACTGUTCTTGGTGCUG
312477388	102688	CAGCTCTAUAAACCCCGAAGCAUA	102689	GCCACGGCAGACUCCTUAAAG
312477596	102690	ATTTCATAUGGAATGCTGUGACCCA	102691	AACCTGTATACCUCTGAGCTGUCA
312477718	102692	CCUGGTTCATTUCCACCCAGAA	102693	GTCCTGCAACUGTGTTCATCTUG
312477735	102694	CCTUGACTAGACUGCAGCGA	102695	TGTTACUAGGGCCTGCTUCCT
312478655	102696	TCCATCTTTAACACUCAACTCCAATUGT	102697	AGTGGATTTUGGAGGCCAUCAAA
312486346	102698	CAGTAATGCAUCCACACATAGCAAUC	102699	GGGATGAGGCCUGAATACTAATTCAAUT
312492624	102700	ACGCTGTTTCUGCTTTTTCACTUT	102701	CATCAGGATAAGGGAUAACGACTCTAUG
312497678	102702	ACTTAGAGACACUTTGCCATTGAUCC	102703	GTGATTGCCUACTGTTAGCTCUAGT
312499430	102704	TCCAGTAATGGAUGGTGCTAGUGA	102705	AGACTGCCTTUTACCTCCAAATUAAACA
312504699	102706	GTTGAGCCGAUAAAGAGGUCCAT	102707	CTCAACTTUGAAAAGCATTGAACGTUT
312510584	102708	GTCACTGGUGAAAGAACCAAAAUGT	102709	GAGGAGTACCAGGUTTGGATTTCATAUT
312512596	102710	TGGAAGACUGTGGCCGGUA	102711	CATTCAAGUTATACACCUGCCAGACT
312513069	102712	GAAGGAGGAACAAGAAAUCCTGUCA	102713	CTTCACTGCTCUCTTTAGACAGCUC
312515056	102714	CCATAGCACTUCCCTTCCAAATACUAAA	102715	CCCTTGGCAGUCATCTTAGTCATUAC
312516097	102716	GGAAGGAGGCCUTTTCTGUGAAT	102717	CAGTAATTGGAAAAUCACACCAGCUT
312517356	102718	CCACAGACCACCCUCCTTTUC	102719	GGAGCUGCTTCUGGAGGT
312519801	102720	CGCUCCGACGUACGGAA	102721	GGGTGTAACUCATCATGUCCAAA
312522652	102722	GTCCAGTAACUGGTTTCTGAGAAUCA	102723	CTTTAGAATGGGAGUATCACAGTGUCAT
312527471	102724	CAGACACATCCUTCTGACCTTUCAAA	102725	CCTGGGCGAAUAGCACTUCC
312529737	102726	CCAGTGGTUCTTCTTCTGGAUCAC	102727	TGCCAAGTTTCUCTCTCCTGTTUT
312534797	102728	AGACAGAGGCCAGGAUGCUA	102729	GGTGCUCCCCGAGTUCC
312534963	102730	GCTGCUGGAGCTGTCUAAAGA	102731	CTGTGGTTUCGTCAATCTUGGG
312539061	102732	AATTTTCCATGGUTCCGAGGCTUA	102733	TGGCTTGGAUCGTAAAACTGTTTUAGA
312539458	102734	GCTGTCUAAAGAGAGCAGUGAAGAAG	102735	GCAACTGACUGTGGTTUCGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
312543496	102736	CTTGTUGCATAAGCUGGACCAC	102737	GCAATGTTTCAUCCATCGTTCAATUACT
312544745	102738	CAGTCTGGAAUACTCTGTCCATTUGT	102739	ACTCTGTATAAAGUGGGTTTGCAAGUT
312545824	102740	TCAGTTTGAUCTGGAGCTUGGG	102741	CCCCTCTCACUTGCTTACTTUCA
312550768	102742	AGAGGCUGGTAAGACACUGGT	102743	GCAGAGTUCGTCTGTTTCUGAAG
312553419	102744	TGAAGAAGTCATTUGTCAACCATGGUAA	102745	CAGAGACUGTCTTCTTAUCCAACCC
312554684	102746	CTGGGCGCUTTTCATCAGUT	102747	GATACTUCTCTATGTTCTUCAGGGAGGA
312568060	102748	CATGCGGUCAGTACTUCCCAT	102749	TGACTTAGGAAAAGUGCCTGGTUT
312568784	102750	TTAACAAAGGAAACCAGUCATGTCUGA	102751	CTTCATTTCTTTAUGCTCTGTCCCTCUT
312569952	102752	GGACTUGAGGAGCCGAAUGG	102753	GTACTGCGGUCCGTCTTUCA
312578601	102754	GGTTGGAAUGTGACUCAGCGT	102755	CGGUCCCUGGACAAAAGGA
312579543	102756	AUGGTGCUAAAAGCCAAGAAAAAGAG	102757	CAGACTCCAUGTGGCTGUCAT
312579661	102758	CTAAGCUCTGGGAAUGCCACA	102759	CTCCAAGAUGACGCTCTUCCAA
312581000	102760	CGCTGTGAAUAATGGGAGGTUAC	102761	GCACGAACATUACTCCTTCGCTUA
312581491	102762	GCTGGCTCUGTCCTCTCUGT	102763	GCGGAGACGGUCTCUGG
312585273	102764	CATGGAAAUCGACTCTGAGACUGT	102765	TGGCAAUCGUCGAGCGT
312586053	102766	TGCCCATGGUTATGCTTTCUAAGAC	102767	CCACTTAGAUAGACCGCGCTUT
312587345	102768	CAGCUGCTCCTAUAGCAACCT	102769	GAGGCCUCUCCACCACAC
312590687	102770	AGGACCAUGATGCCGAUGAC	102771	GCCACAGUCCATTAAGACCUCT
312593063	102772	GCAGCGUCAAGTCTCCUCAAG	102773	CTCTGACCCAUTCGCTCGUA
312597015	102774	CCTCTTTUGCAACGGAACAUGG	102775	TCUGGGAGCGCCCAUAGAT
312602954	102776	GCAACGCCAACAUTGGCTUA	102777	GCTGTAAGGCAAUGAATGATCAAUAAGT
312603468	102778	AAACAAGUGUGGCCAAAAGGAAC	102779	GGCTGGTTTTUCCTTCTGAAGUC
312603580	102780	CCGTCTCTCCUACCTGGCAUA	102781	TCTTGTCGAUCATGTGGAGGUG
312603764	102782	ACCAAAGUCCACAGATUGCCA	102783	GGCACTTTGAUCTGGGCTGAUT
312607621	102784	TTAATGUGCAGCCTGGUCACT	102785	GTTCTTTTGGUCCTGCTTCTGUG
312621257	102786	GCCAAACUGCAGCAGTTAACTAAUAC	102787	GGAGTGUGGAGACTGAGAAAGUT
312622068	102788	ACATGACATUGCCACCACUCT	102789	ACTGTTAGGGAACCUCAGTCTTUAACT
312622664	102790	CTGCCACCCAUCAGUCACAA	102791	CCATTCAUGGCGTTGAGAGUGT
312625899	102792	GCTTGGCUAGGCTGAAGGUG	102793	CCCGCTGUCACAGTGUAGT
312627403	102794	GGUAACAGUGGAAGAACAGAAGGA	102795	TTCTGGTTTTUCACCTGGTGAUGT
312629215	102796	TCTTCGUGGTCGTCCUCAGA	102797	AGCCTGGTGUTCAAGAGTCTTTUT
312635879	102798	GGCTGCUGCTGCTGGTUA	102799	GTCCUCCAGCAGCCUCAC
312636599	102800	CCCTGCTCUGGAAAACAGCUAC	102801	TCGATACUGCCCAGGTCACUA
312639371	102802	TGUACCCGAATCUGACGAGGA	102803	CTCTCCUGGGTCAAAGACUGAAC
312641199	102804	ACCATTAAGUAACACAGGGCTTGUT	102805	GTGAGAGAUGCCAATATTTGAUGCAG
312645099	102806	TGTGCCCCUGTAAGUCCAAAC	102807	GCTTTTAGCACCAUCTGGATCTTTTUC
312645350	102808	CTTTTCCCTACUCTTCTGCATATUAGCA	102809	CUGCAGAGACUGCCCAGA
312648822	102810	TGTCAACTCTGUGAACATGAACAUGA	102811	CCATCUGCATCTGCAUAGGGT
312653412	102812	CAGCGUCGTGGTCGUCAT	102813	AAUAGTCCUGAGACCGAAACCAAG
312654383	102814	AGATGATCUCATCAAACCUGAGGAAGA	102815	TCTTTTTCCGUGGAGATTTCTGGUT
312654869	102816	CGTCATTCUGGGCAGTCUCT	102817	GCAGACAGCAGCAAUAGUCCT
312657678	102818	GGCUATATGAAUCAAACGCCCCAAT	102819	GAGAGACUGTTTGGACAUGCCT
312660165	102820	CAGCAAGTCGUAGACAGTGGAUT	102821	CTCTGTGUCAGACTGCUGGAG
318542737	102822	ACTCAGTGUCCAAATCCAGGTUT	102823	GTCTAACATCCUTCTCCGGCTUG
321637903	102824	TTGCAGGTUAAAAGAATGGCAAATUCA	102825	AGTGGTTGTATGUAAAAACTGCCAAGUA
321650590	102826	CCTGAGATGCUGTTCCTGAUGT	102827	AGCCAGGGUGATGACATTACCUA
321654734	102828	GAATCGGGCACCACUCACUT	102829	TCATGTCTCUCTCCTTCCUCACAG
321678054	102830	AATGACTTCGAGGUCTTGAATGUGT	102831	GCCAGAGGUCCAGGUGGAA
321681470	102832	CTTGTTGGCCUGTGGGTUAC	102833	GATCTGTGAUGCAGCCCUCT
321682712	102834	CUCTGCCAGUCGCCCAA	102835	ACAATCTAUGCCCTCTGCTTTUCC
321697249	102836	GAGTCCAUCAACTGCUGCCT	102837	GCAGUAGCCGCCCTTCUG
321710333	102838	TCCAAACACUACGCCUGCAT	102839	CTGGGAAGAGUTAGTGUCCAAGG
321733811	102840	AGCAGAAAGAAGAAAGGUAAACTGGAUT	102841	GTGCCTCUGCAAACTTTTCCTUAG
321752584	102842	CAGCCAAGCAUCCACCUAGAA	102843	AGTATGCAUGGGAGCCACAUC
321760113	102844	GCAGTAGCGAGUCACGTAGTUG	102845	CCTGGAAGCUTGGCUGAGAG
321766166	102846	GCATUGAGCCGAAGCTCCUC	102847	GGGCTTCTGUCCATCTCTTTUC
321773661	102848	CTGTGGCATCUGCACAAAGTTTUA	102849	GCTCAAAGTAAUGAAGAGGTGGTUCAA
321782137	102850	GCTGTATGGTAUTTTAACAGTACCUGCT	102851	GCAGCTAUCAAAGCAATATUCAAGCAT
321785760	102852	TCCATCGTAGATAUAAACTTAGAATTGGATTUT	102853	TCAUCCGGAATTUGGGAGAACAC
321785802	102854	GCTTTTCTTCAUCAATGTGTTCUCCC	102855	TTGTGTTGCUACCACATTTTTGTGUT
321788972	102856	AGCGGCAAUGACCCCUT	102857	CAGGAGCGCUTACCGAUGT

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amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
321790851	102858	GAAGAGACGAUGAATGAGGTCCUT	102859	GCATCTTUGGCTTGATTTAUGGCT
321814406	102860	CTCTGGTTUGCCACTGGTGUA	102861	GCCTTCTGAACAUTCCAAAAGTTTUGAC
321817574	102862	GGGAAAGAAGAAGUCATGATGTTCCUT	102863	CCTAGAAGCUAGAGTTGGCCATUAC
321831134	102864	GAATTGTTCATACCUTAGTCGTCCACUT	102865	GATCATTTAGTCAUCTTCAGCCGCUA
321842830	102866	GGGCAGAUCCAGTGTTCTGUG	102867	AGCATCTATTTTCUTGACTTTCCCCAUT
321844825	102868	CCTTCAGUCAACAAAGCCAATTATUGA	102869	CCTGCTUACCCCAAAACAAATAAUCAC
321848553	102870	AAGTATAGTCCUACCACTGGGTUGAAT	102871	CATACTGTGAATCUGGGTTCTTCCTUT
321854627	102872	AGGAGAGCUGCTTCGTGAUG	102873	CTGGTTGGCAUTCACACTCCTUA
321877815	102874	TCCTTTAGGAAAUGGATCAGACAAUGG	102875	AAAAAGAGAACGAAAGAUACATCUGCCT
321883467	102876	CAAGGAUGGAACAAGACCAUGGAT	102877	AGTTGACUAACAGTTGCTUAAAGCCT
321896288	102878	CTGACTUGCACTCTGUCACACT	102879	GTTACCTTTAGCUGACCCCTTUCC
321906834	102880	CTCTCCTTGTUTTCTTCTTTCCUCCT	102881	CCAGUGACCCCAGAGCTUAC
321949430	102882	GTCAGCUCCCUCAGCGT	102883	GACCAGCGGCUTCAUGAGA
321949783	102884	CCGATTCUCCTCTGCTCUCCA	102885	GCCCGCAUCCCGUCAAG
321954574	102886	CAGCUCAGCAGGAGTAAGGUT	102887	CTGGAGUGCCCACAGUCAG
321969906	102888	GCAACUCATCCCUCACAAGCAA	102889	AACAAGCCUCAGTGTGAUGGAG
321979748	102890	TGAACUCCAGCAAATCAGUCCAT	102891	CAGATCTGGUGATCTATGTCUACACAAA
321986548	102892	GGGAAATGCTTUCTATATTCTGTGTUCT	102893	GGGCAAGCAUGCUGAACAAT
322046670	102894	CATCCACATTUACTCTAGGCCTTUCC	102895	GCTGTTCAAGAACUACACTTGUCCT
322048474	102896	CCCCCATCUCATCAAGGAGAAUC	102897	GGTAAGGUCAAAGCCCTAAAATUCCT
322062839	102898	GCAGATCCUGGTGGGTGTAUC	102899	ACTTGTTUGTGTGTGUCACCCT
322074609	102900	CCTCAAATTCACAUTTGCTCCTCTCTUA	102901	CGTGAAGCUGCTGAAACTTTUCC
322078141	102902	CCAAACACGCUTCCAGAGUCT	102903	GTAGCTGUGAAGACGTTCTGUGA
322086596	102904	CCTCGCTGUCATAACAAGAUCCC	102905	GGAGCAAGAGCACAUAGAGATTAAUGA
322088606	102906	GACAAGAGACUTCCCGCUGT	102907	CCTATGATUGGCAAACTCAAGTTCTUT
322089461	102908	CACTCATTGACAUCTGCTCCTTUAGAAA	102909	AAAUGAGCAGGGAGGACATUGT
322100511	102910	ACCAUGACGAAGCAGAAGTUCC	102911	GCUGATTAAAGCTGTUCAAAACGAAGAT
322101092	102912	CTGTTTTGCCAUCACTGTCUGT	102913	GGCTATUACGCATCTGCUGCT
322105697	102914	CCTCCTTCTGAAGUATCAGCAATTTUGT	102915	TCUCTCTCAUGGAGCCAAAGAAGA
322107939	102916	GTCTUCAGCAGGAGGGUGAAAA	102917	AACGTGGAGCCAGUACAGATUG
322111662	102918	CAATTGCUGGACCAGGUCAAC	102919	AGTGGTAGCAGGUGGCATTUAC
322114483	102920	TTGACAUCAGCCCCATGGUC	102921	GAAAAAGGACACGUAGAGGTCTUGAA
326726865	102922	TTTCAATGGGTCAUATCACAGATTCUT	102923	GTAAGACTGTUGCTGCCAGUG
326727288	102924	CTTCGACAUCGAGGATGACAUCA	102925	AAGCTGUCCTTGTUGCAGACA
326739570	102926	AAGAGAGAAAUCACAGACAUACAAAGCA	102927	TTTGATCATGGUCCTATCTCTGTCTUCT
326745935	102928	CTCACATUGCCCCTGACAACAUA	102929	ACAGTAAATAACACUCTGGTGTCATUCT
326754327	102930	AATGTACCATGTUAATGTCTTCTTGTUCCT	102931	TGGCTGACCAGUAAATCCATTCUG
326755228	102932	ATCTCTGCTATTACUTTACTAAGAATGATGAUG	102933	CCAACGCGAGAAAUCCCUGAT
326755794	102934	AGAAGATACTCCAAUATGTTTTTCAAGATGUA	102935	AGCTGACCTAGUTCCAATCTTTTCTTUT
326755888	102936	TCATACCTTGCUTAATGGGTGUAGA	102937	CCTATCATCAUAGGTCGTCATGCUT
326771505	102938	AAATTCTGCATTGGUGCTAAAAGTTTCUT	102939	GCAGAGAAUGAGGGAGGAGUACAT
326771844	102940	GTCTAGCCAGAGACAUCAAGAATGAUT	102941	TGCTAAAATGUGTGATATCCCUAGACA
326772204	102942	GTCAGCTUATTATATTCAATTUAAACCCACC	102943	GCAAUGAGGGACCAGTACAUGA
326783366	102944	GGAGAAATUTGCCACTTUGGCT	102945	GCAGCAGACTTUGTGGTCACTAAAAUG
326795490	102946	CGUGGCAGGAAACAUCCCT	102947	ACTGCTCAAAGAAACUAATCAACUGA
326808236	102948	AAAAACTGTGUTGTGGAGUGCAA	102949	CCTGAACAUCCATTTCAAAGUAAGCAA
326815367	102950	TCTTGATTCUGGAACAGATTTGTCTUT	102951	GGGATTCCAUGATTCGATGTUCACAT
326843856	102952	CCTATGGCUTTCCAACCUAGGAA	102953	CAGATCCGUGGGCGUGA
326844609	102954	GCATTAUAAGCCCCAGTGATCTUCCA	102955	TGCAGCTUGCTTAGGUCCAC
326849834	102956	GCTACTGGUGATGCTGUCCAA	102957	TTGTATTCAAGGAGUTTGTTTGTUCCT
326867697	102958	CTGGGAAAATTAUGCTTACTAATGTGGTUT	102959	ACAAGCAGAUTCAAGGTGAUCAGT
326867722	102960	GGACCAACUGATCACCTTGAAUCT	102961	GCACTTATGCUTAAAATCTATTUGCAGT
326881720	102962	TGTAGGAAAGGUACAATGATTTCCACUT	102963	CACAGATTTATAUCATCCAGGCCTUCA
326881828	102964	GGCCTGGAUGATATAAATCTGUGGAT	102965	ACTAATTAATCTTCUTACTTCACACATUGGCT
326889377	102966	TGCGAACAGUGAATATTTCCTTUGA	102967	GGATCTGGATCAUTTGGAACAGTCUAC
326891326	102968	ATGATCTGCTAGUGAATGAGATAAGTCAUA	102969	ACCTACTTACUGTACCTGGUGACA
326913823	102970	CATACTTACCAUGCCACTTTCCCUT	102971	TTTTCTGTTTGGCUTGACTTGACTUT
326918704	102972	GAAGTGGGTCCUATAGATTTCTCUACCA	102973	TCACCAATCTUCTACCAGTGUGT
326921045	102974	CCAGCCUCTCGGGUACAT	102975	CCACAGCCCCCUGUACGA
326922661	102976	TGAGATCAAGATUGCAGATACAGAAUC	102977	TTCACCUTTAGCUGGCAGACC
326932763	102978	AGACAGAAAAGCGGCUGTUAGT	102979	GGTATCCACAUCCTCTTCCUCAG

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
326938015	102980	TGTATTTTTCTTTAAGUGCAAATAGTGTATCUG	102981	CACCTCCUGCTAAGCGAAATUCT
326938567	102982	CCATCTTGAACAUCTTTGTTTCTCTUC	102983	TGCATCACTAACACUACTATCAGGGUAA
326944562	102984	GTGCATTATUGTGATGATTCUGACCT	102985	TCTCCTCAACAACCUTCCACTGUA
326953658	102986	TCCATTTTCTTCUCTCTGACCTTUGG	102987	ATCATCGTCATUCAAGAGAATATTTUCCCT
326977563	102988	GATGGATACGUGGACCCTTCUG	102989	ACATGGGAAAACAUAACCTTGAAUAAAAG
326987374	102990	ATTAAAAACCTTGTUATATAGGCCCAGUT	102991	GCCTGCCCUAGTTCCAAGAUG
327060499	102992	GATTTGGGTGCUTGGGCCTAUA	102993	AGATGATGCCUTCTCCATTTUCAGAC
328198328	102994	AGGACUGCCCATCCACUGA	102995	CCATCGCCTCUTTAACAATTTAGCTAUG
328491218	102996	AATCCGAATTAGUAATTTATCTAAATUGGAGGT	102997	TCACGGTGAACAAUGTACTTTTGAUGA
328491585	102998	AAATTTUAGAGAAGCAAAACATUCAAGGT	102999	CTGTCAGAUGCCCTTCAUGGAAA
328491603	103000	GCAAAACACTUCACGGTACTTTCUAC	103001	ATATCAAAGGAATUATGTGTGGATTGTUACA
328491631	103002	TTCTTGTTCCTUGCACATTGATTTCTUT	103003	AAAAAGTTAAACAAGUGTTTTCTGTATTGTUGA
328492587	103004	ATGTTACATTTCTCUTTAGATGAACAAATGUCT	103005	AGTTAGTTTGTGGUAGTAGTCATGUCAT
328493086	103006	CTGGGCCCUTCTGCTUG	103007	CGGCTGCUGTGCCTUCT
328493136	103008	GCTGACTCGGAGUCTCAGTGATAAAUA	103009	ACATTUAACGACAAGCAAAGCUG
328496807	103010	GCAGAATGAUTTGGACATUGAAGAAGA	103011	ACCGCAGGCUCAATAAATTATUACT
328496855	103012	GGCGAACTUCAGGATCACAGTAAUT	103013	AATGTTGTATATTACCAUTGGCTAAATTTTUGA
328497054	103014	CTCAGGCCGAUGCTTGAAUC	103015	ACTACTAGTAACCUGATATACACTGCTUT
328497062	103016	GCTCCCACTGUTGATTTATCTGAUAGT	103017	AAAAATATGTACGUCAATATTCACAUGAAGAAA
328497846	103018	TCCCGGACUCAAAATCCTCUCA	103019	CCATGAATAAGCAUGTCTTCACATTTUT
328501827	103020	CCTTCACTTUGTTTTGAGGGAUCCAA	103021	GTGCTGTAAGTATUTCAAAAGTACGTTTUCA
328502380	103022	ATTGTTTTCTCTUAGATATGCAATAATTTUCCC	103023	TCCATCGATTCTUGGTGTTCTTTTACUT
328502451	103024	AATTGTTTCCAAUCATTTAGCTUCACCC	103025	GGTGCTTACAAUCCTGATGTTTTCATUC
328565829	103026	GGAAACCCAUCGCCUGAGAAA	103027	GCAAAGTGATUGACTGTGACAGTUC
328645674	103028	ACAUGTTTTCCTCUCGAAAGCCA	103029	GGACAAUGGAAAGGCTGTTATAUGGA
328673846	103030	TTTCAGGGCUGCAACCAAGUA	103031	GGGTCCTGUCACCGTAAGAUG
328700791	103032	CTTAGGCAAGGUTGGGTGUGA	103033	CATCCAAAGACUTTTTGCCACTTGUAG
328806372	103034	GCAATATTUGGCACCACTGGUT	103035	TGTATCAACTGUGGTAAATGCTACAUGA
328847682	103036	TCTGAACAGCUTGCCUAACCC	103037	TCATGTAGCTCAUTGTCAAGTTGGATUT
328862504	103038	CTACTGTATTATTUCTCATGGCAGCUCT	103039	GATTGCTAGCAUTATGTGCAGTUACAAT
328931387	103040	TGTTTCAACAUTGAGAGCUGGGT	103041	TGTATAAGUAGAGCTGGGTTUGGAACT
328932140	103042	CTTGGTGUCAGGCGAATTAAAGTUT	103043	CCAGGAACCTGUACCTTTAATGTCUG
329218262	103044	GGCTCACCCUGTAGATCAGAGAAUAA	103045	ACCTTCTACCUCTTTCCTGCTTUAG
329273555	103046	ATTTTAGACTGCTUAAAGCAATTGTTGTAUAA	103047	CUTCCAUAAGAACGGAGGGACAT
329370991	103048	ATATTCTCTGUAAGAATGGCCCUAGT	103049	ACGGGAAAAGAACUGTGGTTAAATAUGA
329435470	103050	ACCACAUCACCUGCAACCAT	103051	CTGGAAGUGCCTCCTCTTCUG
329445076	103052	GCTCCACATCUCCATGGATACUC	103053	GCCTTAGTAAGUCCACACTTUAAGCA
329445161	103054	CGAACATAUGAACACGAAGCAATGUG	103055	CCAACATACTGAAAUAACCTCAGCACUA
329456901	103056	GGCTTTGACAAACUTGACTTTUGGA	103057	GTGAAGCACAGGUTTTTATCAGTCATUG
329548352	103058	AGCTAUCCAGGATAUGCCACCT	103059	AACACCGGACAAGAGUTTCUGAA
329689140	103060	GGAGGACCUGGACCGUGT	103061	CGCACAGCCACCUCUGT
329739921	103062	AGTGAAAAACAATUCCCTGAAAGCUAGA	103063	ATCTGAAAGCCGAUGTGGUCA
329751229	103064	ATCCATGCAUCTCCTTGCCUAAG	103065	GCAGATGCCCUGGAGTTAAATTTAUCAT
329888112	103066	CCGGTTAUGCACATCATTTAAGUAGG	103067	TCTATCACCAAGUCCAAGTATGUAACCA
329992343	103068	TGGTTCCCCGGAUGATTCUG	103069	AAAATTCCTCUGCAAAAATGUGAGAAGG
330026444	103070	TTCTCTCTCUCCAATAGAAGUGGAACA	103071	TGAAGTUGAGCAGCAGAAGTAGUAAAT
330040169	103072	ACGCGGAGCUGCGUAAG	103073	CCACCGAGGCUGAGGAUG
330045616	103074	CGTAAGTAACCUCATGCTTTCUGAAGT	103075	TCACTGTGTUGTTGTACGGAAUGT
330063817	103076	CCGCGGUTCCCTAGCUC	103077	ACACACGGUCCACAGCUC
330090766	103078	GCAGACTUGCGGCAGTUT	103079	AGCUCGAGGCGTUCAGG
330092138	103080	CTTGGGUGGGTAGAGCAAUCAG	103081	GATACCCCGUGGGCAAGUT
330093466	103082	CTGCTTCCAGGUGTCATATUGGA	103083	GTGGACATUAGCTCAAGTCACUGA
330105732	103084	CCGAAGCCCUATTTCTCTGUCT	103085	TCGTTGAGGAGUGCTGTTUCC
330105985	103086	GGGTAGCACAGUACGTCUCCA	103087	GTGCUAACACGGCTCTCUCT
330129946	103088	CGTCCUCACCGGTCACTCUA	103089	GTGCTGCAUTGCTGCTUACC
330130572	103090	CGCACAGGGUCTCACUGG	103091	CCGCUCACGCCACTUCT
330137554	103092	TGATTGGGTTTUGGCATTTTCAAUACA	103093	GGAGACTAAAGUCAGACAGTGAAGATUT
330144590	103094	CGGGAAACACAGCUCAAAUCC	103095	TCUATGCAAGUCCAACGCACT
330145473	103096	GGATAATGGTUACCCCGTCCUC	103097	AGTGCTTTCTUACATCGTTCAAACUCT
330151528	103098	AGAGATAATGUTGCTGTCAUGGCAA	103099	CATCTGTTCTTTGUTCACTCTCTTCUAT
326727246	103100	TTTCAATGGGTCAUATCACAGATTCUT	103101	TTCCTCAGGAUTGCCTTUACCAC

TABLE 17

amplicon_id	SEQ ID NO	fwdUseq	SEQ ID NO	revUseq
343115165	103102	CACTTTTGGGUAAATACATTCTTCAUACCAGGA	103103	CACGCTCTAUACTGCAAATGCTAUCGA
343115166	103104	GAAGUACCCAGATTUGACAAAGAAAACC	103105	CACAAGTCAGTGUCTTTATCCAAATGUC
343115167	103106	CAATTTTTAATGAUGCTTTCTGGCUGGA	103107	CATACTTTTCTTAUCTGCATAGATTTCUGC
343115168	103108	TTAAATACAGAAGGCAUAAATATUCCAGCAGA	103109	TCAAGAGTTAATUGCAAATTACCTTAATTUCCA
343115169	103110	TATTCTTTCCTTTGUAGTGTCCATAAATTCTUT	103111	GCTGAAGAGUGCAAACAATACATCAUAC
343115170	103112	TGAGTUCCAAGGCCTCATUCAG	103113	TGAACCATCTTTUAACTCAGGTACTGUG
343115171	103114	GGGAAGAAAAGUGTTTTGAAATGUGT	103115	CAAACAAGTTUATATTTCCCCAUGCCA
343115173	103116	TGGGACTTTGGUAATTCACCAGTUAC	103117	CTGCATCGGGUCCACATAAATATATUCA
343115174	103118	CTAUTTTTCCCTTTCUCCCCACAGA	103119	TGACCAAAACUCAGCCTGTTUCT
343115175	103120	CCAGAUAGCCCUGGACAAACC	103121	CAGCATTTACUGCAGCTTGCTUAG

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242431688	chr1	2488047	2488221	2488069	2488201	TNFRSF14	NM_003820	1	8	1	+	2487805	2488172
242161604	chr1	2491297	2491463	2491315	2491444	TNFRSF14	NM_003820	1	8	4	+	2491262	2491417
265722007	chr1	2494277	2494424	2494299	2494401	TNFRSF14	NM_003820	1	8	7	+	2494304	2494335
294020310	chr1	6527797	6527936	6527816	6527915	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294020310	chr1	6527797	6527936	6527816	6527915	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646
294020310	chr1	6527797	6527936	6527816	6527915	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294020310	chr1	6527797	6527936	6527816	6527915	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294020310	chr1	6527797	6527936	6527816	6527915	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
294029495	chr1	6528261	6528428	6528283	6528404	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294029495	chr1	6528261	6528428	6528283	6528404	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646
294029495	chr1	6528261	6528428	6528283	6528404	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294029495	chr1	6528261	6528428	6528283	6528404	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294029495	chr1	6528261	6528428	6528283	6528404	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
294266430	chr1	6529159	6529330	6529179	6529310	PLEKHG5	NM_001042664	2	21	19	-	6529102	6529301
294266430	chr1	6529159	6529330	6529179	6529310	PLEKHG5	NM_001042665	3	21	19	-	6529102	6529301
294266430	chr1	6529159	6529330	6529179	6529310	PLEKHG5	NM_020631	4	21	19	-	6529102	6529301
294266430	chr1	6529159	6529330	6529179	6529310	PLEKHG5	NM_001042663	1	22	20	-	6529102	6529301
294266430	chr1	6529159	6529330	6529179	6529310	PLEKHG5	NM_198681	5	22	20	-	6529102	6529301
295386119	chr1	6529693	6529847	6529713	6529823	PLEKHG5	NM_001042664	2	21	17	-	6529604	6529736
295386119	chr1	6529693	6529847	6529713	6529823	PLEKHG5	NM_001042665	3	21	17	-	6529604	6529736
295386119	chr1	6529693	6529847	6529713	6529823	PLEKHG5	NM_020631	4	21	17	-	6529604	6529736
295386119	chr1	6529693	6529847	6529713	6529823	PLEKHG5	NM_001042663	1	22	18	-	6529604	6529736
295386119	chr1	6529693	6529847	6529713	6529823	PLEKHG5	NM_198681	5	22	18	-	6529604	6529736
294993383	chr1	6530585	6530743	6530605	6530722	PLEKHG5	NM_001042664	2	21	15	-	6530566	6530703
294993383	chr1	6530585	6530743	6530605	6530722	PLEKHG5	NM_001042665	3	21	15	-	6530566	6530703
294993383	chr1	6530585	6530743	6530605	6530722	PLEKHG5	NM_020631	4	21	15	-	6530566	6530703
294993383	chr1	6530585	6530743	6530605	6530722	PLEKHG5	NM_001042663	1	22	16	-	6530566	6530703
294993383	chr1	6530585	6530743	6530605	6530722	PLEKHG5	NM_198681	5	22	16	-	6530566	6530703
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042664	2	21	13	-	6531050	6531160
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042665	3	21	13	-	6531050	6531160
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_020631	4	21	13	-	6531050	6531160
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042663	1	22	14	-	6531050	6531160
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_198681	5	22	14	-	6531050	6531160
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042664	2	21	14	-	6530795	6530944
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042665	3	21	14	-	6530795	6530944
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_020631	4	21	14	-	6530795	6530944
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_001042663	1	22	15	-	6530795	6530944
294268403	chr1	6530909	6531074	6530928	6531056	PLEKHG5	NM_198681	5	22	15	-	6530795	6530944
293958259	chr1	6531622	6531792	6531641	6531774	PLEKHG5	NM_001042664	2	21	12	-	6531548	6531697
293958259	chr1	6531622	6531792	6531641	6531774	PLEKHG5	NM_001042665	3	21	12	-	6531548	6531697
293958259	chr1	6531622	6531792	6531641	6531774	PLEKHG5	NM_020631	4	21	12	-	6531548	6531697

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293958259	chr1	6531622	6531792	6531641	6531774	PLEKHG5	NM_001042663	1	22	13	-	6531548	6531697
293958259	chr1	6531622	6531792	6531641	6531774	PLEKHG5	NM_198681	5	22	13	-	6531548	6531697
294024687	chr1	6532962	6533136	6532985	6533114	PLEKHG5	NM_001042664	2	21	9	-	6533046	6533234
294024687	chr1	6532962	6533136	6532985	6533114	PLEKHG5	NM_001042665	3	21	9	-	6533046	6533234
294024687	chr1	6532962	6533136	6532985	6533114	PLEKHG5	NM_020631	4	21	9	-	6533046	6533234
294024687	chr1	6532962	6533136	6532985	6533114	PLEKHG5	NM_001042663	1	22	10	-	6533046	6533234
294024687	chr1	6532962	6533136	6532985	6533114	PLEKHG5	NM_198681	5	22	10	-	6533046	6533234
294479424	chr1	6533383	6533537	6533401	6533518	PLEKHG5	NM_001042664	2	21	8	-	6533311	6533514
294479424	chr1	6533383	6533537	6533401	6533518	PLEKHG5	NM_001042665	3	21	8	-	6533311	6533514
294479424	chr1	6533383	6533537	6533401	6533518	PLEKHG5	NM_020631	4	21	8	-	6533311	6533514
294479424	chr1	6533383	6533537	6533401	6533518	PLEKHG5	NM_001042663	1	22	9	-	6533311	6533514
294479424	chr1	6533383	6533537	6533401	6533518	PLEKHG5	NM_198681	5	22	9	-	6533311	6533514
293942004	chr1	6534539	6534688	6534559	6534667	PLEKHG5	NM_001042664	2	21	6	-	6534511	6534647
293942004	chr1	6534539	6534688	6534559	6534667	PLEKHG5	NM_001042665	3	21	6	-	6534511	6534647
293942004	chr1	6534539	6534688	6534559	6534667	PLEKHG5	NM_020631	4	21	6	-	6534511	6534647
293942004	chr1	6534539	6534688	6534559	6534667	PLEKHG5	NM_001042663	1	22	7	-	6534511	6534647
293942004	chr1	6534539	6534688	6534559	6534667	PLEKHG5	NM_198681	5	22	7	-	6534511	6534647
294215904	chr1	6537526	6537658	6537551	6537638	PLEKHG5	NM_001042664	2	21	2	-	6537589	6537718
294215904	chr1	6537526	6537658	6537551	6537638	PLEKHG5	NM_001042665	3	21	2	-	6537589	6537718
294215904	chr1	6537526	6537658	6537551	6537638	PLEKHG5	NM_020631	4	21	2	-	6537589	6537718
294215904	chr1	6537526	6537658	6537551	6537638	PLEKHG5	NM_001042663	1	22	3	-	6537589	6537718
294215904	chr1	6537526	6537658	6537551	6537638	PLEKHG5	NM_198681	5	22	3	-	6537589	6537718
295257036	chr1	6579533	6579657	6579553	6579632	PLEKHG5	NM_198681	5	22	1	-	6579505	6580069
294703590	chr1	9775661	9775818	9775682	9775796	PIK3CD	NM_005026	1	24	4	+	9775599	9775827
294139721	chr1	9775964	9776137	9775984	9776116	PIK3CD	NM_005026	1	24	5	+	9775907	9776136
294706844	chr1	9776942	9777086	9776961	9777065	PIK3CD	NM_005026	1	24	7	+	9777017	9777166
294166813	chr1	9778781	9778930	9778801	9778910	PIK3CD	NM_005026	1	24	9	+	9778752	9778973
294987700	chr1	9780209	9780377	9780231	9780357	PIK3CD	NM_005026	1	24	11	+	9780170	9780300
294800194	chr1	9781178	9781349	9781197	9781330	PIK3CD	NM_005026	1	24	14	+	9781185	9781306
294707158	chr1	9781808	9781975	9781828	9781956	PIK3CD	NM_005026	1	24	16	+	9781819	9781918
295395052	chr1	9782329	9782495	9782350	9782474	PIK3CD	NM_005026	1	24	18	+	9782302	9782414
294855667	chr1	9784002	9784149	9784026	9784129	PIK3CD	NM_005026	1	24	21	+	9784027	9784150
294738847	chr1	9784837	9785011	9784858	9784994	PIK3CD	NM_005026	1	24	23	+	9784862	9784994
238086816	chr1	11168215	11168370	11168236	11168344	MTOR	NM_004958	1	58	57	-	11168238	11168343
236630706	chr1	11174350	11174519	11174373	11174495	MTOR	NM_004958	1	58	53	-	11174375	11174510
239281758	chr1	11176985	11177114	11177011	11177091	MTOR	NM_004958	1	58	50	-	11177061	11177143
237764910	chr1	11181936	11182099	11181964	11182078	MTOR	NM_004958	1	58	48	-	11182036	11182183
258715494	chr1	11186586	11186760	11186610	11186737	MTOR	NM_004958	1	58	46	-	11186679	11186853
237144687	chr1	11187629	11187799	11187657	11187776	MTOR	NM_004958	1	58	44	-	11187681	11187863
235998976	chr1	11188466	11188590	11188492	11188568	MTOR	NM_004958	1	58	42	-	11188511	11188609
241036377	chr1	11189756	11189918	11189777	11189895	MTOR	NM_004958	1	58	40	-	11189795	11189895

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236805398	chr1	11190740	11190876	11190764	11190855	MTOR	NM_004958	1	58	39	-	11190586	11190834
237962204	chr1	11194481	11194651	11194503	11194625	MTOR	NM_004958	1	58	37	-	11194408	11194523
236631350	chr1	11204597	11204762	11204620	11204743	MTOR	NM_004958	1	58	34	-	11204705	11204812
236894174	chr1	11210093	11210261	11210114	11210236	MTOR	NM_004958	1	58	31	-	11210183	11210283
241808858	chr1	11227437	11227609	11227457	11227581	MTOR	NM_004958	1	58	29	-	11227499	11227574
236975765	chr1	11259612	11259784	11259638	11259761	MTOR	NM_004958	1	58	27	-	11259598	11259760
237518808	chr1	11269447	11269602	11269467	11269575	MTOR	NM_004958	1	58	25	-	11269369	11269515
241359350	chr1	11272826	11272991	11272847	11272969	MTOR	NM_004958	1	58	22	-	11272853	11272965
237230465	chr1	11288675	11288833	11288697	11288809	MTOR	NM_004958	1	58	19	-	11288725	11288975
238556063	chr1	11291027	11291200	11291047	11291173	MTOR	NM_004958	1	58	18	-	11290982	11291111
235116476	chr1	11293394	11293528	11293421	11293505	MTOR	NM_004958	1	58	15	-	11293455	11293544
237159717	chr1	11297980	11298132	11298000	11298109	MTOR	NM_004958	1	58	13	-	11297900	11298105
242388834	chr1	11300283	11300412	11300311	11300392	MTOR	NM_004958	1	58	11	-	11300360	11300604
239035544	chr1	11301697	11301836	11301719	11301815	MTOR	NM_004958	1	58	10	-	11301610	11301738
235254155	chr1	11307821	11307989	11307843	11307969	MTOR	NM_004958	1	58	7	-	11307876	11308151
236308354	chr1	11313956	11314102	11313977	11314080	MTOR	NM_004958	1	58	6	-	11313896	11314030
241192326	chr1	11317089	11317255	11317108	11317231	MTOR	NM_004958	1	58	4	-	11316990	11317222
258796578	chr1	11319361	11319491	11319384	11319467	MTOR	NM_004958	1	58	2	-	11319305	11319480
262112505	chr1	17349094	17349250	17349114	17349226	SDHB	NM_003000	1	8	7	-	17349103	17349225
264192094	chr1	17354994	17355144	17355019	17355116	SDHB	NM_003000	1	8	4	-	17355095	17355231
238812205	chr1	17371282	17371454	17371305	17371426	SDHB	NM_003000	1	8	2	-	17371256	17371383
237560815	chr1	18960865	18960996	18960885	18960977	PAX7	NM_002584	2	8	2	+	18960797	18961032
237560815	chr1	18960865	18960996	18960885	18960977	PAX7	NM_001135254	1	9	2	+	18960797	18961032
237560815	chr1	18960865	18960996	18960885	18960977	PAX7	NM_013945	3	8	2	+	18960797	18961032
234989587	chr1	18962707	18962881	18962734	18962858	PAX7	NM_013945	3	8	4	+	18962737	18962865
234989587	chr1	18962707	18962881	18962734	18962858	PAX7	NM_002584	2	8	4	+	18962731	18962865
234989587	chr1	18962707	18962881	18962734	18962858	PAX7	NM_001135254	1	9	4	+	18962731	18962865
239390066	chr1	19018367	19018512	19018388	19018488	PAX7	NM_002584	2	8	5	+	19018248	19018447
239390066	chr1	19018367	19018512	19018388	19018488	PAX7	NM_001135254	1	9	5	+	19018248	19018447
239390066	chr1	19018367	19018512	19018388	19018488	PAX7	NM_013945	3	8	5	+	19018248	19018447
235308464	chr1	19029677	19029810	19029695	19029791	PAX7	NM_002584	2	8	7	+	19029588	19029790
235308464	chr1	19029677	19029810	19029695	19029791	PAX7	NM_001135254	1	9	7	+	19029588	19029790
235308464	chr1	19029677	19029810	19029695	19029791	PAX7	NM_013945	3	8	7	+	19029588	19029790
237579843	chr1	19071232	19071362	19071259	19071345	PAX7	NM_001135254	1	9	9	+	19071308	19075360
225016197	chr1	27023223	27023364	27023242	27023347	ARID1A	NM_139135	2	20	1	+	27022522	27024031
225016197	chr1	27023223	27023364	27023242	27023347	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223546357	chr1	27023668	27023829	27023685	27023812	ARID1A	NM_139135	2	20	1	+	27022522	27024031
223546357	chr1	27023668	27023829	27023685	27023812	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223455681	chr1	27056097	27056257	27056120	27056237	ARID1A	NM_139135	2	20	2	+	27056142	27056354
223455681	chr1	27056097	27056257	27056120	27056237	ARID1A	NM_006015	1	20	2	+	27056142	27056354
222720125	chr1	27057814	27057988	27057832	27057969	ARID1A	NM_139135	2	20	3	+	27057643	27058095

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222720125	chr1	27057814	27057988	27057832	27057969	ARID1A	NM_006015	1	20	3	+	27057643	27058095
222485734	chr1	27087355	27087485	27087379	27087463	ARID1A	NM_139135	2	20	5	+	27087347	27087587
222485734	chr1	27087355	27087485	27087379	27087463	ARID1A	NM_006015	1	20	5	+	27087347	27087587
222870435	chr1	27088569	27088739	27088592	27088717	ARID1A	NM_139135	2	20	7	+	27088643	27088810
222870435	chr1	27088569	27088739	27088592	27088717	ARID1A	NM_006015	1	20	7	+	27088643	27088810
224726605	chr1	27089658	27089796	27089678	27089776	ARID1A	NM_139135	2	20	8	+	27089464	27089776
224726605	chr1	27089658	27089796	27089678	27089776	ARID1A	NM_006015	1	20	8	+	27089464	27089776
222743290	chr1	27092981	27093140	27093005	27093112	ARID1A	NM_139135	2	20	10	+	27092948	27093057
222743290	chr1	27092981	27093140	27093005	27093112	ARID1A	NM_006015	1	20	10	+	27092948	27093057
223266972	chr1	27097564	27097725	27097585	27097699	ARID1A	NM_139135	2	20	12	+	27097610	27097817
223266972	chr1	27097564	27097725	27097585	27097699	ARID1A	NM_006015	1	20	12	+	27097610	27097817
222879003	chr1	27099229	27099398	27099251	27099376	ARID1A	NM_139135	2	20	14	+	27099303	27099478
222879003	chr1	27099229	27099398	27099251	27099376	ARID1A	NM_006015	1	20	14	+	27099303	27099478
223578223	chr1	27100019	27100167	27100040	27100144	ARID1A	NM_139135	2	20	16	+	27100071	27100208
223578223	chr1	27100019	27100167	27100040	27100144	ARID1A	NM_006015	1	20	16	+	27100071	27100208
225154888	chr1	27100876	27101024	27100897	27101001	ARID1A	NM_006015	1	20	18	+	27100820	27101711
225137867	chr1	27101291	27101464	27101311	27101441	ARID1A	NM_006015	1	20	18	+	27100820	27101711
223180129	chr1	27102038	27102165	27102060	27102138	ARID1A	NM_139135	2	20	19	+	27102068	27102198
223180129	chr1	27102038	27102165	27102060	27102138	ARID1A	NM_006015	1	20	19	+	27102068	27102198
223532950	chr1	27105619	27105793	27105641	27105769	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223532950	chr1	27105619	27105793	27105641	27105769	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223526953	chr1	27106025	27106195	27106047	27106173	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223526953	chr1	27106025	27106195	27106047	27106173	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223601702	chr1	27106465	27106591	27106491	27106568	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223601702	chr1	27106465	27106591	27106491	27106568	ARID1A	NM_006015	1	20	20	+	27105514	27108601
225009187	chr1	27106828	27106978	27106851	27106958	ARID1A	NM_139135	2	20	20	+	27105514	27108601
225009187	chr1	27106828	27106978	27106851	27106958	ARID1A	NM_006015	1	20	20	+	27105514	27108601
233529536	chr1	32739846	32740006	32739867	32739981	LCK	NM_005356	2	13	2	+	32739926	32740035
233529536	chr1	32739846	32740006	32739867	32739981	LCK	NM_001042771	1	13	2	+	32739926	32740035
232581378	chr1	32740872	32741038	32740890	32741020	LCK	NM_005356	2	13	5	+	32740922	32741020
232581378	chr1	32740872	32741038	32740890	32741020	LCK	NM_001042771	1	13	5	+	32740922	32741020
233369777	chr1	32741595	32741765	32741616	32741742	LCK	NM_005356	2	13	7	+	32741515	32741664
233369777	chr1	32741595	32741765	32741616	32741742	LCK	NM_001042771	1	13	7	+	32741515	32741664
232559259	chr1	32742285	32742429	32742305	32742408	LCK	NM_005356	2	13	9	+	32742208	32742387
232559259	chr1	32742285	32742429	32742305	32742408	LCK	NM_001042771	1	13	9	+	32742208	32742387
233069137	chr1	32745589	32745737	32745609	32745713	LCK	NM_005356	2	13	12	+	32745680	32745811
233069137	chr1	32745589	32745737	32745609	32745713	LCK	NM_001042771	1	13	12	+	32745680	32745811
241554803	chr1	40362941	40363115	40362965	40363092	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
241554803	chr1	40362941	40363115	40362965	40363092	MYCL1	NM_001033081	1	2	2	-	40361096	40363642
241528708	chr1	40363379	40363543	40363406	40363519	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
241528708	chr1	40363379	40363543	40363406	40363519	MYCL1	NM_001033081	1	2	2	-	40361096	40363642

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235126076	chr1	40366575	40366715	40366592	40366698	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235126076	chr1	40366575	40366715	40366592	40366698	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235126076	chr1	40366575	40366715	40366592	40366698	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
235129748	chr1	40366993	40367117	40367013	40367098	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235129748	chr1	40366993	40367117	40367013	40367098	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235129748	chr1	40366993	40367117	40367013	40367098	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
240510235	chr1	43804181	43804312	43804205	43804291	MPL	NM_005373	1	12	3	+	43804213	43804391
238548246	chr1	43805088	43805262	43805108	43805241	MPL	NM_005373	1	12	4	+	43804942	43805240
237658519	chr1	43806043	43806208	43806068	43806185	MPL	NM_005373	1	12	6	+	43806058	43806184
242045868	chr1	43812478	43812642	43812500	43812620	MPL	NM_005373	1	12	8	+	43812463	43812605
235565116	chr1	43817852	43818026	43817873	43818007	MPL	NM_005373	1	12	11	+	43817887	43817974
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_012222	6	16	16	-	45794914	45795109
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_001048171	1	16	16	-	45794914	45795109
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_001128425	5	16	16	-	45794914	45795109
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_001048174	4	16	16	-	45794914	45795109
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_001048173	3	16	16	-	45794914	45795109
239729531	chr1	45794939	45795085	45794963	45795065	MUTYH	NM_001048172	2	16	16	-	45794914	45795109
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_012222	6	16	14	-	45796854	45797006
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_001048171	1	16	14	-	45796854	45797006
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_001128425	5	16	14	-	45796854	45797006
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_001048174	4	16	14	-	45796854	45797006
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_001048173	3	16	14	-	45796854	45797006
235649323	chr1	45796874	45797045	45796894	45797023	MUTYH	NM_001048172	2	16	14	-	45796854	45797006
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_012222	6	16	12	-	45797333	45797521
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_001048171	1	16	12	-	45797333	45797521
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_001128425	5	16	12	-	45797333	45797521
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_001048174	4	16	12	-	45797333	45797521
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_001048173	3	16	12	-	45797333	45797521
237483551	chr1	45797424	45797596	45797441	45797578	MUTYH	NM_001048172	2	16	12	-	45797333	45797521
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_012222	6	16	9	-	45798063	45798160
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_001048171	1	16	9	-	45798063	45798160
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_001128425	5	16	9	-	45798063	45798160
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_001048174	4	16	9	-	45798063	45798160
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_001048173	3	16	9	-	45798063	45798160
239033906	chr1	45798017	45798186	45798038	45798164	MUTYH	NM_001048172	2	16	9	-	45798063	45798160
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_012222	6	16	5	-	45798769	45798842
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_001048171	1	16	5	-	45798769	45798842
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_001128425	5	16	5	-	45798769	45798842
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_001048174	4	16	5	-	45798769	45798842
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_001048173	3	16	5	-	45798769	45798842
235357198	chr1	45798695	45798869	45798716	45798849	MUTYH	NM_001048172	2	16	5	-	45798769	45798842

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_001048172	2	16	3	-	45799085	45799236
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_001048171	1	16	3	-	45799085	45799233
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_001048174	4	16	3	-	45799085	45799233
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_001048173	3	16	3	-	45799085	45799233
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_012222	6	16	3	-	45799085	45799266
237694948	chr1	45799152	45799301	45799176	45799280	MUTYH	NM_001128425	5	16	3	-	45799085	45799275
265136893	chr1	47685463	47685622	47685480	47685604	TAL1	NM_003189	1	4	4	-	47681963	47685846
262487350	chr1	47689569	47689706	47689592	47689683	TAL1	NM_003189	1	4	3	-	47689676	47689770
240388482	chr1	47691274	47691419	47691291	47691401	TAL1	NM_003189	1	4	2	-	47691115	47691561
321949783	chr1	47799687	47799838	47799708	47799821	CMPK1	NM_016308	2	6	1	+	47799469	47799788
321949783	chr1	47799687	47799838	47799708	47799821	CMPK1	NM_001136140	1	5	1	+	47799469	47799788
321883467	chr1	47838708	47838832	47838732	47838806	CMPK1	NM_016308	2	6	3	+	47838627	47838779
321883467	chr1	47838708	47838832	47838732	47838806	CMPK1	NM_001136140	1	5	2	+	47838627	47838779
321782137	chr1	47842316	47842472	47842344	47842445	CMPK1	NM_016308	2	6	6	+	47842376	47844511
321782137	chr1	47842316	47842472	47842344	47842445	CMPK1	NM_001136140	1	5	5	+	47842376	47844511
225601657	chr1	51439604	51439776	51439629	51439756	CDKN2C	NM_001262	1	3	3	+	51439565	51440306
225601657	chr1	51439604	51439776	51439629	51439756	CDKN2C	NM_078626	2	2	2	+	51439565	51440309
232163531	chr1	59247732	59247906	59247754	59247883	JUN	NM_002228	1	1	1	-	59246463	59249785
231957633	chr1	59248485	59248659	59248504	59248635	JUN	NM_002228	1	1	1	-	59246463	59249785
232483118	chr1	65301710	65301845	65301732	65301822	JAK1	NM_002227	1	25	23	-	65301781	65301898
232195697	chr1	65304062	65304236	65304091	65304210	JAK1	NM_002227	1	25	21	-	65304148	65304272
232880320	chr1	65306906	65307055	65306927	65307026	JAK1	NM_002227	1	25	19	-	65306928	65307022
231128649	chr1	65309752	65309926	65309774	65309903	JAK1	NM_002227	1	25	17	-	65309747	65309898
233720804	chr1	65311232	65311357	65311258	65311330	JAK1	NM_002227	1	25	15	-	65311196	65311323
233651269	chr1	65316386	65316526	65316408	65316505	JAK1	NM_002227	1	25	12	-	65316487	65316593
233671009	chr1	65323318	65323486	65323338	65323463	JAK1	NM_002227	1	25	10	-	65323339	65323462
232057111	chr1	65330519	65330691	65330547	65330663	JAK1	NM_002227	1	25	8	-	65330470	65330655
232939739	chr1	65332810	65332982	65332836	65332954	JAK1	NM_002227	1	25	7	-	65332549	65332891
233344731	chr1	65339157	65339330	65339179	65339309	JAK1	NM_002227	1	25	5	-	65339053	65339206
233761441	chr1	65348990	65349131	65349012	65349107	JAK1	NM_002227	1	25	3	-	65348960	65349158
224740447	chr1	85733299	85733450	85733326	85733426	BCL10	NM_003921	1	3	3	-	85731460	85733665
222963426	chr1	85736230	85736404	85736249	85736380	BCL10	NM_003921	1	3	2	-	85736301	85736589
222571047	chr1	85741885	85742010	85741905	85741990	BCL10	NM_003921	1	3	1	-	85741979	85742587
328806372	chr1	97547772	97547936	97547794	97547908	DPYD	NM_000110	1	23	22	-	97547886	97548026
299054807	chr1	97658564	97658714	97658591	97658690	DPYD	NM_000110	1	23	20	-	97658625	97658804
298986546	chr1	97770793	97770963	97770814	97770936	DPYD	NM_000110	1	23	18	-	97770815	97770934
298926721	chr1	97839144	97839274	97839164	97839247	DPYD	NM_000110	1	23	16	-	97839117	97839200
299082503	chr1	97915653	97915785	97915675	97915758	DPYD	NM_000110	1	23	14	-	97915615	97915779
298979697	chr1	97981457	97981589	97981478	97981567	DPYD	NM_000110	1	23	13	-	97981282	97981497
299155916	chr1	98039330	98039484	98039352	98039462	DPYD	NM_000110	1	23	11	-	98039316	98039526
328700791	chr1	98060497	98060659	98060518	98060632	DPYD	NM_000110	1	23	9	-	98060615	98060722

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299171939	chr1	98157225	98157388	98157251	98157362	DPYD	NM_000110	1	23	7	-	98157273	98157354
298942092	chr1	98187010	98187150	98187037	98187123	DPYD	NM_001160301	2	6	5	-	98187066	98187227
298942092	chr1	98187010	98187150	98187037	98187123	DPYD	NM_000110	1	23	5	-	98187066	98187227
299020163	chr1	98205987	98206127	98206012	98206099	DPYD	NM_001160301	2	6	4	-	98205948	98206035
299020163	chr1	98205987	98206127	98206012	98206099	DPYD	NM_000110	1	23	4	-	98205948	98206035
299210923	chr1	98386379	98386508	98386397	98386487	DPYD	NM_001160301	2	6	1	-	98386440	98386615
299210923	chr1	98386379	98386508	98386397	98386487	DPYD	NM_000110	1	23	1	-	98386440	98386615
262880172	chr1	114940527	114940691	114940549	114940663	TRIM33	NM_015906	1	20	19	-	114940562	114940612
239628105	chr1	114945332	114945502	114945354	114945474	TRIM33	NM_015906	1	20	16	-	114945382	114945505
239628105	chr1	114945332	114945502	114945354	114945474	TRIM33	NM_033020	2	19	16	-	114945382	114945505
264743988	chr1	114948123	114948292	114948145	114948264	TRIM33	NM_015906	1	20	15	-	114948032	114948381
264743988	chr1	114948123	114948292	114948145	114948264	TRIM33	NM_033020	2	19	15	-	114948032	114948381
262285544	chr1	114951286	114951431	114951310	114951404	TRIM33	NM_015906	1	20	13	-	114951299	114951362
262285544	chr1	114951286	114951431	114951310	114951404	TRIM33	NM_033020	2	19	13	-	114951299	114951362
242490772	chr1	114964031	114964192	114964059	114964169	TRIM33	NM_015906	1	20	11	-	114964058	114964258
242490772	chr1	114964031	114964192	114964059	114964169	TRIM33	NM_033020	2	19	11	-	114964058	114964258
239379034	chr1	114968011	114968144	114968036	114968119	TRIM33	NM_015906	1	20	9	-	114968071	114968345
239379034	chr1	114968011	114968144	114968036	114968119	TRIM33	NM_033020	2	19	9	-	114968071	114968345
264644990	chr1	114969738	114969873	114969770	114969853	TRIM33	NM_015906	1	20	8	-	114969799	114969916
264644990	chr1	114969738	114969873	114969770	114969853	TRIM33	NM_033020	2	19	8	-	114969799	114969916
241384248	chr1	114970417	114970555	114970445	114970528	TRIM33	NM_015906	1	20	7	-	114970370	114970516
241384248	chr1	114970417	114970555	114970445	114970528	TRIM33	NM_033020	2	19	7	-	114970370	114970516
240574538	chr1	115005679	115005823	115005710	115005800	TRIM33	NM_015906	1	20	4	-	115005726	115005858
240574538	chr1	115005679	115005823	115005710	115005800	TRIM33	NM_033020	2	19	4	-	115005726	115005858
240058778	chr1	115006038	115006204	115006066	115006172	TRIM33	NM_015906	1	20	3	-	115006034	115006178
240058778	chr1	115006038	115006204	115006066	115006172	TRIM33	NM_033020	2	19	3	-	115006034	115006178
266351607	chr1	115053112	115053269	115053133	115053248	TRIM33	NM_015906	1	20	1	-	115053172	115053781
266351607	chr1	115053112	115053269	115053133	115053248	TRIM33	NM_033020	2	19	1	-	115053172	115053781
239816250	chr1	115251036	115251206	115251060	115251184	NRAS	NM_002524	1	7	5	-	115251152	115251275
242632724	chr1	115256375	115256549	115256403	115256523	NRAS	NM_002524	1	7	3	-	115256421	115256599
242179242	chr1	120457906	120458069	120457928	120458047	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242114724	chr1	120458299	120458438	120458318	120458415	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242135314	chr1	120458718	120458875	120458743	120458853	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237131370	chr1	120459212	120459341	120459236	120459317	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237695837	chr1	120461041	120461213	120461061	120461186	NOTCH2	NM_024408	2	34	32	-	120461029	120461176
235497549	chr1	120462761	120462935	120462784	120462916	NOTCH2	NM_024408	2	34	30	-	120462852	120463020
236120687	chr1	120464835	120464963	120464857	120464942	NOTCH2	NM_024408	2	34	28	-	120464859	120465069
235095019	chr1	120466195	120466365	120466220	120466341	NOTCH2	NM_024408	2	34	26	-	120466260	120466607
242726967	chr1	120467861	120468035	120467885	120468012	NOTCH2	NM_024408	2	34	25	-	120467928	120468433
257697991	chr1	120468297	120468464	120468317	120468436	NOTCH2	NM_024408	2	34	25	-	120467928	120468433
241545370	chr1	120471590	120471751	120471613	120471731	NOTCH2	NM_024408	2	34	23	-	120471599	120471835

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235754789	chr1	120478110	120478283	120478132	120478256	NOTCH2	NM_001200001	1	22	22	-	120477736	120478227
235754789	chr1	120478110	120478283	120478132	120478256	NOTCH2	NM_024408	2	34	22	-	120478095	120478227
238518160	chr1	120480488	120480660	120480510	120480639	NOTCH2	NM_001200001	1	22	20	-	120480480	120480633
238518160	chr1	120480488	120480660	120480510	120480639	NOTCH2	NM_024408	2	34	20	-	120480480	120480633
235845092	chr1	120484145	120484301	120484167	120484276	NOTCH2	NM_001200001	1	22	18	-	120484149	120484377
235845092	chr1	120484145	120484301	120484167	120484276	NOTCH2	NM_024408	2	34	18	-	120484149	120484377
238572411	chr1	120491545	120491719	120491570	120491698	NOTCH2	NM_001200001	1	22	16	-	120491630	120491749
238572411	chr1	120491545	120491719	120491570	120491698	NOTCH2	NM_024408	2	34	16	-	120491630	120491749
239912605	chr1	120496092	120496263	120496117	120496236	NOTCH2	NM_001200001	1	22	14	-	120496166	120496311
239912605	chr1	120496092	120496263	120496117	120496236	NOTCH2	NM_024408	2	34	14	-	120496166	120496311
238504964	chr1	120501990	120502147	120502012	120502125	NOTCH2	NM_001200001	1	22	12	-	120502015	120502125
238504964	chr1	120501990	120502147	120502012	120502125	NOTCH2	NM_024408	2	34	12	-	120502015	120502125
236678229	chr1	120508041	120508215	120508067	120508189	NOTCH2	NM_001200001	1	22	10	-	120508076	120508189
236678229	chr1	120508041	120508215	120508067	120508189	NOTCH2	NM_024408	2	34	10	-	120508076	120508189
237341397	chr1	120510118	120510278	120510139	120510251	NOTCH2	NM_001200001	1	22	8	-	120510056	120510244
237341397	chr1	120510118	120510278	120510139	120510251	NOTCH2	NM_024408	2	34	8	-	120510056	120510244
237652368	chr1	120512242	120512409	120512261	120512383	NOTCH2	NM_001200001	1	22	6	-	120512134	120512367
237652368	chr1	120512242	120512409	120512261	120512383	NOTCH2	NM_024408	2	34	6	-	120512134	120512367
238072323	chr1	120539668	120539839	120539688	120539812	NOTCH2	NM_001200001	1	22	4	-	120539620	120539955
238072323	chr1	120539668	120539839	120539688	120539812	NOTCH2	NM_024408	2	34	4	-	120539620	120539955
236950240	chr1	120547904	120548075	120547928	120548054	NOTCH2	NM_001200001	1	22	3	-	120547952	120548211
236950240	chr1	120547904	120548075	120547928	120548054	NOTCH2	NM_024408	2	34	3	-	120547952	120548211
237228504	chr1	144854435	144854588	144854459	144854565	PDE4DIP	NM_001198832	6	46	44	-	144854518	144854656
237228504	chr1	144854435	144854588	144854459	144854565	PDE4DIP	NM_001198834	7	44	42	-	144854518	144854656
237228504	chr1	144854435	144854588	144854459	144854565	PDE4DIP	NM_014644	8	44	42	-	144854518	144854656
236386263	chr1	144856841	144857015	144856859	144856995	PDE4DIP	NM_001198832	6	46	42	-	144856816	144857042
236386263	chr1	144856841	144857015	144856859	144856995	PDE4DIP	NM_001198834	7	44	40	-	144856816	144857042
236386263	chr1	144856841	144857015	144856859	144856995	PDE4DIP	NM_014644	8	44	40	-	144856816	144857042
237362388	chr1	144859694	144859853	144859712	144859836	PDE4DIP	NM_001198832	6	46	40	-	144859759	144859998
237362388	chr1	144859694	144859853	144859712	144859836	PDE4DIP	NM_001198834	7	44	38	-	144859759	144859998
237362388	chr1	144859694	144859853	144859712	144859836	PDE4DIP	NM_014644	8	44	38	-	144859759	144859998
236417817	chr1	144863330	144863500	144863354	144863481	PDE4DIP	NM_001198832	6	46	39	-	144863318	144863442
236417817	chr1	144863330	144863500	144863354	144863481	PDE4DIP	NM_001198834	7	44	37	-	144863318	144863442
236417817	chr1	144863330	144863500	144863354	144863481	PDE4DIP	NM_014644	8	44	37	-	144863318	144863442
236878686	chr1	144865844	144865994	144865866	144865966	PDE4DIP	NM_001198832	6	46	37	-	144865810	144865929
236878686	chr1	144865844	144865994	144865866	144865966	PDE4DIP	NM_001198834	7	44	35	-	144865810	144865929
236878686	chr1	144865844	144865994	144865866	144865966	PDE4DIP	NM_014644	8	44	35	-	144865810	144865929
235840608	chr1	144867968	144868121	144867990	144868100	PDE4DIP	NM_001198832	6	46	35	-	144867921	144868172
235840608	chr1	144867968	144868121	144867990	144868100	PDE4DIP	NM_001198834	7	44	33	-	144867921	144868172
235840608	chr1	144867968	144868121	144867990	144868100	PDE4DIP	NM_014644	8	44	33	-	144867921	144868172
236847672	chr1	144871840	144871990	144871859	144871969	PDE4DIP	NM_001198834	7	44	32	-	144871696	144871881

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236847672	chr1	144871840	144871990	144871859	144871969	PDE4DIP	NM_014644	8	44	32	-	144871696	144871881
237085294	chr1	144874671	144874820	144874692	144874800	PDE4DIP	NM_001198832	6	46	33	-	144874681	144874904
237085294	chr1	144874671	144874820	144874692	144874800	PDE4DIP	NM_001198834	7	44	30	-	144874681	144874904
237085294	chr1	144874671	144874820	144874692	144874800	PDE4DIP	NM_014644	8	44	30	-	144874681	144874904
236572151	chr1	144877164	144877329	144877183	144877301	PDE4DIP	NM_001198832	6	46	31	-	144877036	144877271
236572151	chr1	144877164	144877329	144877183	144877301	PDE4DIP	NM_001198834	7	44	28	-	144877036	144877271
236572151	chr1	144877164	144877329	144877183	144877301	PDE4DIP	NM_014644	8	44	28	-	144877036	144877271
235391473	chr1	144879252	144879423	144879272	144879394	PDE4DIP	NM_001198832	6	46	30	-	144879035	144879563
235391473	chr1	144879252	144879423	144879272	144879394	PDE4DIP	NM_001198834	7	44	27	-	144879035	144879563
235391473	chr1	144879252	144879423	144879272	144879394	PDE4DIP	NM_014644	8	44	27	-	144879035	144879563
237641132	chr1	144881557	144881716	144881578	144881691	PDE4DIP	NM_001198832	6	46	28	-	144881430	144881622
237641132	chr1	144881557	144881716	144881578	144881691	PDE4DIP	NM_001198834	7	44	25	-	144881430	144881622
237641132	chr1	144881557	144881716	144881578	144881691	PDE4DIP	NM_014644	8	44	25	-	144881430	144881622
237770513	chr1	144882729	144882881	144882753	144882860	PDE4DIP	NM_001198832	6	46	27	-	144882776	144882881
237770513	chr1	144882729	144882881	144882753	144882860	PDE4DIP	NM_001198834	7	44	24	-	144882446	144882881
237770513	chr1	144882729	144882881	144882753	144882860	PDE4DIP	NM_014644	8	44	24	-	144882446	144882881
235057537	chr1	144886204	144886362	144886226	144886334	PDE4DIP	NM_001198832	6	46	26	-	144886097	144886329
235057537	chr1	144886204	144886362	144886226	144886334	PDE4DIP	NM_001198834	7	44	23	-	144886097	144886329
235057537	chr1	144886204	144886362	144886226	144886334	PDE4DIP	NM_014644	8	44	23	-	144886097	144886329
236906628	chr1	144903112	144903243	144903133	144903219	PDE4DIP	NM_001198832	6	46	24	-	144903077	144903204
236906628	chr1	144903112	144903243	144903133	144903219	PDE4DIP	NM_001198834	7	44	21	-	144903077	144903204
236906628	chr1	144903112	144903243	144903133	144903219	PDE4DIP	NM_014644	8	44	21	-	144903077	144903204
236906628	chr1	144903112	144903243	144903133	144903219	PDE4DIP	NM_001002812	3	23	21	-	144903077	144903204
236906628	chr1	144903112	144903243	144903133	144903219	PDE4DIP	NM_001002811	2	19	17	-	144903077	144903204
237796245	chr1	144906440	144906564	144906465	144906539	PDE4DIP	NM_001198832	6	46	21	-	144906421	144906537
237796245	chr1	144906440	144906564	144906465	144906539	PDE4DIP	NM_001198834	7	44	18	-	144906421	144906537
237796245	chr1	144906440	144906564	144906465	144906539	PDE4DIP	NM_014644	8	44	18	-	144906421	144906537
237796245	chr1	144906440	144906564	144906465	144906539	PDE4DIP	NM_001002812	3	23	18	-	144906421	144906537
237796245	chr1	144906440	144906564	144906465	144906539	PDE4DIP	NM_001002811	2	19	14	-	144906421	144906537
241077399	chr1	144912004	144912162	144912032	144912144	PDE4DIP	NM_001198832	6	46	18	-	144912130	144912294
241077399	chr1	144912004	144912162	144912032	144912144	PDE4DIP	NM_001198834	7	44	15	-	144912130	144912294
241077399	chr1	144912004	144912162	144912032	144912144	PDE4DIP	NM_014644	8	44	15	-	144912130	144912294
241077399	chr1	144912004	144912162	144912032	144912144	PDE4DIP	NM_001002812	3	23	15	-	144912130	144912294
241077399	chr1	144912004	144912162	144912032	144912144	PDE4DIP	NM_001002811	2	19	11	-	144912130	144912294
234961752	chr1	144915501	144915673	144915528	144915651	PDE4DIP	NM_001198832	6	46	17	-	144915445	144915639
234961752	chr1	144915501	144915673	144915528	144915651	PDE4DIP	NM_001198834	7	44	14	-	144915445	144915639
234961752	chr1	144915501	144915673	144915528	144915651	PDE4DIP	NM_014644	8	44	14	-	144915445	144915639
234961752	chr1	144915501	144915673	144915528	144915651	PDE4DIP	NM_001002812	3	23	14	-	144915445	144915639
234961752	chr1	144915501	144915673	144915528	144915651	PDE4DIP	NM_001002811	2	19	10	-	144915445	144915639
237764726	chr1	144917538	144917666	144917564	144917640	PDE4DIP	NM_001198832	6	46	15	-	144917499	144917636
237764726	chr1	144917538	144917666	144917564	144917640	PDE4DIP	NM_001198834	7	44	12	-	144917499	144917636

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237764726	chr1	144917538	144917666	144917564	144917640	PDE4DIP	NM_014644	8	44	12	-	144917499	144917636
237764726	chr1	144917538	144917666	144917564	144917640	PDE4DIP	NM_001002812	3	23	12	-	144917499	144917636
237764726	chr1	144917538	144917666	144917564	144917640	PDE4DIP	NM_001002811	2	19	8	-	144917499	144917636
236214556	chr1	144921744	144921900	144921768	144921878	PDE4DIP	NM_001198832	6	46	12	-	144921835	144922047
236214556	chr1	144921744	144921900	144921768	144921878	PDE4DIP	NM_001198834	7	44	9	-	144921835	144922047
236214556	chr1	144921744	144921900	144921768	144921878	PDE4DIP	NM_014644	8	44	9	-	144921835	144922047
236214556	chr1	144921744	144921900	144921768	144921878	PDE4DIP	NM_001002812	3	23	9	-	144921835	144922047
236214556	chr1	144921744	144921900	144921768	144921878	PDE4DIP	NM_001002811	2	19	5	-	144921835	144922047
237490590	chr1	144922400	144922573	144922422	144922547	PDE4DIP	NM_001198832	6	46	10	-	144922519	144922638
237490590	chr1	144922400	144922573	144922422	144922547	PDE4DIP	NM_001198834	7	44	7	-	144922519	144922638
237490590	chr1	144922400	144922573	144922422	144922547	PDE4DIP	NM_014644	8	44	7	-	144922519	144922638
237490590	chr1	144922400	144922573	144922422	144922547	PDE4DIP	NM_001002812	3	23	7	-	144922519	144922638
237490590	chr1	144922400	144922573	144922422	144922547	PDE4DIP	NM_001002811	2	19	3	-	144922519	144922638
240326301	chr1	144930530	144930701	144930551	144930676	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
236877645	chr1	144931001	144931174	144931024	144931146	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
236973066	chr1	144931476	144931648	144931497	144931631	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001198834	7	44	1	-	144994591	144995033
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001002810	1	4	1	-	144994591	144995033
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001198832	6	46	4	-	144994591	144994701
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001195261	5	5	2	-	144994591	144994701
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001195260	4	5	2	-	144994591	144994701
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_022359	9	7	4	-	144994591	144994701
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_014644	8	44	1	-	144994591	144995022
235172038	chr1	144994496	144994669	144994519	144994650	PDE4DIP	NM_001002812	3	23	1	-	144994591	144995022
234950021	chr1	145015844	145015997	145015871	145015976	PDE4DIP	NM_001198832	6	46	3	-	145015860	145016011
234950021	chr1	145015844	145015997	145015871	145015976	PDE4DIP	NM_022359	9	7	3	-	145015860	145016011
240103699	chr1	145075611	145075754	145075629	145075737	PDE4DIP	NM_022359	9	7	1	-	145075630	145076186
233576614	chr1	145527512	145527659	145527534	145527637	ITGA10	NM_003637	1	30	2	+	145527613	145527724
233584658	chr1	145528544	145528715	145528567	145528693	ITGA10	NM_003637	1	30	5	+	145528570	145528684
231481274	chr1	145530913	145531076	145530934	145531053	ITGA10	NM_003637	1	30	7	+	145530878	145531026
234441992	chr1	145532486	145532648	145532508	145532622	ITGA10	NM_003637	1	30	9	+	145532457	145532622
233729576	chr1	145533356	145533529	145533378	145533506	ITGA10	NM_003637	1	30	12	+	145533412	145533560
232891795	chr1	145534033	145534196	145534055	145534173	ITGA10	NM_003637	1	30	14	+	145534083	145534286
233561101	chr1	145535791	145535962	145535813	145535940	ITGA10	NM_003637	1	30	16	+	145535735	145535901
231407802	chr1	145537111	145537285	145537137	145537261	ITGA10	NM_003637	1	30	19	+	145537176	145537261
232661279	chr1	145537920	145538093	145537941	145538067	ITGA10	NM_003637	1	30	22	+	145537989	145538065
232233181	chr1	145539326	145539468	145539347	145539445	ITGA10	NM_003637	1	30	26	+	145539365	145539445
231938524	chr1	145541766	145541938	145541794	145541916	ITGA10	NM_003637	1	30	29	+	145541802	145541915
222507899	chr1	147084746	147084903	147084768	147084881	BCL9	NM_004326	1	10	5	+	147084682	147084998
223752673	chr1	147086266	147086439	147086286	147086416	BCL9	NM_004326	1	10	6	+	147086226	147086415
224756301	chr1	147090691	147090846	147090713	147090826	BCL9	NM_004326	1	10	8	+	147090622	147092863

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223204617	chr1	147091070	147091215	147091091	147091192	BCL9	NM_004326	1	10	8	+	147090622	147092863
223254481	chr1	147091548	147091691	147091571	147091670	BCL9	NM_004326	1	10	8	+	147090622	147092863
224783365	chr1	147091932	147092106	147091955	147092084	BCL9	NM_004326	1	10	8	+	147090622	147092863
224801535	chr1	147092418	147092591	147092442	147092571	BCL9	NM_004326	1	10	8	+	147090622	147092863
223312913	chr1	147093980	147094153	147094004	147094125	BCL9	NM_004326	1	10	9	+	147094072	147094332
224488249	chr1	147095661	147095806	147095686	147095786	BCL9	NM_004326	1	10	10	+	147095643	147098015
224486101	chr1	147096113	147096266	147096134	147096245	BCL9	NM_004326	1	10	10	+	147095643	147098015
224512937	chr1	147096511	147096669	147096530	147096647	BCL9	NM_004326	1	10	10	+	147095643	147098015
269761753	chr1	150550613	150550754	150550634	150550730	MCL1	NM_021960	2	3	2	-	150550720	150550967
269761753	chr1	150550613	150550754	150550634	150550730	MCL1	NM_001197320	1	4	3	-	150550720	150550967
271048692	chr1	150551314	150551479	150551334	150551457	MCL1	NM_001197320	1	4	2	-	150551319	150551439
271048692	chr1	150551314	150551479	150551334	150551457	MCL1	NM_021960	2	3	1	-	150551319	150552214
271048692	chr1	150551314	150551479	150551334	150551457	MCL1	NM_182763	3	2	1	-	150551319	150552214
269957907	chr1	150551778	150551906	150551795	150551884	MCL1	NM_021960	2	3	1	-	150551319	150552214
269957907	chr1	150551778	150551906	150551795	150551884	MCL1	NM_182763	3	2	1	-	150551319	150552214
223625037	chr1	150785598	150785728	150785622	150785701	ARNT	NM_001668	2	22	21	-	150785648	150785814
223625037	chr1	150785598	150785728	150785622	150785701	ARNT	NM_178427	3	21	20	-	150785648	150785814
223625037	chr1	150785598	150785728	150785622	150785701	ARNT	NM_001197325	1	21	20	-	150785648	150785814
224497142	chr1	150788706	150788867	150788732	150788845	ARNT	NM_001668	2	22	19	-	150788735	150788882
224497142	chr1	150788706	150788867	150788732	150788845	ARNT	NM_178427	3	21	18	-	150788735	150788882
224497142	chr1	150788706	150788867	150788732	150788845	ARNT	NM_001197325	1	21	18	-	150788735	150788882
224117115	chr1	150789553	150789677	150789579	150789657	ARNT	NM_001668	2	22	17	-	150789558	150789678
224117115	chr1	150789553	150789677	150789579	150789657	ARNT	NM_178427	3	21	16	-	150789558	150789678
224117115	chr1	150789553	150789677	150789579	150789657	ARNT	NM_001197325	1	21	16	-	150789558	150789678
222653756	chr1	150795664	150795825	150795691	150795798	ARNT	NM_001668	2	22	14	-	150795670	150795821
222653756	chr1	150795664	150795825	150795691	150795798	ARNT	NM_178427	3	21	13	-	150795670	150795821
222653756	chr1	150795664	150795825	150795691	150795798	ARNT	NM_001197325	1	21	13	-	150795670	150795821
225132422	chr1	150801604	150801776	150801631	150801748	ARNT	NM_001668	2	22	12	-	150801569	150801703
225132422	chr1	150801604	150801776	150801631	150801748	ARNT	NM_178427	3	21	11	-	150801569	150801703
225132422	chr1	150801604	150801776	150801631	150801748	ARNT	NM_001197325	1	21	11	-	150801569	150801703
222652277	chr1	150804743	150804917	150804771	150804890	ARNT	NM_001668	2	22	9	-	150804810	150804875
222652277	chr1	150804743	150804917	150804771	150804890	ARNT	NM_178427	3	21	8	-	150804810	150804875
222652277	chr1	150804743	150804917	150804771	150804890	ARNT	NM_001197325	1	21	8	-	150804810	150804875
223139147	chr1	150808910	150809063	150808937	150809041	ARNT	NM_001668	2	22	7	-	150808756	150808969
223139147	chr1	150808910	150809063	150808937	150809041	ARNT	NM_178427	3	21	6	-	150808756	150808969
223139147	chr1	150808910	150809063	150808937	150809041	ARNT	NM_001197325	1	21	6	-	150808756	150808969
222543757	chr1	150818661	150818814	150818686	150818786	ARNT	NM_001668	2	22	4	-	150818739	150818783
222543757	chr1	150818661	150818814	150818686	150818786	ARNT	NM_178427	3	21	4	-	150818739	150818783
222543757	chr1	150818661	150818814	150818686	150818786	ARNT	NM_001197325	1	21	4	-	150818739	150818783
225185505	chr1	150830833	150830998	150830854	150830970	ARNT	NM_001668	2	22	2	-	150830825	150830936
225185505	chr1	150830833	150830998	150830854	150830970	ARNT	NM_178427	3	21	2	-	150830825	150830936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225185505	chr1	150830833	150830998	150830854	150830970	ARNT	NM_001197325	1	21	2	-	150830825	150830936
294907170	chr1	154950478	154950636	154950499	154950608	CKS1B	NM_001826	1	3	2	+	154950463	154950590
294907170	chr1	154950478	154950636	154950499	154950608	CKS1B	NR_024163	2	3	2	+	154950463	154950590
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001044391	4	5	4	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001044390	3	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204290	12	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204289	11	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204288	10	8	7	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_002456	20	8	7	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204286	8	9	8	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204294	16	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204293	15	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001044392	5	5	4	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001018017	2	8	7	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001044393	6	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204292	14	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204297	19	5	4	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204296	18	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204295	17	6	5	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204287	9	8	7	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204285	7	9	8	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001204291	13	7	6	-	155159701	155159850
238699253	chr1	155159688	155159839	155159710	155159820	MUC1	NM_001018016	1	8	7	-	155159701	155159850
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204290	12	7	4	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204289	11	7	4	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204288	10	8	5	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_002456	20	8	5	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204286	8	9	6	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204294	16	7	4	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204293	15	7	5	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001018017	2	8	5	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204292	14	7	4	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204287	9	8	5	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204285	7	9	6	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001204291	13	7	4	-	155160198	155160334
237833419	chr1	155160202	155160361	155160223	155160340	MUC1	NM_001018016	1	8	5	-	155160198	155160334
239027529	chr1	155160840	155161013	155160858	155160996	MUC1	NM_001204286	8	9	4	-	155160639	155161063
239027529	chr1	155160840	155161013	155160858	155160996	MUC1	NM_001204285	7	9	4	-	155160639	155161063
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001044391	4	5	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001044390	3	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204290	12	7	1	-	155162577	155162706

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204289	11	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204288	10	8	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_002456	20	8	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204286	8	9	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204294	16	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204293	15	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001044392	5	5	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001018017	2	8	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001044393	6	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204292	14	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204297	19	5	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204296	18	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204295	17	6	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204287	9	8	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204285	7	9	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001204291	13	7	1	-	155162577	155162706
237273712	chr1	155162493	155162658	155162512	155162639	MUC1	NM_001018016	1	8	1	-	155162577	155162706
235683531	chr1	156830789	156830942	156830806	156830920	NTRK1	NM_002529	3	17	1	+	156830671	156830938
235683531	chr1	156830789	156830942	156830806	156830920	NTRK1	NM_001012331	2	16	1	+	156830671	156830938
258000163	chr1	156836645	156836815	156836664	156836794	NTRK1	NM_002529	3	17	4	+	156836702	156836770
258000163	chr1	156836645	156836815	156836664	156836794	NTRK1	NM_001012331	2	16	4	+	156836702	156836770
258000163	chr1	156836645	156836815	156836664	156836794	NTRK1	NM_001007792	1	17	5	+	156836702	156836770
236806692	chr1	156838304	156838459	156838322	156838440	NTRK1	NM_002529	3	17	6	+	156838297	156838439
236806692	chr1	156838304	156838459	156838322	156838440	NTRK1	NM_001012331	2	16	6	+	156838297	156838439
236806692	chr1	156838304	156838459	156838322	156838440	NTRK1	NM_001007792	1	17	7	+	156838297	156838439
236928233	chr1	156843524	156843654	156843544	156843633	NTRK1	NM_002529	3	17	8	+	156843425	156843751
236928233	chr1	156843524	156843654	156843544	156843633	NTRK1	NM_001012331	2	16	8	+	156843425	156843751
236928233	chr1	156843524	156843654	156843544	156843633	NTRK1	NM_001007792	1	17	9	+	156843425	156843751
235612876	chr1	156844629	156844779	156844651	156844758	NTRK1	NM_002529	3	17	11	+	156844698	156844800
235612876	chr1	156844629	156844779	156844651	156844758	NTRK1	NM_001012331	2	16	10	+	156844698	156844800
235612876	chr1	156844629	156844779	156844651	156844758	NTRK1	NM_001007792	1	17	11	+	156844698	156844800
236778526	chr1	156845800	156845968	156845819	156845949	NTRK1	NM_002529	3	17	13	+	156845872	156846002
236778526	chr1	156845800	156845968	156845819	156845949	NTRK1	NM_001012331	2	16	12	+	156845872	156846002
236778526	chr1	156845800	156845968	156845819	156845949	NTRK1	NM_001007792	1	17	13	+	156845872	156846002
238765100	chr1	156848885	156849059	156848909	156849040	NTRK1	NM_002529	3	17	15	+	156848914	156849154
238765100	chr1	156848885	156849059	156848909	156849040	NTRK1	NM_001012331	2	16	14	+	156848914	156849154
238765100	chr1	156848885	156849059	156848909	156849040	NTRK1	NM_001007792	1	17	15	+	156848914	156849154
241832858	chr1	156849888	156850030	156849909	156850008	NTRK1	NM_002529	3	17	16	+	156849791	156849949
241832858	chr1	156849888	156850030	156849909	156850008	NTRK1	NM_001012331	2	16	15	+	156849791	156849949
241832858	chr1	156849888	156850030	156849909	156850008	NTRK1	NM_001007792	1	17	16	+	156849791	156849949
241564438	chr1	161293319	161293457	161293346	161293433	SDHC	NM_003001	4	6	2	+	161293404	161293460

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241564438	chr1	161293319	161293457	161293346	161293433	SDHC	NM_001035512	2	5	2	+	161293404	161293460
241564438	chr1	161293319	161293457	161293346	161293433	SDHC	NM_001035511	1	5	2	+	161293404	161293460
241475892	chr1	161310388	161310556	161310408	161310531	SDHC	NM_003001	4	6	4	+	161310384	161310445
241475892	chr1	161310388	161310556	161310408	161310531	SDHC	NM_001035512	2	5	3	+	161310384	161310445
241475892	chr1	161310388	161310556	161310408	161310531	SDHC	NM_001035513	3	4	2	+	161310384	161310445
241475892	chr1	161310388	161310556	161310408	161310531	SDHC	NM_001035511	1	5	4	+	161310384	161310445
262837793	chr1	161332114	161332288	161332138	161332262	SDHC	NM_003001	4	6	6	+	161332119	161334535
262837793	chr1	161332114	161332288	161332138	161332262	SDHC	NM_001035512	2	5	5	+	161332119	161334535
262837793	chr1	161332114	161332288	161332138	161332262	SDHC	NM_001035513	3	4	4	+	161332119	161334535
262837793	chr1	161332114	161332288	161332138	161332262	SDHC	NM_001035511	1	5	5	+	161332119	161334535
230151333	chr1	162724446	162724608	162724467	162724586	DDR2	NM_006182	2	18	5	+	162724414	162724645
230151333	chr1	162724446	162724608	162724467	162724586	DDR2	NM_001014796	1	19	6	+	162724414	162724645
230122619	chr1	162725427	162725601	162725449	162725572	DDR2	NM_006182	2	18	7	+	162725454	162725559
230122619	chr1	162725427	162725601	162725449	162725572	DDR2	NM_001014796	1	19	8	+	162725454	162725559
230481328	chr1	162731085	162731223	162731108	162731197	DDR2	NM_006182	2	18	9	+	162731001	162731244
230481328	chr1	162731085	162731223	162731108	162731197	DDR2	NM_001014796	1	19	10	+	162731001	162731244
227850556	chr1	162737008	162737182	162737030	162737154	DDR2	NM_006182	2	18	11	+	162737019	162737149
227850556	chr1	162737008	162737182	162737030	162737154	DDR2	NM_001014796	1	19	12	+	162737019	162737149
231036528	chr1	162741866	162742025	162741888	162742002	DDR2	NM_006182	2	18	13	+	162741814	162742037
231036528	chr1	162741866	162742025	162741888	162742002	DDR2	NM_001014796	1	19	14	+	162741814	162742037
228332530	chr1	162745364	162745537	162745385	162745513	DDR2	NM_006182	2	18	15	+	162745442	162745633
228332530	chr1	162745364	162745537	162745385	162745513	DDR2	NM_001014796	1	19	16	+	162745442	162745633
232948025	chr1	162748290	162748457	162748318	162748432	DDR2	NM_006182	2	18	17	+	162748370	162748519
232948025	chr1	162748290	162748457	162748318	162748432	DDR2	NM_001014796	1	19	18	+	162748370	162748519
236908539	chr1	164528934	164529094	164528956	164529074	PBX1	NM_002585	3	9	1	+	164528597	164529250
236908539	chr1	164528934	164529094	164528956	164529074	PBX1	NM_001204963	2	9	1	+	164528597	164529250
236908539	chr1	164528934	164529094	164528956	164529074	PBX1	NM_001204961	1	8	1	+	164528597	164529250
238508034	chr1	164761638	164761811	164761663	164761789	PBX1	NM_002585	3	9	3	+	164761731	164761975
238508034	chr1	164761638	164761811	164761663	164761789	PBX1	NM_001204963	2	9	3	+	164761731	164761975
238508034	chr1	164761638	164761811	164761663	164761789	PBX1	NM_001204961	1	8	3	+	164761731	164761975
240115136	chr1	164769006	164769175	164769028	164769154	PBX1	NM_002585	3	9	4	+	164768936	164769126
240115136	chr1	164769006	164769175	164769028	164769154	PBX1	NM_001204963	2	9	4	+	164768936	164769126
240115136	chr1	164769006	164769175	164769028	164769154	PBX1	NM_001204961	1	8	4	+	164768936	164769126
237474279	chr1	164781288	164781460	164781312	164781433	PBX1	NM_002585	3	9	6	+	164781227	164781386
237474279	chr1	164781288	164781460	164781312	164781433	PBX1	NM_001204963	2	9	6	+	164781227	164781386
237474279	chr1	164781288	164781460	164781312	164781433	PBX1	NM_001204961	1	8	6	+	164781227	164781386
235430726	chr1	164815786	164815939	164815808	164815921	PBX1	NM_002585	3	9	9	+	164815821	164821060
235430726	chr1	164815786	164815939	164815808	164815921	PBX1	NM_001204961	1	8	8	+	164815821	164821060
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_001168239	6	12	12	-	179068462	179078033
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_001168238	5	12	12	-	179068462	179078033
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_001136000	1	13	13	-	179068462	179078033

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_001168237	4	13	13	-	179068462	179078033
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_005158	7	12	12	-	179068462	179078576
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_007314	8	12	12	-	179068462	179078576
224203064	chr1	179077021	179077165	179077042	179077140	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_005158	7	12	12	-	179068462	179078576
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_007314	8	12	12	-	179068462	179078576
223432375	chr1	179077482	179077620	179077504	179077598	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_005158	7	12	12	-	179068462	179078576
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_007314	8	12	12	-	179068462	179078576
223427396	chr1	179077874	179078048	179077897	179078027	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_005158	7	12	12	-	179068462	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_007314	8	12	12	-	179068462	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_001168239	6	12	11	-	179078343	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_001168238	5	12	11	-	179078343	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_001136000	1	13	12	-	179078343	179078576
223133556	chr1	179078335	179078503	179078361	179078482	ABL2	NM_001168237	4	13	12	-	179078343	179078576
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_005158	7	12	10	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001168239	6	12	9	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001168238	5	12	9	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001136001	2	10	9	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001136000	1	13	10	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_007314	8	12	10	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001168237	4	13	10	-	179081444	179081533
223833499	chr1	179081414	179081588	179081441	179081560	ABL2	NM_001168236	3	11	9	-	179081444	179081533
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_005158	7	12	8	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001168239	6	12	7	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001168238	5	12	7	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001136001	2	10	7	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001136000	1	13	8	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_007314	8	12	8	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001168237	4	13	8	-	179086467	179086651
223803795	chr1	179086507	179086680	179086529	179086654	ABL2	NM_001168236	3	11	7	-	179086467	179086651

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_005158	7	12	5	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001168239	6	12	4	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001168238	5	12	4	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001136001	2	10	4	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001136000	1	13	5	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_007314	8	12	5	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001168237	4	13	5	-	179090730	179091002
224114012	chr1	179090635	179090803	179090661	179090783	ABL2	NM_001168236	3	11	4	-	179090730	179091002
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_005158	7	12	4	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001168239	6	12	3	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001168238	5	12	3	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001136001	2	10	3	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001136000	1	13	4	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_007314	8	12	4	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001168237	4	13	4	-	179095512	179095807
222808720	chr1	179095618	179095790	179095641	179095765	ABL2	NM_001168236	3	11	3	-	179095512	179095807
224374237	chr1	179112028	179112202	179112054	179112181	ABL2	NM_005158	7	12	1	-	179112068	179112224
224374237	chr1	179112028	179112202	179112054	179112181	ABL2	NM_001168239	6	12	1	-	179112068	179112224
224374237	chr1	179112028	179112202	179112054	179112181	ABL2	NM_001136000	1	13	1	-	179112068	179112224
321986548	chr1	182544603	182544749	182544631	182544729	RNASEL	NM_021133	1	7	7	-	182542769	182544713
321831134	chr1	182550347	182550512	182550375	182550486	RNASEL	NM_021133	1	7	5	-	182550360	182550492
322046670	chr1	182554357	182554531	182554383	182554506	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322105697	chr1	182554809	182554982	182554837	182554958	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322114483	chr1	182555244	182555413	182555264	182555387	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322100511	chr1	182555696	182555858	182555718	182555830	RNASEL	NM_021133	1	7	2	-	182554462	182556105
312343363	chr1	185060807	185060931	185060835	185060909	RNF2	NM_007212	1	7	3	+	185060711	185060871
312471458	chr1	185067116	185067240	185067143	185067213	RNF2	NM_007212	1	7	5	+	185067204	185067476
312190343	chr1	185068857	185068984	185068890	185068959	RNF2	NM_007212	1	7	6	+	185068923	185069094
312258709	chr1	185069392	185069558	185069416	185069531	RNF2	NM_007212	1	7	7	+	185069332	185071740
266279987	chr1	186286550	186286713	186286577	186286687	TPR	NM_003292	1	51	49	-	186286614	186286732
242033059	chr1	186287688	186287852	186287708	186287824	TPR	NM_003292	1	51	48	-	186287579	186287735
238992810	chr1	186291336	186291495	186291363	186291474	TPR	NM_003292	1	51	45	-	186291450	186291544
242742173	chr1	186292687	186292850	186292715	186292832	TPR	NM_003292	1	51	43	-	186292818	186293002
266299590	chr1	186294780	186294954	186294806	186294930	TPR	NM_003292	1	51	42	-	186294896	186294986
262886432	chr1	186300593	186300766	186300615	186300738	TPR	NM_003292	1	51	39	-	186300630	186300713
264768949	chr1	186302211	186302385	186302239	186302364	TPR	NM_003292	1	51	37	-	186302254	186302526
242310698	chr1	186303452	186303576	186303477	186303552	TPR	NM_003292	1	51	36	-	186303457	186303665
265767832	chr1	186304371	186304527	186304394	186304505	TPR	NM_003292	1	51	34	-	186304470	186304675
262053097	chr1	186305615	186305788	186305643	186305765	TPR	NM_003292	1	51	33	-	186305628	186305826
239499951	chr1	186307044	186307215	186307077	186307187	TPR	NM_003292	1	51	31	-	186307165	186307375
242053016	chr1	186308755	186308905	186308782	186308877	TPR	NM_003292	1	51	30	-	186308774	186308904

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240131794	chr1	186310347	186310498	186310373	186310469	TPR	NM_003292	1	51	28	-	186310384	186310521
265010200	chr1	186312534	186312705	186312556	186312672	TPR	NM_003292	1	51	27	-	186312458	186312605
262988662	chr1	186313620	186313792	186313641	186313765	TPR	NM_003292	1	51	25	-	186313507	186313710
242261527	chr1	186315288	186315423	186315316	186315401	TPR	NM_003292	1	51	23	-	186315267	186315419
240999385	chr1	186319353	186319504	186319379	186319478	TPR	NM_003292	1	51	21	-	186319355	186319520
241008021	chr1	186320977	186321146	186321006	186321120	TPR	NM_003292	1	51	19	-	186321108	186321242
241226921	chr1	186324447	186324612	186324475	186324585	TPR	NM_003292	1	51	17	-	186324542	186324690
240166773	chr1	186325334	186325508	186325360	186325482	TPR	NM_003292	1	51	15	-	186325418	186325581
239078147	chr1	186326702	186326876	186326725	186326851	TPR	NM_003292	1	51	14	-	186326529	186326755
262904909	chr1	186329001	186329150	186329023	186329125	TPR	NM_003292	1	51	12	-	186328931	186329128
239798998	chr1	186329948	186330121	186329977	186330097	TPR	NM_003292	1	51	10	-	186329897	186330037
261731104	chr1	186331354	186331505	186331382	186331476	TPR	NM_003292	1	51	7	-	186331420	186331512
263425494	chr1	186332521	186332689	186332548	186332662	TPR	NM_003292	1	51	5	-	186332474	186332577
239862998	chr1	186340116	186340249	186340139	186340223	TPR	NM_003292	1	51	3	-	186340102	186340175
266371269	chr1	186344065	186344221	186344090	186344199	TPR	NM_003292	1	51	1	-	186344010	186344457
296696534	chr1	186643643	186643796	186643667	186643772	PTGS2	NM_000963	1	10	10	-	186640944	186643894
296091087	chr1	186644964	186645101	186644991	186645073	PTGS2	NM_000963	1	10	8	-	186645030	186645316
297542383	chr1	186645490	186645641	186645518	186645620	PTGS2	NM_000963	1	10	7	-	186645599	186645845
298326130	chr1	186646709	186646852	186646737	186646827	PTGS2	NM_000963	1	10	5	-	186646781	186646962
297715645	chr1	186647460	186647629	186647483	186647602	PTGS2	NM_000963	1	10	4	-	186647393	186647536
295438680	chr1	186648452	186648589	186648475	186648564	PTGS2	NM_000963	1	10	2	-	186648454	186648570
226437988	chr1	193094178	193094352	193094205	193094333	CDC73	NM_024529	1	17	2	+	193094242	193094347
226835964	chr1	193107130	193107297	193107157	193107270	CDC73	NM_024529	1	17	6	+	193107215	193107303
225919823	chr1	193111131	193111299	193111157	193111271	CDC73	NM_024529	1	17	7	+	193110980	193111196
226762848	chr1	193121502	193121626	193121525	193121598	CDC73	NM_024529	1	17	10	+	193121510	193121574
225627040	chr1	193202239	193202367	193202267	193202347	CDC73	NM_024529	1	17	14	+	193202123	193202284
227050525	chr1	193218863	193219033	193218890	193219005	CDC73	NM_024529	1	17	16	+	193218860	193219001
295039807	chr1	204394023	204394197	204394043	204394174	PIK3C2B	NM_002646	1	34	34	-	204391758	204394168
295406268	chr1	204396790	204396915	204396818	204396889	PIK3C2B	NM_002646	1	34	32	-	204396776	204396882
294653180	chr1	204400729	204400865	204400750	204400839	PIK3C2B	NM_002646	1	34	29	-	204400797	204400921
294175231	chr1	204402413	204402581	204402432	204402554	PIK3C2B	NM_002646	1	34	27	-	204402444	204402553
294476455	chr1	204403606	204403776	204403629	204403752	PIK3C2B	NM_002646	1	34	25	-	204403567	204403736
295410224	chr1	204410569	204410716	204410592	204410692	PIK3C2B	NM_002646	1	34	22	-	204410599	204410691
294798402	chr1	204413157	204413328	204413178	204413299	PIK3C2B	NM_002646	1	34	19	-	204413196	204413290
294008875	chr1	204415211	204415374	204415234	204415353	PIK3C2B	NM_002646	1	34	17	-	204415084	204415272
294422981	chr1	204418940	204419101	204418960	204419080	PIK3C2B	NM_002646	1	34	14	-	204418978	204419145
295185831	chr1	204424861	204425031	204424884	204425010	PIK3C2B	NM_002646	1	34	12	-	204424984	204425179
294760272	chr1	204426803	204426976	204426828	204426957	PIK3C2B	NM_002646	1	34	10	-	204426856	204427002
294394252	chr1	204429596	204429744	204429618	204429719	PIK3C2B	NM_002646	1	34	7	-	204429678	204429789
294786444	chr1	204433598	204433771	204433619	204433747	PIK3C2B	NM_002646	1	34	5	-	204433578	204433732
294274209	chr1	204438033	204438206	204438055	204438183	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294303645	chr1	204438402	204438570	204438420	204438549	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
295208552	chr1	204438828	204438985	204438850	204438963	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
233690140	chr1	204499802	204499967	204499825	204499945	MDM4	NM_002393	3	11	4	+	204499812	204499945
233690140	chr1	204499802	204499967	204499825	204499945	MDM4	NR_024171	4	10	4	+	204499812	204499945
233690140	chr1	204499802	204499967	204499825	204499945	MDM4	NM_001204171	1	10	4	+	204499812	204499945
232908308	chr1	204507377	204507544	204507400	204507516	MDM4	NM_002393	3	11	7	+	204507337	204507436
232908308	chr1	204507377	204507544	204507400	204507516	MDM4	NR_024171	4	10	6	+	204507337	204507436
232908308	chr1	204507377	204507544	204507400	204507516	MDM4	NM_001204171	1	10	7	+	204507337	204507436
231494240	chr1	204513681	204513853	204513710	204513825	MDM4	NM_002393	3	11	9	+	204513663	204513812
231494240	chr1	204513681	204513853	204513710	204513825	MDM4	NR_024171	4	10	8	+	204513663	204513812
231926584	chr1	204518247	204518415	204518269	204518386	MDM4	NM_002393	3	11	11	+	204518241	204527248
231926584	chr1	204518247	204518415	204518269	204518386	MDM4	NR_024171	4	10	10	+	204518241	204527248
231926584	chr1	204518247	204518415	204518269	204518386	MDM4	NM_001204171	1	10	10	+	204518241	204527248
231755461	chr1	204518750	204518916	204518772	204518888	MDM4	NM_001204172	2	3	3	+	204518394	204527248
231755461	chr1	204518750	204518916	204518772	204518888	MDM4	NM_002393	3	11	11	+	204518241	204527248
231755461	chr1	204518750	204518916	204518772	204518888	MDM4	NR_024171	4	10	10	+	204518241	204527248
231755461	chr1	204518750	204518916	204518772	204518888	MDM4	NM_001204171	1	10	10	+	204518241	204527248
271542023	chr1	206648187	206648318	206648207	206648298	IKBKE	NM_014002	3	22	5	+	206648208	206648337
271542023	chr1	206648187	206648318	206648207	206648298	IKBKE	NM_001193322	2	21	5	+	206648208	206648337
271542023	chr1	206648187	206648318	206648207	206648298	IKBKE	NM_001193321	1	21	4	+	206648208	206648337
270054738	chr1	206649663	206649824	206649686	206649801	IKBKE	NM_014002	3	22	6	+	206649524	206649705
270054738	chr1	206649663	206649824	206649686	206649801	IKBKE	NM_001193322	2	21	6	+	206649524	206649705
270054738	chr1	206649663	206649824	206649686	206649801	IKBKE	NM_001193321	1	21	5	+	206649524	206649705
270201846	chr1	206651470	206651619	206651490	206651599	IKBKE	NM_014002	3	22	9	+	206651503	206651682
270201846	chr1	206651470	206651619	206651490	206651599	IKBKE	NM_001193322	2	21	9	+	206651503	206651682
270201846	chr1	206651470	206651619	206651490	206651599	IKBKE	NM_001193321	1	21	8	+	206651503	206651682
271829408	chr1	206653186	206653330	206653206	206653310	IKBKE	NM_014002	3	22	11	+	206653213	206653277
271829408	chr1	206653186	206653330	206653206	206653310	IKBKE	NM_001193322	2	21	11	+	206653213	206653277
271829408	chr1	206653186	206653330	206653206	206653310	IKBKE	NM_001193321	1	21	10	+	206653213	206653277
270059322	chr1	206658427	206658583	206658448	206658562	IKBKE	NM_014002	3	22	15	+	206658531	206658643
270059322	chr1	206658427	206658583	206658448	206658562	IKBKE	NM_001193322	2	21	15	+	206658531	206658643
270059322	chr1	206658427	206658583	206658448	206658562	IKBKE	NM_001193321	1	21	14	+	206658531	206658643
272656471	chr1	206664093	206664266	206664116	206664247	IKBKE	NM_014002	3	22	17	+	206664152	206664191
272656471	chr1	206664093	206664266	206664116	206664247	IKBKE	NM_001193322	2	21	17	+	206664152	206664191
272656471	chr1	206664093	206664266	206664116	206664247	IKBKE	NM_001193321	1	21	16	+	206664152	206664191
272194184	chr1	206666573	206666747	206666595	206666723	IKBKE	NM_014002	3	22	20	+	206666599	206666711
272194184	chr1	206666573	206666747	206666595	206666723	IKBKE	NM_001193321	1	21	19	+	206666599	206666711
290906713	chr1	220752562	220752736	220752589	220752713	MARK1	NM_018650	1	18	2	+	220752696	220752899
293615623	chr1	220773079	220773238	220773110	220773211	MARK1	NM_018650	1	18	5	+	220773140	220773205
289851209	chr1	220791509	220791682	220791537	220791654	MARK1	NM_018650	1	18	8	+	220791652	220791888
290529254	chr1	220791866	220792040	220791891	220792013	MARK1	NM_018650	1	18	9	+	220791978	220792097

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
292890365	chr1	220805543	220805670	220805566	220805643	MARK1	NM_018650	1	18	11	+	220805543	220805655
290273258	chr1	220809056	220809229	220809082	220809204	MARK1	NM_018650	1	18	13	+	220809175	220809368
290283794	chr1	220825293	220825455	220825317	220825428	MARK1	NM_018650	1	18	15	+	220825328	220825492
290919521	chr1	220826583	220826726	220826605	220826700	MARK1	NM_018650	1	18	16	+	220826443	220826694
290010324	chr1	220835135	220835309	220835159	220835281	MARK1	NM_018650	1	18	18	+	220835154	220837799
290949272	chr1	226549638	226549812	226549660	226549784	PARP1	NM_001618	1	23	22	-	226549670	226549784
291763535	chr1	226552749	226552923	226552769	226552896	PARP1	NM_001618	1	23	19	-	226552703	226552855
290395517	chr1	226555833	226555982	226555852	226555957	PARP1	NM_001618	1	23	16	-	226555900	226556022
290712597	chr1	226561918	226562088	226561941	226562064	PARP1	NM_001618	1	23	14	-	226561927	226562055
293033067	chr1	226566869	226567043	226566892	226567022	PARP1	NM_001618	1	23	12	-	226566843	226566975
290427059	chr1	226567751	226567876	226567772	226567849	PARP1	NM_001618	1	23	10	-	226567623	226567865
291780361	chr1	226570626	226570762	226570649	226570741	PARP1	NM_001618	1	23	8	-	226570737	226570884
290080751	chr1	226573271	226573418	226573293	226573397	PARP1	NM_001618	1	23	7	-	226573205	226573381
291737171	chr1	226578104	226578272	226578125	226578250	PARP1	NM_001618	1	23	4	-	226578111	226578325
292025909	chr1	226589890	226590043	226589910	226590021	PARP1	NM_001618	1	23	2	-	226589915	226590080
290383347	chr1	236958946	236959117	236958966	236959098	MTR	NM_000254	1	33	1	+	236958581	236959037
290402346	chr1	236969392	236969566	236969418	236969538	MTR	NM_000254	1	33	3	+	236969444	236969533
289584606	chr1	236978857	236979031	236978884	236979003	MTR	NM_000254	1	33	7	+	236978904	236978963
291838975	chr1	236987417	236987591	236987443	236987564	MTR	NM_000254	1	33	9	+	236987419	236987519
290961692	chr1	236992447	236992602	236992480	236992575	MTR	NM_000254	1	33	12	+	236992489	236992568
291481334	chr1	236998887	236999029	236998907	236999001	MTR	NM_000254	1	33	14	+	236998847	236998987
290141860	chr1	237013624	237013788	237013648	237013763	MTR	NM_000254	1	33	16	+	237013644	237013823
289514853	chr1	237016192	237016354	237016219	237016326	MTR	NM_000254	1	33	18	+	237016248	237016388
290944030	chr1	237024447	237024612	237024468	237024585	MTR	NM_000254	1	33	20	+	237024425	237024577
293617632	chr1	237037960	237038094	237037988	237038066	MTR	NM_000254	1	33	24	+	237038026	237038146
290668296	chr1	237048493	237048623	237048519	237048595	MTR	NM_000254	1	33	26	+	237048421	237048519
291892586	chr1	237054371	237054498	237054398	237054470	MTR	NM_000254	1	33	29	+	237054433	237054629
290666500	chr1	237057680	237057828	237057702	237057806	MTR	NM_000254	1	33	30	+	237057657	237057857
291516963	chr1	237058801	237058925	237058821	237058900	MTR	NM_000254	1	33	31	+	237058658	237058850
228214219	chr1	241661016	241661188	241661044	241661166	FH	NM_000143	1	10	10	-	241660857	241661270
227260538	chr1	241663812	241663960	241663832	241663932	FH	NM_000143	1	10	9	-	241663737	241663890
227638719	chr1	241667384	241667552	241667404	241667528	FH	NM_000143	1	10	7	-	241667342	241667545
229377657	chr1	241669412	241669536	241669440	241669505	FH	NM_000143	1	10	6	-	241669303	241669468
227848493	chr1	241675172	241675300	241675200	241675274	FH	NM_000143	1	10	4	-	241675267	241675443
227652440	chr1	241676972	241677105	241676989	241677077	FH	NM_000143	1	10	3	-	241676903	241677013
227280908	chr1	241682889	241683061	241682906	241683040	FH	NM_000143	1	10	1	-	241682891	241683085
270239777	chr1	243675499	243675659	243675526	243675632	AKT3	NM_005465	2	13	12	-	243675626	243675728
270239777	chr1	243675499	243675659	243675526	243675632	AKT3	NM_181690	3	14	12	-	243675626	243675728
270239777	chr1	243675499	243675659	243675526	243675632	AKT3	NM_001206729	1	14	13	-	243675626	243675728
270359457	chr1	243716196	243716366	243716216	243716338	AKT3	NM_005465	2	13	10	-	243716031	243716245
270359457	chr1	243716196	243716366	243716216	243716338	AKT3	NM_181690	3	14	10	-	243716031	243716245

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270359457	chr1	243716196	243716366	243716216	243716338	AKT3	NM_001206729	1	14	11	-	243716031	243716245
270764076	chr1	243736174	243736306	243736202	243736284	AKT3	NM_005465	2	13	8	-	243736228	243736350
270764076	chr1	243736174	243736306	243736202	243736284	AKT3	NM_181690	3	14	8	-	243736228	243736350
270764076	chr1	243736174	243736306	243736202	243736284	AKT3	NM_001206729	1	14	9	-	243736228	243736350
271276449	chr1	243778434	243778558	243778457	243778531	AKT3	NM_005465	2	13	6	-	243778398	243778463
271276449	chr1	243778434	243778558	243778457	243778531	AKT3	NM_181690	3	14	6	-	243778398	243778463
271276449	chr1	243778434	243778558	243778457	243778531	AKT3	NM_001206729	1	14	7	-	243778398	243778463
270904391	chr1	243809287	243809461	243809307	243809436	AKT3	NM_005465	2	13	4	-	243809195	243809339
270904391	chr1	243809287	243809461	243809307	243809436	AKT3	NM_181690	3	14	4	-	243809195	243809339
270904391	chr1	243809287	243809461	243809307	243809436	AKT3	NM_001206729	1	14	5	-	243809195	243809339
272652304	chr1	244006352	244006526	244006379	244006498	AKT3	NM_005465	2	13	1	-	244006427	244006584
272652304	chr1	244006352	244006526	244006379	244006498	AKT3	NM_181690	3	14	1	-	244006427	244006584
272652304	chr1	244006352	244006526	244006379	244006498	AKT3	NM_001206729	1	14	2	-	244006427	244006584
297476094	chr2	5832744	5832888	5832764	5832868	SOX11	NM_003108	1	1	1	+	5832799	5841517
297486312	chr2	5833102	5833274	5833121	5833255	SOX11	NM_003108	1	1	1	+	5832799	5841517
297473986	chr2	5833434	5833586	5833451	5833567	SOX11	NM_003108	1	1	1	+	5832799	5841517
297485609	chr2	5833793	5833961	5833816	5833937	SOX11	NM_003108	1	1	1	+	5832799	5841517
241286465	chr2	16082264	16082438	16082283	16082418	MYCN	NM_005378	1	3	2	+	16082070	16082976
236528446	chr2	16082616	16082786	16082633	16082768	MYCN	NM_005378	1	3	2	+	16082070	16082976
239196385	chr2	16085777	16085939	16085799	16085918	MYCN	NM_005378	1	3	3	+	16085615	16087129
237041445	chr2	24881497	24881667	24881524	24881639	NCOA1	NM_147233	3	21	3	+	24881530	24881635
237041445	chr2	24881497	24881667	24881524	24881639	NCOA1	NM_147223	2	22	3	+	24881530	24881635
237041445	chr2	24881497	24881667	24881524	24881639	NCOA1	NM_003743	1	21	3	+	24881530	24881635
237449633	chr2	24896142	24896288	24896170	24896259	NCOA1	NM_147233	3	21	5	+	24896235	24896332
237449633	chr2	24896142	24896288	24896170	24896259	NCOA1	NM_147223	2	22	5	+	24896235	24896332
237449633	chr2	24896142	24896288	24896170	24896259	NCOA1	NM_003743	1	21	5	+	24896235	24896332
235516957	chr2	24914290	24914424	24914316	24914398	NCOA1	NM_147233	3	21	7	+	24914350	24914529
235516957	chr2	24914290	24914424	24914316	24914398	NCOA1	NM_147223	2	22	7	+	24914350	24914529
235516957	chr2	24914290	24914424	24914316	24914398	NCOA1	NM_003743	1	21	7	+	24914350	24914529
235263129	chr2	24916165	24916325	24916190	24916296	NCOA1	NM_147233	3	21	8	+	24916121	24916216
235263129	chr2	24916165	24916325	24916190	24916296	NCOA1	NM_147223	2	22	8	+	24916121	24916216
235263129	chr2	24916165	24916325	24916190	24916296	NCOA1	NM_003743	1	21	8	+	24916121	24916216
239968651	chr2	24927973	24928102	24927995	24928074	NCOA1	NM_147233	3	21	10	+	24927955	24928102
239968651	chr2	24927973	24928102	24927995	24928074	NCOA1	NM_147223	2	22	10	+	24927955	24928102
239968651	chr2	24927973	24928102	24927995	24928074	NCOA1	NM_003743	1	21	10	+	24927955	24928102
238044968	chr2	24929551	24929711	24929572	24929687	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238044968	chr2	24929551	24929711	24929572	24929687	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238044968	chr2	24929551	24929711	24929572	24929687	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238046994	chr2	24929998	24930168	24930020	24930145	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238046994	chr2	24929998	24930168	24930020	24930145	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238046994	chr2	24929998	24930168	24930020	24930145	NCOA1	NM_003743	1	21	11	+	24929437	24930757

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257712554	chr2	24930476	24930640	24930500	24930612	NCOA1	NM_147233	3	21	11	+	24929437	24930757
257712554	chr2	24930476	24930640	24930500	24930612	NCOA1	NM_147223	2	22	11	+	24929437	24930757
257712554	chr2	24930476	24930640	24930500	24930612	NCOA1	NM_003743	1	21	11	+	24929437	24930757
236651988	chr2	24933854	24934011	24933874	24933985	NCOA1	NM_147233	3	21	12	+	24933800	24933980
236651988	chr2	24933854	24934011	24933874	24933985	NCOA1	NM_147223	2	22	12	+	24933800	24933980
236651988	chr2	24933854	24934011	24933874	24933985	NCOA1	NM_003743	1	21	12	+	24933800	24933980
236921093	chr2	24951218	24951384	24951243	24951356	NCOA1	NM_147233	3	21	14	+	24951177	24951345
236921093	chr2	24951218	24951384	24951243	24951356	NCOA1	NM_147223	2	22	14	+	24951177	24951345
236921093	chr2	24951218	24951384	24951243	24951356	NCOA1	NM_003743	1	21	14	+	24951177	24951345
236390124	chr2	24962181	24962349	24962208	24962325	NCOA1	NM_147233	3	21	16	+	24962301	24962402
236390124	chr2	24962181	24962349	24962208	24962325	NCOA1	NM_147223	2	22	16	+	24962301	24962402
236390124	chr2	24962181	24962349	24962208	24962325	NCOA1	NM_003743	1	21	16	+	24962301	24962402
237541465	chr2	24964772	24964938	24964793	24964915	NCOA1	NM_147233	3	21	17	+	24964653	24965055
237541465	chr2	24964772	24964938	24964793	24964915	NCOA1	NM_147223	2	22	17	+	24964653	24965055
237541465	chr2	24964772	24964938	24964793	24964915	NCOA1	NM_003743	1	21	17	+	24964653	24965055
236831541	chr2	24974933	24975075	24974957	24975047	NCOA1	NM_147233	3	21	18	+	24974851	24975025
236831541	chr2	24974933	24975075	24974957	24975047	NCOA1	NM_147223	2	22	18	+	24974851	24975025
236831541	chr2	24974933	24975075	24974957	24975047	NCOA1	NM_003743	1	21	18	+	24974851	24975025
236324463	chr2	24985560	24985685	24985580	24985661	NCOA1	NM_147233	3	21	20	+	24985556	24985645
236324463	chr2	24985560	24985685	24985580	24985661	NCOA1	NM_147223	2	22	20	+	24985556	24985645
236324463	chr2	24985560	24985685	24985580	24985661	NCOA1	NM_003743	1	21	20	+	24985556	24985645
240778363	chr2	24991221	24991366	24991240	24991339	NCOA1	NM_147223	2	22	22	+	24991090	24993570
240778363	chr2	24991221	24991366	24991240	24991339	NCOA1	NM_003743	1	21	21	+	24991090	24993570
240778363	chr2	24991221	24991366	24991240	24991339	NCOA1	NM_147233	3	21	21	+	24991093	24993570
229288760	chr2	25458561	25458724	25458580	25458696	DNMT3A	NM_022552	1	23	22	-	25458576	25458694
229288760	chr2	25458561	25458724	25458580	25458696	DNMT3A	NM_153759	2	19	18	-	25458576	25458694
229288760	chr2	25458561	25458724	25458580	25458696	DNMT3A	NM_175629	3	23	22	-	25458576	25458694
229972415	chr2	25463083	25463254	25463105	25463233	DNMT3A	NM_022552	1	23	19	-	25463171	25463319
229972415	chr2	25463083	25463254	25463105	25463233	DNMT3A	NM_153759	2	19	15	-	25463171	25463319
229972415	chr2	25463083	25463254	25463105	25463233	DNMT3A	NM_175629	3	23	19	-	25463171	25463319
228887501	chr2	25464529	25464702	25464551	25464678	DNMT3A	NM_022552	1	23	17	-	25464431	25464576
228887501	chr2	25464529	25464702	25464551	25464678	DNMT3A	NM_153759	2	19	13	-	25464431	25464576
228887501	chr2	25464529	25464702	25464551	25464678	DNMT3A	NM_175629	3	23	17	-	25464431	25464576
230818739	chr2	25467094	25467243	25467113	25467221	DNMT3A	NM_022552	1	23	15	-	25467024	25467207
230818739	chr2	25467094	25467243	25467113	25467221	DNMT3A	NM_153759	2	19	11	-	25467024	25467207
230818739	chr2	25467094	25467243	25467113	25467221	DNMT3A	NM_175629	3	23	15	-	25467024	25467207
229811892	chr2	25468865	25469033	25468887	25469012	DNMT3A	NM_022552	1	23	12	-	25468889	25468933
229811892	chr2	25468865	25469033	25468887	25469012	DNMT3A	NM_153759	2	19	8	-	25468889	25468933
229811892	chr2	25468865	25469033	25468887	25469012	DNMT3A	NM_175629	3	23	12	-	25468889	25468933
230304086	chr2	25469466	25469625	25469485	25469607	DNMT3A	NM_022552	1	23	10	-	25469489	25469645
230304086	chr2	25469466	25469625	25469485	25469607	DNMT3A	NM_153759	2	19	6	-	25469489	25469645

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230304086	chr2	25469466	25469625	25469485	25469607	DNMT3A	NM_175629	3	23	10	-	25469489	25469645
229127456	chr2	25470493	25470664	25470510	25470647	DNMT3A	NM_022552	1	23	8	-	25470460	25470618
229127456	chr2	25470493	25470664	25470510	25470647	DNMT3A	NM_153759	2	19	4	-	25470460	25470618
229127456	chr2	25470493	25470664	25470510	25470647	DNMT3A	NM_175629	3	23	8	-	25470460	25470618
228163085	chr2	25472461	25472635	25472488	25472606	DNMT3A	NM_153759	2	19	2	-	25472526	25472593
228637488	chr2	25498309	25498435	25498329	25498412	DNMT3A	NM_022552	1	23	5	-	25498369	25498412
228637488	chr2	25498309	25498435	25498329	25498412	DNMT3A	NM_175629	3	23	5	-	25498369	25498412
228377063	chr2	25522985	25523153	25523007	25523134	DNMT3A	NM_022552	1	23	3	-	25523008	25523112
228377063	chr2	25522985	25523153	25523007	25523134	DNMT3A	NM_175630	4	4	3	-	25523008	25523112
228377063	chr2	25522985	25523153	25523007	25523134	DNMT3A	NM_175629	3	23	3	-	25523008	25523112
222634980	chr2	29416307	29416480	29416328	29416458	ALK	NM_004304	1	29	29	-	29415640	29416788
223932892	chr2	29419568	29419728	29419596	29419703	ALK	NM_004304	1	29	28	-	29419636	29419726
223465409	chr2	29430004	29430168	29430026	29430143	ALK	NM_004304	1	29	26	-	29430037	29430138
224031566	chr2	29443666	29443800	29443689	29443772	ALK	NM_004304	1	29	23	-	29443572	29443701
223054323	chr2	29446207	29446346	29446230	29446325	ALK	NM_004304	1	29	20	-	29446208	29446394
223261736	chr2	29449725	29449897	29449746	29449875	ALK	NM_004304	1	29	18	-	29449788	29449940
223322625	chr2	29451820	29451962	29451840	29451942	ALK	NM_004304	1	29	16	-	29451750	29451932
222824298	chr2	29456477	29456609	29456498	29456587	ALK	NM_004304	1	29	14	-	29456431	29456562
222229645	chr2	29474038	29474163	29474058	29474142	ALK	NM_004304	1	29	12	-	29473971	29474133
223919754	chr2	29498259	29498392	29498281	29498368	ALK	NM_004304	1	29	10	-	29498268	29498362
223332223	chr2	29543547	29543674	29543571	29543654	ALK	NM_004304	1	29	7	-	29543617	29543748
223962614	chr2	29606478	29606633	29606503	29606611	ALK	NM_004304	1	29	5	-	29606598	29606725
222672272	chr2	29754918	29755087	29754939	29755059	ALK	NM_004304	1	29	4	-	29754781	29754982
222559481	chr2	29940325	29940481	29940348	29940458	ALK	NM_004304	1	29	2	-	29940444	29940563
224312077	chr2	30142986	30143160	30143006	30143141	ALK	NM_004304	1	29	1	-	30142859	30144477
222421427	chr2	30143351	30143519	30143373	30143502	ALK	NM_004304	1	29	1	-	30142859	30144477
228013043	chr2	42472654	42472807	42472679	42472784	EML4	NM_019063	2	23	2	+	42472645	42472827
228013043	chr2	42472654	42472807	42472679	42472784	EML4	NM_001145076	1	22	2	+	42472645	42472827
229865486	chr2	42488328	42488479	42488353	42488452	EML4	NM_019063	2	23	4	+	42488261	42488434
230702871	chr2	42491841	42491970	42491869	42491942	EML4	NM_019063	2	23	6	+	42491846	42491871
230702871	chr2	42491841	42491970	42491869	42491942	EML4	NM_001145076	1	22	5	+	42491846	42491871
231130507	chr2	42509969	42510124	42509995	42510097	EML4	NM_019063	2	23	8	+	42509963	42510112
231130507	chr2	42509969	42510124	42509995	42510097	EML4	NM_001145076	1	22	7	+	42509963	42510112
232300074	chr2	42513420	42513585	42513441	42513558	EML4	NM_019063	2	23	10	+	42513409	42513519
232300074	chr2	42513420	42513585	42513441	42513558	EML4	NM_001145076	1	22	9	+	42513409	42513519
230704422	chr2	42522270	42522409	42522295	42522382	EML4	NM_019063	2	23	12	+	42522265	42522399
230704422	chr2	42522270	42522409	42522295	42522382	EML4	NM_001145076	1	22	11	+	42522265	42522399
227685184	chr2	42528391	42528542	42528419	42528514	EML4	NM_019063	2	23	14	+	42528381	42528532
227685184	chr2	42528391	42528542	42528419	42528514	EML4	NM_001145076	1	22	13	+	42528381	42528532
228759872	chr2	42530367	42530522	42530395	42530497	EML4	NM_019063	2	23	16	+	42530455	42530586
228759872	chr2	42530367	42530522	42530395	42530497	EML4	NM_001145076	1	22	15	+	42530455	42530586

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230023992	chr2	42544432	42544588	42544463	42544567	EML4	NM_019063	2	23	19	+	42544567	42544664
230023992	chr2	42544432	42544588	42544463	42544567	EML4	NM_001145076	1	22	18	+	42544567	42544664
230565305	chr2	42553296	42553423	42553321	42553395	EML4	NM_019063	2	23	21	+	42553294	42553392
230565305	chr2	42553296	42553423	42553321	42553395	EML4	NM_001145076	1	22	20	+	42553294	42553392
228767305	chr2	42556929	42557101	42556956	42557076	EML4	NM_019063	2	23	23	+	42556874	42559688
228767305	chr2	42556929	42557101	42556956	42557076	EML4	NM_001145076	1	22	22	+	42556874	42559688
236942817	chr2	47630288	47630444	47630308	47630426	MSH2	NM_000251	1	16	1	+	47630263	47630541
237721702	chr2	47637228	47637400	47637251	47637374	MSH2	NM_000251	1	16	3	+	47637233	47637511
235692136	chr2	47639556	47639692	47639584	47639667	MSH2	NM_000251	1	16	4	+	47639553	47639699
239687739	chr2	47641403	47641541	47641429	47641516	MSH2	NM_000251	1	16	5	+	47641408	47641557
235559334	chr2	47643477	47643631	47643503	47643603	MSH2	NM_000251	1	16	6	+	47643435	47643568
258191574	chr2	47672581	47672755	47672608	47672730	MSH2	NM_000251	1	16	8	+	47672687	47672796
238699348	chr2	47698031	47698189	47698057	47698161	MSH2	NM_000251	1	16	11	+	47698104	47698201
241364904	chr2	47703388	47703552	47703413	47703525	MSH2	NM_000251	1	16	13	+	47703506	47703710
240405521	chr2	47705407	47705542	47705434	47705518	MSH2	NM_000251	1	16	14	+	47705411	47705658
235421010	chr2	47707906	47708033	47707930	47708004	MSH2	NM_000251	1	16	15	+	47707835	47708010
238481521	chr2	48010308	48010449	48010327	48010432	MSH6	NM_000179	1	10	1	+	48010221	48010632
236223903	chr2	48023033	48023162	48023057	48023137	MSH6	NM_000179	1	10	3	+	48023033	48023202
257802730	chr2	48025938	48026079	48025963	48026052	MSH6	NM_000179	1	10	4	+	48025750	48028294
257801277	chr2	48026410	48026579	48026435	48026558	MSH6	NM_000179	1	10	4	+	48025750	48028294
238018062	chr2	48026833	48027004	48026857	48026984	MSH6	NM_000179	1	10	4	+	48025750	48028294
257742460	chr2	48027266	48027404	48027290	48027377	MSH6	NM_000179	1	10	4	+	48025750	48028294
257801983	chr2	48027612	48027761	48027633	48027734	MSH6	NM_000179	1	10	4	+	48025750	48028294
257920839	chr2	48028049	48028218	48028073	48028194	MSH6	NM_000179	1	10	4	+	48025750	48028294
238236064	chr2	48030749	48030910	48030771	48030881	MSH6	NM_000179	1	10	5	+	48030559	48030824
236905420	chr2	48032794	48032967	48032817	48032939	MSH6	NM_000179	1	10	7	+	48032757	48032846
235884794	chr2	48033536	48033680	48033558	48033652	MSH6	NM_000179	1	10	9	+	48033591	48033790
222530987	chr2	60679586	60679754	60679606	60679734	BCL11A	NM_018014	1	5	5	-	60678302	60679801
222530987	chr2	60679586	60679754	60679606	60679734	BCL11A	NM_138559	3	5	5	-	60678302	60679801
224587792	chr2	60687699	60687823	60687720	60687799	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224607366	chr2	60688113	60688272	60688133	60688255	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224607366	chr2	60688113	60688272	60688133	60688255	BCL11A	NM_018014	1	5	4	-	60687817	60689559
224593724	chr2	60688520	60688655	60688538	60688638	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224593724	chr2	60688520	60688655	60688538	60688638	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223035091	chr2	60688993	60689119	60689013	60689099	BCL11A	NM_022893	2	4	4	-	60684329	60689559
223035091	chr2	60688993	60689119	60689013	60689099	BCL11A	NM_018014	1	5	4	-	60687817	60689559
222835503	chr2	60689436	60689603	60689464	60689576	BCL11A	NM_022893	2	4	4	-	60684329	60689559
222835503	chr2	60689436	60689603	60689464	60689576	BCL11A	NM_138559	3	5	4	-	60689417	60689559
222835503	chr2	60689436	60689603	60689464	60689576	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223747275	chr2	60773234	60773368	60773256	60773346	BCL11A	NM_018014	1	5	2	-	60773106	60773435
223747275	chr2	60773234	60773368	60773256	60773346	BCL11A	NM_022893	2	4	2	-	60773106	60773435

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223747275	chr2	60773234	60773368	60773256	60773346	BCL11A	NM_138559	3	5	2	-	60773106	60773435
238477567	chr2	61118773	61118915	61118801	61118896	REL	NM_002908	1	11	2	+	61118818	61118960
242259751	chr2	61143905	61144060	61143931	61144035	REL	NM_002908	1	11	5	+	61144012	61144152
239630735	chr2	61145533	61145685	61145561	61145665	REL	NM_002908	1	11	7	+	61145529	61145741
241921610	chr2	61148772	61148929	61148804	61148903	REL	NM_002908	1	11	11	+	61148898	61150178
241960860	chr2	61149214	61149375	61149236	61149349	REL	NM_002908	1	11	11	+	61148898	61150178
274394971	chr2	61705884	61706038	61705908	61706009	XPO1	NM_003400	1	25	25	-	61705069	61706101
272816705	chr2	61710051	61710179	61710074	61710153	XPO1	NM_003400	1	25	22	-	61710092	61710226
273154335	chr2	61712843	61712975	61712871	61712947	XPO1	NM_003400	1	25	20	-	61712903	61713097
272971139	chr2	61715320	61715490	61715344	61715462	XPO1	NM_003400	1	25	19	-	61715300	61715406
273140702	chr2	61717721	61717887	61717747	61717866	XPO1	NM_003400	1	25	17	-	61717777	61717911
273148752	chr2	61719247	61719381	61719269	61719358	XPO1	NM_003400	1	25	16	-	61719170	61719333
273457358	chr2	61719789	61719923	61719816	61719895	XPO1	NM_003400	1	25	14	-	61719702	61719883
273625083	chr2	61721144	61721307	61721173	61721281	XPO1	NM_003400	1	25	12	-	61721029	61721226
274028676	chr2	61723911	61724083	61723940	61724055	XPO1	NM_003400	1	25	10	-	61724014	61724142
272982782	chr2	61725883	61726053	61725906	61726026	XPO1	NM_003400	1	25	8	-	61726000	61726048
272982782	chr2	61725883	61726053	61725906	61726026	XPO1	NM_003400	1	25	9	-	61725808	61725927
274365520	chr2	61729344	61729499	61729371	61729474	XPO1	NM_003400	1	25	5	-	61729384	61729445
274234778	chr2	61753528	61753657	61753556	61753632	XPO1	NM_003400	1	25	3	-	61753555	61753656
299021195	chr2	85360907	85361074	85360926	85361057	TCF7L1	NM_031283	1	12	1	+	85360583	85361056
299128474	chr2	85510574	85510727	85510595	85510701	TCF7L1	NM_031283	1	12	4	+	85510618	85510701
299193777	chr2	85531329	85531502	85531350	85531480	TCF7L1	NM_031283	1	12	7	+	85531378	85531461
299040700	chr2	85533378	85533508	85533401	85533488	TCF7L1	NM_031283	1	12	9	+	85533329	85533488
299260155	chr2	85536157	85536318	85536176	85536300	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
299266795	chr2	85536550	85536720	85536570	85536697	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
222924649	chr2	100170836	100170975	100170855	100170955	AFF3	NM_002285	2	24	23	-	100170773	100170996
222924649	chr2	100170836	100170975	100170855	100170955	AFF3	NM_001025108	1	24	23	-	100170773	100170996
225144702	chr2	100176760	100176920	100176781	100176898	AFF3	NM_002285	2	24	20	-	100176827	100176898
225144702	chr2	100176760	100176920	100176781	100176898	AFF3	NM_001025108	1	24	20	-	100176827	100176898
224334698	chr2	100194761	100194934	100194788	100194906	AFF3	NM_002285	2	24	17	-	100194789	100194913
224334698	chr2	100194761	100194934	100194788	100194906	AFF3	NM_001025108	1	24	17	-	100194789	100194913
222862702	chr2	100203498	100203644	100203519	100203620	AFF3	NM_002285	2	24	15	-	100203616	100203740
222862702	chr2	100203498	100203644	100203519	100203620	AFF3	NM_001025108	1	24	15	-	100203616	100203740
225176601	chr2	100209797	100209940	100209818	100209920	AFF3	NM_002285	2	24	14	-	100209657	100210751
225176601	chr2	100209797	100209940	100209818	100209920	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223845660	chr2	100210332	100210499	100210349	100210477	AFF3	NM_002285	2	24	14	-	100209657	100210751
223845660	chr2	100210332	100210499	100210349	100210477	AFF3	NM_001025108	1	24	14	-	100209657	100210751
225178542	chr2	100210655	100210787	100210678	100210761	AFF3	NM_002285	2	24	14	-	100209657	100210751
225178542	chr2	100210655	100210787	100210678	100210761	AFF3	NM_001025108	1	24	14	-	100209657	100210751
224395033	chr2	100288906	100289080	100288928	100289052	AFF3	NM_002285	2	24	11	-	100289000	100289051
224395033	chr2	100288906	100289080	100288928	100289052	AFF3	NM_001025108	1	24	11	-	100289000	100289051

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224016278	chr2	100453866	100454035	100453887	100454007	AFF3	NM_002285	2	24	7	-	100453939	100453986
224016278	chr2	100453866	100454035	100453887	100454007	AFF3	NM_001025108	1	24	7	-	100453939	100453986
223106451	chr2	100623429	100623579	100623450	100623551	AFF3	NM_002285	2	24	6	-	100623094	100623479
223106451	chr2	100623429	100623579	100623450	100623551	AFF3	NM_001025108	1	24	6	-	100623094	100623479
223198887	chr2	100625151	100625318	100625173	100625289	AFF3	NM_002285	2	24	4	-	100625274	100625394
223198887	chr2	100625151	100625318	100625173	100625289	AFF3	NM_001025108	1	24	4	-	100625274	100625394
237445497	chr2	113977578	113977751	113977601	113977727	PAX8	NM_003466	1	12	11	-	113977669	113977755
237445497	chr2	113977578	113977751	113977601	113977727	PAX8	NM_013992	4	9	8	-	113977669	113977755
237445497	chr2	113977578	113977751	113977601	113977727	PAX8	NM_013952	2	12	11	-	113977669	113977755
237445497	chr2	113977578	113977751	113977601	113977727	PAX8	NM_013953	3	10	9	-	113977669	113977755
237172749	chr2	113993062	113993197	113993084	113993176	PAX8	NM_003466	1	12	9	-	113992971	113993159
234925392	chr2	113999155	113999312	113999175	113999290	PAX8	NM_003466	1	12	7	-	113999128	113999303
234925392	chr2	113999155	113999312	113999175	113999290	PAX8	NM_013992	4	9	7	-	113999128	113999303
234925392	chr2	113999155	113999312	113999175	113999290	PAX8	NM_013952	2	12	7	-	113999128	113999303
234925392	chr2	113999155	113999312	113999175	113999290	PAX8	NM_013953	3	10	7	-	113999128	113999303
237516735	chr2	114000227	114000382	114000249	114000357	PAX8	NM_003466	1	12	5	-	114000267	114000355
237516735	chr2	114000227	114000382	114000249	114000357	PAX8	NM_013992	4	9	5	-	114000267	114000355
237516735	chr2	114000227	114000382	114000249	114000357	PAX8	NM_013952	2	12	5	-	114000267	114000355
237516735	chr2	114000227	114000382	114000249	114000357	PAX8	NM_013953	3	10	5	-	114000267	114000355
236422771	chr2	114004381	114004552	114004400	114004531	PAX8	NM_003466	1	12	3	-	114004331	114004496
236422771	chr2	114004381	114004552	114004400	114004531	PAX8	NM_013992	4	9	3	-	114004331	114004496
236422771	chr2	114004381	114004552	114004400	114004531	PAX8	NM_013952	2	12	3	-	114004331	114004496
236422771	chr2	114004381	114004552	114004400	114004531	PAX8	NM_013953	3	10	3	-	114004331	114004496
231929356	chr2	128016846	128017020	128016869	128017001	ERCC3	NM_000122	1	15	14	-	128016872	128017024
230524172	chr2	128028873	128029033	128028894	128029009	ERCC3	NM_000122	1	15	12	-	128028912	128029029
232219152	chr2	128036832	128036990	128036855	128036962	ERCC3	NM_000122	1	15	10	-	128036749	128036951
231011331	chr2	128044360	128044503	128044380	128044480	ERCC3	NM_000122	1	15	8	-	128044279	128044593
230495533	chr2	128046808	128046978	128046830	128046953	ERCC3	NM_000122	1	15	6	-	128046913	128047077
230651672	chr2	128047714	128047885	128047736	128047858	ERCC3	NM_000122	1	15	4	-	128047800	128047849
230397849	chr2	128051153	128051323	128051177	128051297	ERCC3	NM_000122	1	15	2	-	128051089	128051294
271151069	chr2	140990836	140990982	140990865	140990954	LRP1B	NM_018557	1	91	91	-	140988996	140990895
270489914	chr2	141004655	141004780	141004680	141004753	LRP1B	NM_018557	1	91	87	-	141004655	141004731
270953646	chr2	141032037	141032161	141032058	141032134	LRP1B	NM_018557	1	91	85	-	141031993	141032167
271815793	chr2	141072503	141072650	141072526	141072624	LRP1B	NM_018557	1	91	83	-	141072504	141072668
272553089	chr2	141079528	141079672	141079549	141079647	LRP1B	NM_018557	1	91	82	-	141079532	141079657
270778060	chr2	141091978	141092148	141092006	141092128	LRP1B	NM_018557	1	91	79	-	141092022	141092128
272182416	chr2	141108361	141108534	141108385	141108505	LRP1B	NM_018557	1	91	77	-	141108366	141108607
271324689	chr2	141113847	141114016	141113873	141113989	LRP1B	NM_018557	1	91	75	-	141113911	141114045
269676123	chr2	141116273	141116434	141116298	141116410	LRP1B	NM_018557	1	91	73	-	141116390	141116515
270378995	chr2	141128178	141128332	141128204	141128307	LRP1B	NM_018557	1	91	71	-	141128279	141128411
270006083	chr2	141130604	141130774	141130629	141130746	LRP1B	NM_018557	1	91	69	-	141130577	141130706

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271018240	chr2	141199942	141200115	141199969	141200093	LRP1B	NM_018557	1	91	66	-	141200073	141200192
271271550	chr2	141202033	141202181	141202061	141202156	LRP1B	NM_018557	1	91	64	-	141202132	141202248
269945957	chr2	141213965	141214097	141213992	141214073	LRP1B	NM_018557	1	91	62	-	141214024	141214172
270035446	chr2	141215145	141215305	141215172	141215278	LRP1B	NM_018557	1	91	61	-	141215032	141215220
270759776	chr2	141242899	141243064	141242925	141243041	LRP1B	NM_018557	1	91	59	-	141242912	141243093
272108799	chr2	141250102	141250276	141250130	141250248	LRP1B	NM_018557	1	91	57	-	141250177	141250262
271996862	chr2	141253281	141253450	141253305	141253426	LRP1B	NM_018557	1	91	56	-	141253134	141253317
269951298	chr2	141260401	141260575	141260426	141260549	LRP1B	NM_018557	1	91	54	-	141260532	141260672
270018834	chr2	141264387	141264541	141264408	141264513	LRP1B	NM_018557	1	91	53	-	141264365	141264487
271224484	chr2	141274360	141274491	141274389	141274466	LRP1B	NM_018557	1	91	50	-	141274458	141274580
270211972	chr2	141283449	141283573	141283471	141283546	LRP1B	NM_018557	1	91	49	-	141283413	141283562
270348272	chr2	141291481	141291653	141291510	141291625	LRP1B	NM_018557	1	91	47	-	141291590	141291709
270785708	chr2	141298475	141298648	141298502	141298624	LRP1B	NM_018557	1	91	45	-	141298542	141298667
270032226	chr2	141299462	141299615	141299485	141299587	LRP1B	NM_018557	1	91	44	-	141299348	141299540
272058794	chr2	141359006	141359149	141359035	141359127	LRP1B	NM_018557	1	91	42	-	141359019	141359208
270643416	chr2	141457872	141457998	141457899	141457970	LRP1B	NM_018557	1	91	41	-	141457819	141458190
269668401	chr2	141459371	141459518	141459392	141459494	LRP1B	NM_018557	1	91	40	-	141459290	141459414
270130098	chr2	141459971	141460099	141460000	141460075	LRP1B	NM_018557	1	91	38	-	141459996	141460122
269547606	chr2	141474214	141474386	141474241	141474358	LRP1B	NM_018557	1	91	36	-	141474251	141474385
272051138	chr2	141528406	141528572	141528433	141528547	LRP1B	NM_018557	1	91	34	-	141528450	141528575
270097980	chr2	141571291	141571445	141571312	141571417	LRP1B	NM_018557	1	91	32	-	141571226	141571375
269724225	chr2	141598582	141598735	141598609	141598708	LRP1B	NM_018557	1	91	30	-	141598487	141598661
271511886	chr2	141609212	141609340	141609241	141609318	LRP1B	NM_018557	1	91	28	-	141609221	141609352
272210303	chr2	141625296	141625461	141625320	141625433	LRP1B	NM_018557	1	91	27	-	141625159	141625403
270747942	chr2	141641385	141641532	141641409	141641510	LRP1B	NM_018557	1	91	25	-	141641386	141641590
270177942	chr2	141660556	141660712	141660577	141660691	LRP1B	NM_018557	1	91	23	-	141660489	141660734
271193101	chr2	141665555	141665726	141665579	141665701	LRP1B	NM_018557	1	91	22	-	141665446	141665646
269616350	chr2	141707803	141707936	141707831	141707908	LRP1B	NM_018557	1	91	20	-	141707804	141707971
272690727	chr2	141739708	141739857	141739734	141739833	LRP1B	NM_018557	1	91	18	-	141739729	141739845
271828833	chr2	141751599	141751757	141751619	141751728	LRP1B	NM_018557	1	91	16	-	141751564	141751704
270830634	chr2	141771123	141771267	141771147	141771238	LRP1B	NM_018557	1	91	14	-	141771125	141771314
270947844	chr2	141773384	141773535	141773409	141773507	LRP1B	NM_018557	1	91	13	-	141773265	141773484
271515969	chr2	141806568	141806711	141806590	141806682	LRP1B	NM_018557	1	91	11	-	141806555	141806791
271073809	chr2	141816367	141816540	141816392	141816512	LRP1B	NM_018557	1	91	9	-	141816452	141816623
270067593	chr2	141819739	141819906	141819761	141819886	LRP1B	NM_018557	1	91	8	-	141819620	141819842
269722190	chr2	141986774	141986926	141986802	141986898	LRP1B	NM_018557	1	91	6	-	141986752	141987009
270482952	chr2	142004790	142004964	142004818	142004936	LRP1B	NM_018557	1	91	5	-	142004795	142004923
269844764	chr2	142237936	142238108	142237960	142238089	LRP1B	NM_018557	1	91	3	-	142237965	142238102
271358429	chr2	142888246	142888414	142888268	142888394	LRP1B	NM_018557	1	91	1	-	142888217	142889270
281673029	chr2	148653882	148654045	148653909	148654017	ACVR2A	NM_001616	1	11	2	+	148653870	148654077
282050328	chr2	148657300	148657438	148657321	148657416	ACVR2A	NM_001616	1	11	4	+	148657313	148657467

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
283559913	chr2	148674832	148674958	148674862	148674937	ACVR2A	NM_001616	1	11	6	+	148674852	148674995
281933393	chr2	148676108	148676276	148676135	148676248	ACVR2A	NM_001616	1	11	7	+	148676016	148676161
283678518	chr2	148680540	148680664	148680559	148680643	ACVR2A	NM_001616	1	11	9	+	148680542	148680680
284556658	chr2	148683696	148683841	148683723	148683814	ACVR2A	NM_001616	1	11	10	+	148683600	148683730
235204393	chr2	178095529	178095693	178095554	178095666	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235204393	chr2	178095529	178095693	178095554	178095666	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235204393	chr2	178095529	178095693	178095554	178095666	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235244146	chr2	178095886	178096059	178095912	178096034	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235244146	chr2	178095886	178096059	178095912	178096034	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235244146	chr2	178095886	178096059	178095912	178096034	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
239915882	chr2	178096385	178096542	178096410	178096515	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
239915882	chr2	178096385	178096542	178096410	178096515	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
239915882	chr2	178096385	178096542	178096410	178096515	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235078261	chr2	178097014	178097178	178097035	178097154	NFE2L2	NM_001145412	1	5	4	-	178097120	178097311
235078261	chr2	178097014	178097178	178097035	178097154	NFE2L2	NM_006164	3	5	4	-	178097120	178097311
235078261	chr2	178097014	178097178	178097035	178097154	NFE2L2	NM_001145413	2	5	4	-	178097120	178097290
241787011	chr2	178098023	178098147	178098050	178098114	NFE2L2	NM_001145412	1	5	3	-	178097978	178098067
241787011	chr2	178098023	178098147	178098050	178098114	NFE2L2	NM_001145413	2	5	3	-	178097978	178098067
241787011	chr2	178098023	178098147	178098050	178098114	NFE2L2	NM_006164	3	5	3	-	178097978	178098067
238586175	chr2	178098931	178099103	178098960	178099082	NFE2L2	NM_001145412	1	5	2	-	178098733	178098999
238586175	chr2	178098931	178099103	178098960	178099082	NFE2L2	NM_001145413	2	5	2	-	178098733	178098999
238586175	chr2	178098931	178099103	178098960	178099082	NFE2L2	NM_006164	3	5	2	-	178098733	178098999
235896708	chr2	190660415	190660550	190660445	190660528	PMS1	NM_001128144	3	12	3	+	190660495	190660677
235896708	chr2	190660415	190660550	190660445	190660528	PMS1	NM_000534	1	13	3	+	190660495	190660677
235896708	chr2	190660415	190660550	190660445	190660528	PMS1	NM_001128143	2	12	3	+	190660495	190660677
236649472	chr2	190670309	190670480	190670337	190670455	PMS1	NM_001128144	3	12	4	+	190670378	190670480
236649472	chr2	190670309	190670480	190670337	190670455	PMS1	NM_000534	1	13	4	+	190670378	190670480
236649472	chr2	190670309	190670480	190670337	190670455	PMS1	NM_001128143	2	12	4	+	190670378	190670480
236696430	chr2	190708579	190708740	190708608	190708716	PMS1	NM_001128144	3	12	6	+	190708690	190708806
236696430	chr2	190708579	190708740	190708608	190708716	PMS1	NM_000534	1	13	6	+	190708690	190708806
239233765	chr2	190718586	190718760	190718614	190718735	PMS1	NM_001128144	3	12	8	+	190718665	190718808
239233765	chr2	190718586	190718760	190718614	190718735	PMS1	NM_000534	1	13	8	+	190718665	190718808
239233765	chr2	190718586	190718760	190718614	190718735	PMS1	NM_001128143	2	12	7	+	190718665	190718808
241089026	chr2	190719291	190719418	190719319	190719392	PMS1	NM_001128144	3	12	9	+	190718965	190719854
241089026	chr2	190719291	190719418	190719319	190719392	PMS1	NM_000534	1	13	9	+	190718965	190719854
241089026	chr2	190719291	190719418	190719319	190719392	PMS1	NM_001128143	2	12	8	+	190718965	190719854
237614436	chr2	190719777	190719901	190719805	190719874	PMS1	NM_001128144	3	12	9	+	190718965	190719854
237614436	chr2	190719777	190719901	190719805	190719874	PMS1	NM_000534	1	13	9	+	190718965	190719854
237614436	chr2	190719777	190719901	190719805	190719874	PMS1	NM_001128143	2	12	8	+	190718965	190719854
238278369	chr2	190728757	190728923	190728785	190728897	PMS1	NM_000534	1	13	10	+	190728469	190728954
238278369	chr2	190728757	190728923	190728785	190728897	PMS1	NM_001128143	2	12	9	+	190728469	190728954

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235549618	chr2	190738126	190738292	190738154	190738268	PMS1	NM_001128144	3	12	11	+	190738222	190738382
235549618	chr2	190738126	190738292	190738154	190738268	PMS1	NM_000534	1	13	12	+	190738222	190738382
235549618	chr2	190738126	190738292	190738154	190738268	PMS1	NM_001128143	2	12	11	+	190738222	190738382
273150923	chr2	198257703	198257850	198257731	198257825	SF3B1	NM_012433	2	25	24	-	198257696	198257912
272797574	chr2	198260813	198260973	198260840	198260946	SF3B1	NM_012433	2	25	23	-	198260780	198261052
273369319	chr2	198262792	198262934	198262817	198262901	SF3B1	NM_012433	2	25	22	-	198262709	198262840
273484011	chr2	198264792	198264965	198264812	198264937	SF3B1	NM_012433	2	25	20	-	198264779	198264890
273894474	chr2	198265439	198265605	198265467	198265580	SF3B1	NM_012433	2	25	18	-	198265439	198265660
273459104	chr2	198266155	198266323	198266179	198266294	SF3B1	NM_012433	2	25	17	-	198266124	198266249
273797805	chr2	198266731	198266886	198266759	198266860	SF3B1	NM_012433	2	25	15	-	198266709	198266854
272738068	chr2	198267568	198267707	198267599	198267685	SF3B1	NM_012433	2	25	13	-	198267673	198267759
272997140	chr2	198268399	198268525	198268422	198268498	SF3B1	NM_012433	2	25	12	-	198268309	198268488
273567045	chr2	198270150	198270322	198270172	198270295	SF3B1	NM_012433	2	25	10	-	198269999	198270196
273051341	chr2	198273065	198273196	198273094	198273172	SF3B1	NM_012433	2	25	8	-	198273093	198273305
272918534	chr2	198274522	198274659	198274547	198274636	SF3B1	NM_012433	2	25	7	-	198274494	198274731
273461017	chr2	198283194	198283346	198283222	198283318	SF3B1	NM_012433	2	25	5	-	198283233	198283312
272960133	chr2	198285221	198285361	198285241	198285332	SF3B1	NM_012433	2	25	4	-	198285152	198285266
272960133	chr2	198285221	198285361	198285241	198285332	SF3B1	NM_001005526	1	5	4	-	198285152	198285266
273838101	chr2	198288531	198288689	198288556	198288663	SF3B1	NM_012433	2	25	2	-	198288532	198288698
273838101	chr2	198288531	198288689	198288556	198288663	SF3B1	NM_001005526	1	5	2	-	198288532	198288698
226048694	chr2	208420390	208420518	208420411	208420492	CREB1	NM_134442	2	9	2	+	208420352	208420473
226048694	chr2	208420390	208420518	208420411	208420492	CREB1	NM_004379	1	8	2	+	208420352	208420473
226300413	chr2	208432047	208432221	208432071	208432196	CREB1	NM_134442	2	9	5	+	208432187	208432287
226300413	chr2	208432047	208432221	208432071	208432196	CREB1	NM_004379	1	8	4	+	208432187	208432287
225343210	chr2	208435004	208435143	208435025	208435117	CREB1	NM_134442	2	9	6	+	208434903	208435045
225343210	chr2	208435004	208435143	208435025	208435117	CREB1	NM_004379	1	8	5	+	208434903	208435045
225571993	chr2	208442267	208442441	208442288	208442418	CREB1	NM_134442	2	9	8	+	208442229	208442379
225571993	chr2	208442267	208442441	208442288	208442418	CREB1	NM_004379	1	8	7	+	208442229	208442379
229588098	chr2	209101814	209101969	209101842	209101941	IDH1	NM_005896	1	10	10	-	209100953	209101893
228844690	chr2	209104592	209104754	209104612	209104730	IDH1	NM_005896	1	10	8	-	209104587	209104727
229309639	chr2	209108183	209108351	209108211	209108328	IDH1	NM_005896	1	10	6	-	209108151	209108328
326755888	chr2	209112973	209113128	209112998	209113103	IDH1	NM_005896	1	10	4	-	209113093	209113384
228491214	chr2	209116102	209116262	209116126	209116244	IDH1	NM_005896	1	10	3	-	209116154	209116291
227734483	chr2	212248443	212248616	212248469	212248590	ERBB4	NM_001042599	1	27	27	-	212240442	212248785
227734483	chr2	212248443	212248616	212248469	212248590	ERBB4	NM_005235	2	28	28	-	212240442	212248785
229603945	chr2	212251665	212251834	212251685	212251814	ERBB4	NM_001042599	1	27	26	-	212251578	212251875
229603945	chr2	212251665	212251834	212251685	212251814	ERBB4	NM_005235	2	28	27	-	212251578	212251875
230418951	chr2	212285161	212285299	212285188	212285271	ERBB4	NM_001042599	1	27	25	-	212285166	212285336
230418951	chr2	212285161	212285299	212285188	212285271	ERBB4	NM_005235	2	28	25	-	212285166	212285336
326755228	chr2	212288821	212288973	212288854	212288952	ERBB4	NM_001042599	1	27	23	-	212288880	212289026
326755228	chr2	212288821	212288973	212288854	212288952	ERBB4	NM_005235	2	28	23	-	212288880	212289026

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230503742	chr2	212295717	212295876	212295740	212295849	ERBB4	NM_001042599	1	27	21	-	212295670	212295825
230503742	chr2	212295717	212295876	212295740	212295849	ERBB4	NM_005235	2	28	21	-	212295670	212295825
230066712	chr2	212483872	212484002	212483894	212483979	ERBB4	NM_001042599	1	27	19	-	212483902	212484000
230066712	chr2	212483872	212484002	212483894	212483979	ERBB4	NM_005235	2	28	19	-	212483902	212484000
232302945	chr2	212495228	212495380	212495255	212495352	ERBB4	NM_001042599	1	27	17	-	212495187	212495319
232302945	chr2	212495228	212495380	212495255	212495352	ERBB4	NM_005235	2	28	17	-	212495187	212495319
231683604	chr2	212537843	212538008	212537871	212537985	ERBB4	NM_001042599	1	27	14	-	212537889	212537982
231683604	chr2	212537843	212538008	212537871	212537985	ERBB4	NM_005235	2	28	14	-	212537889	212537982
231167100	chr2	212566702	212566827	212566724	212566805	ERBB4	NM_001042599	1	27	12	-	212566692	212566891
231167100	chr2	212566702	212566827	212566724	212566805	ERBB4	NM_005235	2	28	12	-	212566692	212566891
230217499	chr2	212570011	212570135	212570032	212570108	ERBB4	NM_001042599	1	27	10	-	212570043	212570116
230217499	chr2	212570011	212570135	212570032	212570108	ERBB4	NM_005235	2	28	10	-	212570043	212570116
326987374	chr2	212578202	212578338	212578231	212578317	ERBB4	NM_001042599	1	27	8	-	212578260	212578373
326987374	chr2	212578202	212578338	212578231	212578317	ERBB4	NM_005235	2	28	8	-	212578260	212578373
230725745	chr2	212589663	212589828	212589686	212589806	ERBB4	NM_001042599	1	27	6	-	212589801	212589919
230725745	chr2	212589663	212589828	212589686	212589806	ERBB4	NM_005235	2	28	6	-	212589801	212589919
232318991	chr2	212652775	212652940	212652797	212652913	ERBB4	NM_001042599	1	27	4	-	212652750	212652884
232318991	chr2	212652775	212652940	212652797	212652913	ERBB4	NM_005235	2	28	4	-	212652750	212652884
230715519	chr2	212989407	212989562	212989429	212989535	ERBB4	NM_001042599	1	27	2	-	212989477	212989628
230715519	chr2	212989407	212989562	212989429	212989535	ERBB4	NM_005235	2	28	2	-	212989477	212989628
280435079	chr2	216226178	216226336	216226205	216226309	FN1	NM_212476	4	44	44	-	216225179	216226349
280435079	chr2	216226178	216226336	216226205	216226309	FN1	NM_212478	5	46	46	-	216225179	216226349
280435079	chr2	216226178	216226336	216226205	216226309	FN1	NM_212482	6	46	46	-	216225179	216226349
280435079	chr2	216226178	216226336	216226205	216226309	FN1	NM_212474	3	44	44	-	216225179	216226349
280435079	chr2	216226178	216226336	216226205	216226309	FN1	NM_002026	1	46	46	-	216225179	216226349
277903609	chr2	216230128	216230302	216230156	216230280	FN1	NM_212476	4	44	41	-	216230228	216230353
277903609	chr2	216230128	216230302	216230156	216230280	FN1	NM_212478	5	46	43	-	216230228	216230353
277903609	chr2	216230128	216230302	216230156	216230280	FN1	NM_212482	6	46	43	-	216230228	216230353
277903609	chr2	216230128	216230302	216230156	216230280	FN1	NM_212474	3	44	41	-	216230228	216230353
277903609	chr2	216230128	216230302	216230156	216230280	FN1	NM_002026	1	46	43	-	216230228	216230353
277883385	chr2	216234911	216235058	216234938	216235037	FN1	NM_212476	4	44	39	-	216235017	216235155
277883385	chr2	216234911	216235058	216234938	216235037	FN1	NM_212478	5	46	41	-	216235017	216235155
277883385	chr2	216234911	216235058	216234938	216235037	FN1	NM_212482	6	46	41	-	216235017	216235155
277883385	chr2	216234911	216235058	216234938	216235037	FN1	NM_212474	3	44	39	-	216235017	216235155
277883385	chr2	216234911	216235058	216234938	216235037	FN1	NM_002026	1	46	41	-	216235017	216235155
278633561	chr2	216236829	216236996	216236848	216236973	FN1	NM_212478	5	46	39	-	216236832	216237023
278633561	chr2	216236829	216236996	216236848	216236973	FN1	NM_002026	1	46	39	-	216236832	216237098
278633561	chr2	216236829	216236996	216236848	216236973	FN1	NM_212476	4	44	38	-	216236632	216237098
278633561	chr2	216236829	216236996	216236848	216236973	FN1	NM_212482	6	46	40	-	216236632	216237098
279241863	chr2	216240014	216240188	216240038	216240166	FN1	NM_212476	4	44	36	-	216239937	216240116
279241863	chr2	216240014	216240188	216240038	216240166	FN1	NM_212478	5	46	37	-	216239937	216240116

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279241863	chr2	216240014	216240188	216240038	216240166	FN1	NM_212482	6	46	38	-	216239937	216240116
279241863	chr2	216240014	216240188	216240038	216240166	FN1	NM_212474	3	44	36	-	216239937	216240116
279241863	chr2	216240014	216240188	216240038	216240166	FN1	NM_002026	1	46	37	-	216239937	216240116
280817280	chr2	216241283	216241430	216241303	216241406	FN1	NM_212476	4	44	34	-	216241221	216241397
280817280	chr2	216241283	216241430	216241303	216241406	FN1	NM_212478	5	46	35	-	216241221	216241397
280817280	chr2	216241283	216241430	216241303	216241406	FN1	NM_212482	6	46	36	-	216241221	216241397
280817280	chr2	216241283	216241430	216241303	216241406	FN1	NM_212474	3	44	34	-	216241221	216241397
280817280	chr2	216241283	216241430	216241303	216241406	FN1	NM_002026	1	46	35	-	216241221	216241397
279847159	chr2	216243934	216244066	216243953	216244040	FN1	NM_212476	4	44	32	-	216243853	216244040
279847159	chr2	216243934	216244066	216243953	216244040	FN1	NM_212478	5	46	33	-	216243853	216244040
279847159	chr2	216243934	216244066	216243953	216244040	FN1	NM_212482	6	46	34	-	216243853	216244040
279847159	chr2	216243934	216244066	216243953	216244040	FN1	NM_212474	3	44	32	-	216243853	216244040
279847159	chr2	216243934	216244066	216243953	216244040	FN1	NM_002026	1	46	33	-	216243853	216244040
280831534	chr2	216246808	216246958	216246836	216246935	FN1	NM_212476	4	44	31	-	216246935	216247048
280831534	chr2	216246808	216246958	216246836	216246935	FN1	NM_212478	5	46	31	-	216246935	216247048
280831534	chr2	216246808	216246958	216246836	216246935	FN1	NM_212482	6	46	32	-	216246935	216247048
280831534	chr2	216246808	216246958	216246836	216246935	FN1	NM_212474	3	44	31	-	216246935	216247048
280831534	chr2	216246808	216246958	216246836	216246935	FN1	NM_002026	1	46	31	-	216246935	216247048
279318659	chr2	216248671	216248844	216248694	216248817	FN1	NM_212476	4	44	29	-	216248743	216248907
279318659	chr2	216248671	216248844	216248694	216248817	FN1	NM_212478	5	46	29	-	216248743	216248907
279318659	chr2	216248671	216248844	216248694	216248817	FN1	NM_212482	6	46	30	-	216248743	216248907
279318659	chr2	216248671	216248844	216248694	216248817	FN1	NM_212474	3	44	29	-	216248743	216248907
279318659	chr2	216248671	216248844	216248694	216248817	FN1	NM_002026	1	46	29	-	216248743	216248907
279051441	chr2	216251477	216251634	216251499	216251610	FN1	NM_212476	4	44	27	-	216251412	216251681
279051441	chr2	216251477	216251634	216251499	216251610	FN1	NM_212478	5	46	27	-	216251412	216251681
279051441	chr2	216251477	216251634	216251499	216251610	FN1	NM_212482	6	46	28	-	216251412	216251681
279051441	chr2	216251477	216251634	216251499	216251610	FN1	NM_212474	3	44	27	-	216251412	216251681
279051441	chr2	216251477	216251634	216251499	216251610	FN1	NM_002026	1	46	27	-	216251412	216251681
277889550	chr2	216256389	216256563	216256413	216256538	FN1	NM_212476	4	44	25	-	216256355	216256537
277889550	chr2	216256389	216256563	216256413	216256538	FN1	NM_212478	5	46	25	-	216256355	216256537
277889550	chr2	216256389	216256563	216256413	216256538	FN1	NM_212482	6	46	26	-	216256355	216256537
277889550	chr2	216256389	216256563	216256413	216256538	FN1	NM_212474	3	44	25	-	216256355	216256537
277889550	chr2	216256389	216256563	216256413	216256538	FN1	NM_002026	1	46	25	-	216256355	216256537
328497054	chr2	216257866	216258023	216257886	216257994	FN1	NM_212482	6	46	25	-	216257654	216257926
278361614	chr2	216262297	216262471	216262319	216262447	FN1	NM_212476	4	44	22	-	216262403	216262571
278361614	chr2	216262297	216262471	216262319	216262447	FN1	NM_212478	5	46	22	-	216262403	216262571
278361614	chr2	216262297	216262471	216262319	216262447	FN1	NM_212482	6	46	22	-	216262403	216262571
278361614	chr2	216262297	216262471	216262319	216262447	FN1	NM_212474	3	44	22	-	216262403	216262571
278361614	chr2	216262297	216262471	216262319	216262447	FN1	NM_002026	1	46	22	-	216262403	216262571
278508199	chr2	216269091	216269240	216269116	216269219	FN1	NM_212476	4	44	20	-	216269112	216269378
278508199	chr2	216269091	216269240	216269116	216269219	FN1	NM_212478	5	46	20	-	216269112	216269378

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278508199	chr2	216269091	216269240	216269116	216269219	FN1	NM_212482	6	46	20	-	216269112	216269378
278508199	chr2	216269091	216269240	216269116	216269219	FN1	NM_212474	3	44	20	-	216269112	216269378
278508199	chr2	216269091	216269240	216269116	216269219	FN1	NM_002026	1	46	20	-	216269112	216269378
278613126	chr2	216271045	216271213	216271063	216271192	FN1	NM_212476	4	44	19	-	216270961	216271233
278613126	chr2	216271045	216271213	216271063	216271192	FN1	NM_212478	5	46	19	-	216270961	216271233
278613126	chr2	216271045	216271213	216271063	216271192	FN1	NM_212482	6	46	19	-	216270961	216271233
278613126	chr2	216271045	216271213	216271063	216271192	FN1	NM_212474	3	44	19	-	216270961	216271233
278613126	chr2	216271045	216271213	216271063	216271192	FN1	NM_002026	1	46	19	-	216270961	216271233
279174197	chr2	216271966	216272091	216271987	216272063	FN1	NM_212476	4	44	18	-	216271850	216272044
279174197	chr2	216271966	216272091	216271987	216272063	FN1	NM_212478	5	46	18	-	216271850	216272044
279174197	chr2	216271966	216272091	216271987	216272063	FN1	NM_212482	6	46	18	-	216271850	216272044
279174197	chr2	216271966	216272091	216271987	216272063	FN1	NM_212474	3	44	18	-	216271850	216272044
279174197	chr2	216271966	216272091	216271987	216272063	FN1	NM_002026	1	46	18	-	216271850	216272044
279161507	chr2	216273050	216273213	216273073	216273188	FN1	NM_212476	4	44	16	-	216273021	216273149
279161507	chr2	216273050	216273213	216273073	216273188	FN1	NM_212478	5	46	16	-	216273021	216273149
279161507	chr2	216273050	216273213	216273073	216273188	FN1	NM_212482	6	46	16	-	216273021	216273149
279161507	chr2	216273050	216273213	216273073	216273188	FN1	NM_212474	3	44	16	-	216273021	216273149
279161507	chr2	216273050	216273213	216273073	216273188	FN1	NM_002026	1	46	16	-	216273021	216273149
278417321	chr2	216274682	216274823	216274703	216274802	FN1	NM_212476	4	44	14	-	216274657	216274837
278417321	chr2	216274682	216274823	216274703	216274802	FN1	NM_212478	5	46	14	-	216274657	216274837
278417321	chr2	216274682	216274823	216274703	216274802	FN1	NM_212482	6	46	14	-	216274657	216274837
278417321	chr2	216274682	216274823	216274703	216274802	FN1	NM_212474	3	44	14	-	216274657	216274837
278417321	chr2	216274682	216274823	216274703	216274802	FN1	NM_002026	1	46	14	-	216274657	216274837
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_212476	4	44	13	-	216279560	216279681
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_212478	5	46	13	-	216279560	216279681
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_212482	6	46	13	-	216279560	216279681
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_212474	3	44	13	-	216279560	216279681
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_002026	1	46	13	-	216279560	216279681
328493136	chr2	216279634	216279791	216279661	216279768	FN1	NM_054034	2	13	13	-	216279384	216279681
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_054034	2	13	11	-	216285396	216285524
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_212476	4	44	11	-	216285396	216285524
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_212478	5	46	11	-	216285396	216285524
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_212482	6	46	11	-	216285396	216285524
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_212474	3	44	11	-	216285396	216285524
279976137	chr2	216285459	216285620	216285482	216285592	FN1	NM_002026	1	46	11	-	216285396	216285524
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_054034	2	13	9	-	216288073	216288249
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_212476	4	44	9	-	216288073	216288249
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_212478	5	46	9	-	216288073	216288249
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_212482	6	46	9	-	216288073	216288249
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_212474	3	44	9	-	216288073	216288249
278155206	chr2	216288137	216288290	216288159	216288262	FN1	NM_002026	1	46	9	-	216288073	216288249

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_054034	2	13	7	-	216289817	216290008
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_212476	4	44	7	-	216289817	216290008
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_212478	5	46	7	-	216289817	216290008
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_212482	6	46	7	-	216289817	216290008
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_212474	3	44	7	-	216289817	216290008
279463595	chr2	216289902	216290071	216289924	216290043	FN1	NM_002026	1	46	7	-	216289817	216290008
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_054034	2	13	5	-	216295438	216295575
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_212476	4	44	5	-	216295438	216295575
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_212478	5	46	5	-	216295438	216295575
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_212482	6	46	5	-	216295438	216295575
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_212474	3	44	5	-	216295438	216295575
279656826	chr2	216295468	216295635	216295491	216295607	FN1	NM_002026	1	46	5	-	216295438	216295575
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_054034	2	13	3	-	216298047	216298184
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_212476	4	44	3	-	216298047	216298184
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_212478	5	46	3	-	216298047	216298184
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_212482	6	46	3	-	216298047	216298184
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_212474	3	44	3	-	216298047	216298184
280230433	chr2	216298086	216298214	216298108	216298191	FN1	NM_002026	1	46	3	-	216298047	216298184
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_054034	2	13	1	-	216300378	216300791
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_212476	4	44	1	-	216300378	216300791
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_212478	5	46	1	-	216300378	216300791
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_212482	6	46	1	-	216300378	216300791
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_212474	3	44	1	-	216300378	216300791
279468539	chr2	216300379	216300544	216300399	216300526	FN1	NM_002026	1	46	1	-	216300378	216300791
264082771	chr2	219538530	219538704	219538552	219538679	STK36	NM_015690	2	27	4	+	219538602	219538679
264082771	chr2	219538530	219538704	219538552	219538679	STK36	NM_001243313	1	27	4	+	219538602	219538679
261136969	chr2	219540781	219540946	219540803	219540924	STK36	NM_015690	2	27	6	+	219540752	219541001
261136969	chr2	219540781	219540946	219540803	219540924	STK36	NM_001243313	1	27	6	+	219540752	219541001
239948812	chr2	219544333	219544491	219544354	219544465	STK36	NM_015690	2	27	8	+	219544283	219544452
239948812	chr2	219544333	219544491	219544354	219544465	STK36	NM_001243313	1	27	8	+	219544283	219544452
262194042	chr2	219549723	219549878	219549747	219549855	STK36	NM_015690	2	27	11	+	219549808	219549951
262194042	chr2	219549723	219549878	219549747	219549855	STK36	NM_001243313	1	27	11	+	219549808	219549951
239298248	chr2	219554535	219554708	219554557	219554680	STK36	NM_015690	2	27	13	+	219554582	219554679
239298248	chr2	219554535	219554708	219554557	219554680	STK36	NM_001243313	1	27	13	+	219554582	219554679
242150889	chr2	219556923	219557055	219556945	219557029	STK36	NM_015690	2	27	15	+	219556866	219557016
242150889	chr2	219556923	219557055	219556945	219557029	STK36	NM_001243313	1	27	15	+	219556866	219557016
242753333	chr2	219558419	219558593	219558440	219558572	STK36	NM_015690	2	27	18	+	219558446	219558544
242753333	chr2	219558419	219558593	219558440	219558572	STK36	NM_001243313	1	27	18	+	219558446	219558544
240370192	chr2	219559261	219559431	219559284	219559407	STK36	NM_015690	2	27	21	+	219559248	219559358
240370192	chr2	219559261	219559431	219559284	219559407	STK36	NM_001243313	1	27	21	+	219559248	219559358
260379124	chr2	219562150	219562297	219562173	219562274	STK36	NM_015690	2	27	24	+	219562186	219562333

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260379124	chr2	219562150	219562297	219562173	219562274	STK36	NM_001243313	1	27	24	+	219562186	219562333
240813108	chr2	219563297	219563463	219563324	219563440	STK36	NM_015690	2	27	26	+	219563325	219564071
240813108	chr2	219563297	219563463	219563324	219563440	STK36	NM_001243313	1	27	26	+	219563325	219564071
240872336	chr2	219563747	219563918	219563769	219563897	STK36	NM_015690	2	27	26	+	219563325	219564071
240872336	chr2	219563747	219563918	219563769	219563897	STK36	NM_001243313	1	27	26	+	219563325	219564071
262691230	chr2	219566607	219566779	219566630	219566757	STK36	NM_015690	2	27	27	+	219566589	219567440
262691230	chr2	219566607	219566779	219566630	219566757	STK36	NM_001243313	1	27	27	+	219566589	219567440
235205672	chr2	223066662	223066825	223066687	223066805	PAX3	NM_001127366	2	9	8	-	223066663	223066909
235205672	chr2	223066662	223066825	223066687	223066805	PAX3	NM_181459	6	10	8	-	223066663	223066909
235205672	chr2	223066662	223066825	223066687	223066805	PAX3	NM_181458	5	9	8	-	223066663	223066909
235205672	chr2	223066662	223066825	223066687	223066805	PAX3	NM_181457	4	8	8	-	223066432	223066909
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_001127366	2	9	6	-	223085941	223086106
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_181461	8	8	6	-	223085941	223086106
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_181459	6	10	6	-	223085941	223086106
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_181460	7	9	6	-	223085941	223086106
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_181458	5	9	6	-	223085941	223086106
234913782	chr2	223085843	223085968	223085865	223085944	PAX3	NM_181457	4	8	6	-	223085941	223086106
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_001127366	2	9	5	-	223096797	223097002
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_181461	8	8	5	-	223096797	223097002
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_181459	6	10	5	-	223096797	223097002
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_181460	7	9	5	-	223096797	223097002
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_181458	5	9	5	-	223096797	223097002
239915654	chr2	223096871	223097026	223096892	223097000	PAX3	NM_181457	4	8	5	-	223096797	223097002
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_000438	1	4	4	-	223158349	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_001127366	2	9	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_181461	8	8	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_181459	6	10	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_013942	3	5	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_181460	7	9	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_181458	5	9	4	-	223158886	223159020
237366859	chr2	223158915	223159076	223158937	223159055	PAX3	NM_181457	4	8	4	-	223158886	223159020
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_000438	1	4	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_181461	8	8	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_181459	6	10	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_013942	3	5	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_181460	7	9	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_181458	5	9	2	-	223161697	223161932
235298329	chr2	223161842	223162014	223161862	223161992	PAX3	NM_181457	4	8	2	-	223161697	223161932
304789820	chr2	234669140	234669308	234669163	234669283	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
304810906	chr2	234669572	234669712	234669596	234669687	UGT1A1	NM_000463	1	5	1	+	234668919	234669797

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300053468	chr2	234675753	234675893	234675779	234675866	UGT1A1	NM_000463	1	5	2	+	234675680	234675811
305719241	chr2	234680853	234681013	234680878	234680992	UGT1A1	NM_000463	1	5	5	+	234680908	234681945
295307439	chr3	3192475	3192630	3192503	3192608	CRBN	NM_016302	2	11	11	-	3191317	3192729
295307439	chr3	3192475	3192630	3192503	3192608	CRBN	NM_001173482	1	11	11	-	3191317	3192729
294787386	chr3	3194171	3194301	3194195	3194273	CRBN	NM_016302	2	11	10	-	3194140	3194271
294787386	chr3	3194171	3194301	3194195	3194273	CRBN	NM_001173482	1	11	10	-	3194140	3194271
294169804	chr3	3195686	3195817	3195713	3195789	CRBN	NM_016302	2	11	8	-	3195644	3195759
294169804	chr3	3195686	3195817	3195713	3195789	CRBN	NM_001173482	1	11	8	-	3195644	3195759
295198786	chr3	3209206	3209370	3209226	3209343	CRBN	NM_016302	2	11	5	-	3209318	3209477
295198786	chr3	3209206	3209370	3209226	3209343	CRBN	NM_001173482	1	11	5	-	3209318	3209477
294173018	chr3	3214448	3214588	3214477	3214563	CRBN	NM_016302	2	11	4	-	3214460	3214609
294173018	chr3	3214448	3214588	3214477	3214563	CRBN	NM_001173482	1	11	4	-	3214460	3214609
294837322	chr3	3215894	3216022	3215914	3215994	CRBN	NM_016302	2	11	3	-	3215743	3215945
294837322	chr3	3215894	3216022	3215914	3215994	CRBN	NM_001173482	1	11	3	-	3215743	3215945
230729795	chr3	10070283	10070455	10070307	10070428	FANCD2	NM_033084	2	43	2	+	10070309	10070405
230729795	chr3	10070283	10070455	10070307	10070428	FANCD2	NM_001018115	1	44	2	+	10070309	10070405
228243184	chr3	10076287	10076438	10076313	10076410	FANCD2	NM_033084	2	43	5	+	10076379	10076482
228243184	chr3	10076287	10076438	10076313	10076410	FANCD2	NM_001018115	1	44	5	+	10076379	10076482
231746486	chr3	10080886	10081058	10080913	10081035	FANCD2	NM_033084	2	43	8	+	10080963	10081041
231746486	chr3	10080886	10081058	10080913	10081035	FANCD2	NM_001018115	1	44	8	+	10080963	10081041
230002244	chr3	10083253	10083422	10083274	10083394	FANCD2	NM_033084	2	43	10	+	10083307	10083394
230002244	chr3	10083253	10083422	10083274	10083394	FANCD2	NM_001018115	1	44	10	+	10083307	10083394
230706997	chr3	10085094	10085268	10085114	10085240	FANCD2	NM_033084	2	43	13	+	10085168	10085276
230706997	chr3	10085094	10085268	10085114	10085240	FANCD2	NM_001018115	1	44	13	+	10085168	10085276
227697858	chr3	10089532	10089666	10089559	10089641	FANCD2	NM_033084	2	43	16	+	10089601	10089735
227697858	chr3	10089532	10089666	10089559	10089641	FANCD2	NM_001018115	1	44	16	+	10089601	10089735
228677473	chr3	10101941	10102113	10101970	10102088	FANCD2	NM_033084	2	43	19	+	10101978	10102087
228677473	chr3	10101941	10102113	10101970	10102088	FANCD2	NM_001018115	1	44	19	+	10101978	10102087
231814171	chr3	10106446	10106620	10106471	10106595	FANCD2	NM_033084	2	43	23	+	10106413	10106559
231814171	chr3	10106446	10106620	10106471	10106595	FANCD2	NM_001018115	1	44	23	+	10106413	10106559
227998881	chr3	10107633	10107768	10107661	10107743	FANCD2	NM_033084	2	43	25	+	10107548	10107663
227998881	chr3	10107633	10107768	10107661	10107743	FANCD2	NM_001018115	1	44	25	+	10107548	10107663
233026000	chr3	10114830	10114990	10114855	10114966	FANCD2	NM_033084	2	43	28	+	10114937	10115046
233026000	chr3	10114830	10114990	10114855	10114966	FANCD2	NM_001018115	1	44	28	+	10114937	10115046
232406547	chr3	10119733	10119906	10119758	10119881	FANCD2	NM_033084	2	43	30	+	10119765	10119881
232406547	chr3	10119733	10119906	10119758	10119881	FANCD2	NM_001018115	1	44	30	+	10119765	10119881
231625177	chr3	10123032	10123174	10123054	10123149	FANCD2	NM_033084	2	43	32	+	10123030	10123148
231625177	chr3	10123032	10123174	10123054	10123149	FANCD2	NM_001018115	1	44	32	+	10123030	10123148
230794960	chr3	10130081	10130255	10130109	10130231	FANCD2	NM_033084	2	43	35	+	10130133	10130226
230794960	chr3	10130081	10130255	10130109	10130231	FANCD2	NM_001018115	1	44	35	+	10130133	10130226
228389587	chr3	10133807	10133981	10133832	10133956	FANCD2	NM_033084	2	43	38	+	10133865	10133936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228389587	chr3	10133807	10133981	10133832	10133956	FANCD2	NM_001018115	1	44	38	+	10133865	10133936
230021341	chr3	10136882	10137015	10136907	10136992	FANCD2	NM_033084	2	43	41	+	10136884	10136958
230021341	chr3	10136882	10137015	10136907	10136992	FANCD2	NM_001018115	1	44	41	+	10136884	10136958
228416250	chr3	10140411	10140572	10140437	10140544	FANCD2	NM_001018115	1	44	43	+	10140404	10140499
228416250	chr3	10140411	10140572	10140437	10140544	FANCD2	NM_033084	2	43	43	+	10140404	10141344
264381571	chr3	10183592	10183766	10183613	10183744	VHL	NM_000551	1	3	1	+	10183319	10183871
264381571	chr3	10183592	10183766	10183613	10183744	VHL	NM_198156	2	2	1	+	10183319	10183871
242644655	chr3	10188244	10188371	10188272	10188343	VHL	NM_000551	1	3	2	+	10188198	10188320
240230629	chr3	12421129	12421286	12421156	12421263	PPARG	NM_138711	3	8	3	+	12421203	12421430
240230629	chr3	12421129	12421286	12421156	12421263	PPARG	NM_015869	2	7	2	+	12421203	12421430
240230629	chr3	12421129	12421286	12421156	12421263	PPARG	NM_138712	4	8	3	+	12421203	12421430
240230629	chr3	12421129	12421286	12421156	12421263	PPARG	NM_005037	1	7	2	+	12421203	12421430
235916094	chr3	12422836	12422992	12422861	12422971	PPARG	NM_138711	3	8	4	+	12422821	12422990
235916094	chr3	12422836	12422992	12422861	12422971	PPARG	NM_015869	2	7	3	+	12422821	12422990
235916094	chr3	12422836	12422992	12422861	12422971	PPARG	NM_138712	4	8	4	+	12422821	12422990
235916094	chr3	12422836	12422992	12422861	12422971	PPARG	NM_005037	1	7	3	+	12422821	12422990
235039262	chr3	12447481	12447616	12447502	12447597	PPARG	NM_138711	3	8	6	+	12447381	12447580
235039262	chr3	12447481	12447616	12447502	12447597	PPARG	NM_015869	2	7	5	+	12447381	12447580
235039262	chr3	12447481	12447616	12447502	12447597	PPARG	NM_138712	4	8	6	+	12447381	12447580
235039262	chr3	12447481	12447616	12447502	12447597	PPARG	NM_005037	1	7	5	+	12447381	12447580
234971181	chr3	12458529	12458696	12458549	12458670	PPARG	NM_138711	3	8	7	+	12458203	12458653
234971181	chr3	12458529	12458696	12458549	12458670	PPARG	NM_015869	2	7	6	+	12458203	12458653
234971181	chr3	12458529	12458696	12458549	12458670	PPARG	NM_138712	4	8	7	+	12458203	12458653
234971181	chr3	12458529	12458696	12458549	12458670	PPARG	NM_005037	1	7	6	+	12458203	12458653
238479377	chr3	12625990	12626150	12626012	12626128	RAF1	NM_002880	1	17	17	-	12625100	12626156
235598029	chr3	12626538	12626699	12626560	12626671	RAF1	NM_002880	1	17	15	-	12626621	12626752
237173770	chr3	12629014	12629187	12629038	12629159	RAF1	NM_002880	1	17	13	-	12629090	12629136
236162756	chr3	12641130	12641260	12641153	12641239	RAF1	NM_002880	1	17	10	-	12641190	12641307
235214651	chr3	12641767	12641940	12641793	12641915	RAF1	NM_002880	1	17	8	-	12641887	12641914
237940579	chr3	12647691	12647853	12647718	12647825	RAF1	NM_002880	1	17	6	-	12647700	12647798
236455510	chr3	12653394	12653540	12653424	12653517	RAF1	NM_002880	1	17	3	-	12653449	12653561
236801565	chr3	12660103	12660250	12660126	12660222	RAF1	NM_002880	1	17	2	-	12660014	12660246
240388560	chr3	14189378	14189527	14189399	14189507	XPC	NR_027299	3	15	13	-	14189408	14189501
240388560	chr3	14189378	14189527	14189399	14189507	XPC	NM_001145769	1	16	14	-	14189408	14189501
240388560	chr3	14189378	14189527	14189399	14189507	XPC	NM_004628	2	16	14	-	14189408	14189501
239521410	chr3	14190339	14190500	14190363	14190478	XPC	NR_027299	3	15	11	-	14190314	14190448
239521410	chr3	14190339	14190500	14190363	14190478	XPC	NM_001145769	1	16	12	-	14190314	14190448
239521410	chr3	14190339	14190500	14190363	14190478	XPC	NM_004628	2	16	12	-	14190314	14190448
239617538	chr3	14197881	14198032	14197901	14198006	XPC	NR_027299	3	15	9	-	14197835	14197995
239617538	chr3	14197881	14198032	14197901	14198006	XPC	NM_001145769	1	16	10	-	14197835	14197995
239617538	chr3	14197881	14198032	14197901	14198006	XPC	NM_004628	2	16	10	-	14197835	14197995

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266269175	chr3	14199858	14200018	14199884	14199995	XPC	NR_027299	3	15	8	-	14199511	14200392
266269175	chr3	14199858	14200018	14199884	14199995	XPC	NM_001145769	1	16	9	-	14199511	14200392
266269175	chr3	14199858	14200018	14199884	14199995	XPC	NM_004628	2	16	9	-	14199511	14200392
262329174	chr3	14200218	14200379	14200241	14200356	XPC	NR_027299	3	15	8	-	14199511	14200392
262329174	chr3	14200218	14200379	14200241	14200356	XPC	NM_001145769	1	16	9	-	14199511	14200392
262329174	chr3	14200218	14200379	14200241	14200356	XPC	NM_004628	2	16	9	-	14199511	14200392
263384504	chr3	14206323	14206461	14206348	14206439	XPC	NR_027299	3	15	6	-	14206313	14206433
263384504	chr3	14206323	14206461	14206348	14206439	XPC	NM_001145769	1	16	7	-	14206313	14206433
263384504	chr3	14206323	14206461	14206348	14206439	XPC	NM_004628	2	16	7	-	14206313	14206433
242048475	chr3	14209718	14209863	14209739	14209842	XPC	NM_004628	2	16	4	-	14209757	14209880
242048475	chr3	14209718	14209863	14209739	14209842	XPC	NM_001145769	1	16	4	-	14209757	14209776
239031429	chr3	14214321	14214470	14214347	14214449	XPC	NR_027299	3	15	2	-	14214367	14214562
239031429	chr3	14214321	14214470	14214347	14214449	XPC	NM_001145769	1	16	2	-	14214367	14214562
239031429	chr3	14214321	14214470	14214347	14214449	XPC	NM_004628	2	16	2	-	14214367	14214562
272552144	chr3	30648343	30648477	30648361	30648456	TGFBR2	NM_001024847	1	8	1	+	30647994	30648469
272552144	chr3	30648343	30648477	30648361	30648456	TGFBR2	NM_003242	2	7	1	+	30647994	30648469
270340917	chr3	30686226	30686378	30686254	30686356	TGFBR2	NM_001024847	1	8	3	+	30686239	30686407
270340917	chr3	30686226	30686378	30686254	30686356	TGFBR2	NM_003242	2	7	2	+	30686239	30686407
272306531	chr3	30713069	30713243	30713095	30713217	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272306531	chr3	30713069	30713243	30713095	30713217	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272293909	chr3	30713551	30713714	30713578	30713695	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272293909	chr3	30713551	30713714	30713578	30713695	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
269572519	chr3	30715603	30715761	30715625	30715739	TGFBR2	NM_001024847	1	8	6	+	30715597	30715738
269572519	chr3	30715603	30715761	30715625	30715739	TGFBR2	NM_003242	2	7	5	+	30715597	30715738
272505648	chr3	30732999	30733155	30733020	30733133	TGFBR2	NM_001024847	1	8	8	+	30732912	30735633
272505648	chr3	30732999	30733155	30733020	30733133	TGFBR2	NM_003242	2	7	7	+	30732912	30735633
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167617	2	19	3	+	37042446	37042539
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167619	4	18	3	+	37042446	37042544
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_001167618	3	19	3	+	37042446	37042544
231118245	chr3	37042357	37042531	37042388	37042503	MLH1	NM_000249	1	19	3	+	37042446	37042544
233175893	chr3	37048421	37048592	37048449	37048564	MLH1	NM_001167619	4	18	5	+	37048482	37048554
233175893	chr3	37048421	37048592	37048449	37048564	MLH1	NM_001167618	3	19	5	+	37048482	37048554
233175893	chr3	37048421	37048592	37048449	37048564	MLH1	NM_001167617	2	19	5	+	37048482	37048554
233175893	chr3	37048421	37048592	37048449	37048564	MLH1	NM_000249	1	19	5	+	37048482	37048554
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167619	4	18	7	+	37053502	37053590
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167618	3	19	8	+	37053502	37053590
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_001167617	2	19	8	+	37053502	37053590
233123150	chr3	37053416	37053582	37053442	37053560	MLH1	NM_000249	1	19	8	+	37053502	37053590
232125747	chr3	37058947	37059115	37058968	37059090	MLH1	NM_001167619	4	18	9	+	37058997	37059090
232125747	chr3	37058947	37059115	37058968	37059090	MLH1	NM_001167618	3	19	10	+	37058997	37059090
232125747	chr3	37058947	37059115	37058968	37059090	MLH1	NM_001167617	2	19	10	+	37058997	37059090

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232125747	chr3	37058947	37059115	37058968	37059090	MLH1	NM_000249	1	19	10	+	37058997	37059090
233218621	chr3	37067119	37067256	37067147	37067235	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233218621	chr3	37067119	37067256	37067147	37067235	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233218621	chr3	37067119	37067256	37067147	37067235	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233218621	chr3	37067119	37067256	37067147	37067235	MLH1	NM_000249	1	19	12	+	37067128	37067498
234247138	chr3	37070179	37070350	37070200	37070327	MLH1	NM_001167619	4	18	12	+	37070275	37070423
234247138	chr3	37070179	37070350	37070200	37070327	MLH1	NM_001167618	3	19	13	+	37070275	37070423
234247138	chr3	37070179	37070350	37070200	37070327	MLH1	NM_001167617	2	19	13	+	37070275	37070423
234247138	chr3	37070179	37070350	37070200	37070327	MLH1	NM_000249	1	19	13	+	37070275	37070423
234336499	chr3	37083645	37083814	37083673	37083787	MLH1	NM_001167619	4	18	14	+	37083759	37083822
234336499	chr3	37083645	37083814	37083673	37083787	MLH1	NM_001167618	3	19	15	+	37083759	37083822
234336499	chr3	37083645	37083814	37083673	37083787	MLH1	NM_001167617	2	19	15	+	37083759	37083822
234336499	chr3	37083645	37083814	37083673	37083787	MLH1	NM_000249	1	19	15	+	37083759	37083822
234602209	chr3	37089963	37090129	37089990	37090101	MLH1	NM_001167619	4	18	16	+	37090008	37090100
234602209	chr3	37089963	37090129	37089990	37090101	MLH1	NM_001167618	3	19	17	+	37090008	37090100
234602209	chr3	37089963	37090129	37089990	37090101	MLH1	NM_001167617	2	19	17	+	37090008	37090100
234602209	chr3	37089963	37090129	37089990	37090101	MLH1	NM_000249	1	19	17	+	37090008	37090100
233393079	chr3	37091998	37092172	37092020	37092144	MLH1	NM_001167619	4	18	18	+	37091977	37092337
233393079	chr3	37091998	37092172	37092020	37092144	MLH1	NM_001167618	3	19	19	+	37091977	37092337
233393079	chr3	37091998	37092172	37092020	37092144	MLH1	NM_001167617	2	19	19	+	37091977	37092337
233393079	chr3	37091998	37092172	37092020	37092144	MLH1	NM_000249	1	19	19	+	37091977	37092337
232982311	chr3	37514798	37514957	37514821	37514936	ITGA9	NM_002207	1	28	3	+	37514845	37514951
230941721	chr3	37535969	37536143	37535991	37536116	ITGA9	NM_002207	1	28	5	+	37535992	37536059
233211325	chr3	37549972	37550123	37549994	37550097	ITGA9	NM_002207	1	28	8	+	37550050	37550118
233068526	chr3	37558964	37559092	37558990	37559069	ITGA9	NM_002207	1	28	10	+	37558995	37559100
232358265	chr3	37567467	37567609	37567490	37567587	ITGA9	NM_002207	1	28	13	+	37567517	37567562
231189965	chr3	37584001	37584152	37584023	37584127	ITGA9	NM_002207	1	28	15	+	37583916	37584076
230840712	chr3	37725288	37725434	37725311	37725409	ITGA9	NM_002207	1	28	18	+	37725356	37725506
231825123	chr3	37783181	37783348	37783201	37783328	ITGA9	NM_002207	1	28	21	+	37783221	37783310
232205193	chr3	37818790	37818936	37818812	37818914	ITGA9	NM_002207	1	28	24	+	37818883	37819008
232290485	chr3	37826405	37826549	37826426	37826527	ITGA9	NM_002207	1	28	26	+	37826468	37826569
274094385	chr3	38180078	38180249	38180095	38180229	MYD88	NM_002468	5	5	1	+	38179969	38180519
274094385	chr3	38180078	38180249	38180095	38180229	MYD88	NM_001172569	4	4	1	+	38179969	38180519
274094385	chr3	38180078	38180249	38180095	38180229	MYD88	NM_001172568	3	4	1	+	38179969	38180519
274094385	chr3	38180078	38180249	38180095	38180229	MYD88	NM_001172567	2	5	1	+	38179969	38180519
274094385	chr3	38180078	38180249	38180095	38180229	MYD88	NM_001172566	1	3	1	+	38179969	38180519
273012109	chr3	38180443	38180602	38180461	38180582	MYD88	NM_002468	5	5	1	+	38179969	38180519
273012109	chr3	38180443	38180602	38180461	38180582	MYD88	NM_001172569	4	4	1	+	38179969	38180519
273012109	chr3	38180443	38180602	38180461	38180582	MYD88	NM_001172568	3	4	1	+	38179969	38180519
273012109	chr3	38180443	38180602	38180461	38180582	MYD88	NM_001172567	2	5	1	+	38179969	38180519
273012109	chr3	38180443	38180602	38180461	38180582	MYD88	NM_001172566	1	3	1	+	38179969	38180519

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273457035	chr3	38181924	38182071	38181944	38182046	MYD88	NM_001172567	2	5	3	+	38181879	38182083
273457035	chr3	38181924	38182071	38181944	38182046	MYD88	NM_002468	5	5	3	+	38181879	38182059
273457035	chr3	38181924	38182071	38181944	38182046	MYD88	NM_001172568	3	4	2	+	38181879	38182059
273946986	chr3	38182663	38182829	38182686	38182805	MYD88	NM_002468	5	5	5	+	38182623	38184512
273946986	chr3	38182663	38182829	38182686	38182805	MYD88	NM_001172569	4	4	4	+	38182623	38184512
273946986	chr3	38182663	38182829	38182686	38182805	MYD88	NM_001172568	3	4	4	+	38182623	38184512
273946986	chr3	38182663	38182829	38182686	38182805	MYD88	NM_001172567	2	5	5	+	38182623	38184512
273946986	chr3	38182663	38182829	38182686	38182805	MYD88	NM_001172566	1	3	3	+	38182623	38184512
225704141	chr3	41266133	41266299	41266158	41266272	CTNNB1	NM_001904	3	15	3	+	41266017	41266244
225704141	chr3	41266133	41266299	41266158	41266272	CTNNB1	NM_001098209	1	16	3	+	41266017	41266244
225704141	chr3	41266133	41266299	41266158	41266272	CTNNB1	NM_001098210	2	16	3	+	41266017	41266244
225692591	chr3	41266761	41266927	41266789	41266902	CTNNB1	NM_001904	3	15	5	+	41266825	41267063
225692591	chr3	41266761	41266927	41266789	41266902	CTNNB1	NM_001098209	1	16	5	+	41266825	41267063
225692591	chr3	41266761	41266927	41266789	41266902	CTNNB1	NM_001098210	2	16	5	+	41266825	41267063
226535422	chr3	41267152	41267314	41267176	41267285	CTNNB1	NM_001904	3	15	6	+	41267151	41267352
226535422	chr3	41267152	41267314	41267176	41267285	CTNNB1	NM_001098209	1	16	6	+	41267151	41267352
226535422	chr3	41267152	41267314	41267176	41267285	CTNNB1	NM_001098210	2	16	6	+	41267151	41267352
226215024	chr3	41274792	41274962	41274820	41274935	CTNNB1	NM_001904	3	15	8	+	41274832	41274935
226215024	chr3	41274792	41274962	41274820	41274935	CTNNB1	NM_001098209	1	16	8	+	41274832	41274935
226215024	chr3	41274792	41274962	41274820	41274935	CTNNB1	NM_001098210	2	16	8	+	41274832	41274935
226054400	chr3	41275276	41275422	41275296	41275394	CTNNB1	NM_001904	3	15	9	+	41275020	41275358
226054400	chr3	41275276	41275422	41275296	41275394	CTNNB1	NM_001098209	1	16	9	+	41275020	41275358
226054400	chr3	41275276	41275422	41275296	41275394	CTNNB1	NM_001098210	2	16	9	+	41275020	41275358
225792353	chr3	41277755	41277929	41277778	41277906	CTNNB1	NM_001904	3	15	12	+	41277840	41277990
225792353	chr3	41277755	41277929	41277778	41277906	CTNNB1	NM_001098209	1	16	12	+	41277840	41277990
225792353	chr3	41277755	41277929	41277778	41277906	CTNNB1	NM_001098210	2	16	12	+	41277840	41277990
226124728	chr3	41279466	41279640	41279494	41279612	CTNNB1	NM_001904	3	15	14	+	41279507	41279567
226124728	chr3	41279466	41279640	41279494	41279612	CTNNB1	NM_001098209	1	16	14	+	41279507	41279567
226124728	chr3	41279466	41279640	41279494	41279612	CTNNB1	NM_001098210	2	16	14	+	41279507	41279567
278279830	chr3	46477636	46477760	46477657	46477732	LTF	NM_002343	2	17	17	-	46477496	46477720
278279830	chr3	46477636	46477760	46477657	46477732	LTF	NM_001199149	1	17	17	-	46477496	46477720
280485800	chr3	46480864	46481003	46480885	46480982	LTF	NM_002343	2	17	15	-	46480787	46480971
280485800	chr3	46480864	46481003	46480885	46480982	LTF	NM_001199149	1	17	15	-	46480787	46480971
279021273	chr3	46486750	46486895	46486770	46486872	LTF	NM_002343	2	17	12	-	46486772	46486927
279021273	chr3	46486750	46486895	46486770	46486872	LTF	NM_001199149	1	17	12	-	46486772	46486927
278419194	chr3	46490267	46490436	46490294	46490414	LTF	NM_002343	2	17	9	-	46490354	46490508
278419194	chr3	46490267	46490436	46490294	46490414	LTF	NM_001199149	1	17	9	-	46490354	46490508
279166018	chr3	46491417	46491565	46491438	46491537	LTF	NM_002343	2	17	8	-	46491344	46491518
279166018	chr3	46491417	46491565	46491438	46491537	LTF	NM_001199149	1	17	8	-	46491344	46491518
279849043	chr3	46496748	46496890	46496768	46496867	LTF	NM_002343	2	17	5	-	46496785	46496932
279849043	chr3	46496748	46496890	46496768	46496867	LTF	NM_001199149	1	17	5	-	46496785	46496932

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279997548	chr3	46497701	46497872	46497723	46497851	LTF	NM_002343	2	17	3	-	46497780	46497888
279997548	chr3	46497701	46497872	46497723	46497851	LTF	NM_001199149	1	17	3	-	46497780	46497888
263230987	chr3	47058515	47058687	47058537	47058660	SETD2	NM_014159	1	21	21	-	47057898	47058744
237982360	chr3	47079128	47079294	47079153	47079268	SETD2	NM_014159	1	21	18	-	47079156	47079267
240516615	chr3	47088035	47088185	47088056	47088157	SETD2	NM_014159	1	21	16	-	47087977	47088111
261261263	chr3	47098627	47098794	47098649	47098772	SETD2	NM_014159	1	21	15	-	47098311	47098980
242058885	chr3	47103703	47103837	47103726	47103815	SETD2	NM_014159	1	21	14	-	47103653	47103836
264194321	chr3	47125277	47125446	47125300	47125419	SETD2	NM_014159	1	21	12	-	47125210	47125872
264195189	chr3	47125716	47125865	47125739	47125843	SETD2	NM_014159	1	21	12	-	47125210	47125872
237818440	chr3	47139336	47139510	47139359	47139488	SETD2	NM_014159	1	21	9	-	47139445	47139571
263875756	chr3	47144778	47144917	47144800	47144889	SETD2	NM_014159	1	21	7	-	47144836	47144913
262367434	chr3	47155361	47155500	47155384	47155475	SETD2	NM_014159	1	21	5	-	47155366	47155494
262431796	chr3	47161702	47161870	47161729	47161845	SETD2	NM_014159	1	21	3	-	47161672	47166038
239033263	chr3	47162102	47162235	47162125	47162213	SETD2	NM_014159	1	21	3	-	47161672	47166038
239168699	chr3	47162539	47162705	47162564	47162679	SETD2	NM_014159	1	21	3	-	47161672	47166038
239108362	chr3	47162928	47163102	47162953	47163077	SETD2	NM_014159	1	21	3	-	47161672	47166038
239181039	chr3	47163352	47163480	47163379	47163455	SETD2	NM_014159	1	21	3	-	47161672	47166038
262454104	chr3	47163721	47163866	47163749	47163840	SETD2	NM_014159	1	21	3	-	47161672	47166038
262517465	chr3	47164088	47164239	47164116	47164209	SETD2	NM_014159	1	21	3	-	47161672	47166038
262481083	chr3	47164527	47164698	47164555	47164671	SETD2	NM_014159	1	21	3	-	47161672	47166038
238822505	chr3	47164922	47165081	47164942	47165053	SETD2	NM_014159	1	21	3	-	47161672	47166038
239080008	chr3	47165247	47165376	47165275	47165350	SETD2	NM_014159	1	21	3	-	47161672	47166038
239134837	chr3	47165584	47165747	47165609	47165724	SETD2	NM_014159	1	21	3	-	47161672	47166038
261578668	chr3	47168015	47168172	47168048	47168144	SETD2	NM_014159	1	21	2	-	47168138	47168153
224029111	chr3	52436575	52436716	52436596	52436690	BAP1	NM_004656	1	17	16	-	52436618	52436690
222316698	chr3	52437387	52437557	52437404	52437540	BAP1	NM_004656	1	17	13	-	52437432	52437910
223085343	chr3	52438387	52438547	52438409	52438524	BAP1	NM_004656	1	17	12	-	52438469	52438602
222886771	chr3	52439743	52439909	52439764	52439887	BAP1	NM_004656	1	17	10	-	52439781	52439928
224037245	chr3	52440774	52440948	52440797	52440925	BAP1	NM_004656	1	17	8	-	52440845	52440923
222253399	chr3	52441451	52441590	52441472	52441567	BAP1	NM_004656	1	17	6	-	52441415	52441476
223498101	chr3	52443478	52443652	52443499	52443628	BAP1	NM_004656	1	17	3	-	52443570	52443624
237380853	chr3	52582001	52582139	52582022	52582118	PBRM1	NM_018165	1	28	28	-	52579368	52582251
237380853	chr3	52582001	52582139	52582022	52582118	PBRM1	NM_018313	2	30	30	-	52579368	52582251
237380853	chr3	52582001	52582139	52582022	52582118	PBRM1	NM_181042	3	28	28	-	52579368	52582251
237261421	chr3	52584502	52584676	52584524	52584654	PBRM1	NM_018165	1	28	27	-	52584437	52584653
237261421	chr3	52584502	52584676	52584524	52584654	PBRM1	NM_018313	2	30	29	-	52584437	52584653
237261421	chr3	52584502	52584676	52584524	52584654	PBRM1	NM_181042	3	28	27	-	52584437	52584653
236323750	chr3	52595742	52595885	52595764	52595864	PBRM1	NM_018165	1	28	24	-	52595783	52595984
236323750	chr3	52595742	52595885	52595764	52595864	PBRM1	NM_018313	2	30	26	-	52595783	52595984
236323750	chr3	52595742	52595885	52595764	52595864	PBRM1	NM_181042	3	28	25	-	52595783	52595984
235398587	chr3	52597431	52597579	52597456	52597556	PBRM1	NM_018165	1	28	23	-	52597299	52597509

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235398587	chr3	52597431	52597579	52597456	52597556	PBRM1	NM_181042	3	28	24	-	52597299	52597509
235398587	chr3	52597431	52597579	52597456	52597556	PBRM1	NM_018313	2	30	25	-	52597380	52597509
237327379	chr3	52610576	52610725	52610602	52610698	PBRM1	NM_018165	1	28	21	-	52610557	52610714
237327379	chr3	52610576	52610725	52610602	52610698	PBRM1	NM_018313	2	30	23	-	52610557	52610714
237327379	chr3	52610576	52610725	52610602	52610698	PBRM1	NM_181042	3	28	22	-	52610557	52610714
237547338	chr3	52620315	52620470	52620339	52620442	PBRM1	NM_018165	1	28	19	-	52620441	52620704
237547338	chr3	52620315	52620470	52620339	52620442	PBRM1	NM_018313	2	30	21	-	52620441	52620704
237547338	chr3	52620315	52620470	52620339	52620442	PBRM1	NM_181042	3	28	20	-	52620441	52620704
237573610	chr3	52620655	52620818	52620681	52620793	PBRM1	NM_018165	1	28	19	-	52620441	52620704
237573610	chr3	52620655	52620818	52620681	52620793	PBRM1	NM_018313	2	30	21	-	52620441	52620704
237573610	chr3	52620655	52620818	52620681	52620793	PBRM1	NM_181042	3	28	20	-	52620441	52620704
238848030	chr3	52623147	52623320	52623172	52623295	PBRM1	NM_018165	1	28	17	-	52623086	52623271
238848030	chr3	52623147	52623320	52623172	52623295	PBRM1	NM_018313	2	30	19	-	52623086	52623271
238848030	chr3	52623147	52623320	52623172	52623295	PBRM1	NM_181042	3	28	18	-	52623086	52623271
239415904	chr3	52643314	52643445	52643341	52643417	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239415904	chr3	52643314	52643445	52643341	52643417	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239415904	chr3	52643314	52643445	52643341	52643417	PBRM1	NM_181042	3	28	16	-	52643329	52643971
239500426	chr3	52643702	52643852	52643727	52643827	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239500426	chr3	52643702	52643852	52643727	52643827	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239500426	chr3	52643702	52643852	52643727	52643827	PBRM1	NM_181042	3	28	16	-	52643329	52643971
235035859	chr3	52651234	52651382	52651254	52651357	PBRM1	NM_018165	1	28	13	-	52651278	52651554
235035859	chr3	52651234	52651382	52651254	52651357	PBRM1	NM_018313	2	30	15	-	52651278	52651554
235035859	chr3	52651234	52651382	52651254	52651357	PBRM1	NM_181042	3	28	14	-	52651278	52651554
237958271	chr3	52662821	52662989	52662849	52662961	PBRM1	NM_018165	1	28	11	-	52662910	52663051
237958271	chr3	52662821	52662989	52662849	52662961	PBRM1	NM_018313	2	30	13	-	52662910	52663051
237958271	chr3	52662821	52662989	52662849	52662961	PBRM1	NM_181042	3	28	12	-	52662910	52663051
237521751	chr3	52668712	52668883	52668732	52668856	PBRM1	NM_018165	1	28	10	-	52668618	52668831
237521751	chr3	52668712	52668883	52668732	52668856	PBRM1	NM_018313	2	30	12	-	52668618	52668831
237521751	chr3	52668712	52668883	52668732	52668856	PBRM1	NM_181042	3	28	11	-	52668618	52668831
237737626	chr3	52678692	52678863	52678717	52678834	PBRM1	NM_018165	1	28	8	-	52678720	52678805
237737626	chr3	52678692	52678863	52678717	52678834	PBRM1	NM_018313	2	30	9	-	52678720	52678805
237737626	chr3	52678692	52678863	52678717	52678834	PBRM1	NM_181042	3	28	8	-	52678720	52678805
240593833	chr3	52692298	52692433	52692322	52692402	PBRM1	NM_018165	1	28	5	-	52692215	52692331
240593833	chr3	52692298	52692433	52692322	52692402	PBRM1	NM_018313	2	30	6	-	52692215	52692331
240593833	chr3	52692298	52692433	52692322	52692402	PBRM1	NM_181042	3	28	5	-	52692215	52692331
235641061	chr3	52712398	52712544	52712421	52712522	PBRM1	NM_018165	1	28	2	-	52712516	52712613
235641061	chr3	52712398	52712544	52712421	52712522	PBRM1	NM_018313	2	30	3	-	52712516	52712613
235641061	chr3	52712398	52712544	52712421	52712522	PBRM1	NM_181042	3	28	2	-	52712516	52712613
312578601	chr3	65342031	65342205	65342052	65342186	MAGI1	NM_015520	3	25	25	-	65339906	65342807
312578601	chr3	65342031	65342205	65342052	65342186	MAGI1	NM_001033057	1	23	23	-	65339906	65342807
312314033	chr3	65342670	65342831	65342693	65342808	MAGI1	NM_015520	3	25	25	-	65339906	65342807

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312314033	chr3	65342670	65342831	65342693	65342808	MAGI1	NM_001033057	1	23	23	-	65339906	65342807
312466648	chr3	65349111	65349245	65349132	65349222	MAGI1	NM_004742	2	23	22	-	65349140	65349283
312466648	chr3	65349111	65349245	65349132	65349222	MAGI1	NM_015520	3	25	22	-	65349140	65349283
312466648	chr3	65349111	65349245	65349132	65349222	MAGI1	NM_001033057	1	23	21	-	65349140	65349283
312164499	chr3	65361312	65361474	65361340	65361451	MAGI1	NM_015520	3	25	19	-	65361420	65361620
312164499	chr3	65361312	65361474	65361340	65361451	MAGI1	NM_001033057	1	23	18	-	65361420	65361620
312164499	chr3	65361312	65361474	65361340	65361451	MAGI1	NM_004742	2	23	19	-	65361420	65361623
312400070	chr3	65364922	65365046	65364942	65365029	MAGI1	NM_004742	2	23	18	-	65364936	65365229
312400070	chr3	65364922	65365046	65364942	65365029	MAGI1	NM_015520	3	25	18	-	65364936	65365229
312400070	chr3	65364922	65365046	65364942	65365029	MAGI1	NM_001033057	1	23	17	-	65364936	65365229
312543496	chr3	65367606	65367778	65367628	65367750	MAGI1	NM_004742	2	23	17	-	65367552	65367744
312543496	chr3	65367606	65367778	65367628	65367750	MAGI1	NM_015520	3	25	17	-	65367552	65367744
312543496	chr3	65367606	65367778	65367628	65367750	MAGI1	NM_001033057	1	23	16	-	65367552	65367744
312534797	chr3	65376792	65376938	65376812	65376921	MAGI1	NM_004742	2	23	14	-	65376817	65377033
312534797	chr3	65376792	65376938	65376812	65376921	MAGI1	NM_015520	3	25	14	-	65376817	65377033
312534797	chr3	65376792	65376938	65376812	65376921	MAGI1	NM_001033057	1	23	14	-	65376817	65377033
312355686	chr3	65415276	65415416	65415303	65415394	MAGI1	NM_004742	2	23	12	-	65415195	65415815
312355686	chr3	65415276	65415416	65415303	65415394	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312355686	chr3	65415276	65415416	65415303	65415394	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312347560	chr3	65415669	65415837	65415693	65415815	MAGI1	NM_004742	2	23	12	-	65415195	65415815
312347560	chr3	65415669	65415837	65415693	65415815	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312347560	chr3	65415669	65415837	65415693	65415815	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312273490	chr3	65422859	65423027	65422880	65422998	MAGI1	NM_004742	2	23	10	-	65422830	65422922
312273490	chr3	65422859	65423027	65422880	65422998	MAGI1	NM_015520	3	25	10	-	65422830	65422922
312273490	chr3	65422859	65423027	65422880	65422998	MAGI1	NM_001033057	1	23	10	-	65422830	65422922
312290346	chr3	65433586	65433758	65433611	65433732	MAGI1	NM_004742	2	23	7	-	65433697	65433732
312290346	chr3	65433586	65433758	65433611	65433732	MAGI1	NM_015520	3	25	7	-	65433697	65433732
312290346	chr3	65433586	65433758	65433611	65433732	MAGI1	NM_001033057	1	23	7	-	65433697	65433732
312343653	chr3	65456059	65456191	65456081	65456166	MAGI1	NM_004742	2	23	5	-	65455958	65456159
312343653	chr3	65456059	65456191	65456081	65456166	MAGI1	NM_015520	3	25	5	-	65455958	65456159
312343653	chr3	65456059	65456191	65456081	65456166	MAGI1	NM_001033057	1	23	5	-	65455958	65456159
312474645	chr3	65479218	65479342	65479238	65479315	MAGI1	NM_004742	2	23	3	-	65479187	65479306
312474645	chr3	65479218	65479342	65479238	65479315	MAGI1	NM_015520	3	25	3	-	65479187	65479306
312474645	chr3	65479218	65479342	65479238	65479315	MAGI1	NM_001033057	1	23	3	-	65479187	65479306
312519801	chr3	66023846	66023997	66023863	66023974	MAGI1	NM_004742	2	23	1	-	66023671	66024509
312519801	chr3	66023846	66023997	66023863	66023974	MAGI1	NM_015520	3	25	1	-	66023671	66024509
312519801	chr3	66023846	66023997	66023863	66023974	MAGI1	NM_001033057	1	23	1	-	66023671	66024509
231857517	chr3	69915368	69915535	69915389	69915510	MITF	NM_198177	7	10	1	+	69915375	69915497
233656538	chr3	69985776	69985926	69985800	69985896	MITF	NM_001184968	3	3	1	+	69985751	69985906
233656538	chr3	69985776	69985926	69985800	69985896	MITF	NM_000248	1	9	1	+	69985751	69985906
233656538	chr3	69985776	69985926	69985800	69985896	MITF	NM_198178	8	9	1	+	69985751	69985906

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233656538	chr3	69985776	69985926	69985800	69985896	MITF	NM_198158	5	9	1	+	69985751	69985906
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_001184968	3	3	2	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_001184967	2	10	3	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_006722	4	10	3	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_000248	1	9	2	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_198177	7	10	3	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_198159	6	10	3	+	69986973	69987200
232624440	chr3	69987171	69987296	69987198	69987269	MITF	NM_198158	5	9	2	+	69986973	69987200
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_001184967	2	10	6	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_006722	4	10	6	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_000248	1	9	5	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_198177	7	10	6	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_198159	6	10	6	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_198178	8	9	5	+	69998202	69998319
232176106	chr3	69998117	69998251	69998150	69998226	MITF	NM_198158	5	9	5	+	69998202	69998319
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_001184967	2	10	8	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_006722	4	10	8	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_000248	1	9	7	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_198177	7	10	8	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_198159	6	10	8	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_198178	8	9	7	+	70005606	70005681
231111493	chr3	70005544	70005711	70005568	70005686	MITF	NM_198158	5	9	7	+	70005606	70005681
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_001184967	2	10	10	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_006722	4	10	10	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_000248	1	9	9	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_198177	7	10	10	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_198159	6	10	10	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_198178	8	9	9	+	70013998	70017488
233941387	chr3	70014129	70014292	70014151	70014270	MITF	NM_198158	5	9	9	+	70013998	70017488
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244816	8	20	19	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244815	7	16	15	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244814	6	17	16	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244813	5	15	14	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_032682	9	21	20	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244812	4	16	15	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244808	2	21	20	-	71015041	71015207
227777011	chr3	71015013	71015180	71015034	71015157	FOXP1	NM_001244810	3	21	20	-	71015041	71015207
227775974	chr3	71021219	71021355	71021239	71021334	FOXP1	NM_001244810	3	21	18	-	71021162	71021331
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244816	8	20	16	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244815	7	16	12	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244814	6	17	13	-	71026092	71026193

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244813	5	15	11	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_032682	9	21	17	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244812	4	16	12	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244808	2	21	17	-	71026092	71026193
227836292	chr3	71026104	71026246	71026122	71026219	FOXP1	NM_001244810	3	21	17	-	71026092	71026193
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244816	8	20	14	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244815	7	16	10	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244814	6	17	11	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244813	5	15	9	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_032682	9	21	15	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244812	4	16	10	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244808	2	21	15	-	71026979	71027180
229400517	chr3	71026981	71027143	71027000	71027123	FOXP1	NM_001244810	3	21	15	-	71026979	71027180
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244816	8	20	12	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244815	7	16	8	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244814	6	17	9	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244813	5	15	7	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_032682	9	21	13	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244812	4	16	8	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244808	2	21	13	-	71050123	71050210
228938894	chr3	71050016	71050178	71050043	71050152	FOXP1	NM_001244810	3	21	13	-	71050123	71050210
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244816	8	20	10	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244815	7	16	6	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244814	6	17	7	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244813	5	15	5	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_032682	9	21	11	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244812	4	16	6	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244808	2	21	11	-	71090479	71090683
227367167	chr3	71090440	71090611	71090462	71090588	FOXP1	NM_001244810	3	21	11	-	71090479	71090683
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244816	8	20	8	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244815	7	16	4	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244814	6	17	5	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244813	5	15	3	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_032682	9	21	9	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244808	2	21	9	-	71101688	71101777
228909796	chr3	71101630	71101803	71101653	71101777	FOXP1	NM_001244810	3	21	9	-	71101688	71101777
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244816	8	20	6	-	71161687	71161788
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244815	7	16	2	-	71161687	71161788
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244814	6	17	3	-	71161687	71161788
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_032682	9	21	7	-	71161687	71161788
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244812	4	16	4	-	71161687	71161788

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244808	2	21	7	-	71161687	71161788
230156850	chr3	71161674	71161829	71161700	71161801	FOXP1	NM_001244810	3	21	7	-	71161687	71161788
229057986	chr3	71247126	71247280	71247146	71247259	FOXP1	NM_001012505	1	7	7	-	71247034	71247219
269971442	chr3	89156925	89157094	89156947	89157073	EPHA3	NM_005233	1	17	1	+	89156674	89156986
269971442	chr3	89156925	89157094	89156947	89157073	EPHA3	NM_182644	2	7	1	+	89156674	89156986
271527129	chr3	89259095	89259268	89259117	89259245	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271527129	chr3	89259095	89259268	89259117	89259245	EPHA3	NM_182644	2	7	3	+	89259010	89259670
271509369	chr3	89259588	89259762	89259609	89259734	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271509369	chr3	89259588	89259762	89259609	89259734	EPHA3	NM_182644	2	7	3	+	89259010	89259670
270712946	chr3	89390853	89391005	89390880	89390985	EPHA3	NM_005233	1	17	5	+	89390905	89391240
270712946	chr3	89390853	89391005	89390880	89390985	EPHA3	NM_182644	2	7	5	+	89390905	89391240
270887491	chr3	89444897	89445023	89444921	89444998	EPHA3	NM_005233	1	17	6	+	89444987	89445111
270887491	chr3	89444897	89445023	89444921	89444998	EPHA3	NM_182644	2	7	6	+	89444987	89445111
271971042	chr3	89448609	89448762	89448637	89448734	EPHA3	NM_182644	2	7	7	+	89448468	89449495
270068877	chr3	89462248	89462375	89462272	89462350	EPHA3	NM_005233	1	17	10	+	89462291	89462416
270161268	chr3	89478136	89478299	89478163	89478273	EPHA3	NM_005233	1	17	12	+	89478256	89478317
272709783	chr3	89480367	89480504	89480390	89480479	EPHA3	NM_005233	1	17	13	+	89480300	89480509
271447913	chr3	89498475	89498609	89498500	89498585	EPHA3	NM_005233	1	17	14	+	89498375	89498524
271730159	chr3	89521652	89521824	89521673	89521797	EPHA3	NM_005233	1	17	16	+	89521614	89521769
229865373	chr3	128199946	128200109	128199965	128200084	GATA2	NM_032638	3	6	6	-	128198265	128200161
229865373	chr3	128199946	128200109	128199965	128200084	GATA2	NM_001145661	1	7	7	-	128198265	128200161
229865373	chr3	128199946	128200109	128199965	128200084	GATA2	NM_001145662	2	6	6	-	128198265	128200161
227455083	chr3	128202608	128202782	128202630	128202761	GATA2	NM_032638	3	6	4	-	128202703	128202848
227455083	chr3	128202608	128202782	128202630	128202761	GATA2	NM_001145661	1	7	5	-	128202703	128202848
227455083	chr3	128202608	128202782	128202630	128202761	GATA2	NM_001145662	2	6	4	-	128202703	128202848
229076909	chr3	128204757	128204913	128204779	128204892	GATA2	NM_032638	3	6	3	-	128204570	128205211
229076909	chr3	128204757	128204913	128204779	128204892	GATA2	NM_001145661	1	7	4	-	128204570	128205211
229076909	chr3	128204757	128204913	128204779	128204892	GATA2	NM_001145662	2	6	3	-	128204570	128205211
227188630	chr3	128205608	128205762	128205626	128205745	GATA2	NM_032638	3	6	2	-	128205646	128205919
227188630	chr3	128205608	128205762	128205626	128205745	GATA2	NM_001145661	1	7	3	-	128205646	128205919
227188630	chr3	128205608	128205762	128205626	128205745	GATA2	NM_001145662	2	6	2	-	128205646	128205919
270961681	chr3	134670089	134670258	134670110	134670237	EPHB1	NM_004441	1	16	3	+	134670213	134670894
271023250	chr3	134670555	134670720	134670581	134670694	EPHB1	NM_004441	1	16	3	+	134670213	134670894
271949934	chr3	134825372	134825499	134825390	134825479	EPHB1	NM_004441	1	16	4	+	134825290	134825445
271223793	chr3	134872887	134873058	134872909	134873036	EPHB1	NM_004441	1	16	6	+	134872994	134873118
272706532	chr3	134884779	134884941	134884802	134884919	EPHB1	NM_004441	1	16	8	+	134884810	134884918
272361742	chr3	134911329	134911486	134911352	134911465	EPHB1	NM_004441	1	16	11	+	134911418	134911665
269832136	chr3	134920417	134920565	134920439	134920539	EPHB1	NM_004441	1	16	12	+	134920316	134920531
269537809	chr3	134967225	134967396	134967245	134967369	EPHB1	NM_004441	1	16	14	+	134967158	134967351
294538206	chr3	138374201	138374341	138374226	138374313	PIK3CB	NM_001256045	1	13	13	-	138371540	138374368
294538206	chr3	138374201	138374341	138374226	138374313	PIK3CB	NM_006219	2	22	22	-	138371540	138374368

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294896998	chr3	138376452	138376614	138376475	138376589	PIK3CB	NM_001256045	1	13	11	-	138376532	138376677
294896998	chr3	138376452	138376614	138376475	138376589	PIK3CB	NM_006219	2	22	20	-	138376532	138376677
293909646	chr3	138383815	138383984	138383841	138383958	PIK3CB	NM_001256045	1	13	9	-	138383878	138384045
293909646	chr3	138383815	138383984	138383841	138383958	PIK3CB	NM_006219	2	22	18	-	138383878	138384045
294682509	chr3	138402460	138402590	138402487	138402563	PIK3CB	NM_001256045	1	13	7	-	138402520	138402629
294682509	chr3	138402460	138402590	138402487	138402563	PIK3CB	NM_006219	2	22	16	-	138402520	138402629
294046833	chr3	138407648	138407806	138407676	138407782	PIK3CB	NM_001256045	1	13	5	-	138407717	138407816
294046833	chr3	138407648	138407806	138407676	138407782	PIK3CB	NM_006219	2	22	14	-	138407717	138407816
294711329	chr3	138413528	138413678	138413555	138413657	PIK3CB	NM_001256045	1	13	3	-	138413628	138413749
294711329	chr3	138413528	138413678	138413555	138413657	PIK3CB	NM_006219	2	22	12	-	138413628	138413749
293920779	chr3	138417860	138417997	138417885	138417975	PIK3CB	NM_001256045	1	13	2	-	138417749	138417937
293920779	chr3	138417860	138417997	138417885	138417975	PIK3CB	NM_006219	2	22	11	-	138417749	138417937
294796312	chr3	138426056	138426228	138426084	138426201	PIK3CB	NM_006219	2	22	9	-	138426001	138426131
294796312	chr3	138426056	138426228	138426084	138426201	PIK3CB	NM_001256045	1	13	1	-	138426001	138426463
294667806	chr3	138433322	138433481	138433350	138433453	PIK3CB	NM_006219	2	22	7	-	138433310	138433561
294593009	chr3	138453376	138453548	138453403	138453523	PIK3CB	NM_006219	2	22	5	-	138453476	138453646
294168910	chr3	138461309	138461439	138461332	138461418	PIK3CB	NM_006219	2	22	3	-	138461400	138461623
293964855	chr3	138474622	138474750	138474646	138474722	PIK3CB	NM_006219	2	22	2	-	138474596	138474821
229732310	chr3	138664389	138664540	138664407	138664523	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229750319	chr3	138665144	138665311	138665166	138665291	FOXL2	NM_023067	1	1	1	-	138663066	138665982
282986707	chr3	142168287	142168454	142168315	142168430	ATR	NM_001184	1	47	47	-	142168077	142168444
284756111	chr3	142176388	142176512	142176415	142176486	ATR	NM_001184	1	47	45	-	142176446	142176597
281326836	chr3	142177828	142177973	142177853	142177946	ATR	NM_001184	1	47	44	-	142177800	142177953
284434129	chr3	142178121	142178245	142178141	142178221	ATR	NM_001184	1	47	43	-	142178069	142178225
282579870	chr3	142180895	142181046	142180920	142181018	ATR	NM_001184	1	47	42	-	142180782	142180932
281325934	chr3	142185060	142185193	142185092	142185167	ATR	NM_001184	1	47	40	-	142185166	142185375
282077769	chr3	142186760	142186891	142186791	142186865	ATR	NM_001184	1	47	39	-	142186776	142186910
283083996	chr3	142188256	142188408	142188284	142188391	ATR	NM_001184	1	47	38	-	142188179	142188411
283975281	chr3	142203956	142204089	142203981	142204061	ATR	NM_001184	1	47	36	-	142203982	142204124
283770404	chr3	142215179	142215310	142215201	142215289	ATR	NM_001184	1	47	34	-	142215203	142215362
282687788	chr3	142217375	142217530	142217400	142217502	ATR	NM_001184	1	47	32	-	142217439	142217616
283060597	chr3	142222195	142222353	142222222	142222325	ATR	NM_001184	1	47	30	-	142222204	142222295
283386731	chr3	142226707	142226847	142226734	142226819	ATR	NM_001184	1	47	28	-	142226773	142226951
282735525	chr3	142231225	142231399	142231249	142231371	ATR	NM_001184	1	47	27	-	142231102	142231312
281796022	chr3	142234269	142234442	142234296	142234415	ATR	NM_001184	1	47	25	-	142234237	142234357
281813764	chr3	142242783	142242943	142242811	142242923	ATR	NM_001184	1	47	22	-	142242835	142243041
285747265	chr3	142253944	142254113	142253971	142254085	ATR	NM_001184	1	47	21	-	142253922	142254047
282256911	chr3	142259683	142259814	142259711	142259790	ATR	NM_001184	1	47	18	-	142259746	142259876
282607198	chr3	142266560	142266728	142266587	142266704	ATR	NM_001184	1	47	16	-	142266567	142266752
282014738	chr3	142268437	142268562	142268464	142268536	ATR	NM_001184	1	47	15	-	142268321	142268515
284365870	chr3	142272124	142272258	142272148	142272232	ATR	NM_001184	1	47	13	-	142272069	142272240

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
283403090	chr3	142272621	142272761	142272648	142272733	ATR	NM_001184	1	47	11	-	142272667	142272857
284574029	chr3	142274819	142274987	142274844	142274959	ATR	NM_001184	1	47	10	-	142274719	142274981
284379455	chr3	142277441	142277572	142277464	142277546	ATR	NM_001184	1	47	8	-	142277466	142277618
282759508	chr3	142278218	142278382	142278246	142278354	ATR	NM_001184	1	47	7	-	142278093	142278283
282195023	chr3	142280135	142280265	142280155	142280244	ATR	NM_001184	1	47	5	-	142280085	142280263
281397300	chr3	142281245	142281407	142281267	142281378	ATR	NM_001184	1	47	4	-	142281074	142281951
283776005	chr3	142281553	142281726	142281581	142281699	ATR	NM_001184	1	47	4	-	142281074	142281951
283788910	chr3	142281885	142282033	142281910	142282005	ATR	NM_001184	1	47	4	-	142281074	142281951
281897799	chr3	142297441	142297582	142297461	142297565	ATR	NM_001184	1	47	1	-	142297488	142297668
237453745	chr3	178916886	178917025	178916912	178916999	PIK3CA	NM_006218	1	21	2	+	178916538	178916965
241323204	chr3	178919023	178919162	178919050	178919136	PIK3CA	NM_006218	1	21	4	+	178919078	178919328
235936473	chr3	178921389	178921553	178921415	178921525	PIK3CA	NM_006218	1	21	5	+	178921332	178921577
236803779	chr3	178927969	178928095	178927992	178928068	PIK3CA	NM_006218	1	21	8	+	178927974	178928126
236070736	chr3	178928316	178928473	178928341	178928445	PIK3CA	NM_006218	1	21	9	+	178928219	178928353
235352525	chr3	178937016	178937145	178937044	178937114	PIK3CA	NM_006218	1	21	11	+	178936984	178937065
236818943	chr3	178941768	178941942	178941793	178941920	PIK3CA	NM_006218	1	21	15	+	178941869	178941975
235222326	chr3	178943684	178943853	178943705	178943829	PIK3CA	NM_006218	1	21	17	+	178943750	178943828
235749304	chr3	178947674	178947832	178947702	178947809	PIK3CA	NM_006218	1	21	19	+	178947792	178947909
237325070	chr3	178948084	178948226	178948112	178948198	PIK3CA	NM_006218	1	21	20	+	178948013	178948164
263667014	chr3	181430140	181430265	181430157	181430246	SOX2	NM_003106	1	1	1	+	181429712	181432223
263687220	chr3	181430489	181430661	181430511	181430643	SOX2	NM_003106	1	1	1	+	181429712	181432223
263687508	chr3	181430870	181431042	181430889	181431020	SOX2	NM_003106	1	1	1	+	181429712	181432223
224737416	chr3	187440220	187440394	187440243	187440371	BCL6	NM_001706	3	10	10	-	187439165	187440389
224737416	chr3	187440220	187440394	187440243	187440371	BCL6	NM_001134738	2	8	8	-	187439165	187440389
224737416	chr3	187440220	187440394	187440243	187440371	BCL6	NM_001130845	1	10	10	-	187439165	187440389
223592024	chr3	187443293	187443426	187443312	187443399	BCL6	NM_001706	3	10	8	-	187443287	187443417
223592024	chr3	187443293	187443426	187443312	187443399	BCL6	NM_001134738	2	8	6	-	187443287	187443417
223592024	chr3	187443293	187443426	187443312	187443399	BCL6	NM_001130845	1	10	8	-	187443287	187443417
224044937	chr3	187446104	187446260	187446124	187446242	BCL6	NM_001706	3	10	6	-	187446148	187446332
224044937	chr3	187446104	187446260	187446124	187446242	BCL6	NM_001134738	2	8	5	-	187446148	187446332
224044937	chr3	187446104	187446260	187446124	187446242	BCL6	NM_001130845	1	10	6	-	187446148	187446332
225169206	chr3	187447038	187447197	187447059	187447176	BCL6	NM_001706	3	10	5	-	187446838	187447809
225169206	chr3	187447038	187447197	187447059	187447176	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225169206	chr3	187447038	187447197	187447059	187447176	BCL6	NM_001130845	1	10	5	-	187446838	187447809
225170056	chr3	187447463	187447625	187447483	187447605	BCL6	NM_001706	3	10	5	-	187446838	187447809
225170056	chr3	187447463	187447625	187447483	187447605	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225170056	chr3	187447463	187447625	187447483	187447605	BCL6	NM_001130845	1	10	5	-	187446838	187447809
223613821	chr3	187449485	187449651	187449506	187449628	BCL6	NM_001706	3	10	4	-	187449497	187449718
223613821	chr3	187449485	187449651	187449506	187449628	BCL6	NM_001134738	2	8	3	-	187449497	187449718
223613821	chr3	187449485	187449651	187449506	187449628	BCL6	NM_001130845	1	10	4	-	187449497	187449718
234281990	chr3	188123878	188124040	188123906	188124017	LPP	NM_001167672	2	10	2	+	188123900	188124101

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234281990	chr3	188123878	188124040	188123906	188124017	LPP	NM_001167671	1	11	3	+	188123900	188124101
234281990	chr3	188123878	188124040	188123906	188124017	LPP	NM_005578	3	11	3	+	188123900	188124101
233388008	chr3	188242424	188242598	188242449	188242576	LPP	NM_001167672	2	10	4	+	188242453	188242575
233388008	chr3	188242424	188242598	188242449	188242576	LPP	NM_001167671	1	11	5	+	188242453	188242575
233388008	chr3	188242424	188242598	188242449	188242576	LPP	NM_005578	3	11	5	+	188242453	188242575
233644441	chr3	188327269	188327435	188327293	188327415	LPP	NM_001167671	1	11	6	+	188326949	188327632
233644441	chr3	188327269	188327435	188327293	188327415	LPP	NM_005578	3	11	6	+	188326949	188327632
234450346	chr3	188426118	188426269	188426142	188426244	LPP	NM_001167672	2	10	6	+	188426055	188426181
234450346	chr3	188426118	188426269	188426142	188426244	LPP	NM_001167671	1	11	7	+	188426055	188426181
234450346	chr3	188426118	188426269	188426142	188426244	LPP	NM_005578	3	11	7	+	188426055	188426181
233727562	chr3	188584047	188584190	188584067	188584169	LPP	NM_001167672	2	10	8	+	188583988	188584166
233727562	chr3	188584047	188584190	188584067	188584169	LPP	NM_001167671	1	11	9	+	188583988	188584166
233727562	chr3	188584047	188584190	188584067	188584169	LPP	NM_005578	3	11	9	+	188583988	188584166
299641367	chr3	195590913	195591081	195590931	195591059	TNK2	NM_001010938	1	15	15	-	195590236	195591058
299641367	chr3	195590913	195591081	195590931	195591059	TNK2	NM_005781	2	15	15	-	195590236	195591058
304433322	chr3	195594218	195594386	195594235	195594369	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304433322	chr3	195594218	195594386	195594235	195594369	TNK2	NM_005781	2	15	12	-	195594232	195595580
300729851	chr3	195594654	195594778	195594673	195594761	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300729851	chr3	195594654	195594778	195594673	195594761	TNK2	NM_005781	2	15	12	-	195594232	195595580
300732179	chr3	195594970	195595125	195594990	195595104	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300732179	chr3	195594970	195595125	195594990	195595104	TNK2	NM_005781	2	15	12	-	195594232	195595580
304440530	chr3	195595393	195595565	195595410	195595546	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304440530	chr3	195595393	195595565	195595410	195595546	TNK2	NM_005781	2	15	12	-	195594232	195595580
304616799	chr3	195599112	195599253	195599129	195599235	TNK2	NM_001010938	1	15	10	-	195599147	195599341
304616799	chr3	195599112	195599253	195599129	195599235	TNK2	NM_005781	2	15	10	-	195599147	195599341
302223380	chr3	195605376	195605507	195605395	195605489	TNK2	NM_001010938	1	15	8	-	195605317	195605463
302223380	chr3	195605376	195605507	195605395	195605489	TNK2	NM_005781	2	15	8	-	195605317	195605463
301188352	chr3	195608993	195609164	195609013	195609145	TNK2	NM_001010938	1	15	6	-	195608922	195609199
301188352	chr3	195608993	195609164	195609013	195609145	TNK2	NM_005781	2	15	6	-	195608922	195609199
300544785	chr3	195611640	195611793	195611657	195611774	TNK2	NM_001010938	1	15	4	-	195611683	195611904
300544785	chr3	195611640	195611793	195611657	195611774	TNK2	NM_005781	2	15	4	-	195611683	195611904
299913316	chr3	195615228	195615388	195615248	195615371	TNK2	NM_001010938	1	15	2	-	195615297	195615477
299913316	chr3	195615228	195615388	195615248	195615371	TNK2	NM_005781	2	15	2	-	195615297	195615477
227844936	chr4	1800946	1801116	1800964	1801099	FGFR3	NM_000142	1	18	3	+	1800981	1801250
227844936	chr4	1800946	1801116	1800964	1801099	FGFR3	NM_022965	3	16	3	+	1800981	1801250
227844936	chr4	1800946	1801116	1800964	1801099	FGFR3	NM_001163213	2	18	3	+	1800981	1801250
229022653	chr4	1803059	1803233	1803078	1803213	FGFR3	NM_000142	1	18	5	+	1803094	1803263
229022653	chr4	1803059	1803233	1803078	1803213	FGFR3	NM_022965	3	16	5	+	1803094	1803263
229022653	chr4	1803059	1803233	1803078	1803213	FGFR3	NM_001163213	2	18	5	+	1803094	1803263
227442256	chr4	1803535	1803667	1803552	1803646	FGFR3	NM_000142	1	18	7	+	1803562	1803752
227442256	chr4	1803535	1803667	1803552	1803646	FGFR3	NM_022965	3	16	7	+	1803562	1803752

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227442256	chr4	1803535	1803667	1803552	1803646	FGFR3	NM_001163213	2	18	7	+	1803562	1803752
227471428	chr4	1804639	1804812	1804661	1804792	FGFR3	NM_001163213	2	18	8	+	1804641	1804791
227641799	chr4	1806126	1806279	1806149	1806255	FGFR3	NM_000142	1	18	9	+	1806057	1806247
227641799	chr4	1806126	1806279	1806149	1806255	FGFR3	NM_001163213	2	18	9	+	1806057	1806247
227877076	chr4	1807174	1807303	1807193	1807282	FGFR3	NM_000142	1	18	11	+	1807082	1807203
227877076	chr4	1807174	1807303	1807193	1807282	FGFR3	NM_022965	3	16	9	+	1807082	1807203
227877076	chr4	1807174	1807303	1807193	1807282	FGFR3	NM_001163213	2	18	11	+	1807082	1807203
228570701	chr4	1807511	1807667	1807530	1807646	FGFR3	NM_000142	1	18	13	+	1807477	1807667
228570701	chr4	1807511	1807667	1807530	1807646	FGFR3	NM_022965	3	16	11	+	1807477	1807667
228570701	chr4	1807511	1807667	1807530	1807646	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
227629274	chr4	1807965	1808094	1807983	1808077	FGFR3	NM_000142	1	18	15	+	1807984	1808054
227629274	chr4	1807965	1808094	1807983	1808077	FGFR3	NM_022965	3	16	13	+	1807984	1808054
227629274	chr4	1807965	1808094	1807983	1808077	FGFR3	NM_001163213	2	18	15	+	1807984	1808054
329689140	chr4	1808622	1808796	1808640	1808779	FGFR3	NM_000142	1	18	17	+	1808556	1808661
329689140	chr4	1808622	1808796	1808640	1808779	FGFR3	NM_022965	3	16	15	+	1808556	1808661
329689140	chr4	1808622	1808796	1808640	1808779	FGFR3	NM_001163213	2	18	17	+	1808556	1808661
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_007331	2	11	4	+	1902353	1902978
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_133330	3	24	4	+	1902353	1902978
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_133335	6	22	2	+	1902353	1902978
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_133334	5	9	1	+	1902353	1902978
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_133331	4	23	3	+	1902353	1902978
294598488	chr4	1902480	1902639	1902498	1902616	WHSC1	NM_001042424	1	22	2	+	1902353	1902978
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_007331	2	11	5	+	1905943	1906105
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_133330	3	24	5	+	1905943	1906105
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_133335	6	22	3	+	1905943	1906105
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_133334	5	9	2	+	1905943	1906105
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_133331	4	23	4	+	1905943	1906105
294839781	chr4	1905878	1906046	1905903	1906025	WHSC1	NM_001042424	1	22	3	+	1905943	1906105
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_007331	2	11	7	+	1919868	1920350
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_133330	3	24	7	+	1919868	1920350
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_133335	6	22	5	+	1919868	1920350
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_133334	5	9	4	+	1919868	1920350
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_133331	4	23	6	+	1919868	1920350
294397342	chr4	1919788	1919949	1919816	1919927	WHSC1	NM_001042424	1	22	5	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_007331	2	11	7	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_133330	3	24	7	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_133335	6	22	5	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_133334	5	9	4	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_133331	4	23	6	+	1919868	1920350
294434028	chr4	1920231	1920403	1920253	1920375	WHSC1	NM_001042424	1	22	5	+	1919868	1920350
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_007331	2	11	10	+	1940178	1940259

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_133330	3	24	10	+	1940178	1940259
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_133335	6	22	8	+	1940178	1940259
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_133334	5	9	7	+	1940178	1940259
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_133331	4	23	9	+	1940178	1940259
294301094	chr4	1940043	1940216	1940065	1940196	WHSC1	NM_001042424	1	22	8	+	1940178	1940259
295153438	chr4	1943957	1944101	1943979	1944078	WHSC1	NM_007331	2	11	11	+	1941381	1944302
295153438	chr4	1943957	1944101	1943979	1944078	WHSC1	NM_133334	5	9	9	+	1944066	1950545
294958418	chr4	1953879	1954042	1953897	1954024	WHSC1	NM_133330	3	24	13	+	1953835	1953958
294958418	chr4	1953879	1954042	1953897	1954024	WHSC1	NM_133335	6	22	11	+	1953835	1953958
294958418	chr4	1953879	1954042	1953897	1954024	WHSC1	NM_133331	4	23	12	+	1953835	1953958
294958418	chr4	1953879	1954042	1953897	1954024	WHSC1	NM_001042424	1	22	11	+	1953835	1953958
294765259	chr4	1956957	1957126	1956976	1957105	WHSC1	NM_133330	3	24	15	+	1956888	1957067
294765259	chr4	1956957	1957126	1956976	1957105	WHSC1	NM_133335	6	22	13	+	1956888	1957067
294765259	chr4	1956957	1957126	1956976	1957105	WHSC1	NM_133331	4	23	14	+	1956888	1957067
294765259	chr4	1956957	1957126	1956976	1957105	WHSC1	NM_001042424	1	22	13	+	1956888	1957067
294344119	chr4	1957774	1957945	1957801	1957917	WHSC1	NM_133330	3	24	17	+	1957710	1957915
294344119	chr4	1957774	1957945	1957801	1957917	WHSC1	NM_133335	6	22	15	+	1957710	1957915
294344119	chr4	1957774	1957945	1957801	1957917	WHSC1	NM_133331	4	23	16	+	1957710	1957915
294344119	chr4	1957774	1957945	1957801	1957917	WHSC1	NM_001042424	1	22	15	+	1957710	1957915
294322908	chr4	1961265	1961436	1961287	1961414	WHSC1	NM_133330	3	24	19	+	1961198	1961467
294322908	chr4	1961265	1961436	1961287	1961414	WHSC1	NM_133335	6	22	17	+	1961198	1961467
294322908	chr4	1961265	1961436	1961287	1961414	WHSC1	NM_133331	4	23	18	+	1961198	1961467
294322908	chr4	1961265	1961436	1961287	1961414	WHSC1	NM_001042424	1	22	17	+	1961198	1961467
294772032	chr4	1976610	1976751	1976634	1976732	WHSC1	NM_133330	3	24	21	+	1976590	1976731
294772032	chr4	1976610	1976751	1976634	1976732	WHSC1	NM_133335	6	22	19	+	1976590	1976731
294772032	chr4	1976610	1976751	1976634	1976732	WHSC1	NM_133331	4	23	20	+	1976590	1976731
294772032	chr4	1976610	1976751	1976634	1976732	WHSC1	NM_001042424	1	22	19	+	1976590	1976731
294967549	chr4	1978196	1978357	1978217	1978337	WHSC1	NM_133330	3	24	23	+	1978202	1978406
294967549	chr4	1978196	1978357	1978217	1978337	WHSC1	NM_133335	6	22	21	+	1978202	1978406
294967549	chr4	1978196	1978357	1978217	1978337	WHSC1	NM_133331	4	23	22	+	1978202	1978406
294967549	chr4	1978196	1978357	1978217	1978337	WHSC1	NM_001042424	1	22	21	+	1978202	1978406
294958761	chr4	1980500	1980666	1980523	1980649	WHSC1	NM_133335	6	22	22	+	1980365	1983934
294958761	chr4	1980500	1980666	1980523	1980649	WHSC1	NM_001042424	1	22	22	+	1980365	1983934
294958761	chr4	1980500	1980666	1980523	1980649	WHSC1	NM_133330	3	24	24	+	1980365	1983930
294958761	chr4	1980500	1980666	1980523	1980649	WHSC1	NM_133331	4	23	23	+	1980365	1983930
262053249	chr4	40245285	40245450	40245312	40245429	RHOH	NM_004310	1	3	3	+	40244798	40246281
235717580	chr4	41747683	41747851	41747705	41747826	PHOX2B	NM_003924	1	3	3	-	41746099	41748339
238035319	chr4	41749271	41749441	41749292	41749421	PHOX2B	NM_003924	1	3	2	-	41749366	41749553
238144512	chr4	41750489	41750651	41750511	41750630	PHOX2B	NM_003924	1	3	1	-	41750387	41750987
240042436	chr4	55127452	55127621	55127475	55127598	PDGFRA	NM_006206	1	23	3	+	55127262	55127579
239199535	chr4	55131020	55131146	55131048	55131118	PDGFRA	NM_006206	1	23	5	+	55131086	55131216

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235488274	chr4	55133636	55133807	55133661	55133783	PDGFRA	NM_006206	1	23	7	+	55133719	55133908
240212404	chr4	55138443	55138609	55138463	55138586	PDGFRA	NM_006206	1	23	9	+	55138561	55138687
235159279	chr4	55140670	55140843	55140693	55140818	PDGFRA	NM_006206	1	23	11	+	55140698	55140792
238237773	chr4	55144007	55144155	55144031	55144128	PDGFRA	NM_006206	1	23	14	+	55144063	55144173
235803433	chr4	55146447	55146600	55146470	55146572	PDGFRA	NM_006206	1	23	16	+	55146483	55146649
236734860	chr4	55151923	55152083	55151944	55152058	PDGFRA	NM_006206	1	23	18	+	55152008	55152130
236601663	chr4	55155145	55155306	55155166	55155284	PDGFRA	NM_006206	1	23	21	+	55155176	55155281
235742125	chr4	55161198	55161371	55161220	55161348	PDGFRA	NM_006206	1	23	23	+	55161292	55164412
233149050	chr4	55561717	55561862	55561740	55561833	KIT	NM_000222	1	21	2	+	55561678	55561947
233149050	chr4	55561717	55561862	55561740	55561833	KIT	NM_001093772	2	21	2	+	55561678	55561947
233650883	chr4	55564644	55564815	55564664	55564789	KIT	NM_000222	1	21	3	+	55564450	55564731
233650883	chr4	55564644	55564815	55564664	55564789	KIT	NM_001093772	2	21	3	+	55564450	55564731
233221153	chr4	55569871	55570041	55569898	55570013	KIT	NM_000222	1	21	5	+	55569890	55570058
233221153	chr4	55569871	55570041	55569898	55570013	KIT	NM_001093772	2	21	5	+	55569890	55570058
234335248	chr4	55575628	55575779	55575650	55575756	KIT	NM_000222	1	21	7	+	55575590	55575705
234335248	chr4	55575628	55575779	55575650	55575756	KIT	NM_001093772	2	21	7	+	55575590	55575705
232621917	chr4	55592083	55592257	55592109	55592230	KIT	NM_001093772	2	21	9	+	55592023	55592204
232621917	chr4	55592083	55592257	55592109	55592230	KIT	NM_000222	1	21	9	+	55592023	55592216
231140516	chr4	55593948	55594119	55593970	55594093	KIT	NM_000222	1	21	12	+	55593989	55594093
231140516	chr4	55593948	55594119	55593970	55594093	KIT	NM_001093772	2	21	12	+	55593989	55594093
231487299	chr4	55597441	55597614	55597463	55597588	KIT	NM_000222	1	21	15	+	55597494	55597585
231487299	chr4	55597441	55597614	55597463	55597588	KIT	NM_001093772	2	21	15	+	55597494	55597585
326771844	chr4	55599309	55599480	55599336	55599453	KIT	NM_000222	1	21	17	+	55599236	55599358
326771844	chr4	55599309	55599480	55599336	55599453	KIT	NM_001093772	2	21	17	+	55599236	55599358
232496838	chr4	55602902	55603065	55602922	55603037	KIT	NM_000222	1	21	19	+	55602887	55602986
232496838	chr4	55602902	55603065	55602922	55603037	KIT	NM_001093772	2	21	19	+	55602887	55602986
233965041	chr4	55604572	55604746	55604597	55604724	KIT	NM_000222	1	21	21	+	55604595	55606881
233965041	chr4	55604572	55604746	55604597	55604724	KIT	NM_001093772	2	21	21	+	55604595	55606881
231418373	chr4	55948112	55948236	55948139	55948208	KDR	NM_002253	1	30	29	-	55948123	55948208
233956100	chr4	55953807	55953967	55953829	55953941	KDR	NM_002253	1	30	27	-	55953774	55953925
231439803	chr4	55955822	55955995	55955844	55955969	KDR	NM_002253	1	30	24	-	55955858	55955969
232730231	chr4	55960939	55961078	55960961	55961056	KDR	NM_002253	1	30	21	-	55960969	55961122
232575060	chr4	55962402	55962550	55962424	55962521	KDR	NM_002253	1	30	19	-	55962396	55962509
232275914	chr4	55964325	55964470	55964346	55964442	KDR	NM_002253	1	30	17	-	55964304	55964439
231261405	chr4	55968167	55968297	55968188	55968269	KDR	NM_002253	1	30	15	-	55968064	55968195
232833435	chr4	55970827	55970967	55970849	55970940	KDR	NM_002253	1	30	13	-	55970810	55971151
233140601	chr4	55972799	55972973	55972827	55972950	KDR	NM_002253	1	30	11	-	55972854	55972977
230956099	chr4	55976492	55976665	55976512	55976638	KDR	NM_002253	1	30	9	-	55976570	55976733
232589275	chr4	55979420	55979570	55979447	55979545	KDR	NM_002253	1	30	7	-	55979471	55979648
233168222	chr4	55980958	55981120	55980987	55981098	KDR	NM_002253	1	30	5	-	55981041	55981209
233404700	chr4	55981486	55981655	55981511	55981627	KDR	NM_002253	1	30	4	-	55981448	55981578

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233746178	chr4	55991373	55991499	55991393	55991479	KDR	NM_002253	1	30	1	-	55991394	55991762
294438408	chr4	62453093	62453227	62453117	62453199	LPHN3	NM_015236	1	23	2	+	62452945	62453158
294444129	chr4	62598378	62598533	62598405	62598508	LPHN3	NM_015236	1	23	5	+	62598472	62599272
294495323	chr4	62598818	62598988	62598844	62598965	LPHN3	NM_015236	1	23	5	+	62598472	62599272
294720984	chr4	62758329	62758497	62758353	62758473	LPHN3	NM_015236	1	23	7	+	62758374	62758676
294193562	chr4	62761470	62761623	62761493	62761597	LPHN3	NM_015236	1	23	8	+	62761449	62761552
294316318	chr4	62778403	62778530	62778432	62778503	LPHN3	NM_015236	1	23	10	+	62778437	62778475
293715656	chr4	62801716	62801840	62801737	62801812	LPHN3	NM_015236	1	23	12	+	62801641	62801763
293992602	chr4	62813873	62813998	62813900	62813974	LPHN3	NM_015236	1	23	14	+	62813818	62813994
294784561	chr4	62849120	62849284	62849146	62849263	LPHN3	NM_015236	1	23	16	+	62849101	62849321
294869532	chr4	62863950	62864107	62863974	62864079	LPHN3	NM_015236	1	23	18	+	62863892	62863983
294354433	chr4	62897239	62897385	62897261	62897357	LPHN3	NM_015236	1	23	20	+	62897160	62897328
294321965	chr4	62910204	62910357	62910227	62910329	LPHN3	NM_015236	1	23	22	+	62910171	62910267
294735320	chr4	62936108	62936260	62936132	62936237	LPHN3	NM_015236	1	23	23	+	62935827	62938168
294714880	chr4	62936529	62936653	62936551	62936627	LPHN3	NM_015236	1	23	23	+	62935827	62938168
223862626	chr4	87967296	87967470	87967322	87967441	AFF1	NM_005935	2	20	2	+	87967318	87967438
223862626	chr4	87967296	87967470	87967322	87967441	AFF1	NM_001166693	1	21	3	+	87967318	87967438
223649266	chr4	87968116	87968254	87968138	87968233	AFF1	NM_005935	2	20	3	+	87967847	87968746
223649266	chr4	87968116	87968254	87968138	87968233	AFF1	NM_001166693	1	21	4	+	87967847	87968746
225075308	chr4	87968554	87968728	87968576	87968705	AFF1	NM_005935	2	20	3	+	87967847	87968746
225075308	chr4	87968554	87968728	87968576	87968705	AFF1	NM_001166693	1	21	4	+	87967847	87968746
223069902	chr4	88012928	88013095	88012959	88013071	AFF1	NM_005935	2	20	6	+	88012945	88012981
223069902	chr4	88012928	88013095	88012959	88013071	AFF1	NM_001166693	1	21	7	+	88012945	88012981
222290732	chr4	88026834	88027001	88026857	88026979	AFF1	NM_005935	2	20	9	+	88026960	88026997
222290732	chr4	88026834	88027001	88026857	88026979	AFF1	NM_001166693	1	21	10	+	88026960	88026997
225140519	chr4	88035421	88035574	88035441	88035553	AFF1	NM_005935	2	20	11	+	88035519	88036451
225140519	chr4	88035421	88035574	88035441	88035553	AFF1	NM_001166693	1	21	12	+	88035519	88036451
225164669	chr4	88035899	88036064	88035918	88036044	AFF1	NM_005935	2	20	11	+	88035519	88036451
225164669	chr4	88035899	88036064	88035918	88036044	AFF1	NM_001166693	1	21	12	+	88035519	88036451
223734469	chr4	88036304	88036468	88036327	88036447	AFF1	NM_005935	2	20	11	+	88035519	88036451
223734469	chr4	88036304	88036468	88036327	88036447	AFF1	NM_001166693	1	21	12	+	88035519	88036451
222535192	chr4	88047184	88047351	88047206	88047330	AFF1	NM_005935	2	20	13	+	88047251	88047488
222535192	chr4	88047184	88047351	88047206	88047330	AFF1	NM_001166693	1	21	14	+	88047251	88047488
222815094	chr4	88048174	88048299	88048197	88048271	AFF1	NM_005935	2	20	14	+	88048178	88048269
222815094	chr4	88048174	88048299	88048197	88048271	AFF1	NM_001166693	1	21	15	+	88048178	88048269
223663943	chr4	88052879	88053035	88052907	88053007	AFF1	NM_005935	2	20	17	+	88052945	88053016
223663943	chr4	88052879	88053035	88052907	88053007	AFF1	NM_001166693	1	21	18	+	88052945	88053016
222840927	chr4	88055535	88055695	88055559	88055675	AFF1	NM_005935	2	20	19	+	88055626	88055846
222840927	chr4	88055535	88055695	88055559	88055675	AFF1	NM_001166693	1	21	20	+	88055623	88055846
222742627	chr4	88056748	88056892	88056769	88056864	AFF1	NM_005935	2	20	20	+	88056732	88062191
222742627	chr4	88056748	88056892	88056769	88056864	AFF1	NM_001166693	1	21	21	+	88056732	88062206

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293009296	chr4	103455009	103455183	103455038	103455155	NFKB1	NM_001165412	1	24	4	+	103455005	103455042
293009296	chr4	103455009	103455183	103455038	103455155	NFKB1	NM_003998	2	24	4	+	103455002	103455042
292519688	chr4	103497952	103498118	103497976	103498096	NFKB1	NM_001165412	1	24	7	+	103498033	103498196
292519688	chr4	103497952	103498118	103497976	103498096	NFKB1	NM_003998	2	24	7	+	103498033	103498196
291562146	chr4	103501662	103501835	103501690	103501810	NFKB1	NM_001165412	1	24	9	+	103501692	103501796
291562146	chr4	103501662	103501835	103501690	103501810	NFKB1	NM_003998	2	24	9	+	103501692	103501796
293363369	chr4	103514509	103514641	103514531	103514616	NFKB1	NM_001165412	1	24	12	+	103514582	103514725
293363369	chr4	103514509	103514641	103514531	103514616	NFKB1	NM_003998	2	24	12	+	103514582	103514725
291788766	chr4	103517190	103517358	103517213	103517330	NFKB1	NM_001165412	1	24	14	+	103517295	103517489
291788766	chr4	103517190	103517358	103517213	103517330	NFKB1	NM_003998	2	24	14	+	103517295	103517489
290252269	chr4	103518681	103518853	103518706	103518828	NFKB1	NM_001165412	1	24	15	+	103518677	103518818
290252269	chr4	103518681	103518853	103518706	103518828	NFKB1	NM_003998	2	24	15	+	103518677	103518818
292354879	chr4	103527731	103527882	103527750	103527856	NFKB1	NM_001165412	1	24	17	+	103527653	103527854
292354879	chr4	103527731	103527882	103527750	103527856	NFKB1	NM_003998	2	24	17	+	103527653	103527854
292883975	chr4	103531619	103531793	103531640	103531769	NFKB1	NM_001165412	1	24	20	+	103531732	103531856
292883975	chr4	103531619	103531793	103531640	103531769	NFKB1	NM_003998	2	24	20	+	103531732	103531856
292234822	chr4	103533670	103533826	103533690	103533798	NFKB1	NM_001165412	1	24	22	+	103533591	103533763
292234822	chr4	103533670	103533826	103533690	103533798	NFKB1	NM_003998	2	24	22	+	103533591	103533763
291962472	chr4	103537629	103537776	103537650	103537755	NFKB1	NM_001165412	1	24	24	+	103537591	103538459
291962472	chr4	103537629	103537776	103537650	103537755	NFKB1	NM_003998	2	24	24	+	103537591	103538459
242257004	chr4	106155384	106155539	106155407	106155512	TET2	NM_001127208	1	11	3	+	106155054	106158508
242257004	chr4	106155384	106155539	106155407	106155512	TET2	NM_017628	2	3	3	+	106155054	106163928
265716641	chr4	106155828	106155957	106155856	106155936	TET2	NM_001127208	1	11	3	+	106155054	106158508
265716641	chr4	106155828	106155957	106155856	106155936	TET2	NM_017628	2	3	3	+	106155054	106163928
265734166	chr4	106156235	106156384	106156259	106156360	TET2	NM_001127208	1	11	3	+	106155054	106158508
265734166	chr4	106156235	106156384	106156259	106156360	TET2	NM_017628	2	3	3	+	106155054	106163928
242210546	chr4	106156684	106156858	106156706	106156833	TET2	NM_001127208	1	11	3	+	106155054	106158508
242210546	chr4	106156684	106156858	106156706	106156833	TET2	NM_017628	2	3	3	+	106155054	106163928
242737641	chr4	106157130	106157304	106157159	106157281	TET2	NM_001127208	1	11	3	+	106155054	106158508
242737641	chr4	106157130	106157304	106157159	106157281	TET2	NM_017628	2	3	3	+	106155054	106163928
242133528	chr4	106157539	106157691	106157567	106157666	TET2	NM_001127208	1	11	3	+	106155054	106158508
242133528	chr4	106157539	106157691	106157567	106157666	TET2	NM_017628	2	3	3	+	106155054	106163928
242224871	chr4	106157928	106158063	106157951	106158041	TET2	NM_001127208	1	11	3	+	106155054	106158508
242224871	chr4	106157928	106158063	106157951	106158041	TET2	NM_017628	2	3	3	+	106155054	106163928
242239227	chr4	106158343	106158517	106158368	106158493	TET2	NM_001127208	1	11	3	+	106155054	106158508
242239227	chr4	106158343	106158517	106158368	106158493	TET2	NM_017628	2	3	3	+	106155054	106163928
242661219	chr4	106162555	106162723	106162581	106162695	TET2	NM_001127208	1	11	4	+	106162496	106162586
242661219	chr4	106162555	106162723	106162581	106162695	TET2	NM_017628	2	3	3	+	106155054	106163928
263012473	chr4	106164819	106164984	106164841	106164963	TET2	NM_001127208	1	11	6	+	106164727	106164935
241022784	chr4	106182914	106183044	106182940	106183017	TET2	NM_001127208	1	11	8	+	106182916	106183005
240636079	chr4	106193762	106193931	106193784	106193910	TET2	NM_001127208	1	11	10	+	106193721	106194075

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241675304	chr4	106196194	106196365	106196216	106196340	TET2	NM_001127208	1	11	11	+	106196205	106200960
265184509	chr4	106196636	106196809	106196663	106196782	TET2	NM_001127208	1	11	11	+	106196205	106200960
265168325	chr4	106197116	106197286	106197144	106197261	TET2	NM_001127208	1	11	11	+	106196205	106200960
265286355	chr4	106197549	106197714	106197569	106197686	TET2	NM_001127208	1	11	11	+	106196205	106200960
233789450	chr4	123374959	123375132	123374987	123375105	IL2	NM_000586	1	4	3	-	123374865	123375008
233255824	chr4	123377467	123377601	123377494	123377578	IL2	NM_000586	1	4	1	-	123377449	123377650
231833624	chr4	153244128	153244279	153244148	153244253	FBXW7	NM_033632	3	12	12	-	153242410	153244301
231833624	chr4	153244128	153244279	153244148	153244253	FBXW7	NM_001013415	1	11	11	-	153242410	153244301
231833624	chr4	153244128	153244279	153244148	153244253	FBXW7	NM_018315	2	11	11	-	153242410	153244301
232210669	chr4	153245469	153245627	153245492	153245599	FBXW7	NM_033632	3	12	11	-	153245336	153245546
232210669	chr4	153245469	153245627	153245492	153245599	FBXW7	NM_001013415	1	11	10	-	153245336	153245546
232210669	chr4	153245469	153245627	153245492	153245599	FBXW7	NM_018315	2	11	10	-	153245336	153245546
229694068	chr4	153249385	153249558	153249407	153249530	FBXW7	NM_033632	3	12	9	-	153249360	153249541
229694068	chr4	153249385	153249558	153249407	153249530	FBXW7	NM_001013415	1	11	8	-	153249360	153249541
229694068	chr4	153249385	153249558	153249407	153249530	FBXW7	NM_018315	2	11	8	-	153249360	153249541
230511947	chr4	153251805	153251946	153251832	153251919	FBXW7	NM_033632	3	12	7	-	153251884	153252020
230511947	chr4	153251805	153251946	153251832	153251919	FBXW7	NM_001013415	1	11	6	-	153251884	153252020
230511947	chr4	153251805	153251946	153251832	153251919	FBXW7	NM_018315	2	11	6	-	153251884	153252020
230790215	chr4	153253840	153253966	153253864	153253933	FBXW7	NM_033632	3	12	6	-	153253748	153253871
230790215	chr4	153253840	153253966	153253864	153253933	FBXW7	NM_001013415	1	11	5	-	153253748	153253871
230790215	chr4	153253840	153253966	153253864	153253933	FBXW7	NM_018315	2	11	5	-	153253748	153253871
228995302	chr4	153268078	153268224	153268105	153268203	FBXW7	NM_033632	3	12	4	-	153268082	153268223
228995302	chr4	153268078	153268224	153268105	153268203	FBXW7	NM_001013415	1	11	3	-	153268082	153268223
228995302	chr4	153268078	153268224	153268105	153268203	FBXW7	NM_018315	2	11	3	-	153268082	153268223
229419673	chr4	153273588	153273761	153273616	153273733	FBXW7	NM_018315	2	11	1	-	153273622	153274110
229308196	chr4	153303366	153303517	153303394	153303489	FBXW7	NM_001013415	1	11	1	-	153303341	153303664
228155185	chr4	153332716	153332882	153332740	153332857	FBXW7	NM_033632	3	12	2	-	153332455	153333024
294482420	chr5	223489	223662	223516	223641	SDHA	NM_004168	1	15	2	+	223597	223683
294183039	chr5	225408	225561	225428	225541	SDHA	NM_004168	1	15	4	+	225534	225677
294363585	chr5	226039	226172	226064	226151	SDHA	NM_004168	1	15	5	+	225998	226162
294538491	chr5	230927	231099	230950	231076	SDHA	NM_004168	1	15	7	+	230991	231115
294304577	chr5	235217	235357	235236	235336	SDHA	NM_004168	1	15	9	+	235259	235454
293973398	chr5	236435	236602	236456	236585	SDHA	NM_004168	1	15	10	+	236543	236714
294451535	chr5	256413	256572	256440	256547	SDHA	NM_004168	1	15	15	+	256449	256814
289319185	chr5	7873369	7873538	7873397	7873517	MTRR	NM_002454	1	15	3	+	7873486	7873639
289319185	chr5	7873369	7873538	7873397	7873517	MTRR	NM_024010	2	15	3	+	7873486	7873639
293585649	chr5	7877977	7878146	7878003	7878121	MTRR	NM_002454	1	15	5	+	7878057	7878435
293585649	chr5	7877977	7878146	7878003	7878121	MTRR	NM_024010	2	15	5	+	7878057	7878435
293372605	chr5	7883147	7883314	7883173	7883288	MTRR	NM_002454	1	15	6	+	7883268	7883390
293372605	chr5	7883147	7883314	7883173	7883288	MTRR	NM_024010	2	15	6	+	7883268	7883390
290616155	chr5	7886687	7886818	7886712	7886791	MTRR	NM_002454	1	15	8	+	7886728	7886816

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
290616155	chr5	7886687	7886818	7886712	7886791	MTRR	NM_024010	2	15	8	+	7886728	7886816
290702459	chr5	7892771	7892944	7892797	7892922	MTRR	NM_002454	1	15	11	+	7892840	7893026
290702459	chr5	7892771	7892944	7892797	7892922	MTRR	NM_024010	2	15	11	+	7892840	7893026
291721642	chr5	7896847	7897018	7896874	7896994	MTRR	NM_002454	1	15	13	+	7896977	7897069
291721642	chr5	7896847	7897018	7896874	7896994	MTRR	NM_024010	2	15	13	+	7896977	7897069
291232913	chr5	7899982	7900126	7900008	7900103	MTRR	NM_002454	1	15	15	+	7900027	7901235
291232913	chr5	7899982	7900126	7900008	7900103	MTRR	NM_024010	2	15	15	+	7900027	7901235
273263268	chr5	35860842	35861006	35860870	35860979	IL7R	NM_002185	1	8	2	+	35860954	35861092
272993305	chr5	35867492	35867616	35867520	35867592	IL7R	NM_002185	1	8	3	+	35867408	35867565
274260440	chr5	35873628	35873778	35873648	35873750	IL7R	NM_002185	1	8	5	+	35873582	35873750
274642953	chr5	35876159	35876317	35876184	35876295	IL7R	NM_002185	1	8	8	+	35876085	35876923
298994759	chr5	37815693	37815850	37815716	37815828	GDNF	NM_199231	4	3	3	-	37812779	37816237
298994759	chr5	37815693	37815850	37815716	37815828	GDNF	NM_001190468	2	3	3	-	37812779	37816237
298994759	chr5	37815693	37815850	37815716	37815828	GDNF	NM_001190469	3	3	3	-	37812779	37816237
298994759	chr5	37815693	37815850	37815716	37815828	GDNF	NM_000514	1	3	3	-	37812779	37816237
299026699	chr5	37816110	37816274	37816131	37816247	GDNF	NM_199231	4	3	3	-	37812779	37816237
299026699	chr5	37816110	37816274	37816131	37816247	GDNF	NM_001190468	2	3	3	-	37812779	37816237
299026699	chr5	37816110	37816274	37816131	37816247	GDNF	NM_001190469	3	3	3	-	37812779	37816237
299026699	chr5	37816110	37816274	37816131	37816247	GDNF	NM_000514	1	3	3	-	37812779	37816237
299143228	chr5	37835648	37835787	37835673	37835760	GDNF	NM_001190468	2	3	1	-	37835736	37835929
299143228	chr5	37835648	37835787	37835673	37835760	GDNF	NM_001190469	3	3	1	-	37835736	37835929
234463603	chr5	38482001	38482170	38482029	38482148	LIFR	NM_001127671	1	20	20	-	38475065	38482320
234463603	chr5	38482001	38482170	38482029	38482148	LIFR	NM_002310	2	20	20	-	38475065	38482320
231232885	chr5	38484842	38484968	38484870	38484940	LIFR	NM_001127671	1	20	18	-	38484877	38484970
231232885	chr5	38484842	38484968	38484870	38484940	LIFR	NM_002310	2	20	18	-	38484877	38484970
231506139	chr5	38489150	38489321	38489179	38489293	LIFR	NM_001127671	1	20	16	-	38489180	38489347
231506139	chr5	38489150	38489321	38489179	38489293	LIFR	NM_002310	2	20	16	-	38489180	38489347
232845472	chr5	38493639	38493769	38493661	38493747	LIFR	NM_001127671	1	20	14	-	38493708	38493887
232845472	chr5	38493639	38493769	38493661	38493747	LIFR	NM_002310	2	20	14	-	38493708	38493887
233105508	chr5	38496589	38496741	38496612	38496713	LIFR	NM_001127671	1	20	13	-	38496484	38496697
233105508	chr5	38496589	38496741	38496612	38496713	LIFR	NM_002310	2	20	13	-	38496484	38496697
232120095	chr5	38502789	38502916	38502817	38502890	LIFR	NM_001127671	1	20	11	-	38502739	38502901
232120095	chr5	38502789	38502916	38502817	38502890	LIFR	NM_002310	2	20	11	-	38502739	38502901
233689904	chr5	38506024	38506160	38506052	38506132	LIFR	NM_001127671	1	20	9	-	38506007	38506176
233689904	chr5	38506024	38506160	38506052	38506132	LIFR	NM_002310	2	20	9	-	38506007	38506176
230841011	chr5	38510579	38510703	38510606	38510681	LIFR	NM_001127671	1	20	7	-	38510566	38510820
230841011	chr5	38510579	38510703	38510606	38510681	LIFR	NM_002310	2	20	7	-	38510566	38510820
233383554	chr5	38511999	38512124	38512019	38512097	LIFR	NM_001127671	1	20	6	-	38511892	38512066
233383554	chr5	38511999	38512124	38512019	38512097	LIFR	NM_002310	2	20	6	-	38511892	38512066
232770623	chr5	38527190	38527357	38527216	38527333	LIFR	NM_001127671	1	20	4	-	38527257	38527396
232770623	chr5	38527190	38527357	38527216	38527333	LIFR	NM_002310	2	20	4	-	38527257	38527396

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231654221	chr5	55236880	55237017	55236905	55236989	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231654221	chr5	55236880	55237017	55236905	55236989	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231654221	chr5	55236880	55237017	55236905	55236989	IL6ST	NM_002184	2	17	17	-	55230925	55237647
231701903	chr5	55237224	55237397	55237244	55237373	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231701903	chr5	55237224	55237397	55237244	55237373	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231701903	chr5	55237224	55237397	55237244	55237373	IL6ST	NM_002184	2	17	17	-	55230925	55237647
233465569	chr5	55238479	55238617	55238505	55238589	IL6ST	NM_175767	3	16	15	-	55238498	55238579
233465569	chr5	55238479	55238617	55238505	55238589	IL6ST	NM_001190981	1	16	15	-	55238498	55238579
233465569	chr5	55238479	55238617	55238505	55238589	IL6ST	NM_002184	2	17	16	-	55238498	55238579
233156332	chr5	55247807	55247934	55247834	55247906	IL6ST	NM_175767	3	16	12	-	55247757	55247903
233156332	chr5	55247807	55247934	55247834	55247906	IL6ST	NM_001190981	1	16	12	-	55247757	55247903
233156332	chr5	55247807	55247934	55247834	55247906	IL6ST	NM_002184	2	17	13	-	55247757	55247903
233693014	chr5	55250651	55250814	55250671	55250787	IL6ST	NM_175767	3	16	10	-	55250638	55250820
233693014	chr5	55250651	55250814	55250671	55250787	IL6ST	NM_002184	2	17	11	-	55250638	55250820
232481594	chr5	55253046	55253220	55253071	55253192	IL6ST	NM_001190981	1	16	9	-	55253037	55253119
232481594	chr5	55253046	55253220	55253071	55253192	IL6ST	NM_002184	2	17	9	-	55253037	55253119
231591385	chr5	55259194	55259332	55259222	55259313	IL6ST	NM_175767	3	16	7	-	55259180	55259334
231591385	chr5	55259194	55259332	55259222	55259313	IL6ST	NM_001190981	1	16	7	-	55259180	55259334
231591385	chr5	55259194	55259332	55259222	55259313	IL6ST	NM_002184	2	17	7	-	55259180	55259334
234383721	chr5	55264183	55264314	55264211	55264290	IL6ST	NM_175767	3	16	5	-	55264104	55264224
234383721	chr5	55264183	55264314	55264211	55264290	IL6ST	NM_001190981	1	16	5	-	55264104	55264224
234383721	chr5	55264183	55264314	55264211	55264290	IL6ST	NM_002184	2	17	5	-	55264104	55264224
241012843	chr5	67522596	67522763	67522624	67522742	PIK3R1	NM_181523	3	16	2	+	67522118	67522837
239344631	chr5	67575341	67575465	67575368	67575442	PIK3R1	NM_181523	3	16	5	+	67575430	67575561
235803778	chr5	67576665	67576836	67576691	67576819	PIK3R1	NM_181523	3	16	7	+	67576755	67576834
236186027	chr5	67586607	67586746	67586635	67586717	PIK3R1	NM_181504	2	10	1	+	67586467	67586662
235021056	chr5	67589033	67589199	67589059	67589174	PIK3R1	NM_181523	3	16	10	+	67589131	67589311
235021056	chr5	67589033	67589199	67589059	67589174	PIK3R1	NM_001242466	1	9	3	+	67589131	67589311
235021056	chr5	67589033	67589199	67589059	67589174	PIK3R1	NM_181524	4	10	4	+	67589131	67589311
235021056	chr5	67589033	67589199	67589059	67589174	PIK3R1	NM_181504	2	10	4	+	67589131	67589311
237481914	chr5	67590925	67591076	67590947	67591054	PIK3R1	NM_181523	3	16	13	+	67590976	67591152
237481914	chr5	67590925	67591076	67590947	67591054	PIK3R1	NM_001242466	1	9	6	+	67590976	67591152
237481914	chr5	67590925	67591076	67590947	67591054	PIK3R1	NM_181524	4	10	7	+	67590976	67591152
237481914	chr5	67590925	67591076	67590947	67591054	PIK3R1	NM_181504	2	10	7	+	67590976	67591152
238528568	chr5	67591950	67592123	67591974	67592102	PIK3R1	NM_181523	3	16	15	+	67591999	67592169
238528568	chr5	67591950	67592123	67591974	67592102	PIK3R1	NM_001242466	1	9	8	+	67591999	67592169
238528568	chr5	67591950	67592123	67591974	67592102	PIK3R1	NM_181524	4	10	9	+	67591999	67592169
238528568	chr5	67591950	67592123	67591974	67592102	PIK3R1	NM_181504	2	10	9	+	67591999	67592169
222560115	chr5	112043318	112043483	112043336	112043463	APC	NM_001127511	3	14	1	+	112043202	112043579
223304037	chr5	112101906	112102080	112101930	112102057	APC	NM_000038	1	16	3	+	112102023	112102107
223304037	chr5	112101906	112102080	112101930	112102057	APC	NM_001127510	2	17	4	+	112102023	112102107

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223304037	chr5	112101906	112102080	112101930	112102057	APC	NM_001127511	3	14	2	+	112102023	112102107
225058119	chr5	112102995	112103132	112103018	112103106	APC	NM_000038	1	16	4	+	112102886	112103087
225058119	chr5	112102995	112103132	112103018	112103106	APC	NM_001127510	2	17	5	+	112102886	112103087
225058119	chr5	112102995	112103132	112103018	112103106	APC	NM_001127511	3	14	3	+	112102886	112103087
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_000038	1	16	6	+	112116487	112116600
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_001127510	2	17	7	+	112116487	112116600
223193687	chr5	112116492	112116639	112116519	112116611	APC	NM_001127511	3	14	5	+	112116487	112116600
222615042	chr5	112151098	112151252	112151125	112151225	APC	NM_000038	1	16	9	+	112151192	112151290
222615042	chr5	112151098	112151252	112151125	112151225	APC	NM_001127510	2	17	10	+	112151192	112151290
222615042	chr5	112151098	112151252	112151125	112151225	APC	NM_001127511	3	14	7	+	112151192	112151290
222884262	chr5	112154800	112154974	112154823	112154951	APC	NM_000038	1	16	10	+	112154663	112155041
222884262	chr5	112154800	112154974	112154823	112154951	APC	NM_001127510	2	17	11	+	112154663	112155041
222884262	chr5	112154800	112154974	112154823	112154951	APC	NM_001127511	3	14	8	+	112154663	112155041
224047523	chr5	112162823	112162951	112162851	112162926	APC	NM_000038	1	16	12	+	112162805	112162944
224047523	chr5	112162823	112162951	112162851	112162926	APC	NM_001127510	2	17	13	+	112162805	112162944
224047523	chr5	112162823	112162951	112162851	112162926	APC	NM_001127511	3	14	10	+	112162805	112162944
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_000038	1	16	14	+	112164553	112164669
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_001127510	2	17	15	+	112164553	112164669
223605033	chr5	112164625	112164779	112164650	112164747	APC	NM_001127511	3	14	12	+	112164553	112164669
224518902	chr5	112173194	112173365	112173222	112173338	APC	NM_000038	1	16	16	+	112173250	112181936
224518902	chr5	112173194	112173365	112173222	112173338	APC	NM_001127510	2	17	17	+	112173250	112181936
224518902	chr5	112173194	112173365	112173222	112173338	APC	NM_001127511	3	14	14	+	112173250	112181936
224579200	chr5	112173619	112173792	112173645	112173766	APC	NM_000038	1	16	16	+	112173250	112181936
224579200	chr5	112173619	112173792	112173645	112173766	APC	NM_001127510	2	17	17	+	112173250	112181936
224579200	chr5	112173619	112173792	112173645	112173766	APC	NM_001127511	3	14	14	+	112173250	112181936
224582579	chr5	112174073	112174240	112174101	112174215	APC	NM_000038	1	16	16	+	112173250	112181936
224582579	chr5	112174073	112174240	112174101	112174215	APC	NM_001127510	2	17	17	+	112173250	112181936
224582579	chr5	112174073	112174240	112174101	112174215	APC	NM_001127511	3	14	14	+	112173250	112181936
222826428	chr5	112174516	112174682	112174544	112174654	APC	NM_000038	1	16	16	+	112173250	112181936
222826428	chr5	112174516	112174682	112174544	112174654	APC	NM_001127510	2	17	17	+	112173250	112181936
222826428	chr5	112174516	112174682	112174544	112174654	APC	NM_001127511	3	14	14	+	112173250	112181936
222777284	chr5	112174901	112175027	112174929	112175006	APC	NM_000038	1	16	16	+	112173250	112181936
222777284	chr5	112174901	112175027	112174929	112175006	APC	NM_001127510	2	17	17	+	112173250	112181936
222777284	chr5	112174901	112175027	112174929	112175006	APC	NM_001127511	3	14	14	+	112173250	112181936
222768447	chr5	112175296	112175468	112175321	112175442	APC	NM_000038	1	16	16	+	112173250	112181936
222768447	chr5	112175296	112175468	112175321	112175442	APC	NM_001127510	2	17	17	+	112173250	112181936
222768447	chr5	112175296	112175468	112175321	112175442	APC	NM_001127511	3	14	14	+	112173250	112181936
224551347	chr5	112175789	112175953	112175813	112175928	APC	NM_000038	1	16	16	+	112173250	112181936
224551347	chr5	112175789	112175953	112175813	112175928	APC	NM_001127510	2	17	17	+	112173250	112181936
224551347	chr5	112175789	112175953	112175813	112175928	APC	NM_001127511	3	14	14	+	112173250	112181936
224544591	chr5	112176229	112176398	112176257	112176374	APC	NM_000038	1	16	16	+	112173250	112181936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224544591	chr5	112176229	112176398	112176257	112176374	APC	NM_001127510	2	17	17	+	112173250	112181936
224544591	chr5	112176229	112176398	112176257	112176374	APC	NM_001127511	3	14	14	+	112173250	112181936
222794331	chr5	112176751	112176916	112176776	112176888	APC	NM_000038	1	16	16	+	112173250	112181936
222794331	chr5	112176751	112176916	112176776	112176888	APC	NM_001127510	2	17	17	+	112173250	112181936
222794331	chr5	112176751	112176916	112176776	112176888	APC	NM_001127511	3	14	14	+	112173250	112181936
222840073	chr5	112177124	112177296	112177150	112177273	APC	NM_000038	1	16	16	+	112173250	112181936
222840073	chr5	112177124	112177296	112177150	112177273	APC	NM_001127510	2	17	17	+	112173250	112181936
222840073	chr5	112177124	112177296	112177150	112177273	APC	NM_001127511	3	14	14	+	112173250	112181936
224561892	chr5	112177559	112177721	112177585	112177695	APC	NM_000038	1	16	16	+	112173250	112181936
224561892	chr5	112177559	112177721	112177585	112177695	APC	NM_001127510	2	17	17	+	112173250	112181936
224561892	chr5	112177559	112177721	112177585	112177695	APC	NM_001127511	3	14	14	+	112173250	112181936
224556289	chr5	112178047	112178216	112178071	112178193	APC	NM_000038	1	16	16	+	112173250	112181936
224556289	chr5	112178047	112178216	112178071	112178193	APC	NM_001127510	2	17	17	+	112173250	112181936
224556289	chr5	112178047	112178216	112178071	112178193	APC	NM_001127511	3	14	14	+	112173250	112181936
224584997	chr5	112178480	112178639	112178509	112178616	APC	NM_000038	1	16	16	+	112173250	112181936
224584997	chr5	112178480	112178639	112178509	112178616	APC	NM_001127510	2	17	17	+	112173250	112181936
224584997	chr5	112178480	112178639	112178509	112178616	APC	NM_001127511	3	14	14	+	112173250	112181936
222808332	chr5	112178927	112179086	112178947	112179058	APC	NM_000038	1	16	16	+	112173250	112181936
222808332	chr5	112178927	112179086	112178947	112179058	APC	NM_001127510	2	17	17	+	112173250	112181936
222808332	chr5	112178927	112179086	112178947	112179058	APC	NM_001127511	3	14	14	+	112173250	112181936
224564510	chr5	112179343	112179509	112179369	112179481	APC	NM_000038	1	16	16	+	112173250	112181936
224564510	chr5	112179343	112179509	112179369	112179481	APC	NM_001127510	2	17	17	+	112173250	112181936
224564510	chr5	112179343	112179509	112179369	112179481	APC	NM_001127511	3	14	14	+	112173250	112181936
224540558	chr5	112179788	112179960	112179808	112179932	APC	NM_000038	1	16	16	+	112173250	112181936
224540558	chr5	112179788	112179960	112179808	112179932	APC	NM_001127510	2	17	17	+	112173250	112181936
224540558	chr5	112179788	112179960	112179808	112179932	APC	NM_001127511	3	14	14	+	112173250	112181936
236072010	chr5	131911407	131911576	131911430	131911548	RAD50	NM_005732	1	25	3	+	131911469	131911620
236520987	chr5	131915112	131915260	131915140	131915235	RAD50	NM_005732	1	25	4	+	131915009	131915194
241351770	chr5	131923302	131923468	131923330	131923442	RAD50	NM_005732	1	25	6	+	131923254	131923382
235121433	chr5	131924449	131924573	131924472	131924549	RAD50	NM_005732	1	25	8	+	131924379	131924572
239765682	chr5	131926790	131926947	131926817	131926922	RAD50	NM_005732	1	25	10	+	131926916	131927098
239915353	chr5	131927557	131927710	131927588	131927682	RAD50	NM_005732	1	25	11	+	131927569	131927726
237572732	chr5	131930646	131930813	131930671	131930789	RAD50	NM_005732	1	25	12	+	131930561	131930736
235180559	chr5	131931426	131931569	131931455	131931545	RAD50	NM_005732	1	25	13	+	131931265	131931502
236784511	chr5	131940397	131940559	131940424	131940536	RAD50	NM_005732	1	25	16	+	131940498	131940691
235129332	chr5	131944853	131945024	131944885	131944996	RAD50	NM_005732	1	25	19	+	131944975	131945088
235129332	chr5	131944853	131945024	131944885	131944996	RAD50	NM_005732	1	25	18	+	131944809	131944901
235668046	chr5	131953766	131953890	131953794	131953863	RAD50	NM_005732	1	25	21	+	131953762	131953986
239923667	chr5	131972851	131972991	131972875	131972971	RAD50	NM_005732	1	25	22	+	131972807	131972892
236405706	chr5	131976396	131976523	131976416	131976497	RAD50	NM_005732	1	25	24	+	131976364	131976497
273122844	chr5	138117516	138117672	138117541	138117643	CTNNA1	NM_001903	1	18	2	+	138117612	138117718

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273204257	chr5	138118958	138119101	138118985	138119080	CTNNA1	NM_001903	1	18	3	+	138118866	138119061
272859192	chr5	138147906	138148078	138147934	138148049	CTNNA1	NM_001903	1	18	5	+	138147872	138147991
272981640	chr5	138163139	138163302	138163167	138163282	CTNNA1	NM_001903	1	18	7	+	138163204	138163407
273741341	chr5	138223074	138223216	138223103	138223191	CTNNA1	NM_001903	1	18	9	+	138223179	138223331
272789065	chr5	138240042	138240167	138240063	138240144	CTNNA1	NM_001903	1	18	10	+	138240038	138240130
273120194	chr5	138260157	138260329	138260181	138260305	CTNNA1	NM_001903	1	18	12	+	138260199	138260399
273545827	chr5	138264896	138265064	138264920	138265045	CTNNA1	NM_001903	1	18	14	+	138264935	138265045
273692250	chr5	138268242	138268412	138268265	138268387	CTNNA1	NM_001903	1	18	17	+	138268267	138268401
273996984	chr5	138269620	138269785	138269643	138269762	CTNNA1	NM_001903	1	18	18	+	138269491	138270723
225708536	chr5	149433865	149434019	149433883	149433997	CSF1R	NM_005211	1	22	21	-	149433885	149433993
225526048	chr5	149435640	149435810	149435664	149435785	CSF1R	NM_005211	1	22	18	-	149435782	149435904
225526048	chr5	149435640	149435810	149435664	149435785	CSF1R	NM_005211	1	22	19	-	149435589	149435700
226105400	chr5	149439228	149439395	149439251	149439375	CSF1R	NM_005211	1	22	15	-	149439263	149439425
225398125	chr5	149440959	149441093	149440983	149441072	CSF1R	NM_005211	1	22	13	-	149441054	149441158
253767227	chr5	149447671	149447837	149447693	149447817	CSF1R	NM_005211	1	22	11	-	149447778	149447893
227068030	chr5	149449713	149449886	149449732	149449865	CSF1R	NM_005211	1	22	9	-	149449745	149449865
226547181	chr5	149452914	149453083	149452936	149453060	CSF1R	NM_005211	1	22	7	-	149452864	149453056
226286447	chr5	149457667	149457829	149457688	149457811	CSF1R	NM_005211	1	22	5	-	149457675	149457811
225382577	chr5	149460254	149460426	149460280	149460406	CSF1R	NM_005211	1	22	3	-	149460330	149460587
239135386	chr5	149495229	149495392	149495247	149495373	PDGFRB	NM_002609	1	23	23	-	149493402	149495509
240139636	chr5	149497208	149497336	149497225	149497316	PDGFRB	NM_002609	1	23	22	-	149497181	149497413
235404741	chr5	149499509	149499651	149499529	149499628	PDGFRB	NM_002609	1	23	19	-	149499575	149499686
236468092	chr5	149500645	149500800	149500668	149500779	PDGFRB	NM_002609	1	23	17	-	149500767	149500885
237293263	chr5	149502558	149502731	149502582	149502711	PDGFRB	NM_002609	1	23	15	-	149502605	149502764
235569608	chr5	149504269	149504418	149504289	149504394	PDGFRB	NM_002609	1	23	13	-	149504290	149504394
240536427	chr5	149509208	149509351	149509229	149509332	PDGFRB	NM_002609	1	23	10	-	149509320	149509531
236586117	chr5	149510095	149510252	149510117	149510229	PDGFRB	NM_002609	1	23	9	-	149510102	149510225
236946028	chr5	149512379	149512526	149512402	149512509	PDGFRB	NM_002609	1	23	7	-	149512313	149512505
235221814	chr5	149513459	149513597	149513480	149513572	PDGFRB	NM_002609	1	23	5	-	149513444	149513571
237363403	chr5	149515059	149515229	149515081	149515208	PDGFRB	NM_002609	1	23	3	-	149515118	149515441
241721407	chr5	170814914	170815087	170814934	170815070	NPM1	NM_002520	2	11	1	+	170814708	170815010
241721407	chr5	170814914	170815087	170814934	170815070	NPM1	NM_001037738	1	10	1	+	170814708	170815010
241721407	chr5	170814914	170815087	170814934	170815070	NPM1	NM_199185	3	10	1	+	170814708	170815010
257858086	chr5	170818329	170818465	170818355	170818437	NPM1	NM_002520	2	11	3	+	170818309	170818428
257858086	chr5	170818329	170818465	170818355	170818437	NPM1	NM_001037738	1	10	3	+	170818309	170818428
257858086	chr5	170818329	170818465	170818355	170818437	NPM1	NM_199185	3	10	3	+	170818309	170818428
237091653	chr5	170819736	170819887	170819760	170819858	NPM1	NM_002520	2	11	5	+	170819714	170819820
237091653	chr5	170819736	170819887	170819760	170819858	NPM1	NM_001037738	1	10	5	+	170819714	170819820
237091653	chr5	170819736	170819887	170819760	170819858	NPM1	NM_199185	3	10	5	+	170819714	170819820
238853469	chr5	170834646	170834804	170834674	170834778	NPM1	NM_002520	2	11	10	+	170834704	170834778
238853469	chr5	170834646	170834804	170834674	170834778	NPM1	NM_199185	3	10	9	+	170834704	170834778

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270015340	chr5	176517452	176517591	176517469	176517573	FGFR4	NM_022963	2	16	2	+	176517391	176517654
270015340	chr5	176517452	176517591	176517469	176517573	FGFR4	NM_002011	1	18	3	+	176517391	176517654
270015340	chr5	176517452	176517591	176517469	176517573	FGFR4	NM_213647	3	18	3	+	176517391	176517654
272540646	chr5	176518003	176518128	176518022	176518106	FGFR4	NM_022963	2	16	4	+	176517939	176518105
272540646	chr5	176518003	176518128	176518022	176518106	FGFR4	NM_002011	1	18	5	+	176517939	176518105
272540646	chr5	176518003	176518128	176518022	176518106	FGFR4	NM_213647	3	18	5	+	176517939	176518105
271361547	chr5	176519404	176519566	176519424	176519544	FGFR4	NM_022963	2	16	6	+	176519322	176519512
271361547	chr5	176519404	176519566	176519424	176519544	FGFR4	NM_002011	1	18	7	+	176519322	176519512
271361547	chr5	176519404	176519566	176519424	176519544	FGFR4	NM_213647	3	18	7	+	176519322	176519512
269926378	chr5	176520170	176520336	176520191	176520318	FGFR4	NM_002011	1	18	9	+	176520139	176520332
269926378	chr5	176520170	176520336	176520191	176520318	FGFR4	NM_213647	3	18	9	+	176520139	176520332
270140171	chr5	176520622	176520789	176520642	176520771	FGFR4	NM_022963	2	16	9	+	176520655	176520776
270140171	chr5	176520622	176520789	176520642	176520771	FGFR4	NM_002011	1	18	11	+	176520655	176520776
270140171	chr5	176520622	176520789	176520642	176520771	FGFR4	NM_213647	3	18	11	+	176520655	176520776
270157963	chr5	176522654	176522811	176522674	176522790	FGFR4	NM_022963	2	16	11	+	176522534	176522724
270157963	chr5	176522654	176522811	176522674	176522790	FGFR4	NM_002011	1	18	13	+	176522534	176522724
270157963	chr5	176522654	176522811	176522674	176522790	FGFR4	NM_213647	3	18	13	+	176522534	176522724
269959691	chr5	176523501	176523674	176523520	176523656	FGFR4	NM_022963	2	16	14	+	176523605	176523742
269959691	chr5	176523501	176523674	176523520	176523656	FGFR4	NM_002011	1	18	16	+	176523605	176523742
269959691	chr5	176523501	176523674	176523520	176523656	FGFR4	NM_213647	3	18	16	+	176523605	176523742
271564224	chr5	176524503	176524651	176524520	176524631	FGFR4	NM_022963	2	16	16	+	176524528	176525126
271564224	chr5	176524503	176524651	176524520	176524631	FGFR4	NM_002011	1	18	18	+	176524528	176525126
271564224	chr5	176524503	176524651	176524520	176524631	FGFR4	NM_213647	3	18	18	+	176524528	176525126
240553831	chr5	176562304	176562458	176562327	176562436	NSD1	NM_022455	1	23	2	+	176562088	176563031
235810701	chr5	176562752	176562897	176562772	176562872	NSD1	NM_022455	1	23	2	+	176562088	176563031
238375735	chr5	176618891	176619059	176618916	176619031	NSD1	NM_022455	1	23	3	+	176618885	176619020
238375735	chr5	176618891	176619059	176618916	176619031	NSD1	NM_172349	2	24	4	+	176618885	176619020
257520581	chr5	176636668	176636839	176636689	176636817	NSD1	NM_022455	1	23	5	+	176636637	176639196
257520581	chr5	176636668	176636839	176636689	176636817	NSD1	NM_172349	2	24	6	+	176636637	176639196
237603280	chr5	176637128	176637293	176637156	176637268	NSD1	NM_022455	1	23	5	+	176636637	176639196
237603280	chr5	176637128	176637293	176637156	176637268	NSD1	NM_172349	2	24	6	+	176636637	176639196
237667648	chr5	176637571	176637695	176637596	176637669	NSD1	NM_022455	1	23	5	+	176636637	176639196
237667648	chr5	176637571	176637695	176637596	176637669	NSD1	NM_172349	2	24	6	+	176636637	176639196
242670631	chr5	176637973	176638132	176637998	176638104	NSD1	NM_022455	1	23	5	+	176636637	176639196
242670631	chr5	176637973	176638132	176637998	176638104	NSD1	NM_172349	2	24	6	+	176636637	176639196
242608952	chr5	176638367	176638538	176638388	176638512	NSD1	NM_022455	1	23	5	+	176636637	176639196
242608952	chr5	176638367	176638538	176638388	176638512	NSD1	NM_172349	2	24	6	+	176636637	176639196
257588464	chr5	176638802	176638926	176638823	176638905	NSD1	NM_022455	1	23	5	+	176636637	176639196
257588464	chr5	176638802	176638926	176638823	176638905	NSD1	NM_172349	2	24	6	+	176636637	176639196
238505227	chr5	176662708	176662855	176662736	176662832	NSD1	NM_022455	1	23	6	+	176662822	176662946
238505227	chr5	176662708	176662855	176662736	176662832	NSD1	NM_172349	2	24	7	+	176662822	176662946

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236202098	chr5	176665379	176665541	176665400	176665518	NSD1	NM_022455	1	23	7	+	176665238	176665508
236202098	chr5	176665379	176665541	176665400	176665518	NSD1	NM_172349	2	24	8	+	176665238	176665508
258590893	chr5	176673547	176673712	176673568	176673687	NSD1	NM_022455	1	23	10	+	176673679	176673797
258590893	chr5	176673547	176673712	176673568	176673687	NSD1	NM_172349	2	24	11	+	176673679	176673797
238236245	chr5	176678736	176678885	176678758	176678860	NSD1	NM_022455	1	23	12	+	176678731	176678854
238236245	chr5	176678736	176678885	176678758	176678860	NSD1	NM_172349	2	24	13	+	176678731	176678854
238539831	chr5	176686958	176687106	176686983	176687077	NSD1	NM_022455	1	23	14	+	176686990	176687169
238539831	chr5	176686958	176687106	176686983	176687077	NSD1	NM_172349	2	24	15	+	176686990	176687169
237718482	chr5	176694592	176694747	176694615	176694720	NSD1	NM_022455	1	23	15	+	176694563	176694719
237718482	chr5	176694592	176694747	176694615	176694720	NSD1	NM_172349	2	24	16	+	176694563	176694719
257731081	chr5	176700637	176700809	176700663	176700787	NSD1	NM_022455	1	23	17	+	176700673	176700785
257731081	chr5	176700637	176700809	176700663	176700787	NSD1	NM_172349	2	24	18	+	176700673	176700785
235147324	chr5	176709403	176709527	176709429	176709502	NSD1	NM_022455	1	23	19	+	176709466	176709582
235147324	chr5	176709403	176709527	176709429	176709502	NSD1	NM_172349	2	24	20	+	176709466	176709582
258736567	chr5	176715728	176715858	176715752	176715830	NSD1	NM_022455	1	23	21	+	176715820	176715926
258736567	chr5	176715728	176715858	176715752	176715830	NSD1	NM_172349	2	24	22	+	176715820	176715926
239742375	chr5	176720765	176720928	176720787	176720905	NSD1	NM_022455	1	23	23	+	176720833	176727214
239742375	chr5	176720765	176720928	176720787	176720905	NSD1	NM_172349	2	24	24	+	176720833	176727214
239900679	chr5	176721182	176721312	176721204	176721292	NSD1	NM_022455	1	23	23	+	176720833	176727214
239900679	chr5	176721182	176721312	176721204	176721292	NSD1	NM_172349	2	24	24	+	176720833	176727214
235299066	chr5	176721585	176721741	176721606	176721716	NSD1	NM_022455	1	23	23	+	176720833	176727214
235299066	chr5	176721585	176721741	176721606	176721716	NSD1	NM_172349	2	24	24	+	176720833	176727214
239822292	chr5	176722005	176722176	176722031	176722151	NSD1	NM_022455	1	23	23	+	176720833	176727214
239822292	chr5	176722005	176722176	176722031	176722151	NSD1	NM_172349	2	24	24	+	176720833	176727214
272463029	chr5	180030055	180030222	180030077	180030198	FLT4	NM_182925	2	30	30	-	180028506	180030390
271851622	chr5	180036883	180037048	180036904	180037025	FLT4	NM_182925	2	30	28	-	180036905	180037025
271851622	chr5	180036883	180037048	180036904	180037025	FLT4	NM_002020	1	30	28	-	180036905	180037025
270136520	chr5	180039967	180040131	180039986	180040111	FLT4	NM_182925	2	30	25	-	180040011	180040110
270136520	chr5	180039967	180040131	180039986	180040111	FLT4	NM_002020	1	30	25	-	180040011	180040110
271079628	chr5	180043856	180044014	180043876	180043995	FLT4	NM_182925	2	30	22	-	180043900	180043994
271079628	chr5	180043856	180044014	180043876	180043995	FLT4	NM_002020	1	30	22	-	180043900	180043994
271833181	chr5	180046293	180046454	180046312	180046435	FLT4	NM_182925	2	30	19	-	180046253	180046366
271833181	chr5	180046293	180046454	180046312	180046435	FLT4	NM_002020	1	30	19	-	180046253	180046366
272407668	chr5	180047201	180047365	180047220	180047343	FLT4	NM_182925	2	30	17	-	180047173	180047308
272407668	chr5	180047201	180047365	180047220	180047343	FLT4	NM_002020	1	30	17	-	180047173	180047308
272200687	chr5	180047888	180048055	180047905	180048036	FLT4	NM_182925	2	30	15	-	180047876	180048007
272200687	chr5	180047888	180048055	180047905	180048036	FLT4	NM_002020	1	30	15	-	180047876	180048007
271349198	chr5	180048487	180048661	180048509	180048642	FLT4	NM_182925	2	30	13	-	180048542	180048904
271349198	chr5	180048487	180048661	180048509	180048642	FLT4	NM_002020	1	30	13	-	180048542	180048904
269966374	chr5	180049653	180049809	180049675	180049787	FLT4	NM_182925	2	30	12	-	180049731	180049839
269966374	chr5	180049653	180049809	180049675	180049787	FLT4	NM_002020	1	30	12	-	180049731	180049839

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269950911	chr5	180052846	180053004	180052866	180052987	FLT4	NM_182925	2	30	10	-	180052869	180053031
269950911	chr5	180052846	180053004	180052866	180052987	FLT4	NM_002020	1	30	10	-	180052869	180053031
270919466	chr5	180055804	180055945	180055824	180055925	FLT4	NM_182925	2	30	8	-	180055882	180055999
270919466	chr5	180055804	180055945	180055824	180055925	FLT4	NM_002020	1	30	8	-	180055882	180055999
271335625	chr5	180056632	180056756	180056653	180056736	FLT4	NM_182925	2	30	6	-	180056696	180056835
271335625	chr5	180056632	180056756	180056653	180056736	FLT4	NM_002020	1	30	6	-	180056696	180056835
272522366	chr5	180057187	180057359	180057204	180057338	FLT4	NM_182925	2	30	4	-	180057225	180057337
272522366	chr5	180057187	180057359	180057204	180057338	FLT4	NM_002020	1	30	4	-	180057225	180057337
233364459	chr6	393071	393234	393090	393217	IRF4	NM_001195286	1	9	2	+	393098	393368
233364459	chr6	393071	393234	393090	393217	IRF4	NR_046000	4	10	2	+	393098	393368
233364459	chr6	393071	393234	393090	393217	IRF4	NM_002460	2	9	2	+	393098	393368
233276468	chr6	394898	395039	394919	395014	IRF4	NM_001195286	1	9	3	+	394821	395007
233276468	chr6	394898	395039	394919	395014	IRF4	NR_046000	4	10	3	+	394821	395007
233276468	chr6	394898	395039	394919	395014	IRF4	NM_002460	2	9	3	+	394821	395007
233276468	chr6	394898	395039	394919	395014	IRF4	NR_036585	3	8	2	+	394821	395007
232068160	chr6	397174	397303	397193	397275	IRF4	NM_002460	2	9	5	+	397108	397252
232068160	chr6	397174	397303	397193	397275	IRF4	NM_001195286	1	9	5	+	397111	397252
232068160	chr6	397174	397303	397193	397275	IRF4	NR_046000	4	10	5	+	397111	397252
232068160	chr6	397174	397303	397193	397275	IRF4	NR_036585	3	8	4	+	397111	397252
234180940	chr6	401431	401599	401452	401574	IRF4	NM_001195286	1	9	7	+	401424	401777
234180940	chr6	401431	401599	401452	401574	IRF4	NR_046000	4	10	7	+	401424	401777
234180940	chr6	401431	401599	401452	401574	IRF4	NM_002460	2	9	7	+	401424	401777
234180940	chr6	401431	401599	401452	401574	IRF4	NR_036585	3	8	6	+	401424	401777
233834986	chr6	407350	407512	407375	407485	IRF4	NM_001195286	1	9	9	+	407455	411443
233834986	chr6	407350	407512	407375	407485	IRF4	NR_046000	4	10	10	+	407455	411443
233834986	chr6	407350	407512	407375	407485	IRF4	NM_002460	2	9	9	+	407455	411443
233834986	chr6	407350	407512	407375	407485	IRF4	NR_036585	3	8	8	+	407455	411443
227684640	chr6	18237511	18237679	18237534	18237651	DEK	NM_003472	2	11	8	-	18237612	18237747
227684640	chr6	18237511	18237679	18237534	18237651	DEK	NM_001134709	1	10	7	-	18237612	18237747
227714278	chr6	18249997	18250156	18250019	18250124	DEK	NM_003472	2	11	7	-	18249882	18250070
227714278	chr6	18249997	18250156	18250019	18250124	DEK	NM_001134709	1	10	6	-	18249882	18250070
230482671	chr6	18256637	18256773	18256661	18256744	DEK	NM_003472	2	11	5	-	18256592	18256686
230482671	chr6	18256637	18256773	18256661	18256744	DEK	NM_001134709	1	10	4	-	18256592	18256686
237826280	chr6	31132530	31132689	31132548	31132661	POU5F1	NM_002701	2	5	5	-	31132114	31132644
237826280	chr6	31132530	31132689	31132548	31132661	POU5F1	NM_203289	3	4	4	-	31132114	31132644
237826280	chr6	31132530	31132689	31132548	31132661	POU5F1	NM_001173531	1	5	5	-	31132114	31132644
235538801	chr6	31133339	31133513	31133365	31133488	POU5F1	NM_002701	2	5	3	-	31133348	31133478
235538801	chr6	31133339	31133513	31133365	31133488	POU5F1	NM_203289	3	4	2	-	31133348	31133478
235538801	chr6	31133339	31133513	31133365	31133488	POU5F1	NM_001173531	1	5	3	-	31133348	31133478
237537864	chr6	31137988	31138151	31138006	31138134	POU5F1	NM_002701	2	5	1	-	31137993	31138451
290133183	chr6	32163418	32163584	32163442	32163564	NOTCH4	NM_004557	1	30	30	-	32162620	32163927

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
291071884	chr6	32164071	32164227	32164091	32164207	NOTCH4	NM_004557	1	30	29	-	32164101	32164198
290767711	chr6	32165150	32165306	32165168	32165286	NOTCH4	NM_004557	1	30	27	-	32165076	32165371
292668983	chr6	32166356	32166530	32166379	32166508	NOTCH4	NM_004557	1	30	25	-	32166426	32166507
290455147	chr6	32168668	32168822	32168685	32168799	NOTCH4	NM_004557	1	30	23	-	32168608	32168783
293610572	chr6	32169169	32169341	32169189	32169315	NOTCH4	NM_004557	1	30	22	-	32168894	32169277
292919812	chr6	32170162	32170328	32170182	32170310	NOTCH4	NM_004557	1	30	21	-	32169853	32170376
291436248	chr6	32171923	32172096	32171943	32172075	NOTCH4	NM_004557	1	30	19	-	32171914	32172166
291673984	chr6	32180128	32180300	32180154	32180279	NOTCH4	NM_004557	1	30	17	-	32180251	32180404
291132545	chr6	32180892	32181052	32180909	32181033	NOTCH4	NM_004557	1	30	15	-	32180912	32181029
290965893	chr6	32181976	32182142	32181997	32182119	NOTCH4	NM_004557	1	30	13	-	32181887	32182032
291484886	chr6	32184787	32184946	32184807	32184925	NOTCH4	NM_004557	1	30	11	-	32184722	32184844
290926352	chr6	32187432	32187591	32187451	32187571	NOTCH4	NM_004557	1	30	8	-	32187369	32187563
293009476	chr6	32188272	32188417	32188293	32188397	NOTCH4	NM_004557	1	30	6	-	32188182	32188418
290055503	chr6	32188818	32188990	32188839	32188969	NOTCH4	NM_004557	1	30	4	-	32188755	32189102
291664931	chr6	32190326	32190468	32190343	32190449	NOTCH4	NM_004557	1	30	3	-	32190288	32190583
273508667	chr6	33286435	33286609	33286457	33286584	DAXX	NM_001254717	3	7	7	-	33286335	33286579
273508667	chr6	33286435	33286609	33286457	33286584	DAXX	NM_001350	4	8	8	-	33286335	33286579
273508667	chr6	33286435	33286609	33286457	33286584	DAXX	NM_001141969	1	8	8	-	33286335	33286579
273508667	chr6	33286435	33286609	33286457	33286584	DAXX	NM_001141970	2	8	8	-	33286335	33286579
273064258	chr6	33287244	33287382	33287265	33287362	DAXX	NM_001254717	3	7	5	-	33287157	33287631
273064258	chr6	33287244	33287382	33287265	33287362	DAXX	NM_001350	4	8	6	-	33287157	33287631
273064258	chr6	33287244	33287382	33287265	33287362	DAXX	NM_001141969	1	8	6	-	33287157	33287631
273064258	chr6	33287244	33287382	33287265	33287362	DAXX	NM_001141970	2	8	6	-	33287157	33287631
273088245	chr6	33287766	33287937	33287791	33287914	DAXX	NM_001254717	3	7	4	-	33287788	33288001
273088245	chr6	33287766	33287937	33287791	33287914	DAXX	NM_001350	4	8	5	-	33287788	33288001
273088245	chr6	33287766	33287937	33287791	33287914	DAXX	NM_001141969	1	8	5	-	33287788	33288001
273088245	chr6	33287766	33287937	33287791	33287914	DAXX	NM_001141970	2	8	5	-	33287788	33288001
273246947	chr6	33288243	33288402	33288266	33288376	DAXX	NM_001254717	3	7	3	-	33288157	33288368
273246947	chr6	33288243	33288402	33288266	33288376	DAXX	NM_001350	4	8	4	-	33288157	33288368
273246947	chr6	33288243	33288402	33288266	33288376	DAXX	NM_001141969	1	8	4	-	33288157	33288368
273246947	chr6	33288243	33288402	33288266	33288376	DAXX	NM_001141970	2	8	4	-	33288157	33288368
274355724	chr6	33288805	33288940	33288828	33288918	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274355724	chr6	33288805	33288940	33288828	33288918	DAXX	NM_001350	4	8	3	-	33288513	33289344
274355724	chr6	33288805	33288940	33288828	33288918	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274355724	chr6	33288805	33288940	33288828	33288918	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274336321	chr6	33289218	33289362	33289241	33289339	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274336321	chr6	33289218	33289362	33289241	33289339	DAXX	NM_001350	4	8	3	-	33288513	33289344
274336321	chr6	33289218	33289362	33289241	33289339	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274336321	chr6	33289218	33289362	33289241	33289339	DAXX	NM_001141970	2	8	3	-	33288513	33289344
272983732	chr6	33289647	33289820	33289672	33289798	DAXX	NM_001141970	2	8	2	-	33289496	33289685
272983732	chr6	33289647	33289820	33289672	33289798	DAXX	NM_001350	4	8	2	-	33289496	33289751

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272983732	chr6	33289647	33289820	33289672	33289798	DAXX	NM_001141969	1	8	2	-	33289496	33289754
235087070	chr6	37138518	37138649	37138536	37138631	PIM1	NM_002648	2	6	2	+	37138549	37138655
235087070	chr6	37138518	37138649	37138536	37138631	PIM1	NM_001243186	1	6	2	+	37138549	37138655
238246970	chr6	37138940	37139072	37138961	37139051	PIM1	NM_002648	2	6	4	+	37138901	37139267
238246970	chr6	37138940	37139072	37138961	37139051	PIM1	NM_001243186	1	6	4	+	37138901	37139267
236679736	chr6	37140849	37141007	37140872	37140979	PIM1	NM_002648	2	6	5	+	37140772	37140948
236679736	chr6	37140849	37141007	37140872	37140979	PIM1	NM_001243186	1	6	5	+	37140772	37140948
269496234	chr6	41533566	41533722	41533584	41533703	FOXP4	NM_138457	3	17	2	+	41533483	41533702
269496234	chr6	41533566	41533722	41533584	41533703	FOXP4	NM_001012427	2	17	2	+	41533483	41533702
269496234	chr6	41533566	41533722	41533584	41533703	FOXP4	NM_001012426	1	17	2	+	41533483	41533702
270155482	chr6	41552538	41552711	41552557	41552689	FOXP4	NM_138457	3	17	4	+	41552507	41552629
270155482	chr6	41552538	41552711	41552557	41552689	FOXP4	NM_001012427	2	17	4	+	41552507	41552629
270155482	chr6	41552538	41552711	41552557	41552689	FOXP4	NM_001012426	1	17	4	+	41552507	41552629
269967648	chr6	41554979	41555120	41554999	41555101	FOXP4	NM_138457	3	17	7	+	41555040	41555250
269967648	chr6	41554979	41555120	41554999	41555101	FOXP4	NM_001012427	2	17	7	+	41555037	41555250
269967648	chr6	41554979	41555120	41554999	41555101	FOXP4	NM_001012426	1	17	7	+	41555037	41555250
271026325	chr6	41555597	41555768	41555619	41555747	FOXP4	NM_138457	3	17	8	+	41555531	41555635
271026325	chr6	41555597	41555768	41555619	41555747	FOXP4	NM_001012427	2	17	8	+	41555531	41555635
271026325	chr6	41555597	41555768	41555619	41555747	FOXP4	NM_001012426	1	17	8	+	41555531	41555635
270274207	chr6	41557717	41557889	41557739	41557867	FOXP4	NM_138457	3	17	11	+	41557737	41557908
270274207	chr6	41557717	41557889	41557739	41557867	FOXP4	NM_001012427	2	17	11	+	41557701	41557908
270274207	chr6	41557717	41557889	41557739	41557867	FOXP4	NM_001012426	1	17	11	+	41557701	41557908
271946062	chr6	41559000	41559168	41559028	41559144	FOXP4	NM_138457	3	17	13	+	41558959	41559060
271946062	chr6	41559000	41559168	41559028	41559144	FOXP4	NM_001012427	2	17	13	+	41558959	41559060
271946062	chr6	41559000	41559168	41559028	41559144	FOXP4	NM_001012426	1	17	13	+	41558959	41559060
270526630	chr6	41565416	41565577	41565435	41565559	FOXP4	NM_138457	3	17	16	+	41565519	41565688
270526630	chr6	41565416	41565577	41565435	41565559	FOXP4	NM_001012427	2	17	16	+	41565519	41565688
270526630	chr6	41565416	41565577	41565435	41565559	FOXP4	NM_001012426	1	17	16	+	41565519	41565688
227392160	chr6	44216267	44216433	44216294	44216412	HSP90AB1	NM_007355	1	12	2	+	44216367	44216513
228790709	chr6	44217318	44217487	44217341	44217466	HSP90AB1	NM_007355	1	12	4	+	44217412	44217571
228071498	chr6	44218210	44218359	44218238	44218337	HSP90AB1	NM_007355	1	12	6	+	44218028	44218336
229322587	chr6	44219151	44219312	44219175	44219286	HSP90AB1	NM_007355	1	12	8	+	44219155	44219345
228566289	chr6	44219718	44219892	44219746	44219871	HSP90AB1	NM_007355	1	12	10	+	44219736	44220004
227204054	chr6	44220793	44220967	44220819	44220949	HSP90AB1	NM_007355	1	12	11	+	44220782	44221115
272208089	chr6	51483826	51483994	51483852	51483972	PKHD1	NM_138694	1	67	67	-	51480145	51484318
270541179	chr6	51484235	51484401	51484258	51484372	PKHD1	NM_138694	1	67	67	-	51480145	51484318
271522952	chr6	51497361	51497493	51497387	51497470	PKHD1	NM_138694	1	67	65	-	51497363	51497521
270057907	chr6	51512776	51512942	51512800	51512917	PKHD1	NM_138694	1	67	63	-	51512829	51512916
271087718	chr6	51523805	51523931	51523831	51523908	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271071245	chr6	51524227	51524372	51524248	51524350	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271140785	chr6	51524678	51524849	51524703	51524821	PKHD1	NM_138694	1	67	61	-	51523750	51524767

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270380084	chr6	51611452	51611626	51611478	51611601	PKHD1	NM_138694	1	67	59	-	51611519	51611687
270380084	chr6	51611452	51611626	51611478	51611601	PKHD1	NM_170724	2	61	59	-	51611519	51611687
272287639	chr6	51612751	51612924	51612773	51612898	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272287639	chr6	51612751	51612924	51612773	51612898	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270549382	chr6	51613234	51613403	51613258	51613376	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270549382	chr6	51613234	51613403	51613258	51613376	PKHD1	NM_170724	2	61	58	-	51612585	51613463
271896899	chr6	51619505	51619669	51619525	51619648	PKHD1	NM_138694	1	67	56	-	51619582	51619736
271896899	chr6	51619505	51619669	51619525	51619648	PKHD1	NM_170724	2	61	56	-	51619582	51619736
270899357	chr6	51640672	51640842	51640700	51640814	PKHD1	NM_138694	1	67	54	-	51640606	51640719
270899357	chr6	51640672	51640842	51640700	51640814	PKHD1	NM_170724	2	61	54	-	51640606	51640719
271908017	chr6	51695736	51695880	51695758	51695854	PKHD1	NM_138694	1	67	52	-	51695659	51695787
271908017	chr6	51695736	51695880	51695758	51695854	PKHD1	NM_170724	2	61	52	-	51695659	51695787
271513143	chr6	51720643	51720813	51720669	51720786	PKHD1	NM_138694	1	67	49	-	51720691	51720868
271513143	chr6	51720643	51720813	51720669	51720786	PKHD1	NM_170724	2	61	49	-	51720691	51720868
272239352	chr6	51732798	51732963	51732820	51732935	PKHD1	NM_138694	1	67	48	-	51732661	51732907
272239352	chr6	51732798	51732963	51732820	51732935	PKHD1	NM_170724	2	61	48	-	51732661	51732907
269797772	chr6	51747899	51748056	51747927	51748030	PKHD1	NM_138694	1	67	46	-	51747891	51748025
269797772	chr6	51747899	51748056	51747927	51748030	PKHD1	NM_170724	2	61	46	-	51747891	51748025
270529388	chr6	51751931	51752102	51751956	51752077	PKHD1	NM_138694	1	67	44	-	51751931	51752043
270529388	chr6	51751931	51752102	51751956	51752077	PKHD1	NM_170724	2	61	44	-	51751931	51752043
270625116	chr6	51768796	51768924	51768818	51768901	PKHD1	NM_138694	1	67	42	-	51768784	51768840
270625116	chr6	51768796	51768924	51768818	51768901	PKHD1	NM_170724	2	61	42	-	51768784	51768840
271124280	chr6	51774151	51774313	51774172	51774287	PKHD1	NM_138694	1	67	40	-	51774081	51774272
271124280	chr6	51774151	51774313	51774172	51774287	PKHD1	NM_170724	2	61	40	-	51774081	51774272
271355820	chr6	51777224	51777396	51777244	51777374	PKHD1	NM_138694	1	67	38	-	51777164	51777374
271355820	chr6	51777224	51777396	51777244	51777374	PKHD1	NM_170724	2	61	38	-	51777164	51777374
269499037	chr6	51824674	51824847	51824697	51824825	PKHD1	NM_138694	1	67	36	-	51824668	51824824
269499037	chr6	51824674	51824847	51824697	51824825	PKHD1	NM_170724	2	61	36	-	51824668	51824824
269722160	chr6	51882206	51882372	51882228	51882350	PKHD1	NM_138694	1	67	34	-	51882208	51882427
269722160	chr6	51882206	51882372	51882228	51882350	PKHD1	NM_170724	2	61	34	-	51882208	51882427
270336366	chr6	51887671	51887841	51887692	51887818	PKHD1	NM_138694	1	67	33	-	51887599	51887742
270336366	chr6	51887671	51887841	51887692	51887818	PKHD1	NM_170724	2	61	33	-	51887599	51887742
271925889	chr6	51889636	51889810	51889660	51889789	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271925889	chr6	51889636	51889810	51889660	51889789	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271900511	chr6	51890094	51890227	51890117	51890206	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271900511	chr6	51890094	51890227	51890117	51890206	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271920948	chr6	51890489	51890656	51890512	51890634	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271920948	chr6	51890489	51890656	51890512	51890634	PKHD1	NM_170724	2	61	32	-	51889372	51890979
270088513	chr6	51890948	51891096	51890972	51891072	PKHD1	NM_138694	1	67	32	-	51889372	51890979
270088513	chr6	51890948	51891096	51890972	51891072	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271394809	chr6	51893079	51893211	51893100	51893187	PKHD1	NM_138694	1	67	30	-	51892954	51893149

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271394809	chr6	51893079	51893211	51893100	51893187	PKHD1	NM_170724	2	61	30	-	51892954	51893149
272501825	chr6	51900330	51900460	51900357	51900438	PKHD1	NM_138694	1	67	28	-	51900389	51900519
272501825	chr6	51900330	51900460	51900357	51900438	PKHD1	NM_170724	2	61	28	-	51900389	51900519
271971583	chr6	51907847	51908017	51907871	51907991	PKHD1	NM_138694	1	67	27	-	51907657	51907932
271971583	chr6	51907847	51908017	51907871	51907991	PKHD1	NM_170724	2	61	27	-	51907657	51907932
269702681	chr6	51909849	51909995	51909869	51909967	PKHD1	NM_138694	1	67	25	-	51909764	51909886
269702681	chr6	51909849	51909995	51909869	51909967	PKHD1	NM_170724	2	61	25	-	51909764	51909886
270366671	chr6	51914896	51915046	51914918	51915024	PKHD1	NM_138694	1	67	22	-	51914955	51915093
270366671	chr6	51914896	51915046	51914918	51915024	PKHD1	NM_170724	2	61	22	-	51914955	51915093
271837489	chr6	51918732	51918905	51918759	51918877	PKHD1	NM_138694	1	67	20	-	51918836	51918963
271837489	chr6	51918732	51918905	51918759	51918877	PKHD1	NM_170724	2	61	20	-	51918836	51918963
318542737	chr6	51921356	51921530	51921379	51921507	PKHD1	NM_138694	1	67	18	-	51921496	51921586
318542737	chr6	51921356	51921530	51921379	51921507	PKHD1	NM_170724	2	61	18	-	51921496	51921586
271458895	chr6	51923158	51923319	51923178	51923298	PKHD1	NM_138694	1	67	16	-	51923121	51923399
271458895	chr6	51923158	51923319	51923178	51923298	PKHD1	NM_170724	2	61	16	-	51923121	51923399
271826894	chr6	51927236	51927364	51927260	51927341	PKHD1	NM_138694	1	67	14	-	51927317	51927458
271826894	chr6	51927236	51927364	51927260	51927341	PKHD1	NM_170724	2	61	14	-	51927317	51927458
270170324	chr6	51930837	51931000	51930854	51930972	PKHD1	NM_138694	1	67	12	-	51930774	51930875
270170324	chr6	51930837	51931000	51930854	51930972	PKHD1	NM_170724	2	61	12	-	51930774	51930875
271524350	chr6	51935729	51935900	51935752	51935872	PKHD1	NM_138694	1	67	9	-	51935804	51935868
271524350	chr6	51935729	51935900	51935752	51935872	PKHD1	NM_170724	2	61	9	-	51935804	51935868
269775341	chr6	51940998	51941165	51941020	51941138	PKHD1	NM_138694	1	67	6	-	51941074	51941131
269775341	chr6	51940998	51941165	51941020	51941138	PKHD1	NM_170724	2	61	6	-	51941074	51941131
269582581	chr6	51947940	51948108	51947968	51948083	PKHD1	NM_138694	1	67	3	-	51947976	51948053
269582581	chr6	51947940	51948108	51947968	51948083	PKHD1	NM_170724	2	61	3	-	51947976	51948053
280424627	chr6	52871116	52871288	52871136	52871265	ICK	NM_016513	2	15	14	-	52871113	52871235
280424627	chr6	52871116	52871288	52871136	52871265	ICK	NM_014920	1	14	13	-	52871113	52871235
277976185	chr6	52876567	52876739	52876588	52876716	ICK	NM_016513	2	15	12	-	52876567	52876715
277976185	chr6	52876567	52876739	52876588	52876716	ICK	NM_014920	1	14	11	-	52876567	52876715
279479868	chr6	52878533	52878703	52878555	52878680	ICK	NM_016513	2	15	10	-	52878460	52878780
279479868	chr6	52878533	52878703	52878555	52878680	ICK	NM_014920	1	14	9	-	52878460	52878780
279512947	chr6	52883100	52883265	52883123	52883244	ICK	NM_016513	2	15	8	-	52883128	52883299
279512947	chr6	52883100	52883265	52883123	52883244	ICK	NM_014920	1	14	7	-	52883128	52883299
281256717	chr6	52895808	52895969	52895837	52895943	ICK	NM_016513	2	15	6	-	52895863	52895942
281256717	chr6	52895808	52895969	52895837	52895943	ICK	NM_014920	1	14	5	-	52895863	52895942
279328640	chr6	52905904	52906072	52905931	52906053	ICK	NM_016513	2	15	3	-	52905934	52906206
279328640	chr6	52905904	52906072	52905931	52906053	ICK	NM_014920	1	14	2	-	52905934	52906206
287417544	chr6	56324860	56325033	56324887	56325008	DST	NM_015548	2	84	83	-	56324929	56325052
286782031	chr6	56328335	56328501	56328360	56328482	DST	NM_015548	2	84	81	-	56328363	56328562
287317606	chr6	56333675	56333843	56333697	56333815	DST	NM_015548	2	84	79	-	56333780	56333797
287605867	chr6	56334979	56335146	56335003	56335118	DST	NM_015548	2	84	77	-	56334926	56335080

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287677940	chr6	56336806	56336980	56336830	56336952	DST	NM_015548	2	84	75	-	56336857	56337020
286734136	chr6	56338770	56338894	56338795	56338864	DST	NM_015548	2	84	74	-	56338671	56338800
287115071	chr6	56342036	56342200	56342059	56342175	DST	NM_015548	2	84	72	-	56342143	56342286
287816156	chr6	56347452	56347620	56347475	56347598	DST	NM_015548	2	84	70	-	56347481	56347675
286889530	chr6	56350211	56350377	56350235	56350355	DST	NM_015548	2	84	69	-	56350110	56350269
287542466	chr6	56354286	56354411	56354312	56354384	DST	NM_015548	2	84	67	-	56354288	56354407
286269397	chr6	56357169	56357312	56357195	56357285	DST	NM_015548	2	84	66	-	56357025	56357231
285867622	chr6	56358801	56358968	56358829	56358940	DST	NM_015548	2	84	64	-	56358808	56358978
285702008	chr6	56362595	56362720	56362622	56362697	DST	NM_015548	2	84	62	-	56362654	56362851
288694773	chr6	56365895	56366034	56365920	56366011	DST	NM_015548	2	84	61	-	56365878	56366033
285237447	chr6	56366369	56366493	56366396	56366466	DST	NM_015548	2	84	60	-	56366318	56366491
286036580	chr6	56371285	56371459	56371309	56371432	DST	NM_015548	2	84	58	-	56371241	56371342
289162138	chr6	56373329	56373487	56373353	56373464	DST	NM_015548	2	84	56	-	56373327	56373553
286586248	chr6	56374527	56374686	56374554	56374663	DST	NM_015548	2	84	55	-	56374440	56374671
284803520	chr6	56376112	56376236	56376134	56376210	DST	NM_015548	2	84	54	-	56375995	56376198
286969677	chr6	56381966	56382096	56381987	56382067	DST	NM_015548	2	84	52	-	56381996	56382103
286963775	chr6	56391082	56391231	56391109	56391209	DST	NM_015548	2	84	50	-	56391159	56391365
289072448	chr6	56392367	56392500	56392388	56392474	DST	NM_015548	2	84	49	-	56392291	56392532
287496006	chr6	56394241	56394391	56394264	56394364	DST	NM_015548	2	84	47	-	56394246	56394572
287638090	chr6	56394719	56394846	56394747	56394821	DST	NM_015548	2	84	46	-	56394772	56394931
288839234	chr6	56397272	56397438	56397296	56397410	DST	NM_015548	2	84	45	-	56397142	56397308
285316519	chr6	56401586	56401711	56401607	56401684	DST	NM_015548	2	84	43	-	56401577	56401738
285840722	chr6	56417124	56417270	56417146	56417243	DST	NM_015548	2	84	42	-	56416982	56418453
288155528	chr6	56417552	56417719	56417573	56417698	DST	NM_015548	2	84	42	-	56416982	56418453
288122432	chr6	56418021	56418190	56418044	56418161	DST	NM_015548	2	84	42	-	56416982	56418453
288154806	chr6	56418418	56418581	56418436	56418558	DST	NM_015548	2	84	42	-	56416982	56418453
287296769	chr6	56420406	56420553	56420430	56420529	DST	NM_015548	2	84	41	-	56420143	56420638
286188371	chr6	56422233	56422397	56422261	56422366	DST	NM_015548	2	84	40	-	56422117	56422316
285174978	chr6	56426165	56426295	56426191	56426272	DST	NM_015548	2	84	38	-	56426106	56426347
286429620	chr6	56433144	56433302	56433172	56433282	DST	NM_015548	2	84	36	-	56433267	56433393
287153345	chr6	56434751	56434899	56434779	56434871	DST	NM_015548	2	84	35	-	56434654	56434810
285834532	chr6	56437631	56437762	56437655	56437738	DST	NM_015548	2	84	33	-	56437545	56437862
287233657	chr6	56438498	56438658	56438524	56438630	DST	NM_015548	2	84	32	-	56438477	56438685
287568532	chr6	56443643	56443772	56443670	56443745	DST	NM_015548	2	84	31	-	56443612	56443735
288808606	chr6	56458509	56458673	56458529	56458647	DST	NM_015548	2	84	29	-	56458461	56458991
286992019	chr6	56462486	56462659	56462514	56462637	DST	NM_015548	2	84	28	-	56462538	56462804
286392707	chr6	56463350	56463489	56463378	56463469	DST	NM_015548	2	84	27	-	56463274	56463507
288496689	chr6	56464929	56465072	56464951	56465045	DST	NM_015548	2	84	26	-	56464867	56465019
286959885	chr6	56476331	56476496	56476359	56476468	DST	NM_015548	2	84	24	-	56476306	56476394
287155042	chr6	56480384	56480541	56480412	56480513	DST	NM_001723	1	24	24	-	56479375	56482216
289052018	chr6	56480836	56480993	56480860	56480966	DST	NM_001723	1	24	24	-	56479375	56482216

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289045998	chr6	56481275	56481425	56481299	56481401	DST	NM_001723	1	24	24	-	56479375	56482216
289086730	chr6	56481734	56481871	56481756	56481849	DST	NM_001723	1	24	24	-	56479375	56482216
287489042	chr6	56482130	56482292	56482152	56482263	DST	NM_001723	1	24	24	-	56479375	56482216
288303413	chr6	56483064	56483219	56483086	56483197	DST	NM_001723	1	24	23	-	56482784	56485513
288281106	chr6	56483493	56483652	56483521	56483630	DST	NM_001723	1	24	23	-	56482784	56485513
286204365	chr6	56483949	56484099	56483973	56484070	DST	NM_001723	1	24	23	-	56482784	56485513
288255489	chr6	56484326	56484498	56484354	56484472	DST	NM_001723	1	24	23	-	56482784	56485513
286144600	chr6	56484760	56484924	56484782	56484897	DST	NM_001723	1	24	23	-	56482784	56485513
286096063	chr6	56485196	56485363	56485217	56485339	DST	NM_001723	1	24	23	-	56482784	56485513
287169659	chr6	56489384	56489528	56489404	56489500	DST	NM_015548	2	84	22	-	56489328	56489426
287169659	chr6	56489384	56489528	56489404	56489500	DST	NM_001723	1	24	22	-	56489328	56489426
288339648	chr6	56492025	56492190	56492051	56492162	DST	NM_015548	2	84	20	-	56492002	56492085
288339648	chr6	56492025	56492190	56492051	56492162	DST	NM_001723	1	24	20	-	56492002	56492085
284785802	chr6	56494097	56494221	56494121	56494196	DST	NM_015548	2	84	18	-	56494048	56494241
284785802	chr6	56494097	56494221	56494121	56494196	DST	NM_001723	1	24	18	-	56494048	56494241
287382957	chr6	56496559	56496713	56496582	56496685	DST	NM_015548	2	84	15	-	56496681	56496838
287382957	chr6	56496559	56496713	56496582	56496685	DST	NM_001723	1	24	15	-	56496681	56496838
286263175	chr6	56497712	56497867	56497740	56497839	DST	NM_015548	2	84	14	-	56497652	56497835
286263175	chr6	56497712	56497867	56497740	56497839	DST	NM_001723	1	24	14	-	56497652	56497835
285886847	chr6	56499309	56499454	56499330	56499426	DST	NM_015548	2	84	12	-	56499260	56499414
285886847	chr6	56499309	56499454	56499330	56499426	DST	NM_001723	1	24	12	-	56499260	56499414
286477428	chr6	56501286	56501414	56501313	56501392	DST	NM_015548	2	84	9	-	56501355	56501450
286477428	chr6	56501286	56501414	56501313	56501392	DST	NM_001723	1	24	9	-	56501355	56501450
287926571	chr6	56504203	56504354	56504229	56504326	DST	NM_015548	2	84	7	-	56504248	56504409
287926571	chr6	56504203	56504354	56504229	56504326	DST	NM_001723	1	24	7	-	56504248	56504409
287182336	chr6	56504655	56504819	56504682	56504791	DST	NM_015548	2	84	5	-	56504727	56504855
287182336	chr6	56504655	56504819	56504682	56504791	DST	NM_001723	1	24	5	-	56504727	56504855
286991964	chr6	56504934	56505089	56504959	56505063	DST	NM_015548	2	84	4	-	56504941	56505403
286991964	chr6	56504934	56505089	56504959	56505063	DST	NM_001723	1	24	4	-	56504941	56505403
285058216	chr6	56506714	56506877	56506742	56506854	DST	NM_015548	2	84	3	-	56506745	56506899
285058216	chr6	56506714	56506877	56506742	56506854	DST	NM_001723	1	24	3	-	56506745	56506899
288426005	chr6	56507392	56507562	56507416	56507534	DST	NM_015548	2	84	1	-	56507420	56507694
288426005	chr6	56507392	56507562	56507416	56507534	DST	NM_001723	1	24	1	-	56507420	56507694
284139668	chr6	69348671	69348837	69348700	69348811	BAI3	NM_001704	1	32	3	+	69348553	69349324
284114386	chr6	69348961	69349135	69348990	69349108	BAI3	NM_001704	1	32	3	+	69348553	69349324
283075626	chr6	69640488	69640637	69640511	69640609	BAI3	NM_001704	1	32	4	+	69640451	69640561
281806662	chr6	69653766	69653912	69653788	69653886	BAI3	NM_001704	1	32	6	+	69653722	69653886
281428145	chr6	69666631	69666797	69666653	69666768	BAI3	NM_001704	1	32	8	+	69666537	69666701
284252379	chr6	69703722	69703878	69703750	69703854	BAI3	NM_001704	1	32	11	+	69703660	69703854
283545243	chr6	69758103	69758227	69758128	69758205	BAI3	NM_001704	1	32	14	+	69758077	69758226
284096998	chr6	69772836	69773005	69772864	69772977	BAI3	NM_001704	1	32	16	+	69772826	69772928

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
283342781	chr6	69943182	69943334	69943203	69943309	BAI3	NM_001704	1	32	18	+	69943182	69943308
282577341	chr6	69948996	69949120	69949022	69949093	BAI3	NM_001704	1	32	20	+	69949016	69949118
283926830	chr6	70037676	70037846	70037702	70037818	BAI3	NM_001704	1	32	22	+	70037712	70037781
283219268	chr6	70048719	70048866	70048747	70048843	BAI3	NM_001704	1	32	25	+	70048808	70048906
285673634	chr6	70064044	70064217	70064065	70064192	BAI3	NM_001704	1	32	27	+	70064125	70064220
284250590	chr6	70070777	70070918	70070794	70070891	BAI3	NM_001704	1	32	29	+	70070761	70071404
282148423	chr6	70071166	70071315	70071186	70071295	BAI3	NM_001704	1	32	29	+	70070761	70071404
283476215	chr6	70082297	70082431	70082327	70082407	BAI3	NM_001704	1	32	30	+	70082298	70082333
294769870	chr6	91226191	91226346	91226219	91226321	MAP3K7	NM_145333	4	15	15	-	91225353	91226400
294769870	chr6	91226191	91226346	91226219	91226321	MAP3K7	NM_145332	3	16	16	-	91225353	91226400
294769870	chr6	91226191	91226346	91226219	91226321	MAP3K7	NM_145331	2	17	17	-	91225353	91226400
294769870	chr6	91226191	91226346	91226219	91226321	MAP3K7	NM_003188	1	16	16	-	91225353	91226400
293921749	chr6	91228854	91229013	91228880	91228988	MAP3K7	NM_145333	4	15	14	-	91228977	91229038
293921749	chr6	91228854	91229013	91228880	91228988	MAP3K7	NM_145332	3	16	15	-	91228977	91229038
293921749	chr6	91228854	91229013	91228880	91228988	MAP3K7	NM_145331	2	17	15	-	91228977	91229038
293921749	chr6	91228854	91229013	91228880	91228988	MAP3K7	NM_003188	1	16	14	-	91228977	91229038
294800605	chr6	91246042	91246179	91246067	91246151	MAP3K7	NM_145333	4	15	12	-	91246056	91246120
294800605	chr6	91246042	91246179	91246067	91246151	MAP3K7	NM_145332	3	16	13	-	91246056	91246120
294800605	chr6	91246042	91246179	91246067	91246151	MAP3K7	NM_145331	2	17	13	-	91246056	91246120
294800605	chr6	91246042	91246179	91246067	91246151	MAP3K7	NM_003188	1	16	12	-	91246056	91246120
294198794	chr6	91257643	91257810	91257670	91257782	MAP3K7	NM_145333	4	15	10	-	91257766	91257896
294198794	chr6	91257643	91257810	91257670	91257782	MAP3K7	NM_145332	3	16	10	-	91257766	91257896
294198794	chr6	91257643	91257810	91257670	91257782	MAP3K7	NM_145331	2	17	10	-	91257766	91257896
294198794	chr6	91257643	91257810	91257670	91257782	MAP3K7	NM_003188	1	16	10	-	91257766	91257896
294980917	chr6	91263109	91263246	91263130	91263227	MAP3K7	NM_145333	4	15	7	-	91263177	91263305
294980917	chr6	91263109	91263246	91263130	91263227	MAP3K7	NM_145332	3	16	7	-	91263177	91263305
294980917	chr6	91263109	91263246	91263130	91263227	MAP3K7	NM_145331	2	17	7	-	91263177	91263305
294980917	chr6	91263109	91263246	91263130	91263227	MAP3K7	NM_003188	1	16	7	-	91263177	91263305
293823138	chr6	91269733	91269875	91269755	91269852	MAP3K7	NM_145333	4	15	5	-	91269795	91269933
293823138	chr6	91269733	91269875	91269755	91269852	MAP3K7	NM_145332	3	16	5	-	91269795	91269933
293823138	chr6	91269733	91269875	91269755	91269852	MAP3K7	NM_145331	2	17	5	-	91269795	91269933
293823138	chr6	91269733	91269875	91269755	91269852	MAP3K7	NM_003188	1	16	5	-	91269795	91269933
293703679	chr6	91278204	91278358	91278232	91278332	MAP3K7	NM_145333	4	15	3	-	91278277	91278342
293703679	chr6	91278204	91278358	91278232	91278332	MAP3K7	NM_145332	3	16	3	-	91278277	91278342
293703679	chr6	91278204	91278358	91278232	91278332	MAP3K7	NM_145331	2	17	3	-	91278277	91278342
293703679	chr6	91278204	91278358	91278232	91278332	MAP3K7	NM_003188	1	16	3	-	91278277	91278342
293709361	chr6	91296490	91296664	91296513	91296646	MAP3K7	NM_145331	2	17	1	-	91296483	91296764
293709361	chr6	91296490	91296664	91296513	91296646	MAP3K7	NM_145333	4	15	1	-	91296483	91296907
293709361	chr6	91296490	91296664	91296513	91296646	MAP3K7	NM_145332	3	16	1	-	91296483	91296907
293709361	chr6	91296490	91296664	91296513	91296646	MAP3K7	NM_003188	1	16	1	-	91296483	91296907
270554573	chr6	93955090	93955221	93955118	93955193	EPHA7	NM_004440	1	17	16	-	93955016	93955171

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270971861	chr6	93964368	93964505	93964396	93964483	EPHA7	NM_004440	1	17	14	-	93964365	93964514
269641833	chr6	93965648	93965789	93965671	93965761	EPHA7	NM_004440	1	17	13	-	93965546	93965755
270132419	chr6	93967892	93968026	93967920	93968003	EPHA7	NM_004440	1	17	11	-	93967817	93968002
271358747	chr6	93974295	93974421	93974320	93974399	EPHA7	NM_004440	1	17	8	-	93974312	93974420
271187315	chr6	93981964	93982134	93981987	93982110	EPHA7	NM_004440	1	17	6	-	93982016	93982140
270922240	chr6	94066604	94066764	94066627	94066742	EPHA7	NM_004440	1	17	5	-	94066435	94066770
270597439	chr6	94120101	94120275	94120123	94120249	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270641566	chr6	94120524	94120650	94120547	94120623	EPHA7	NM_004440	1	17	3	-	94120219	94120888
271203745	chr6	94124337	94124488	94124362	94124462	EPHA7	NM_004440	1	17	2	-	94124421	94124485
273496401	chr6	106534411	106534583	106534437	106534557	PRDM1	NM_001198	1	7	1	+	106534195	106534470
273825722	chr6	106543481	106543606	106543508	106543578	PRDM1	NM_001198	1	7	3	+	106543490	106543609
274599636	chr6	106547224	106547378	106547246	106547357	PRDM1	NM_182907	2	5	2	+	106547175	106547427
274599636	chr6	106547224	106547378	106547246	106547357	PRDM1	NM_001198	1	7	4	+	106547175	106547427
272802093	chr6	106552855	106553017	106552879	106552997	PRDM1	NM_182907	2	5	3	+	106552700	106553808
272802093	chr6	106552855	106553017	106552879	106552997	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273920439	chr6	106553313	106553466	106553332	106553448	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273920439	chr6	106553313	106553466	106553332	106553448	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273937210	chr6	106553719	106553876	106553740	106553848	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273937210	chr6	106553719	106553876	106553740	106553848	PRDM1	NM_001198	1	7	5	+	106552700	106553808
272991963	chr6	106554833	106555001	106554854	106554979	PRDM1	NM_182907	2	5	5	+	106554786	106557814
272991963	chr6	106554833	106555001	106554854	106554979	PRDM1	NM_001198	1	7	7	+	106554786	106557814
274104082	chr6	106555271	106555445	106555293	106555419	PRDM1	NM_182907	2	5	5	+	106554786	106557814
274104082	chr6	106555271	106555445	106555293	106555419	PRDM1	NM_001198	1	7	7	+	106554786	106557814
229547905	chr6	108985012	108985186	108985032	108985161	FOXO3	NM_001455	1	3	2	+	108984658	108986092
229547905	chr6	108985012	108985186	108985032	108985161	FOXO3	NM_201559	2	4	3	+	108984658	108986092
227547667	chr6	108985599	108985772	108985619	108985752	FOXO3	NM_001455	1	3	2	+	108984658	108986092
227547667	chr6	108985599	108985772	108985619	108985752	FOXO3	NM_201559	2	4	3	+	108984658	108986092
242642962	chr6	117609848	117609973	117609869	117609951	ROS1	NM_002944	1	43	43	-	117609530	117609965
238483218	chr6	117629906	117630035	117629928	117630008	ROS1	NM_002944	1	43	41	-	117629957	117630091
262646118	chr6	117631393	117631524	117631417	117631496	ROS1	NM_002944	1	43	40	-	117631244	117631444
242305483	chr6	117639294	117639456	117639321	117639428	ROS1	NM_002944	1	43	37	-	117639351	117639415
260940878	chr6	117642471	117642642	117642491	117642614	ROS1	NM_002944	1	43	35	-	117642422	117642557
264105590	chr6	117647428	117647556	117647456	117647528	ROS1	NM_002944	1	43	33	-	117647387	117647577
240770544	chr6	117658289	117658458	117658319	117658430	ROS1	NM_002944	1	43	31	-	117658335	117658503
241304372	chr6	117662340	117662514	117662366	117662486	ROS1	NM_002944	1	43	30	-	117662298	117662474
261120733	chr6	117663541	117663711	117663564	117663684	ROS1	NM_002944	1	43	28	-	117663563	117663707
239552003	chr6	117674062	117674215	117674084	117674193	ROS1	NM_002944	1	43	26	-	117674153	117674332
238529896	chr6	117677910	117678049	117677935	117678022	ROS1	NM_002944	1	43	25	-	117677792	117678078
242320957	chr6	117680964	117681096	117680988	117681073	ROS1	NM_002944	1	43	23	-	117680972	117681174
262165652	chr6	117683657	117683827	117683683	117683802	ROS1	NM_002944	1	43	21	-	117683766	117684028
261844125	chr6	117686204	117686372	117686231	117686345	ROS1	NM_002944	1	43	20	-	117686223	117686367

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262556941	chr6	117687196	117687329	117687222	117687302	ROS1	NM_002944	1	43	18	-	117687239	117687453
264291684	chr6	117700251	117700389	117700279	117700362	ROS1	NM_002944	1	43	17	-	117700222	117700322
261917790	chr6	117706819	117706984	117706843	117706963	ROS1	NM_002944	1	43	15	-	117706846	117707024
241751409	chr6	117708993	117709141	117709018	117709116	ROS1	NM_002944	1	43	13	-	117708943	117709197
260285074	chr6	117710619	117710791	117710643	117710767	ROS1	NM_002944	1	43	12	-	117710513	117711009
241012838	chr6	117714386	117714560	117714412	117714532	ROS1	NM_002944	1	43	11	-	117714387	117714484
241426372	chr6	117717307	117717463	117717330	117717438	ROS1	NM_002944	1	43	8	-	117717351	117717427
262174235	chr6	117724378	117724548	117724402	117724524	ROS1	NM_002944	1	43	6	-	117724302	117724440
241339083	chr6	117737341	117737513	117737366	117737486	ROS1	NM_002944	1	43	3	-	117737421	117737480
294198660	chr6	134491345	134491519	134491372	134491499	SGK1	NM_001143676	1	14	14	-	134490384	134491573
294198660	chr6	134491345	134491519	134491372	134491499	SGK1	NM_001143677	2	12	12	-	134490384	134491573
294198660	chr6	134491345	134491519	134491372	134491499	SGK1	NM_005627	4	12	12	-	134490384	134491573
294198660	chr6	134491345	134491519	134491372	134491499	SGK1	NM_001143678	3	12	12	-	134490384	134491573
293937895	chr6	134492215	134492370	134492235	134492342	SGK1	NM_001143676	1	14	12	-	134492161	134492316
293937895	chr6	134492215	134492370	134492235	134492342	SGK1	NM_001143677	2	12	10	-	134492161	134492316
293937895	chr6	134492215	134492370	134492235	134492342	SGK1	NM_005627	4	12	10	-	134492161	134492316
293937895	chr6	134492215	134492370	134492235	134492342	SGK1	NM_001143678	3	12	10	-	134492161	134492316
294331153	chr6	134493778	134493949	134493799	134493924	SGK1	NM_001143676	1	14	9	-	134493800	134493912
294331153	chr6	134493778	134493949	134493799	134493924	SGK1	NM_001143677	2	12	7	-	134493800	134493912
294331153	chr6	134493778	134493949	134493799	134493924	SGK1	NM_005627	4	12	7	-	134493800	134493912
294331153	chr6	134493778	134493949	134493799	134493924	SGK1	NM_001143678	3	12	7	-	134493800	134493912
294646266	chr6	134494518	134494656	134494545	134494628	SGK1	NM_001143676	1	14	6	-	134494600	134494704
294646266	chr6	134494518	134494656	134494545	134494628	SGK1	NM_001143677	2	12	4	-	134494600	134494704
294646266	chr6	134494518	134494656	134494545	134494628	SGK1	NM_005627	4	12	4	-	134494600	134494704
294646266	chr6	134494518	134494656	134494545	134494628	SGK1	NM_001143678	3	12	4	-	134494600	134494704
294594349	chr6	134495813	134495982	134495838	134495960	SGK1	NM_005627	4	12	1	-	134495870	134496034
293894756	chr6	134528414	134528557	134528437	134528533	SGK1	NM_001143676	1	14	3	-	134528494	134528569
294801120	chr6	134583235	134583392	134583257	134583369	SGK1	NM_001143676	1	14	2	-	134583071	134583286
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001130173	2	16	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001130172	1	15	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001161657	4	14	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001161656	3	16	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_005375	8	15	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001161658	5	16	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001161660	7	14	3	+	135508972	135509043
235071919	chr6	135508889	135509052	135508917	135509024	MYB	NM_001161659	6	14	3	+	135508972	135509043
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001130173	2	16	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001130172	1	15	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001161657	4	14	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001161656	3	16	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_005375	8	15	5	+	135511265	135511485

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001161658	5	16	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001161660	7	14	5	+	135511265	135511485
238985136	chr6	135511137	135511300	135511163	135511278	MYB	NM_001161659	6	14	5	+	135511265	135511485
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001130173	2	16	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001130172	1	15	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001161657	4	14	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001161656	3	16	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_005375	8	15	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001161658	5	16	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001161660	7	14	6	+	135513462	135513696
235775103	chr6	135513464	135513636	135513492	135513616	MYB	NM_001161659	6	14	6	+	135513462	135513696
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001130173	2	16	8	+	135515494	135515598
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001161657	4	14	8	+	135515494	135515598
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_005375	8	15	8	+	135515494	135515598
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001161658	5	16	8	+	135515494	135515598
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001161659	6	14	8	+	135515494	135515598
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001130172	1	15	8	+	135515494	135515589
238298078	chr6	135515515	135515640	135515542	135515617	MYB	NM_001161656	3	16	8	+	135515494	135515589
239254211	chr6	135518077	135518251	135518098	135518230	MYB	NM_001130173	2	16	10	+	135518099	135518461
239254211	chr6	135518077	135518251	135518098	135518230	MYB	NM_001161656	3	16	10	+	135518099	135518461
239254211	chr6	135518077	135518251	135518098	135518230	MYB	NM_001161658	5	16	10	+	135518099	135518461
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001130173	2	16	11	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001130172	1	15	10	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001161657	4	14	9	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001161656	3	16	11	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_005375	8	15	10	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001161658	5	16	11	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001161660	7	14	9	+	135520046	135520188
237812542	chr6	135520108	135520275	135520130	135520247	MYB	NM_001161659	6	14	10	+	135520046	135520188
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001130173	2	16	13	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001130172	1	15	12	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001161657	4	14	11	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001161656	3	16	13	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_005375	8	15	12	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001161658	5	16	13	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001161660	7	14	11	+	135521428	135521553
235587712	chr6	135521412	135521576	135521433	135521554	MYB	NM_001161659	6	14	12	+	135521428	135521553
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001130173	2	16	16	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001130172	1	15	15	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001161657	4	14	14	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001161656	3	16	16	+	135539002	135540311

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001161658	5	16	16	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001161660	7	14	14	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_001161659	6	14	14	+	135539002	135540311
235563881	chr6	135538893	135539052	135538914	135539030	MYB	NM_005375	8	15	15	+	135539002	135540310
238909849	chr6	138192529	138192703	138192553	138192680	TNFAIP3	NM_006290	1	9	2	+	138192350	138192659
264860488	chr6	138196892	138197017	138196920	138196990	TNFAIP3	NM_006290	1	9	4	+	138196825	138196972
241405421	chr6	138198219	138198381	138198244	138198359	TNFAIP3	NM_006290	1	9	6	+	138198213	138198393
263784219	chr6	138199751	138199914	138199772	138199893	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
263790945	chr6	138200159	138200333	138200185	138200311	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
240725368	chr6	138201291	138201447	138201312	138201425	TNFAIP3	NM_006290	1	9	8	+	138201208	138201389
272090110	chr6	152128954	152129106	152128974	152129084	ESR1	NM_000125	1	8	1	+	152128814	152129499
272090110	chr6	152128954	152129106	152128974	152129084	ESR1	NM_001122740	2	9	2	+	152128978	152129499
272090110	chr6	152128954	152129106	152128974	152129084	ESR1	NM_001122742	4	10	3	+	152128978	152129499
272090110	chr6	152128954	152129106	152128974	152129084	ESR1	NM_001122741	3	9	2	+	152128978	152129499
272097513	chr6	152129345	152129477	152129364	152129460	ESR1	NM_000125	1	8	1	+	152128814	152129499
272097513	chr6	152129345	152129477	152129364	152129460	ESR1	NM_001122740	2	9	2	+	152128978	152129499
272097513	chr6	152129345	152129477	152129364	152129460	ESR1	NM_001122742	4	10	3	+	152128978	152129499
272097513	chr6	152129345	152129477	152129364	152129460	ESR1	NM_001122741	3	9	2	+	152128978	152129499
272597081	chr6	152163838	152163981	152163861	152163957	ESR1	NM_000125	1	8	2	+	152163732	152163922
272597081	chr6	152163838	152163981	152163861	152163957	ESR1	NM_001122740	2	9	3	+	152163732	152163922
272597081	chr6	152163838	152163981	152163861	152163957	ESR1	NM_001122742	4	10	4	+	152163732	152163922
272597081	chr6	152163838	152163981	152163861	152163957	ESR1	NM_001122741	3	9	3	+	152163732	152163922
269916151	chr6	152265293	152265465	152265316	152265443	ESR1	NM_000125	1	8	4	+	152265308	152265643
269916151	chr6	152265293	152265465	152265316	152265443	ESR1	NM_001122740	2	9	5	+	152265308	152265643
269916151	chr6	152265293	152265465	152265316	152265443	ESR1	NM_001122742	4	10	6	+	152265308	152265643
269916151	chr6	152265293	152265465	152265316	152265443	ESR1	NM_001122741	3	9	5	+	152265308	152265643
270060550	chr6	152332792	152332953	152332816	152332931	ESR1	NM_000125	1	8	5	+	152332791	152332929
270060550	chr6	152332792	152332953	152332816	152332931	ESR1	NM_001122740	2	9	6	+	152332791	152332929
270060550	chr6	152332792	152332953	152332816	152332931	ESR1	NM_001122742	4	10	7	+	152332791	152332929
270060550	chr6	152332792	152332953	152332816	152332931	ESR1	NM_001122741	3	9	6	+	152332791	152332929
269795813	chr6	152415576	152415742	152415596	152415717	ESR1	NM_000125	1	8	7	+	152415520	152415703
269795813	chr6	152415576	152415742	152415596	152415717	ESR1	NM_001122740	2	9	8	+	152415520	152415703
269795813	chr6	152415576	152415742	152415596	152415717	ESR1	NM_001122742	4	10	9	+	152415520	152415703
269795813	chr6	152415576	152415742	152415596	152415717	ESR1	NM_001122741	3	9	8	+	152415520	152415703
305007169	chr6	152443512	152443685	152443533	152443664	SYNE1	NM_033071	1	146	146	-	152442819	152443811
305007169	chr6	152443512	152443685	152443533	152443664	SYNE1	NM_182961	2	146	146	-	152442819	152443811
303953345	chr6	152453218	152453389	152453238	152453362	SYNE1	NM_033071	1	146	144	-	152453257	152453349
303953345	chr6	152453218	152453389	152453238	152453362	SYNE1	NM_182961	2	146	144	-	152453257	152453349
301209189	chr6	152456176	152456346	152456202	152456321	SYNE1	NM_033071	1	146	142	-	152456239	152456367
301209189	chr6	152456176	152456346	152456202	152456321	SYNE1	NM_182961	2	146	142	-	152456239	152456367
302298317	chr6	152457905	152458070	152457928	152458044	SYNE1	NM_033071	1	146	141	-	152457753	152457953

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
302298317	chr6	152457905	152458070	152457928	152458044	SYNE1	NM_182961	2	146	141	-	152457753	152457953
301990526	chr6	152462315	152462489	152462336	152462467	SYNE1	NM_033071	1	146	139	-	152462338	152462464
301990526	chr6	152462315	152462489	152462336	152462467	SYNE1	NM_182961	2	146	139	-	152462338	152462464
302541733	chr6	152469137	152469310	152469162	152469291	SYNE1	NM_033071	1	146	136	-	152469180	152469513
302541733	chr6	152469137	152469310	152469162	152469291	SYNE1	NM_182961	2	146	137	-	152469180	152469513
299896526	chr6	152470671	152470845	152470691	152470817	SYNE1	NM_033071	1	146	135	-	152470612	152470803
299896526	chr6	152470671	152470845	152470691	152470817	SYNE1	NM_182961	2	146	136	-	152470612	152470803
300917802	chr6	152473139	152473301	152473159	152473276	SYNE1	NM_033071	1	146	133	-	152473094	152473276
300917802	chr6	152473139	152473301	152473159	152473276	SYNE1	NM_182961	2	146	134	-	152473094	152473276
304473740	chr6	152477097	152477263	152477118	152477238	SYNE1	NM_033071	1	146	131	-	152477045	152477232
304473740	chr6	152477097	152477263	152477118	152477238	SYNE1	NM_182961	2	146	132	-	152477045	152477232
301031167	chr6	152497560	152497731	152497579	152497703	SYNE1	NM_033071	1	146	129	-	152497529	152497695
301031167	chr6	152497560	152497731	152497579	152497703	SYNE1	NM_182961	2	146	130	-	152497529	152497695
300487434	chr6	152510423	152510576	152510450	152510550	SYNE1	NM_033071	1	146	127	-	152510387	152510542
300487434	chr6	152510423	152510576	152510450	152510550	SYNE1	NM_182961	2	146	128	-	152510387	152510542
301948281	chr6	152527344	152527469	152527365	152527448	SYNE1	NM_033071	1	146	125	-	152527303	152527497
301948281	chr6	152527344	152527469	152527365	152527448	SYNE1	NM_182961	2	146	126	-	152527303	152527497
301474480	chr6	152529285	152529415	152529305	152529389	SYNE1	NM_033071	1	146	124	-	152529107	152529341
301474480	chr6	152529285	152529415	152529305	152529389	SYNE1	NM_182961	2	146	125	-	152529107	152529341
304013814	chr6	152534767	152534922	152534794	152534899	SYNE1	NM_033071	1	146	122	-	152534747	152534894
304013814	chr6	152534767	152534922	152534794	152534899	SYNE1	NM_182961	2	146	123	-	152534747	152534894
300942470	chr6	152539484	152539622	152539507	152539594	SYNE1	NM_033071	1	146	120	-	152539392	152539538
300942470	chr6	152539484	152539622	152539507	152539594	SYNE1	NM_182961	2	146	121	-	152539392	152539538
300440327	chr6	152542064	152542210	152542084	152542182	SYNE1	NM_033071	1	146	118	-	152541977	152542181
300440327	chr6	152542064	152542210	152542084	152542182	SYNE1	NM_182961	2	146	119	-	152541977	152542181
305429443	chr6	152545624	152545780	152545648	152545757	SYNE1	NM_033071	1	146	116	-	152545629	152545799
305429443	chr6	152545624	152545780	152545648	152545757	SYNE1	NM_182961	2	146	117	-	152545629	152545799
303962554	chr6	152551599	152551729	152551625	152551704	SYNE1	NM_033071	1	146	114	-	152551682	152551837
303962554	chr6	152551599	152551729	152551625	152551704	SYNE1	NM_182961	2	146	115	-	152551682	152551837
300519042	chr6	152552597	152552766	152552625	152552739	SYNE1	NM_033071	1	146	113	-	152552526	152552702
300519042	chr6	152552597	152552766	152552625	152552739	SYNE1	NM_182961	2	146	114	-	152552526	152552702
303818800	chr6	152555723	152555868	152555748	152555846	SYNE1	NM_033071	1	146	110	-	152555803	152555935
303818800	chr6	152555723	152555868	152555748	152555846	SYNE1	NM_182961	2	146	111	-	152555803	152555935
299713684	chr6	152557367	152557534	152557395	152557508	SYNE1	NM_033071	1	146	109	-	152557242	152557438
299713684	chr6	152557367	152557534	152557395	152557508	SYNE1	NM_182961	2	146	110	-	152557242	152557438
303882817	chr6	152560733	152560875	152560756	152560850	SYNE1	NM_033071	1	146	107	-	152560668	152560841
303882817	chr6	152560733	152560875	152560756	152560850	SYNE1	NM_182961	2	146	108	-	152560668	152560841
299812034	chr6	152565728	152565897	152565755	152565871	SYNE1	NM_033071	1	146	105	-	152565672	152565791
299812034	chr6	152565728	152565897	152565755	152565871	SYNE1	NM_182961	2	146	106	-	152565672	152565791
305975318	chr6	152576032	152576162	152576060	152576134	SYNE1	NM_033071	1	146	103	-	152576015	152576224
305975318	chr6	152576032	152576162	152576060	152576134	SYNE1	NM_182961	2	146	104	-	152576015	152576224

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300624330	chr6	152577647	152577795	152577669	152577774	SYNE1	NM_033071	1	146	101	-	152577769	152577900
300624330	chr6	152577647	152577795	152577669	152577774	SYNE1	NM_182961	2	146	102	-	152577769	152577900
305203765	chr6	152583270	152583408	152583293	152583387	SYNE1	NM_033071	1	146	100	-	152583167	152583323
305203765	chr6	152583270	152583408	152583293	152583387	SYNE1	NM_182961	2	146	101	-	152583167	152583323
305400176	chr6	152599095	152599257	152599116	152599236	SYNE1	NM_033071	1	146	97	-	152599224	152599415
305400176	chr6	152599095	152599257	152599116	152599236	SYNE1	NM_182961	2	146	98	-	152599224	152599415
302972689	chr6	152602986	152603116	152603004	152603092	SYNE1	NM_033071	1	146	96	-	152602942	152603115
302972689	chr6	152602986	152603116	152603004	152603092	SYNE1	NM_182961	2	146	97	-	152602942	152603115
302737551	chr6	152614780	152614914	152614801	152614886	SYNE1	NM_033071	1	146	94	-	152614723	152614884
302737551	chr6	152614780	152614914	152614801	152614886	SYNE1	NM_182961	2	146	95	-	152614723	152614884
301805355	chr6	152621766	152621938	152621788	152621917	SYNE1	NM_033071	1	146	92	-	152621776	152621916
301805355	chr6	152621766	152621938	152621788	152621917	SYNE1	NM_182961	2	146	93	-	152621776	152621916
299344663	chr6	152629531	152629686	152629555	152629664	SYNE1	NM_182961	2	146	91	-	152629624	152629767
299344663	chr6	152629531	152629686	152629555	152629664	SYNE1	NM_033071	1	146	90	-	152629624	152629763
304288819	chr6	152631438	152631581	152631463	152631559	SYNE1	NM_033071	1	146	88	-	152631531	152631653
304288819	chr6	152631438	152631581	152631463	152631559	SYNE1	NM_182961	2	146	89	-	152631531	152631653
305989530	chr6	152631922	152632048	152631945	152632024	SYNE1	NM_033071	1	146	87	-	152631823	152632008
305989530	chr6	152631922	152632048	152631945	152632024	SYNE1	NM_182961	2	146	88	-	152631823	152632008
301878712	chr6	152639301	152639466	152639321	152639442	SYNE1	NM_033071	1	146	85	-	152639216	152639398
301878712	chr6	152639301	152639466	152639321	152639442	SYNE1	NM_182961	2	146	86	-	152639216	152639398
305630293	chr6	152642415	152642589	152642444	152642564	SYNE1	NM_033071	1	146	83	-	152642373	152642525
305630293	chr6	152642415	152642589	152642444	152642564	SYNE1	NM_182961	2	146	84	-	152642373	152642525
305540868	chr6	152644724	152644874	152644741	152644847	SYNE1	NM_033071	1	146	81	-	152644613	152644872
305540868	chr6	152644724	152644874	152644741	152644847	SYNE1	NM_182961	2	146	82	-	152644613	152644872
302966788	chr6	152647073	152647230	152647095	152647207	SYNE1	NM_033071	1	146	79	-	152647093	152647237
302966788	chr6	152647073	152647230	152647095	152647207	SYNE1	NM_182961	2	146	80	-	152647093	152647237
303829326	chr6	152647507	152647680	152647530	152647660	SYNE1	NM_033071	1	146	78	-	152647431	152647768
303829326	chr6	152647507	152647680	152647530	152647660	SYNE1	NM_182961	2	146	79	-	152647431	152647768
305433045	chr6	152651013	152651176	152651037	152651151	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305433045	chr6	152651013	152651176	152651037	152651151	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305417542	chr6	152651469	152651634	152651491	152651611	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305417542	chr6	152651469	152651634	152651491	152651611	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305403909	chr6	152651892	152652050	152651916	152652023	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305403909	chr6	152651892	152652050	152651916	152652023	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305400709	chr6	152652314	152652473	152652336	152652451	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305400709	chr6	152652314	152652473	152652336	152652451	SYNE1	NM_182961	2	146	78	-	152650865	152653025
302225794	chr6	152652784	152652909	152652806	152652881	SYNE1	NM_033071	1	146	77	-	152650865	152653025
302225794	chr6	152652784	152652909	152652806	152652881	SYNE1	NM_182961	2	146	78	-	152650865	152653025
299884941	chr6	152655320	152655491	152655347	152655462	SYNE1	NM_033071	1	146	76	-	152655143	152655408
299884941	chr6	152655320	152655491	152655347	152655462	SYNE1	NM_182961	2	146	77	-	152655143	152655408
300332825	chr6	152660276	152660421	152660304	152660398	SYNE1	NM_033071	1	146	74	-	152660376	152660501

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300332825	chr6	152660276	152660421	152660304	152660398	SYNE1	NM_182961	2	146	75	-	152660376	152660501
300453352	chr6	152668141	152668297	152668164	152668278	SYNE1	NM_033071	1	146	72	-	152668194	152668370
300453352	chr6	152668141	152668297	152668164	152668278	SYNE1	NM_182961	2	146	73	-	152668194	152668370
299995896	chr6	152671720	152671853	152671746	152671829	SYNE1	NM_033071	1	146	71	-	152671753	152671905
299995896	chr6	152671720	152671853	152671746	152671829	SYNE1	NM_182961	2	146	71	-	152671753	152671905
301072386	chr6	152673343	152673515	152673366	152673488	SYNE1	NM_033071	1	146	70	-	152673162	152673488
301072386	chr6	152673343	152673515	152673366	152673488	SYNE1	NM_182961	2	146	70	-	152673162	152673488
300825118	chr6	152674797	152674935	152674818	152674907	SYNE1	NM_033071	1	146	68	-	152674724	152674879
300825118	chr6	152674797	152674935	152674818	152674907	SYNE1	NM_182961	2	146	68	-	152674724	152674879
302169660	chr6	152679381	152679532	152679407	152679508	SYNE1	NM_033071	1	146	66	-	152679508	152679672
302169660	chr6	152679381	152679532	152679407	152679508	SYNE1	NM_182961	2	146	66	-	152679508	152679672
300328794	chr6	152680459	152680633	152680483	152680606	SYNE1	NM_033071	1	146	65	-	152680450	152680593
300328794	chr6	152680459	152680633	152680483	152680606	SYNE1	NM_182961	2	146	65	-	152680450	152680593
304383326	chr6	152686048	152686185	152686071	152686157	SYNE1	NM_033071	1	146	63	-	152685982	152686154
304383326	chr6	152686048	152686185	152686071	152686157	SYNE1	NM_182961	2	146	63	-	152685982	152686154
304731908	chr6	152690195	152690345	152690218	152690323	SYNE1	NM_033071	1	146	61	-	152690107	152690262
304731908	chr6	152690195	152690345	152690218	152690323	SYNE1	NM_182961	2	146	61	-	152690107	152690262
301682789	chr6	152694231	152694355	152694253	152694327	SYNE1	NM_033071	1	146	59	-	152694172	152694354
301682789	chr6	152694231	152694355	152694253	152694327	SYNE1	NM_182961	2	146	59	-	152694172	152694354
302023451	chr6	152697890	152698054	152697918	152698029	SYNE1	NM_033071	1	146	57	-	152697911	152698047
302023451	chr6	152697890	152698054	152697918	152698029	SYNE1	NM_182961	2	146	57	-	152697911	152698047
304671880	chr6	152702303	152702443	152702325	152702423	SYNE1	NM_033071	1	146	56	-	152702141	152702497
304671880	chr6	152702303	152702443	152702325	152702423	SYNE1	NM_182961	2	146	56	-	152702141	152702497
304590642	chr6	152708106	152708277	152708129	152708253	SYNE1	NM_033071	1	146	54	-	152708207	152708516
304590642	chr6	152708106	152708277	152708129	152708253	SYNE1	NM_182961	2	146	54	-	152708207	152708516
305958208	chr6	152711337	152711493	152711359	152711467	SYNE1	NM_033071	1	146	53	-	152711415	152711587
305958208	chr6	152711337	152711493	152711359	152711467	SYNE1	NM_182961	2	146	53	-	152711415	152711587
300497277	chr6	152712559	152712705	152712580	152712679	SYNE1	NM_033071	1	146	52	-	152712412	152712703
300497277	chr6	152712559	152712705	152712580	152712679	SYNE1	NM_182961	2	146	52	-	152712412	152712703
305262984	chr6	152717847	152717991	152717875	152717963	SYNE1	NM_033071	1	146	50	-	152717910	152718115
305262984	chr6	152717847	152717991	152717875	152717963	SYNE1	NM_182961	2	146	50	-	152717910	152718115
303775477	chr6	152719765	152719931	152719790	152719902	SYNE1	NM_033071	1	146	49	-	152719754	152719866
303775477	chr6	152719765	152719931	152719790	152719902	SYNE1	NM_182961	2	146	49	-	152719754	152719866
305778514	chr6	152722293	152722427	152722316	152722402	SYNE1	NM_033071	1	146	47	-	152722273	152722476
305778514	chr6	152722293	152722427	152722316	152722402	SYNE1	NM_182961	2	146	47	-	152722273	152722476
302386216	chr6	152728181	152728355	152728203	152728332	SYNE1	NM_033071	1	146	45	-	152728149	152728331
302386216	chr6	152728181	152728355	152728203	152728332	SYNE1	NM_182961	2	146	45	-	152728149	152728331
305934920	chr6	152730645	152730772	152730674	152730746	SYNE1	NM_033071	1	146	43	-	152730694	152730844
305934920	chr6	152730645	152730772	152730674	152730746	SYNE1	NM_182961	2	146	43	-	152730694	152730844
302647920	chr6	152734517	152734645	152734538	152734618	SYNE1	NM_033071	1	146	42	-	152734487	152734666
302647920	chr6	152734517	152734645	152734538	152734618	SYNE1	NM_182961	2	146	42	-	152734487	152734666

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305288088	chr6	152737724	152737848	152737745	152737821	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305288088	chr6	152737724	152737848	152737745	152737821	SYNE1	NM_182961	2	146	41	-	152737522	152738150
304003029	chr6	152740691	152740857	152740716	152740829	SYNE1	NM_033071	1	146	40	-	152740704	152740857
304003029	chr6	152740691	152740857	152740716	152740829	SYNE1	NM_182961	2	146	40	-	152740704	152740857
301393443	chr6	152746592	152746721	152746617	152746694	SYNE1	NM_033071	1	146	39	-	152746516	152746682
301393443	chr6	152746592	152746721	152746617	152746694	SYNE1	NM_182961	2	146	39	-	152746516	152746682
302704072	chr6	152751257	152751398	152751286	152751370	SYNE1	NM_033071	1	146	36	-	152751247	152751345
302704072	chr6	152751257	152751398	152751286	152751370	SYNE1	NM_182961	2	146	36	-	152751247	152751345
303998678	chr6	152754833	152754964	152754853	152754941	SYNE1	NM_033071	1	146	34	-	152754930	152755080
303998678	chr6	152754833	152754964	152754853	152754941	SYNE1	NM_182961	2	146	34	-	152754930	152755080
302780121	chr6	152757163	152757305	152757185	152757279	SYNE1	NM_033071	1	146	33	-	152757076	152757236
302780121	chr6	152757163	152757305	152757185	152757279	SYNE1	NM_182961	2	146	33	-	152757076	152757236
302005814	chr6	152763282	152763448	152763299	152763420	SYNE1	NM_033071	1	146	31	-	152763210	152763380
302005814	chr6	152763282	152763448	152763299	152763420	SYNE1	NM_182961	2	146	31	-	152763210	152763380
301411748	chr6	152768628	152768790	152768653	152768762	SYNE1	NM_033071	1	146	29	-	152768593	152768757
301411748	chr6	152768628	152768790	152768653	152768762	SYNE1	NM_182961	2	146	29	-	152768593	152768757
300645540	chr6	152771759	152771928	152771783	152771904	SYNE1	NM_033071	1	146	27	-	152771760	152771968
300645540	chr6	152771759	152771928	152771783	152771904	SYNE1	NM_182961	2	146	27	-	152771760	152771968
300521072	chr6	152774598	152774750	152774625	152774728	SYNE1	NM_033071	1	146	25	-	152774721	152774855
300521072	chr6	152774598	152774750	152774625	152774728	SYNE1	NM_182961	2	146	25	-	152774721	152774855
302571677	chr6	152776957	152777131	152776980	152777105	SYNE1	NM_033071	1	146	23	-	152777021	152777179
302571677	chr6	152776957	152777131	152776980	152777105	SYNE1	NM_182961	2	146	23	-	152777021	152777179
302814351	chr6	152779983	152780112	152780009	152780084	SYNE1	NM_033071	1	146	22	-	152779892	152780065
302814351	chr6	152779983	152780112	152780009	152780084	SYNE1	NM_182961	2	146	22	-	152779892	152780065
305252685	chr6	152783935	152784061	152783957	152784039	SYNE1	NM_033071	1	146	20	-	152783873	152784025
305252685	chr6	152783935	152784061	152783957	152784039	SYNE1	NM_182961	2	146	20	-	152783873	152784025
299668735	chr6	152786313	152786487	152786333	152786464	SYNE1	NM_033071	1	146	18	-	152786393	152786595
299668735	chr6	152786313	152786487	152786333	152786464	SYNE1	NM_182961	2	146	18	-	152786393	152786595
302894553	chr6	152792676	152792844	152792700	152792818	SYNE1	NM_033071	1	146	16	-	152792732	152792900
302894553	chr6	152792676	152792844	152792700	152792818	SYNE1	NM_182961	2	146	16	-	152792732	152792900
302690987	chr6	152804136	152804281	152804157	152804261	SYNE1	NM_033071	1	146	14	-	152804220	152804384
302690987	chr6	152804136	152804281	152804157	152804261	SYNE1	NM_182961	2	146	14	-	152804220	152804384
300029390	chr6	152809418	152809582	152809450	152809558	SYNE1	NM_033071	1	146	12	-	152809531	152809638
300029390	chr6	152809418	152809582	152809450	152809558	SYNE1	NM_182961	2	146	12	-	152809531	152809638
305421301	chr6	152826227	152826391	152826249	152826369	SYNE1	NM_033071	1	146	9	-	152826336	152826532
305421301	chr6	152826227	152826391	152826249	152826369	SYNE1	NM_182961	2	146	9	-	152826336	152826532
300593355	chr6	152831361	152831530	152831386	152831507	SYNE1	NM_033071	1	146	8	-	152831328	152831506
300593355	chr6	152831361	152831530	152831386	152831507	SYNE1	NM_182961	2	146	8	-	152831328	152831506
301083808	chr6	152832698	152832836	152832721	152832808	SYNE1	NM_033071	1	146	6	-	152832706	152832726
305916191	chr6	152860978	152861132	152861004	152861104	SYNE1	NM_033071	1	146	3	-	152861095	152861156
305916191	chr6	152860978	152861132	152861004	152861104	SYNE1	NM_182961	2	146	4	-	152861095	152861156

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270255086	chr6	160412224	160412390	160412252	160412363	IGF2R	NM_000876	1	48	2	+	160412216	160412355
271927356	chr6	160445483	160445643	160445509	160445617	IGF2R	NM_000876	1	48	5	+	160445604	160445736
271072795	chr6	160450555	160450727	160450579	160450706	IGF2R	NM_000876	1	48	7	+	160450582	160450687
270758012	chr6	160454021	160454167	160454049	160454143	IGF2R	NM_000876	1	48	9	+	160453974	160454139
270343911	chr6	160464055	160464226	160464077	160464205	IGF2R	NM_000876	1	48	12	+	160464180	160464320
271990833	chr6	160466671	160466833	160466693	160466812	IGF2R	NM_000876	1	48	14	+	160466777	160466914
271511836	chr6	160467638	160467771	160467658	160467743	IGF2R	NM_000876	1	48	15	+	160467530	160467677
272423994	chr6	160468810	160468982	160468831	160468960	IGF2R	NM_000876	1	48	17	+	160468824	160468939
271153651	chr6	160471585	160471749	160471608	160471727	IGF2R	NM_000876	1	48	19	+	160471505	160471684
271564168	chr6	160479907	160480073	160479931	160480050	IGF2R	NM_000876	1	48	22	+	160479938	160480130
271108652	chr6	160482443	160482593	160482464	160482571	IGF2R	NM_000876	1	48	24	+	160482535	160482678
271412312	chr6	160483528	160483670	160483550	160483652	IGF2R	NM_000876	1	48	26	+	160483564	160483651
271633165	chr6	160485392	160485544	160485413	160485520	IGF2R	NM_000876	1	48	28	+	160485433	160485563
269840573	chr6	160489227	160489401	160489256	160489380	IGF2R	NM_000876	1	48	30	+	160489281	160489417
270417167	chr6	160492920	160493094	160492944	160493075	IGF2R	NM_000876	1	48	32	+	160492942	160493068
270563727	chr6	160494330	160494464	160494350	160494442	IGF2R	NM_000876	1	48	34	+	160494245	160494501
270868760	chr6	160496825	160496994	160496851	160496972	IGF2R	NM_000876	1	48	36	+	160496879	160497028
270076341	chr6	160500532	160500706	160500556	160500687	IGF2R	NM_000876	1	48	38	+	160500612	160500819
270416751	chr6	160501203	160501376	160501224	160501354	IGF2R	NM_000876	1	48	39	+	160501161	160501307
270685641	chr6	160506124	160506292	160506144	160506268	IGF2R	NM_000876	1	48	41	+	160506027	160506163
270811617	chr6	160510222	160510347	160510243	160510322	IGF2R	NM_000876	1	48	43	+	160510139	160510285
272682572	chr6	160517508	160517682	160517531	160517658	IGF2R	NM_000876	1	48	45	+	160517471	160517657
272071222	chr6	160525676	160525841	160525696	160525821	IGF2R	NM_000876	1	48	48	+	160525706	160527583
240460973	chr6	166826196	166826366	166826215	166826348	RPS6KA2	NM_001006932	1	22	22	-	166822854	166826375
240460973	chr6	166826196	166826366	166826215	166826348	RPS6KA2	NM_021135	2	21	21	-	166822854	166826375
238830974	chr6	166831638	166831810	166831660	166831791	RPS6KA2	NM_001006932	1	22	20	-	166831713	166831830
238830974	chr6	166831638	166831810	166831660	166831791	RPS6KA2	NM_021135	2	21	19	-	166831713	166831830
237976541	chr6	166836765	166836921	166836786	166836899	RPS6KA2	NM_001006932	1	22	18	-	166836744	166836905
237976541	chr6	166836765	166836921	166836786	166836899	RPS6KA2	NM_021135	2	21	17	-	166836744	166836905
241979902	chr6	166844057	166844191	166844080	166844169	RPS6KA2	NM_001006932	1	22	17	-	166843941	166844099
241979902	chr6	166844057	166844191	166844080	166844169	RPS6KA2	NM_021135	2	21	16	-	166843941	166844099
238012575	chr6	166864466	166864620	166864489	166864599	RPS6KA2	NM_001006932	1	22	14	-	166864591	166864721
238012575	chr6	166864466	166864620	166864489	166864599	RPS6KA2	NM_021135	2	21	13	-	166864591	166864721
261793303	chr6	166902195	166902358	166902219	166902338	RPS6KA2	NM_001006932	1	22	11	-	166902321	166902409
261793303	chr6	166902195	166902358	166902219	166902338	RPS6KA2	NM_021135	2	21	10	-	166902321	166902409
260595572	chr6	166912035	166912201	166912052	166912183	RPS6KA2	NM_001006932	1	22	9	-	166911996	166912138
260595572	chr6	166912035	166912201	166912052	166912183	RPS6KA2	NM_021135	2	21	8	-	166911996	166912138
241419544	chr6	166921631	166921798	166921651	166921777	RPS6KA2	NM_001006932	1	22	6	-	166921691	166921770
241419544	chr6	166921631	166921798	166921651	166921777	RPS6KA2	NM_021135	2	21	5	-	166921691	166921770
237834866	chr6	166952212	166952366	166952234	166952346	RPS6KA2	NM_001006932	1	22	3	-	166952156	166952272
237834866	chr6	166952212	166952366	166952234	166952346	RPS6KA2	NM_021135	2	21	2	-	166952156	166952272

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225214807	chr7	2946211	2946381	2946230	2946361	CARD11	NM_032415	1	25	25	-	2945710	2946476
225184395	chr7	2951751	2951916	2951771	2951892	CARD11	NM_032415	1	25	23	-	2951806	2951930
223388896	chr7	2954853	2955026	2954870	2955006	CARD11	NM_032415	1	25	21	-	2954871	2955006
224125467	chr7	2958954	2959126	2958977	2959106	CARD11	NM_032415	1	25	18	-	2959006	2959246
223242236	chr7	2962703	2962838	2962725	2962819	CARD11	NM_032415	1	25	16	-	2962766	2962967
223067622	chr7	2963865	2964037	2963889	2964018	CARD11	NM_032415	1	25	15	-	2963867	2963999
222444647	chr7	2969677	2969833	2969694	2969813	CARD11	NM_032415	1	25	12	-	2969626	2969708
225191021	chr7	2976562	2976731	2976580	2976710	CARD11	NM_032415	1	25	9	-	2976671	2976868
222456063	chr7	2978228	2978382	2978247	2978363	CARD11	NM_032415	1	25	7	-	2978313	2978465
223910120	chr7	2979495	2979627	2979521	2979603	CARD11	NM_032415	1	25	6	-	2979383	2979562
222305856	chr7	2984113	2984237	2984133	2984216	CARD11	NM_032415	1	25	5	-	2983846	2984171
222979401	chr7	2987302	2987467	2987325	2987439	CARD11	NM_032415	1	25	3	-	2987209	2987421
240533768	chr7	6026545	6026700	6026573	6026678	PMS2	NM_000535	1	15	11	-	6026390	6027251
240533768	chr7	6026545	6026700	6026573	6026678	PMS2	NR_003085	2	15	11	-	6026390	6027251
240508899	chr7	6026908	6027041	6026925	6027016	PMS2	NM_000535	1	15	11	-	6026390	6027251
240508899	chr7	6026908	6027041	6026925	6027016	PMS2	NR_003085	2	15	11	-	6026390	6027251
236121503	chr7	6029394	6029523	6029422	6029496	PMS2	NM_000535	1	15	10	-	6029431	6029586
236121503	chr7	6029394	6029523	6029422	6029496	PMS2	NR_003085	2	15	10	-	6029431	6029586
235343819	chr7	6036923	6037052	6036949	6037027	PMS2	NM_000535	1	15	7	-	6036957	6037054
235343819	chr7	6036923	6037052	6036949	6037027	PMS2	NR_003085	2	15	7	-	6036957	6037054
235525634	chr7	6042021	6042148	6042050	6042127	PMS2	NM_000535	1	15	5	-	6042084	6042267
235525634	chr7	6042021	6042148	6042050	6042127	PMS2	NR_003085	2	15	5	-	6042084	6042267
237920365	chr7	6043515	6043684	6043540	6043656	PMS2	NM_000535	1	15	3	-	6043603	6043689
237920365	chr7	6043515	6043684	6043540	6043656	PMS2	NR_003085	2	15	3	-	6043603	6043689
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163151	5	9	9	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163150	4	10	10	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163149	3	12	12	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163148	2	13	13	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163147	1	12	12	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_004956	7	14	14	-	13930856	13935712
232322908	chr7	13935581	13935746	13935602	13935719	ETV1	NM_001163152	6	9	9	-	13930856	13935712
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163151	5	9	7	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163150	4	10	8	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163149	3	12	10	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163148	2	13	11	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163147	1	12	10	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_004956	7	14	12	-	13946055	13946224
227945219	chr7	13946163	13946337	13946183	13946310	ETV1	NM_001163152	6	9	7	-	13946055	13946224
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163151	5	9	4	-	13971127	13971374
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163150	4	10	5	-	13971127	13971374
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163149	3	12	7	-	13971127	13971374

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163148	2	13	8	-	13971127	13971374
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163147	1	12	8	-	13971127	13971374
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_004956	7	14	9	-	13971127	13971374
230184933	chr7	13971201	13971357	13971223	13971333	ETV1	NM_001163152	6	9	4	-	13971127	13971374
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163151	5	9	2	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163150	4	10	3	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163149	3	12	5	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163148	2	13	6	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163147	1	12	6	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_004956	7	14	7	-	13978742	13978871
231656746	chr7	13978715	13978839	13978738	13978817	ETV1	NM_001163152	6	9	3	-	13978742	13978871
229050467	chr7	14025620	14025776	14025648	14025751	ETV1	NM_001163151	5	9	1	-	14025741	14026139
229050467	chr7	14025620	14025776	14025648	14025751	ETV1	NM_001163150	4	10	1	-	14025741	14026139
229050467	chr7	14025620	14025776	14025648	14025751	ETV1	NM_001163152	6	9	1	-	14025741	14026139
229317323	chr7	14028583	14028707	14028602	14028684	ETV1	NM_001163149	3	12	2	-	14028633	14028764
229317323	chr7	14028583	14028707	14028602	14028684	ETV1	NM_001163148	2	13	3	-	14028633	14028764
229317323	chr7	14028583	14028707	14028602	14028684	ETV1	NM_001163147	1	12	2	-	14028633	14028764
229317323	chr7	14028583	14028707	14028602	14028684	ETV1	NM_004956	7	14	3	-	14028633	14028764
227681814	chr7	50444294	50444438	50444314	50444410	IKZF1	NM_006060	13	8	4	+	50444231	50444491
227681814	chr7	50444294	50444438	50444314	50444410	IKZF1	NM_001220771	7	5	4	+	50444231	50444491
227681814	chr7	50444294	50444438	50444314	50444410	IKZF1	NM_001220768	4	6	4	+	50444231	50444491
227681814	chr7	50444294	50444438	50444314	50444410	IKZF1	NM_001220765	1	7	4	+	50444231	50444491
227462486	chr7	50454968	50455141	50454992	50455119	IKZF1	NM_006060	13	8	6	+	50455043	50455168
227462486	chr7	50454968	50455141	50454992	50455119	IKZF1	NM_001220774	10	5	3	+	50455043	50455168
227462486	chr7	50454968	50455141	50454992	50455119	IKZF1	NM_001220773	9	5	3	+	50455043	50455168
227462486	chr7	50454968	50455141	50454992	50455119	IKZF1	NM_001220767	3	7	5	+	50455043	50455168
227462486	chr7	50454968	50455141	50454992	50455119	IKZF1	NM_001220766	2	7	5	+	50455043	50455168
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_006060	13	8	8	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
228274503	chr7	50467591	50467722	50467611	50467702	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_006060	13	8	8	+	50467616	50472798

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
228285053	chr7	50467996	50468157	50468020	50468133	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
229910389	chr7	55209899	55210071	55209921	55210045	EGFR	NM_005228	1	28	2	+	55209979	55210130
229910389	chr7	55209899	55210071	55209921	55210045	EGFR	NM_201284	4	16	2	+	55209979	55210130
229910389	chr7	55209899	55210071	55209921	55210045	EGFR	NM_201283	3	10	2	+	55209979	55210130
229910389	chr7	55209899	55210071	55209921	55210045	EGFR	NM_201282	2	16	2	+	55209979	55210130
227801665	chr7	55214232	55214398	55214259	55214376	EGFR	NM_005228	1	28	4	+	55214299	55214433
227801665	chr7	55214232	55214398	55214259	55214376	EGFR	NM_201284	4	16	4	+	55214299	55214433
227801665	chr7	55214232	55214398	55214259	55214376	EGFR	NM_201283	3	10	4	+	55214299	55214433
227801665	chr7	55214232	55214398	55214259	55214376	EGFR	NM_201282	2	16	4	+	55214299	55214433
229055506	chr7	55220293	55220457	55220312	55220436	EGFR	NM_005228	1	28	6	+	55220239	55220357
229055506	chr7	55220293	55220457	55220312	55220436	EGFR	NM_201284	4	16	6	+	55220239	55220357
229055506	chr7	55220293	55220457	55220312	55220436	EGFR	NM_201283	3	10	6	+	55220239	55220357
229055506	chr7	55220293	55220457	55220312	55220436	EGFR	NM_201282	2	16	6	+	55220239	55220357
230397881	chr7	55223573	55223717	55223597	55223696	EGFR	NM_005228	1	28	8	+	55223523	55223639
230397881	chr7	55223573	55223717	55223597	55223696	EGFR	NM_201284	4	16	8	+	55223523	55223639
230397881	chr7	55223573	55223717	55223597	55223696	EGFR	NM_201283	3	10	8	+	55223523	55223639
230397881	chr7	55223573	55223717	55223597	55223696	EGFR	NM_201282	2	16	8	+	55223523	55223639
230175199	chr7	55224432	55224605	55224456	55224577	EGFR	NM_005228	1	28	10	+	55224452	55224525
230175199	chr7	55224432	55224605	55224456	55224577	EGFR	NM_201284	4	16	10	+	55224452	55224525
230175199	chr7	55224432	55224605	55224456	55224577	EGFR	NM_201282	2	16	10	+	55224452	55224525
230175199	chr7	55224432	55224605	55224456	55224577	EGFR	NM_201283	3	10	10	+	55224452	55224644
230195609	chr7	55227923	55228080	55227951	55228057	EGFR	NM_005228	1	28	12	+	55227832	55228031
230195609	chr7	55227923	55228080	55227951	55228057	EGFR	NM_201284	4	16	12	+	55227832	55228031
230195609	chr7	55227923	55228080	55227951	55228057	EGFR	NM_201282	2	16	12	+	55227832	55228031
228630698	chr7	55232925	55233080	55232954	55233059	EGFR	NM_005228	1	28	15	+	55232973	55233130
228630698	chr7	55232925	55233080	55232954	55233059	EGFR	NM_201284	4	16	15	+	55232973	55233130
228630698	chr7	55232925	55233080	55232954	55233059	EGFR	NM_201282	2	16	15	+	55232973	55233130
230632980	chr7	55237990	55238160	55238012	55238139	EGFR	NM_201284	4	16	16	+	55238000	55238738
227722022	chr7	55240745	55240902	55240764	55240882	EGFR	NM_005228	1	28	17	+	55240676	55240817
232978808	chr7	55248956	55249123	55248975	55249100	EGFR	NM_005228	1	28	20	+	55248986	55249171

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231616816	chr7	55260405	55260574	55260432	55260548	EGFR	NM_005228	1	28	22	+	55260459	55260534
230481741	chr7	55268797	55268962	55268818	55268939	EGFR	NM_005228	1	28	25	+	55268881	55269048
231198336	chr7	55272860	55273025	55272883	55273000	EGFR	NM_005228	1	28	28	+	55272949	55275031
241375102	chr7	66453306	66453470	66453326	66453450	SBDS	NM_016038	1	5	5	-	66452690	66453486
261484241	chr7	66458197	66458326	66458220	66458300	SBDS	NM_016038	1	5	3	-	66458204	66458404
242591678	chr7	66460159	66460327	66460177	66460306	SBDS	NM_016038	1	5	1	-	66460277	66460588
224092577	chr7	91603025	91603153	91603047	91603125	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224092577	chr7	91603025	91603153	91603047	91603125	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224642543	chr7	91609612	91609739	91609636	91609711	AKAP9	NM_005751	1	50	3	+	91609603	91609647
224642543	chr7	91609612	91609739	91609636	91609711	AKAP9	NM_147185	2	50	3	+	91609603	91609647
223433634	chr7	91622240	91622405	91622260	91622377	AKAP9	NM_005751	1	50	5	+	91622199	91622369
223433634	chr7	91622240	91622405	91622260	91622377	AKAP9	NM_147185	2	50	5	+	91622199	91622369
224412167	chr7	91624855	91625025	91624882	91625001	AKAP9	NM_005751	1	50	7	+	91624917	91625114
224412167	chr7	91624855	91625025	91624882	91625001	AKAP9	NM_147185	2	50	7	+	91624917	91625114
222725328	chr7	91630597	91630761	91630619	91630733	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222725328	chr7	91630597	91630761	91630619	91630733	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224476901	chr7	91630908	91631073	91630935	91631045	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224476901	chr7	91630908	91631073	91630935	91631045	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224470258	chr7	91631333	91631467	91631361	91631439	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224470258	chr7	91631333	91631467	91631361	91631439	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224481857	chr7	91631721	91631861	91631749	91631834	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224481857	chr7	91631721	91631861	91631749	91631834	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222660555	chr7	91632259	91632432	91632287	91632403	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222660555	chr7	91632259	91632432	91632287	91632403	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222262253	chr7	91641741	91641903	91641769	91641877	AKAP9	NM_005751	1	50	9	+	91641743	91641956
222262253	chr7	91641741	91641903	91641769	91641877	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222977422	chr7	91645345	91645515	91645366	91645487	AKAP9	NM_005751	1	50	11	+	91645443	91645581
222977422	chr7	91645345	91645515	91645366	91645487	AKAP9	NM_147185	2	50	11	+	91645443	91645581
223294348	chr7	91651635	91651760	91651662	91651731	AKAP9	NM_005751	1	50	13	+	91651552	91651666
223294348	chr7	91651635	91651760	91651662	91651731	AKAP9	NM_147185	2	50	13	+	91651552	91651666
222488576	chr7	91660820	91660973	91660848	91660945	AKAP9	NM_005751	1	50	16	+	91660826	91660918
222488576	chr7	91660820	91660973	91660848	91660945	AKAP9	NM_147185	2	50	16	+	91660826	91660918
222554659	chr7	91667896	91668048	91667924	91668021	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222554659	chr7	91667896	91668048	91667924	91668021	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222183051	chr7	91670107	91670279	91670130	91670255	AKAP9	NM_005751	1	50	18	+	91669988	91670212
222183051	chr7	91670107	91670279	91670130	91670255	AKAP9	NM_147185	2	50	18	+	91669988	91670212
223556064	chr7	91671996	91672157	91672024	91672127	AKAP9	NM_005751	1	50	20	+	91671982	91672085
223556064	chr7	91671996	91672157	91672024	91672127	AKAP9	NM_147185	2	50	20	+	91671982	91672085
222670784	chr7	91682048	91682202	91682076	91682175	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222670784	chr7	91682048	91682202	91682076	91682175	AKAP9	NM_147185	2	50	22	+	91682040	91682272
222905503	chr7	91690646	91690815	91690668	91690792	AKAP9	NM_005751	1	50	23	+	91690574	91690736

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222905503	chr7	91690646	91690815	91690668	91690792	AKAP9	NM_147185	2	50	23	+	91690574	91690736
224492841	chr7	91694592	91694739	91694618	91694713	AKAP9	NM_005751	1	50	25	+	91694545	91694777
224492841	chr7	91694592	91694739	91694618	91694713	AKAP9	NM_147185	2	50	25	+	91694545	91694777
222446210	chr7	91699326	91699478	91699354	91699450	AKAP9	NM_005751	1	50	27	+	91699344	91699520
222446210	chr7	91699326	91699478	91699354	91699450	AKAP9	NM_147185	2	50	27	+	91699344	91699496
224425364	chr7	91706917	91707053	91706947	91707028	AKAP9	NM_005751	1	50	30	+	91707010	91707189
224425364	chr7	91706917	91707053	91706947	91707028	AKAP9	NM_147185	2	50	30	+	91707010	91707189
223484756	chr7	91708411	91708569	91708437	91708542	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223484756	chr7	91708411	91708569	91708437	91708542	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223504149	chr7	91708816	91708959	91708841	91708932	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223504149	chr7	91708816	91708959	91708841	91708932	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223524609	chr7	91709135	91709302	91709163	91709274	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223524609	chr7	91709135	91709302	91709163	91709274	AKAP9	NM_147185	2	50	31	+	91708393	91709466
222337017	chr7	91711911	91712084	91711933	91712053	AKAP9	NM_005751	1	50	32	+	91711836	91711976
222337017	chr7	91711911	91712084	91711933	91712053	AKAP9	NM_147185	2	50	32	+	91711836	91711976
224066656	chr7	91712695	91712868	91712723	91712840	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224066656	chr7	91712695	91712868	91712723	91712840	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224321448	chr7	91713978	91714152	91714006	91714124	AKAP9	NM_005751	1	50	34	+	91713954	91714017
224321448	chr7	91713978	91714152	91714006	91714124	AKAP9	NM_147185	2	50	34	+	91713954	91714017
222353493	chr7	91714847	91715019	91714872	91714992	AKAP9	NM_005751	1	50	36	+	91714809	91715000
222353493	chr7	91714847	91715019	91714872	91714992	AKAP9	NM_147185	2	50	36	+	91714809	91715000
224695921	chr7	91718647	91718773	91718674	91718745	AKAP9	NM_005751	1	50	38	+	91718699	91718843
224695921	chr7	91718647	91718773	91718674	91718745	AKAP9	NM_147185	2	50	38	+	91718699	91718843
222472100	chr7	91724288	91724456	91724313	91724435	AKAP9	NM_005751	1	50	40	+	91724337	91724487
222472100	chr7	91724288	91724456	91724313	91724435	AKAP9	NM_147185	2	50	40	+	91724337	91724487
224248945	chr7	91726187	91726346	91726213	91726322	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224248945	chr7	91726187	91726346	91726213	91726322	AKAP9	NM_147185	2	50	41	+	91726003	91726671
222175536	chr7	91726576	91726721	91726599	91726700	AKAP9	NM_005751	1	50	41	+	91726003	91726671
222175536	chr7	91726576	91726721	91726599	91726700	AKAP9	NM_147185	2	50	41	+	91726003	91726671
223799394	chr7	91727365	91727525	91727390	91727507	AKAP9	NM_005751	1	50	43	+	91727423	91727528
223799394	chr7	91727365	91727525	91727390	91727507	AKAP9	NM_147185	2	50	43	+	91727423	91727528
223247682	chr7	91730237	91730401	91730265	91730375	AKAP9	NM_005751	1	50	45	+	91730170	91730370
223247682	chr7	91730237	91730401	91730265	91730375	AKAP9	NM_147185	2	50	45	+	91730170	91730370
223471334	chr7	91734954	91735094	91734981	91735066	AKAP9	NM_005751	1	50	47	+	91734992	91735077
223471334	chr7	91734954	91735094	91734981	91735066	AKAP9	NM_147185	2	50	47	+	91734992	91735077
222701931	chr7	91737816	91737975	91737838	91737951	AKAP9	NM_005751	1	50	49	+	91737808	91737947
222701931	chr7	91737816	91737975	91737838	91737951	AKAP9	NM_147185	2	50	49	+	91737808	91737947
226056969	chr7	92247269	92247443	92247291	92247416	CDK6	NM_001145306	1	8	7	-	92247386	92247521
226056969	chr7	92247269	92247443	92247291	92247416	CDK6	NM_001259	2	8	7	-	92247386	92247521
226073334	chr7	92300703	92300872	92300730	92300852	CDK6	NM_001145306	1	8	5	-	92300740	92300849
226073334	chr7	92300703	92300872	92300730	92300852	CDK6	NM_001259	2	8	5	-	92300740	92300849

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253674340	chr7	92404028	92404180	92404050	92404154	CDK6	NM_001145306	1	8	3	-	92404010	92404145
253674340	chr7	92404028	92404180	92404050	92404154	CDK6	NM_001259	2	8	3	-	92404010	92404145
294119837	chr7	92730601	92730761	92730627	92730738	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294119837	chr7	92730601	92730761	92730627	92730738	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294124173	chr7	92731036	92731209	92731064	92731181	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294124173	chr7	92731036	92731209	92731064	92731181	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294039509	chr7	92731410	92731584	92731435	92731561	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294039509	chr7	92731410	92731584	92731435	92731561	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294087847	chr7	92731896	92732051	92731924	92732022	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294087847	chr7	92731896	92732051	92731924	92732022	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295052989	chr7	92732301	92732461	92732326	92732434	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295052989	chr7	92732301	92732461	92732326	92732434	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295079833	chr7	92732660	92732834	92732683	92732807	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295079833	chr7	92732660	92732834	92732683	92732807	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295051597	chr7	92733038	92733167	92733060	92733144	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295051597	chr7	92733038	92733167	92733060	92733144	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294135762	chr7	92733364	92733511	92733391	92733483	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294135762	chr7	92733364	92733511	92733391	92733483	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294064195	chr7	92733756	92733924	92733780	92733896	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294064195	chr7	92733756	92733924	92733780	92733896	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294094253	chr7	92734144	92734318	92734172	92734292	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294094253	chr7	92734144	92734318	92734172	92734292	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295057289	chr7	92734459	92734605	92734483	92734577	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295057289	chr7	92734459	92734605	92734483	92734577	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294134941	chr7	92734864	92735037	92734893	92735012	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294134941	chr7	92734864	92735037	92734893	92735012	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294170580	chr7	92735261	92735425	92735287	92735399	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294170580	chr7	92735261	92735425	92735287	92735399	SAMD9	NM_017654	2	3	3	-	92728826	92735418
300631294	chr7	98487944	98488104	98487972	98488077	TRRAP	NM_003496	2	71	4	+	98487958	98488068
300631294	chr7	98487944	98488104	98487972	98488077	TRRAP	NM_001244580	1	72	4	+	98487958	98488068
301519383	chr7	98491478	98491606	98491497	98491579	TRRAP	NM_003496	2	71	6	+	98491421	98491504
301519383	chr7	98491478	98491606	98491497	98491579	TRRAP	NM_001244580	1	72	6	+	98491421	98491504
304596938	chr7	98496989	98497151	98497014	98497123	TRRAP	NM_003496	2	71	9	+	98497045	98497122
304596938	chr7	98496989	98497151	98497014	98497123	TRRAP	NM_001244580	1	72	9	+	98497045	98497122
305447106	chr7	98498245	98498370	98498271	98498342	TRRAP	NM_003496	2	71	11	+	98498247	98498343
305447106	chr7	98498245	98498370	98498271	98498342	TRRAP	NM_001244580	1	72	11	+	98498247	98498343
302895148	chr7	98506320	98506491	98506343	98506471	TRRAP	NM_003496	2	71	14	+	98506351	98506585
302895148	chr7	98506320	98506491	98506343	98506471	TRRAP	NM_001244580	1	72	14	+	98506351	98506585
301108315	chr7	98507766	98507930	98507784	98507906	TRRAP	NM_003496	2	71	15	+	98507679	98508042
301108315	chr7	98507766	98507930	98507784	98507906	TRRAP	NM_001244580	1	72	15	+	98507679	98508042
301961251	chr7	98508129	98508303	98508152	98508275	TRRAP	NM_003496	2	71	16	+	98508133	98508230

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
301961251	chr7	98508129	98508303	98508152	98508275	TRRAP	NM_001244580	1	72	16	+	98508133	98508230
302195640	chr7	98509603	98509774	98509630	98509752	TRRAP	NM_003496	2	71	18	+	98509645	98509836
302195640	chr7	98509603	98509774	98509630	98509752	TRRAP	NM_001244580	1	72	18	+	98509645	98509836
305212205	chr7	98514965	98515093	98514988	98515072	TRRAP	NM_003496	2	71	20	+	98515046	98515302
305212205	chr7	98514965	98515093	98514988	98515072	TRRAP	NM_001244580	1	72	20	+	98515046	98515302
303557509	chr7	98519438	98519601	98519458	98519578	TRRAP	NM_003496	2	71	21	+	98519376	98519576
303557509	chr7	98519438	98519601	98519458	98519578	TRRAP	NM_001244580	1	72	21	+	98519376	98519576
305987171	chr7	98524827	98524977	98524847	98524956	TRRAP	NM_003496	2	71	23	+	98524790	98524989
305987171	chr7	98524827	98524977	98524847	98524956	TRRAP	NM_001244580	1	72	23	+	98524790	98524989
302449744	chr7	98528225	98528399	98528250	98528377	TRRAP	NM_003496	2	71	25	+	98528256	98528453
302449744	chr7	98528225	98528399	98528250	98528377	TRRAP	NM_001244580	1	72	25	+	98528256	98528453
300080283	chr7	98529171	98529324	98529192	98529298	TRRAP	NM_003496	2	71	26	+	98529028	98529288
300080283	chr7	98529171	98529324	98529192	98529298	TRRAP	NM_001244580	1	72	26	+	98529028	98529288
303594928	chr7	98533239	98533365	98533263	98533339	TRRAP	NM_003496	2	71	28	+	98533202	98533298
303594928	chr7	98533239	98533365	98533263	98533339	TRRAP	NM_001244580	1	72	28	+	98533202	98533298
301767580	chr7	98535288	98535459	98535314	98535435	TRRAP	NM_003496	2	71	30	+	98535273	98535443
301767580	chr7	98535288	98535459	98535314	98535435	TRRAP	NM_001244580	1	72	30	+	98535273	98535443
301994373	chr7	98545735	98545893	98545757	98545866	TRRAP	NM_003496	2	71	32	+	98545844	98545963
301994373	chr7	98545735	98545893	98545757	98545866	TRRAP	NM_001244580	1	72	33	+	98545844	98545963
301467557	chr7	98547063	98547208	98547082	98547187	TRRAP	NM_003496	2	71	34	+	98547040	98547204
301467557	chr7	98547063	98547208	98547082	98547187	TRRAP	NM_001244580	1	72	35	+	98547040	98547204
300787345	chr7	98547662	98547833	98547686	98547812	TRRAP	NM_003496	2	71	36	+	98547687	98547885
300787345	chr7	98547662	98547833	98547686	98547812	TRRAP	NM_001244580	1	72	37	+	98547687	98547885
300998200	chr7	98550747	98550921	98550772	98550902	TRRAP	NM_003496	2	71	38	+	98550790	98551056
300998200	chr7	98550747	98550921	98550772	98550902	TRRAP	NM_001244580	1	72	39	+	98550790	98551056
299830736	chr7	98552702	98552873	98552729	98552852	TRRAP	NM_003496	2	71	39	+	98552721	98552927
299830736	chr7	98552702	98552873	98552729	98552852	TRRAP	NM_001244580	1	72	40	+	98552721	98552927
301173223	chr7	98553881	98554055	98553903	98554033	TRRAP	NM_003496	2	71	41	+	98554022	98554156
301173223	chr7	98553881	98554055	98553903	98554033	TRRAP	NM_001244580	1	72	42	+	98554022	98554156
301173223	chr7	98553881	98554055	98553903	98554033	TRRAP	NM_003496	2	71	40	+	98553769	98553927
301173223	chr7	98553881	98554055	98553903	98554033	TRRAP	NM_001244580	1	72	41	+	98553769	98553927
300637911	chr7	98557063	98557218	98557084	98557194	TRRAP	NM_003496	2	71	43	+	98556967	98557113
300637911	chr7	98557063	98557218	98557084	98557194	TRRAP	NM_001244580	1	72	44	+	98556967	98557113
301194496	chr7	98559989	98560162	98560012	98560141	TRRAP	NM_003496	2	71	45	+	98559925	98560050
301194496	chr7	98559989	98560162	98560012	98560141	TRRAP	NM_001244580	1	72	46	+	98559925	98560050
305304782	chr7	98563410	98563550	98563432	98563530	TRRAP	NM_003496	2	71	47	+	98563319	98563518
305304782	chr7	98563410	98563550	98563432	98563530	TRRAP	NM_001244580	1	72	48	+	98563319	98563518
301700401	chr7	98565183	98565343	98565204	98565321	TRRAP	NM_003496	2	71	49	+	98565108	98565321
301700401	chr7	98565183	98565343	98565204	98565321	TRRAP	NM_001244580	1	72	50	+	98565108	98565321
300615331	chr7	98569504	98569634	98569525	98569608	TRRAP	NM_003496	2	71	51	+	98569422	98569568
300615331	chr7	98569504	98569634	98569525	98569608	TRRAP	NM_001244580	1	72	52	+	98569422	98569568

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
301231155	chr7	98574188	98574353	98574208	98574329	TRRAP	NM_003496	2	71	53	+	98574106	98574393
301231155	chr7	98574188	98574353	98574208	98574329	TRRAP	NM_001244580	1	72	54	+	98574106	98574393
299567575	chr7	98575834	98575982	98575858	98575961	TRRAP	NM_003496	2	71	55	+	98575834	98575946
299567575	chr7	98575834	98575982	98575858	98575961	TRRAP	NM_001244580	1	72	56	+	98575834	98575946
299829519	chr7	98579418	98579591	98579439	98579572	TRRAP	NM_003496	2	71	57	+	98579392	98579583
299829519	chr7	98579418	98579591	98579439	98579572	TRRAP	NM_001244580	1	72	58	+	98579392	98579583
300802274	chr7	98581051	98581223	98581072	98581197	TRRAP	NM_003496	2	71	58	+	98580887	98581082
300802274	chr7	98581051	98581223	98581072	98581197	TRRAP	NM_001244580	1	72	59	+	98580887	98581115
302222337	chr7	98582467	98582641	98582494	98582617	TRRAP	NM_003496	2	71	60	+	98582567	98582667
302222337	chr7	98582467	98582641	98582494	98582617	TRRAP	NM_001244580	1	72	61	+	98582567	98582667
301632637	chr7	98588013	98588157	98588036	98588137	TRRAP	NM_003496	2	71	62	+	98588078	98588242
301632637	chr7	98588013	98588157	98588036	98588137	TRRAP	NM_001244580	1	72	63	+	98588078	98588242
301474962	chr7	98591180	98591352	98591202	98591327	TRRAP	NM_003496	2	71	64	+	98591215	98591360
301474962	chr7	98591180	98591352	98591202	98591327	TRRAP	NM_001244580	1	72	65	+	98591215	98591360
299808646	chr7	98592425	98592558	98592447	98592532	TRRAP	NM_003496	2	71	65	+	98592210	98592471
299808646	chr7	98592425	98592558	98592447	98592532	TRRAP	NM_001244580	1	72	66	+	98592210	98592471
303176134	chr7	98602686	98602860	98602711	98602838	TRRAP	NM_003496	2	71	67	+	98602754	98602971
303176134	chr7	98602686	98602860	98602711	98602838	TRRAP	NM_001244580	1	72	68	+	98602754	98602971
299993106	chr7	98606101	98606274	98606120	98606251	TRRAP	NM_003496	2	71	68	+	98606000	98606184
299993106	chr7	98606101	98606274	98606120	98606251	TRRAP	NM_001244580	1	72	69	+	98606000	98606184
304659463	chr7	98609048	98609181	98609067	98609161	TRRAP	NM_003496	2	71	70	+	98608964	98609158
304659463	chr7	98609048	98609181	98609067	98609161	TRRAP	NM_001244580	1	72	71	+	98608964	98609158
271879916	chr7	100401026	100401193	100401044	100401175	EPHB4	NM_004444	1	17	17	-	100400187	100401212
271417570	chr7	100403092	100403261	100403111	100403242	EPHB4	NM_004444	1	17	15	-	100403123	100403316
270999325	chr7	100404949	100405094	100404970	100405071	EPHB4	NM_004444	1	17	13	-	100404987	100405202
271679741	chr7	100410492	100410642	100410512	100410621	EPHB4	NM_004444	1	17	12	-	100410369	100410616
271062811	chr7	100411520	100411670	100411540	100411648	EPHB4	NM_004444	1	17	9	-	100411541	100411643
271688300	chr7	100416156	100416315	100416176	100416293	EPHB4	NM_004444	1	17	7	-	100416142	100416266
270006533	chr7	100417701	100417863	100417721	100417842	EPHB4	NM_004444	1	17	5	-	100417763	100417918
270689808	chr7	100420081	100420237	100420104	100420218	EPHB4	NM_004444	1	17	4	-	100419893	100420289
269704559	chr7	100421410	100421580	100421427	100421561	EPHB4	NM_004444	1	17	3	-	100421266	100421553
294974068	chr7	106508115	106508279	106508135	106508260	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294976400	chr7	106508513	106508679	106508534	106508654	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
293994032	chr7	106509021	106509174	106509041	106509152	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294011102	chr7	106509428	106509583	106509447	106509562	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294072504	chr7	106509853	106510027	106509875	106510002	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294551632	chr7	106513274	106513411	106513294	106513385	PIK3CG	NM_002649	1	11	4	+	106513158	106513383
294563749	chr7	106522466	106522590	106522499	106522562	PIK3CG	NM_002649	1	11	7	+	106522562	106522652
293859426	chr7	106524491	106524663	106524517	106524640	PIK3CG	NM_002649	1	11	9	+	106524600	106524711
294601567	chr7	106545428	106545582	106545451	106545557	PIK3CG	NM_002649	1	11	11	+	106545554	106547592
234538490	chr7	116339105	116339274	116339127	116339246	MET	NM_001127500	2	21	2	+	116339125	116340338

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234538490	chr7	116339105	116339274	116339127	116339246	MET	NM_000245	1	21	2	+	116339125	116340338
234539541	chr7	116339565	116339720	116339588	116339695	MET	NM_001127500	2	21	2	+	116339125	116340338
234539541	chr7	116339565	116339720	116339588	116339695	MET	NM_000245	1	21	2	+	116339125	116340338
234573363	chr7	116339934	116340078	116339960	116340050	MET	NM_001127500	2	21	2	+	116339125	116340338
234573363	chr7	116339934	116340078	116339960	116340050	MET	NM_000245	1	21	2	+	116339125	116340338
231560176	chr7	116371681	116371831	116371709	116371808	MET	NM_001127500	2	21	3	+	116371722	116371913
231560176	chr7	116371681	116371831	116371709	116371808	MET	NM_000245	1	21	3	+	116371722	116371913
232341031	chr7	116380862	116381022	116380886	116381001	MET	NM_001127500	2	21	5	+	116380906	116381079
232341031	chr7	116380862	116381022	116380886	116381001	MET	NM_000245	1	21	5	+	116380906	116381079
233659281	chr7	116397430	116397602	116397457	116397574	MET	NM_001127500	2	21	7	+	116397491	116397593
233659281	chr7	116397430	116397602	116397457	116397574	MET	NM_000245	1	21	7	+	116397491	116397593
231824265	chr7	116398506	116398646	116398534	116398620	MET	NM_001127500	2	21	9	+	116398513	116398674
231824265	chr7	116398506	116398646	116398534	116398620	MET	NM_000245	1	21	9	+	116398513	116398674
234436793	chr7	116403026	116403157	116403054	116403135	MET	NM_001127500	2	21	11	+	116403104	116403322
234436793	chr7	116403026	116403157	116403054	116403135	MET	NM_000245	1	21	11	+	116403104	116403322
232303549	chr7	116409715	116409874	116409743	116409849	MET	NM_001127500	2	21	12	+	116409699	116409845
232303549	chr7	116409715	116409874	116409743	116409849	MET	NM_000245	1	21	12	+	116409699	116409845
233164486	chr7	116411853	116411978	116411873	116411956	MET	NM_001127500	2	21	14	+	116411903	116412043
233164486	chr7	116411853	116411978	116411873	116411956	MET	NM_000245	1	21	14	+	116411903	116412043
230894755	chr7	116415057	116415228	116415078	116415200	MET	NM_001127500	2	21	15	+	116414935	116415165
230894755	chr7	116415057	116415228	116415078	116415200	MET	NM_000245	1	21	15	+	116414935	116415165
233658487	chr7	116422016	116422181	116422043	116422155	MET	NM_001127500	2	21	18	+	116422042	116422151
233658487	chr7	116422016	116422181	116422043	116422155	MET	NM_000245	1	21	18	+	116422042	116422151
233318723	chr7	116435757	116435899	116435784	116435871	MET	NM_001127500	2	21	20	+	116435709	116435845
233318723	chr7	116435757	116435899	116435784	116435871	MET	NM_000245	1	21	20	+	116435709	116435845
295289765	chr7	124463945	124464119	124463969	124464098	POT1	NR_003103	4	18	18	-	124462440	124464128
295289765	chr7	124463945	124464119	124463969	124464098	POT1	NR_003104	5	20	20	-	124462440	124464128
295289765	chr7	124463945	124464119	124463969	124464098	POT1	NR_003102	3	20	20	-	124462440	124464128
295289765	chr7	124463945	124464119	124463969	124464098	POT1	NM_001042594	1	18	18	-	124462440	124464128
295289765	chr7	124463945	124464119	124463969	124464098	POT1	NM_015450	2	19	19	-	124462440	124464128
294418399	chr7	124469205	124469352	124469233	124469328	POT1	NR_003104	5	20	17	-	124469308	124469396
294418399	chr7	124469205	124469352	124469233	124469328	POT1	NR_003102	3	20	17	-	124469308	124469396
294418399	chr7	124469205	124469352	124469233	124469328	POT1	NM_001042594	1	18	15	-	124469308	124469396
294418399	chr7	124469205	124469352	124469233	124469328	POT1	NM_015450	2	19	16	-	124469308	124469396
293935877	chr7	124481102	124481226	124481130	124481205	POT1	NR_003103	4	18	14	-	124481027	124481232
293935877	chr7	124481102	124481226	124481130	124481205	POT1	NR_003104	5	20	14	-	124481027	124481232
293935877	chr7	124481102	124481226	124481130	124481205	POT1	NR_003102	3	20	15	-	124481027	124481232
293935877	chr7	124481102	124481226	124481130	124481205	POT1	NM_001042594	1	18	13	-	124481027	124481232
293935877	chr7	124481102	124481226	124481130	124481205	POT1	NM_015450	2	19	14	-	124481027	124481232
293833673	chr7	124486924	124487070	124486947	124487043	POT1	NR_003103	4	18	12	-	124486996	124487052
293833673	chr7	124486924	124487070	124486947	124487043	POT1	NR_003104	5	20	12	-	124486996	124487052

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293833673	chr7	124486924	124487070	124486947	124487043	POT1	NR_003102	3	20	13	-	124486996	124487052
293833673	chr7	124486924	124487070	124486947	124487043	POT1	NM_001042594	1	18	11	-	124486996	124487052
293833673	chr7	124486924	124487070	124486947	124487043	POT1	NM_015450	2	19	12	-	124486996	124487052
294632404	chr7	124498992	124499154	124499024	124499131	POT1	NR_003103	4	18	9	-	124499011	124499166
294632404	chr7	124498992	124499154	124499024	124499131	POT1	NR_003104	5	20	9	-	124499011	124499166
294632404	chr7	124498992	124499154	124499024	124499131	POT1	NR_003102	3	20	9	-	124499011	124499166
294632404	chr7	124498992	124499154	124499024	124499131	POT1	NM_001042594	1	18	8	-	124499011	124499166
294632404	chr7	124498992	124499154	124499024	124499131	POT1	NM_015450	2	19	9	-	124499011	124499166
293878958	chr7	124503461	124503627	124503486	124503605	POT1	NR_003103	4	18	8	-	124503404	124503694
293878958	chr7	124503461	124503627	124503486	124503605	POT1	NR_003104	5	20	8	-	124503404	124503694
293878958	chr7	124503461	124503627	124503486	124503605	POT1	NR_003102	3	20	8	-	124503404	124503694
293878958	chr7	124503461	124503627	124503486	124503605	POT1	NM_001042594	1	18	7	-	124503404	124503694
293878958	chr7	124503461	124503627	124503486	124503605	POT1	NM_015450	2	19	8	-	124503404	124503694
294000388	chr7	124511046	124511193	124511074	124511165	POT1	NR_003103	4	18	7	-	124510965	124511095
294000388	chr7	124511046	124511193	124511074	124511165	POT1	NR_003104	5	20	7	-	124510965	124511095
294000388	chr7	124511046	124511193	124511074	124511165	POT1	NR_003102	3	20	7	-	124510965	124511095
294000388	chr7	124511046	124511193	124511074	124511165	POT1	NM_015450	2	19	7	-	124510965	124511095
294445583	chr7	124537159	124537326	124537185	124537298	POT1	NR_003103	4	18	5	-	124537219	124537266
294445583	chr7	124537159	124537326	124537185	124537298	POT1	NR_003104	5	20	5	-	124537219	124537266
294445583	chr7	124537159	124537326	124537185	124537298	POT1	NR_003102	3	20	5	-	124537219	124537266
294445583	chr7	124537159	124537326	124537185	124537298	POT1	NM_001042594	1	18	5	-	124537219	124537266
294445583	chr7	124537159	124537326	124537185	124537298	POT1	NM_015450	2	19	5	-	124537219	124537266
294602226	chr7	126086246	126086413	126086269	126086387	GRM8	NR_028041	3	11	10	-	126086180	126086426
294602226	chr7	126086246	126086413	126086269	126086387	GRM8	NM_000845	1	10	9	-	126086180	126086426
294602226	chr7	126086246	126086413	126086269	126086387	GRM8	NM_001127323	2	11	10	-	126086125	126086426
293776398	chr7	126173110	126173281	126173133	126173256	GRM8	NR_028041	3	11	9	-	126173006	126173941
293776398	chr7	126173110	126173281	126173133	126173256	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293776398	chr7	126173110	126173281	126173133	126173256	GRM8	NM_000845	1	10	8	-	126173006	126173941
293813543	chr7	126173590	126173731	126173612	126173710	GRM8	NR_028041	3	11	9	-	126173006	126173941
293813543	chr7	126173590	126173731	126173612	126173710	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293813543	chr7	126173590	126173731	126173612	126173710	GRM8	NM_000845	1	10	8	-	126173006	126173941
294810772	chr7	126249363	126249488	126249383	126249460	GRM8	NR_028041	3	11	8	-	126249416	126249552
294810772	chr7	126249363	126249488	126249383	126249460	GRM8	NM_001127323	2	11	8	-	126249416	126249552
294810772	chr7	126249363	126249488	126249383	126249460	GRM8	NM_000845	1	10	7	-	126249416	126249552
293849179	chr7	126410056	126410224	126410084	126410197	GRM8	NR_028041	3	11	6	-	126409919	126410119
293849179	chr7	126410056	126410224	126410084	126410197	GRM8	NM_001127323	2	11	7	-	126409919	126410119
293849179	chr7	126410056	126410224	126410084	126410197	GRM8	NM_000845	1	10	6	-	126409919	126410119
294497195	chr7	126544561	126544735	126544589	126544714	GRM8	NR_028041	3	11	3	-	126544602	126544737
294497195	chr7	126544561	126544735	126544589	126544714	GRM8	NM_001127323	2	11	4	-	126544602	126544737
294497195	chr7	126544561	126544735	126544589	126544714	GRM8	NM_000845	1	10	3	-	126544602	126544737
295212341	chr7	126882717	126882867	126882744	126882843	GRM8	NR_028041	3	11	1	-	126882749	126883569

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295212341	chr7	126882717	126882867	126882744	126882843	GRM8	NM_001127323	2	11	2	-	126882749	126883569
295212341	chr7	126882717	126882867	126882744	126882843	GRM8	NM_000845	1	10	1	-	126882749	126883569
295279322	chr7	126883112	126883284	126883135	126883261	GRM8	NR_028041	3	11	1	-	126882749	126883569
295279322	chr7	126883112	126883284	126883135	126883261	GRM8	NM_001127323	2	11	2	-	126882749	126883569
295279322	chr7	126883112	126883284	126883135	126883261	GRM8	NM_000845	1	10	1	-	126882749	126883569
238684044	chr7	128843294	128843458	128843313	128843438	SMO	NM_005631	1	12	2	+	128843225	128843430
238034820	chr7	128845350	128845517	128845372	128845490	SMO	NM_005631	1	12	4	+	128845451	128845623
238669801	chr7	128846199	128846357	128846219	128846334	SMO	NM_005631	1	12	6	+	128846305	128846428
262096080	chr7	128850180	128850354	128850202	128850335	SMO	NM_005631	1	12	9	+	128850204	128850389
263563567	chr7	128851447	128851621	128851472	128851599	SMO	NM_005631	1	12	11	+	128851477	128851611
241169869	chr7	128851988	128852149	128852005	128852130	SMO	NM_005631	1	12	12	+	128851865	128853385
273202791	chr7	138145511	138145671	138145530	138145654	TRIM24	NM_015905	2	19	1	+	138145079	138145657
273202791	chr7	138145511	138145671	138145530	138145654	TRIM24	NM_003852	1	19	1	+	138145079	138145657
273462333	chr7	138200009	138200182	138200031	138200154	TRIM24	NM_015905	2	19	3	+	138199957	138200104
273462333	chr7	138200009	138200182	138200031	138200154	TRIM24	NM_003852	1	19	3	+	138199957	138200104
273065601	chr7	138223327	138223490	138223354	138223465	TRIM24	NM_015905	2	19	7	+	138223402	138223548
273065601	chr7	138223327	138223490	138223354	138223465	TRIM24	NM_003852	1	19	7	+	138223402	138223548
274258653	chr7	138239342	138239514	138239368	138239491	TRIM24	NM_003852	1	19	9	+	138239443	138239609
274258653	chr7	138239342	138239514	138239368	138239491	TRIM24	NM_015905	2	19	9	+	138239443	138239711
273666313	chr7	138252235	138252386	138252263	138252364	TRIM24	NM_015905	2	19	10	+	138252226	138252399
273666313	chr7	138252235	138252386	138252263	138252364	TRIM24	NM_003852	1	19	10	+	138252226	138252399
273208434	chr7	138258191	138258323	138258224	138258295	TRIM24	NM_015905	2	19	12	+	138258252	138258387
273208434	chr7	138258191	138258323	138258224	138258295	TRIM24	NM_003852	1	19	12	+	138258252	138258387
272921861	chr7	138262226	138262366	138262252	138262338	TRIM24	NM_015905	2	19	14	+	138262165	138262333
272921861	chr7	138262226	138262366	138262252	138262338	TRIM24	NM_003852	1	19	14	+	138262165	138262333
273621515	chr7	138264165	138264307	138264187	138264280	TRIM24	NM_015905	2	19	15	+	138263949	138264277
273621515	chr7	138264165	138264307	138264187	138264280	TRIM24	NM_003852	1	19	15	+	138263949	138264277
273678059	chr7	138266437	138266567	138266463	138266540	TRIM24	NM_015905	2	19	17	+	138266442	138266516
273678059	chr7	138266437	138266567	138266463	138266540	TRIM24	NM_003852	1	19	17	+	138266442	138266516
273271271	chr7	138269479	138269648	138269501	138269625	TRIM24	NM_015905	2	19	19	+	138269487	138270332
273271271	chr7	138269479	138269648	138269501	138269625	TRIM24	NM_003852	1	19	19	+	138269487	138270332
222636793	chr7	140434542	140434690	140434560	140434661	BRAF	NM_004333	1	18	18	-	140433813	140434570
223460541	chr7	140452996	140453123	140453024	140453102	BRAF	NM_004333	1	18	15	-	140453075	140453193
223967627	chr7	140476724	140476891	140476753	140476865	BRAF	NM_004333	1	18	13	-	140476712	140476888
326913823	chr7	140481367	140481537	140481392	140481511	BRAF	NM_004333	1	18	11	-	140481376	140481493
223739184	chr7	140494084	140494242	140494112	140494215	BRAF	NM_004333	1	18	8	-	140494108	140494267
223944056	chr7	140501106	140501280	140501131	140501252	BRAF	NM_004333	1	18	6	-	140501212	140501360
224404546	chr7	140508661	140508792	140508689	140508770	BRAF	NM_004333	1	18	4	-	140508692	140508795
222922922	chr7	140534497	140534645	140534525	140534620	BRAF	NM_004333	1	18	3	-	140534409	140534672
224119138	chr7	140624286	140624459	140624308	140624441	BRAF	NM_004333	1	18	1	-	140624366	140624564
271193956	chr7	142561639	142561781	142561666	142561761	EPHB6	NM_004445	1	20	7	+	142561724	142562504

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271216864	chr7	142562012	142562163	142562033	142562143	EPHB6	NM_004445	1	20	7	+	142561724	142562504
270779535	chr7	142563209	142563373	142563229	142563354	EPHB6	NM_004445	1	20	8	+	142563230	142563385
271801030	chr7	142563892	142564020	142563912	142564000	EPHB6	NM_004445	1	20	9	+	142563715	142564071
272729343	chr7	142564634	142564808	142564654	142564785	EPHB6	NM_004445	1	20	11	+	142564661	142564823
270538522	chr7	142565658	142565832	142565681	142565811	EPHB6	NM_004445	1	20	13	+	142565752	142565804
270717446	chr7	142566343	142566512	142566362	142566494	EPHB6	NM_004445	1	20	15	+	142566247	142566494
269950627	chr7	142567639	142567777	142567663	142567757	EPHB6	NM_004445	1	20	17	+	142567570	142567719
269981169	chr7	142568234	142568391	142568259	142568369	EPHB6	NM_004445	1	20	19	+	142568283	142568438
232433557	chr7	148506098	148506269	148506123	148506247	EZH2	NM_001203248	2	20	19	-	148506163	148506247
232433557	chr7	148506098	148506269	148506123	148506247	EZH2	NM_152998	5	19	18	-	148506163	148506247
232433557	chr7	148506098	148506269	148506123	148506247	EZH2	NM_001203247	1	20	19	-	148506163	148506247
232433557	chr7	148506098	148506269	148506123	148506247	EZH2	NM_001203249	3	19	18	-	148506163	148506247
232433557	chr7	148506098	148506269	148506123	148506247	EZH2	NM_004456	4	20	19	-	148506163	148506247
228775790	chr7	148508737	148508886	148508765	148508861	EZH2	NM_001203248	2	20	16	-	148508717	148508812
228775790	chr7	148508737	148508886	148508765	148508861	EZH2	NM_152998	5	19	15	-	148508717	148508812
228775790	chr7	148508737	148508886	148508765	148508861	EZH2	NM_001203247	1	20	16	-	148508717	148508812
228775790	chr7	148508737	148508886	148508765	148508861	EZH2	NM_001203249	3	19	15	-	148508717	148508812
228775790	chr7	148508737	148508886	148508765	148508861	EZH2	NM_004456	4	20	16	-	148508717	148508812
231499823	chr7	148512082	148512227	148512103	148512201	EZH2	NM_001203248	2	20	14	-	148512006	148512131
231499823	chr7	148512082	148512227	148512103	148512201	EZH2	NM_152998	5	19	13	-	148512006	148512131
231499823	chr7	148512082	148512227	148512103	148512201	EZH2	NM_001203247	1	20	14	-	148512006	148512131
231499823	chr7	148512082	148512227	148512103	148512201	EZH2	NM_004456	4	20	14	-	148512006	148512131
228399362	chr7	148514340	148514510	148514364	148514483	EZH2	NM_001203248	2	20	11	-	148514314	148514483
228399362	chr7	148514340	148514510	148514364	148514483	EZH2	NM_152998	5	19	10	-	148514314	148514483
228399362	chr7	148514340	148514510	148514364	148514483	EZH2	NM_001203247	1	20	11	-	148514314	148514483
228399362	chr7	148514340	148514510	148514364	148514483	EZH2	NM_001203249	3	19	11	-	148514314	148514483
228399362	chr7	148514340	148514510	148514364	148514483	EZH2	NM_004456	4	20	11	-	148514314	148514483
229711434	chr7	148516589	148516732	148516611	148516708	EZH2	NM_001203248	2	20	9	-	148516688	148516779
229711434	chr7	148516589	148516732	148516611	148516708	EZH2	NM_152998	5	19	8	-	148516688	148516779
229711434	chr7	148516589	148516732	148516611	148516708	EZH2	NM_001203247	1	20	9	-	148516688	148516779
229711434	chr7	148516589	148516732	148516611	148516708	EZH2	NM_001203249	3	19	9	-	148516688	148516779
229711434	chr7	148516589	148516732	148516611	148516708	EZH2	NM_004456	4	20	9	-	148516688	148516779
230200993	chr7	148523691	148523849	148523708	148523821	EZH2	NM_001203248	2	20	8	-	148523561	148523724
230200993	chr7	148523691	148523849	148523708	148523821	EZH2	NM_152998	5	19	7	-	148523561	148523724
230200993	chr7	148523691	148523849	148523708	148523821	EZH2	NM_001203247	1	20	8	-	148523561	148523724
230200993	chr7	148523691	148523849	148523708	148523821	EZH2	NM_001203249	3	19	8	-	148523561	148523724
230200993	chr7	148523691	148523849	148523708	148523821	EZH2	NM_004456	4	20	8	-	148523546	148523724
230653984	chr7	148526767	148526902	148526793	148526875	EZH2	NM_001203248	2	20	5	-	148526820	148526940
230653984	chr7	148526767	148526902	148526793	148526875	EZH2	NM_152998	5	19	4	-	148526820	148526940
230653984	chr7	148526767	148526902	148526793	148526875	EZH2	NM_001203247	1	20	5	-	148526820	148526940
230653984	chr7	148526767	148526902	148526793	148526875	EZH2	NM_001203249	3	19	5	-	148526820	148526940

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230653984	chr7	148526767	148526902	148526793	148526875	EZH2	NM_004456	4	20	5	-	148526820	148526940
227687344	chr7	148543454	148543618	148543476	148543597	EZH2	NM_152998	5	19	3	-	148543562	148543690
227687344	chr7	148543454	148543618	148543476	148543597	EZH2	NM_001203247	1	20	3	-	148543562	148543690
227687344	chr7	148543454	148543618	148543476	148543597	EZH2	NM_004456	4	20	3	-	148543562	148543690
227687344	chr7	148543454	148543618	148543476	148543597	EZH2	NM_001203248	2	20	3	-	148543589	148543690
227687344	chr7	148543454	148543618	148543476	148543597	EZH2	NM_001203249	3	19	3	-	148543589	148543690
274618569	chr7	151833892	151834040	151833912	151834017	MLL3	NM_170606	1	59	59	-	151832010	151834009
273253708	chr7	151836784	151836958	151836808	151836934	MLL3	NM_170606	1	59	56	-	151836760	151836876
273225209	chr7	151842238	151842405	151842263	151842380	MLL3	NM_170606	1	59	54	-	151842238	151842380
273084658	chr7	151845199	151845342	151845221	151845321	MLL3	NM_170606	1	59	52	-	151845118	151846237
274152802	chr7	151845665	151845813	151845689	151845786	MLL3	NM_170606	1	59	52	-	151845118	151846237
273000365	chr7	151846134	151846268	151846155	151846240	MLL3	NM_170606	1	59	52	-	151845118	151846237
273588870	chr7	151848560	151848719	151848582	151848691	MLL3	NM_170606	1	59	50	-	151848527	151848666
273406105	chr7	151850982	151851148	151851006	151851120	MLL3	NM_170606	1	59	48	-	151851095	151851231
273105339	chr7	151851406	151851564	151851427	151851536	MLL3	NM_170606	1	59	47	-	151851352	151851530
273192425	chr7	151853220	151853354	151853244	151853332	MLL3	NM_170606	1	59	45	-	151853290	151853431
274521144	chr7	151859124	151859276	151859150	151859248	MLL3	NM_170606	1	59	43	-	151859202	151860911
274563218	chr7	151859530	151859690	151859554	151859669	MLL3	NM_170606	1	59	43	-	151859202	151860911
274558184	chr7	151859922	151860077	151859950	151860053	MLL3	NM_170606	1	59	43	-	151859202	151860911
274583113	chr7	151860362	151860528	151860384	151860507	MLL3	NM_170606	1	59	43	-	151859202	151860911
273632887	chr7	151860741	151860912	151860761	151860884	MLL3	NM_170606	1	59	43	-	151859202	151860911
273817847	chr7	151864402	151864569	151864423	151864542	MLL3	NM_170606	1	59	42	-	151864231	151864463
273355766	chr7	151871241	151871399	151871267	151871366	MLL3	NM_170606	1	59	39	-	151871216	151871327
274310649	chr7	151873568	151873702	151873590	151873679	MLL3	NM_170606	1	59	38	-	151873276	151875095
273358689	chr7	151873917	151874042	151873944	151874014	MLL3	NM_170606	1	59	38	-	151873276	151875095
273275901	chr7	151874237	151874361	151874262	151874334	MLL3	NM_170606	1	59	38	-	151873276	151875095
273357997	chr7	151874638	151874801	151874660	151874777	MLL3	NM_170606	1	59	38	-	151873276	151875095
274294675	chr7	151875049	151875213	151875069	151875185	MLL3	NM_170606	1	59	38	-	151873276	151875095
273812908	chr7	151877728	151877901	151877755	151877878	MLL3	NM_170606	1	59	36	-	151877796	151879679
273813570	chr7	151878206	151878340	151878228	151878317	MLL3	NM_170606	1	59	36	-	151877796	151879679
273883185	chr7	151878602	151878759	151878624	151878738	MLL3	NM_170606	1	59	36	-	151877796	151879679
273895867	chr7	151879032	151879199	151879055	151879176	MLL3	NM_170606	1	59	36	-	151877796	151879679
273874657	chr7	151879487	151879653	151879510	151879627	MLL3	NM_170606	1	59	36	-	151877796	151879679
273460280	chr7	151882638	151882763	151882665	151882736	MLL3	NM_170606	1	59	34	-	151882643	151882716
273702375	chr7	151884518	151884684	151884545	151884651	MLL3	NM_170606	1	59	33	-	151884347	151884561
274324061	chr7	151891008	151891180	151891033	151891159	MLL3	NM_170606	1	59	31	-	151891094	151891213
273850796	chr7	151892931	151893098	151892953	151893079	MLL3	NM_170606	1	59	28	-	151892992	151893096
272912413	chr7	151896417	151896563	151896442	151896535	MLL3	NM_170606	1	59	27	-	151896364	151896544
273584216	chr7	151902123	151902247	151902154	151902220	MLL3	NM_170606	1	59	25	-	151902191	151902310
273268091	chr7	151917620	151917794	151917644	151917771	MLL3	NM_170606	1	59	23	-	151917608	151917820
272797249	chr7	151932892	151933056	151932913	151933031	MLL3	NM_170606	1	59	16	-	151932902	151933018

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273464031	chr7	151945046	151945219	151945071	151945192	MLL3	NM_170606	1	59	14	-	151944987	151945705
273232951	chr7	151946875	151947001	151946902	151946975	MLL3	NM_170606	1	59	13	-	151946961	151947038
274426231	chr7	151948959	151949128	151948985	151949100	MLL3	NM_170606	1	59	11	-	151949024	151949175
272928668	chr7	151949747	151949914	151949769	151949881	MLL3	NM_170606	1	59	10	-	151949631	151949800
274045627	chr7	151970903	151971070	151970927	151971043	MLL3	NM_170606	1	59	7	-	151970790	151970952
273718435	chr7	152008925	152009077	152008947	152009049	MLL3	NM_170606	1	59	5	-	152008883	152009031
273255079	chr7	152055598	152055747	152055624	152055727	MLL3	NM_170606	1	59	2	-	152055672	152055760
293863398	chr7	152345815	152345971	152345840	152345950	XRCC2	NM_005431	1	3	3	-	152343587	152346448
294975555	chr7	152346261	152346399	152346283	152346372	XRCC2	NM_005431	1	3	3	-	152343587	152346448
239086483	chr8	30915936	30916090	30915962	30916062	WRN	NM_000553	1	35	2	+	30915888	30916059
241452310	chr8	30921875	30922046	30921900	30922019	WRN	NM_000553	1	35	4	+	30921805	30921950
262063993	chr8	30924499	30924623	30924527	30924598	WRN	NM_000553	1	35	6	+	30924549	30924698
265754052	chr8	30925801	30925969	30925828	30925945	WRN	NM_000553	1	35	7	+	30925774	30925843
240011200	chr8	30938425	30938585	30938451	30938557	WRN	NM_000553	1	35	9	+	30938383	30938812
262203681	chr8	30945230	30945374	30945256	30945347	WRN	NM_000553	1	35	12	+	30945292	30945436
330151528	chr8	30948021	30948193	30948046	30948165	WRN	NM_000553	1	35	14	+	30947981	30948048
239543300	chr8	30954273	30954441	30954302	30954415	WRN	NM_000553	1	35	17	+	30954284	30954366
264527429	chr8	30969280	30969447	30969301	30969418	WRN	NM_000553	1	35	19	+	30969131	30969315
262303528	chr8	30977771	30977905	30977795	30977879	WRN	NM_000553	1	35	21	+	30977759	30977940
238374239	chr8	30982300	30982466	30982328	30982440	WRN	NM_000553	1	35	23	+	30982424	30982516
240546347	chr8	30998857	30998992	30998887	30998968	WRN	NM_000553	1	35	25	+	30998946	30999116
262591353	chr8	30999224	30999383	30999247	30999355	WRN	NM_000553	1	35	26	+	30999197	30999291
238709446	chr8	31004500	31004646	31004529	31004625	WRN	NM_000553	1	35	29	+	31004569	31004644
264729265	chr8	31007753	31007904	31007781	31007878	WRN	NM_000553	1	35	31	+	31007857	31007971
241864381	chr8	31014914	31015085	31014936	31015061	WRN	NM_000553	1	35	33	+	31014884	31015046
239372670	chr8	31030411	31030551	31030434	31030526	WRN	NM_000553	1	35	35	+	31030511	31031277
228355903	chr8	37654892	37655062	37654909	37655041	GPR124	NM_032777	1	19	1	+	37654401	37655052
227241414	chr8	37686399	37686553	37686418	37686536	GPR124	NM_032777	1	19	3	+	37686406	37686477
229778181	chr8	37687427	37687572	37687444	37687553	GPR124	NM_032777	1	19	6	+	37687369	37687532
228130219	chr8	37689019	37689187	37689040	37689166	GPR124	NM_032777	1	19	8	+	37688941	37689105
228742456	chr8	37691177	37691313	37691200	37691288	GPR124	NM_032777	1	19	10	+	37691206	37691355
227888727	chr8	37692611	37692783	37692632	37692765	GPR124	NM_032777	1	19	12	+	37692692	37692916
227132288	chr8	37693167	37693306	37693186	37693283	GPR124	NM_032777	1	19	13	+	37693072	37693288
229081669	chr8	37695394	37695564	37695412	37695538	GPR124	NM_032777	1	19	14	+	37695249	37695457
229017893	chr8	37697584	37697729	37697603	37697708	GPR124	NM_032777	1	19	17	+	37697639	37697784
227507280	chr8	37698691	37698847	37698708	37698826	GPR124	NM_032777	1	19	19	+	37698604	37701504
229574891	chr8	37699169	37699337	37699186	37699320	GPR124	NM_032777	1	19	19	+	37698604	37701504
227560900	chr8	37699733	37699870	37699751	37699849	GPR124	NM_032777	1	19	19	+	37698604	37701504
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_001174066	4	17	16	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_001174065	3	18	17	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_001174063	1	18	17	-	38271436	38271541

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_023110	9	18	17	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_023106	8	17	16	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_023105	7	17	16	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_015850	6	18	17	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_001174067	5	19	18	-	38271436	38271541
229661294	chr8	38271406	38271572	38271423	38271551	FGFR1	NM_001174064	2	19	18	-	38271436	38271541
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_001174066	4	17	14	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_001174065	3	18	15	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_001174063	1	18	15	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_023110	9	18	15	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_023106	8	17	14	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_023105	7	17	14	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_015850	6	18	15	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_001174067	5	19	16	-	38272077	38272147
230113015	chr8	38272089	38272263	38272114	38272239	FGFR1	NM_001174064	2	19	16	-	38272077	38272147
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_001174066	4	17	12	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_001174065	3	18	13	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_001174063	1	18	13	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_023110	9	18	13	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_023106	8	17	12	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_023105	7	17	12	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_015850	6	18	13	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_001174067	5	19	14	-	38273388	38273578
228267757	chr8	38273459	38273606	38273478	38273587	FGFR1	NM_001174064	2	19	14	-	38273388	38273578
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_001174066	4	17	10	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_001174065	3	18	11	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_001174063	1	18	11	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_023110	9	18	11	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_023106	8	17	10	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_023105	7	17	10	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_015850	6	18	11	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_001174067	5	19	12	-	38275388	38275509
231796159	chr8	38275421	38275573	38275442	38275551	FGFR1	NM_001174064	2	19	12	-	38275388	38275509
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_001174063	1	18	9	-	38277057	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_001174064	2	19	10	-	38277057	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_001174066	4	17	8	-	38277051	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_001174065	3	18	9	-	38277051	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_023110	9	18	9	-	38277051	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_023106	8	17	8	-	38277051	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_023105	7	17	8	-	38277051	38277253
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_015850	6	18	9	-	38277051	38277253

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229718864	chr8	38277115	38277279	38277141	38277258	FGFR1	NM_001174067	5	19	10	-	38277051	38277253
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174066	4	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174065	3	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174063	1	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023110	9	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023106	8	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_023105	7	17	6	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_015850	6	18	7	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174067	5	19	8	-	38282027	38282217
229208392	chr8	38282113	38282274	38282133	38282252	FGFR1	NM_001174064	2	19	8	-	38282027	38282217
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_001174066	4	17	4	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_001174065	3	18	5	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_001174063	1	18	5	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_023110	9	18	5	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_023106	8	17	4	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_023105	7	17	4	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_015850	6	18	5	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_001174067	5	19	6	-	38285439	38285611
228295080	chr8	38285480	38285641	38285502	38285620	FGFR1	NM_001174064	2	19	6	-	38285439	38285611
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_023110	9	18	3	-	38287200	38287466
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_015850	6	18	3	-	38287200	38287466
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
227979101	chr8	38287299	38287456	38287318	38287439	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_001174066	4	17	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_001174065	3	18	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_001174063	1	18	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_023110	9	18	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_023106	8	17	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_023105	7	17	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_015850	6	18	2	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_001174067	5	19	3	-	38314874	38315052
230732661	chr8	38314865	38315039	38314887	38315019	FGFR1	NM_001174064	2	19	2	-	38314874	38315052
312176746	chr8	41789730	41789854	41789753	41789833	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312176746	chr8	41789730	41789854	41789753	41789833	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312176746	chr8	41789730	41789854	41789753	41789833	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312191961	chr8	41790099	41790271	41790119	41790248	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312191961	chr8	41790099	41790271	41790119	41790248	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312191961	chr8	41790099	41790271	41790119	41790248	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312635879	chr8	41790786	41790959	41790804	41790941	KAT6A	NM_001099412	1	18	18	-	41786997	41792385

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312635879	chr8	41790786	41790959	41790804	41790941	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312635879	chr8	41790786	41790959	41790804	41790941	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312367415	chr8	41791185	41791349	41791207	41791328	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312367415	chr8	41791185	41791349	41791207	41791328	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312367415	chr8	41791185	41791349	41791207	41791328	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312645350	chr8	41791652	41791824	41791680	41791806	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312645350	chr8	41791652	41791824	41791680	41791806	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312645350	chr8	41791652	41791824	41791680	41791806	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312326784	chr8	41791992	41792163	41792011	41792139	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312326784	chr8	41791992	41792163	41792011	41792139	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312326784	chr8	41791992	41792163	41792011	41792139	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312345929	chr8	41794731	41794868	41794760	41794847	KAT6A	NM_001099412	1	18	17	-	41794774	41795086
312345929	chr8	41794731	41794868	41794760	41794847	KAT6A	NM_006766	3	17	16	-	41794774	41795086
312345929	chr8	41794731	41794868	41794760	41794847	KAT6A	NM_001099413	2	18	17	-	41794774	41795086
312387756	chr8	41798272	41798399	41798301	41798377	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312387756	chr8	41798272	41798399	41798301	41798377	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312387756	chr8	41798272	41798399	41798301	41798377	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312443105	chr8	41798682	41798852	41798710	41798826	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312443105	chr8	41798682	41798852	41798710	41798826	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312443105	chr8	41798682	41798852	41798710	41798826	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312461369	chr8	41800419	41800593	41800442	41800565	KAT6A	NM_001099412	1	18	15	-	41800311	41800518
312461369	chr8	41800419	41800593	41800442	41800565	KAT6A	NM_006766	3	17	14	-	41800311	41800518
312461369	chr8	41800419	41800593	41800442	41800565	KAT6A	NM_001099413	2	18	15	-	41800311	41800518
312276454	chr8	41804056	41804226	41804078	41804202	KAT6A	NM_001099412	1	18	13	-	41804109	41804202
312276454	chr8	41804056	41804226	41804078	41804202	KAT6A	NM_006766	3	17	12	-	41804109	41804202
312276454	chr8	41804056	41804226	41804078	41804202	KAT6A	NM_001099413	2	18	13	-	41804109	41804202
312354081	chr8	41806765	41806892	41806790	41806872	KAT6A	NM_001099412	1	18	11	-	41806740	41806881
312354081	chr8	41806765	41806892	41806790	41806872	KAT6A	NM_006766	3	17	10	-	41806740	41806881
312354081	chr8	41806765	41806892	41806790	41806872	KAT6A	NM_001099413	2	18	11	-	41806740	41806881
312472013	chr8	41832226	41832377	41832254	41832353	KAT6A	NM_001099412	1	18	9	-	41832222	41832340
312472013	chr8	41832226	41832377	41832254	41832353	KAT6A	NM_006766	3	17	8	-	41832222	41832340
312472013	chr8	41832226	41832377	41832254	41832353	KAT6A	NM_001099413	2	18	9	-	41832222	41832340
312446293	chr8	41834723	41834850	41834752	41834824	KAT6A	NM_001099412	1	18	8	-	41834526	41834845
312446293	chr8	41834723	41834850	41834752	41834824	KAT6A	NM_006766	3	17	7	-	41834526	41834845
312446293	chr8	41834723	41834850	41834752	41834824	KAT6A	NM_001099413	2	18	8	-	41834526	41834845
312256589	chr8	41838384	41838510	41838404	41838483	KAT6A	NM_001099412	1	18	6	-	41838364	41838445
312256589	chr8	41838384	41838510	41838404	41838483	KAT6A	NM_006766	3	17	5	-	41838364	41838445
312256589	chr8	41838384	41838510	41838404	41838483	KAT6A	NM_001099413	2	18	6	-	41838364	41838445
312504699	chr8	41905986	41906151	41906009	41906124	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312504699	chr8	41905986	41906151	41906009	41906124	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312504699	chr8	41905986	41906151	41906009	41906124	KAT6A	NM_001099413	2	18	3	-	41905896	41906820

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312492624	chr8	41906418	41906543	41906442	41906515	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312492624	chr8	41906418	41906543	41906442	41906515	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312492624	chr8	41906418	41906543	41906442	41906515	KAT6A	NM_001099413	2	18	3	-	41905896	41906820
279410685	chr8	42146127	42146286	42146146	42146267	IKBKB	NR_033819	5	21	3	+	42146152	42146246
279410685	chr8	42146127	42146286	42146146	42146267	IKBKB	NR_033818	4	22	3	+	42146152	42146246
279410685	chr8	42146127	42146286	42146146	42146267	IKBKB	NM_001556	3	22	3	+	42146152	42146246
279410685	chr8	42146127	42146286	42146146	42146267	IKBKB	NM_001190720	1	21	2	+	42146152	42146246
279410685	chr8	42146127	42146286	42146146	42146267	IKBKB	NR_040009	6	22	3	+	42146152	42146246
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NM_001242778	2	21	5	+	42162705	42162793
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NR_033819	5	21	6	+	42162705	42162793
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NR_033818	4	22	6	+	42162705	42162793
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NM_001556	3	22	6	+	42162705	42162793
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NM_001190720	1	21	5	+	42162705	42162793
278810810	chr8	42162616	42162748	42162639	42162721	IKBKB	NR_040009	6	22	6	+	42162705	42162793
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NM_001242778	2	21	7	+	42166419	42166543
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NR_033819	5	21	8	+	42166419	42166543
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NR_033818	4	22	8	+	42166419	42166543
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NM_001556	3	22	8	+	42166419	42166543
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NM_001190720	1	21	7	+	42166419	42166543
279302681	chr8	42166439	42166613	42166460	42166589	IKBKB	NR_040009	6	22	8	+	42166419	42166543
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NM_001242778	2	21	10	+	42174228	42174422
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NR_033819	5	21	11	+	42174228	42174422
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NR_033818	4	22	11	+	42174228	42174422
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NM_001556	3	22	11	+	42174228	42174422
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NM_001190720	1	21	10	+	42174228	42174422
279943274	chr8	42174283	42174450	42174305	42174430	IKBKB	NR_040009	6	22	11	+	42174228	42174422
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NM_001242778	2	21	12	+	42176070	42176193
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NR_033819	5	21	13	+	42176070	42176193
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NR_033818	4	22	13	+	42176070	42176193
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NM_001556	3	22	13	+	42176070	42176193
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NM_001190720	1	21	12	+	42176070	42176193
278494027	chr8	42176132	42176304	42176152	42176281	IKBKB	NR_040009	6	22	13	+	42176070	42176193
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NM_001242778	2	21	15	+	42178253	42178362
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NR_033819	5	21	15	+	42178253	42178362
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NR_033818	4	22	16	+	42178253	42178362
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NM_001556	3	22	16	+	42178253	42178362
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NM_001190720	1	21	15	+	42178253	42178362
279526366	chr8	42178206	42178380	42178225	42178362	IKBKB	NR_040009	6	22	16	+	42178253	42178362
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NM_001242778	2	21	18	+	42179865	42180012
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NR_033819	5	21	18	+	42179865	42180012
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NR_033818	4	22	19	+	42179865	42180012

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NM_001556	3	22	19	+	42179865	42180012
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NM_001190720	1	21	18	+	42179865	42180012
277938767	chr8	42179911	42180081	42179933	42180061	IKBKB	NR_040009	6	22	19	+	42179865	42180012
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NM_001242778	2	21	21	+	42188432	42190171
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NR_033819	5	21	21	+	42188432	42190171
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NR_033818	4	22	22	+	42188432	42190171
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NM_001556	3	22	22	+	42188432	42190171
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NM_001190720	1	21	21	+	42188432	42190171
277842284	chr8	42188383	42188552	42188406	42188532	IKBKB	NR_040009	6	22	22	+	42188432	42190171
228710582	chr8	42780604	42780774	42780632	42780746	HOOK3	NM_032410	1	22	3	+	42780700	42780772
228162598	chr8	42798464	42798600	42798492	42798572	HOOK3	NM_032410	1	22	5	+	42798456	42798588
227127662	chr8	42812231	42812359	42812259	42812331	HOOK3	NM_032410	1	22	7	+	42812237	42812299
227471681	chr8	42819459	42819627	42819484	42819598	HOOK3	NM_032410	1	22	9	+	42819454	42819617
229794068	chr8	42823205	42823356	42823233	42823328	HOOK3	NM_032410	1	22	11	+	42823156	42823357
227170428	chr8	42829207	42829372	42829231	42829345	HOOK3	NM_032410	1	22	13	+	42829250	42829337
227932896	chr8	42852643	42852815	42852666	42852787	HOOK3	NM_032410	1	22	16	+	42852693	42852780
227339237	chr8	42868346	42868516	42868375	42868488	HOOK3	NM_032410	1	22	21	+	42868472	42868543
270860163	chr8	48686696	48686844	48686724	48686823	PRKDC	NM_001081640	1	85	85	-	48685669	48686938
270860163	chr8	48686696	48686844	48686724	48686823	PRKDC	NM_006904	2	86	86	-	48685669	48686938
270353765	chr8	48690201	48690373	48690225	48690349	PRKDC	NM_001081640	1	85	83	-	48690247	48690435
270353765	chr8	48690201	48690373	48690225	48690349	PRKDC	NM_006904	2	86	84	-	48690247	48690435
269461790	chr8	48691186	48691360	48691206	48691340	PRKDC	NM_001081640	1	85	82	-	48691020	48691221
269461790	chr8	48691186	48691360	48691206	48691340	PRKDC	NM_006904	2	86	83	-	48691020	48691221
269461790	chr8	48691186	48691360	48691206	48691340	PRKDC	NM_001081640	1	85	81	-	48691289	48691360
269461790	chr8	48691186	48691360	48691206	48691340	PRKDC	NM_006904	2	86	82	-	48691289	48691360
269596117	chr8	48694658	48694785	48694677	48694758	PRKDC	NM_006904	2	86	80	-	48694723	48694815
269854377	chr8	48696257	48696398	48696278	48696371	PRKDC	NM_001081640	1	85	78	-	48696303	48696370
269854377	chr8	48696257	48696398	48696278	48696371	PRKDC	NM_006904	2	86	78	-	48696303	48696370
269631191	chr8	48701447	48701616	48701466	48701593	PRKDC	NM_001081640	1	85	76	-	48701467	48701610
269631191	chr8	48701447	48701616	48701466	48701593	PRKDC	NM_006904	2	86	76	-	48701467	48701610
269997797	chr8	48706769	48706901	48706792	48706874	PRKDC	NM_001081640	1	85	74	-	48706851	48707062
269997797	chr8	48706769	48706901	48706792	48706874	PRKDC	NM_006904	2	86	74	-	48706851	48707062
272582037	chr8	48710822	48710985	48710851	48710958	PRKDC	NM_001081640	1	85	73	-	48710798	48710958
272582037	chr8	48710822	48710985	48710851	48710958	PRKDC	NM_006904	2	86	73	-	48710798	48710958
271700839	chr8	48713407	48713554	48713429	48713530	PRKDC	NM_001081640	1	85	71	-	48713354	48713547
271700839	chr8	48713407	48713554	48713429	48713530	PRKDC	NM_006904	2	86	71	-	48713354	48713547
270824007	chr8	48719653	48719807	48719674	48719787	PRKDC	NM_001081640	1	85	69	-	48719698	48719887
270824007	chr8	48719653	48719807	48719674	48719787	PRKDC	NM_006904	2	86	69	-	48719698	48719887
270247911	chr8	48731977	48732136	48732003	48732108	PRKDC	NM_001081640	1	85	67	-	48731963	48732071
270247911	chr8	48731977	48732136	48732003	48732108	PRKDC	NM_006904	2	86	67	-	48731963	48732071
270319415	chr8	48734163	48734310	48734191	48734286	PRKDC	NM_001081640	1	85	65	-	48734165	48734353

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270319415	chr8	48734163	48734310	48734191	48734286	PRKDC	NM_006904	2	86	65	-	48734165	48734353
270776726	chr8	48739192	48739363	48739212	48739346	PRKDC	NM_001081640	1	85	63	-	48739217	48739422
270776726	chr8	48739192	48739363	48739212	48739346	PRKDC	NM_006904	2	86	63	-	48739217	48739422
272001333	chr8	48740852	48741012	48740880	48740984	PRKDC	NM_001081640	1	85	62	-	48740729	48740908
272001333	chr8	48740852	48741012	48740880	48740984	PRKDC	NM_006904	2	86	62	-	48740729	48740908
271553763	chr8	48744394	48744564	48744415	48744542	PRKDC	NM_001081640	1	85	60	-	48744375	48744487
271553763	chr8	48744394	48744564	48744415	48744542	PRKDC	NM_006904	2	86	60	-	48744375	48744487
271208936	chr8	48748907	48749081	48748929	48749057	PRKDC	NM_001081640	1	85	58	-	48748899	48749088
271208936	chr8	48748907	48749081	48748929	48749057	PRKDC	NM_006904	2	86	58	-	48748899	48749088
270223018	chr8	48749916	48750040	48749937	48750016	PRKDC	NM_001081640	1	85	57	-	48749773	48749980
270223018	chr8	48749916	48750040	48749937	48750016	PRKDC	NM_006904	2	86	57	-	48749773	48749980
269671511	chr8	48761794	48761957	48761817	48761935	PRKDC	NM_001081640	1	85	54	-	48761715	48761864
269671511	chr8	48761794	48761957	48761817	48761935	PRKDC	NM_006904	2	86	54	-	48761715	48761864
270375409	chr8	48765283	48765443	48765311	48765415	PRKDC	NM_001081640	1	85	52	-	48765234	48765345
270375409	chr8	48765283	48765443	48765311	48765415	PRKDC	NM_006904	2	86	52	-	48765234	48765345
270042734	chr8	48767800	48767931	48767821	48767903	PRKDC	NM_001081640	1	85	50	-	48767783	48767934
270042734	chr8	48767800	48767931	48767821	48767903	PRKDC	NM_006904	2	86	50	-	48767783	48767934
272507389	chr8	48769826	48769990	48769844	48769969	PRKDC	NM_001081640	1	85	49	-	48769717	48769860
272507389	chr8	48769826	48769990	48769844	48769969	PRKDC	NM_006904	2	86	49	-	48769717	48769860
270231340	chr8	48772047	48772221	48772072	48772198	PRKDC	NM_001081640	1	85	46	-	48772172	48772320
270231340	chr8	48772047	48772221	48772072	48772198	PRKDC	NM_006904	2	86	46	-	48772172	48772320
270507919	chr8	48773480	48773613	48773508	48773584	PRKDC	NM_001081640	1	85	45	-	48773460	48773532
270507919	chr8	48773480	48773613	48773508	48773584	PRKDC	NM_006904	2	86	45	-	48773460	48773532
271077690	chr8	48775983	48776114	48776009	48776086	PRKDC	NM_001081640	1	85	42	-	48775960	48776138
271077690	chr8	48775983	48776114	48776009	48776086	PRKDC	NM_006904	2	86	42	-	48775960	48776138
270586094	chr8	48777138	48777302	48777159	48777282	PRKDC	NM_001081640	1	85	41	-	48777117	48777324
270586094	chr8	48777138	48777302	48777159	48777282	PRKDC	NM_006904	2	86	41	-	48777117	48777324
269700947	chr8	48792046	48792176	48792072	48792154	PRKDC	NM_001081640	1	85	39	-	48792052	48792219
269700947	chr8	48792046	48792176	48792072	48792154	PRKDC	NM_006904	2	86	39	-	48792052	48792219
271839566	chr8	48794523	48794684	48794543	48794658	PRKDC	NM_001081640	1	85	37	-	48794473	48794658
271839566	chr8	48794523	48794684	48794543	48794658	PRKDC	NM_006904	2	86	37	-	48794473	48794658
271296874	chr8	48800150	48800292	48800172	48800267	PRKDC	NM_001081640	1	85	35	-	48800108	48800266
271296874	chr8	48800150	48800292	48800172	48800267	PRKDC	NM_006904	2	86	35	-	48800108	48800266
271700920	chr8	48801647	48801821	48801674	48801795	PRKDC	NM_001081640	1	85	33	-	48801575	48801783
271700920	chr8	48801647	48801821	48801674	48801795	PRKDC	NM_006904	2	86	33	-	48801575	48801783
271163409	chr8	48805673	48805836	48805695	48805819	PRKDC	NM_001081640	1	85	31	-	48805700	48805947
271163409	chr8	48805673	48805836	48805695	48805819	PRKDC	NM_006904	2	86	31	-	48805700	48805947
271948984	chr8	48809716	48809887	48809743	48809862	PRKDC	NM_001081640	1	85	30	-	48809721	48809854
271948984	chr8	48809716	48809887	48809743	48809862	PRKDC	NM_006904	2	86	30	-	48809721	48809854
271540092	chr8	48815071	48815244	48815095	48815221	PRKDC	NM_001081640	1	85	27	-	48815129	48815355
271540092	chr8	48815071	48815244	48815095	48815221	PRKDC	NM_006904	2	86	27	-	48815129	48815355

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272422709	chr8	48817474	48817606	48817501	48817582	PRKDC	NM_001081640	1	85	26	-	48817429	48817536
272422709	chr8	48817474	48817606	48817501	48817582	PRKDC	NM_006904	2	86	26	-	48817429	48817536
271153129	chr8	48826480	48826628	48826501	48826605	PRKDC	NM_001081640	1	85	24	-	48826461	48826624
271153129	chr8	48826480	48826628	48826501	48826605	PRKDC	NM_006904	2	86	24	-	48826461	48826624
269732650	chr8	48830774	48830944	48830802	48830918	PRKDC	NM_001081640	1	85	22	-	48830837	48830943
269732650	chr8	48830774	48830944	48830802	48830918	PRKDC	NM_006904	2	86	22	-	48830837	48830943
271289831	chr8	48839812	48839952	48839841	48839926	PRKDC	NM_001081640	1	85	21	-	48839754	48839913
271289831	chr8	48839812	48839952	48839841	48839926	PRKDC	NM_006904	2	86	21	-	48839754	48839913
270095264	chr8	48842309	48842479	48842336	48842451	PRKDC	NM_001081640	1	85	18	-	48842413	48842572
270095264	chr8	48842309	48842479	48842336	48842451	PRKDC	NM_006904	2	86	18	-	48842413	48842572
271057856	chr8	48843242	48843400	48843265	48843372	PRKDC	NM_001081640	1	85	17	-	48843232	48843347
271057856	chr8	48843242	48843400	48843265	48843372	PRKDC	NM_006904	2	86	17	-	48843232	48843347
270631219	chr8	48846523	48846650	48846545	48846628	PRKDC	NM_001081640	1	85	15	-	48846525	48846650
270631219	chr8	48846523	48846650	48846545	48846628	PRKDC	NM_006904	2	86	15	-	48846525	48846650
270598395	chr8	48848171	48848332	48848200	48848312	PRKDC	NM_001081640	1	85	13	-	48848292	48848460
270598395	chr8	48848171	48848332	48848200	48848312	PRKDC	NM_006904	2	86	13	-	48848292	48848460
272424557	chr8	48848940	48849074	48848961	48849046	PRKDC	NM_001081640	1	85	12	-	48848913	48849077
272424557	chr8	48848940	48849074	48848961	48849046	PRKDC	NM_006904	2	86	12	-	48848913	48849077
270050024	chr8	48852226	48852379	48852249	48852351	PRKDC	NM_001081640	1	85	11	-	48852111	48852257
270050024	chr8	48852226	48852379	48852249	48852351	PRKDC	NM_006904	2	86	11	-	48852111	48852257
272554310	chr8	48856412	48856548	48856432	48856520	PRKDC	NM_001081640	1	85	9	-	48856413	48856443
272554310	chr8	48856412	48856548	48856432	48856520	PRKDC	NM_006904	2	86	9	-	48856413	48856443
270250182	chr8	48866320	48866445	48866344	48866417	PRKDC	NM_001081640	1	85	6	-	48866367	48866479
270250182	chr8	48866320	48866445	48866344	48866417	PRKDC	NM_006904	2	86	6	-	48866367	48866479
270305857	chr8	48868441	48868588	48868460	48868561	PRKDC	NM_001081640	1	85	4	-	48868434	48868508
270305857	chr8	48868441	48868588	48868460	48868561	PRKDC	NM_006904	2	86	4	-	48868434	48868508
272560316	chr8	48872474	48872646	48872493	48872628	PRKDC	NM_001081640	1	85	1	-	48872533	48872743
272560316	chr8	48872474	48872646	48872493	48872628	PRKDC	NM_006904	2	86	1	-	48872533	48872743
240836244	chr8	57079047	57079203	57079071	57079180	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240836244	chr8	57079047	57079203	57079071	57079180	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
240836244	chr8	57079047	57079203	57079071	57079180	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
237140469	chr8	57079523	57079692	57079545	57079671	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237140469	chr8	57079523	57079692	57079545	57079671	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237140469	chr8	57079523	57079692	57079545	57079671	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
240838357	chr8	57079964	57080133	57079991	57080104	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240838357	chr8	57079964	57080133	57079991	57080104	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
240838357	chr8	57079964	57080133	57079991	57080104	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
240280763	chr8	71025781	71025955	71025807	71025929	NCOA2	NM_006540	1	23	23	-	71024267	71025878
236438905	chr8	71036190	71036362	71036212	71036337	NCOA2	NM_006540	1	23	21	-	71036119	71036317
237358500	chr8	71039031	71039181	71039057	71039156	NCOA2	NM_006540	1	23	19	-	71039048	71039282
235635266	chr8	71040913	71041087	71040933	71041063	NCOA2	NM_006540	1	23	17	-	71040937	71041215

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237636338	chr8	71044102	71044265	71044125	71044240	NCOA2	NM_006540	1	23	16	-	71044072	71044237
237266818	chr8	71053502	71053674	71053525	71053646	NCOA2	NM_006540	1	23	14	-	71053419	71053634
236259532	chr8	71060472	71060613	71060498	71060589	NCOA2	NM_006540	1	23	12	-	71060508	71060718
240170962	chr8	71068260	71068434	71068284	71068410	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240149366	chr8	71068674	71068817	71068695	71068795	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240243366	chr8	71069076	71069236	71069099	71069213	NCOA2	NM_006540	1	23	11	-	71068206	71069475
238161337	chr8	71071722	71071882	71071750	71071856	NCOA2	NM_006540	1	23	10	-	71071740	71071887
235437417	chr8	71075598	71075754	71075626	71075730	NCOA2	NM_006540	1	23	8	-	71075700	71075801
235540590	chr8	71082311	71082469	71082332	71082446	NCOA2	NM_006540	1	23	6	-	71082437	71082614
240418729	chr8	71126052	71126201	71126077	71126172	NCOA2	NM_006540	1	23	4	-	71126138	71126310
235606585	chr8	71128927	71129060	71128949	71129035	NCOA2	NM_006540	1	23	3	-	71128895	71128999
239149627	chr8	90955523	90955696	90955550	90955667	NBN	NM_002485	1	16	14	-	90955481	90955594
258685330	chr8	90965383	90965541	90965412	90965513	NBN	NM_002485	1	16	11	-	90965472	90965919
258743804	chr8	90965768	90965892	90965790	90965864	NBN	NM_002485	1	16	11	-	90965472	90965919
235657309	chr8	90967624	90967769	90967652	90967744	NBN	NM_002485	1	16	10	-	90967511	90967783
238364112	chr8	90976547	90976721	90976574	90976694	NBN	NM_002485	1	16	8	-	90976638	90976735
236516996	chr8	90982723	90982895	90982749	90982869	NBN	NM_002485	1	16	7	-	90982592	90982785
239084421	chr8	90992968	90993094	90992996	90993066	NBN	NM_002485	1	16	4	-	90992962	90993121
235151286	chr8	90993657	90993809	90993681	90993782	NBN	NM_002485	1	16	3	-	90993603	90993751
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_004349	12	11	11	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198625	1	15	15	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198626	2	13	13	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198627	3	14	14	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198679	11	12	12	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_175636	15	10	10	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198630	6	13	13	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_175635	14	11	11	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_175634	13	12	12	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198633	9	11	11	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198632	8	12	12	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198631	7	12	12	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198634	10	11	11	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198629	5	12	12	-	92967195	92972745
240155197	chr8	92972420	92972592	92972440	92972572	RUNX1T1	NM_001198628	4	12	12	-	92967195	92972745
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_004349	12	11	10	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198625	1	15	14	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198626	2	13	12	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198627	3	14	13	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198679	11	12	11	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_175636	15	10	9	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198630	6	13	12	-	92982886	92983076

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_175635	14	11	10	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_175634	13	12	11	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198633	9	11	10	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198632	8	12	11	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198631	7	12	11	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198634	10	11	10	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198629	5	12	11	-	92982886	92983076
240878212	chr8	92982966	92983106	92982986	92983085	RUNX1T1	NM_001198628	4	12	11	-	92982886	92983076
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_004349	12	11	7	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198625	1	15	11	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198626	2	13	9	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198627	3	14	10	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198679	11	12	8	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_175636	15	10	6	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198630	6	13	9	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_175635	14	11	7	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_175634	13	12	8	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198633	9	11	7	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198632	8	12	8	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198631	7	12	8	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198634	10	11	7	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198629	5	12	8	-	92999115	92999200
264415393	chr8	92999000	92999159	92999025	92999134	RUNX1T1	NM_001198628	4	12	8	-	92999115	92999200
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_004349	12	11	6	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198625	1	15	10	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198626	2	13	8	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198627	3	14	9	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198679	11	12	7	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_175636	15	10	5	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198630	6	13	8	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_175635	14	11	6	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_175634	13	12	7	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198633	9	11	6	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198632	8	12	7	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198631	7	12	7	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198634	10	11	6	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198629	5	12	7	-	93003867	93004117
260795354	chr8	93004055	93004182	93004075	93004160	RUNX1T1	NM_001198628	4	12	7	-	93003867	93004117
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_004349	12	11	4	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198625	1	15	8	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198626	2	13	6	-	93023230	93023319

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198627	3	14	7	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198679	11	12	5	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_175636	15	10	3	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198630	6	13	6	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_175635	14	11	4	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_175634	13	12	5	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198633	9	11	4	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198632	8	12	5	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198631	7	12	5	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198634	10	11	4	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198629	5	12	5	-	93023230	93023319
242064024	chr8	93023273	93023444	93023300	93023416	RUNX1T1	NM_001198628	4	12	5	-	93023230	93023319
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_175636	15	10	1	-	93029454	93029908
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_004349	12	11	2	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198625	1	15	6	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198626	2	13	4	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198627	3	14	5	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198679	11	12	3	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198630	6	13	4	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_175635	14	11	2	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_175634	13	12	3	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198633	9	11	2	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198632	8	12	3	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198631	7	12	3	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198634	10	11	2	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198629	5	12	3	-	93029454	93029591
238563169	chr8	93029422	93029552	93029448	93029529	RUNX1T1	NM_001198628	4	12	3	-	93029454	93029591
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198630	6	13	1	-	93107256	93107490
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_175635	14	11	1	-	93107256	93107490
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198632	8	12	1	-	93107256	93107490
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198629	5	12	1	-	93107256	93107490
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198625	1	15	2	-	93107256	93107399
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198626	2	13	2	-	93107256	93107399
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198627	3	14	2	-	93107256	93107399
239372821	chr8	93107139	93107298	93107159	93107276	RUNX1T1	NM_001198679	11	12	2	-	93107256	93107399
238490871	chr8	93114967	93115140	93114987	93115119	RUNX1T1	NM_175634	13	12	1	-	93115085	93115454
238490871	chr8	93114967	93115140	93114987	93115119	RUNX1T1	NM_001198633	9	11	1	-	93115085	93115454
301709078	chr8	103269772	103269930	103269800	103269910	UBR5	NM_015902	1	59	58	-	103269860	103269945
302524675	chr8	103273311	103273456	103273339	103273429	UBR5	NM_015902	1	59	56	-	103273374	103273487
304016435	chr8	103277230	103277393	103277257	103277369	UBR5	NM_015902	1	59	53	-	103277328	103277506
303208424	chr8	103279206	103279365	103279233	103279338	UBR5	NM_015902	1	59	52	-	103279175	103279235

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
302621685	chr8	103282353	103282520	103282375	103282492	UBR5	NM_015902	1	59	50	-	103282267	103282411
300376389	chr8	103284867	103285011	103284888	103284984	UBR5	NM_015902	1	59	48	-	103284757	103285000
302470016	chr8	103289158	103289331	103289186	103289310	UBR5	NM_015902	1	59	45	-	103289200	103289420
302184737	chr8	103291110	103291279	103291137	103291258	UBR5	NM_015902	1	59	44	-	103291054	103291167
305199938	chr8	103292591	103292765	103292619	103292737	UBR5	NM_015902	1	59	42	-	103292622	103292695
302251740	chr8	103297340	103297501	103297366	103297475	UBR5	NM_015902	1	59	40	-	103297355	103297566
300478975	chr8	103297867	103298039	103297888	103298015	UBR5	NM_015902	1	59	39	-	103297741	103298009
299340592	chr8	103299697	103299847	103299718	103299819	UBR5	NM_015902	1	59	37	-	103299661	103299792
302796177	chr8	103301664	103301833	103301691	103301805	UBR5	NM_015902	1	59	35	-	103301681	103301804
302143481	chr8	103306029	103306198	103306053	103306170	UBR5	NM_015902	1	59	34	-	103305833	103306072
300232246	chr8	103307140	103307280	103307166	103307260	UBR5	NM_015902	1	59	32	-	103307210	103307339
301962183	chr8	103307529	103307688	103307557	103307667	UBR5	NM_015902	1	59	30	-	103307642	103307760
301962183	chr8	103307529	103307688	103307557	103307667	UBR5	NM_015902	1	59	31	-	103307432	103307558
305556322	chr8	103307962	103308108	103307988	103308080	UBR5	NM_015902	1	59	29	-	103307864	103308010
304430848	chr8	103310561	103310718	103310589	103310698	UBR5	NM_015902	1	59	26	-	103310620	103310717
305697237	chr8	103311569	103311721	103311594	103311700	UBR5	NM_015902	1	59	24	-	103311680	103311775
303251635	chr8	103316178	103316315	103316203	103316293	UBR5	NM_015902	1	59	22	-	103316271	103316397
301657951	chr8	103317350	103317481	103317375	103317452	UBR5	NM_015902	1	59	21	-	103317313	103317523
301808273	chr8	103323688	103323852	103323714	103323819	UBR5	NM_015902	1	59	20	-	103323527	103323724
301891979	chr8	103324320	103324489	103324347	103324466	UBR5	NM_015902	1	59	18	-	103324362	103324473
300640675	chr8	103324686	103324839	103324713	103324809	UBR5	NM_015902	1	59	17	-	103324570	103324713
300455164	chr8	103335492	103335663	103335514	103335635	UBR5	NM_015902	1	59	14	-	103335539	103335723
300901713	chr8	103339924	103340076	103339952	103340054	UBR5	NM_015902	1	59	12	-	103339970	103340124
303515953	chr8	103341406	103341580	103341434	103341558	UBR5	NM_015902	1	59	10	-	103341511	103341627
302679131	chr8	103354787	103354935	103354809	103354914	UBR5	NM_015902	1	59	9	-	103354701	103354912
305665606	chr8	103358551	103358709	103358580	103358685	UBR5	NM_015902	1	59	7	-	103358464	103358623
300487785	chr8	103372317	103372455	103372338	103372427	UBR5	NM_015902	1	59	5	-	103372299	103372418
301589434	chr8	103373727	103373888	103373746	103373860	UBR5	NM_015902	1	59	2	-	103373810	103373854
299058466	chr8	113240910	113241066	113240941	113241038	CSMD3	NM_052900	1	69	68	-	113240985	113241120
299058466	chr8	113240910	113241066	113240941	113241038	CSMD3	NM_198123	2	71	70	-	113240985	113241120
299058466	chr8	113240910	113241066	113240941	113241038	CSMD3	NM_198124	3	72	71	-	113240985	113241120
287562697	chr8	113246668	113246840	113246689	113246813	CSMD3	NM_052900	1	69	66	-	113246594	113246706
287562697	chr8	113246668	113246840	113246689	113246813	CSMD3	NM_198123	2	71	68	-	113246594	113246706
287562697	chr8	113246668	113246840	113246689	113246813	CSMD3	NM_198124	3	72	69	-	113246594	113246706
286196692	chr8	113256562	113256707	113256586	113256685	CSMD3	NM_052900	1	69	63	-	113256623	113256802
286196692	chr8	113256562	113256707	113256586	113256685	CSMD3	NM_198123	2	71	65	-	113256623	113256802
286196692	chr8	113256562	113256707	113256586	113256685	CSMD3	NM_198124	3	72	66	-	113256623	113256802
285924937	chr8	113266417	113266543	113266441	113266521	CSMD3	NM_052900	1	69	61	-	113266482	113266555
285924937	chr8	113266417	113266543	113266441	113266521	CSMD3	NM_198123	2	71	63	-	113266482	113266555
285924937	chr8	113266417	113266543	113266441	113266521	CSMD3	NM_198124	3	72	64	-	113266482	113266555
285261665	chr8	113275773	113275907	113275801	113275886	CSMD3	NM_052900	1	69	59	-	113275868	113276041

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
285261665	chr8	113275773	113275907	113275801	113275886	CSMD3	NM_198123	2	71	61	-	113275868	113276041
285261665	chr8	113275773	113275907	113275801	113275886	CSMD3	NM_198124	3	72	62	-	113275868	113276041
286450143	chr8	113277725	113277849	113277747	113277821	CSMD3	NM_052900	1	69	58	-	113277640	113277819
286450143	chr8	113277725	113277849	113277747	113277821	CSMD3	NM_198123	2	71	60	-	113277640	113277819
286450143	chr8	113277725	113277849	113277747	113277821	CSMD3	NM_198124	3	72	61	-	113277640	113277819
286706277	chr8	113299166	113299331	113299194	113299310	CSMD3	NM_052900	1	69	56	-	113299293	113299475
286706277	chr8	113299166	113299331	113299194	113299310	CSMD3	NM_198123	2	71	58	-	113299293	113299475
286706277	chr8	113299166	113299331	113299194	113299310	CSMD3	NM_198124	3	72	59	-	113299293	113299475
287340985	chr8	113301680	113301832	113301708	113301807	CSMD3	NM_052900	1	69	55	-	113301594	113301767
287340985	chr8	113301680	113301832	113301708	113301807	CSMD3	NM_198123	2	71	57	-	113301594	113301767
287340985	chr8	113301680	113301832	113301708	113301807	CSMD3	NM_198124	3	72	58	-	113301594	113301767
286339402	chr8	113303897	113304048	113303921	113304016	CSMD3	NM_052900	1	69	54	-	113303739	113303924
286339402	chr8	113303897	113304048	113303921	113304016	CSMD3	NM_198123	2	71	56	-	113303739	113303924
286339402	chr8	113303897	113304048	113303921	113304016	CSMD3	NM_198124	3	72	57	-	113303739	113303924
287197072	chr8	113308075	113308239	113308096	113308218	CSMD3	NM_052900	1	69	52	-	113308062	113308235
287197072	chr8	113308075	113308239	113308096	113308218	CSMD3	NM_198123	2	71	54	-	113308062	113308235
287197072	chr8	113308075	113308239	113308096	113308218	CSMD3	NM_198124	3	72	55	-	113308062	113308235
288082703	chr8	113314120	113314260	113314145	113314235	CSMD3	NM_052900	1	69	51	-	113314022	113314195
288082703	chr8	113314120	113314260	113314145	113314235	CSMD3	NM_198123	2	71	53	-	113314022	113314195
288082703	chr8	113314120	113314260	113314145	113314235	CSMD3	NM_198124	3	72	54	-	113314022	113314195
288582514	chr8	113318208	113318355	113318233	113318327	CSMD3	NM_052900	1	69	50	-	113318236	113318421
288582514	chr8	113318208	113318355	113318233	113318327	CSMD3	NM_198123	2	71	51	-	113318236	113318421
288582514	chr8	113318208	113318355	113318233	113318327	CSMD3	NM_198124	3	72	52	-	113318236	113318421
287838183	chr8	113323333	113323483	113323354	113323460	CSMD3	NM_052900	1	69	49	-	113323207	113323395
287838183	chr8	113323333	113323483	113323354	113323460	CSMD3	NM_198123	2	71	50	-	113323207	113323395
287838183	chr8	113323333	113323483	113323354	113323460	CSMD3	NM_198124	3	72	51	-	113323207	113323395
286396598	chr8	113326739	113326894	113326762	113326867	CSMD3	NM_052900	1	69	47	-	113326658	113326846
286396598	chr8	113326739	113326894	113326762	113326867	CSMD3	NM_198123	2	71	48	-	113326658	113326846
286396598	chr8	113326739	113326894	113326762	113326867	CSMD3	NM_198124	3	72	49	-	113326658	113326846
288756103	chr8	113347519	113347684	113347548	113347662	CSMD3	NM_052900	1	69	44	-	113347558	113347703
288756103	chr8	113347519	113347684	113347548	113347662	CSMD3	NM_198123	2	71	45	-	113347558	113347703
288756103	chr8	113347519	113347684	113347548	113347662	CSMD3	NM_198124	3	72	46	-	113347558	113347703
288723163	chr8	113349676	113349814	113349700	113349788	CSMD3	NM_052900	1	69	42	-	113349772	113349960
288723163	chr8	113349676	113349814	113349700	113349788	CSMD3	NM_198123	2	71	43	-	113349772	113349960
288723163	chr8	113349676	113349814	113349700	113349788	CSMD3	NM_198124	3	72	44	-	113349772	113349960
287945714	chr8	113353779	113353921	113353807	113353893	CSMD3	NM_052900	1	69	41	-	113353706	113353915
287945714	chr8	113353779	113353921	113353807	113353893	CSMD3	NM_198123	2	71	42	-	113353706	113353915
287945714	chr8	113353779	113353921	113353807	113353893	CSMD3	NM_198124	3	72	43	-	113353706	113353915
287150997	chr8	113363301	113363458	113363334	113363434	CSMD3	NM_052900	1	69	39	-	113363404	113363473
287150997	chr8	113363301	113363458	113363334	113363434	CSMD3	NM_198123	2	71	40	-	113363404	113363473
287150997	chr8	113363301	113363458	113363334	113363434	CSMD3	NM_198124	3	72	41	-	113363404	113363473

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287582163	chr8	113392537	113392687	113392565	113392659	CSMD3	NM_052900	1	69	37	-	113392581	113392685
287582163	chr8	113392537	113392687	113392565	113392659	CSMD3	NM_198123	2	71	38	-	113392581	113392685
287582163	chr8	113392537	113392687	113392565	113392659	CSMD3	NM_198124	3	72	39	-	113392581	113392685
286748733	chr8	113402782	113402955	113402808	113402927	CSMD3	NM_052900	1	69	35	-	113402893	113403017
286748733	chr8	113402782	113402955	113402808	113402927	CSMD3	NM_198123	2	71	36	-	113402893	113403017
286748733	chr8	113402782	113402955	113402808	113402927	CSMD3	NM_198124	3	72	37	-	113402893	113403017
288474492	chr8	113418914	113419071	113418935	113419038	CSMD3	NM_052900	1	69	34	-	113418753	113418956
288474492	chr8	113418914	113419071	113418935	113419038	CSMD3	NM_198123	2	71	35	-	113418753	113418956
288474492	chr8	113418914	113419071	113418935	113419038	CSMD3	NM_198124	3	72	36	-	113418753	113418956
285177034	chr8	113484759	113484903	113484789	113484875	CSMD3	NM_052900	1	69	31	-	113484820	113484936
285177034	chr8	113484759	113484903	113484789	113484875	CSMD3	NM_198123	2	71	32	-	113484820	113484936
285177034	chr8	113484759	113484903	113484789	113484875	CSMD3	NM_198124	3	72	33	-	113484820	113484936
286768488	chr8	113504795	113504921	113504823	113504897	CSMD3	NM_052900	1	69	30	-	113504718	113504912
286768488	chr8	113504795	113504921	113504823	113504897	CSMD3	NM_198123	2	71	31	-	113504718	113504912
286768488	chr8	113504795	113504921	113504823	113504897	CSMD3	NM_198124	3	72	32	-	113504718	113504912
288891043	chr8	113518849	113518975	113518877	113518953	CSMD3	NM_052900	1	69	28	-	113518920	113519058
288891043	chr8	113518849	113518975	113518877	113518953	CSMD3	NM_198123	2	71	29	-	113518920	113519058
288891043	chr8	113518849	113518975	113518877	113518953	CSMD3	NM_198124	3	72	30	-	113518920	113519058
286889655	chr8	113529395	113529522	113529416	113529489	CSMD3	NM_052900	1	69	27	-	113529263	113529454
286889655	chr8	113529395	113529522	113529416	113529489	CSMD3	NM_198123	2	71	28	-	113529263	113529454
286889655	chr8	113529395	113529522	113529416	113529489	CSMD3	NM_198124	3	72	29	-	113529263	113529454
286429364	chr8	113564766	113564899	113564786	113564873	CSMD3	NM_052900	1	69	25	-	113564823	113564949
286429364	chr8	113564766	113564899	113564786	113564873	CSMD3	NM_198123	2	71	26	-	113564823	113564949
286429364	chr8	113564766	113564899	113564786	113564873	CSMD3	NM_198124	3	72	27	-	113564823	113564949
286262269	chr8	113569069	113569193	113569093	113569169	CSMD3	NM_052900	1	69	24	-	113568992	113569183
286262269	chr8	113569069	113569193	113569093	113569169	CSMD3	NM_198123	2	71	25	-	113568992	113569183
286262269	chr8	113569069	113569193	113569093	113569169	CSMD3	NM_198124	3	72	26	-	113568992	113569183
287547429	chr8	113585839	113586013	113585866	113585986	CSMD3	NM_052900	1	69	23	-	113585730	113585886
287547429	chr8	113585839	113586013	113585866	113585986	CSMD3	NM_198123	2	71	24	-	113585730	113585886
287547429	chr8	113585839	113586013	113585866	113585986	CSMD3	NM_198124	3	72	25	-	113585730	113585886
288892329	chr8	113648959	113649131	113648988	113649107	CSMD3	NM_052900	1	69	21	-	113649046	113649234
288892329	chr8	113648959	113649131	113648988	113649107	CSMD3	NM_198123	2	71	22	-	113649046	113649234
288892329	chr8	113648959	113649131	113648988	113649107	CSMD3	NM_198124	3	72	23	-	113649046	113649234
288126519	chr8	113650973	113651110	113650994	113651083	CSMD3	NM_052900	1	69	20	-	113650925	113651140
288126519	chr8	113650973	113651110	113650994	113651083	CSMD3	NM_198123	2	71	21	-	113650925	113651140
288126519	chr8	113650973	113651110	113650994	113651083	CSMD3	NM_198124	3	72	22	-	113650925	113651140
286812883	chr8	113662368	113662504	113662397	113662476	CSMD3	NM_052900	1	69	18	-	113662390	113662578
286812883	chr8	113662368	113662504	113662397	113662476	CSMD3	NM_198123	2	71	19	-	113662390	113662578
286812883	chr8	113662368	113662504	113662397	113662476	CSMD3	NM_198124	3	72	20	-	113662390	113662578
284964094	chr8	113668514	113668642	113668539	113668610	CSMD3	NM_052900	1	69	17	-	113668383	113668570
284964094	chr8	113668514	113668642	113668539	113668610	CSMD3	NM_198123	2	71	18	-	113668383	113668570

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
284964094	chr8	113668514	113668642	113668539	113668610	CSMD3	NM_198124	3	72	19	-	113668383	113668570
286411892	chr8	113694580	113694714	113694605	113694689	CSMD3	NM_052900	1	69	15	-	113694671	113694865
286411892	chr8	113694580	113694714	113694605	113694689	CSMD3	NM_198123	2	71	16	-	113694671	113694865
286411892	chr8	113694580	113694714	113694605	113694689	CSMD3	NM_198124	3	72	17	-	113694671	113694865
285080116	chr8	113697547	113697687	113697576	113697664	CSMD3	NM_052900	1	69	14	-	113697635	113697961
285080116	chr8	113697547	113697687	113697576	113697664	CSMD3	NM_198123	2	71	15	-	113697635	113697961
285080116	chr8	113697547	113697687	113697576	113697664	CSMD3	NM_198124	3	72	16	-	113697635	113697961
288674113	chr8	113702067	113702222	113702091	113702194	CSMD3	NM_052900	1	69	13	-	113702097	113702279
288674113	chr8	113702067	113702222	113702091	113702194	CSMD3	NM_198123	2	71	14	-	113702097	113702279
288674113	chr8	113702067	113702222	113702091	113702194	CSMD3	NM_198124	3	72	15	-	113702097	113702279
286645813	chr8	113841871	113842044	113841893	113842019	CSMD3	NM_052900	1	69	11	-	113841915	113842018
286645813	chr8	113841871	113842044	113841893	113842019	CSMD3	NM_198123	2	71	12	-	113841915	113842018
286645813	chr8	113841871	113842044	113841893	113842019	CSMD3	NM_198124	3	72	13	-	113841915	113842018
286417430	chr8	113933878	113934052	113933901	113934024	CSMD3	NM_052900	1	69	9	-	113933856	113933980
286417430	chr8	113933878	113934052	113933901	113934024	CSMD3	NM_198123	2	71	10	-	113933856	113933980
286417430	chr8	113933878	113934052	113933901	113934024	CSMD3	NM_198124	3	72	11	-	113933856	113933980
287590652	chr8	113988025	113988152	113988049	113988127	CSMD3	NM_198123	2	71	7	-	113988066	113988377
287590652	chr8	113988025	113988152	113988049	113988127	CSMD3	NM_198124	3	72	8	-	113988066	113988377
288560080	chr8	114031343	114031477	114031365	114031449	CSMD3	NM_052900	1	69	6	-	114031296	114031408
288560080	chr8	114031343	114031477	114031365	114031449	CSMD3	NM_198123	2	71	6	-	114031296	114031408
288560080	chr8	114031343	114031477	114031365	114031449	CSMD3	NM_198124	3	72	7	-	114031296	114031408
286363980	chr8	114185898	114186063	114185926	114186041	CSMD3	NM_052900	1	69	4	-	114185951	114186145
286363980	chr8	114185898	114186063	114185926	114186041	CSMD3	NM_198123	2	71	4	-	114185951	114186145
286363980	chr8	114185898	114186063	114185926	114186041	CSMD3	NM_198124	3	72	5	-	114185951	114186145
288172829	chr8	114326754	114326928	114326781	114326900	CSMD3	NM_052900	1	69	2	-	114326800	114327022
288172829	chr8	114326754	114326928	114326781	114326900	CSMD3	NM_198123	2	71	2	-	114326800	114327022
288172829	chr8	114326754	114326928	114326781	114326900	CSMD3	NM_198124	3	72	3	-	114326800	114327022
287770886	chr8	114388850	114389014	114388874	114388991	CSMD3	NM_198124	3	72	2	-	114388967	114389114
232648306	chr8	118811902	118812057	118811922	118812038	EXT1	NM_000127	1	11	11	-	118811602	118812136
229552513	chr8	118819358	118819514	118819385	118819492	EXT1	NM_000127	1	11	9	-	118819456	118819616
230794363	chr8	118831894	118832067	118831914	118832039	EXT1	NM_000127	1	11	6	-	118831915	118832033
228298283	chr8	118847649	118847821	118847670	118847798	EXT1	NM_000127	1	11	3	-	118847683	118847790
231389553	chr8	119122526	119122694	119122549	119122674	EXT1	NM_000127	1	11	1	-	119122324	119124058
231403266	chr8	119122966	119123096	119122989	119123073	EXT1	NM_000127	1	11	1	-	119122324	119124058
240718058	chr8	128750439	128750580	128750461	128750559	MYC	NM_002467	1	3	2	+	128750494	128751265
240736615	chr8	128750819	128750993	128750838	128750976	MYC	NM_002467	1	3	2	+	128750494	128751265
242575364	chr8	128752525	128752695	128752553	128752670	MYC	NM_002467	1	3	3	+	128752642	128753680
242641813	chr8	128752953	128753120	128752973	128753099	MYC	NM_002467	1	3	3	+	128752642	128753680
240784630	chr8	145736937	145737104	145736956	145737086	RECQL4	NM_004260	1	22	21	-	145737064	145737172
260714778	chr8	145737480	145737641	145737497	145737623	RECQL4	NM_004260	1	22	19	-	145737527	145737707
239187331	chr8	145737984	145738158	145738006	145738138	RECQL4	NM_004260	1	22	17	-	145738025	145738154

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264245598	chr8	145738424	145738551	145738441	145738530	RECQL4	NM_004260	1	22	16	-	145738230	145738521
262830009	chr8	145738889	145739059	145738909	145739031	RECQL4	NM_004260	1	22	13	-	145738955	145739096
238541001	chr8	145739435	145739582	145739453	145739562	RECQL4	NM_004260	1	22	12	-	145739312	145739491
263791196	chr8	145739835	145740008	145739856	145739986	RECQL4	NM_004260	1	22	10	-	145739826	145739909
260975900	chr8	145740539	145740666	145740558	145740644	RECQL4	NM_004260	1	22	8	-	145740534	145740626
238518712	chr8	145741175	145741307	145741197	145741287	RECQL4	NM_004260	1	22	6	-	145741148	145741274
264078010	chr8	145741609	145741782	145741631	145741760	RECQL4	NM_004260	1	22	5	-	145741372	145742148
264082996	chr8	145742022	145742178	145742044	145742156	RECQL4	NM_004260	1	22	5	-	145741372	145742148
240872942	chr8	145742854	145743028	145742873	145743007	RECQL4	NM_004260	1	22	2	-	145742986	145743019
240872942	chr8	145742854	145743028	145742873	145743007	RECQL4	NM_004260	1	22	3	-	145742798	145742892
233784977	chr9	5021948	5022119	5021976	5022091	JAK2	NM_004972	1	25	3	+	5021963	5022213
234597125	chr9	5029829	5029954	5029853	5029926	JAK2	NM_004972	1	25	4	+	5029783	5029906
232451247	chr9	5050752	5050922	5050777	5050897	JAK2	NM_004972	1	25	6	+	5050686	5050831
233554755	chr9	5054732	5054884	5054757	5054856	JAK2	NM_004972	1	25	7	+	5054563	5054884
233184441	chr9	5064911	5065041	5064940	5065019	JAK2	NM_004972	1	25	9	+	5064883	5065040
232748454	chr9	5068967	5069116	5068992	5069091	JAK2	NM_004972	1	25	11	+	5069022	5069208
231992790	chr9	5072430	5072570	5072456	5072547	JAK2	NM_004972	1	25	13	+	5072492	5072626
233378243	chr9	5077457	5077586	5077485	5077561	JAK2	NM_004972	1	25	15	+	5077453	5077580
232461347	chr9	5080230	5080375	5080254	5080350	JAK2	NM_004972	1	25	17	+	5080229	5080380
231843011	chr9	5081631	5081805	5081660	5081783	JAK2	NM_004972	1	25	19	+	5081725	5081861
233441081	chr9	5090407	5090575	5090435	5090547	JAK2	NM_004972	1	25	21	+	5090446	5090570
233001226	chr9	5122936	5123060	5122964	5123039	JAK2	NM_004972	1	25	23	+	5123004	5123121
234768466	chr9	5126622	5126790	5126646	5126763	JAK2	NM_004972	1	25	25	+	5126684	5128183
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_001040712	1	30	29	-	8319831	8319966
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_001171025	2	29	28	-	8319831	8319966
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_130393	6	29	28	-	8319831	8319966
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_130392	5	31	30	-	8319831	8319966
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_130391	4	31	30	-	8319831	8319966
272623718	chr9	8319834	8319998	8319856	8319977	PTPRD	NM_002839	3	46	45	-	8319831	8319966
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_001040712	1	30	27	-	8338922	8339047
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_001171025	2	29	26	-	8338922	8339047
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_130393	6	29	26	-	8338922	8339047
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_130392	5	31	28	-	8338922	8339047
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_130391	4	31	28	-	8338922	8339047
270949147	chr9	8338914	8339040	8338936	8339020	PTPRD	NM_002839	3	46	43	-	8338922	8339047
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_001040712	1	30	25	-	8341090	8341268
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_001171025	2	29	24	-	8341090	8341268
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_130393	6	29	24	-	8341090	8341268
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_130392	5	31	26	-	8341090	8341268
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_130391	4	31	26	-	8341090	8341268
271890430	chr9	8341119	8341280	8341147	8341258	PTPRD	NM_002839	3	46	41	-	8341090	8341268

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_001040712	1	30	24	-	8341693	8341978
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_001171025	2	29	23	-	8341693	8341978
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_130393	6	29	23	-	8341693	8341978
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_130392	5	31	25	-	8341693	8341978
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_130391	4	31	25	-	8341693	8341978
271265143	chr9	8341838	8342008	8341866	8341980	PTPRD	NM_002839	3	46	40	-	8341693	8341978
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_001040712	1	30	22	-	8376607	8376726
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_001171025	2	29	21	-	8376607	8376726
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_130393	6	29	21	-	8376607	8376726
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_130392	5	31	23	-	8376607	8376726
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_130391	4	31	23	-	8376607	8376726
270645116	chr9	8376601	8376755	8376627	8376731	PTPRD	NM_002839	3	46	38	-	8376607	8376726
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_001040712	1	30	20	-	8404537	8404660
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_001171025	2	29	19	-	8404537	8404660
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_130393	6	29	19	-	8404537	8404660
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_130392	5	31	21	-	8404537	8404660
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_130391	4	31	21	-	8404537	8404660
270944411	chr9	8404582	8404712	8404609	8404684	PTPRD	NM_002839	3	46	36	-	8404537	8404660
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_001040712	1	30	18	-	8449725	8449837
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_001171025	2	29	16	-	8449725	8449837
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_130393	6	29	17	-	8449725	8449837
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_130392	5	31	19	-	8449725	8449837
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_130391	4	31	19	-	8449725	8449837
270383857	chr9	8449664	8449795	8449690	8449770	PTPRD	NM_002839	3	46	34	-	8449725	8449837
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_001040712	1	30	16	-	8460411	8460571
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_001171025	2	29	15	-	8460411	8460571
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_130393	6	29	16	-	8460411	8460571
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_130392	5	31	17	-	8460411	8460571
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_130391	4	31	17	-	8460411	8460571
271212045	chr9	8460429	8460595	8460456	8460567	PTPRD	NM_002839	3	46	33	-	8460411	8460571
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_001040712	1	30	15	-	8465466	8465675
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_001171025	2	29	14	-	8465466	8465675
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_130393	6	29	15	-	8465466	8465675
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_130392	5	31	16	-	8465466	8465675
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_130391	4	31	16	-	8465466	8465675
270234188	chr9	8465618	8465776	8465644	8465750	PTPRD	NM_002839	3	46	32	-	8465466	8465675
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_001040712	1	30	13	-	8484119	8484378
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_001171025	2	29	12	-	8484119	8484378
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_130393	6	29	13	-	8484119	8484378
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_130392	5	31	14	-	8484119	8484378
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_130391	4	31	14	-	8484119	8484378

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270035026	chr9	8484310	8484470	8484335	8484443	PTPRD	NM_002839	3	46	30	-	8484119	8484378
272563016	chr9	8485858	8486027	8485884	8486007	PTPRD	NM_002839	3	46	28	-	8485762	8486349
271948419	chr9	8492784	8492937	8492808	8492917	PTPRD	NM_002839	3	46	27	-	8492862	8492979
272605102	chr9	8499735	8499898	8499760	8499877	PTPRD	NM_002839	3	46	25	-	8499647	8499840
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_001040712	1	30	11	-	8504261	8504405
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_001171025	2	29	10	-	8504261	8504405
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_130393	6	29	11	-	8504261	8504405
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_130392	5	31	12	-	8504261	8504405
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_130391	4	31	12	-	8504261	8504405
271978951	chr9	8504173	8504306	8504196	8504282	PTPRD	NM_002839	3	46	23	-	8504261	8504405
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_130393	6	29	9	-	8517848	8518429
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_130392	5	31	10	-	8517848	8518429
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_130391	4	31	10	-	8517848	8518429
269838076	chr9	8517820	8517985	8517842	8517961	PTPRD	NM_002839	3	46	21	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_130393	6	29	9	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_130392	5	31	10	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_130391	4	31	10	-	8517848	8518429
269908799	chr9	8518270	8518436	8518294	8518414	PTPRD	NM_002839	3	46	21	-	8517848	8518429
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_001040712	1	30	8	-	8521277	8521546
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_001171025	2	29	7	-	8521277	8521546
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_130393	6	29	8	-	8521277	8521546
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_130392	5	31	9	-	8521277	8521546
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_130391	4	31	9	-	8521277	8521546
271248611	chr9	8521410	8521575	8521431	8521547	PTPRD	NM_002839	3	46	20	-	8521277	8521546
269709893	chr9	8526533	8526707	8526555	8526679	PTPRD	NM_001040712	1	30	5	-	8526627	8526644
269709893	chr9	8526533	8526707	8526555	8526679	PTPRD	NM_130392	5	31	6	-	8526627	8526644
269709893	chr9	8526533	8526707	8526555	8526679	PTPRD	NM_130391	4	31	6	-	8526627	8526644
269709893	chr9	8526533	8526707	8526555	8526679	PTPRD	NM_002839	3	46	17	-	8526627	8526644
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_001040712	1	30	3	-	8633317	8633458
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_001171025	2	29	3	-	8633317	8633458
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_130393	6	29	3	-	8633317	8633458
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_130392	5	31	3	-	8633317	8633458
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_130391	4	31	3	-	8633317	8633458
270182242	chr9	8633205	8633371	8633230	8633342	PTPRD	NM_002839	3	46	14	-	8633317	8633458
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_001040712	1	30	1	-	8733780	8733946
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_001171025	2	29	1	-	8733780	8733946
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_130393	6	29	1	-	8733780	8733946

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_130392	5	31	1	-	8733780	8733946
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_130391	4	31	1	-	8733780	8733946
270411923	chr9	8733721	8733892	8733747	8733871	PTPRD	NM_002839	3	46	12	-	8733780	8733946
235602904	chr9	15468681	15468852	15468706	15468828	PSIP1	NM_001128217	1	16	14	-	15468628	15468841
235602904	chr9	15468681	15468852	15468706	15468828	PSIP1	NM_033222	3	16	14	-	15468628	15468841
238340206	chr9	15471119	15471282	15471145	15471257	PSIP1	NM_021144	2	10	10	-	15470642	15471229
235619062	chr9	15474046	15474196	15474068	15474168	PSIP1	NM_001128217	1	16	9	-	15474007	15474235
235619062	chr9	15474046	15474196	15474068	15474168	PSIP1	NM_033222	3	16	9	-	15474007	15474235
235619062	chr9	15474046	15474196	15474068	15474168	PSIP1	NM_021144	2	10	8	-	15474007	15474235
238725795	chr9	15485918	15486053	15485946	15486026	PSIP1	NM_001128217	1	16	6	-	15486004	15486066
238725795	chr9	15485918	15486053	15485946	15486026	PSIP1	NM_033222	3	16	6	-	15486004	15486066
238725795	chr9	15485918	15486053	15485946	15486026	PSIP1	NM_021144	2	10	5	-	15486004	15486066
235801541	chr9	15489919	15490087	15489946	15490058	PSIP1	NM_001128217	1	16	4	-	15489984	15490122
235801541	chr9	15489919	15490087	15489946	15490058	PSIP1	NM_033222	3	16	4	-	15489984	15490122
235801541	chr9	15489919	15490087	15489946	15490058	PSIP1	NM_021144	2	10	3	-	15489984	15490122
225436497	chr9	21968152	21968278	21968172	21968252	CDKN2A	NM_058195	3	3	3	-	21967751	21968241
225436497	chr9	21968152	21968278	21968172	21968252	CDKN2A	NM_058197	4	3	3	-	21967751	21968241
225436497	chr9	21968152	21968278	21968172	21968252	CDKN2A	NM_001195132	2	4	4	-	21967751	21968241
225436497	chr9	21968152	21968278	21968172	21968252	CDKN2A	NM_000077	1	3	3	-	21967751	21968241
225943133	chr9	21971112	21971273	21971129	21971251	CDKN2A	NM_058195	3	3	2	-	21970901	21971207
225943133	chr9	21971112	21971273	21971129	21971251	CDKN2A	NM_058197	4	3	2	-	21970901	21971207
225943133	chr9	21971112	21971273	21971129	21971251	CDKN2A	NM_001195132	2	4	2	-	21970901	21971207
225943133	chr9	21971112	21971273	21971129	21971251	CDKN2A	NM_000077	1	3	2	-	21970901	21971207
226642480	chr9	21994113	21994280	21994132	21994263	CDKN2A	NM_058195	3	3	1	-	21994138	21994490
226281085	chr9	22006035	22006179	22006052	22006161	CDKN2B	NM_004936	1	2	2	-	22002902	22006246
226281085	chr9	22006035	22006179	22006052	22006161	CDKN2B	NM_078487	2	2	2	-	22002902	22006246
226596194	chr9	22008859	22009004	22008880	22008982	CDKN2B	NM_078487	2	2	1	-	22008674	22009312
226596194	chr9	22008859	22009004	22008880	22008982	CDKN2B	NM_004936	1	2	1	-	22008797	22009312
261447187	chr9	32630291	32630448	32630313	32630426	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261360222	chr9	32630676	32630840	32630704	32630813	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237832277	chr9	32631049	32631179	32631076	32631152	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237925481	chr9	32631395	32631551	32631423	32631524	TAF1L	NM_153809	1	1	1	-	32629452	32635667
238055360	chr9	32631798	32631935	32631821	32631910	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237881643	chr9	32632151	32632324	32632171	32632300	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261244802	chr9	32632549	32632700	32632573	32632679	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261245009	chr9	32632942	32633093	32632963	32633066	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261400233	chr9	32633266	32633437	32633288	32633410	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237868220	chr9	32633718	32633888	32633740	32633868	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237905828	chr9	32634140	32634304	32634162	32634284	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261317962	chr9	32634554	32634703	32634578	32634682	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261340568	chr9	32635019	32635182	32635046	32635154	TAF1L	NM_153809	1	1	1	-	32629452	32635667

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261296169	chr9	32635439	32635598	32635461	32635571	TAF1L	NM_153809	1	1	1	-	32629452	32635667
230669015	chr9	35074362	35074532	35074384	35074504	FANCG	NM_004629	1	14	13	-	35074368	35074491
228765905	chr9	35075432	35075596	35075451	35075574	FANCG	NM_004629	1	14	10	-	35075462	35075751
228462338	chr9	35076379	35076550	35076401	35076525	FANCG	NM_004629	1	14	8	-	35076429	35076580
229652260	chr9	35076934	35077099	35076955	35077078	FANCG	NM_004629	1	14	6	-	35076968	35077098
230950419	chr9	35078112	35078286	35078135	35078266	FANCG	NM_004629	1	14	4	-	35078138	35078340
227758327	chr9	35078656	35078795	35078677	35078767	FANCG	NM_004629	1	14	3	-	35078602	35078733
235922099	chr9	36846792	36846954	36846811	36846931	PAX5	NM_016734	1	10	9	-	36846840	36846926
237358588	chr9	36966469	36966616	36966489	36966597	PAX5	NM_016734	1	10	6	-	36966546	36966721
238851990	chr9	37006359	37006532	37006384	37006509	PAX5	NM_016734	1	10	4	-	37006470	37006534
241232257	chr9	37020568	37020734	37020592	37020714	PAX5	NM_016734	1	10	2	-	37020633	37020798
227232971	chr9	80336328	80336459	80336348	80336436	GNAQ	NM_002072	1	7	7	-	80335191	80336429
326953658	chr9	80409465	80409621	80409491	80409591	GNAQ	NM_002072	1	7	5	-	80409379	80409508
229847418	chr9	80430628	80430795	80430653	80430767	GNAQ	NM_002072	1	7	3	-	80430532	80430686
227583662	chr9	80646004	80646169	80646023	80646148	GNAQ	NM_002072	1	7	1	-	80646016	80646219
238002595	chr9	93606361	93606507	93606382	93606486	SYK	NM_001135052	1	13	2	+	93606140	93606597
238002595	chr9	93606361	93606507	93606382	93606486	SYK	NM_001174167	2	14	2	+	93606140	93606597
238002595	chr9	93606361	93606507	93606382	93606486	SYK	NM_001174168	3	13	2	+	93606140	93606597
238002595	chr9	93606361	93606507	93606382	93606486	SYK	NM_003177	4	14	2	+	93606140	93606597
240574060	chr9	93607804	93607959	93607827	93607934	SYK	NM_001135052	1	13	3	+	93607716	93607876
240574060	chr9	93607804	93607959	93607827	93607934	SYK	NM_001174167	2	14	3	+	93607716	93607876
240574060	chr9	93607804	93607959	93607827	93607934	SYK	NM_001174168	3	13	3	+	93607716	93607876
240574060	chr9	93607804	93607959	93607827	93607934	SYK	NM_003177	4	14	3	+	93607716	93607876
239649723	chr9	93627235	93627408	93627263	93627381	SYK	NM_001135052	1	13	6	+	93627330	93627379
239649723	chr9	93627235	93627408	93627263	93627381	SYK	NM_001174167	2	14	6	+	93627330	93627379
239649723	chr9	93627235	93627408	93627263	93627381	SYK	NM_001174168	3	13	6	+	93627330	93627379
239649723	chr9	93627235	93627408	93627263	93627381	SYK	NM_003177	4	14	6	+	93627330	93627379
242596413	chr9	93637037	93637187	93637058	93637162	SYK	NM_001135052	1	13	8	+	93636954	93637131
242596413	chr9	93637037	93637187	93637058	93637162	SYK	NM_001174167	2	14	9	+	93636954	93637131
242596413	chr9	93637037	93637187	93637058	93637162	SYK	NM_001174168	3	13	8	+	93636954	93637131
242596413	chr9	93637037	93637187	93637058	93637162	SYK	NM_003177	4	14	9	+	93636954	93637131
262064950	chr9	93640972	93641141	93640993	93641117	SYK	NM_001135052	1	13	10	+	93641046	93641235
262064950	chr9	93640972	93641141	93640993	93641117	SYK	NM_001174167	2	14	11	+	93641046	93641235
262064950	chr9	93640972	93641141	93640993	93641117	SYK	NM_001174168	3	13	10	+	93641046	93641235
262064950	chr9	93640972	93641141	93640993	93641117	SYK	NM_003177	4	14	11	+	93641046	93641235
238022124	chr9	93650718	93650847	93650742	93650824	SYK	NM_001135052	1	13	12	+	93650797	93650909
238022124	chr9	93650718	93650847	93650742	93650824	SYK	NM_001174167	2	14	13	+	93650797	93650909
238022124	chr9	93650718	93650847	93650742	93650824	SYK	NM_001174168	3	13	12	+	93650797	93650909
238022124	chr9	93650718	93650847	93650742	93650824	SYK	NM_003177	4	14	13	+	93650797	93650909
232214841	chr9	97863995	97864166	97864018	97864138	FANCC	NM_001243743	2	15	15	-	97861336	97864132
232214841	chr9	97863995	97864166	97864018	97864138	FANCC	NM_000136	1	15	15	-	97861336	97864132

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232442361	chr9	97873501	97873661	97873524	97873640	FANCC	NM_001243744	3	14	14	-	97872508	97873627
230729295	chr9	97879539	97879695	97879563	97879673	FANCC	NM_001243744	3	14	11	-	97879597	97879672
230729295	chr9	97879539	97879695	97879563	97879673	FANCC	NM_001243743	2	15	11	-	97879597	97879672
230729295	chr9	97879539	97879695	97879563	97879673	FANCC	NM_000136	1	15	11	-	97879597	97879672
228766717	chr9	97897618	97897786	97897645	97897761	FANCC	NM_001243744	3	14	8	-	97897628	97897784
228766717	chr9	97897618	97897786	97897645	97897761	FANCC	NM_001243743	2	15	8	-	97897628	97897784
228766717	chr9	97897618	97897786	97897645	97897761	FANCC	NM_000136	1	15	8	-	97897628	97897784
232095994	chr9	97933317	97933457	97933345	97933429	FANCC	NM_001243744	3	14	6	-	97933361	97933425
232095994	chr9	97933317	97933457	97933345	97933429	FANCC	NM_001243743	2	15	6	-	97933361	97933425
232095994	chr9	97933317	97933457	97933345	97933429	FANCC	NM_000136	1	15	6	-	97933361	97933425
230985927	chr9	98009680	98009842	98009702	98009814	FANCC	NM_001243744	3	14	3	-	98009714	98009798
230985927	chr9	98009680	98009842	98009702	98009814	FANCC	NM_001243743	2	15	3	-	98009714	98009798
230985927	chr9	98009680	98009842	98009702	98009814	FANCC	NM_000136	1	15	3	-	98009714	98009798
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237368433	chr9	98209255	98209421	98209275	98209403	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_000264	1	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
240868639	chr9	98209687	98209841	98209705	98209819	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083605	5	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083602	2	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_000264	1	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083604	4	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083606	6	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083607	7	24	21	-	98212123	98212222
235860581	chr9	98212098	98212249	98212118	98212226	PTCH1	NM_001083603	3	24	21	-	98212123	98212222
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083605	5	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083602	2	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_000264	1	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083604	4	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083606	6	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083607	7	24	19	-	98218558	98218695
236588734	chr9	98218625	98218796	98218648	98218774	PTCH1	NM_001083603	3	24	19	-	98218558	98218695

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083605	5	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083602	2	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_000264	1	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083604	4	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083606	6	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083607	7	24	17	-	98221882	98222065
236315401	chr9	98221857	98222031	98221880	98222005	PTCH1	NM_001083603	3	24	17	-	98221882	98222065
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083602	2	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_000264	1	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
235665327	chr9	98229333	98229507	98229356	98229479	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235325808	chr9	98231060	98231209	98231084	98231189	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083605	5	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083602	2	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_000264	1	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083604	4	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083606	6	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083607	7	24	13	-	98232095	98232213
237953277	chr9	98232123	98232251	98232142	98232226	PTCH1	NM_001083603	3	24	13	-	98232095	98232213
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083605	5	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083602	2	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_000264	1	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083604	4	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083606	6	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083607	7	24	10	-	98239829	98239984
235827061	chr9	98239707	98239881	98239728	98239862	PTCH1	NM_001083603	3	24	10	-	98239829	98239984
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083605	5	24	8	-	98241282	98241429
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083602	2	24	8	-	98241282	98241429
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_000264	1	24	8	-	98241282	98241429
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083604	4	24	8	-	98241282	98241429
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083606	6	24	8	-	98241282	98241429
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083607	7	24	8	-	98241282	98241429

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237006286	chr9	98241225	98241365	98241252	98241342	PTCH1	NM_001083603	3	24	8	-	98241282	98241429
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083605	5	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083602	2	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_000264	1	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083604	4	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083606	6	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083607	7	24	6	-	98242672	98242870
237549971	chr9	98242625	98242779	98242647	98242754	PTCH1	NM_001083603	3	24	6	-	98242672	98242870
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083605	5	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083602	2	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_000264	1	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083604	4	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083606	6	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083607	7	24	3	-	98247967	98248156
237009052	chr9	98247922	98248085	98247943	98248057	PTCH1	NM_001083603	3	24	3	-	98247967	98248156
235585454	chr9	98270384	98270512	98270406	98270494	PTCH1	NM_000264	1	24	1	-	98270443	98270831
237349937	chr9	98278986	98279149	98279012	98279129	PTCH1	NM_001083603	3	24	1	-	98278905	98279247
237349937	chr9	98278986	98279149	98279012	98279129	PTCH1	NM_001083602	2	24	1	-	98278751	98279247
239474830	chr9	100447128	100447291	100447156	100447264	XPA	NR_027302	2	7	5	-	100447205	100447322
239474830	chr9	100447128	100447291	100447156	100447264	XPA	NM_000380	1	6	5	-	100447205	100447322
241664054	chr9	100449488	100449632	100449517	100449612	XPA	NR_027302	2	7	4	-	100449378	100449543
241664054	chr9	100449488	100449632	100449517	100449612	XPA	NM_000380	1	6	4	-	100449378	100449543
262318506	chr9	100455838	100456004	100455868	100455979	XPA	NR_027302	2	7	2	-	100455931	100456041
262318506	chr9	100455838	100456004	100455868	100455979	XPA	NM_000380	1	6	2	-	100455931	100456041
294023878	chr9	120466723	120466887	120466746	120466863	TLR4	NR_024169	5	2	1	+	120466460	120466843
294023878	chr9	120466723	120466887	120466746	120466863	TLR4	NR_024168	4	4	1	+	120466460	120466843
294023878	chr9	120466723	120466887	120466746	120466863	TLR4	NM_003266	1	4	1	+	120466453	120466843
294023878	chr9	120466723	120466887	120466746	120466863	TLR4	NM_138554	2	3	1	+	120466453	120466843
294023878	chr9	120466723	120466887	120466746	120466863	TLR4	NM_138557	3	2	1	+	120466453	120466843
295061082	chr9	120474654	120474804	120474682	120474779	TLR4	NM_003266	1	4	4	+	120474667	120479769
295061082	chr9	120474654	120474804	120474682	120474779	TLR4	NM_138554	2	3	3	+	120474667	120479769
295061082	chr9	120474654	120474804	120474682	120474779	TLR4	NM_138557	3	2	2	+	120474667	120479769
295061082	chr9	120474654	120474804	120474682	120474779	TLR4	NR_024169	5	2	2	+	120474667	120479766
295061082	chr9	120474654	120474804	120474682	120474779	TLR4	NR_024168	4	4	4	+	120474667	120479766
295101783	chr9	120475021	120475187	120475046	120475165	TLR4	NM_003266	1	4	4	+	120474667	120479769
295101783	chr9	120475021	120475187	120475046	120475165	TLR4	NM_138554	2	3	3	+	120474667	120479769
295101783	chr9	120475021	120475187	120475046	120475165	TLR4	NM_138557	3	2	2	+	120474667	120479769
295101783	chr9	120475021	120475187	120475046	120475165	TLR4	NR_024169	5	2	2	+	120474667	120479766
295101783	chr9	120475021	120475187	120475046	120475165	TLR4	NR_024168	4	4	4	+	120474667	120479766
294065610	chr9	120475449	120475606	120475478	120475583	TLR4	NM_003266	1	4	4	+	120474667	120479769
294065610	chr9	120475449	120475606	120475478	120475583	TLR4	NM_138554	2	3	3	+	120474667	120479769

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294065610	chr9	120475449	120475606	120475478	120475583	TLR4	NM_138557	3	2	2	+	120474667	120479769
294065610	chr9	120475449	120475606	120475478	120475583	TLR4	NR_024169	5	2	2	+	120474667	120479766
294065610	chr9	120475449	120475606	120475478	120475583	TLR4	NR_024168	4	4	4	+	120474667	120479766
295102835	chr9	120475867	120476041	120475893	120476013	TLR4	NM_003266	1	4	4	+	120474667	120479769
295102835	chr9	120475867	120476041	120475893	120476013	TLR4	NM_138554	2	3	3	+	120474667	120479769
295102835	chr9	120475867	120476041	120475893	120476013	TLR4	NM_138557	3	2	2	+	120474667	120479769
295102835	chr9	120475867	120476041	120475893	120476013	TLR4	NR_024169	5	2	2	+	120474667	120479766
295102835	chr9	120475867	120476041	120475893	120476013	TLR4	NR_024168	4	4	4	+	120474667	120479766
294150435	chr9	120476317	120476480	120476339	120476457	TLR4	NM_003266	1	4	4	+	120474667	120479769
294150435	chr9	120476317	120476480	120476339	120476457	TLR4	NM_138554	2	3	3	+	120474667	120479769
294150435	chr9	120476317	120476480	120476339	120476457	TLR4	NM_138557	3	2	2	+	120474667	120479769
294150435	chr9	120476317	120476480	120476339	120476457	TLR4	NR_024169	5	2	2	+	120474667	120479766
294150435	chr9	120476317	120476480	120476339	120476457	TLR4	NR_024168	4	4	4	+	120474667	120479766
295102367	chr9	120476817	120476962	120476838	120476939	TLR4	NM_003266	1	4	4	+	120474667	120479769
295102367	chr9	120476817	120476962	120476838	120476939	TLR4	NM_138554	2	3	3	+	120474667	120479769
295102367	chr9	120476817	120476962	120476838	120476939	TLR4	NM_138557	3	2	2	+	120474667	120479769
295102367	chr9	120476817	120476962	120476838	120476939	TLR4	NR_024169	5	2	2	+	120474667	120479766
295102367	chr9	120476817	120476962	120476838	120476939	TLR4	NR_024168	4	4	4	+	120474667	120479766
222672154	chr9	133729435	133729605	133729456	133729578	ABL1	NM_005157	1	11	2	+	133729451	133729624
222672154	chr9	133729435	133729605	133729456	133729578	ABL1	NM_007313	2	11	2	+	133729451	133729624
222610938	chr9	133730411	133730585	133730431	133730560	ABL1	NM_005157	1	11	3	+	133730188	133730483
222610938	chr9	133730411	133730585	133730431	133730560	ABL1	NM_007313	2	11	3	+	133730188	133730483
224096113	chr9	133738382	133738511	133738404	133738489	ABL1	NM_005157	1	11	4	+	133738150	133738422
224096113	chr9	133738382	133738511	133738404	133738489	ABL1	NM_007313	2	11	4	+	133738150	133738422
223939737	chr9	133748258	133748431	133748277	133748408	ABL1	NM_005157	1	11	6	+	133748247	133748424
223939737	chr9	133748258	133748431	133748277	133748408	ABL1	NM_007313	2	11	6	+	133748247	133748424
223726849	chr9	133753706	133753846	133753727	133753824	ABL1	NM_005157	1	11	8	+	133753802	133753954
223726849	chr9	133753706	133753846	133753727	133753824	ABL1	NM_007313	2	11	8	+	133753802	133753954
223629856	chr9	133755970	133756137	133755989	133756118	ABL1	NM_005157	1	11	10	+	133755887	133756051
223629856	chr9	133755970	133756137	133755989	133756118	ABL1	NM_007313	2	11	10	+	133755887	133756051
224384992	chr9	133759617	133759761	133759637	133759744	ABL1	NM_005157	1	11	11	+	133759356	133763062
224384992	chr9	133759617	133759761	133759637	133759744	ABL1	NM_007313	2	11	11	+	133759356	133763062
224378547	chr9	133760027	133760191	133760050	133760169	ABL1	NM_005157	1	11	11	+	133759356	133763062
224378547	chr9	133760027	133760191	133760050	133760169	ABL1	NM_007313	2	11	11	+	133759356	133763062
224374140	chr9	133760345	133760518	133760367	133760499	ABL1	NM_005157	1	11	11	+	133759356	133763062
224374140	chr9	133760345	133760518	133760367	133760499	ABL1	NM_007313	2	11	11	+	133759356	133763062
224374299	chr9	133760795	133760949	133760815	133760927	ABL1	NM_005157	1	11	11	+	133759356	133763062
224374299	chr9	133760795	133760949	133760815	133760927	ABL1	NM_007313	2	11	11	+	133759356	133763062
238790181	chr9	134001100	134001259	134001122	134001239	NUP214	NM_005085	1	36	1	+	134000981	134001136
234997753	chr9	134003658	134003828	134003683	134003803	NUP214	NM_005085	1	36	3	+	134003719	134003870
241121618	chr9	134004768	134004894	134004789	134004866	NUP214	NM_005085	1	36	4	+	134004666	134004864

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236887217	chr9	134008368	134008528	134008392	134008505	NUP214	NM_005085	1	36	7	+	134008493	134008596
235596049	chr9	134011257	134011404	134011278	134011376	NUP214	NM_005085	1	36	9	+	134011327	134011393
237525900	chr9	134015956	134016129	134015979	134016106	NUP214	NM_005085	1	36	11	+	134015936	134016097
237105765	chr9	134019919	134020084	134019942	134020058	NUP214	NM_005085	1	36	12	+	134019667	134020141
235136880	chr9	134021643	134021784	134021664	134021756	NUP214	NM_005085	1	36	13	+	134021516	134021691
239899236	chr9	134025913	134026068	134025936	134026046	NUP214	NM_005085	1	36	16	+	134026003	134026152
237471074	chr9	134034710	134034863	134034738	134034839	NUP214	NM_005085	1	36	18	+	134034770	134034873
235393372	chr9	134039326	134039492	134039350	134039468	NUP214	NM_005085	1	36	21	+	134039448	134039531
236826296	chr9	134049642	134049795	134049666	134049769	NUP214	NM_005085	1	36	22	+	134049442	134049705
236460622	chr9	134062594	134062766	134062616	134062741	NUP214	NM_005085	1	36	25	+	134062676	134062751
235485169	chr9	134067644	134067794	134067666	134067766	NUP214	NM_005085	1	36	27	+	134067595	134067679
238053843	chr9	134072770	134072894	134072791	134072873	NUP214	NM_005085	1	36	29	+	134072603	134074402
234929551	chr9	134073153	134073316	134073177	134073293	NUP214	NM_005085	1	36	29	+	134072603	134074402
237982785	chr9	134073604	134073743	134073621	134073724	NUP214	NM_005085	1	36	29	+	134072603	134074402
237984110	chr9	134074037	134074202	134074059	134074181	NUP214	NM_005085	1	36	29	+	134072603	134074402
236889408	chr9	134090543	134090696	134090566	134090674	NUP214	NM_005085	1	36	31	+	134090599	134090755
235023816	chr9	134103513	134103687	134103539	134103667	NUP214	NM_005085	1	36	33	+	134103547	134103718
236511685	chr9	134107609	134107759	134107631	134107731	NUP214	NM_005085	1	36	35	+	134107671	134107695
265423383	chr9	135771827	135771989	135771853	135771968	TSC1	NM_000368	1	23	23	-	135766735	135772141
265423383	chr9	135771827	135771989	135771853	135771968	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265423383	chr9	135771827	135771989	135771853	135771968	TSC1	NM_001162426	2	23	23	-	135766735	135772141
262375644	chr9	135772590	135772761	135772616	135772733	TSC1	NM_000368	1	23	22	-	135772571	135772732
262375644	chr9	135772590	135772761	135772616	135772733	TSC1	NM_001162427	3	22	21	-	135772571	135772732
262375644	chr9	135772590	135772761	135772616	135772733	TSC1	NM_001162426	2	23	22	-	135772571	135772732
241481319	chr9	135775981	135776133	135776001	135776111	TSC1	NM_000368	1	23	20	-	135776102	135776224
241481319	chr9	135775981	135776133	135776001	135776111	TSC1	NM_001162427	3	22	19	-	135776102	135776224
241481319	chr9	135775981	135776133	135776001	135776111	TSC1	NM_001162426	2	23	20	-	135776102	135776224
263297186	chr9	135778086	135778217	135778111	135778189	TSC1	NM_000368	1	23	18	-	135777992	135778174
263297186	chr9	135778086	135778217	135778111	135778189	TSC1	NM_001162427	3	22	17	-	135777992	135778174
263297186	chr9	135778086	135778217	135778111	135778189	TSC1	NM_001162426	2	23	18	-	135777992	135778174
240476469	chr9	135780948	135781119	135780967	135781095	TSC1	NM_000368	1	23	15	-	135780968	135781526
240476469	chr9	135780948	135781119	135780967	135781095	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240476469	chr9	135780948	135781119	135780967	135781095	TSC1	NM_001162426	2	23	15	-	135780968	135781526
240621248	chr9	135781428	135781567	135781450	135781542	TSC1	NM_000368	1	23	15	-	135780968	135781526
240621248	chr9	135781428	135781567	135781450	135781542	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240621248	chr9	135781428	135781567	135781450	135781542	TSC1	NM_001162426	2	23	15	-	135780968	135781526
266359771	chr9	135786258	135786421	135786284	135786395	TSC1	NM_000368	1	23	11	-	135786389	135786500
266359771	chr9	135786258	135786421	135786284	135786395	TSC1	NM_001162427	3	22	10	-	135786389	135786500
266359771	chr9	135786258	135786421	135786284	135786395	TSC1	NM_001162426	2	23	11	-	135786389	135786500
240250526	chr9	135787734	135787878	135787757	135787850	TSC1	NM_000368	1	23	9	-	135787669	135787844
240250526	chr9	135787734	135787878	135787757	135787850	TSC1	NM_001162427	3	22	8	-	135787669	135787844

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240250526	chr9	135787734	135787878	135787757	135787850	TSC1	NM_001162426	2	23	9	-	135787669	135787844
239734819	chr9	135797213	135797386	135797241	135797361	TSC1	NM_000368	1	23	7	-	135797206	135797360
239734819	chr9	135797213	135797386	135797241	135797361	TSC1	NM_001162427	3	22	6	-	135797206	135797360
239734819	chr9	135797213	135797386	135797241	135797361	TSC1	NM_001162426	2	23	7	-	135797206	135797360
262589944	chr9	135800985	135801154	135801011	135801127	TSC1	NM_000368	1	23	5	-	135800974	135801126
262589944	chr9	135800985	135801154	135801011	135801127	TSC1	NM_001162426	2	23	5	-	135800974	135801126
241689145	chr9	135804212	135804376	135804233	135804354	TSC1	NM_000368	1	23	3	-	135804154	135804339
241689145	chr9	135804212	135804376	135804233	135804354	TSC1	NM_001162427	3	22	3	-	135804154	135804339
241689145	chr9	135804212	135804376	135804233	135804354	TSC1	NM_001162426	2	23	3	-	135804154	135804339
273024683	chr9	135976858	135977026	135976875	135977007	RALGDS	NM_001042368	1	18	16	-	135976907	135977149
273024683	chr9	135976858	135977026	135976875	135977007	RALGDS	NM_006266	2	18	16	-	135976907	135977149
273260789	chr9	135977322	135977479	135977344	135977459	RALGDS	NM_001042368	1	18	15	-	135977325	135977526
273260789	chr9	135977322	135977479	135977344	135977459	RALGDS	NM_006266	2	18	15	-	135977325	135977526
272948297	chr9	135978259	135978404	135978279	135978384	RALGDS	NM_001042368	1	18	13	-	135978166	135978287
272948297	chr9	135978259	135978404	135978279	135978384	RALGDS	NM_006266	2	18	13	-	135978166	135978287
273288034	chr9	135981306	135981430	135981323	135981406	RALGDS	NM_001042368	1	18	9	-	135981319	135981403
273288034	chr9	135981306	135981430	135981323	135981406	RALGDS	NM_006266	2	18	9	-	135981319	135981403
273175090	chr9	135982549	135982721	135982569	135982699	RALGDS	NM_001042368	1	18	7	-	135982472	135982687
273175090	chr9	135982549	135982721	135982569	135982699	RALGDS	NM_006266	2	18	7	-	135982472	135982687
273405354	chr9	135984017	135984191	135984037	135984171	RALGDS	NM_001042368	1	18	5	-	135984060	135984253
273405354	chr9	135984017	135984191	135984037	135984171	RALGDS	NM_006266	2	18	5	-	135984060	135984253
273491642	chr9	135985738	135985909	135985760	135985888	RALGDS	NM_001042368	1	18	3	-	135985683	135985876
273491642	chr9	135985738	135985909	135985760	135985888	RALGDS	NM_006266	2	18	3	-	135985683	135985876
273885232	chr9	135996391	135996556	135996409	135996539	RALGDS	NM_006266	2	18	1	-	135996359	135996561
223264297	chr9	136899862	136899996	136899883	136899977	BRD3	NM_007371	1	12	11	-	136899823	136899951
224454757	chr9	136905074	136905205	136905094	136905186	BRD3	NM_007371	1	12	9	-	136905156	136905391
223285617	chr9	136906939	136907078	136906959	136907058	BRD3	NM_007371	1	12	8	-	136906882	136907073
222638754	chr9	136913093	136913262	136913111	136913244	BRD3	NM_007371	1	12	6	-	136913205	136913576
224438950	chr9	136915468	136915616	136915486	136915596	BRD3	NM_007371	1	12	5	-	136915496	136915710
222176282	chr9	136917377	136917502	136917396	136917476	BRD3	NM_007371	1	12	3	-	136917428	136917565
240910644	chr9	139390420	139390555	139390445	139390538	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236034284	chr9	139390852	139391025	139390869	139391003	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240921691	chr9	139391302	139391463	139391321	139391446	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240924470	chr9	139391634	139391769	139391654	139391752	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
242099919	chr9	139393306	139393477	139393326	139393454	NOTCH1	NM_017617	1	34	33	-	139393351	139393448
236195969	chr9	139395050	139395214	139395067	139395190	NOTCH1	NM_017617	1	34	31	-	139395004	139395299
241773106	chr9	139396352	139396507	139396372	139396485	NOTCH1	NM_017617	1	34	29	-	139396453	139396540
237190087	chr9	139397537	139397672	139397557	139397652	NOTCH1	NM_017617	1	34	27	-	139397634	139397782
241012723	chr9	139399520	139399686	139399541	139399664	NOTCH1	NM_017617	1	34	26	-	139399125	139399556
235687627	chr9	139400051	139400208	139400072	139400190	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
239233519	chr9	139401051	139401211	139401072	139401191	NOTCH1	NM_017617	1	34	24	-	139400979	139401091

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239233519	chr9	139401051	139401211	139401072	139401191	NOTCH1	NM_017617	1	34	23	-	139401168	139401425
236012554	chr9	139401631	139401801	139401653	139401780	NOTCH1	NM_017617	1	34	22	-	139401757	139401889
236748733	chr9	139402628	139402772	139402648	139402754	NOTCH1	NM_017617	1	34	20	-	139402684	139402837
236505138	chr9	139404057	139404225	139404076	139404202	NOTCH1	NM_017617	1	34	18	-	139404185	139404413
238238929	chr9	139405112	139405239	139405130	139405218	NOTCH1	NM_017617	1	34	17	-	139405105	139405257
236462348	chr9	139407417	139407589	139407434	139407571	NOTCH1	NM_017617	1	34	15	-	139407473	139407586
236457248	chr9	139408915	139409087	139408937	139409067	NOTCH1	NM_017617	1	34	13	-	139408962	139409154
235380681	chr9	139409826	139409976	139409848	139409957	NOTCH1	NM_017617	1	34	11	-	139409935	139410168
235380681	chr9	139409826	139409976	139409848	139409957	NOTCH1	NM_017617	1	34	12	-	139409742	139409852
239498335	chr9	139410474	139410603	139410495	139410582	NOTCH1	NM_017617	1	34	10	-	139410433	139410546
237716507	chr9	139412571	139412715	139412588	139412694	NOTCH1	NM_017617	1	34	7	-	139412589	139412744
241560385	chr9	139413827	139413998	139413851	139413972	NOTCH1	NM_017617	1	34	5	-	139413895	139414017
238631254	chr9	139417375	139417508	139417392	139417488	NOTCH1	NM_017617	1	34	4	-	139417302	139417640
237663341	chr9	139418184	139418355	139418202	139418337	NOTCH1	NM_017617	1	34	3	-	139418169	139418431
234819805	chr10	3821683	3821807	3821705	3821785	KLF6	NM_001300	3	4	4	-	3818188	3821782
234819805	chr10	3821683	3821807	3821705	3821785	KLF6	NR_027653	4	4	4	-	3818188	3821782
234819805	chr10	3821683	3821807	3821705	3821785	KLF6	NM_001160125	2	3	3	-	3818188	3821782
234819805	chr10	3821683	3821807	3821705	3821785	KLF6	NM_001160124	1	4	4	-	3818188	3821782
233074228	chr10	3823944	3824099	3823965	3824077	KLF6	NM_001160124	1	4	2	-	3823959	3824406
233074228	chr10	3823944	3824099	3823965	3824077	KLF6	NR_027653	4	4	2	-	3823987	3824406
233074228	chr10	3823944	3824099	3823965	3824077	KLF6	NM_001300	3	4	2	-	3823833	3824406
233074228	chr10	3823944	3824099	3823965	3824077	KLF6	NM_001160125	2	3	2	-	3823833	3824406
232697762	chr10	3827030	3827204	3827048	3827186	KLF6	NM_001300	3	4	1	-	3827105	3827473
232697762	chr10	3827030	3827204	3827048	3827186	KLF6	NR_027653	4	4	1	-	3827105	3827473
232697762	chr10	3827030	3827204	3827048	3827186	KLF6	NM_001160125	2	3	1	-	3827105	3827473
232697762	chr10	3827030	3827204	3827048	3827186	KLF6	NM_001160124	1	4	1	-	3827105	3827473
229309471	chr10	8097799	8097963	8097819	8097943	GATA3	NM_002051	2	6	2	+	8097250	8097859
229309471	chr10	8097799	8097963	8097819	8097943	GATA3	NM_001002295	1	6	2	+	8097250	8097859
229540304	chr10	8100564	8100715	8100587	8100696	GATA3	NM_002051	2	6	3	+	8100268	8100804
229540304	chr10	8100564	8100715	8100587	8100696	GATA3	NM_001002295	1	6	3	+	8100268	8100804
228739614	chr10	8111399	8111549	8111424	8111527	GATA3	NM_002051	2	6	5	+	8111436	8111561
228739614	chr10	8111399	8111549	8111424	8111527	GATA3	NM_001002295	1	6	5	+	8111436	8111561
228232085	chr10	8115844	8116001	8115865	8115981	GATA3	NM_002051	2	6	6	+	8115702	8117164
228232085	chr10	8115844	8116001	8115865	8115981	GATA3	NM_001002295	1	6	6	+	8115702	8117164
232313481	chr10	21827653	21827795	21827681	21827771	MLLT10	NM_004641	5	24	3	+	21827762	21827841
232313481	chr10	21827653	21827795	21827681	21827771	MLLT10	NM_001195627	2	5	3	+	21827762	21827841
232313481	chr10	21827653	21827795	21827681	21827771	MLLT10	NM_001195626	1	22	2	+	21827762	21827841
232313481	chr10	21827653	21827795	21827681	21827771	MLLT10	NM_001195628	3	4	3	+	21827762	21827841
232313481	chr10	21827653	21827795	21827681	21827771	MLLT10	NM_001195630	4	4	3	+	21827762	21827841
231661039	chr10	21884137	21884296	21884165	21884272	MLLT10	NM_004641	5	24	5	+	21884260	21884369
231661039	chr10	21884137	21884296	21884165	21884272	MLLT10	NM_001195626	1	22	4	+	21884260	21884369

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231130641	chr10	21903659	21903827	21903686	21903803	MLLT10	NM_004641	5	24	7	+	21903760	21903853
231130641	chr10	21903659	21903827	21903686	21903803	MLLT10	NM_001195626	1	22	6	+	21903760	21903853
233625669	chr10	21940646	21940803	21940666	21940778	MLLT10	NM_004641	5	24	9	+	21940602	21940697
233625669	chr10	21940646	21940803	21940666	21940778	MLLT10	NM_001195626	1	22	8	+	21940602	21940697
232526973	chr10	21959597	21959737	21959619	21959704	MLLT10	NM_004641	5	24	10	+	21959378	21959633
232526973	chr10	21959597	21959737	21959619	21959704	MLLT10	NM_001195626	1	22	9	+	21959378	21959633
234545644	chr10	21962489	21962662	21962514	21962637	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234545644	chr10	21962489	21962662	21962514	21962637	MLLT10	NM_001195626	1	22	10	+	21962279	21962848
232641302	chr10	21971086	21971234	21971115	21971207	MLLT10	NM_004641	5	24	13	+	21971154	21971186
232641302	chr10	21971086	21971234	21971115	21971207	MLLT10	NM_001195626	1	22	12	+	21971154	21971186
231844568	chr10	22015050	22015220	22015081	22015197	MLLT10	NM_004641	5	24	16	+	22015173	22015284
231844568	chr10	22015050	22015220	22015081	22015197	MLLT10	NM_001195626	1	22	14	+	22015173	22015284
231561702	chr10	22019855	22020026	22019877	22019998	MLLT10	NM_004641	5	24	18	+	22019829	22019983
231561702	chr10	22019855	22020026	22019877	22019998	MLLT10	NM_001195626	1	22	16	+	22019829	22019983
232245242	chr10	22022324	22022486	22022346	22022462	MLLT10	NM_004641	5	24	20	+	22022433	22022521
232245242	chr10	22022324	22022486	22022346	22022462	MLLT10	NM_001195626	1	22	18	+	22022433	22022521
234684624	chr10	22023002	22023131	22023022	22023107	MLLT10	NM_004641	5	24	21	+	22022697	22023058
234684624	chr10	22023002	22023131	22023022	22023107	MLLT10	NM_001195626	1	22	19	+	22022697	22023058
232266636	chr10	22029037	22029164	22029058	22029136	MLLT10	NM_001195626	1	22	21	+	22028959	22029165
232266636	chr10	22029037	22029164	22029058	22029136	MLLT10	NM_004641	5	24	23	+	22029083	22029165
240742669	chr10	43595941	43596108	43595963	43596088	RET	NM_020630	1	19	2	+	43595907	43596170
240742669	chr10	43595941	43596108	43595963	43596088	RET	NM_020975	2	20	2	+	43595907	43596170
242218663	chr10	43597970	43598096	43597989	43598077	RET	NM_020630	1	19	3	+	43597790	43598077
242218663	chr10	43597970	43598096	43597989	43598077	RET	NM_020975	2	20	3	+	43597790	43598077
261502879	chr10	43601800	43601970	43601817	43601953	RET	NM_020630	1	19	5	+	43601824	43602019
261502879	chr10	43601800	43601970	43601817	43601953	RET	NM_020975	2	20	5	+	43601824	43602019
238674262	chr10	43606567	43606713	43606588	43606692	RET	NM_020630	1	19	7	+	43606655	43606913
238674262	chr10	43606567	43606713	43606588	43606692	RET	NM_020975	2	20	7	+	43606655	43606913
238023895	chr10	43607516	43607690	43607535	43607672	RET	NM_020630	1	19	8	+	43607547	43607672
238023895	chr10	43607516	43607690	43607535	43607672	RET	NM_020975	2	20	8	+	43607547	43607672
264063512	chr10	43609895	43610052	43609912	43610035	RET	NM_020630	1	19	11	+	43609928	43610184
264063512	chr10	43609895	43610052	43609912	43610035	RET	NM_020975	2	20	11	+	43609928	43610184
239633572	chr10	43612026	43612187	43612049	43612164	RET	NM_020630	1	19	12	+	43612032	43612179
239633572	chr10	43612026	43612187	43612049	43612164	RET	NM_020975	2	20	12	+	43612032	43612179
241504553	chr10	43614856	43615015	43614877	43614995	RET	NM_020630	1	19	14	+	43614979	43615193
241504553	chr10	43614856	43615015	43614877	43614995	RET	NM_020975	2	20	14	+	43614979	43615193
241633877	chr10	43615576	43615742	43615601	43615719	RET	NM_020630	1	19	15	+	43615529	43615651
241633877	chr10	43615576	43615742	43615601	43615719	RET	NM_020975	2	20	15	+	43615529	43615651
241726831	chr10	43620293	43620466	43620315	43620443	RET	NM_020630	1	19	18	+	43620331	43620430
241726831	chr10	43620293	43620466	43620315	43620443	RET	NM_020975	2	20	18	+	43620331	43620430
262812737	chr10	43623587	43623751	43623608	43623727	RET	NM_020975	2	20	20	+	43623560	43625797

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295398339	chr10	49612897	49613036	49612923	49613004	MAPK8	NM_002750	1	11	2	+	49612895	49613024
295398339	chr10	49612897	49613036	49612923	49613004	MAPK8	NM_139049	4	11	2	+	49612895	49613024
295398339	chr10	49612897	49613036	49612923	49613004	MAPK8	NM_139046	2	11	2	+	49612895	49613024
295398339	chr10	49612897	49613036	49612923	49613004	MAPK8	NM_139047	3	11	2	+	49612895	49613024
293719256	chr10	49618109	49618233	49618134	49618205	MAPK8	NM_002750	1	11	4	+	49618073	49618211
293719256	chr10	49618109	49618233	49618134	49618205	MAPK8	NM_139049	4	11	4	+	49618073	49618211
293719256	chr10	49618109	49618233	49618134	49618205	MAPK8	NM_139046	2	11	4	+	49618073	49618211
293719256	chr10	49618109	49618233	49618134	49618205	MAPK8	NM_139047	3	11	4	+	49618073	49618211
294161405	chr10	49632083	49632246	49632109	49632219	MAPK8	NM_002750	1	11	6	+	49632131	49632202
294161405	chr10	49632083	49632246	49632109	49632219	MAPK8	NM_139049	4	11	6	+	49632131	49632202
294682136	chr10	49633971	49634100	49633998	49634077	MAPK8	NM_002750	1	11	7	+	49633931	49634113
294682136	chr10	49633971	49634100	49633998	49634077	MAPK8	NM_139049	4	11	7	+	49633931	49634113
294682136	chr10	49633971	49634100	49633998	49634077	MAPK8	NM_139046	2	11	7	+	49633931	49634113
294682136	chr10	49633971	49634100	49633998	49634077	MAPK8	NM_139047	3	11	7	+	49633931	49634113
293827129	chr10	49635066	49635216	49635094	49635188	MAPK8	NM_002750	1	11	9	+	49635123	49635186
293827129	chr10	49635066	49635216	49635094	49635188	MAPK8	NM_139049	4	11	9	+	49635123	49635186
293827129	chr10	49635066	49635216	49635094	49635188	MAPK8	NM_139046	2	11	9	+	49635123	49635186
293827129	chr10	49635066	49635216	49635094	49635188	MAPK8	NM_139047	3	11	9	+	49635123	49635186
293736615	chr10	49642944	49643118	49642967	49643098	MAPK8	NM_002750	1	11	11	+	49642922	49643183
293736615	chr10	49642944	49643118	49642967	49643098	MAPK8	NM_139046	2	11	11	+	49642922	49643183
293736615	chr10	49642944	49643118	49642967	49643098	MAPK8	NM_139049	4	11	11	+	49642927	49643183
293736615	chr10	49642944	49643118	49642967	49643098	MAPK8	NM_139047	3	11	11	+	49642927	49643183
239075640	chr10	51580500	51580634	51580528	51580610	NCOA4	NM_001145261	2	11	4	+	51580556	51580696
239075640	chr10	51580500	51580634	51580528	51580610	NCOA4	NM_005437	5	10	3	+	51580556	51580696
239075640	chr10	51580500	51580634	51580528	51580610	NCOA4	NM_001145262	3	10	3	+	51580556	51580696
239075640	chr10	51580500	51580634	51580528	51580610	NCOA4	NM_001145263	4	10	3	+	51580556	51580696
239075640	chr10	51580500	51580634	51580528	51580610	NCOA4	NM_001145260	1	12	4	+	51580556	51580696
237235325	chr10	51581141	51581310	51581170	51581284	NCOA4	NM_001145261	2	11	6	+	51581270	51581378
237235325	chr10	51581141	51581310	51581170	51581284	NCOA4	NM_005437	5	10	5	+	51581270	51581378
237235325	chr10	51581141	51581310	51581170	51581284	NCOA4	NM_001145262	3	10	5	+	51581270	51581378
237235325	chr10	51581141	51581310	51581170	51581284	NCOA4	NM_001145263	4	10	5	+	51581270	51581378
237235325	chr10	51581141	51581310	51581170	51581284	NCOA4	NM_001145260	1	12	6	+	51581270	51581378
239239197	chr10	51582847	51582985	51582868	51582959	NCOA4	NM_001145261	2	11	8	+	51582796	51582939
239239197	chr10	51582847	51582985	51582868	51582959	NCOA4	NM_005437	5	10	7	+	51582796	51582939
239239197	chr10	51582847	51582985	51582868	51582959	NCOA4	NM_001145262	3	10	7	+	51582796	51582939
239239197	chr10	51582847	51582985	51582868	51582959	NCOA4	NM_001145263	4	10	7	+	51582796	51582939
239239197	chr10	51582847	51582985	51582868	51582959	NCOA4	NM_001145260	1	12	8	+	51582796	51582939
241433419	chr10	51584845	51585005	51584866	51584983	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
241433419	chr10	51584845	51585005	51584866	51584983	NCOA4	NM_005437	5	10	8	+	51584616	51585599
241433419	chr10	51584845	51585005	51584866	51584983	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
241433419	chr10	51584845	51585005	51584866	51584983	NCOA4	NM_001145263	4	10	8	+	51584616	51585599

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241433419	chr10	51584845	51585005	51584866	51584983	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
236621504	chr10	51585270	51585431	51585298	51585405	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
236621504	chr10	51585270	51585431	51585298	51585405	NCOA4	NM_005437	5	10	8	+	51584616	51585599
236621504	chr10	51585270	51585431	51585298	51585405	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
236621504	chr10	51585270	51585431	51585298	51585405	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
236621504	chr10	51585270	51585431	51585298	51585405	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
237317048	chr10	51586330	51586502	51586351	51586474	NCOA4	NM_001145261	2	11	10	+	51586271	51586411
237317048	chr10	51586330	51586502	51586351	51586474	NCOA4	NM_005437	5	10	9	+	51586271	51586411
237317048	chr10	51586330	51586502	51586351	51586474	NCOA4	NM_001145262	3	10	9	+	51586271	51586411
237317048	chr10	51586330	51586502	51586351	51586474	NCOA4	NM_001145263	4	10	9	+	51586271	51586411
237317048	chr10	51586330	51586502	51586351	51586474	NCOA4	NM_001145260	1	12	10	+	51586271	51586411
262774095	chr10	70332078	70332237	70332106	70332213	TET1	NM_030625	1	12	2	+	70331974	70334009
262767522	chr10	70332463	70332593	70332491	70332572	TET1	NM_030625	1	12	2	+	70331974	70334009
262798603	chr10	70332911	70333078	70332936	70333050	TET1	NM_030625	1	12	2	+	70331974	70334009
262760138	chr10	70333391	70333545	70333415	70333518	TET1	NM_030625	1	12	2	+	70331974	70334009
262960694	chr10	70333804	70333941	70333830	70333916	TET1	NM_030625	1	12	2	+	70331974	70334009
262664342	chr10	70404503	70404667	70404527	70404639	TET1	NM_030625	1	12	4	+	70404455	70406762
262724007	chr10	70404893	70405054	70404919	70405027	TET1	NM_030625	1	12	4	+	70404455	70406762
262859114	chr10	70405335	70405469	70405363	70405446	TET1	NM_030625	1	12	4	+	70404455	70406762
262731591	chr10	70405665	70405806	70405692	70405782	TET1	NM_030625	1	12	4	+	70404455	70406762
262738213	chr10	70406046	70406209	70406071	70406185	TET1	NM_030625	1	12	4	+	70404455	70406762
262757383	chr10	70406501	70406665	70406527	70406644	TET1	NM_030625	1	12	4	+	70404455	70406762
241706064	chr10	70412262	70412402	70412288	70412375	TET1	NM_030625	1	12	6	+	70412258	70412351
262658266	chr10	70432595	70432726	70432623	70432700	TET1	NM_030625	1	12	8	+	70432652	70432802
241357747	chr10	70442691	70442833	70442714	70442800	TET1	NM_030625	1	12	10	+	70442593	70442730
238922335	chr10	70446337	70446494	70446360	70446470	TET1	NM_030625	1	12	11	+	70446113	70446464
239137380	chr10	70450797	70450948	70450817	70450927	TET1	NM_030625	1	12	12	+	70450565	70454239
239216152	chr10	70451242	70451379	70451262	70451350	TET1	NM_030625	1	12	12	+	70450565	70454239
312544745	chr10	76602496	76602649	76602522	76602622	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312544745	chr10	76602496	76602649	76602522	76602622	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312544745	chr10	76602496	76602649	76602522	76602622	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312569952	chr10	76602964	76603131	76602984	76603111	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312569952	chr10	76602964	76603131	76602984	76603111	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312569952	chr10	76602964	76603131	76602984	76603111	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312207041	chr10	76729373	76729507	76729395	76729485	KAT6B	NM_012330	3	18	5	+	76729418	76729533
312207041	chr10	76729373	76729507	76729395	76729485	KAT6B	NM_001256468	1	18	5	+	76729418	76729533
312207041	chr10	76729373	76729507	76729395	76729485	KAT6B	NM_001256469	2	18	5	+	76729418	76729533
312296554	chr10	76732155	76732328	76732178	76732300	KAT6B	NM_012330	3	18	7	+	76732265	76732397
312296554	chr10	76732155	76732328	76732178	76732300	KAT6B	NM_001256468	1	18	7	+	76732265	76732397
312296554	chr10	76732155	76732328	76732178	76732300	KAT6B	NM_001256469	2	18	7	+	76732265	76732397
312398407	chr10	76735161	76735306	76735188	76735285	KAT6B	NM_001256468	1	18	8	+	76735157	76735539

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312398407	chr10	76735161	76735306	76735188	76735285	KAT6B	NM_001256469	2	18	8	+	76735157	76735212
312398407	chr10	76735161	76735306	76735188	76735285	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312450988	chr10	76735519	76735673	76735543	76735652	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312443102	chr10	76735941	76736113	76735962	76736088	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312512596	chr10	76739004	76739134	76739023	76739108	KAT6B	NM_012330	3	18	10	+	76738982	76739097
312512596	chr10	76739004	76739134	76739023	76739108	KAT6B	NM_001256468	1	18	10	+	76738982	76739097
312512596	chr10	76739004	76739134	76739023	76739108	KAT6B	NM_001256469	2	18	10	+	76738982	76739097
312393379	chr10	76744833	76744985	76744862	76744963	KAT6B	NM_012330	3	18	12	+	76744838	76744999
312393379	chr10	76744833	76744985	76744862	76744963	KAT6B	NM_001256468	1	18	12	+	76744838	76744999
312393379	chr10	76744833	76744985	76744862	76744963	KAT6B	NM_001256469	2	18	12	+	76744838	76744999
312603580	chr10	76780404	76780561	76780425	76780539	KAT6B	NM_012330	3	18	14	+	76780340	76780571
312603580	chr10	76780404	76780561	76780425	76780539	KAT6B	NM_001256468	1	18	14	+	76780340	76780571
312603580	chr10	76780404	76780561	76780425	76780539	KAT6B	NM_001256469	2	18	14	+	76780340	76780571
312497678	chr10	76781551	76781723	76781577	76781698	KAT6B	NM_012330	3	18	16	+	76781639	76781989
312497678	chr10	76781551	76781723	76781577	76781698	KAT6B	NM_001256468	1	18	16	+	76781639	76781989
312497678	chr10	76781551	76781723	76781577	76781698	KAT6B	NM_001256469	2	18	16	+	76781639	76781989
312231292	chr10	76784676	76784845	76784705	76784822	KAT6B	NM_012330	3	18	17	+	76784716	76785007
312231292	chr10	76784676	76784845	76784705	76784822	KAT6B	NM_001256468	1	18	17	+	76784716	76785007
312231292	chr10	76784676	76784845	76784705	76784822	KAT6B	NM_001256469	2	18	17	+	76784716	76785007
312603468	chr10	76788315	76788486	76788338	76788463	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312603468	chr10	76788315	76788486	76788338	76788463	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312603468	chr10	76788315	76788486	76788338	76788463	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312579543	chr10	76788730	76788891	76788756	76788870	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312579543	chr10	76788730	76788891	76788756	76788870	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312579543	chr10	76788730	76788891	76788756	76788870	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312585273	chr10	76789184	76789357	76789208	76789340	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312585273	chr10	76789184	76789357	76789208	76789340	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312585273	chr10	76789184	76789357	76789208	76789340	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312587345	chr10	76789688	76789860	76789709	76789842	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312587345	chr10	76789688	76789860	76789709	76789842	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312587345	chr10	76789688	76789860	76789709	76789842	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312641199	chr10	76790135	76790309	76790160	76790283	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312641199	chr10	76790135	76790309	76790160	76790283	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312641199	chr10	76790135	76790309	76790160	76790283	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312657678	chr10	76790613	76790780	76790638	76790758	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312657678	chr10	76790613	76790780	76790638	76790758	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312657678	chr10	76790613	76790780	76790638	76790758	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
223123591	chr10	88649755	88649904	88649782	88649876	BMPR1A	NM_004329	1	13	4	+	88649819	88649981
223979161	chr10	88659444	88659611	88659466	88659583	BMPR1A	NM_004329	1	13	6	+	88659551	88659647
222389561	chr10	88671885	88672058	88671911	88672032	BMPR1A	NM_004329	1	13	8	+	88671997	88672141
328932140	chr10	88678795	88678966	88678820	88678940	BMPR1A	NM_004329	1	13	10	+	88678929	88679226

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223061587	chr10	88679201	88679333	88679224	88679302	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
223012141	chr10	88683134	88683308	88683158	88683283	BMPR1A	NM_004329	1	13	12	+	88683133	88683263
236721179	chr10	89653816	89653970	89653839	89653942	PTEN	NM_000314	1	9	2	+	89653782	89653866
235012738	chr10	89692749	89692885	89692776	89692860	PTEN	NM_000314	1	9	5	+	89692770	89693008
236536646	chr10	89711889	89712047	89711918	89712021	PTEN	NM_000314	1	9	6	+	89711875	89712016
236874615	chr10	89720538	89720708	89720568	89720687	PTEN	NM_000314	1	9	8	+	89720651	89720875
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NM_152872	3	8	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NM_152871	2	8	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NR_028036	7	8	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NR_028035	6	7	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NR_028034	5	6	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NR_028033	4	7	1	+	90750288	90750663
228268495	chr10	90750578	90750719	90750597	90750699	FAS	NM_000043	1	9	1	+	90750288	90750663
228720538	chr10	90767535	90767687	90767559	90767666	FAS	NM_152872	3	8	3	+	90767457	90767594
228720538	chr10	90767535	90767687	90767559	90767666	FAS	NM_152871	2	8	3	+	90767457	90767594
228720538	chr10	90767535	90767687	90767559	90767666	FAS	NR_028036	7	8	3	+	90767457	90767594
228720538	chr10	90767535	90767687	90767559	90767666	FAS	NR_028033	4	7	3	+	90767457	90767594
228720538	chr10	90767535	90767687	90767559	90767666	FAS	NM_000043	1	9	3	+	90767457	90767594
232445812	chr10	90770504	90770645	90770529	90770617	FAS	NM_152872	3	8	6	+	90770510	90770572
232445812	chr10	90770504	90770645	90770529	90770617	FAS	NR_028036	7	8	5	+	90770510	90770572
232445812	chr10	90770504	90770645	90770529	90770617	FAS	NR_028035	6	7	4	+	90770510	90770572
232445812	chr10	90770504	90770645	90770529	90770617	FAS	NM_000043	1	9	6	+	90770510	90770572
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NM_152872	3	8	8	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NM_152871	2	8	8	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NR_028036	7	8	8	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NR_028035	6	7	7	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NR_028034	5	6	6	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NR_028033	4	7	7	+	90773876	90775542
231215052	chr10	90773984	90774121	90774010	90774095	FAS	NM_000043	1	9	9	+	90773876	90775542
286774778	chr10	96522469	96522636	96522491	96522608	CYP2C19	NM_000769	1	9	1	+	96522463	96522630
287025945	chr10	96535025	96535195	96535050	96535175	CYP2C19	NM_000769	1	9	3	+	96535147	96535296
328502451	chr10	96540236	96540404	96540264	96540376	CYP2C19	NM_000769	1	9	4	+	96540256	96540416
286933824	chr10	96580256	96580407	96580282	96580383	CYP2C19	NM_000769	1	9	6	+	96580253	96580394
285361767	chr10	96609642	96609816	96609667	96609792	CYP2C19	NM_000769	1	9	8	+	96609674	96609815
294676361	chr10	97951685	97951834	97951707	97951806	BLNK	NM_013314	2	17	17	-	97951455	97951848
294676361	chr10	97951685	97951834	97951707	97951806	BLNK	NM_001114094	1	16	16	-	97951455	97951848
294030465	chr10	97956777	97956923	97956798	97956892	BLNK	NM_013314	2	17	16	-	97956664	97956819
294030465	chr10	97956777	97956923	97956798	97956892	BLNK	NM_001114094	1	16	15	-	97956664	97956819
294442204	chr10	97963797	97963925	97963821	97963897	BLNK	NM_013314	2	17	13	-	97963813	97963844
294442204	chr10	97963797	97963925	97963821	97963897	BLNK	NM_001114094	1	16	12	-	97963813	97963844
294645661	chr10	97967526	97967695	97967548	97967668	BLNK	NM_013314	2	17	10	-	97967628	97967655

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294645661	chr10	97967526	97967695	97967548	97967668	BLNK	NM_001114094	1	16	9	-	97967628	97967655
294455648	chr10	97976380	97976554	97976401	97976526	BLNK	NM_013314	2	17	7	-	97976409	97976490
294455648	chr10	97976380	97976554	97976401	97976526	BLNK	NM_001114094	1	16	7	-	97976409	97976490
293858398	chr10	97987209	97987354	97987231	97987334	BLNK	NM_013314	2	17	5	-	97987166	97987322
293858398	chr10	97987209	97987354	97987231	97987334	BLNK	NM_001114094	1	16	5	-	97987166	97987322
294997324	chr10	98031030	98031194	98031057	98031166	BLNK	NM_013314	2	17	1	-	98031109	98031333
294997324	chr10	98031030	98031194	98031057	98031166	BLNK	NM_001114094	1	16	1	-	98031109	98031333
264726008	chr10	102891451	102891625	102891470	102891607	TLX1	NM_005521	2	3	1	+	102891061	102891866
264726008	chr10	102891451	102891625	102891470	102891607	TLX1	NM_001195517	1	3	1	+	102891061	102891866
262943493	chr10	102894066	102894198	102894085	102894178	TLX1	NM_005521	2	3	2	+	102893932	102894133
262943493	chr10	102894066	102894198	102894085	102894178	TLX1	NM_001195517	1	3	2	+	102893932	102894133
235644275	chr10	104155591	104155747	104155612	104155724	NFKB2	NM_002502	3	23	2	+	104155645	104155737
235644275	chr10	104155591	104155747	104155612	104155724	NFKB2	NM_001077494	2	23	2	+	104155645	104155737
235644275	chr10	104155591	104155747	104155612	104155724	NFKB2	NM_001077493	1	23	2	+	104155645	104155737
235530627	chr10	104156452	104156625	104156475	104156606	NFKB2	NM_002502	3	23	5	+	104156482	104156580
235530627	chr10	104156452	104156625	104156475	104156606	NFKB2	NM_001077494	2	23	5	+	104156482	104156580
235530627	chr10	104156452	104156625	104156475	104156606	NFKB2	NM_001077493	1	23	5	+	104156482	104156580
236610199	chr10	104157071	104157235	104157091	104157215	NFKB2	NM_002502	3	23	7	+	104157059	104157165
236610199	chr10	104157071	104157235	104157091	104157215	NFKB2	NM_001077494	2	23	7	+	104157059	104157165
236610199	chr10	104157071	104157235	104157091	104157215	NFKB2	NM_001077493	1	23	7	+	104157059	104157165
240141039	chr10	104157945	104158117	104157968	104158091	NFKB2	NM_002502	3	23	10	+	104157969	104158054
240141039	chr10	104157945	104158117	104157968	104158091	NFKB2	NM_001077494	2	23	10	+	104157969	104158054
240141039	chr10	104157945	104158117	104157968	104158091	NFKB2	NM_001077493	1	23	10	+	104157969	104158054
237164446	chr10	104158539	104158673	104158557	104158651	NFKB2	NM_002502	3	23	12	+	104158496	104158621
237164446	chr10	104158539	104158673	104158557	104158651	NFKB2	NM_001077494	2	23	12	+	104158496	104158621
237164446	chr10	104158539	104158673	104158557	104158651	NFKB2	NM_001077493	1	23	12	+	104158496	104158621
239932589	chr10	104159327	104159494	104159347	104159476	NFKB2	NM_002502	3	23	14	+	104159334	104159475
239932589	chr10	104159327	104159494	104159347	104159476	NFKB2	NM_001077494	2	23	14	+	104159334	104159475
239932589	chr10	104159327	104159494	104159347	104159476	NFKB2	NM_001077493	1	23	14	+	104159334	104159475
241363321	chr10	104160113	104160278	104160131	104160257	NFKB2	NM_002502	3	23	16	+	104160035	104160248
241363321	chr10	104160113	104160278	104160131	104160257	NFKB2	NM_001077494	2	23	16	+	104160035	104160248
241363321	chr10	104160113	104160278	104160131	104160257	NFKB2	NM_001077493	1	23	16	+	104160035	104160248
237291537	chr10	104160871	104161031	104160893	104161010	NFKB2	NM_002502	3	23	19	+	104160937	104161088
237291537	chr10	104160871	104161031	104160893	104161010	NFKB2	NM_001077494	2	23	19	+	104160937	104161088
237291537	chr10	104160871	104161031	104160893	104161010	NFKB2	NM_001077493	1	23	19	+	104160937	104161088
257978516	chr10	104161610	104161783	104161629	104161761	NFKB2	NM_002502	3	23	21	+	104161502	104161674
257978516	chr10	104161610	104161783	104161629	104161761	NFKB2	NM_001077494	2	23	21	+	104161502	104161674
257978516	chr10	104161610	104161783	104161629	104161761	NFKB2	NM_001077493	1	23	21	+	104161502	104161674
237777185	chr10	104263983	104264152	104264002	104264132	SUFU	NM_016169	2	12	1	+	104263719	104264091
237777185	chr10	104263983	104264152	104264002	104264132	SUFU	NM_001178133	1	11	1	+	104263719	104264091
238611800	chr10	104309743	104309916	104309765	104309895	SUFU	NM_016169	2	12	3	+	104309727	104309863

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238611800	chr10	104309743	104309916	104309765	104309895	SUFU	NM_001178133	1	11	3	+	104309727	104309863
241942552	chr10	104353705	104353850	104353726	104353822	SUFU	NM_016169	2	12	6	+	104353750	104353822
241942552	chr10	104353705	104353850	104353726	104353822	SUFU	NM_001178133	1	11	6	+	104353750	104353822
240604230	chr10	104359212	104359379	104359233	104359358	SUFU	NM_016169	2	12	8	+	104359190	104359301
240604230	chr10	104359212	104359379	104359233	104359358	SUFU	NM_001178133	1	11	8	+	104359190	104359301
238824466	chr10	104377156	104377318	104377175	104377296	SUFU	NM_016169	2	12	10	+	104377047	104377185
238824466	chr10	104377156	104377318	104377175	104377296	SUFU	NM_001178133	1	11	10	+	104377047	104377185
242731302	chr10	104389834	104389981	104389856	104389957	SUFU	NM_016169	2	12	12	+	104389823	104393214
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001146283	2	13	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198526	7	13	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_030756	13	14	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001146286	5	12	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001146285	4	13	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198530	11	11	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198529	10	13	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198525	6	15	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198531	12	13	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001146274	1	14	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198528	9	15	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001198527	8	15	2	+	114710966	114711032
274022240	chr10	114710877	114711044	114710896	114711024	TCF7L2	NM_001146284	3	13	2	+	114710966	114711032
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001146283	2	13	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198526	7	13	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_030756	13	14	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001146286	5	12	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001146285	4	13	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198529	10	13	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198525	6	15	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198531	12	13	5	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001146274	1	14	5	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198528	9	15	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001198527	8	15	4	+	114799784	114799885
273856957	chr10	114799763	114799910	114799788	114799885	TCF7L2	NM_001146284	3	13	4	+	114799784	114799885
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001146283	2	13	6	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198526	7	13	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_030756	13	14	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001146286	5	12	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001146285	4	13	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198530	11	11	4	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198529	10	13	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198525	6	15	5	+	114900943	114901075

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198531	12	13	6	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001146274	1	14	6	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198528	9	15	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001198527	8	15	5	+	114900943	114901075
272985784	chr10	114901001	114901149	114901025	114901129	TCF7L2	NM_001146284	3	13	5	+	114900943	114901075
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001146283	2	13	9	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198526	7	13	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_030756	13	14	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001146286	5	12	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001146285	4	13	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198530	11	11	7	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198529	10	13	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198531	12	13	9	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001146274	1	14	9	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198528	9	15	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198527	8	15	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001146284	3	13	8	+	114910757	114910882
273787680	chr10	114910637	114910790	114910659	114910769	TCF7L2	NM_001198525	6	15	8	+	114910742	114910882
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001146283	2	13	11	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198526	7	13	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_030756	13	14	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001146286	5	12	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001146285	4	13	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198530	11	11	9	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198529	10	13	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198525	6	15	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198531	12	13	11	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001146274	1	14	11	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198528	9	15	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001198527	8	15	10	+	114912092	114912199
274104685	chr10	114912061	114912231	114912084	114912204	TCF7L2	NM_001146284	3	13	10	+	114912092	114912199
273356036	chr10	114919647	114919781	114919668	114919757	TCF7L2	NM_030756	13	14	13	+	114919679	114919751
273356036	chr10	114919647	114919781	114919668	114919757	TCF7L2	NM_001146285	4	13	12	+	114919679	114919751
273356036	chr10	114919647	114919781	114919668	114919757	TCF7L2	NM_001198525	6	15	13	+	114919679	114919751
273356036	chr10	114919647	114919781	114919668	114919757	TCF7L2	NM_001198528	9	15	13	+	114919679	114919751
273356036	chr10	114919647	114919781	114919668	114919757	TCF7L2	NM_001198527	8	15	13	+	114919679	114919751
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001146283	2	13	13	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198526	7	13	13	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_030756	13	14	14	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001146286	5	12	12	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001146285	4	13	13	+	114925314	114927436

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198530	11	11	11	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198529	10	13	13	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198525	6	15	15	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198531	12	13	13	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001146274	1	14	14	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198528	9	15	15	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001198527	8	15	15	+	114925314	114927436
274212392	chr10	114925290	114925463	114925316	114925441	TCF7L2	NM_001146284	3	13	13	+	114925314	114927436
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_001144915	4	17	17	-	123237844	123239184
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_001144918	7	16	16	-	123237844	123239535
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_000141	1	18	18	-	123237844	123239535
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_001144917	6	16	16	-	123237844	123239535
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_001144916	5	15	15	-	123237844	123239535
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_022970	9	18	18	-	123237844	123239535
231456023	chr10	123239158	123239297	123239181	123239276	FGFR2	NM_001144914	3	15	15	-	123237844	123239535
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144913	2	17	16	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144918	7	16	15	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_000141	1	18	17	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144917	6	16	15	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144916	5	15	14	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_022970	9	18	17	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144914	3	15	14	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144915	4	17	16	-	123243212	123243317
231679983	chr10	123243092	123243250	123243120	123243224	FGFR2	NM_001144919	8	17	16	-	123243212	123243317
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144913	2	17	14	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144918	7	16	13	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_000141	1	18	15	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144917	6	16	13	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144916	5	15	12	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_022970	9	18	15	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144914	3	15	12	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144915	4	17	14	-	123246868	123246938
228309377	chr10	123246767	123246928	123246789	123246907	FGFR2	NM_001144919	8	17	14	-	123246868	123246938
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144913	2	17	12	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144918	7	16	11	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_000141	1	18	13	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144917	6	16	11	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144916	5	15	10	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_022970	9	18	13	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144914	3	15	10	-	123256046	123256236
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144915	4	17	12	-	123256046	123256236

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230732778	chr10	123255965	123256131	123255987	123256110	FGFR2	NM_001144919	8	17	12	-	123256046	123256236
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144913	2	17	10	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144918	7	16	9	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_000141	1	18	11	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144917	6	16	9	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144916	5	15	8	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_022970	9	18	11	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144914	3	15	8	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144915	4	17	10	-	123260340	123260461
227816152	chr10	123260382	123260530	123260406	123260505	FGFR2	NM_001144919	8	17	10	-	123260340	123260461
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144918	7	16	7	-	123274637	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144913	2	17	8	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_000141	1	18	9	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144916	5	15	6	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_022970	9	18	9	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144914	3	15	6	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144915	4	17	8	-	123274631	123274833
228055971	chr10	123274691	123274858	123274712	123274834	FGFR2	NM_001144919	8	17	8	-	123274631	123274833
232644790	chr10	123278200	123278374	123278221	123278347	FGFR2	NM_001144913	2	17	7	-	123278196	123278343
232644790	chr10	123278200	123278374	123278221	123278347	FGFR2	NM_022970	9	18	8	-	123278196	123278343
232644790	chr10	123278200	123278374	123278221	123278347	FGFR2	NM_001144919	8	17	7	-	123278196	123278343
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144913	2	17	5	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144918	7	16	4	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_000141	1	18	6	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144917	6	16	6	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144916	5	15	3	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_022970	9	18	6	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144914	3	15	5	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144915	4	17	5	-	123298106	123298229
232481890	chr10	123298095	123298253	123298116	123298230	FGFR2	NM_001144919	8	17	5	-	123298106	123298229
231591859	chr10	123324840	123325011	123324861	123324987	FGFR2	NM_001144913	2	17	2	-	123324952	123325218
231591859	chr10	123324840	123325011	123324861	123324987	FGFR2	NM_000141	1	18	3	-	123324952	123325218
231591859	chr10	123324840	123325011	123324861	123324987	FGFR2	NM_001144917	6	16	3	-	123324952	123325218
231591859	chr10	123324840	123325011	123324861	123324987	FGFR2	NM_022970	9	18	3	-	123324952	123325218
231591859	chr10	123324840	123325011	123324861	123324987	FGFR2	NM_001144914	3	15	2	-	123324952	123325218
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144916	5	15	1	-	123353223	123353772
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144913	2	17	1	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144918	7	16	2	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_000141	1	18	2	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144917	6	16	2	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_022970	9	18	2	-	123353223	123353481

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144914	3	15	1	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144915	4	17	2	-	123353223	123353481
227732000	chr10	123353218	123353386	123353242	123353360	FGFR2	NM_001144919	8	17	2	-	123353223	123353481
228573792	chr11	532613	532779	532630	532758	HRAS	NM_005343	2	6	5	-	532631	532755
228573792	chr11	532613	532779	532630	532758	HRAS	NM_001130442	1	5	5	-	532242	532755
228573792	chr11	532613	532779	532630	532758	HRAS	NM_176795	3	6	6	-	532242	532755
227465156	chr11	533662	533809	533681	533786	HRAS	NM_001130442	1	5	3	-	533766	533944
227465156	chr11	533662	533809	533681	533786	HRAS	NM_176795	3	6	3	-	533766	533944
227465156	chr11	533662	533809	533681	533786	HRAS	NM_005343	2	6	3	-	533766	533944
227445718	chr11	534223	534371	534247	534351	HRAS	NM_001130442	1	5	2	-	534212	534375
227445718	chr11	534223	534371	534247	534351	HRAS	NM_176795	3	6	2	-	534212	534375
227445718	chr11	534223	534371	534247	534351	HRAS	NM_005343	2	6	2	-	534212	534375
330105732	chr11	2154692	2154856	2154714	2154835	IGF2	NM_000612	1	4	3	-	2154747	2154895
330105732	chr11	2154692	2154856	2154714	2154835	IGF2	NM_001127598	3	5	4	-	2154747	2154895
330105732	chr11	2154692	2154856	2154714	2154835	IGF2	NM_001007139	2	5	4	-	2154747	2154895
330144590	chr11	2161341	2161472	2161362	2161451	IGF2	NM_001127598	3	5	2	-	2161365	2161529
235802952	chr11	3697530	3697688	3697553	3697664	NUP98	NM_016320	2	33	33	-	3696240	3697606
235802952	chr11	3697530	3697688	3697553	3697664	NUP98	NM_139132	4	32	32	-	3696240	3697606
235804125	chr11	3704336	3704509	3704362	3704485	NUP98	NM_016320	2	33	30	-	3704430	3704671
235804125	chr11	3704336	3704509	3704362	3704485	NUP98	NM_139132	4	32	29	-	3704430	3704671
236061864	chr11	3707294	3707468	3707315	3707446	NUP98	NM_016320	2	33	29	-	3707203	3707424
240186875	chr11	3714490	3714647	3714512	3714618	NUP98	NM_016320	2	33	27	-	3714462	3714605
240186875	chr11	3714490	3714647	3714512	3714618	NUP98	NM_139132	4	32	27	-	3714462	3714605
236086000	chr11	3720337	3720508	3720359	3720485	NUP98	NM_016320	2	33	25	-	3720312	3720578
236086000	chr11	3720337	3720508	3720359	3720485	NUP98	NM_139132	4	32	25	-	3720312	3720578
236655957	chr11	3721969	3722123	3721992	3722095	NUP98	NM_016320	2	33	24	-	3721840	3722069
236655957	chr11	3721969	3722123	3721992	3722095	NUP98	NM_139132	4	32	24	-	3721840	3722069
237371812	chr11	3723995	3724145	3724017	3724122	NUP98	NM_016320	2	33	23	-	3723693	3724122
237371812	chr11	3723995	3724145	3724017	3724122	NUP98	NM_139132	4	32	23	-	3723693	3724122
237671425	chr11	3727725	3727885	3727747	3727860	NUP98	NM_016320	2	33	21	-	3727675	3727857
237671425	chr11	3727725	3727885	3727747	3727860	NUP98	NM_139132	4	32	21	-	3727675	3727857
238862774	chr11	3735064	3735195	3735085	3735169	NUP98	NM_005387	1	20	19	-	3735048	3735225
238862774	chr11	3735064	3735195	3735085	3735169	NUP98	NM_139131	3	20	19	-	3735048	3735225
238862774	chr11	3735064	3735195	3735085	3735169	NUP98	NM_016320	2	33	19	-	3735048	3735225
238862774	chr11	3735064	3735195	3735085	3735169	NUP98	NM_139132	4	32	19	-	3735048	3735225
235438071	chr11	3744315	3744471	3744342	3744443	NUP98	NM_005387	1	20	16	-	3744387	3744685
235438071	chr11	3744315	3744471	3744342	3744443	NUP98	NM_139131	3	20	16	-	3744387	3744685
235438071	chr11	3744315	3744471	3744342	3744443	NUP98	NM_016320	2	33	16	-	3744387	3744685
235438071	chr11	3744315	3744471	3744342	3744443	NUP98	NM_139132	4	32	16	-	3744387	3744685
236525354	chr11	3746383	3746556	3746410	3746535	NUP98	NM_005387	1	20	15	-	3746333	3746449
236525354	chr11	3746383	3746556	3746410	3746535	NUP98	NM_139131	3	20	15	-	3746333	3746449

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236525354	chr11	3746383	3746556	3746410	3746535	NUP98	NM_016320	2	33	15	-	3746333	3746449
236525354	chr11	3746383	3746556	3746410	3746535	NUP98	NM_139132	4	32	15	-	3746333	3746449
236966293	chr11	3756461	3756635	3756484	3756610	NUP98	NM_005387	1	20	13	-	3756421	3756554
236966293	chr11	3756461	3756635	3756484	3756610	NUP98	NM_139131	3	20	13	-	3756421	3756554
236966293	chr11	3756461	3756635	3756484	3756610	NUP98	NM_016320	2	33	13	-	3756421	3756554
236966293	chr11	3756461	3756635	3756484	3756610	NUP98	NM_139132	4	32	13	-	3756421	3756554
236855933	chr11	3781643	3781816	3781668	3781796	NUP98	NM_139131	3	20	10	-	3781769	3781856
236855933	chr11	3781643	3781816	3781668	3781796	NUP98	NM_016320	2	33	10	-	3781769	3781856
236855933	chr11	3781643	3781816	3781668	3781796	NUP98	NM_139132	4	32	10	-	3781769	3781856
236855933	chr11	3781643	3781816	3781668	3781796	NUP98	NM_005387	1	20	10	-	3781718	3781856
235630364	chr11	3789780	3789940	3789805	3789918	NUP98	NM_005387	1	20	8	-	3789811	3789974
235630364	chr11	3789780	3789940	3789805	3789918	NUP98	NM_139131	3	20	8	-	3789811	3789974
235630364	chr11	3789780	3789940	3789805	3789918	NUP98	NM_016320	2	33	8	-	3789811	3789974
235630364	chr11	3789780	3789940	3789805	3789918	NUP98	NM_139132	4	32	8	-	3789811	3789974
235600016	chr11	3794748	3794910	3794776	3794882	NUP98	NM_005387	1	20	6	-	3794862	3794969
235600016	chr11	3794748	3794910	3794776	3794882	NUP98	NM_139131	3	20	6	-	3794862	3794969
235600016	chr11	3794748	3794910	3794776	3794882	NUP98	NM_016320	2	33	6	-	3794862	3794969
235600016	chr11	3794748	3794910	3794776	3794882	NUP98	NM_139132	4	32	6	-	3794862	3794969
238353484	chr11	3800062	3800214	3800091	3800189	NUP98	NM_005387	1	20	4	-	3800103	3800279
238353484	chr11	3800062	3800214	3800091	3800189	NUP98	NM_139131	3	20	4	-	3800103	3800279
238353484	chr11	3800062	3800214	3800091	3800189	NUP98	NM_016320	2	33	4	-	3800103	3800279
238353484	chr11	3800062	3800214	3800091	3800189	NUP98	NM_139132	4	32	4	-	3800103	3800279
235772323	chr11	3803189	3803314	3803214	3803297	NUP98	NM_005387	1	20	2	-	3803272	3803375
235772323	chr11	3803189	3803314	3803214	3803297	NUP98	NM_139131	3	20	2	-	3803272	3803375
235772323	chr11	3803189	3803314	3803214	3803297	NUP98	NM_016320	2	33	2	-	3803272	3803375
235772323	chr11	3803189	3803314	3803214	3803297	NUP98	NM_139132	4	32	2	-	3803272	3803375
294190524	chr11	4123228	4123382	4123249	4123356	RRM1	NM_001033	1	19	2	+	4123223	4123311
294099299	chr11	4130790	4130946	4130810	4130919	RRM1	NM_001033	1	19	5	+	4130874	4130933
294684130	chr11	4133154	4133319	4133179	4133293	RRM1	NM_001033	1	19	7	+	4133130	4133292
294256807	chr11	4142763	4142924	4142787	4142896	RRM1	NM_001033	1	19	10	+	4142834	4142995
293703468	chr11	4144340	4144484	4144372	4144458	RRM1	NM_001033	1	19	12	+	4144413	4144614
294170586	chr11	4147900	4148025	4147924	4148000	RRM1	NM_001033	1	19	13	+	4147914	4148063
295375594	chr11	4150216	4150389	4150238	4150361	RRM1	NM_001033	1	19	15	+	4150304	4150380
294094470	chr11	4154831	4154956	4154851	4154932	RRM1	NM_001033	1	19	17	+	4154793	4154888
293717503	chr11	4159361	4159503	4159388	4159475	RRM1	NM_001033	1	19	19	+	4159425	4160106
232921730	chr11	22646253	22646408	22646277	22646386	FANCF	NM_022725	1	1	1	-	22644079	22647387
230651948	chr11	22646738	22646908	22646760	22646882	FANCF	NM_022725	1	1	1	-	22644079	22647387
230567627	chr11	22647180	22647332	22647198	22647311	FANCF	NM_022725	1	1	1	-	22644079	22647387
239702231	chr11	32413387	32413546	32413414	32413522	WT1	NM_001198552	3	9	8	-	32413518	32413610
239702231	chr11	32413387	32413546	32413414	32413522	WT1	NM_024426	5	10	9	-	32413518	32413610
240698061	chr11	32417821	32417988	32417843	32417963	WT1	NM_000378	1	9	6	-	32417803	32417953

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240698061	chr11	32417821	32417988	32417843	32417963	WT1	NM_001198552	3	9	6	-	32417803	32417953
240698061	chr11	32417821	32417988	32417843	32417963	WT1	NM_001198551	2	10	7	-	32417803	32417953
240698061	chr11	32417821	32417988	32417843	32417963	WT1	NM_024426	5	10	7	-	32417803	32417953
240698061	chr11	32417821	32417988	32417843	32417963	WT1	NM_024424	4	10	7	-	32417803	32417953
242597530	chr11	32439001	32439165	32439022	32439141	WT1	NM_000378	1	9	4	-	32439123	32439200
242597530	chr11	32439001	32439165	32439022	32439141	WT1	NM_001198552	3	9	4	-	32439123	32439200
242597530	chr11	32439001	32439165	32439022	32439141	WT1	NM_001198551	2	10	4	-	32439123	32439200
242597530	chr11	32439001	32439165	32439022	32439141	WT1	NM_024426	5	10	4	-	32439123	32439200
242597530	chr11	32439001	32439165	32439022	32439141	WT1	NM_024424	4	10	4	-	32439123	32439200
238596959	chr11	32449932	32450100	32449956	32450078	WT1	NM_000378	1	9	2	-	32450043	32450165
238596959	chr11	32449932	32450100	32449956	32450078	WT1	NM_001198552	3	9	2	-	32450043	32450165
238596959	chr11	32449932	32450100	32449956	32450078	WT1	NM_001198551	2	10	2	-	32450043	32450165
238596959	chr11	32449932	32450100	32449956	32450078	WT1	NM_024426	5	10	2	-	32450043	32450165
238596959	chr11	32449932	32450100	32449956	32450078	WT1	NM_024424	4	10	2	-	32450043	32450165
262319133	chr11	32456255	32456424	32456273	32456406	WT1	NM_000378	1	9	1	-	32456246	32457081
262319133	chr11	32456255	32456424	32456273	32456406	WT1	NM_024426	5	10	1	-	32456246	32457081
262319133	chr11	32456255	32456424	32456273	32456406	WT1	NM_024424	4	10	1	-	32456246	32457081
266346407	chr11	32456759	32456912	32456779	32456891	WT1	NM_000378	1	9	1	-	32456246	32457081
266346407	chr11	32456759	32456912	32456779	32456891	WT1	NM_024426	5	10	1	-	32456246	32457081
266346407	chr11	32456759	32456912	32456779	32456891	WT1	NM_024424	4	10	1	-	32456246	32457081
230546735	chr11	44129299	44129473	44129322	44129454	EXT2	NM_000401	1	14	2	+	44129233	44129798
230546735	chr11	44129299	44129473	44129322	44129454	EXT2	NM_001178083	2	15	2	+	44129233	44129798
230546735	chr11	44129299	44129473	44129322	44129454	EXT2	NM_207122	3	14	2	+	44129233	44129798
230112426	chr11	44130608	44130781	44130630	44130755	EXT2	NM_000401	1	14	3	+	44130744	44130833
230112426	chr11	44130608	44130781	44130630	44130755	EXT2	NM_001178083	2	15	3	+	44130744	44130833
230112426	chr11	44130608	44130781	44130630	44130755	EXT2	NM_207122	3	14	3	+	44130744	44130833
230696791	chr11	44146284	44146436	44146308	44146413	EXT2	NM_000401	1	14	5	+	44146339	44146534
230696791	chr11	44146284	44146436	44146308	44146413	EXT2	NM_001178083	2	15	5	+	44146339	44146534
230696791	chr11	44146284	44146436	44146308	44146413	EXT2	NM_207122	3	14	5	+	44146339	44146534
229420008	chr11	44151545	44151719	44151568	44151698	EXT2	NM_000401	1	14	7	+	44151595	44151688
229420008	chr11	44151545	44151719	44151568	44151698	EXT2	NM_001178083	2	15	7	+	44151595	44151688
229420008	chr11	44151545	44151719	44151568	44151698	EXT2	NM_207122	3	14	7	+	44151595	44151688
230797643	chr11	44193166	44193316	44193186	44193292	EXT2	NM_000401	1	14	8	+	44193161	44193292
230797643	chr11	44193166	44193316	44193186	44193292	EXT2	NM_207122	3	14	8	+	44193161	44193292
230797643	chr11	44193166	44193316	44193186	44193292	EXT2	NM_001178083	2	15	9	+	44193224	44193292
231615718	chr11	44228361	44228533	44228385	44228508	EXT2	NM_000401	1	14	10	+	44228343	44228509
231615718	chr11	44228361	44228533	44228385	44228508	EXT2	NM_001178083	2	15	11	+	44228343	44228509
231615718	chr11	44228361	44228533	44228385	44228508	EXT2	NM_207122	3	14	10	+	44228343	44228509
230709646	chr11	44255609	44255768	44255637	44255748	EXT2	NM_000401	1	14	12	+	44255665	44255793
230709646	chr11	44255609	44255768	44255637	44255748	EXT2	NM_001178083	2	15	13	+	44255665	44255793
230709646	chr11	44255609	44255768	44255637	44255748	EXT2	NM_207122	3	14	12	+	44255665	44255793

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229063412	chr11	47236595	47236768	47236615	47236748	DDB2	NM_000107	1	10	1	+	47236493	47236814
230300946	chr11	47238294	47238467	47238315	47238441	DDB2	NM_000107	1	10	3	+	47238409	47238600
229494595	chr11	47254414	47254572	47254435	47254552	DDB2	NM_000107	1	10	4	+	47254365	47254510
228705004	chr11	47256281	47256424	47256300	47256403	DDB2	NM_000107	1	10	6	+	47256308	47256485
228799359	chr11	47259314	47259485	47259342	47259460	DDB2	NM_000107	1	10	8	+	47259388	47259552
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130800	3	10	10	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130803	6	10	10	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130802	5	10	10	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130801	4	10	10	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130804	7	11	11	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_000244	1	10	10	-	64570986	64572288
233334974	chr11	64571730	64571869	64571751	64571847	MEN1	NM_130799	2	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130800	3	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130803	6	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130802	5	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130801	4	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130804	7	11	11	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_000244	1	10	10	-	64570986	64572288
234684097	chr11	64572206	64572358	64572223	64572339	MEN1	NM_130799	2	10	10	-	64570986	64572288
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130800	3	10	8	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130803	6	10	8	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130802	5	10	8	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130801	4	10	8	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130804	7	11	9	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_000244	1	10	8	-	64573107	64573242
231870761	chr11	64573099	64573271	64573118	64573251	MEN1	NM_130799	2	10	8	-	64573107	64573242
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130800	3	10	5	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130803	6	10	5	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130802	5	10	5	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130801	4	10	5	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130804	7	11	6	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_000244	1	10	5	-	64574651	64574691
232002826	chr11	64574565	64574720	64574592	64574698	MEN1	NM_130799	2	10	5	-	64574651	64574691
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130800	3	10	2	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130803	6	10	2	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130802	5	10	2	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130801	4	10	2	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130804	7	11	3	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_000244	1	10	2	-	64577122	64577604
231174510	chr11	64577076	64577233	64577100	64577212	MEN1	NM_130799	2	10	2	-	64577137	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130800	3	10	2	-	64577122	64577604

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130803	6	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130802	5	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130801	4	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130804	7	11	3	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_000244	1	10	2	-	64577122	64577604
231208212	chr11	64577522	64577688	64577540	64577670	MEN1	NM_130799	2	10	2	-	64577137	64577604
226293222	chr11	69457786	69457942	69457804	69457918	CCND1	NM_053056	1	5	2	+	69457799	69458014
226438348	chr11	69458657	69458824	69458682	69458807	CCND1	NM_053056	1	5	3	+	69458600	69458759
226973363	chr11	69465900	69466054	69465919	69466035	CCND1	NM_053056	1	5	5	+	69465886	69469242
237740556	chr11	71715017	71715181	71715036	71715163	NUMA1	NM_006185	1	27	26	-	71714933	71715145
237460755	chr11	71716212	71716336	71716233	71716318	NUMA1	NM_006185	1	27	23	-	71716279	71716415
235523412	chr11	71718168	71718307	71718190	71718287	NUMA1	NM_006185	1	27	21	-	71718235	71718481
237973507	chr11	71719815	71719939	71719836	71719916	NUMA1	NM_006185	1	27	20	-	71719734	71719891
237540399	chr11	71720200	71720374	71720226	71720352	NUMA1	NM_006185	1	27	19	-	71720013	71720231
237540399	chr11	71720200	71720374	71720226	71720352	NUMA1	NM_006185	1	27	18	-	71720314	71720433
258135082	chr11	71723866	71724036	71723887	71724016	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258188852	chr11	71724303	71724464	71724322	71724445	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238456991	chr11	71724755	71724883	71724777	71724858	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258156745	chr11	71725132	71725296	71725152	71725274	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238406953	chr11	71725568	71725704	71725585	71725686	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258203202	chr11	71726015	71726140	71726038	71726117	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258176054	chr11	71726381	71726538	71726401	71726520	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238102632	chr11	71726857	71727025	71726878	71727005	NUMA1	NM_006185	1	27	15	-	71723941	71727306
235552965	chr11	71727430	71727604	71727452	71727579	NUMA1	NM_006185	1	27	14	-	71727454	71727576
238737627	chr11	71729211	71729380	71729234	71729356	NUMA1	NM_006185	1	27	12	-	71729229	71729346
236331089	chr11	71729906	71730056	71729927	71730034	NUMA1	NM_006185	1	27	10	-	71729869	71730026
258566881	chr11	71733314	71733487	71733339	71733466	NUMA1	NM_006185	1	27	7	-	71733385	71733465
236815163	chr11	71746853	71747011	71746875	71746990	NUMA1	NM_006185	1	27	3	-	71746948	71747021
237066023	chr11	94168909	94169056	94168938	94169028	MRE11A	NM_005591	2	20	18	-	94168998	94169065
237066023	chr11	94168909	94169056	94168938	94169028	MRE11A	NM_005590	1	19	17	-	94168998	94169065
238285758	chr11	94180333	94180506	94180354	94180479	MRE11A	NM_005591	2	20	15	-	94180385	94180604
238285758	chr11	94180333	94180506	94180354	94180479	MRE11A	NM_005590	1	19	15	-	94180385	94180604
238882920	chr11	94192644	94192775	94192671	94192747	MRE11A	NM_005591	2	20	13	-	94192574	94192747
238882920	chr11	94192644	94192775	94192671	94192747	MRE11A	NM_005590	1	19	13	-	94192574	94192747
236172524	chr11	94200882	94201020	94200907	94200996	MRE11A	NM_005591	2	20	10	-	94200979	94201059
236172524	chr11	94200882	94201020	94200907	94200996	MRE11A	NM_005590	1	19	10	-	94200979	94201059
237423394	chr11	94203742	94203868	94203771	94203843	MRE11A	NM_005591	2	20	9	-	94203637	94203808
237423394	chr11	94203742	94203868	94203771	94203843	MRE11A	NM_005590	1	19	9	-	94203637	94203808
237363624	chr11	94211784	94211931	94211811	94211909	MRE11A	NM_005591	2	20	6	-	94211901	94212042
237363624	chr11	94211784	94211931	94211811	94211909	MRE11A	NM_005590	1	19	6	-	94211901	94212042
235924030	chr11	94212830	94212975	94212855	94212950	MRE11A	NM_005591	2	20	5	-	94212840	94212927

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235924030	chr11	94212830	94212975	94212855	94212950	MRE11A	NM_005590	1	19	5	-	94212840	94212927
235310363	chr11	94223984	94224112	94224010	94224080	MRE11A	NM_005591	2	20	3	-	94223999	94224131
235310363	chr11	94223984	94224112	94224010	94224080	MRE11A	NM_005590	1	19	3	-	94223999	94224131
234489065	chr11	95712236	95712406	95712260	95712379	MAML2	NM_032427	1	5	5	-	95711440	95713127
234498876	chr11	95712693	95712840	95712715	95712812	MAML2	NM_032427	1	5	5	-	95711440	95713127
232275139	chr11	95718685	95718848	95718712	95718820	MAML2	NM_032427	1	5	4	-	95718695	95718806
233067705	chr11	95825425	95825595	95825447	95825572	MAML2	NM_032427	1	5	2	-	95825056	95826681
234519125	chr11	95825853	95826003	95825873	95825981	MAML2	NM_032427	1	5	2	-	95825056	95826681
234532728	chr11	95826334	95826483	95826357	95826462	MAML2	NM_032427	1	5	2	-	95825056	95826681
233181164	chr11	96074481	96074652	96074505	96074632	MAML2	NM_032427	1	5	1	-	96074547	96076344
223894851	chr11	102195163	102195334	102195187	102195308	BIRC3	NM_182962	2	10	3	+	102195192	102196093
223894851	chr11	102195163	102195334	102195187	102195308	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222410260	chr11	102195603	102195777	102195627	102195749	BIRC3	NM_182962	2	10	3	+	102195192	102196093
222410260	chr11	102195603	102195777	102195627	102195749	BIRC3	NM_001165	1	9	2	+	102192568	102196093
224029287	chr11	102196055	102196220	102196075	102196192	BIRC3	NM_182962	2	10	3	+	102195192	102196093
224029287	chr11	102196055	102196220	102196075	102196192	BIRC3	NM_001165	1	9	2	+	102192568	102196093
223940638	chr11	102198800	102198951	102198826	102198923	BIRC3	NM_182962	2	10	5	+	102198783	102198861
223940638	chr11	102198800	102198951	102198826	102198923	BIRC3	NM_001165	1	9	4	+	102198783	102198861
223004537	chr11	102201802	102201974	102201826	102201947	BIRC3	NM_182962	2	10	7	+	102201730	102201972
223004537	chr11	102201802	102201974	102201826	102201947	BIRC3	NM_001165	1	9	6	+	102201730	102201972
224612376	chr11	102207368	102207539	102207393	102207511	BIRC3	NM_182962	2	10	9	+	102207491	102207532
224612376	chr11	102207368	102207539	102207393	102207511	BIRC3	NM_001165	1	9	8	+	102207491	102207532
224051474	chr11	102207744	102207871	102207771	102207838	BIRC3	NM_182962	2	10	10	+	102207640	102210135
224051474	chr11	102207744	102207871	102207771	102207838	BIRC3	NM_001165	1	9	9	+	102207640	102210135
294226207	chr11	102220821	102220976	102220845	102220951	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294272777	chr11	102221251	102221378	102221272	102221350	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294933611	chr11	102221569	102221731	102221592	102221703	BIRC2	NM_001166	1	9	3	+	102221575	102221674
294106837	chr11	102248129	102248297	102248154	102248272	BIRC2	NM_001166	1	9	7	+	102248227	102248481
293816419	chr11	102248611	102248763	102248640	102248739	BIRC2	NM_001166	1	9	9	+	102248721	102249401
271880524	chr11	106558359	106558519	106558380	106558490	GUCY1A2	NM_000855	1	8	8	-	106544738	106558482
271880524	chr11	106558359	106558519	106558380	106558490	GUCY1A2	NM_001256424	2	9	9	-	106544738	106558482
271810162	chr11	106647165	106647339	106647187	106647312	GUCY1A2	NM_000855	1	8	6	-	106647165	106647308
271810162	chr11	106647165	106647339	106647187	106647312	GUCY1A2	NM_001256424	2	9	6	-	106647165	106647308
272152114	chr11	106681055	106681182	106681075	106681155	GUCY1A2	NM_000855	1	8	5	-	106680719	106681204
272152114	chr11	106681055	106681182	106681075	106681155	GUCY1A2	NM_001256424	2	9	5	-	106680719	106681204
272653271	chr11	106810289	106810451	106810314	106810428	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
272653271	chr11	106810289	106810451	106810314	106810428	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
271265303	chr11	106810770	106810933	106810793	106810906	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
271265303	chr11	106810770	106810933	106810793	106810906	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
270183661	chr11	106856802	106856935	106856830	106856912	GUCY1A2	NM_000855	1	8	2	-	106856796	106856857
270183661	chr11	106856802	106856935	106856830	106856912	GUCY1A2	NM_001256424	2	9	2	-	106856796	106856857

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223696973	chr11	108098368	108098526	108098389	108098498	ATM	NM_000051	1	63	2	+	108098322	108098423
222444283	chr11	108106320	108106481	108106348	108106453	ATM	NM_000051	1	63	5	+	108106397	108106561
222536518	chr11	108114683	108114842	108114707	108114818	ATM	NM_000051	1	63	6	+	108114680	108114845
222997242	chr11	108115575	108115744	108115600	108115725	ATM	NM_000051	1	63	7	+	108115515	108115753
224035069	chr11	108117792	108117954	108117820	108117928	ATM	NM_000051	1	63	8	+	108117691	108117854
223533762	chr11	108121506	108121630	108121530	108121602	ATM	NM_000051	1	63	10	+	108121428	108121799
223269928	chr11	108122590	108122759	108122613	108122737	ATM	NM_000051	1	63	11	+	108122564	108122758
223073479	chr11	108124487	108124624	108124511	108124596	ATM	NM_000051	1	63	13	+	108124541	108124766
222203805	chr11	108126948	108127072	108126972	108127045	ATM	NM_000051	1	63	14	+	108126942	108127067
222204488	chr11	108129635	108129785	108129662	108129757	ATM	NM_000051	1	63	16	+	108129713	108129802
223659859	chr11	108139210	108139384	108139236	108139356	ATM	NM_000051	1	63	18	+	108139137	108139336
223516717	chr11	108142060	108142191	108142087	108142163	ATM	NM_000051	1	63	20	+	108141978	108142133
223781850	chr11	108143437	108143564	108143462	108143544	ATM	NM_000051	1	63	22	+	108143449	108143579
222171152	chr11	108151605	108151756	108151633	108151731	ATM	NM_000051	1	63	24	+	108151722	108151895
224359488	chr11	108154966	108155115	108154994	108155086	ATM	NM_000051	1	63	26	+	108154954	108155200
224114318	chr11	108159628	108159760	108159656	108159736	ATM	NM_000051	1	63	28	+	108159704	108159830
222740386	chr11	108160446	108160581	108160474	108160553	ATM	NM_000051	1	63	29	+	108160329	108160528
224735920	chr11	108165603	108165733	108165627	108165705	ATM	NM_000051	1	63	32	+	108165654	108165786
326918704	chr11	108170464	108170616	108170492	108170593	ATM	NM_000051	1	63	34	+	108170441	108170612
326881828	chr11	108173622	108173774	108173648	108173742	ATM	NM_000051	1	63	36	+	108173580	108173756
223039345	chr11	108175517	108175673	108175539	108175646	ATM	NM_000051	1	63	37	+	108175402	108175579
223583369	chr11	108183016	108183183	108183044	108183155	ATM	NM_000051	1	63	40	+	108183138	108183225
224007686	chr11	108186678	108186806	108186708	108186779	ATM	NM_000051	1	63	42	+	108186738	108186840
222547294	chr11	108190678	108190852	108190704	108190824	ATM	NM_000051	1	63	44	+	108190681	108190785
223483293	chr11	108196089	108196254	108196110	108196227	ATM	NM_000051	1	63	46	+	108196037	108196271
223672105	chr11	108198302	108198433	108198324	108198412	ATM	NM_000051	1	63	48	+	108198372	108198485
222358631	chr11	108199888	108200036	108199912	108200008	ATM	NM_000051	1	63	49	+	108199748	108199965
224645888	chr11	108202069	108202241	108202093	108202220	ATM	NM_000051	1	63	51	+	108202171	108202284
222592843	chr11	108202727	108202875	108202755	108202847	ATM	NM_000051	1	63	52	+	108202606	108202764
223221577	chr11	108204568	108204704	108204596	108204673	ATM	NM_000051	1	63	54	+	108204613	108204695
224373216	chr11	108206576	108206748	108206599	108206720	ATM	NM_000051	1	63	56	+	108206572	108206688
223808104	chr11	108216578	108216732	108216603	108216705	ATM	NM_000051	1	63	58	+	108216470	108216635
223536280	chr11	108224493	108224667	108224515	108224645	ATM	NM_000051	1	63	60	+	108224493	108224607
224465893	chr11	108236015	108236185	108236039	108236163	ATM	NM_000051	1	63	63	+	108236052	108239826
239793456	chr11	111958599	111958745	111958620	111958720	SDHD	NM_003002	1	4	2	+	111958581	111958697
233663118	chr11	118307470	118307638	118307487	118307621	MLL	NM_005933	2	36	1	+	118307205	118307659
233663118	chr11	118307470	118307638	118307487	118307621	MLL	NM_001197104	1	36	1	+	118307205	118307659
234013494	chr11	118342372	118342505	118342400	118342477	MLL	NM_005933	2	36	3	+	118342377	118345030
234013494	chr11	118342372	118342505	118342400	118342477	MLL	NM_001197104	1	36	3	+	118342377	118345030
234025894	chr11	118342765	118342936	118342789	118342916	MLL	NM_005933	2	36	3	+	118342377	118345030
234025894	chr11	118342765	118342936	118342789	118342916	MLL	NM_001197104	1	36	3	+	118342377	118345030

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231639161	chr11	118343148	118343317	118343171	118343291	MLL	NM_005933	2	36	3	+	118342377	118345030
231639161	chr11	118343148	118343317	118343171	118343291	MLL	NM_001197104	1	36	3	+	118342377	118345030
231697556	chr11	118343598	118343762	118343620	118343739	MLL	NM_005933	2	36	3	+	118342377	118345030
231697556	chr11	118343598	118343762	118343620	118343739	MLL	NM_001197104	1	36	3	+	118342377	118345030
234027022	chr11	118344013	118344157	118344039	118344134	MLL	NM_005933	2	36	3	+	118342377	118345030
234027022	chr11	118344013	118344157	118344039	118344134	MLL	NM_001197104	1	36	3	+	118342377	118345030
234027183	chr11	118344437	118344596	118344456	118344568	MLL	NM_005933	2	36	3	+	118342377	118345030
234027183	chr11	118344437	118344596	118344456	118344568	MLL	NM_001197104	1	36	3	+	118342377	118345030
234021275	chr11	118344794	118344949	118344811	118344930	MLL	NM_005933	2	36	3	+	118342377	118345030
234021275	chr11	118344794	118344949	118344811	118344930	MLL	NM_001197104	1	36	3	+	118342377	118345030
233581662	chr11	118348633	118348807	118348658	118348788	MLL	NM_005933	2	36	5	+	118348682	118348916
233581662	chr11	118348633	118348807	118348658	118348788	MLL	NM_001197104	1	36	5	+	118348682	118348916
233118315	chr11	118352390	118352553	118352419	118352531	MLL	NM_005933	2	36	7	+	118352430	118352807
233118315	chr11	118352390	118352553	118352419	118352531	MLL	NM_001197104	1	36	7	+	118352430	118352807
231859493	chr11	118353073	118353245	118353099	118353218	MLL	NM_005933	2	36	8	+	118353137	118353210
231859493	chr11	118353073	118353245	118353099	118353218	MLL	NM_001197104	1	36	8	+	118353137	118353210
233477072	chr11	118359225	118359391	118359247	118359367	MLL	NM_005933	2	36	11	+	118359329	118359475
233477072	chr11	118359225	118359391	118359247	118359367	MLL	NM_001197104	1	36	11	+	118359329	118359475
232708524	chr11	118360721	118360881	118360748	118360860	MLL	NM_005933	2	36	13	+	118360844	118360964
232708524	chr11	118360721	118360881	118360748	118360860	MLL	NM_001197104	1	36	13	+	118360844	118360964
231611127	chr11	118362426	118362597	118362451	118362572	MLL	NM_005933	2	36	15	+	118362459	118362643
231611127	chr11	118362426	118362597	118362451	118362572	MLL	NM_001197104	1	36	15	+	118362459	118362643
231030592	chr11	118364944	118365117	118364968	118365094	MLL	NM_005933	2	36	17	+	118365003	118365113
231030592	chr11	118364944	118365117	118364968	118365094	MLL	NM_001197104	1	36	17	+	118365003	118365113
233266616	chr11	118366292	118366445	118366320	118366425	MLL	NM_005933	2	36	19	+	118366415	118366608
233266616	chr11	118366292	118366445	118366320	118366425	MLL	NM_001197104	1	36	19	+	118366415	118366608
231636552	chr11	118368553	118368718	118368579	118368694	MLL	NM_005933	2	36	21	+	118368651	118368788
231636552	chr11	118368553	118368718	118368579	118368694	MLL	NM_001197104	1	36	21	+	118368651	118368788
234382961	chr11	118369898	118370047	118369925	118370019	MLL	NM_005933	2	36	23	+	118370018	118370135
234382961	chr11	118369898	118370047	118369925	118370019	MLL	NM_001197104	1	36	23	+	118370018	118370135
233308287	chr11	118371733	118371890	118371751	118371862	MLL	NM_005933	2	36	25	+	118371702	118371862
233308287	chr11	118371733	118371890	118371751	118371862	MLL	NM_001197104	1	36	25	+	118371702	118371862
231221292	chr11	118373049	118373222	118373078	118373197	MLL	NM_005933	2	36	27	+	118373113	118377361
231221292	chr11	118373049	118373222	118373078	118373197	MLL	NM_001197104	1	36	27	+	118373113	118377361
231306411	chr11	118373504	118373669	118373525	118373641	MLL	NM_005933	2	36	27	+	118373113	118377361
231306411	chr11	118373504	118373669	118373525	118373641	MLL	NM_001197104	1	36	27	+	118373113	118377361
233884531	chr11	118373957	118374090	118373977	118374062	MLL	NM_005933	2	36	27	+	118373113	118377361
233884531	chr11	118373957	118374090	118373977	118374062	MLL	NM_001197104	1	36	27	+	118373113	118377361
231343720	chr11	118374379	118374539	118374405	118374512	MLL	NM_005933	2	36	27	+	118373113	118377361
231343720	chr11	118374379	118374539	118374405	118374512	MLL	NM_001197104	1	36	27	+	118373113	118377361
233872925	chr11	118374751	118374901	118374776	118374873	MLL	NM_005933	2	36	27	+	118373113	118377361

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233872925	chr11	118374751	118374901	118374776	118374873	MLL	NM_001197104	1	36	27	+	118373113	118377361
233873154	chr11	118375148	118375291	118375172	118375265	MLL	NM_005933	2	36	27	+	118373113	118377361
233873154	chr11	118375148	118375291	118375172	118375265	MLL	NM_001197104	1	36	27	+	118373113	118377361
233884426	chr11	118375610	118375784	118375633	118375762	MLL	NM_005933	2	36	27	+	118373113	118377361
233884426	chr11	118375610	118375784	118375633	118375762	MLL	NM_001197104	1	36	27	+	118373113	118377361
233903822	chr11	118376107	118376275	118376128	118376252	MLL	NM_005933	2	36	27	+	118373113	118377361
233903822	chr11	118376107	118376275	118376128	118376252	MLL	NM_001197104	1	36	27	+	118373113	118377361
233897537	chr11	118376560	118376697	118376583	118376677	MLL	NM_005933	2	36	27	+	118373113	118377361
233897537	chr11	118376560	118376697	118376583	118376677	MLL	NM_001197104	1	36	27	+	118373113	118377361
233924929	chr11	118376923	118377091	118376944	118377068	MLL	NM_005933	2	36	27	+	118373113	118377361
233924929	chr11	118376923	118377091	118376944	118377068	MLL	NM_001197104	1	36	27	+	118373113	118377361
231601697	chr11	118378201	118378375	118378228	118378351	MLL	NM_005933	2	36	28	+	118378244	118378324
231601697	chr11	118378201	118378375	118378228	118378351	MLL	NM_001197104	1	36	28	+	118378244	118378324
234591297	chr11	118382593	118382764	118382620	118382740	MLL	NM_005933	2	36	31	+	118382666	118382740
234591297	chr11	118382593	118382764	118382620	118382740	MLL	NM_001197104	1	36	31	+	118382666	118382740
231726202	chr11	118390650	118390801	118390674	118390779	MLL	NM_005933	2	36	33	+	118390672	118390779
231726202	chr11	118390650	118390801	118390674	118390779	MLL	NM_001197104	1	36	33	+	118390672	118390779
230969521	chr11	118392028	118392166	118392055	118392142	MLL	NM_005933	2	36	35	+	118392003	118392132
230969521	chr11	118392028	118392166	118392055	118392142	MLL	NM_001197104	1	36	35	+	118392003	118392132
253777269	chr11	119077048	119077221	119077067	119077200	CBL	NM_005188	1	16	1	+	119076990	119077322
226472872	chr11	119103183	119103356	119103204	119103328	CBL	NM_005188	1	16	2	+	119103158	119103405
226313178	chr11	119142556	119142730	119142579	119142704	CBL	NM_005188	1	16	3	+	119142445	119142591
226092825	chr11	119145532	119145693	119145555	119145664	CBL	NM_005188	1	16	5	+	119145542	119145663
226426452	chr11	119148790	119148917	119148821	119148896	CBL	NM_005188	1	16	8	+	119148876	119149007
226242022	chr11	119149274	119149448	119149296	119149424	CBL	NM_005188	1	16	9	+	119149220	119149423
225893938	chr11	119155950	119156100	119155972	119156081	CBL	NM_005188	1	16	11	+	119155899	119156276
226184349	chr11	119158557	119158710	119158581	119158682	CBL	NM_005188	1	16	12	+	119158562	119158656
225399677	chr11	119168156	119168281	119168175	119168254	CBL	NM_005188	1	16	14	+	119168094	119168191
226355988	chr11	119170259	119170428	119170283	119170406	CBL	NM_005188	1	16	16	+	119170205	119178859
226460535	chr11	125497492	125497666	125497519	125497638	CHEK1	NM_001244846	3	12	3	+	125497502	125497725
226460535	chr11	125497492	125497666	125497519	125497638	CHEK1	NR_045205	6	13	3	+	125497502	125497725
226460535	chr11	125497492	125497666	125497519	125497638	CHEK1	NM_001114121	1	14	3	+	125497502	125497725
226460535	chr11	125497492	125497666	125497519	125497638	CHEK1	NM_001114122	2	13	3	+	125497502	125497725
226460535	chr11	125497492	125497666	125497519	125497638	CHEK1	NM_001274	4	13	3	+	125497502	125497725
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NM_001244846	3	12	4	+	125499127	125499191
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NR_045205	6	13	4	+	125499127	125499191
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NM_001114121	1	14	4	+	125499127	125499191
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NM_001114122	2	13	4	+	125499127	125499191
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NM_001274	4	13	4	+	125499127	125499191
226115158	chr11	125499140	125499274	125499160	125499246	CHEK1	NR_045204	5	12	3	+	125499127	125499191
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NM_001244846	3	12	6	+	125503058	125503246

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NR_045205	6	13	6	+	125503058	125503246
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NM_001114121	1	14	6	+	125503058	125503246
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NM_001114122	2	13	6	+	125503058	125503246
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NM_001274	4	13	6	+	125503058	125503246
225722148	chr11	125503068	125503199	125503090	125503172	CHEK1	NR_045204	5	12	5	+	125503058	125503246
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NM_001244846	3	12	8	+	125507344	125507439
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NR_045205	6	13	8	+	125507344	125507439
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NM_001114121	1	14	8	+	125507344	125507439
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NM_001114122	2	13	8	+	125507344	125507439
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NM_001274	4	13	8	+	125507344	125507439
226571694	chr11	125507264	125507390	125507291	125507362	CHEK1	NR_045204	5	12	7	+	125507344	125507439
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NM_001244846	3	12	10	+	125513986	125514163
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NR_045205	6	13	10	+	125513986	125514163
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NM_001114121	1	14	10	+	125513986	125514163
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NM_001114122	2	13	10	+	125513986	125514163
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NM_001274	4	13	10	+	125513986	125514163
225532534	chr11	125513965	125514127	125513992	125514101	CHEK1	NR_045204	5	12	9	+	125513986	125514163
225439546	chr11	125523603	125523750	125523625	125523723	CHEK1	NR_045205	6	13	12	+	125523641	125523742
225439546	chr11	125523603	125523750	125523625	125523723	CHEK1	NM_001114121	1	14	12	+	125523641	125523742
225439546	chr11	125523603	125523750	125523625	125523723	CHEK1	NM_001114122	2	13	12	+	125523641	125523742
225439546	chr11	125523603	125523750	125523625	125523723	CHEK1	NM_001274	4	13	12	+	125523641	125523742
225439546	chr11	125523603	125523750	125523625	125523723	CHEK1	NR_045204	5	12	11	+	125523641	125523742
294564652	chr11	128332177	128332344	128332205	128332323	ETS1	NM_005238	3	8	8	-	128328656	128332471
294564652	chr11	128332177	128332344	128332205	128332323	ETS1	NM_001143820	1	10	10	-	128328656	128332471
294564652	chr11	128332177	128332344	128332205	128332323	ETS1	NM_001162422	2	4	4	-	128328656	128332471
294377010	chr11	128333415	128333555	128333440	128333530	ETS1	NM_005238	3	8	7	-	128333404	128333522
294377010	chr11	128333415	128333555	128333440	128333530	ETS1	NM_001143820	1	10	9	-	128333404	128333522
294377010	chr11	128333415	128333555	128333440	128333530	ETS1	NM_001162422	2	4	3	-	128333404	128333522
293781512	chr11	128354661	128354796	128354689	128354772	ETS1	NM_005238	3	8	5	-	128354718	128354966
293781512	chr11	128354661	128354796	128354689	128354772	ETS1	NM_001143820	1	10	7	-	128354718	128354966
293802587	chr11	128359148	128359320	128359171	128359294	ETS1	NM_005238	3	8	3	-	128359185	128359385
293802587	chr11	128359148	128359320	128359171	128359294	ETS1	NM_001143820	1	10	5	-	128359185	128359385
293927180	chr11	128391693	128391866	128391713	128391845	ETS1	NM_005238	3	8	1	-	128391808	128392205
293927180	chr11	128391693	128391866	128391713	128391845	ETS1	NM_001162422	2	4	1	-	128391808	128392205
294712737	chr11	128442909	128443058	128442931	128443038	ETS1	NM_001143820	1	10	2	-	128442957	128443039
228000054	chr11	128628150	128628319	128628172	128628297	FLI1	NM_002017	2	9	2	+	128628010	128628221
228000054	chr11	128628150	128628319	128628172	128628297	FLI1	NM_001167681	1	10	3	+	128628010	128628221
227157666	chr11	128642738	128642900	128642761	128642880	FLI1	NM_002017	2	9	4	+	128642677	128642880
227157666	chr11	128642738	128642900	128642761	128642880	FLI1	NM_001167681	1	10	5	+	128642677	128642880
228520120	chr11	128676986	128677160	128677011	128677136	FLI1	NM_002017	2	9	7	+	128677075	128677134
228520120	chr11	128676986	128677160	128677011	128677136	FLI1	NM_001167681	1	10	8	+	128677075	128677134

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229106647	chr11	128680533	128680686	128680559	128680660	FLI1	NM_002017	2	9	9	+	128680354	128683162
229106647	chr11	128680533	128680686	128680559	128680660	FLI1	NM_001167681	1	10	10	+	128680354	128683162
226082697	chr12	4383120	4383277	4383140	4383259	CCND2	NM_001759	1	5	1	+	4382902	4383401
226191167	chr12	4385201	4385356	4385222	4385334	CCND2	NM_001759	1	5	2	+	4385171	4385386
226697631	chr12	4397924	4398059	4397947	4398039	CCND2	NM_001759	1	5	4	+	4398008	4398156
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_001127584	3	8	8	-	6759704	6760400
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_001127583	2	8	8	-	6759704	6760400
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_016162	6	8	8	-	6759704	6760400
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_001127582	1	8	8	-	6759704	6760400
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_001127586	5	7	7	-	6759704	6760400
280575152	chr12	6760321	6760445	6760343	6760420	ING4	NM_001127585	4	7	7	-	6759704	6760400
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_001127584	3	8	5	-	6761828	6761933
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_016162	6	8	5	-	6761828	6761933
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_001127583	2	8	5	-	6761828	6761936
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_001127582	1	8	5	-	6761828	6761936
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_001127586	5	7	5	-	6761828	6761936
278029449	chr12	6761786	6761958	6761808	6761937	ING4	NM_001127585	4	7	4	-	6761828	6761936
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_001127584	3	8	3	-	6762396	6762562
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_001127583	2	8	3	-	6762396	6762562
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_016162	6	8	3	-	6762396	6762562
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_001127582	1	8	3	-	6762396	6762562
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_001127586	5	7	3	-	6762396	6762562
279593714	chr12	6762422	6762585	6762444	6762563	ING4	NM_001127585	4	7	2	-	6762396	6762562
264667922	chr12	6776797	6776964	6776821	6776943	ZNF384	NM_133476	3	10	10	-	6775643	6777281
264667922	chr12	6776797	6776964	6776821	6776943	ZNF384	NM_001135734	2	11	11	-	6775643	6777281
264667922	chr12	6776797	6776964	6776821	6776943	ZNF384	NM_001039920	1	9	9	-	6775643	6777281
240869925	chr12	6778135	6778289	6778158	6778268	ZNF384	NM_133476	3	10	9	-	6778197	6778355
240869925	chr12	6778135	6778289	6778158	6778268	ZNF384	NM_001135734	2	11	10	-	6778197	6778355
240869925	chr12	6778135	6778289	6778158	6778268	ZNF384	NM_001039920	1	9	8	-	6778197	6778355
262004398	chr12	6781550	6781703	6781570	6781682	ZNF384	NM_001135734	2	11	8	-	6781516	6781698
240106142	chr12	6782554	6782694	6782575	6782672	ZNF384	NM_133476	3	10	7	-	6782382	6782606
240106142	chr12	6782554	6782694	6782575	6782672	ZNF384	NM_001135734	2	11	7	-	6782382	6782606
240106142	chr12	6782554	6782694	6782575	6782672	ZNF384	NM_001039920	1	9	6	-	6782382	6782606
262562639	chr12	6787537	6787689	6787558	6787660	ZNF384	NM_133476	3	10	6	-	6787293	6787626
262562639	chr12	6787537	6787689	6787558	6787660	ZNF384	NM_001135734	2	11	6	-	6787293	6787626
240626366	chr12	6788295	6788463	6788316	6788441	ZNF384	NM_133476	3	10	4	-	6788112	6788349
240626366	chr12	6788295	6788463	6788316	6788441	ZNF384	NM_001135734	2	11	4	-	6788112	6788349
240626366	chr12	6788295	6788463	6788316	6788441	ZNF384	NM_001039920	1	9	4	-	6788112	6788349
233361228	chr12	25368409	25368536	25368436	25368508	KRAS	NM_033360	2	6	5	-	25368371	25368494
234355242	chr12	25380223	25380385	25380241	25380358	KRAS	NM_004985	1	5	3	-	25380168	25380346
234355242	chr12	25380223	25380385	25380241	25380358	KRAS	NM_033360	2	6	3	-	25380168	25380346

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
281405650	chr12	43747994	43748164	43748022	43748137	ADAMTS20	NM_025003	1	39	39	-	43748012	43748101
284270209	chr12	43763078	43763230	43763105	43763203	ADAMTS20	NM_025003	1	39	37	-	43763093	43763184
282553462	chr12	43769919	43770092	43769941	43770063	ADAMTS20	NM_025003	1	39	35	-	43769860	43769951
282553462	chr12	43769919	43770092	43769941	43770063	ADAMTS20	NM_025003	1	39	34	-	43770039	43770133
282529330	chr12	43770336	43770467	43770364	43770443	ADAMTS20	NM_025003	1	39	33	-	43770327	43770456
282846816	chr12	43777244	43777402	43777265	43777376	ADAMTS20	NM_025003	1	39	31	-	43777361	43777531
283686814	chr12	43777641	43777814	43777663	43777786	ADAMTS20	NM_025003	1	39	30	-	43777607	43777780
328491603	chr12	43792989	43793142	43793015	43793111	ADAMTS20	NM_025003	1	39	29	-	43792869	43793036
283397837	chr12	43821107	43821234	43821133	43821212	ADAMTS20	NM_025003	1	39	27	-	43821111	43821272
328496855	chr12	43822235	43822371	43822260	43822338	ADAMTS20	NM_025003	1	39	26	-	43822044	43822334
281752141	chr12	43823338	43823485	43823366	43823457	ADAMTS20	NM_025003	1	39	24	-	43823420	43823527
283368852	chr12	43824142	43824285	43824169	43824261	ADAMTS20	NM_025003	1	39	23	-	43824155	43824274
284454677	chr12	43826037	43826170	43826070	43826144	ADAMTS20	NM_025003	1	39	21	-	43826107	43826271
282527970	chr12	43826402	43826532	43826427	43826507	ADAMTS20	NM_025003	1	39	20	-	43826404	43826614
283911093	chr12	43828047	43828193	43828074	43828170	ADAMTS20	NM_025003	1	39	19	-	43828048	43828174
282761434	chr12	43833617	43833774	43833650	43833746	ADAMTS20	NM_025003	1	39	17	-	43833700	43833872
284018566	chr12	43837559	43837733	43837583	43837705	ADAMTS20	NM_025003	1	39	16	-	43837594	43837686
282062920	chr12	43846067	43846210	43846093	43846182	ADAMTS20	NM_025003	1	39	14	-	43846077	43846213
282132617	chr12	43846392	43846549	43846414	43846521	ADAMTS20	NM_025003	1	39	13	-	43846317	43846498
281977331	chr12	43858353	43858479	43858382	43858452	ADAMTS20	NM_025003	1	39	10	-	43858394	43858535
281835645	chr12	43862337	43862494	43862363	43862466	ADAMTS20	NM_025003	1	39	8	-	43862403	43862508
281560886	chr12	43886331	43886502	43886352	43886474	ADAMTS20	NM_025003	1	39	6	-	43886308	43886432
284548790	chr12	43925818	43925948	43925847	43925920	ADAMTS20	NM_025003	1	39	3	-	43925839	43925998
283603108	chr12	43944837	43945009	43944856	43944988	ADAMTS20	NM_025003	1	39	2	-	43944712	43945073
273048706	chr12	46123787	46123914	46123804	46123889	ARID2	NM_152641	1	21	2	+	46123827	46123920
272828560	chr12	46205172	46205306	46205196	46205280	ARID2	NM_152641	1	21	4	+	46205201	46205334
273380946	chr12	46211553	46211689	46211580	46211660	ARID2	NM_152641	1	21	5	+	46211453	46211671
273416843	chr12	46230386	46230544	46230413	46230516	ARID2	NM_152641	1	21	7	+	46230372	46230438
273700480	chr12	46231055	46231217	46231079	46231191	ARID2	NM_152641	1	21	9	+	46231104	46231200
273583443	chr12	46231443	46231571	46231464	46231539	ARID2	NM_152641	1	21	10	+	46231281	46231490
273456802	chr12	46240631	46240772	46240657	46240748	ARID2	NM_152641	1	21	12	+	46240639	46240720
273510104	chr12	46243351	46243477	46243379	46243452	ARID2	NM_152641	1	21	14	+	46243363	46243559
274435304	chr12	46243874	46244044	46243900	46244018	ARID2	NM_152641	1	21	15	+	46243819	46246679
274438194	chr12	46244324	46244495	46244351	46244467	ARID2	NM_152641	1	21	15	+	46243819	46246679
274434358	chr12	46244772	46244920	46244794	46244898	ARID2	NM_152641	1	21	15	+	46243819	46246679
274506632	chr12	46245213	46245377	46245233	46245354	ARID2	NM_152641	1	21	15	+	46243819	46246679
273582289	chr12	46245698	46245866	46245718	46245838	ARID2	NM_152641	1	21	15	+	46243819	46246679
273586664	chr12	46246094	46246218	46246121	46246197	ARID2	NM_152641	1	21	15	+	46243819	46246679
274467277	chr12	46246483	46246654	46246510	46246632	ARID2	NM_152641	1	21	15	+	46243819	46246679
272837313	chr12	46254682	46254827	46254708	46254795	ARID2	NM_152641	1	21	16	+	46254584	46254732
273705807	chr12	46285669	46285827	46285693	46285805	ARID2	NM_152641	1	21	17	+	46285563	46285701

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273705807	chr12	46285669	46285827	46285693	46285805	ARID2	NM_152641	1	21	18	+	46285794	46285879
274561382	chr12	46287343	46287516	46287370	46287492	ARID2	NM_152641	1	21	20	+	46287413	46287504
274052411	chr12	49415793	49415967	49415817	49415946	MLL2	NM_003482	1	54	53	-	49415826	49415934
273903439	chr12	49416544	49416699	49416567	49416678	MLL2	NM_003482	1	54	51	-	49416373	49416658
273569839	chr12	49418639	49418785	49418660	49418764	MLL2	NM_003482	1	54	49	-	49418593	49418729
273647981	chr12	49420265	49420431	49420284	49420412	MLL2	NM_003482	1	54	48	-	49419965	49421105
274617857	chr12	49420665	49420837	49420684	49420816	MLL2	NM_003482	1	54	48	-	49419965	49421105
273334035	chr12	49421564	49421738	49421584	49421716	MLL2	NM_003482	1	54	47	-	49421586	49421713
274173378	chr12	49422644	49422779	49422665	49422757	MLL2	NM_003482	1	54	45	-	49422611	49422741
273023377	chr12	49423990	49424155	49424016	49424133	MLL2	NM_003482	1	54	42	-	49424063	49424222
273480691	chr12	49424588	49424753	49424608	49424732	MLL2	NM_003482	1	54	40	-	49424676	49424816
274244696	chr12	49425164	49425293	49425184	49425272	MLL2	NM_003482	1	54	39	-	49424958	49427747
274231927	chr12	49425553	49425717	49425572	49425699	MLL2	NM_003482	1	54	39	-	49424958	49427747
273251335	chr12	49425971	49426133	49425996	49426110	MLL2	NM_003482	1	54	39	-	49424958	49427747
273265942	chr12	49426344	49426485	49426363	49426465	MLL2	NM_003482	1	54	39	-	49424958	49427747
273254086	chr12	49426928	49427052	49426948	49427034	MLL2	NM_003482	1	54	39	-	49424958	49427747
273263426	chr12	49427294	49427447	49427312	49427425	MLL2	NM_003482	1	54	39	-	49424958	49427747
273532346	chr12	49427743	49427916	49427763	49427894	MLL2	NM_003482	1	54	38	-	49427850	49428082
273120186	chr12	49428319	49428480	49428340	49428455	MLL2	NM_003482	1	54	36	-	49428365	49428449
274295628	chr12	49431101	49431268	49431118	49431251	MLL2	NM_003482	1	54	34	-	49430908	49432772
273268855	chr12	49431581	49431707	49431600	49431688	MLL2	NM_003482	1	54	34	-	49430908	49432772
273324919	chr12	49432001	49432173	49432021	49432154	MLL2	NM_003482	1	54	34	-	49430908	49432772
274263725	chr12	49432472	49432644	49432496	49432623	MLL2	NM_003482	1	54	34	-	49430908	49432772
273599646	chr12	49432999	49433169	49433019	49433142	MLL2	NM_003482	1	54	33	-	49433005	49433141
274185630	chr12	49433483	49433634	49433505	49433612	MLL2	NM_003482	1	54	31	-	49433507	49435318
273166522	chr12	49433909	49434034	49433931	49434015	MLL2	NM_003482	1	54	31	-	49433507	49435318
273183948	chr12	49434295	49434468	49434315	49434445	MLL2	NM_003482	1	54	31	-	49433507	49435318
273151624	chr12	49434626	49434796	49434648	49434774	MLL2	NM_003482	1	54	31	-	49433507	49435318
274185591	chr12	49435028	49435182	49435046	49435161	MLL2	NM_003482	1	54	31	-	49433507	49435318
273949224	chr12	49435658	49435806	49435679	49435781	MLL2	NM_003482	1	54	29	-	49435700	49435773
273022342	chr12	49436278	49436452	49436300	49436428	MLL2	NM_003482	1	54	27	-	49436344	49436428
272892115	chr12	49437045	49437201	49437066	49437175	MLL2	NM_003482	1	54	24	-	49437146	49437211
273949545	chr12	49437572	49437746	49437595	49437725	MLL2	NM_003482	1	54	22	-	49437651	49437781
273372027	chr12	49438191	49438365	49438216	49438338	MLL2	NM_003482	1	54	20	-	49438186	49438305
274280525	chr12	49439695	49439862	49439716	49439840	MLL2	NM_003482	1	54	18	-	49439703	49439750
273279966	chr12	49440311	49440484	49440336	49440457	MLL2	NM_003482	1	54	15	-	49440392	49440573
274590562	chr12	49442858	49443026	49442880	49443002	MLL2	NM_003482	1	54	12	-	49442888	49443001
273770211	chr12	49443731	49443885	49443756	49443863	MLL2	NM_003482	1	54	11	-	49443465	49444573
273750309	chr12	49444173	49444337	49444194	49444317	MLL2	NM_003482	1	54	11	-	49443465	49444573
273076612	chr12	49444626	49444800	49444653	49444777	MLL2	NM_003482	1	54	10	-	49444669	49446207
273084857	chr12	49445048	49445200	49445068	49445179	MLL2	NM_003482	1	54	10	-	49444669	49446207

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273135891	chr12	49445503	49445634	49445521	49445614	MLL2	NM_003482	1	54	10	-	49444669	49446207
273098904	chr12	49445773	49445910	49445794	49445891	MLL2	NM_003482	1	54	10	-	49444669	49446207
273098681	chr12	49446141	49446285	49446158	49446267	MLL2	NM_003482	1	54	10	-	49444669	49446207
272852885	chr12	49446763	49446897	49446784	49446875	MLL2	NM_003482	1	54	8	-	49446698	49446855
273547169	chr12	49447705	49447870	49447727	49447849	MLL2	NM_003482	1	54	5	-	49447761	49447923
273188169	chr12	49448318	49448471	49448337	49448454	MLL2	NM_003482	1	54	3	-	49448311	49448534
273056345	chr12	49448989	49449163	49449010	49449142	MLL2	NM_003482	1	54	1	-	49449059	49449107
224749788	chr12	51203285	51203429	51203309	51203401	ATF1	NM_005171	1	7	4	+	51203239	51203372
223284405	chr12	51208054	51208184	51208077	51208158	ATF1	NM_005171	1	7	6	+	51208063	51208222
321678054	chr12	54575832	54576006	54575857	54575987	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321678054	chr12	54575832	54576006	54575857	54575987	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321678054	chr12	54575832	54576006	54575857	54575987	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NR_045039	7	5	4	-	54576288	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_001243791	5	4	3	-	54576288	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_001243790	4	5	4	-	54576288	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_001243789	3	6	5	-	54576288	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321654734	chr12	54576270	54576431	54576290	54576407	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
269936381	chr12	56474010	56474184	56474030	56474166	ERBB3	NM_001005915	1	3	1	+	56473892	56474166
269936381	chr12	56474010	56474184	56474030	56474166	ERBB3	NM_001982	2	28	1	+	56473809	56474166
269980499	chr12	56478799	56478932	56478820	56478909	ERBB3	NM_001005915	1	3	3	+	56478779	56479401
269980499	chr12	56478799	56478932	56478820	56478909	ERBB3	NM_001982	2	28	3	+	56478779	56478965
270243847	chr12	56481290	56481463	56481315	56481435	ERBB3	NM_001982	2	28	5	+	56481361	56481426
269981327	chr12	56482297	56482466	56482321	56482441	ERBB3	NM_001982	2	28	8	+	56482327	56482440
272723516	chr12	56487084	56487242	56487110	56487215	ERBB3	NM_001982	2	28	12	+	56487129	56487334
271818352	chr12	56487830	56488001	56487853	56487974	ERBB3	NM_001982	2	28	14	+	56487883	56487973
269619802	chr12	56489398	56489539	56489421	56489517	ERBB3	NM_001982	2	28	17	+	56489449	56489590
270979703	chr12	56490779	56490950	56490805	56490929	ERBB3	NM_001982	2	28	20	+	56490829	56491014
270864377	chr12	56492257	56492389	56492285	56492367	ERBB3	NM_001982	2	28	22	+	56492284	56492359
270555623	chr12	56493574	56493737	56493595	56493713	ERBB3	NM_001982	2	28	25	+	56493622	56493813
270315674	chr12	56494913	56495074	56494934	56495052	ERBB3	NM_001982	2	28	27	+	56494845	56495145
269759504	chr12	56495444	56495616	56495465	56495588	ERBB3	NM_001982	2	28	28	+	56495313	56497291
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_001195055	3	4	4	-	57910371	57910963
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_001195054	2	4	4	-	57910371	57910963
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_001195053	1	4	4	-	57910371	57910963
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_001195057	5	4	4	-	57910371	57910963
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_001195056	4	3	3	-	57910371	57910963
231102396	chr12	57910475	57910630	57910496	57910607	DDIT3	NM_004083	6	4	4	-	57910371	57910963
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_001195053	1	4	3	-	57911052	57911378
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_001195056	4	3	2	-	57911052	57911536

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_001195057	5	4	3	-	57911052	57911207
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_001195054	2	4	3	-	57911052	57911325
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_001195055	3	4	3	-	57911052	57911302
228161862	chr12	57910965	57911114	57910991	57911089	DDIT3	NM_004083	6	4	3	-	57911052	57911221
226187887	chr12	58142945	58143110	58142964	58143092	CDK4	NM_000075	1	8	7	-	58142965	58143100
226053197	chr12	58144643	58144813	58144665	58144790	CDK4	NM_000075	1	8	4	-	58144706	58144873
226582103	chr12	58145188	58145351	58145209	58145330	CDK4	NM_000075	1	8	2	-	58145283	58145519
231419236	chr12	69202871	69203035	69202892	69203011	MDM2	NM_002392	1	11	2	+	69202988	69203072
233565032	chr12	69210684	69210810	69210705	69210783	MDM2	NM_002392	1	11	4	+	69210592	69210725
232577674	chr12	69218339	69218470	69218363	69218443	MDM2	NM_002392	1	11	7	+	69218335	69218431
233169266	chr12	69229540	69229714	69229568	69229686	MDM2	NM_002392	1	11	9	+	69229609	69229764
234781199	chr12	69233139	69233276	69233164	69233248	MDM2	NM_002392	1	11	11	+	69233054	69239212
234773109	chr12	69233564	69233737	69233585	69233709	MDM2	NM_002392	1	11	11	+	69233054	69239212
326783366	chr12	112888188	112888351	112888210	112888324	PTPN11	NM_002834	1	16	3	+	112888122	112888316
241320313	chr12	112893639	112893813	112893665	112893785	PTPN11	NM_002834	1	16	6	+	112893754	112893867
236207114	chr12	112915407	112915576	112915430	112915548	PTPN11	NM_002834	1	16	8	+	112915455	112915534
240094066	chr12	112919879	112920048	112919906	112920021	PTPN11	NM_002834	1	16	10	+	112919878	112920009
238258168	chr12	112926781	112926947	112926804	112926919	PTPN11	NM_002834	1	16	13	+	112926828	112926979
227190154	chr12	121416459	121416598	121416481	121416577	HNF1A	NM_000545	1	10	1	+	121416549	121416897
227192489	chr12	121416825	121416967	121416847	121416949	HNF1A	NM_000545	1	10	1	+	121416549	121416897
227410308	chr12	121431233	121431393	121431258	121431372	HNF1A	NM_000545	1	10	3	+	121431323	121431509
227614048	chr12	121431954	121432119	121431975	121432102	HNF1A	NM_000545	1	10	4	+	121431967	121432208
227974277	chr12	121434316	121434486	121434334	121434469	HNF1A	NM_000545	1	10	6	+	121434344	121434545
227443439	chr12	121437040	121437211	121437058	121437192	HNF1A	NM_000545	1	10	8	+	121437071	121437192
229011428	chr12	121438955	121439117	121438977	121439098	HNF1A	NM_000545	1	10	10	+	121438868	121440314
280118997	chr12	123214083	123214227	123214107	123214206	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280151388	chr12	123214529	123214682	123214553	123214655	HCAR1	NM_032554	1	1	1	-	123212153	123215129
288132265	chr12	132445313	132445437	132445331	132445416	EP400	NM_015409	1	53	2	+	132445130	132446499
328496807	chr12	132446421	132446594	132446448	132446569	EP400	NM_015409	1	53	2	+	132445130	132446499
287505349	chr12	132466685	132466858	132466707	132466838	EP400	NM_015409	1	53	5	+	132466638	132467023
287553807	chr12	132471051	132471222	132471075	132471201	EP400	NM_015409	1	53	6	+	132471059	132471352
287829890	chr12	132472354	132472510	132472376	132472489	EP400	NM_015409	1	53	7	+	132472250	132472435
286986693	chr12	132475918	132476050	132475938	132476027	EP400	NM_015409	1	53	10	+	132475952	132476001
287668873	chr12	132489640	132489791	132489662	132489767	EP400	NM_015409	1	53	13	+	132489622	132489729
287331434	chr12	132491307	132491480	132491327	132491453	EP400	NM_015409	1	53	15	+	132491245	132491422
289169798	chr12	132497589	132497754	132497612	132497732	EP400	NM_015409	1	53	17	+	132497554	132497723
285025396	chr12	132498269	132498443	132498293	132498418	EP400	NM_015409	1	53	19	+	132498322	132498458
288509870	chr12	132502210	132502361	132502230	132502338	EP400	NM_015409	1	53	20	+	132502080	132502266
287902080	chr12	132504688	132504840	132504705	132504819	EP400	NM_015409	1	53	22	+	132504594	132504763
288761879	chr12	132505821	132505959	132505839	132505939	EP400	NM_015409	1	53	23	+	132505624	132505866
288747331	chr12	132510241	132510415	132510258	132510390	EP400	NM_015409	1	53	25	+	132510191	132510349

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288238542	chr12	132512646	132512817	132512670	132512797	EP400	NM_015409	1	53	27	+	132512562	132512833
286403466	chr12	132514497	132514658	132514518	132514630	EP400	NM_015409	1	53	29	+	132514534	132514703
285378603	chr12	132522191	132522365	132522220	132522339	EP400	NM_015409	1	53	31	+	132522227	132522338
288964890	chr12	132527840	132528014	132527862	132527993	EP400	NM_015409	1	53	33	+	132527849	132528007
284851999	chr12	132528816	132528963	132528835	132528937	EP400	NM_015409	1	53	35	+	132528722	132528856
289024169	chr12	132529825	132529989	132529850	132529964	EP400	NM_015409	1	53	38	+	132529864	132530105
285965281	chr12	132530294	132530467	132530316	132530446	EP400	NM_015409	1	53	39	+	132530272	132530445
286228770	chr12	132535120	132535271	132535145	132535243	EP400	NM_015409	1	53	41	+	132535144	132535200
288919719	chr12	132539517	132539672	132539540	132539648	EP400	NM_015409	1	53	45	+	132539644	132539753
288919719	chr12	132539517	132539672	132539540	132539648	EP400	NM_015409	1	53	44	+	132539519	132539564
286310192	chr12	132546935	132547070	132546958	132547049	EP400	NM_015409	1	53	47	+	132547011	132547246
288811151	chr12	132549199	132549368	132549227	132549350	EP400	NM_015409	1	53	48	+	132549213	132549431
289056233	chr12	132551815	132551967	132551839	132551948	EP400	NM_015409	1	53	50	+	132551907	132552031
286571384	chr12	132561001	132561162	132561028	132561138	EP400	NM_015409	1	53	52	+	132561061	132561138
269669232	chr13	26828760	26828894	26828778	26828872	CDK8	NM_001260	1	13	1	+	26828756	26828906
271154889	chr13	26927765	26927934	26927792	26927909	CDK8	NM_001260	1	13	4	+	26927877	26928017
270246849	chr13	26959227	26959398	26959253	26959370	CDK8	NM_001260	1	13	6	+	26959348	26959479
272645173	chr13	26967606	26967765	26967634	26967736	CDK8	NM_001260	1	13	7	+	26967504	26967647
271184333	chr13	26975388	26975520	26975416	26975493	CDK8	NM_001260	1	13	11	+	26975406	26975484
269723679	chr13	26978076	26978250	26978098	26978227	CDK8	NM_001260	1	13	13	+	26978093	26978569
227495405	chr13	28588577	28588729	28588600	28588700	FLT3	NM_004119	1	24	23	-	28588589	28588694
326745935	chr13	28592599	28592760	28592622	28592732	FLT3	NM_004119	1	24	20	-	28592604	28592726
228702319	chr13	28601188	28601358	28601214	28601330	FLT3	NM_004119	1	24	17	-	28601225	28601378
228905712	chr13	28607981	28608155	28608006	28608131	FLT3	NM_004119	1	24	15	-	28608024	28608128
228162941	chr13	28608442	28608582	28608468	28608558	FLT3	NM_004119	1	24	13	-	28608438	28608544
227611083	chr13	28610086	28610214	28610109	28610191	FLT3	NM_004119	1	24	11	-	28610072	28610180
227331767	chr13	28623500	28623674	28623520	28623646	FLT3	NM_004119	1	24	8	-	28623521	28623674
227646644	chr13	28624138	28624311	28624163	28624283	FLT3	NM_004119	1	24	6	-	28624232	28624359
227749241	chr13	28631550	28631686	28631571	28631658	FLT3	NM_004119	1	24	4	-	28631484	28631599
227394142	chr13	28644534	28644703	28644557	28644675	FLT3	NM_004119	1	24	2	-	28644628	28644749
228857053	chr13	28877384	28877521	28877403	28877492	FLT1	NM_002019	4	30	30	-	28874483	28877505
227132856	chr13	28885717	28885849	28885745	28885821	FLT1	NM_002019	4	30	27	-	28885727	28885869
227840780	chr13	28891623	28891794	28891645	28891767	FLT1	NM_002019	4	30	25	-	28891635	28891734
227527976	chr13	28895623	28895772	28895649	28895744	FLT1	NM_002019	4	30	23	-	28895600	28895722
227399931	chr13	28896937	28897107	28896966	28897085	FLT1	NM_002019	4	30	21	-	28896927	28897083
227223245	chr13	28908123	28908295	28908144	28908267	FLT1	NM_002019	4	30	18	-	28908162	28908266
227989373	chr13	28931608	28931779	28931631	28931755	FLT1	NM_002019	4	30	15	-	28931691	28931822
229638019	chr13	28963756	28963912	28963776	28963883	FLT1	NM_001159920	1	13	13	-	28959688	28964241
227298253	chr13	28964190	28964330	28964211	28964302	FLT1	NM_001159920	1	13	13	-	28959688	28964241
227298253	chr13	28964190	28964330	28964211	28964302	FLT1	NM_002019	4	30	13	-	28963933	28964241
227298253	chr13	28964190	28964330	28964211	28964302	FLT1	NM_001160030	2	15	13	-	28963933	28964241

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227418506	chr13	28979927	28980069	28979951	28980042	FLT1	NM_002019	4	30	11	-	28979917	28980031
227418506	chr13	28979927	28980069	28979951	28980042	FLT1	NM_001159920	1	13	11	-	28979917	28980031
227418506	chr13	28979927	28980069	28979951	28980042	FLT1	NM_001160031	3	12	11	-	28979917	28980031
227418506	chr13	28979927	28980069	28979951	28980042	FLT1	NM_001160030	2	15	11	-	28979917	28980031
228001553	chr13	29001923	29002097	29001950	29002070	FLT1	NM_002019	4	30	9	-	29001889	29002058
228001553	chr13	29001923	29002097	29001950	29002070	FLT1	NM_001159920	1	13	9	-	29001889	29002058
228001553	chr13	29001923	29002097	29001950	29002070	FLT1	NM_001160031	3	12	9	-	29001889	29002058
228001553	chr13	29001923	29002097	29001950	29002070	FLT1	NM_001160030	2	15	9	-	29001889	29002058
228418200	chr13	29005341	29005501	29005370	29005475	FLT1	NM_002019	4	30	7	-	29005273	29005447
228418200	chr13	29005341	29005501	29005370	29005475	FLT1	NM_001159920	1	13	7	-	29005273	29005447
228418200	chr13	29005341	29005501	29005370	29005475	FLT1	NM_001160031	3	12	7	-	29005273	29005447
228418200	chr13	29005341	29005501	29005370	29005475	FLT1	NM_001160030	2	15	7	-	29005273	29005447
228928112	chr13	29008226	29008383	29008249	29008357	FLT1	NM_002019	4	30	5	-	29008195	29008357
228928112	chr13	29008226	29008383	29008249	29008357	FLT1	NM_001159920	1	13	5	-	29008195	29008357
228928112	chr13	29008226	29008383	29008249	29008357	FLT1	NM_001160031	3	12	5	-	29008195	29008357
228928112	chr13	29008226	29008383	29008249	29008357	FLT1	NM_001160030	2	15	5	-	29008195	29008357
227420097	chr13	29041055	29041189	29041084	29041165	FLT1	NM_002019	4	30	3	-	29041040	29041266
227420097	chr13	29041055	29041189	29041084	29041165	FLT1	NM_001159920	1	13	3	-	29041040	29041266
227420097	chr13	29041055	29041189	29041084	29041165	FLT1	NM_001160031	3	12	3	-	29041040	29041266
227420097	chr13	29041055	29041189	29041084	29041165	FLT1	NM_001160030	2	15	3	-	29041040	29041266
229045339	chr13	29068802	29068944	29068819	29068927	FLT1	NM_002019	4	30	1	-	29068917	29069265
229045339	chr13	29068802	29068944	29068819	29068927	FLT1	NM_001159920	1	13	1	-	29068917	29069265
229045339	chr13	29068802	29068944	29068819	29068927	FLT1	NM_001160031	3	12	1	-	29068917	29069265
229045339	chr13	29068802	29068944	29068819	29068927	FLT1	NM_001160030	2	15	1	-	29068917	29069265
230284630	chr13	41133803	41133976	41133824	41133956	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230274674	chr13	41134223	41134387	41134247	41134364	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230250500	chr13	41134605	41134730	41134629	41134706	FOXO1	NM_002015	1	3	2	-	41133646	41134997
229108204	chr13	41239623	41239772	41239641	41239753	FOXO1	NM_002015	1	3	1	-	41239720	41240734
227234918	chr13	41240229	41240398	41240246	41240379	FOXO1	NM_002015	1	3	1	-	41239720	41240734
242616297	chr13	48916662	48916795	48916695	48916767	RB1	NM_000321	1	27	3	+	48916735	48916850
326771505	chr13	48923107	48923276	48923136	48923252	RB1	NM_000321	1	27	6	+	48923092	48923159
239977367	chr13	48942570	48942736	48942598	48942711	RB1	NM_000321	1	27	11	+	48942663	48942740
326815367	chr13	48955399	48955565	48955426	48955539	RB1	NM_000321	1	27	17	+	48955383	48955579
238058188	chr13	49030300	49030468	49030326	49030440	RB1	NM_000321	1	27	19	+	49030340	49030485
242362921	chr13	49037881	49038045	49037909	49038012	RB1	NM_000321	1	27	21	+	49037867	49037971
238926081	chr13	49039363	49039532	49039385	49039504	RB1	NM_000321	1	27	23	+	49039341	49039504
240874975	chr13	49051401	49051536	49051429	49051511	RB1	NM_000321	1	27	26	+	49051491	49051540
230803047	chr13	103504402	103504563	103504430	103504538	ERCC5	NM_000123	1	15	2	+	103504468	103504643
229219217	chr13	103506516	103506675	103506537	103506651	ERCC5	NM_000123	1	15	4	+	103506638	103506724
227918651	chr13	103513755	103513894	103513779	103513871	ERCC5	NM_000123	1	15	7	+	103513857	103514064
227737199	chr13	103514335	103514509	103514362	103514485	ERCC5	NM_000123	1	15	8	+	103514380	103515453

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227819221	chr13	103514773	103514945	103514795	103514923	ERCC5	NM_000123	1	15	8	+	103514380	103515453
231006814	chr13	103515199	103515373	103515227	103515352	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230620724	chr13	103518201	103518345	103518224	103518318	ERCC5	NM_000123	1	15	9	+	103518017	103518261
230534130	chr13	103519067	103519196	103519088	103519168	ERCC5	NM_000123	1	15	11	+	103518982	103519195
231229243	chr13	103520538	103520708	103520561	103520682	ERCC5	NM_000123	1	15	12	+	103520463	103520607
229736609	chr13	103525496	103525643	103525524	103525623	ERCC5	NM_000123	1	15	14	+	103525609	103525693
231481279	chr13	103527809	103527983	103527834	103527960	ERCC5	NM_000123	1	15	15	+	103527657	103528351
271610687	chr13	110408508	110408682	110408532	110408655	IRS2	NM_003749	1	2	2	-	110406184	110408655
272382972	chr13	110434624	110434798	110434642	110434780	IRS2	NM_003749	1	2	1	-	110434389	110438914
272381649	chr13	110435059	110435230	110435077	110435213	IRS2	NM_003749	1	2	1	-	110434389	110438914
272382164	chr13	110435625	110435774	110435649	110435757	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383262	chr13	110435982	110436155	110436001	110436135	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383908	chr13	110436324	110436495	110436343	110436477	IRS2	NM_003749	1	2	1	-	110434389	110438914
272388395	chr13	110436768	110436922	110436791	110436904	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383949	chr13	110437410	110437544	110437429	110437525	IRS2	NM_003749	1	2	1	-	110434389	110438914
272384882	chr13	110437840	110438011	110437857	110437993	IRS2	NM_003749	1	2	1	-	110434389	110438914
279832077	chr13	113960775	113960942	113960797	113960921	LAMP1	NM_005561	1	9	2	+	113960800	113960921
280861146	chr13	113973720	113973894	113973748	113973871	LAMP1	NM_005561	1	9	5	+	113973784	113973971
279393263	chr13	113974673	113974845	113974697	113974821	LAMP1	NM_005561	1	9	6	+	113974660	113974785
280896801	chr13	113976571	113976734	113976592	113976713	LAMP1	NM_005561	1	9	9	+	113976597	113977741
269575787	chr14	23776879	23777053	23776901	23777030	BCL2L2	NM_004050	2	4	3	+	23776969	23777408
269575787	chr14	23776879	23777053	23776901	23777030	BCL2L2	NM_001199839	1	4	3	+	23776969	23777408
269599584	chr14	23777305	23777463	23777328	23777442	BCL2L2	NM_004050	2	4	3	+	23776969	23777408
269599584	chr14	23777305	23777463	23777328	23777442	BCL2L2	NM_001199839	1	4	3	+	23776969	23777408
238984450	chr14	36986550	36986692	36986569	36986675	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
238984450	chr14	36986550	36986692	36986569	36986675	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
258663329	chr14	36987177	36987349	36987197	36987332	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
258663329	chr14	36987177	36987349	36987197	36987332	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
237522143	chr14	36988472	36988596	36988495	36988575	NKX2-1	NM_003317	2	2	1	-	36988190	36988903
237522143	chr14	36988472	36988596	36988495	36988575	NKX2-1	NM_001079668	1	3	2	-	36988190	36988575
237128232	chr14	51192505	51192637	51192529	51192612	NIN	NM_016350	1	29	29	-	51192546	51192784
237128232	chr14	51192505	51192637	51192529	51192612	NIN	NM_182946	4	30	30	-	51192546	51192784
242344565	chr14	51196150	51196308	51196175	51196285	NIN	NM_016350	1	29	28	-	51196241	51196441
242344565	chr14	51196150	51196308	51196175	51196285	NIN	NM_182946	4	30	29	-	51196241	51196441
242344565	chr14	51196150	51196308	51196175	51196285	NIN	NM_182944	3	30	29	-	51196241	51196441
242344565	chr14	51196150	51196308	51196175	51196285	NIN	NM_020921	2	31	29	-	51196241	51196441
239356288	chr14	51202264	51202438	51202291	51202412	NIN	NM_016350	1	29	27	-	51202234	51202335
239356288	chr14	51202264	51202438	51202291	51202412	NIN	NM_182946	4	30	28	-	51202234	51202335
239356288	chr14	51202264	51202438	51202291	51202412	NIN	NM_182944	3	30	28	-	51202234	51202335
239356288	chr14	51202264	51202438	51202291	51202412	NIN	NM_020921	2	31	28	-	51202234	51202335
242136822	chr14	51206081	51206236	51206104	51206208	NIN	NM_016350	1	29	25	-	51206026	51206205

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242136822	chr14	51206081	51206236	51206104	51206208	NIN	NM_182946	4	30	26	-	51206026	51206205
242136822	chr14	51206081	51206236	51206104	51206208	NIN	NM_182944	3	30	26	-	51206026	51206205
242136822	chr14	51206081	51206236	51206104	51206208	NIN	NM_020921	2	31	26	-	51206026	51206205
235411576	chr14	51210840	51211005	51210862	51210978	NIN	NM_016350	1	29	22	-	51210961	51211083
235411576	chr14	51210840	51211005	51210862	51210978	NIN	NM_182946	4	30	23	-	51210961	51211083
235411576	chr14	51210840	51211005	51210862	51210978	NIN	NM_182944	3	30	23	-	51210961	51211083
235411576	chr14	51210840	51211005	51210862	51210978	NIN	NM_020921	2	31	23	-	51210961	51211083
237340319	chr14	51219215	51219381	51219235	51219353	NIN	NM_016350	1	29	20	-	51219236	51219451
237340319	chr14	51219215	51219381	51219235	51219353	NIN	NM_182946	4	30	21	-	51219236	51219451
237340319	chr14	51219215	51219381	51219235	51219353	NIN	NM_182944	3	30	21	-	51219236	51219451
237340319	chr14	51219215	51219381	51219235	51219353	NIN	NM_020921	2	31	21	-	51219236	51219451
235955471	chr14	51223725	51223864	51223743	51223836	NIN	NM_182946	4	30	18	-	51223210	51225348
235955471	chr14	51223725	51223864	51223743	51223836	NIN	NM_182944	3	30	18	-	51223210	51225348
235955471	chr14	51223725	51223864	51223743	51223836	NIN	NM_020921	2	31	18	-	51223210	51225348
236024721	chr14	51224124	51224282	51224149	51224261	NIN	NM_182946	4	30	18	-	51223210	51225348
236024721	chr14	51224124	51224282	51224149	51224261	NIN	NM_182944	3	30	18	-	51223210	51225348
236024721	chr14	51224124	51224282	51224149	51224261	NIN	NM_020921	2	31	18	-	51223210	51225348
240904201	chr14	51224552	51224724	51224574	51224700	NIN	NM_182946	4	30	18	-	51223210	51225348
240904201	chr14	51224552	51224724	51224574	51224700	NIN	NM_182944	3	30	18	-	51223210	51225348
240904201	chr14	51224552	51224724	51224574	51224700	NIN	NM_020921	2	31	18	-	51223210	51225348
236157757	chr14	51225021	51225195	51225047	51225174	NIN	NM_182946	4	30	18	-	51223210	51225348
236157757	chr14	51225021	51225195	51225047	51225174	NIN	NM_182944	3	30	18	-	51223210	51225348
236157757	chr14	51225021	51225195	51225047	51225174	NIN	NM_020921	2	31	18	-	51223210	51225348
235472176	chr14	51226669	51226811	51226690	51226788	NIN	NM_016350	1	29	17	-	51226575	51227077
235472176	chr14	51226669	51226811	51226690	51226788	NIN	NM_182946	4	30	17	-	51226575	51227077
235472176	chr14	51226669	51226811	51226690	51226788	NIN	NM_182944	3	30	17	-	51226575	51227077
235472176	chr14	51226669	51226811	51226690	51226788	NIN	NM_020921	2	31	17	-	51226575	51227077
241148461	chr14	51228483	51228657	51228504	51228632	NIN	NM_016350	1	29	16	-	51228508	51228629
241148461	chr14	51228483	51228657	51228504	51228632	NIN	NM_182946	4	30	16	-	51228508	51228629
241148461	chr14	51228483	51228657	51228504	51228632	NIN	NM_182944	3	30	16	-	51228508	51228629
241148461	chr14	51228483	51228657	51228504	51228632	NIN	NM_020921	2	31	16	-	51228508	51228629
235553834	chr14	51233422	51233562	51233444	51233534	NIN	NM_016350	1	29	13	-	51233498	51233608
235553834	chr14	51233422	51233562	51233444	51233534	NIN	NM_182946	4	30	13	-	51233498	51233608
235553834	chr14	51233422	51233562	51233444	51233534	NIN	NM_182944	3	30	13	-	51233498	51233608
235553834	chr14	51233422	51233562	51233444	51233534	NIN	NM_020921	2	31	13	-	51233498	51233608
237468729	chr14	51237460	51237625	51237480	51237604	NIN	NM_016350	1	29	11	-	51237570	51237710
237468729	chr14	51237460	51237625	51237480	51237604	NIN	NM_182946	4	30	11	-	51237570	51237710
237468729	chr14	51237460	51237625	51237480	51237604	NIN	NM_182944	3	30	11	-	51237570	51237710
237468729	chr14	51237460	51237625	51237480	51237604	NIN	NM_020921	2	31	11	-	51237570	51237710
257581111	chr14	51238971	51239120	51238996	51239098	NIN	NM_016350	1	29	9	-	51239019	51239186
257581111	chr14	51238971	51239120	51238996	51239098	NIN	NM_182946	4	30	9	-	51239019	51239186

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257581111	chr14	51238971	51239120	51238996	51239098	NIN	NM_182944	3	30	9	-	51239019	51239186
257581111	chr14	51238971	51239120	51238996	51239098	NIN	NM_020921	2	31	9	-	51239019	51239186
239231892	chr14	51239767	51239898	51239791	51239870	NIN	NM_016350	1	29	8	-	51239667	51239813
239231892	chr14	51239767	51239898	51239791	51239870	NIN	NM_182946	4	30	8	-	51239667	51239813
239231892	chr14	51239767	51239898	51239791	51239870	NIN	NM_182944	3	30	8	-	51239667	51239813
239231892	chr14	51239767	51239898	51239791	51239870	NIN	NM_020921	2	31	8	-	51239667	51239813
235634279	chr14	51259384	51259510	51259406	51259488	NIN	NM_016350	1	29	5	-	51259430	51259599
235634279	chr14	51259384	51259510	51259406	51259488	NIN	NM_182946	4	30	5	-	51259430	51259599
235634279	chr14	51259384	51259510	51259406	51259488	NIN	NM_182944	3	30	5	-	51259430	51259599
235634279	chr14	51259384	51259510	51259406	51259488	NIN	NM_020921	2	31	5	-	51259430	51259599
236031502	chr14	51288644	51288806	51288665	51288784	NIN	NM_016350	1	29	3	-	51288592	51288795
236031502	chr14	51288644	51288806	51288665	51288784	NIN	NM_182946	4	30	3	-	51288592	51288795
236031502	chr14	51288644	51288806	51288665	51288784	NIN	NM_182944	3	30	3	-	51288592	51288795
236031502	chr14	51288644	51288806	51288665	51288784	NIN	NM_020921	2	31	3	-	51288592	51288795
279362090	chr14	62186984	62187144	62187010	62187123	HIF1A	NM_001530	2	15	2	+	62187100	62187290
279362090	chr14	62186984	62187144	62187010	62187123	HIF1A	NM_181054	3	14	2	+	62187100	62187290
279362090	chr14	62186984	62187144	62187010	62187123	HIF1A	NM_001243084	1	15	2	+	62187097	62187290
279181511	chr14	62188247	62188399	62188272	62188371	HIF1A	NM_001243084	1	15	3	+	62188227	62188372
279181511	chr14	62188247	62188399	62188272	62188371	HIF1A	NM_001530	2	15	3	+	62188227	62188372
279181511	chr14	62188247	62188399	62188272	62188371	HIF1A	NM_181054	3	14	3	+	62188227	62188372
279350737	chr14	62193417	62193541	62193444	62193514	HIF1A	NM_001243084	1	15	5	+	62193424	62193536
279350737	chr14	62193417	62193541	62193444	62193514	HIF1A	NM_001530	2	15	5	+	62193424	62193536
279350737	chr14	62193417	62193541	62193444	62193514	HIF1A	NM_181054	3	14	5	+	62193424	62193536
279960948	chr14	62194305	62194456	62194333	62194430	HIF1A	NM_001243084	1	15	6	+	62194171	62194373
279960948	chr14	62194305	62194456	62194333	62194430	HIF1A	NM_001530	2	15	6	+	62194171	62194373
279960948	chr14	62194305	62194456	62194333	62194430	HIF1A	NM_181054	3	14	6	+	62194171	62194373
280849998	chr14	62200868	62201011	62200890	62200983	HIF1A	NM_001243084	1	15	8	+	62200856	62201003
280849998	chr14	62200868	62201011	62200890	62200983	HIF1A	NM_001530	2	15	8	+	62200856	62201003
280849998	chr14	62200868	62201011	62200890	62200983	HIF1A	NM_181054	3	14	8	+	62200856	62201003
279042260	chr14	62203729	62203877	62203757	62203851	HIF1A	NM_001243084	1	15	9	+	62203607	62203827
279042260	chr14	62203729	62203877	62203757	62203851	HIF1A	NM_001530	2	15	9	+	62203607	62203827
279042260	chr14	62203729	62203877	62203757	62203851	HIF1A	NM_181054	3	14	9	+	62203607	62203827
280785881	chr14	62207170	62207323	62207198	62207299	HIF1A	NM_001243084	1	15	11	+	62207223	62207345
280785881	chr14	62207170	62207323	62207198	62207299	HIF1A	NM_001530	2	15	11	+	62207223	62207345
280785881	chr14	62207170	62207323	62207198	62207299	HIF1A	NM_181054	3	14	11	+	62207223	62207345
278397493	chr14	62207505	62207664	62207532	62207642	HIF1A	NM_001243084	1	15	12	+	62207473	62207906
278397493	chr14	62207505	62207664	62207532	62207642	HIF1A	NM_001530	2	15	12	+	62207473	62207906
278397493	chr14	62207505	62207664	62207532	62207642	HIF1A	NM_181054	3	14	12	+	62207473	62207906
278852243	chr14	62211346	62211482	62211374	62211457	HIF1A	NM_001243084	1	15	13	+	62211423	62211531
278852243	chr14	62211346	62211482	62211374	62211457	HIF1A	NM_001530	2	15	13	+	62211423	62211531
278852243	chr14	62211346	62211482	62211374	62211457	HIF1A	NM_181054	3	14	13	+	62211423	62211531

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280855226	chr14	62213672	62213802	62213695	62213774	HIF1A	NM_001243084	1	15	15	+	62213652	62214977
280855226	chr14	62213672	62213802	62213695	62213774	HIF1A	NM_001530	2	15	15	+	62213652	62214977
280855226	chr14	62213672	62213802	62213695	62213774	HIF1A	NM_181054	3	14	14	+	62213652	62214977
266318562	chr14	81528378	81528550	81528405	81528525	TSHR	NM_001142626	3	9	2	+	81528492	81528563
266318562	chr14	81528378	81528550	81528405	81528525	TSHR	NM_000369	1	10	2	+	81528492	81528563
266318562	chr14	81528378	81528550	81528405	81528525	TSHR	NM_001018036	2	9	2	+	81528492	81528563
266356714	chr14	81554248	81554407	81554276	81554379	TSHR	NM_001142626	3	9	4	+	81554298	81554372
266356714	chr14	81554248	81554407	81554276	81554379	TSHR	NM_000369	1	10	4	+	81554298	81554372
266356714	chr14	81554248	81554407	81554276	81554379	TSHR	NM_001018036	2	9	4	+	81554298	81554372
264039859	chr14	81574739	81574878	81574767	81574850	TSHR	NM_001142626	3	9	8	+	81574719	81574796
264039859	chr14	81574739	81574878	81574767	81574850	TSHR	NM_000369	1	10	8	+	81574719	81574796
264039859	chr14	81574739	81574878	81574767	81574850	TSHR	NM_001018036	2	9	8	+	81574719	81574796
266487335	chr14	81606090	81606252	81606116	81606228	TSHR	NM_000369	1	10	9	+	81606023	81606211
262765572	chr14	81609611	81609735	81609633	81609712	TSHR	NM_000369	1	10	10	+	81609284	81612646
266518026	chr14	81610061	81610232	81610083	81610205	TSHR	NM_000369	1	10	10	+	81609284	81612646
262846572	chr14	81610532	81610673	81610553	81610650	TSHR	NM_000369	1	10	10	+	81609284	81612646
264397356	chr14	92436147	92436283	92436172	92436252	TRIP11	NM_004239	1	21	21	-	92434243	92436237
239476554	chr14	92441489	92441660	92441511	92441632	TRIP11	NM_004239	1	21	18	-	92441516	92441630
241320099	chr14	92460205	92460363	92460233	92460335	TRIP11	NM_004239	1	21	15	-	92460153	92460256
238406511	chr14	92465680	92465841	92465708	92465815	TRIP11	NM_004239	1	21	13	-	92465584	92465777
266112012	chr14	92469661	92469825	92469683	92469803	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266132617	chr14	92470109	92470240	92470135	92470212	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266147562	chr14	92470512	92470642	92470541	92470619	TRIP11	NM_004239	1	21	11	-	92469763	92472792
242766062	chr14	92470907	92471044	92470932	92471016	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266131393	chr14	92471231	92471400	92471260	92471374	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266151312	chr14	92471600	92471724	92471625	92471700	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266159706	chr14	92471898	92472053	92471920	92472027	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266166547	chr14	92472231	92472355	92472258	92472326	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266165999	chr14	92472505	92472631	92472533	92472606	TRIP11	NM_004239	1	21	11	-	92469763	92472792
240288789	chr14	92473988	92474136	92474015	92474107	TRIP11	NM_004239	1	21	10	-	92473984	92474196
263040682	chr14	92478058	92478232	92478086	92478204	TRIP11	NM_004239	1	21	8	-	92478099	92478139
263130522	chr14	92483942	92484107	92483970	92484079	TRIP11	NM_004239	1	21	5	-	92484026	92484094
240250230	chr14	92488136	92488307	92488158	92488280	TRIP11	NM_004239	1	21	4	-	92487900	92488175
240233431	chr14	92499531	92499704	92499558	92499675	TRIP11	NM_004239	1	21	2	-	92499536	92499597
229999963	chr14	95556831	95556969	95556854	95556944	DICER1	NM_177438	3	27	27	-	95552565	95557000
229999963	chr14	95556831	95556969	95556854	95556944	DICER1	NM_001195573	1	25	25	-	95552565	95557000
229999963	chr14	95556831	95556969	95556854	95556944	DICER1	NM_030621	2	28	28	-	95552565	95557000
231485590	chr14	95557390	95557561	95557414	95557540	DICER1	NM_177438	3	27	26	-	95557371	95557446
231485590	chr14	95557390	95557561	95557414	95557540	DICER1	NM_001195573	1	25	24	-	95557371	95557446
231485590	chr14	95557390	95557561	95557414	95557540	DICER1	NM_030621	2	28	27	-	95557371	95557446
231485590	chr14	95557390	95557561	95557414	95557540	DICER1	NM_177438	3	27	25	-	95557540	95557702

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231485590	chr14	95557390	95557561	95557414	95557540	DICER1	NM_030621	2	28	26	-	95557540	95557702
229767104	chr14	95560297	95560461	95560320	95560436	DICER1	NM_177438	3	27	24	-	95560225	95560493
229767104	chr14	95560297	95560461	95560320	95560436	DICER1	NM_001195573	1	25	23	-	95560225	95560493
229767104	chr14	95560297	95560461	95560320	95560436	DICER1	NM_030621	2	28	25	-	95560225	95560493
232993028	chr14	95562281	95562445	95562309	95562421	DICER1	NM_177438	3	27	23	-	95562162	95563050
232993028	chr14	95562281	95562445	95562309	95562421	DICER1	NM_001195573	1	25	22	-	95562162	95563050
232993028	chr14	95562281	95562445	95562309	95562421	DICER1	NM_030621	2	28	24	-	95562162	95563050
230663761	chr14	95562702	95562856	95562725	95562829	DICER1	NM_177438	3	27	23	-	95562162	95563050
230663761	chr14	95562702	95562856	95562725	95562829	DICER1	NM_001195573	1	25	22	-	95562162	95563050
230663761	chr14	95562702	95562856	95562725	95562829	DICER1	NM_030621	2	28	24	-	95562162	95563050
232750814	chr14	95566130	95566265	95566157	95566238	DICER1	NM_177438	3	27	22	-	95566117	95566272
232750814	chr14	95566130	95566265	95566157	95566238	DICER1	NM_001195573	1	25	21	-	95566117	95566272
232750814	chr14	95566130	95566265	95566157	95566238	DICER1	NM_030621	2	28	23	-	95566117	95566272
228171934	chr14	95569865	95570039	95569891	95570011	DICER1	NM_177438	3	27	21	-	95569683	95570463
228171934	chr14	95569865	95570039	95569891	95570011	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228171934	chr14	95569865	95570039	95569891	95570011	DICER1	NM_030621	2	28	22	-	95569683	95570463
228132843	chr14	95570291	95570459	95570319	95570433	DICER1	NM_177438	3	27	21	-	95569683	95570463
228132843	chr14	95570291	95570459	95570319	95570433	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228132843	chr14	95570291	95570459	95570319	95570433	DICER1	NM_030621	2	28	22	-	95569683	95570463
228736616	chr14	95571971	95572109	95572003	95572083	DICER1	NM_177438	3	27	19	-	95572015	95572120
228736616	chr14	95571971	95572109	95572003	95572083	DICER1	NM_001195573	1	25	18	-	95572015	95572120
228736616	chr14	95571971	95572109	95572003	95572083	DICER1	NM_030621	2	28	20	-	95572015	95572120
228396900	chr14	95573881	95574031	95573907	95574002	DICER1	NM_177438	3	27	17	-	95573945	95574098
228396900	chr14	95573881	95574031	95573907	95574002	DICER1	NM_001195573	1	25	16	-	95573945	95574098
228396900	chr14	95573881	95574031	95573907	95574002	DICER1	NM_030621	2	28	18	-	95573945	95574098
228801564	chr14	95574220	95574370	95574248	95574342	DICER1	NM_177438	3	27	16	-	95574217	95574430
228801564	chr14	95574220	95574370	95574248	95574342	DICER1	NM_001195573	1	25	15	-	95574217	95574430
228801564	chr14	95574220	95574370	95574248	95574342	DICER1	NM_030621	2	28	17	-	95574217	95574430
228295996	chr14	95574695	95574869	95574719	95574841	DICER1	NM_177438	3	27	15	-	95574661	95574840
228295996	chr14	95574695	95574869	95574719	95574841	DICER1	NM_001195573	1	25	14	-	95574661	95574840
228295996	chr14	95574695	95574869	95574719	95574841	DICER1	NM_030621	2	28	16	-	95574661	95574840
228098565	chr14	95578496	95578626	95578523	95578598	DICER1	NM_177438	3	27	13	-	95578509	95578584
228098565	chr14	95578496	95578626	95578523	95578598	DICER1	NM_001195573	1	25	12	-	95578509	95578584
228098565	chr14	95578496	95578626	95578523	95578598	DICER1	NM_030621	2	28	14	-	95578509	95578584
230468120	chr14	95582050	95582206	95582072	95582178	DICER1	NM_177438	3	27	11	-	95582004	95582158
230468120	chr14	95582050	95582206	95582072	95582178	DICER1	NM_001195573	1	25	10	-	95582004	95582158
230468120	chr14	95582050	95582206	95582072	95582178	DICER1	NM_030621	2	28	12	-	95582004	95582158
229812654	chr14	95583887	95584013	95583909	95583990	DICER1	NM_177438	3	27	9	-	95583959	95584091
229812654	chr14	95583887	95584013	95583909	95583990	DICER1	NM_001195573	1	25	8	-	95583959	95584091
229812654	chr14	95583887	95584013	95583909	95583990	DICER1	NM_030621	2	28	10	-	95583959	95584091
232516804	chr14	95590725	95590895	95590749	95590869	DICER1	NM_177438	3	27	8	-	95590533	95591005

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232516804	chr14	95590725	95590895	95590749	95590869	DICER1	NM_001195573	1	25	7	-	95590533	95591005
232516804	chr14	95590725	95590895	95590749	95590869	DICER1	NM_030621	2	28	9	-	95590533	95591005
227743000	chr14	95595783	95595943	95595807	95595920	DICER1	NM_177438	3	27	6	-	95595809	95595969
227743000	chr14	95595783	95595943	95595807	95595920	DICER1	NM_001195573	1	25	5	-	95595809	95595969
227743000	chr14	95595783	95595943	95595807	95595920	DICER1	NM_030621	2	28	7	-	95595809	95595969
230504735	chr14	95597768	95597942	95597795	95597917	DICER1	NM_177438	3	27	4	-	95597846	95597976
230504735	chr14	95597768	95597942	95597795	95597917	DICER1	NM_001195573	1	25	3	-	95597846	95597976
230504735	chr14	95597768	95597942	95597795	95597917	DICER1	NM_030621	2	28	5	-	95597846	95597976
230028966	chr14	95598979	95599125	95599005	95599093	DICER1	NM_177438	3	27	3	-	95598852	95599014
230028966	chr14	95598979	95599125	95599005	95599093	DICER1	NM_001195573	1	25	2	-	95598852	95599014
230028966	chr14	95598979	95599125	95599005	95599093	DICER1	NM_030621	2	28	4	-	95598852	95599014
239818584	chr14	96178465	96178638	96178488	96178616	TCL1A	NM_021966	2	4	2	-	96178557	96178733
239818584	chr14	96178465	96178638	96178488	96178616	TCL1A	NM_001098725	1	4	2	-	96178557	96178733
223913735	chr14	99640421	99640578	99640442	99640557	BCL11B	NM_138576	2	4	4	-	99635625	99642532
223913735	chr14	99640421	99640578	99640442	99640557	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225215608	chr14	99640940	99641073	99640957	99641054	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225215608	chr14	99640940	99641073	99640957	99641054	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225207010	chr14	99641602	99641767	99641619	99641748	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225207010	chr14	99641602	99641767	99641619	99641748	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225209736	chr14	99642099	99642236	99642117	99642219	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225209736	chr14	99642099	99642236	99642117	99642219	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225217519	chr14	99642435	99642578	99642453	99642560	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225217519	chr14	99642435	99642578	99642453	99642560	BCL11B	NM_022898	1	3	3	-	99635625	99642532
222955640	chr14	99723788	99723922	99723807	99723902	BCL11B	NM_138576	2	4	2	-	99723808	99724176
222955640	chr14	99723788	99723922	99723807	99723902	BCL11B	NM_022898	1	3	2	-	99723808	99724176
223646417	chr14	99737478	99737602	99737496	99737583	BCL11B	NM_138576	2	4	1	-	99737498	99737822
223646417	chr14	99737478	99737602	99737496	99737583	BCL11B	NM_022898	1	3	1	-	99737498	99737822
227272362	chr14	102548495	102548667	102548516	102548645	HSP90AA1	NM_005348	2	11	10	-	102548448	102548781
227272362	chr14	102548495	102548667	102548516	102548645	HSP90AA1	NM_001017963	1	12	11	-	102548448	102548781
228110560	chr14	102549340	102549514	102549368	102549490	HSP90AA1	NM_005348	2	11	9	-	102549371	102549639
228110560	chr14	102549340	102549514	102549368	102549490	HSP90AA1	NM_001017963	1	12	10	-	102549371	102549639
227153276	chr14	102549947	102550114	102549969	102550086	HSP90AA1	NM_005348	2	11	8	-	102549883	102550030
227153276	chr14	102549947	102550114	102549969	102550086	HSP90AA1	NM_001017963	1	12	9	-	102549883	102550030
227699352	chr14	102550675	102550849	102550696	102550826	HSP90AA1	NM_005348	2	11	6	-	102550736	102550901
227699352	chr14	102550675	102550849	102550696	102550826	HSP90AA1	NM_001017963	1	12	7	-	102550736	102550901
227311817	chr14	102551127	102551253	102551155	102551229	HSP90AA1	NM_005348	2	11	5	-	102551018	102551335
227311817	chr14	102551127	102551253	102551155	102551229	HSP90AA1	NM_001017963	1	12	6	-	102551018	102551335
227718952	chr14	102551981	102552148	102552005	102552128	HSP90AA1	NM_005348	2	11	3	-	102552095	102552461
227718952	chr14	102551981	102552148	102552005	102552128	HSP90AA1	NM_001017963	1	12	4	-	102552095	102552461
227239284	chr14	102552498	102552668	102552521	102552648	HSP90AA1	NM_005348	2	11	2	-	102552554	102552715
227239284	chr14	102552498	102552668	102552521	102552648	HSP90AA1	NM_001017963	1	12	3	-	102552554	102552715

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227421567	chr14	102568340	102568464	102568363	102568438	HSP90AA1	NM_001017963	1	12	2	-	102568212	102568422
225027382	chr14	105237025	105237154	105237048	105237133	AKT1	NM_005163	3	14	13	-	105237082	105237184
225027382	chr14	105237025	105237154	105237048	105237133	AKT1	NM_001014432	2	15	14	-	105237082	105237184
225027382	chr14	105237025	105237154	105237048	105237133	AKT1	NM_001014431	1	14	13	-	105237082	105237184
223599813	chr14	105239182	105239342	105239203	105239318	AKT1	NM_005163	3	14	11	-	105239215	105239429
223599813	chr14	105239182	105239342	105239203	105239318	AKT1	NM_001014432	2	15	12	-	105239215	105239429
223599813	chr14	105239182	105239342	105239203	105239318	AKT1	NM_001014431	1	14	11	-	105239215	105239429
223838981	chr14	105239789	105239947	105239807	105239930	AKT1	NM_005163	3	14	9	-	105239792	105239917
223838981	chr14	105239789	105239947	105239807	105239930	AKT1	NM_001014432	2	15	10	-	105239792	105239917
223838981	chr14	105239789	105239947	105239807	105239930	AKT1	NM_001014431	1	14	9	-	105239792	105239917
224404303	chr14	105241417	105241552	105241439	105241531	AKT1	NM_005163	3	14	6	-	105241413	105241544
224404303	chr14	105241417	105241552	105241439	105241531	AKT1	NM_001014432	2	15	7	-	105241413	105241544
224404303	chr14	105241417	105241552	105241439	105241531	AKT1	NM_001014431	1	14	6	-	105241413	105241544
223790319	chr14	105242887	105243039	105242907	105243019	AKT1	NM_005163	3	14	4	-	105242996	105243107
223790319	chr14	105242887	105243039	105242907	105243019	AKT1	NM_001014432	2	15	5	-	105242996	105243107
223790319	chr14	105242887	105243039	105242907	105243019	AKT1	NM_001014431	1	14	4	-	105242996	105243107
223636632	chr14	105246479	105246603	105246501	105246583	AKT1	NM_005163	3	14	3	-	105246425	105246553
223636632	chr14	105246479	105246603	105246501	105246583	AKT1	NM_001014432	2	15	4	-	105246425	105246553
223636632	chr14	105246479	105246603	105246501	105246583	AKT1	NM_001014431	1	14	3	-	105246425	105246553
305315326	chr15	39873979	39874149	39874000	39874126	THBS1	NM_003246	1	22	2	+	39874030	39874125
304194449	chr15	39874604	39874767	39874626	39874745	THBS1	NM_003246	1	22	3	+	39874394	39874953
300817556	chr15	39876067	39876221	39876087	39876199	THBS1	NM_003246	1	22	5	+	39876189	39876388
304748200	chr15	39877640	39877800	39877662	39877772	THBS1	NM_003246	1	22	7	+	39877671	39877764
301735206	chr15	39880271	39880439	39880291	39880419	THBS1	NM_003246	1	22	9	+	39880243	39880419
300812073	chr15	39881302	39881461	39881324	39881442	THBS1	NM_003246	1	22	12	+	39881403	39881555
304971504	chr15	39882634	39882781	39882655	39882757	THBS1	NM_003246	1	22	14	+	39882717	39882824
305674229	chr15	39883674	39883848	39883697	39883825	THBS1	NM_003246	1	22	16	+	39883706	39883824
299914498	chr15	39885219	39885384	39885244	39885363	THBS1	NM_003246	1	22	18	+	39885201	39885428
301640193	chr15	39885768	39885892	39885788	39885870	THBS1	NM_003246	1	22	19	+	39885598	39885869
300958522	chr15	39887440	39887613	39887471	39887585	THBS1	NM_003246	1	22	22	+	39887563	39889668
223590454	chr15	40462216	40462386	40462240	40462359	BUB1B	NM_001211	1	23	3	+	40462263	40462322
223929840	chr15	40468734	40468905	40468757	40468876	BUB1B	NM_001211	1	23	5	+	40468678	40468874
223696232	chr15	40477254	40477403	40477281	40477378	BUB1B	NM_001211	1	23	7	+	40477366	40477580
223793368	chr15	40477773	40477922	40477794	40477898	BUB1B	NM_001211	1	23	8	+	40477752	40477843
224142869	chr15	40488887	40489034	40488912	40489012	BUB1B	NM_001211	1	23	9	+	40488746	40488975
224859727	chr15	40492442	40492586	40492464	40492560	BUB1B	NM_001211	1	23	11	+	40492445	40492560
223442548	chr15	40494849	40495001	40494873	40494974	BUB1B	NM_001211	1	23	14	+	40494790	40494895
222411296	chr15	40498582	40498721	40498607	40498693	BUB1B	NM_001211	1	23	15	+	40498385	40498659
223134257	chr15	40502216	40502383	40502239	40502364	BUB1B	NM_001211	1	23	18	+	40502311	40502411
222941690	chr15	40505472	40505642	40505500	40505617	BUB1B	NM_001211	1	23	20	+	40505533	40505675
222386339	chr15	40510626	40510792	40510654	40510764	BUB1B	NM_001211	1	23	22	+	40510657	40510763

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225928617	chr15	40894995	40895153	40895020	40895133	CASC5	NM_144508	1	26	2	+	40895113	40895164
225928617	chr15	40894995	40895153	40895020	40895133	CASC5	NM_170589	2	27	2	+	40895113	40895164
226138905	chr15	40898460	40898634	40898488	40898613	CASC5	NM_144508	1	26	4	+	40898591	40898650
226138905	chr15	40898460	40898634	40898488	40898613	CASC5	NM_170589	2	27	4	+	40898591	40898650
226251204	chr15	40902306	40902476	40902333	40902448	CASC5	NM_144508	1	26	6	+	40902443	40902495
226251204	chr15	40902306	40902476	40902333	40902448	CASC5	NM_170589	2	27	6	+	40902443	40902495
225330478	chr15	40912857	40913005	40912878	40912979	CASC5	NM_144508	1	26	10	+	40912838	40917838
225330478	chr15	40912857	40913005	40912878	40912979	CASC5	NM_170589	2	27	11	+	40912838	40917838
225345574	chr15	40913146	40913314	40913171	40913286	CASC5	NM_144508	1	26	10	+	40912838	40917838
225345574	chr15	40913146	40913314	40913171	40913286	CASC5	NM_170589	2	27	11	+	40912838	40917838
226628010	chr15	40913515	40913682	40913543	40913658	CASC5	NM_144508	1	26	10	+	40912838	40917838
226628010	chr15	40913515	40913682	40913543	40913658	CASC5	NM_170589	2	27	11	+	40912838	40917838
226621758	chr15	40913853	40913989	40913878	40913960	CASC5	NM_144508	1	26	10	+	40912838	40917838
226621758	chr15	40913853	40913989	40913878	40913960	CASC5	NM_170589	2	27	11	+	40912838	40917838
226633046	chr15	40914213	40914368	40914236	40914340	CASC5	NM_144508	1	26	10	+	40912838	40917838
226633046	chr15	40914213	40914368	40914236	40914340	CASC5	NM_170589	2	27	11	+	40912838	40917838
226630001	chr15	40914562	40914719	40914590	40914694	CASC5	NM_144508	1	26	10	+	40912838	40917838
226630001	chr15	40914562	40914719	40914590	40914694	CASC5	NM_170589	2	27	11	+	40912838	40917838
226629130	chr15	40915006	40915162	40915028	40915143	CASC5	NM_144508	1	26	10	+	40912838	40917838
226629130	chr15	40915006	40915162	40915028	40915143	CASC5	NM_170589	2	27	11	+	40912838	40917838
225345681	chr15	40915413	40915550	40915440	40915525	CASC5	NM_144508	1	26	10	+	40912838	40917838
225345681	chr15	40915413	40915550	40915440	40915525	CASC5	NM_170589	2	27	11	+	40912838	40917838
225366909	chr15	40915766	40915925	40915793	40915902	CASC5	NM_144508	1	26	10	+	40912838	40917838
225366909	chr15	40915766	40915925	40915793	40915902	CASC5	NM_170589	2	27	11	+	40912838	40917838
225390503	chr15	40916207	40916344	40916231	40916318	CASC5	NM_144508	1	26	10	+	40912838	40917838
225390503	chr15	40916207	40916344	40916231	40916318	CASC5	NM_170589	2	27	11	+	40912838	40917838
226633134	chr15	40916536	40916701	40916560	40916673	CASC5	NM_144508	1	26	10	+	40912838	40917838
226633134	chr15	40916536	40916701	40916560	40916673	CASC5	NM_170589	2	27	11	+	40912838	40917838
226629282	chr15	40916955	40917080	40916977	40917054	CASC5	NM_144508	1	26	10	+	40912838	40917838
226629282	chr15	40916955	40917080	40916977	40917054	CASC5	NM_170589	2	27	11	+	40912838	40917838
226635582	chr15	40917294	40917440	40917322	40917416	CASC5	NM_144508	1	26	10	+	40912838	40917838
226635582	chr15	40917294	40917440	40917322	40917416	CASC5	NM_170589	2	27	11	+	40912838	40917838
226642008	chr15	40917619	40917769	40917647	40917743	CASC5	NM_144508	1	26	10	+	40912838	40917838
226642008	chr15	40917619	40917769	40917647	40917743	CASC5	NM_170589	2	27	11	+	40912838	40917838
226418238	chr15	40920265	40920393	40920294	40920373	CASC5	NM_144508	1	26	11	+	40920268	40920406
226418238	chr15	40920265	40920393	40920294	40920373	CASC5	NM_170589	2	27	12	+	40920268	40920406
225427967	chr15	40921426	40921595	40921453	40921569	CASC5	NM_144508	1	26	13	+	40921471	40921569
225427967	chr15	40921426	40921595	40921453	40921569	CASC5	NM_170589	2	27	14	+	40921471	40921569
226268593	chr15	40937779	40937953	40937804	40937931	CASC5	NM_144508	1	26	16	+	40937854	40937970
226268593	chr15	40937779	40937953	40937804	40937931	CASC5	NM_170589	2	27	17	+	40937854	40937970
226537898	chr15	40942483	40942612	40942516	40942584	CASC5	NM_144508	1	26	18	+	40942499	40942576

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226537898	chr15	40942483	40942612	40942516	40942584	CASC5	NM_170589	2	27	19	+	40942499	40942576
225401088	chr15	40944115	40944245	40944138	40944221	CASC5	NM_144508	1	26	21	+	40944203	40944303
225401088	chr15	40944115	40944245	40944138	40944221	CASC5	NM_170589	2	27	22	+	40944203	40944303
253687433	chr15	40954249	40954412	40954275	40954390	CASC5	NM_144508	1	26	26	+	40954272	40954881
253687433	chr15	40954249	40954412	40954275	40954390	CASC5	NM_170589	2	27	27	+	40954272	40954881
270754565	chr15	41796501	41796655	41796525	41796635	LTK	NM_001135685	1	18	17	-	41796540	41796630
270754565	chr15	41796501	41796655	41796525	41796635	LTK	NM_002344	2	20	19	-	41796540	41796630
270754565	chr15	41796501	41796655	41796525	41796635	LTK	NM_206961	3	19	18	-	41796540	41796630
270231771	chr15	41796955	41797116	41796976	41797091	LTK	NM_001135685	1	18	15	-	41796971	41797072
270231771	chr15	41796955	41797116	41796976	41797091	LTK	NM_002344	2	20	17	-	41796971	41797072
270231771	chr15	41796955	41797116	41796976	41797091	LTK	NM_206961	3	19	16	-	41796971	41797072
271970372	chr15	41797527	41797668	41797550	41797644	LTK	NM_001135685	1	18	12	-	41797599	41797728
271970372	chr15	41797527	41797668	41797550	41797644	LTK	NM_002344	2	20	14	-	41797599	41797728
271970372	chr15	41797527	41797668	41797550	41797644	LTK	NM_206961	3	19	13	-	41797599	41797728
270474824	chr15	41799249	41799417	41799273	41799397	LTK	NM_002344	2	20	11	-	41799293	41799488
270474824	chr15	41799249	41799417	41799273	41799397	LTK	NM_206961	3	19	10	-	41799293	41799488
270474824	chr15	41799249	41799417	41799273	41799397	LTK	NM_001135685	1	18	10	-	41799293	41799372
269532916	chr15	41800343	41800491	41800365	41800466	LTK	NM_001135685	1	18	8	-	41800267	41800419
269532916	chr15	41800343	41800491	41800365	41800466	LTK	NM_002344	2	20	9	-	41800267	41800419
269532916	chr15	41800343	41800491	41800365	41800466	LTK	NM_206961	3	19	8	-	41800267	41800419
270279532	chr15	41804007	41804153	41804027	41804135	LTK	NM_001135685	1	18	5	-	41804015	41804161
270279532	chr15	41804007	41804153	41804027	41804135	LTK	NM_002344	2	20	5	-	41804015	41804161
270279532	chr15	41804007	41804153	41804027	41804135	LTK	NM_206961	3	19	5	-	41804015	41804161
270164271	chr15	41804376	41804542	41804400	41804523	LTK	NM_001135685	1	18	4	-	41804313	41804463
270164271	chr15	41804376	41804542	41804400	41804523	LTK	NM_002344	2	20	4	-	41804313	41804463
270164271	chr15	41804376	41804542	41804400	41804523	LTK	NM_206961	3	19	4	-	41804313	41804463
269615314	chr15	41805129	41805287	41805150	41805266	LTK	NM_001135685	1	18	2	-	41805175	41805318
269615314	chr15	41805129	41805287	41805150	41805266	LTK	NM_002344	2	20	2	-	41805175	41805318
269615314	chr15	41805129	41805287	41805150	41805266	LTK	NM_206961	3	19	2	-	41805175	41805318
295338993	chr15	43568664	43568836	43568685	43568813	TGM7	NM_052955	1	13	13	-	43568479	43568812
294742730	chr15	43571330	43571503	43571353	43571475	TGM7	NM_052955	1	13	11	-	43571315	43571475
294689387	chr15	43573982	43574130	43574005	43574110	TGM7	NM_052955	1	13	9	-	43574042	43574284
294856790	chr15	43576904	43577065	43576926	43577042	TGM7	NM_052955	1	13	7	-	43577012	43577150
294912284	chr15	43579694	43579832	43579716	43579809	TGM7	NM_052955	1	13	5	-	43579739	43579867
295303273	chr15	43584940	43585087	43584959	43585065	TGM7	NM_052955	1	13	3	-	43584907	43585152
295268787	chr15	43594319	43594489	43594344	43594467	TGM7	NM_052955	1	13	1	-	43594439	43594453
242604823	chr15	57355947	57356071	57355974	57356043	TCF12	NM_207038	4	20	4	+	57355948	57356021
242604823	chr15	57355947	57356071	57355974	57356043	TCF12	NM_207036	2	21	4	+	57355948	57356021
242604823	chr15	57355947	57356071	57355974	57356043	TCF12	NM_003205	1	20	4	+	57355948	57356021
242604823	chr15	57355947	57356071	57355974	57356043	TCF12	NM_207037	3	21	4	+	57355948	57356021
264271689	chr15	57484300	57484441	57484322	57484414	TCF12	NM_207038	4	20	7	+	57484356	57484491

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264271689	chr15	57484300	57484441	57484322	57484414	TCF12	NM_207036	2	21	7	+	57484356	57484491
264271689	chr15	57484300	57484441	57484322	57484414	TCF12	NM_003205	1	20	7	+	57484356	57484491
264271689	chr15	57484300	57484441	57484322	57484414	TCF12	NM_207037	3	21	7	+	57484356	57484491
242118719	chr15	57511631	57511795	57511654	57511767	TCF12	NM_207040	5	13	1	+	57511655	57511788
242121580	chr15	57524358	57524531	57524381	57524504	TCF12	NM_207038	4	20	10	+	57524489	57524628
242121580	chr15	57524358	57524531	57524381	57524504	TCF12	NM_207036	2	21	10	+	57524489	57524628
242121580	chr15	57524358	57524531	57524381	57524504	TCF12	NM_003205	1	20	10	+	57524489	57524628
242121580	chr15	57524358	57524531	57524381	57524504	TCF12	NM_207037	3	21	10	+	57524489	57524628
242121580	chr15	57524358	57524531	57524381	57524504	TCF12	NM_207040	5	13	3	+	57524489	57524628
238782752	chr15	57524982	57525109	57525002	57525085	TCF12	NM_207038	4	20	11	+	57524910	57525054
238782752	chr15	57524982	57525109	57525002	57525085	TCF12	NM_207036	2	21	11	+	57524910	57525054
238782752	chr15	57524982	57525109	57525002	57525085	TCF12	NM_003205	1	20	11	+	57524910	57525054
238782752	chr15	57524982	57525109	57525002	57525085	TCF12	NM_207037	3	21	11	+	57524910	57525054
238782752	chr15	57524982	57525109	57525002	57525085	TCF12	NM_207040	5	13	4	+	57524910	57525054
242621141	chr15	57544536	57544673	57544564	57544648	TCF12	NM_207036	2	21	15	+	57544619	57544690
242621141	chr15	57544536	57544673	57544564	57544648	TCF12	NM_207037	3	21	15	+	57544619	57544690
242550361	chr15	57545611	57545775	57545638	57545750	TCF12	NM_207038	4	20	15	+	57545460	57545666
242550361	chr15	57545611	57545775	57545638	57545750	TCF12	NM_207036	2	21	16	+	57545460	57545666
242550361	chr15	57545611	57545775	57545638	57545750	TCF12	NM_003205	1	20	15	+	57545460	57545666
242550361	chr15	57545611	57545775	57545638	57545750	TCF12	NM_207037	3	21	16	+	57545460	57545666
242550361	chr15	57545611	57545775	57545638	57545750	TCF12	NM_207040	5	13	8	+	57545460	57545666
238684295	chr15	57555294	57555467	57555316	57555439	TCF12	NM_207038	4	20	17	+	57555310	57555472
238684295	chr15	57555294	57555467	57555316	57555439	TCF12	NM_207036	2	21	18	+	57555310	57555472
238684295	chr15	57555294	57555467	57555316	57555439	TCF12	NM_003205	1	20	17	+	57555310	57555472
238684295	chr15	57555294	57555467	57555316	57555439	TCF12	NM_207037	3	21	18	+	57555310	57555472
238684295	chr15	57555294	57555467	57555316	57555439	TCF12	NM_207040	5	13	10	+	57555310	57555472
264108923	chr15	57565314	57565488	57565332	57565460	TCF12	NM_207038	4	20	18	+	57565228	57565460
264108923	chr15	57565314	57565488	57565332	57565460	TCF12	NM_207036	2	21	19	+	57565228	57565460
264108923	chr15	57565314	57565488	57565332	57565460	TCF12	NM_003205	1	20	18	+	57565228	57565460
264108923	chr15	57565314	57565488	57565332	57565460	TCF12	NM_207037	3	21	19	+	57565228	57565460
264108923	chr15	57565314	57565488	57565332	57565460	TCF12	NM_207040	5	13	11	+	57565228	57565460
233518656	chr15	66727300	66727474	66727325	66727453	MAP2K1	NM_002755	1	11	2	+	66727365	66727575
233667219	chr15	66735542	66735669	66735563	66735643	MAP2K1	NM_002755	1	11	4	+	66735618	66735695
233365243	chr15	66774013	66774153	66774036	66774129	MAP2K1	NM_002755	1	11	6	+	66774093	66774217
233998454	chr15	66779494	66779668	66779515	66779641	MAP2K1	NM_002755	1	11	8	+	66779566	66779630
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033250	9	7	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033249	8	7	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033247	7	5	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033246	6	6	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033244	5	8	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033240	4	7	1	+	74287014	74287282

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033239	3	8	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_033238	2	9	1	+	74287014	74287282
236999718	chr15	74287098	74287256	74287119	74287239	PML	NM_002675	1	8	1	+	74287014	74287282
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033250	9	7	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033249	8	7	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033247	7	5	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033246	6	6	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033244	5	8	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033240	4	7	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033239	3	8	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_033238	2	9	2	+	74290345	74290817
237953344	chr15	74290520	74290680	74290540	74290661	PML	NM_002675	1	8	2	+	74290345	74290817
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033250	9	7	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033249	8	7	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033247	7	5	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033246	6	6	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033244	5	8	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033240	4	7	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033239	3	8	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_033238	2	9	3	+	74315169	74315749
239373717	chr15	74315225	74315352	74315244	74315335	PML	NM_002675	1	8	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033250	9	7	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033249	8	7	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033247	7	5	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033246	6	6	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033244	5	8	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033240	4	7	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033239	3	8	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_033238	2	9	3	+	74315169	74315749
239368878	chr15	74315579	74315745	74315596	74315726	PML	NM_002675	1	8	3	+	74315169	74315749
241278551	chr15	74324974	74325119	74324996	74325097	PML	NM_033244	5	8	5	+	74324913	74325056
241278551	chr15	74324974	74325119	74324996	74325097	PML	NM_033240	4	7	5	+	74324913	74325056
241278551	chr15	74324974	74325119	74324996	74325097	PML	NM_033239	3	8	5	+	74324913	74325056
241278551	chr15	74324974	74325119	74324996	74325097	PML	NM_033238	2	9	5	+	74324913	74325056
241278551	chr15	74324974	74325119	74324996	74325097	PML	NM_002675	1	8	5	+	74324913	74325056
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033240	4	7	7	+	74326819	74328735
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033250	9	7	6	+	74326819	74326871
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033249	8	7	6	+	74326819	74326871
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033246	6	6	5	+	74326819	74326871
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033244	5	8	7	+	74326819	74326871
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033239	3	8	7	+	74326819	74326871

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_033238	2	9	7	+	74326819	74326871
235886703	chr15	74326728	74326892	74326749	74326872	PML	NM_002675	1	8	7	+	74326819	74326871
238139142	chr15	74327769	74327925	74327791	74327905	PML	NM_033250	9	7	7	+	74327513	74328735
238139142	chr15	74327769	74327925	74327791	74327905	PML	NM_033244	5	8	8	+	74327513	74328735
238139142	chr15	74327769	74327925	74327791	74327905	PML	NM_033239	3	8	8	+	74327513	74328735
238139142	chr15	74327769	74327925	74327791	74327905	PML	NM_033240	4	7	7	+	74326819	74328735
234995979	chr15	74328154	74328328	74328175	74328306	PML	NM_033250	9	7	7	+	74327513	74328735
234995979	chr15	74328154	74328328	74328175	74328306	PML	NM_033244	5	8	8	+	74327513	74328735
234995979	chr15	74328154	74328328	74328175	74328306	PML	NM_033239	3	8	8	+	74327513	74328735
234995979	chr15	74328154	74328328	74328175	74328306	PML	NM_033240	4	7	7	+	74326819	74328735
239443530	chr15	74336533	74336703	74336551	74336681	PML	NM_033238	2	9	9	+	74336562	74340155
239442640	chr15	74336992	74337136	74337011	74337118	PML	NM_033238	2	9	9	+	74336562	74340155
236336144	chr15	88420235	88420398	88420255	88420377	NTRK3	NM_002530	4	19	19	-	88419988	88420351
236336144	chr15	88420235	88420398	88420255	88420377	NTRK3	NM_001012338	2	20	20	-	88419988	88420351
236336144	chr15	88420235	88420398	88420255	88420377	NTRK3	NM_001243101	3	18	18	-	88419988	88420351
235943014	chr15	88472421	88472587	88472446	88472566	NTRK3	NM_002530	4	19	17	-	88472422	88472665
235943014	chr15	88472421	88472587	88472446	88472566	NTRK3	NM_001012338	2	20	17	-	88472422	88472665
235943014	chr15	88472421	88472587	88472446	88472566	NTRK3	NM_001243101	3	18	16	-	88472422	88472665
242473896	chr15	88483745	88483907	88483771	88483887	NTRK3	NM_002530	4	19	15	-	88483854	88483984
242473896	chr15	88483745	88483907	88483771	88483887	NTRK3	NM_001012338	2	20	15	-	88483854	88483984
242473896	chr15	88483745	88483907	88483771	88483887	NTRK3	NM_001243101	3	18	14	-	88483854	88483984
235150326	chr15	88576012	88576179	88576034	88576158	NTRK3	NM_002530	4	19	14	-	88576088	88576276
235150326	chr15	88576012	88576179	88576034	88576158	NTRK3	NM_001007156	1	16	14	-	88576088	88576276
235150326	chr15	88576012	88576179	88576034	88576158	NTRK3	NM_001012338	2	20	14	-	88576088	88576276
235150326	chr15	88576012	88576179	88576034	88576158	NTRK3	NM_001243101	3	18	13	-	88576088	88576276
258000703	chr15	88671910	88672035	88671935	88672011	NTRK3	NM_002530	4	19	11	-	88671942	88671965
258000703	chr15	88671910	88672035	88671935	88672011	NTRK3	NM_001007156	1	16	11	-	88671942	88671965
258000703	chr15	88671910	88672035	88671935	88672011	NTRK3	NM_001012338	2	20	11	-	88671942	88671965
239019050	chr15	88679098	88679240	88679119	88679218	NTRK3	NM_002530	4	19	9	-	88679130	88679271
239019050	chr15	88679098	88679240	88679119	88679218	NTRK3	NM_001007156	1	16	9	-	88679130	88679271
239019050	chr15	88679098	88679240	88679119	88679218	NTRK3	NM_001012338	2	20	9	-	88679130	88679271
239019050	chr15	88679098	88679240	88679119	88679218	NTRK3	NM_001243101	3	18	9	-	88679130	88679271
242001174	chr15	88680543	88680715	88680563	88680695	NTRK3	NM_002530	4	19	7	-	88680635	88680792
242001174	chr15	88680543	88680715	88680563	88680695	NTRK3	NM_001007156	1	16	7	-	88680635	88680792
242001174	chr15	88680543	88680715	88680563	88680695	NTRK3	NM_001012338	2	20	7	-	88680635	88680792
242001174	chr15	88680543	88680715	88680563	88680695	NTRK3	NM_001243101	3	18	7	-	88680635	88680792
236728810	chr15	88727433	88727560	88727451	88727538	NTRK3	NM_002530	4	19	4	-	88727456	88727530
236728810	chr15	88727433	88727560	88727451	88727538	NTRK3	NM_001007156	1	16	4	-	88727456	88727530
236728810	chr15	88727433	88727560	88727451	88727538	NTRK3	NM_001012338	2	20	4	-	88727456	88727530
236728810	chr15	88727433	88727560	88727451	88727538	NTRK3	NM_001243101	3	18	4	-	88727456	88727530
227635538	chr15	90627469	90627611	90627486	90627589	IDH2	NM_002168	1	11	11	-	90627212	90627585

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227257676	chr15	90628507	90628649	90628527	90628627	IDH2	NM_002168	1	11	8	-	90628507	90628619
227668336	chr15	90630695	90630860	90630714	90630843	IDH2	NM_002168	1	11	6	-	90630671	90630807
229766197	chr15	90631877	90632014	90631901	90631991	IDH2	NM_002168	1	11	4	-	90631819	90631979
227439869	chr15	90634717	90634870	90634738	90634848	IDH2	NM_002168	1	11	2	-	90634785	90634876
222681059	chr15	91292640	91292764	91292670	91292741	BLM	NM_000057	1	22	3	+	91292597	91293297
222706131	chr15	91293006	91293179	91293028	91293153	BLM	NM_000057	1	22	3	+	91292597	91293297
223082955	chr15	91295148	91295312	91295176	91295282	BLM	NM_000057	1	22	4	+	91295017	91295176
224448993	chr15	91303381	91303514	91303406	91303491	BLM	NM_000057	1	22	6	+	91303377	91303509
225080165	chr15	91304011	91304177	91304035	91304150	BLM	NM_000057	1	22	7	+	91303824	91304485
225052638	chr15	91304416	91304577	91304440	91304549	BLM	NM_000057	1	22	7	+	91303824	91304485
222981204	chr15	91308478	91308650	91308500	91308624	BLM	NM_000057	1	22	9	+	91308526	91308644
222970328	chr15	91312395	91312555	91312421	91312533	BLM	NM_000057	1	22	11	+	91312363	91312461
225103085	chr15	91328118	91328292	91328147	91328270	BLM	NM_000057	1	22	14	+	91328151	91328311
223299103	chr15	91337333	91337489	91337366	91337461	BLM	NM_000057	1	22	16	+	91337397	91337587
222442079	chr15	91341426	91341566	91341452	91341539	BLM	NM_000057	1	22	17	+	91341420	91341567
222533287	chr15	91346882	91347036	91346902	91347007	BLM	NM_000057	1	22	18	+	91346751	91346950
224061751	chr15	91352380	91352544	91352406	91352522	BLM	NM_000057	1	22	20	+	91352367	91352489
223786588	chr15	91358362	91358536	91358385	91358510	BLM	NM_000057	1	22	22	+	91358332	91358686
269828795	chr15	99250816	99250966	99250838	99250945	IGF1R	NM_000875	1	21	2	+	99250791	99251336
271801215	chr15	99251255	99251428	99251275	99251407	IGF1R	NM_000875	1	21	2	+	99250791	99251336
270836318	chr15	99439929	99440101	99439956	99440079	IGF1R	NM_000875	1	21	4	+	99439986	99440134
270998080	chr15	99451881	99452051	99451901	99452023	IGF1R	NM_000875	1	21	6	+	99451914	99452128
270089806	chr15	99456238	99456404	99456261	99456384	IGF1R	NM_000875	1	21	8	+	99456273	99456511
271001881	chr15	99459250	99459423	99459271	99459399	IGF1R	NM_000875	1	21	9	+	99459193	99459360
271289107	chr15	99465346	99465501	99465372	99465479	IGF1R	NM_000875	1	21	11	+	99465377	99465660
269733428	chr15	99467143	99467298	99467165	99467270	IGF1R	NM_000875	1	21	12	+	99467105	99467241
272356431	chr15	99472857	99473029	99472881	99473001	IGF1R	NM_000875	1	21	14	+	99472787	99472889
269902530	chr15	99478149	99478312	99478170	99478283	IGF1R	NM_000875	1	21	16	+	99478053	99478282
272045255	chr15	99482455	99482616	99482479	99482595	IGF1R	NM_000875	1	21	18	+	99482430	99482589
269558510	chr15	99491857	99491988	99491876	99491960	IGF1R	NM_000875	1	21	20	+	99491803	99491937
272143373	chr15	99500512	99500643	99500530	99500626	IGF1R	NM_000875	1	21	21	+	99500290	99507759
262455562	chr16	2098542	2098676	2098563	2098648	TSC2	NM_000548	1	42	2	+	2098588	2098754
262455562	chr16	2098542	2098676	2098563	2098648	TSC2	NM_001077183	2	40	2	+	2098588	2098754
262455562	chr16	2098542	2098676	2098563	2098648	TSC2	NM_001114382	3	41	2	+	2098588	2098754
238383974	chr16	2104223	2104369	2104244	2104346	TSC2	NM_000548	1	42	5	+	2104297	2104441
238383974	chr16	2104223	2104369	2104244	2104346	TSC2	NM_001077183	2	40	5	+	2104297	2104441
238383974	chr16	2104223	2104369	2104244	2104346	TSC2	NM_001114382	3	41	5	+	2104297	2104441
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_000548	1	42	7	+	2106197	2106245
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_001077183	2	40	7	+	2106197	2106245
241709768	chr16	2106103	2106253	2106131	2106232	TSC2	NM_001114382	3	41	7	+	2106197	2106245
264520055	chr16	2108845	2108995	2108866	2108973	TSC2	NM_000548	1	42	10	+	2108748	2108874

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264520055	chr16	2108845	2108995	2108866	2108973	TSC2	NM_001077183	2	40	10	+	2108748	2108874
264520055	chr16	2108845	2108995	2108866	2108973	TSC2	NM_001114382	3	41	10	+	2108748	2108874
262865126	chr16	2111846	2112018	2111866	2112001	TSC2	NM_000548	1	42	12	+	2111872	2112009
262865126	chr16	2111846	2112018	2111866	2112001	TSC2	NM_001077183	2	40	12	+	2111872	2112009
262865126	chr16	2111846	2112018	2111866	2112001	TSC2	NM_001114382	3	41	12	+	2111872	2112009
240603573	chr16	2114308	2114447	2114328	2114429	TSC2	NM_000548	1	42	15	+	2114273	2114428
240603573	chr16	2114308	2114447	2114328	2114429	TSC2	NM_001077183	2	40	15	+	2114273	2114428
240603573	chr16	2114308	2114447	2114328	2114429	TSC2	NM_001114382	3	41	15	+	2114273	2114428
265942848	chr16	2121487	2121615	2121510	2121595	TSC2	NM_000548	1	42	18	+	2121511	2121617
265942848	chr16	2121487	2121615	2121510	2121595	TSC2	NM_001077183	2	40	18	+	2121511	2121617
265942848	chr16	2121487	2121615	2121510	2121595	TSC2	NM_001114382	3	41	18	+	2121511	2121617
238416100	chr16	2121911	2122062	2121929	2122044	TSC2	NM_000548	1	42	19	+	2121785	2121935
238416100	chr16	2121911	2122062	2121929	2122044	TSC2	NM_001077183	2	40	19	+	2121785	2121935
238416100	chr16	2121911	2122062	2121929	2122044	TSC2	NM_001114382	3	41	19	+	2121785	2121935
262298381	chr16	2122927	2123083	2122949	2123055	TSC2	NM_000548	1	42	21	+	2122850	2122984
262298381	chr16	2122927	2123083	2122949	2123055	TSC2	NM_001077183	2	40	21	+	2122850	2122984
262298381	chr16	2122927	2123083	2122949	2123055	TSC2	NM_001114382	3	41	21	+	2122850	2122984
263179840	chr16	2125814	2125957	2125834	2125939	TSC2	NM_000548	1	42	23	+	2125800	2125893
263179840	chr16	2125814	2125957	2125834	2125939	TSC2	NM_001077183	2	40	23	+	2125800	2125893
263179840	chr16	2125814	2125957	2125834	2125939	TSC2	NM_001114382	3	41	23	+	2125800	2125893
239207701	chr16	2127578	2127733	2127598	2127716	TSC2	NM_000548	1	42	26	+	2127599	2127727
239207701	chr16	2127578	2127733	2127598	2127716	TSC2	NM_001114382	3	41	26	+	2127599	2127727
240072080	chr16	2129143	2129276	2129166	2129254	TSC2	NM_001077183	2	40	26	+	2129036	2129197
240072080	chr16	2129143	2129276	2129166	2129254	TSC2	NM_000548	1	42	27	+	2129033	2129197
240072080	chr16	2129143	2129276	2129166	2129254	TSC2	NM_001114382	3	41	27	+	2129033	2129197
264190201	chr16	2129573	2129742	2129594	2129723	TSC2	NM_000548	1	42	29	+	2129558	2129670
264190201	chr16	2129573	2129742	2129594	2129723	TSC2	NM_001077183	2	40	28	+	2129558	2129670
264190201	chr16	2129573	2129742	2129594	2129723	TSC2	NM_001114382	3	41	29	+	2129558	2129670
241059125	chr16	2131639	2131804	2131663	2131785	TSC2	NM_000548	1	42	31	+	2131596	2131799
241059125	chr16	2131639	2131804	2131663	2131785	TSC2	NM_001077183	2	40	30	+	2131596	2131799
241059125	chr16	2131639	2131804	2131663	2131785	TSC2	NM_001114382	3	41	31	+	2131596	2131799
262597423	chr16	2134125	2134265	2134145	2134246	TSC2	NM_000548	1	42	34	+	2134229	2134716
262597423	chr16	2134125	2134265	2134145	2134246	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262597423	chr16	2134125	2134265	2134145	2134246	TSC2	NM_001114382	3	41	33	+	2134229	2134716
262624798	chr16	2134598	2134762	2134620	2134745	TSC2	NM_000548	1	42	34	+	2134229	2134716
262624798	chr16	2134598	2134762	2134620	2134745	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262624798	chr16	2134598	2134762	2134620	2134745	TSC2	NM_001114382	3	41	33	+	2134229	2134716
242589434	chr16	2136074	2136247	2136095	2136227	TSC2	NM_000548	1	42	37	+	2136194	2136380
242589434	chr16	2136074	2136247	2136095	2136227	TSC2	NM_001077183	2	40	35	+	2136194	2136380
242589434	chr16	2136074	2136247	2136095	2136227	TSC2	NM_001114382	3	41	36	+	2136194	2136380
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_000548	1	42	38	+	2136733	2136872

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_001077183	2	40	36	+	2136733	2136872
262175904	chr16	2136807	2136974	2136827	2136955	TSC2	NM_001114382	3	41	37	+	2136733	2136872
242283169	chr16	2138183	2138350	2138203	2138330	TSC2	NM_000548	1	42	41	+	2138228	2138326
242283169	chr16	2138183	2138350	2138203	2138330	TSC2	NM_001077183	2	40	39	+	2138228	2138326
242283169	chr16	2138183	2138350	2138203	2138330	TSC2	NM_001114382	3	41	40	+	2138228	2138326
225467996	chr16	3777772	3777922	3777790	3777903	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225467996	chr16	3777772	3777922	3777790	3777903	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225491190	chr16	3778224	3778361	3778242	3778342	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225491190	chr16	3778224	3778361	3778242	3778342	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226717821	chr16	3778604	3778778	3778621	3778755	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226717821	chr16	3778604	3778778	3778621	3778755	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226717930	chr16	3779019	3779193	3779036	3779176	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226717930	chr16	3779019	3779193	3779036	3779176	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226719562	chr16	3779534	3779692	3779558	3779675	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226719562	chr16	3779534	3779692	3779558	3779675	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225890191	chr16	3781217	3781365	3781235	3781348	CREBBP	NM_001079846	1	30	29	-	3781193	3781474
225890191	chr16	3781217	3781365	3781235	3781348	CREBBP	NM_004380	2	31	30	-	3781193	3781474
226605363	chr16	3786014	3786140	3786036	3786118	CREBBP	NM_001079846	1	30	27	-	3786037	3786204
226605363	chr16	3786014	3786140	3786036	3786118	CREBBP	NM_004380	2	31	28	-	3786037	3786204
225399757	chr16	3788446	3788613	3788475	3788587	CREBBP	NM_001079846	1	30	25	-	3788560	3788673
225399757	chr16	3788446	3788613	3788475	3788587	CREBBP	NM_004380	2	31	26	-	3788560	3788673
225744031	chr16	3790297	3790467	3790322	3790446	CREBBP	NM_001079846	1	30	23	-	3790400	3790550
225744031	chr16	3790297	3790467	3790322	3790446	CREBBP	NM_004380	2	31	24	-	3790400	3790550
226263553	chr16	3799490	3799657	3799518	3799629	CREBBP	NM_001079846	1	30	20	-	3799628	3799684
226263553	chr16	3799490	3799657	3799518	3799629	CREBBP	NM_004380	2	31	21	-	3799628	3799684
226492928	chr16	3807812	3807964	3807833	3807945	CREBBP	NM_001079846	1	30	17	-	3807810	3808049
226492928	chr16	3807812	3807964	3807833	3807945	CREBBP	NM_004380	2	31	18	-	3807810	3808049
226200498	chr16	3817643	3817781	3817670	3817759	CREBBP	NM_001079846	1	30	15	-	3817721	3817910
226200498	chr16	3817643	3817781	3817670	3817759	CREBBP	NM_004380	2	31	16	-	3817721	3817910
226656623	chr16	3819227	3819384	3819247	3819360	CREBBP	NM_001079846	1	30	14	-	3819175	3819354
226656623	chr16	3819227	3819384	3819247	3819360	CREBBP	NM_004380	2	31	15	-	3819175	3819354
226570291	chr16	3820816	3820970	3820836	3820946	CREBBP	NM_001079846	1	30	13	-	3820571	3820987
226570291	chr16	3820816	3820970	3820836	3820946	CREBBP	NM_004380	2	31	14	-	3820571	3820987
225602292	chr16	3824467	3824598	3824492	3824577	CREBBP	NM_001079846	1	30	11	-	3824570	3824694
225602292	chr16	3824467	3824598	3824492	3824577	CREBBP	NM_004380	2	31	12	-	3824570	3824694
225402179	chr16	3827975	3828123	3827996	3828101	CREBBP	NM_001079846	1	30	9	-	3828012	3828183
225402179	chr16	3827975	3828123	3827996	3828101	CREBBP	NM_004380	2	31	10	-	3828012	3828183
225912626	chr16	3830673	3830831	3830695	3830808	CREBBP	NM_001079846	1	30	7	-	3830733	3830879
225912626	chr16	3830673	3830831	3830695	3830808	CREBBP	NM_004380	2	31	8	-	3830733	3830879
226165080	chr16	3832659	3832825	3832684	3832808	CREBBP	NM_001079846	1	30	5	-	3832685	3832927
226165080	chr16	3832659	3832825	3832684	3832808	CREBBP	NM_004380	2	31	6	-	3832685	3832927

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225699618	chr16	3843295	3843455	3843316	3843432	CREBBP	NM_001079846	1	30	4	-	3843387	3843627
225699618	chr16	3843295	3843455	3843316	3843432	CREBBP	NM_004380	2	31	4	-	3843387	3843627
226389671	chr16	3860664	3860814	3860686	3860791	CREBBP	NM_001079846	1	30	3	-	3860604	3860780
226389671	chr16	3860664	3860814	3860686	3860791	CREBBP	NM_004380	2	31	3	-	3860604	3860780
226010800	chr16	3900613	3900752	3900633	3900733	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
226010800	chr16	3900613	3900752	3900633	3900733	CREBBP	NM_004380	2	31	2	-	3900298	3901010
226461443	chr16	3929764	3929928	3929784	3929907	CREBBP	NM_001079846	1	30	1	-	3929833	3930121
226461443	chr16	3929764	3929928	3929784	3929907	CREBBP	NM_004380	2	31	1	-	3929833	3930121
264718505	chr16	11348879	11349044	11348897	11349027	SOCS1	NM_003745	1	2	2	-	11348274	11349385
264724734	chr16	11349282	11349413	11349302	11349392	SOCS1	NM_003745	1	2	2	-	11348274	11349385
231874283	chr16	14015825	14015968	14015853	14015940	ERCC4	NM_005236	1	11	2	+	14015888	14016068
228017886	chr16	14020449	14020583	14020476	14020555	ERCC4	NM_005236	1	11	3	+	14020418	14020613
232856074	chr16	14021964	14022093	14021991	14022065	ERCC4	NM_005236	1	11	4	+	14021885	14022092
229979714	chr16	14025912	14026084	14025935	14026058	ERCC4	NM_005236	1	11	6	+	14026014	14026142
232136271	chr16	14028908	14029078	14028929	14029055	ERCC4	NM_005236	1	11	8	+	14029003	14029600
232173336	chr16	14029364	14029521	14029389	14029498	ERCC4	NM_005236	1	11	8	+	14029003	14029600
228363818	chr16	14038551	14038724	14038577	14038703	ERCC4	NM_005236	1	11	10	+	14038580	14038692
232539411	chr16	14041714	14041864	14041736	14041844	ERCC4	NM_005236	1	11	11	+	14041471	14046205
237725262	chr16	15797812	15797937	15797833	15797909	MYH11	NM_022844	4	42	42	-	15796992	15797980
237725262	chr16	15797812	15797937	15797833	15797909	MYH11	NM_002474	3	41	41	-	15796992	15797980
237725262	chr16	15797812	15797937	15797833	15797909	MYH11	NM_001040113	1	43	43	-	15796992	15797980
237725262	chr16	15797812	15797937	15797833	15797909	MYH11	NM_001040114	2	42	42	-	15796992	15797980
236543000	chr16	15808842	15808968	15808859	15808947	MYH11	NM_022844	4	42	40	-	15808766	15808938
236543000	chr16	15808842	15808968	15808859	15808947	MYH11	NM_002474	3	41	40	-	15808766	15808938
236543000	chr16	15808842	15808968	15808859	15808947	MYH11	NM_001040113	1	43	41	-	15808766	15808938
236543000	chr16	15808842	15808968	15808859	15808947	MYH11	NM_001040114	2	42	41	-	15808766	15808938
240646660	chr16	15811017	15811165	15811038	15811144	MYH11	NM_022844	4	42	38	-	15810997	15811205
240646660	chr16	15811017	15811165	15811038	15811144	MYH11	NM_002474	3	41	38	-	15810997	15811205
240646660	chr16	15811017	15811165	15811038	15811144	MYH11	NM_001040113	1	43	39	-	15810997	15811205
240646660	chr16	15811017	15811165	15811038	15811144	MYH11	NM_001040114	2	42	39	-	15810997	15811205
238367077	chr16	15813051	15813206	15813076	15813185	MYH11	NM_022844	4	42	36	-	15813077	15813165
238367077	chr16	15813051	15813206	15813076	15813185	MYH11	NM_002474	3	41	36	-	15813077	15813165
238367077	chr16	15813051	15813206	15813076	15813185	MYH11	NM_001040113	1	43	37	-	15813077	15813165
238367077	chr16	15813051	15813206	15813076	15813185	MYH11	NM_001040114	2	42	37	-	15813077	15813165
242142842	chr16	15814612	15814786	15814635	15814767	MYH11	NM_022844	4	42	33	-	15814696	15814908
242142842	chr16	15814612	15814786	15814635	15814767	MYH11	NM_002474	3	41	33	-	15814696	15814908
242142842	chr16	15814612	15814786	15814635	15814767	MYH11	NM_001040113	1	43	34	-	15814696	15814908
242142842	chr16	15814612	15814786	15814635	15814767	MYH11	NM_001040114	2	42	34	-	15814696	15814908
240423779	chr16	15815345	15815519	15815365	15815497	MYH11	NM_022844	4	42	32	-	15815279	15815491
240423779	chr16	15815345	15815519	15815365	15815497	MYH11	NM_002474	3	41	32	-	15815279	15815491
240423779	chr16	15815345	15815519	15815365	15815497	MYH11	NM_001040113	1	43	33	-	15815279	15815491

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240423779	chr16	15815345	15815519	15815365	15815497	MYH11	NM_001040114	2	42	33	-	15815279	15815491
236859943	chr16	15818455	15818626	15818478	15818605	MYH11	NM_022844	4	42	30	-	15818504	15818656
236859943	chr16	15818455	15818626	15818478	15818605	MYH11	NM_002474	3	41	30	-	15818504	15818656
236859943	chr16	15818455	15818626	15818478	15818605	MYH11	NM_001040113	1	43	31	-	15818504	15818656
236859943	chr16	15818455	15818626	15818478	15818605	MYH11	NM_001040114	2	42	31	-	15818504	15818656
237073441	chr16	15820702	15820826	15820721	15820804	MYH11	NM_022844	4	42	28	-	15820705	15820911
237073441	chr16	15820702	15820826	15820721	15820804	MYH11	NM_002474	3	41	28	-	15820705	15820911
237073441	chr16	15820702	15820826	15820721	15820804	MYH11	NM_001040113	1	43	29	-	15820705	15820911
237073441	chr16	15820702	15820826	15820721	15820804	MYH11	NM_001040114	2	42	29	-	15820705	15820911
235988482	chr16	15829126	15829290	15829147	15829270	MYH11	NM_022844	4	42	26	-	15829223	15829435
235988482	chr16	15829126	15829290	15829147	15829270	MYH11	NM_002474	3	41	26	-	15829223	15829435
235988482	chr16	15829126	15829290	15829147	15829270	MYH11	NM_001040113	1	43	27	-	15829223	15829435
235988482	chr16	15829126	15829290	15829147	15829270	MYH11	NM_001040114	2	42	27	-	15829223	15829435
238415755	chr16	15831349	15831508	15831371	15831487	MYH11	NM_022844	4	42	25	-	15831306	15831477
238415755	chr16	15831349	15831508	15831371	15831487	MYH11	NM_002474	3	41	25	-	15831306	15831477
238415755	chr16	15831349	15831508	15831371	15831487	MYH11	NM_001040113	1	43	26	-	15831306	15831477
238415755	chr16	15831349	15831508	15831371	15831487	MYH11	NM_001040114	2	42	26	-	15831306	15831477
241726314	chr16	15833893	15834067	15833913	15834043	MYH11	NM_022844	4	42	23	-	15833908	15834045
241726314	chr16	15833893	15834067	15833913	15834043	MYH11	NM_002474	3	41	23	-	15833908	15834045
241726314	chr16	15833893	15834067	15833913	15834043	MYH11	NM_001040113	1	43	24	-	15833908	15834045
241726314	chr16	15833893	15834067	15833913	15834043	MYH11	NM_001040114	2	42	24	-	15833908	15834045
235599637	chr16	15835463	15835634	15835486	15835613	MYH11	NM_022844	4	42	22	-	15835320	15835526
235599637	chr16	15835463	15835634	15835486	15835613	MYH11	NM_002474	3	41	22	-	15835320	15835526
235599637	chr16	15835463	15835634	15835486	15835613	MYH11	NM_001040113	1	43	23	-	15835320	15835526
235599637	chr16	15835463	15835634	15835486	15835613	MYH11	NM_001040114	2	42	23	-	15835320	15835526
241172995	chr16	15839011	15839185	15839031	15839165	MYH11	NM_022844	4	42	20	-	15838986	15839094
241172995	chr16	15839011	15839185	15839031	15839165	MYH11	NM_002474	3	41	20	-	15838986	15839094
241172995	chr16	15839011	15839185	15839031	15839165	MYH11	NM_001040113	1	43	21	-	15838986	15839094
241172995	chr16	15839011	15839185	15839031	15839165	MYH11	NM_001040114	2	42	21	-	15838986	15839094
235852487	chr16	15841884	15842050	15841903	15842029	MYH11	NM_022844	4	42	17	-	15841904	15842025
235852487	chr16	15841884	15842050	15841903	15842029	MYH11	NM_002474	3	41	17	-	15841904	15842025
235852487	chr16	15841884	15842050	15841903	15842029	MYH11	NM_001040113	1	43	18	-	15841904	15842025
235852487	chr16	15841884	15842050	15841903	15842029	MYH11	NM_001040114	2	42	18	-	15841904	15842025
235077422	chr16	15847188	15847336	15847212	15847313	MYH11	NM_022844	4	42	15	-	15847251	15847365
235077422	chr16	15847188	15847336	15847212	15847313	MYH11	NM_002474	3	41	15	-	15847251	15847365
235077422	chr16	15847188	15847336	15847212	15847313	MYH11	NM_001040113	1	43	16	-	15847251	15847365
235077422	chr16	15847188	15847336	15847212	15847313	MYH11	NM_001040114	2	42	16	-	15847251	15847365
239213918	chr16	15850303	15850464	15850323	15850442	MYH11	NM_022844	4	42	14	-	15850198	15850371
239213918	chr16	15850303	15850464	15850323	15850442	MYH11	NM_002474	3	41	14	-	15850198	15850371
239213918	chr16	15850303	15850464	15850323	15850442	MYH11	NM_001040113	1	43	15	-	15850198	15850371
239213918	chr16	15850303	15850464	15850323	15850442	MYH11	NM_001040114	2	42	15	-	15850198	15850371

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235880810	chr16	15853512	15853653	15853531	15853630	MYH11	NM_022844	4	42	12	-	15853433	15853585
235880810	chr16	15853512	15853653	15853531	15853630	MYH11	NM_002474	3	41	12	-	15853433	15853585
235880810	chr16	15853512	15853653	15853531	15853630	MYH11	NM_001040113	1	43	13	-	15853433	15853585
235880810	chr16	15853512	15853653	15853531	15853630	MYH11	NM_001040114	2	42	13	-	15853433	15853585
242728936	chr16	15865521	15865646	15865543	15865623	MYH11	NM_022844	4	42	9	-	15865426	15865569
242728936	chr16	15865521	15865646	15865543	15865623	MYH11	NM_002474	3	41	9	-	15865426	15865569
242728936	chr16	15865521	15865646	15865543	15865623	MYH11	NM_001040113	1	43	10	-	15865426	15865569
242728936	chr16	15865521	15865646	15865543	15865623	MYH11	NM_001040114	2	42	10	-	15865426	15865569
239097318	chr16	15878444	15878613	15878466	15878584	MYH11	NM_001040113	1	43	6	-	15878555	15878575
239097318	chr16	15878444	15878613	15878466	15878584	MYH11	NM_001040114	2	42	6	-	15878555	15878575
235281037	chr16	15917148	15917300	15917168	15917278	MYH11	NM_022844	4	42	3	-	15917112	15917268
235281037	chr16	15917148	15917300	15917168	15917278	MYH11	NM_002474	3	41	3	-	15917112	15917268
235281037	chr16	15917148	15917300	15917168	15917278	MYH11	NM_001040113	1	43	3	-	15917112	15917268
235281037	chr16	15917148	15917300	15917168	15917278	MYH11	NM_001040114	2	42	3	-	15917112	15917268
235129090	chr16	15931994	15932162	15932014	15932140	MYH11	NM_022844	4	42	2	-	15931765	15932126
235129090	chr16	15931994	15932162	15932014	15932140	MYH11	NM_002474	3	41	2	-	15931765	15932126
235129090	chr16	15931994	15932162	15932014	15932140	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235129090	chr16	15931994	15932162	15932014	15932140	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235350858	chr16	23619127	23619269	23619148	23619243	PALB2	NM_024675	1	13	12	-	23619185	23619333
235277634	chr16	23634197	23634369	23634225	23634344	PALB2	NM_024675	1	13	9	-	23634290	23634451
238130907	chr16	23637461	23637626	23637483	23637600	PALB2	NM_024675	1	13	7	-	23637557	23637718
236524480	chr16	23640990	23641158	23641015	23641133	PALB2	NM_024675	1	13	5	-	23640961	23641790
239919433	chr16	23641434	23641603	23641460	23641578	PALB2	NM_024675	1	13	5	-	23640961	23641790
238215553	chr16	23646205	23646378	23646229	23646353	PALB2	NM_024675	1	13	4	-	23646183	23647655
235061529	chr16	23646710	23646860	23646733	23646832	PALB2	NM_024675	1	13	4	-	23646183	23647655
235067513	chr16	23646996	23647149	23647024	23647126	PALB2	NM_024675	1	13	4	-	23646183	23647655
238251018	chr16	23647361	23647530	23647384	23647502	PALB2	NM_024675	1	13	4	-	23646183	23647655
236423262	chr16	23649385	23649510	23649405	23649488	PALB2	NM_024675	1	13	2	-	23649391	23649450
227432455	chr16	27441352	27441501	27441373	27441481	IL21R	NM_181079	3	10	3	+	27441377	27441441
227432455	chr16	27441352	27441501	27441373	27441481	IL21R	NM_181078	2	9	2	+	27441377	27441441
227432455	chr16	27441352	27441501	27441373	27441481	IL21R	NM_021798	1	9	2	+	27441377	27441441
227769296	chr16	27454202	27454374	27454223	27454350	IL21R	NM_181079	3	10	6	+	27454283	27454437
227769296	chr16	27454202	27454374	27454223	27454350	IL21R	NM_181078	2	9	5	+	27454283	27454437
227769296	chr16	27454202	27454374	27454223	27454350	IL21R	NM_021798	1	9	5	+	27454283	27454437
228359079	chr16	27456441	27456573	27456464	27456551	IL21R	NM_181079	3	10	8	+	27456498	27456597
228359079	chr16	27456441	27456573	27456464	27456551	IL21R	NM_181078	2	9	7	+	27456498	27456597
228359079	chr16	27456441	27456573	27456464	27456551	IL21R	NM_021798	1	9	7	+	27456498	27456597
228960740	chr16	27459891	27460031	27459908	27460013	IL21R	NM_181079	3	10	10	+	27459855	27463363
228960740	chr16	27459891	27460031	27459908	27460013	IL21R	NM_181078	2	9	9	+	27459855	27463363
228960740	chr16	27459891	27460031	27459908	27460013	IL21R	NM_021798	1	9	9	+	27459855	27463363
228955869	chr16	27460315	27460470	27460337	27460448	IL21R	NM_181079	3	10	10	+	27459855	27463363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228955869	chr16	27460315	27460470	27460337	27460448	IL21R	NM_181078	2	9	9	+	27459855	27463363
228955869	chr16	27460315	27460470	27460337	27460448	IL21R	NM_021798	1	9	9	+	27459855	27463363
225419196	chr16	50783605	50783735	50783630	50783708	CYLD	NM_015247	3	20	4	+	50783487	50784113
225419196	chr16	50783605	50783735	50783630	50783708	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225419196	chr16	50783605	50783735	50783630	50783708	CYLD	NM_001042412	2	18	3	+	50783487	50784113
225418705	chr16	50783979	50784105	50784000	50784079	CYLD	NM_015247	3	20	4	+	50783487	50784113
225418705	chr16	50783979	50784105	50784000	50784079	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225418705	chr16	50783979	50784105	50784000	50784079	CYLD	NM_001042412	2	18	3	+	50783487	50784113
226607155	chr16	50785684	50785832	50785711	50785805	CYLD	NM_015247	3	20	5	+	50785515	50785817
226607155	chr16	50785684	50785832	50785711	50785805	CYLD	NM_001042355	1	18	4	+	50785515	50785817
226607155	chr16	50785684	50785832	50785711	50785805	CYLD	NM_001042412	2	18	4	+	50785515	50785817
226567767	chr16	50813656	50813794	50813676	50813769	CYLD	NM_015247	3	20	10	+	50813576	50813955
226567767	chr16	50813656	50813794	50813676	50813769	CYLD	NM_001042355	1	18	8	+	50813576	50813955
226567767	chr16	50813656	50813794	50813676	50813769	CYLD	NM_001042412	2	18	8	+	50813576	50813955
225897075	chr16	50815172	50815297	50815192	50815277	CYLD	NM_015247	3	20	11	+	50815157	50815322
225897075	chr16	50815172	50815297	50815192	50815277	CYLD	NM_001042355	1	18	9	+	50815157	50815322
225897075	chr16	50815172	50815297	50815192	50815277	CYLD	NM_001042412	2	18	9	+	50815157	50815322
225735429	chr16	50818137	50818277	50818168	50818249	CYLD	NM_015247	3	20	13	+	50818240	50818362
225735429	chr16	50818137	50818277	50818168	50818249	CYLD	NM_001042355	1	18	11	+	50818240	50818362
225735429	chr16	50818137	50818277	50818168	50818249	CYLD	NM_001042412	2	18	11	+	50818240	50818362
226524117	chr16	50821687	50821845	50821715	50821818	CYLD	NM_015247	3	20	15	+	50821697	50821763
226524117	chr16	50821687	50821845	50821715	50821818	CYLD	NM_001042355	1	18	13	+	50821697	50821763
226524117	chr16	50821687	50821845	50821715	50821818	CYLD	NM_001042412	2	18	13	+	50821697	50821763
225875907	chr16	50826520	50826669	50826547	50826641	CYLD	NM_015247	3	20	17	+	50826508	50826616
225875907	chr16	50826520	50826669	50826547	50826641	CYLD	NM_001042355	1	18	15	+	50826508	50826616
225875907	chr16	50826520	50826669	50826547	50826641	CYLD	NM_001042412	2	18	15	+	50826508	50826616
226723901	chr16	50830174	50830347	50830199	50830326	CYLD	NM_015247	3	20	20	+	50830235	50835846
226723901	chr16	50830174	50830347	50830199	50830326	CYLD	NM_001042355	1	18	18	+	50830235	50835846
226723901	chr16	50830174	50830347	50830199	50830326	CYLD	NM_001042412	2	18	18	+	50830235	50835846
289199472	chr16	55516753	55516915	55516774	55516890	MMP2	NM_001127891	1	13	2	+	55516821	55517047
289199472	chr16	55516753	55516915	55516774	55516890	MMP2	NM_004530	2	13	2	+	55516821	55517047
291518494	chr16	55518015	55518187	55518037	55518166	MMP2	NM_001127891	1	13	3	+	55517928	55518076
291518494	chr16	55518015	55518187	55518037	55518166	MMP2	NM_004530	2	13	3	+	55517928	55518076
291265557	chr16	55519548	55519710	55519570	55519690	MMP2	NM_001127891	1	13	5	+	55519516	55519689
291265557	chr16	55519548	55519710	55519570	55519690	MMP2	NM_004530	2	13	5	+	55519516	55519689
289592872	chr16	55523478	55523652	55523503	55523632	MMP2	NM_001127891	1	13	7	+	55523563	55523736
289592872	chr16	55523478	55523652	55523503	55523632	MMP2	NM_004530	2	13	7	+	55523563	55523736
289604994	chr16	55527029	55527167	55527051	55527142	MMP2	NM_001127891	1	13	9	+	55527070	55527205
289604994	chr16	55527029	55527167	55527051	55527142	MMP2	NM_004530	2	13	9	+	55527070	55527205
289915453	chr16	55532175	55532349	55532196	55532322	MMP2	NM_001127891	1	13	11	+	55532201	55532360
289915453	chr16	55532175	55532349	55532196	55532322	MMP2	NM_004530	2	13	11	+	55532201	55532360

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293177385	chr16	55539237	55539403	55539261	55539381	MMP2	NM_001127891	1	13	13	+	55539251	55540586
293177385	chr16	55539237	55539403	55539261	55539381	MMP2	NM_004530	2	13	13	+	55539251	55540586
226972570	chr16	64981777	64981941	64981801	64981917	CDH11	NM_001797	1	13	13	-	64980683	64982002
226581053	chr16	64984831	64984978	64984851	64984956	CDH11	NM_001797	1	13	12	-	64984670	64984921
226021474	chr16	65005824	65005990	65005847	65005968	CDH11	NM_001797	1	13	10	-	65005834	65005967
225507865	chr16	65016011	65016136	65016032	65016111	CDH11	NM_001797	1	13	8	-	65015951	65016204
225612611	chr16	65022178	65022316	65022206	65022287	CDH11	NM_001797	1	13	7	-	65022060	65022247
225988226	chr16	65026865	65027038	65026889	65027011	CDH11	NM_001797	1	13	5	-	65026818	65026937
253679742	chr16	65032697	65032822	65032718	65032799	CDH11	NM_001797	1	13	4	-	65032465	65032759
272541602	chr16	66413322	66413493	66413340	66413474	CDH5	NM_001795	1	12	2	+	66413222	66413450
271724623	chr16	66422195	66422369	66422216	66422346	CDH5	NM_001795	1	12	4	+	66422227	66422343
271172654	chr16	66424363	66424535	66424386	66424515	CDH5	NM_001795	1	12	6	+	66424306	66424493
271247586	chr16	66429909	66430083	66429935	66430060	CDH5	NM_001795	1	12	8	+	66429962	66430104
271446489	chr16	66432323	66432495	66432345	66432470	CDH5	NM_001795	1	12	10	+	66432359	66432464
271650199	chr16	66436518	66436691	66436539	66436670	CDH5	NM_001795	1	12	12	+	66436555	66438689
271651731	chr16	66437006	66437170	66437027	66437149	CDH5	NM_001795	1	12	12	+	66436555	66438689
226304836	chr16	68835434	68835604	68835460	68835585	CDH1	NM_004360	1	16	3	+	68835573	68835796
226174495	chr16	68842336	68842507	68842359	68842484	CDH1	NM_004360	1	16	4	+	68842327	68842470
226259787	chr16	68844127	68844301	68844150	68844278	CDH1	NM_004360	1	16	6	+	68844100	68844244
226010327	chr16	68846113	68846263	68846134	68846239	CDH1	NM_004360	1	16	8	+	68846038	68846166
225856876	chr16	68849473	68849597	68849497	68849577	CDH1	NM_004360	1	16	10	+	68849418	68849662
225493995	chr16	68855809	68855938	68855833	68855917	CDH1	NM_004360	1	16	12	+	68855904	68856128
226604741	chr16	68857376	68857550	68857404	68857529	CDH1	NM_004360	1	16	13	+	68857302	68857529
254170750	chr16	68863601	68863746	68863624	68863722	CDH1	NM_004360	1	16	15	+	68863557	68863700
232681357	chr16	79628357	79628513	79628385	79628493	MAF	NM_001031804	1	1	1	-	79627745	79634622
232681357	chr16	79628357	79628513	79628385	79628493	MAF	NM_005360	2	2	2	-	79627745	79628450
232466547	chr16	79632894	79633039	79632912	79633022	MAF	NM_001031804	1	1	1	-	79627745	79634622
232466547	chr16	79632894	79633039	79632912	79633022	MAF	NM_005360	2	2	1	-	79632682	79634622
233799616	chr16	79633668	79633793	79633686	79633771	MAF	NM_001031804	1	1	1	-	79627745	79634622
233799616	chr16	79633668	79633793	79633686	79633771	MAF	NM_005360	2	2	1	-	79632682	79634622
227835840	chr16	89805234	89805408	89805256	89805384	FANCA	NM_000135	1	43	42	-	89805290	89805382
228001706	chr16	89806380	89806528	89806401	89806507	FANCA	NM_000135	1	43	39	-	89806402	89806507
227700387	chr16	89811346	89811506	89811366	89811486	FANCA	NM_000135	1	43	36	-	89811367	89811479
232904479	chr16	89815027	89815198	89815047	89815176	FANCA	NM_000135	1	43	33	-	89815067	89815175
230482015	chr16	89824964	89825122	89824988	89825100	FANCA	NM_000135	1	43	30	-	89824985	89825113
228971628	chr16	89831308	89831482	89831330	89831455	FANCA	NM_000135	1	43	28	-	89831298	89831474
227858404	chr16	89836214	89836384	89836234	89836366	FANCA	NM_000135	1	43	26	-	89836245	89836432
230399983	chr16	89836996	89837156	89837016	89837132	FANCA	NM_000135	1	43	24	-	89836972	89837042
228914987	chr16	89842070	89842243	89842092	89842219	FANCA	NM_000135	1	43	21	-	89842150	89842223
231804623	chr16	89849185	89849352	89849212	89849327	FANCA	NM_000135	1	43	17	-	89849267	89849326
230168113	chr16	89857800	89857974	89857824	89857947	FANCA	NM_000135	1	43	14	-	89857811	89857944

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230803994	chr16	89862258	89862408	89862280	89862387	FANCA	NM_000135	1	43	11	-	89862314	89862426
227815112	chr16	89865935	89866108	89865962	89866079	FANCA	NM_000135	1	43	9	-	89866013	89866046
227815112	chr16	89865935	89866108	89865962	89866079	FANCA	NM_001018112	2	11	9	-	89866013	89866046
229937482	chr16	89874725	89874897	89874749	89874869	FANCA	NM_000135	1	43	6	-	89874702	89874775
229937482	chr16	89874725	89874897	89874749	89874869	FANCA	NM_001018112	2	11	6	-	89874702	89874775
230674767	chr16	89877389	89877561	89877409	89877535	FANCA	NM_000135	1	43	4	-	89877337	89877479
230674767	chr16	89877389	89877561	89877409	89877535	FANCA	NM_001018112	2	11	4	-	89877337	89877479
229299501	chr16	89882861	89883016	89882878	89882998	FANCA	NM_000135	1	43	1	-	89882945	89883065
229299501	chr16	89882861	89883016	89882878	89882998	FANCA	NM_001018112	2	11	1	-	89882945	89883065
237428388	chr17	5405061	5405216	5405082	5405193	NLRP1	NM_001033053	1	16	16	-	5404719	5405192
237421255	chr17	5418692	5418866	5418715	5418840	NLRP1	NM_014922	2	16	15	-	5418793	5418837
237421255	chr17	5418692	5418866	5418715	5418840	NLRP1	NM_033007	5	15	14	-	5418793	5418837
237421255	chr17	5418692	5418866	5418715	5418840	NLRP1	NM_033006	4	16	15	-	5418793	5418837
237421255	chr17	5418692	5418866	5418715	5418840	NLRP1	NM_033004	3	17	16	-	5418793	5418837
236182835	chr17	5424206	5424364	5424230	5424336	NLRP1	NM_001033053	1	16	14	-	5424201	5424332
236182835	chr17	5424206	5424364	5424230	5424336	NLRP1	NM_033006	4	16	13	-	5424201	5424332
236182835	chr17	5424206	5424364	5424230	5424336	NLRP1	NM_033004	3	17	14	-	5424201	5424332
236148340	chr17	5433775	5433949	5433797	5433924	NLRP1	NM_014922	2	16	12	-	5433801	5434024
236148340	chr17	5433775	5433949	5433797	5433924	NLRP1	NM_001033053	1	16	12	-	5433801	5434024
236148340	chr17	5433775	5433949	5433797	5433924	NLRP1	NM_033007	5	15	11	-	5433801	5434024
236148340	chr17	5433775	5433949	5433797	5433924	NLRP1	NM_033006	4	16	11	-	5433801	5434024
236148340	chr17	5433775	5433949	5433797	5433924	NLRP1	NM_033004	3	17	12	-	5433801	5434024
235093047	chr17	5436218	5436382	5436239	5436361	NLRP1	NM_014922	2	16	11	-	5436142	5436304
235093047	chr17	5436218	5436382	5436239	5436361	NLRP1	NM_001033053	1	16	11	-	5436142	5436304
235093047	chr17	5436218	5436382	5436239	5436361	NLRP1	NM_033007	5	15	10	-	5436142	5436304
235093047	chr17	5436218	5436382	5436239	5436361	NLRP1	NM_033006	4	16	10	-	5436142	5436304
235093047	chr17	5436218	5436382	5436239	5436361	NLRP1	NM_033004	3	17	11	-	5436142	5436304
238981724	chr17	5442793	5442961	5442815	5442941	NLRP1	NM_014922	2	16	7	-	5442735	5442905
238981724	chr17	5442793	5442961	5442815	5442941	NLRP1	NM_001033053	1	16	7	-	5442735	5442905
238981724	chr17	5442793	5442961	5442815	5442941	NLRP1	NM_033007	5	15	7	-	5442735	5442905
238981724	chr17	5442793	5442961	5442815	5442941	NLRP1	NM_033006	4	16	7	-	5442735	5442905
238981724	chr17	5442793	5442961	5442815	5442941	NLRP1	NM_033004	3	17	7	-	5442735	5442905
238308177	chr17	5456785	5456915	5456807	5456891	NLRP1	NM_014922	2	16	5	-	5456706	5456876
238308177	chr17	5456785	5456915	5456807	5456891	NLRP1	NM_001033053	1	16	5	-	5456706	5456876
238308177	chr17	5456785	5456915	5456807	5456891	NLRP1	NM_033007	5	15	5	-	5456706	5456876
238308177	chr17	5456785	5456915	5456807	5456891	NLRP1	NM_033006	4	16	5	-	5456706	5456876
238308177	chr17	5456785	5456915	5456807	5456891	NLRP1	NM_033004	3	17	5	-	5456706	5456876
257624546	chr17	5461972	5462141	5461995	5462116	NLRP1	NM_014922	2	16	4	-	5461659	5463363
257624546	chr17	5461972	5462141	5461995	5462116	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
257624546	chr17	5461972	5462141	5461995	5462116	NLRP1	NM_033007	5	15	4	-	5461659	5463363
257624546	chr17	5461972	5462141	5461995	5462116	NLRP1	NM_033006	4	16	4	-	5461659	5463363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257624546	chr17	5461972	5462141	5461995	5462116	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237511209	chr17	5462472	5462598	5462494	5462578	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237511209	chr17	5462472	5462598	5462494	5462578	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237511209	chr17	5462472	5462598	5462494	5462578	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237511209	chr17	5462472	5462598	5462494	5462578	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237511209	chr17	5462472	5462598	5462494	5462578	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237721437	chr17	5462875	5463044	5462896	5463019	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237721437	chr17	5462875	5463044	5462896	5463019	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237721437	chr17	5462875	5463044	5462896	5463019	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237721437	chr17	5462875	5463044	5462896	5463019	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237721437	chr17	5462875	5463044	5462896	5463019	NLRP1	NM_033004	3	17	4	-	5461659	5463363
235633011	chr17	5485157	5485331	5485178	5485311	NLRP1	NM_014922	2	16	3	-	5485179	5485382
235633011	chr17	5485157	5485331	5485178	5485311	NLRP1	NM_001033053	1	16	3	-	5485179	5485382
235633011	chr17	5485157	5485331	5485178	5485311	NLRP1	NM_033007	5	15	3	-	5485179	5485382
235633011	chr17	5485157	5485331	5485178	5485311	NLRP1	NM_033006	4	16	3	-	5485179	5485382
235633011	chr17	5485157	5485331	5485178	5485311	NLRP1	NM_033004	3	17	3	-	5485179	5485382
235907293	chr17	5486988	5487137	5487006	5487119	NLRP1	NM_014922	2	16	1	-	5487007	5487832
235907293	chr17	5486988	5487137	5487006	5487119	NLRP1	NM_001033053	1	16	1	-	5487007	5487832
235907293	chr17	5486988	5487137	5487006	5487119	NLRP1	NM_033007	5	15	1	-	5487007	5487832
235907293	chr17	5486988	5487137	5487006	5487119	NLRP1	NM_033006	4	16	1	-	5487007	5487832
235907293	chr17	5486988	5487137	5487006	5487119	NLRP1	NM_033004	3	17	1	-	5487007	5487832
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126117	7	8	8	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126116	6	8	8	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126113	3	12	12	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_000546	1	11	11	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126118	8	10	10	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126114	4	12	12	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126112	2	11	11	-	7571720	7573008
239807548	chr17	7572911	7573063	7572937	7573040	TP53	NM_001126115	5	7	7	-	7571720	7573008
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126117	7	8	4	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126116	6	8	4	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126113	3	12	8	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_000546	1	11	8	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126118	8	10	7	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126114	4	12	8	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126112	2	11	8	-	7577019	7577155
242292875	chr17	7576987	7577148	7577007	7577127	TP53	NM_001126115	5	7	4	-	7577019	7577155
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126117	7	8	2	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126116	6	8	2	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126113	3	12	6	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_000546	1	11	6	-	7578177	7578289

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126118	8	10	5	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126114	4	12	6	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126112	2	11	6	-	7578177	7578289
262327837	chr17	7578121	7578245	7578142	7578219	TP53	NM_001126115	5	7	2	-	7578177	7578289
263757129	chr17	7579259	7579407	7579279	7579385	TP53	NM_001126113	3	12	4	-	7579312	7579590
263757129	chr17	7579259	7579407	7579279	7579385	TP53	NM_000546	1	11	4	-	7579312	7579590
263757129	chr17	7579259	7579407	7579279	7579385	TP53	NM_001126118	8	10	3	-	7579312	7579590
263757129	chr17	7579259	7579407	7579279	7579385	TP53	NM_001126114	4	12	4	-	7579312	7579590
263757129	chr17	7579259	7579407	7579279	7579385	TP53	NM_001126112	2	11	4	-	7579312	7579590
242494828	chr17	7579815	7579971	7579835	7579949	TP53	NM_001126113	3	12	2	-	7579839	7579940
242494828	chr17	7579815	7579971	7579835	7579949	TP53	NM_000546	1	11	2	-	7579839	7579940
242494828	chr17	7579815	7579971	7579835	7579949	TP53	NM_001126114	4	12	2	-	7579839	7579940
242494828	chr17	7579815	7579971	7579835	7579949	TP53	NM_001126112	2	11	2	-	7579839	7579937
242494828	chr17	7579815	7579971	7579835	7579949	TP53	NM_001126118	8	10	2	-	7579700	7579940
236314691	chr17	8045102	8045237	8045119	8045219	PER1	NM_002616	1	23	22	-	8045123	8045273
236745812	chr17	8045931	8046104	8045950	8046084	PER1	NM_002616	1	23	20	-	8045967	8046153
237929352	chr17	8046719	8046885	8046741	8046860	PER1	NM_002616	1	23	19	-	8046584	8047194
237926434	chr17	8047086	8047245	8047105	8047225	PER1	NM_002616	1	23	19	-	8046584	8047194
234914302	chr17	8049216	8049369	8049236	8049349	PER1	NM_002616	1	23	17	-	8049276	8049455
237285690	chr17	8049893	8050021	8049911	8050003	PER1	NM_002616	1	23	15	-	8049912	8050083
239353953	chr17	8050590	8050737	8050608	8050717	PER1	NM_002616	1	23	13	-	8050568	8050699
236956067	chr17	8051069	8051235	8051090	8051213	PER1	NM_002616	1	23	11	-	8050992	8051145
235237916	chr17	8051897	8052060	8051919	8052040	PER1	NM_002616	1	23	8	-	8051962	8052104
237439208	chr17	8052813	8052976	8052834	8052954	PER1	NM_002616	1	23	6	-	8052780	8052981
237005787	chr17	8053267	8053416	8053288	8053393	PER1	NM_002616	1	23	4	-	8053289	8053443
236695701	chr17	8053724	8053898	8053749	8053878	PER1	NM_002616	1	23	2	-	8053750	8054163
270882259	chr17	8108289	8108437	8108310	8108410	AURKB	NM_004217	1	9	9	-	8108049	8108362
272529702	chr17	8109745	8109887	8109766	8109863	AURKB	NM_004217	1	9	7	-	8109809	8109957
269855707	chr17	8110353	8110526	8110373	8110504	AURKB	NM_004217	1	9	5	-	8110494	8110685
269990714	chr17	8111026	8111196	8111045	8111176	AURKB	NM_004217	1	9	3	-	8111056	8111158
233282771	chr17	11958107	11958263	11958129	11958235	MAP2K4	NM_003010	1	11	2	+	11958206	11958308
230937396	chr17	11984779	11984920	11984801	11984893	MAP2K4	NM_003010	1	11	3	+	11984673	11984847
232500629	chr17	12011128	12011297	12011156	12011274	MAP2K4	NM_003010	1	11	5	+	12011107	12011226
233550986	chr17	12016540	12016711	12016567	12016689	MAP2K4	NM_003010	1	11	7	+	12016550	12016677
232635876	chr17	12043033	12043207	12043057	12043180	MAP2K4	NM_003010	1	11	10	+	12043156	12043201
228471264	chr17	17116943	17117086	17116965	17117064	FLCN	NM_144997	2	14	14	-	17115527	17117170
227624023	chr17	17118373	17118547	17118397	17118524	FLCN	NM_144997	2	14	13	-	17118299	17118404
227624023	chr17	17118373	17118547	17118397	17118524	FLCN	NM_144997	2	14	12	-	17118499	17118630
227398087	chr17	17120354	17120522	17120376	17120499	FLCN	NM_144997	2	14	10	-	17120383	17120496
227427736	chr17	17124727	17124882	17124748	17124859	FLCN	NM_144606	1	8	8	-	17124485	17124942
227427736	chr17	17124727	17124882	17124748	17124859	FLCN	NM_144997	2	14	8	-	17124851	17124942

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227301377	chr17	17127212	17127350	17127233	17127326	FLCN	NM_144997	2	14	6	-	17127236	17127457
227301377	chr17	17127212	17127350	17127233	17127326	FLCN	NM_144606	1	8	6	-	17127236	17127457
227380079	chr17	17129562	17129735	17129590	17129710	FLCN	NM_144997	2	14	5	-	17129490	17129636
227380079	chr17	17129562	17129735	17129590	17129710	FLCN	NM_144606	1	8	5	-	17129490	17129636
258118626	chr17	29422203	29422371	29422221	29422354	NF1	NM_000267	1	57	1	+	29421945	29422387
258118626	chr17	29422203	29422371	29422221	29422354	NF1	NM_001128147	3	15	1	+	29421945	29422387
258118626	chr17	29422203	29422371	29422221	29422354	NF1	NM_001042492	2	58	1	+	29421945	29422387
236393544	chr17	29485969	29486143	29485996	29486114	NF1	NM_000267	1	57	3	+	29486028	29486111
236393544	chr17	29485969	29486143	29485996	29486114	NF1	NM_001128147	3	15	3	+	29486028	29486111
236393544	chr17	29485969	29486143	29485996	29486114	NF1	NM_001042492	2	58	3	+	29486028	29486111
240265457	chr17	29508341	29508486	29508371	29508465	NF1	NM_000267	1	57	6	+	29508440	29508507
240265457	chr17	29508341	29508486	29508371	29508465	NF1	NM_001128147	3	15	6	+	29508440	29508507
240265457	chr17	29508341	29508486	29508371	29508465	NF1	NM_001042492	2	58	6	+	29508440	29508507
237444341	chr17	29509584	29509746	29509603	29509717	NF1	NM_000267	1	57	8	+	29509526	29509683
237444341	chr17	29509584	29509746	29509603	29509717	NF1	NM_001128147	3	15	8	+	29509526	29509683
237444341	chr17	29509584	29509746	29509603	29509717	NF1	NM_001042492	2	58	8	+	29509526	29509683
235109734	chr17	29527571	29527743	29527598	29527715	NF1	NM_000267	1	57	9	+	29527440	29527613
235109734	chr17	29527571	29527743	29527598	29527715	NF1	NM_001128147	3	15	9	+	29527440	29527613
235109734	chr17	29527571	29527743	29527598	29527715	NF1	NM_001042492	2	58	9	+	29527440	29527613
236498026	chr17	29528347	29528517	29528374	29528489	NF1	NM_000267	1	57	11	+	29528429	29528503
236498026	chr17	29528347	29528517	29528374	29528489	NF1	NM_001128147	3	15	11	+	29528429	29528503
236498026	chr17	29528347	29528517	29528374	29528489	NF1	NM_001042492	2	58	11	+	29528429	29528503
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_000267	1	57	13	+	29541469	29541603
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_001128147	3	15	13	+	29541469	29541603
257923164	chr17	29541511	29541670	29541535	29541648	NF1	NM_001042492	2	58	13	+	29541469	29541603
237782771	chr17	29550526	29550698	29550547	29550672	NF1	NM_000267	1	57	16	+	29550462	29550585
237782771	chr17	29550526	29550698	29550547	29550672	NF1	NM_001042492	2	58	16	+	29550462	29550585
236053758	chr17	29553515	29553680	29553537	29553654	NF1	NM_000267	1	57	18	+	29553453	29553702
236053758	chr17	29553515	29553680	29553537	29553654	NF1	NM_001042492	2	58	18	+	29553453	29553702
236360765	chr17	29555951	29556110	29555979	29556088	NF1	NM_000267	1	57	21	+	29556043	29556483
236360765	chr17	29555951	29556110	29555979	29556088	NF1	NM_001042492	2	58	21	+	29556043	29556483
236390724	chr17	29556292	29556438	29556315	29556410	NF1	NM_000267	1	57	21	+	29556043	29556483
236390724	chr17	29556292	29556438	29556315	29556410	NF1	NM_001042492	2	58	21	+	29556043	29556483
235504565	chr17	29557341	29557497	29557367	29557469	NF1	NM_000267	1	57	23	+	29557278	29557400
235504565	chr17	29557341	29557497	29557367	29557469	NF1	NM_001042492	2	58	23	+	29557278	29557400
236201541	chr17	29559619	29559786	29559644	29559763	NF1	NM_000267	1	57	26	+	29559718	29559899
236201541	chr17	29559619	29559786	29559644	29559763	NF1	NM_001042492	2	58	26	+	29559718	29559899
237112721	chr17	29560094	29560257	29560120	29560231	NF1	NM_000267	1	57	27	+	29560020	29560231
237112721	chr17	29560094	29560257	29560120	29560231	NF1	NM_001042492	2	58	27	+	29560020	29560231
236762074	chr17	29562963	29563133	29562991	29563112	NF1	NM_000267	1	57	29	+	29562936	29563039
236762074	chr17	29562963	29563133	29562991	29563112	NF1	NM_001042492	2	58	29	+	29562936	29563039

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257713066	chr17	29579946	29580118	29579967	29580090	NF1	NM_001042492	2	58	31	+	29579956	29580018
237203098	chr17	29585942	29586104	29585975	29586080	NF1	NM_000267	1	57	32	+	29586050	29586147
237203098	chr17	29585942	29586104	29585975	29586080	NF1	NM_001042492	2	58	33	+	29586050	29586147
236394928	chr17	29588630	29588796	29588655	29588774	NF1	NM_000267	1	57	34	+	29588729	29588875
236394928	chr17	29588630	29588796	29588655	29588774	NF1	NM_001042492	2	58	35	+	29588729	29588875
235391588	chr17	29592313	29592440	29592335	29592412	NF1	NM_000267	1	57	35	+	29592247	29592357
235391588	chr17	29592313	29592440	29592335	29592412	NF1	NM_001042492	2	58	36	+	29592247	29592357
239326308	chr17	29653139	29653299	29653160	29653273	NF1	NM_000267	1	57	36	+	29652838	29653270
239326308	chr17	29653139	29653299	29653160	29653273	NF1	NM_001042492	2	58	37	+	29652838	29653270
239868286	chr17	29654818	29654979	29654846	29654951	NF1	NM_000267	1	57	37	+	29654517	29654857
239868286	chr17	29654818	29654979	29654846	29654951	NF1	NM_001042492	2	58	38	+	29654517	29654857
242466922	chr17	29657460	29657624	29657483	29657593	NF1	NM_000267	1	57	38	+	29657314	29657516
242466922	chr17	29657460	29657624	29657483	29657593	NF1	NM_001042492	2	58	39	+	29657314	29657516
238334827	chr17	29663357	29663491	29663384	29663464	NF1	NM_000267	1	57	40	+	29663351	29663491
238334827	chr17	29663357	29663491	29663384	29663464	NF1	NM_001042492	2	58	41	+	29663351	29663491
240038917	chr17	29663807	29663964	29663830	29663935	NF1	NM_000267	1	57	41	+	29663653	29663932
240038917	chr17	29663807	29663964	29663830	29663935	NF1	NM_001042492	2	58	42	+	29663653	29663932
239661439	chr17	29664720	29664894	29664744	29664872	NF1	NM_000267	1	57	43	+	29664837	29664898
239661439	chr17	29664720	29664894	29664744	29664872	NF1	NM_001042492	2	58	44	+	29664837	29664898
237654770	chr17	29667437	29667609	29667464	29667587	NF1	NM_000267	1	57	46	+	29667523	29667663
237654770	chr17	29667437	29667609	29667464	29667587	NF1	NM_001042492	2	58	47	+	29667523	29667663
235992734	chr17	29676061	29676227	29676084	29676199	NF1	NM_000267	1	57	48	+	29676138	29676269
235992734	chr17	29676061	29676227	29676084	29676199	NF1	NM_001042492	2	58	49	+	29676138	29676269
239718463	chr17	29677237	29677411	29677265	29677390	NF1	NM_000267	1	57	49	+	29677201	29677336
239718463	chr17	29677237	29677411	29677265	29677390	NF1	NM_001042492	2	58	50	+	29677201	29677336
235935272	chr17	29683358	29683530	29683386	29683504	NF1	NM_000267	1	57	51	+	29683478	29683600
235935272	chr17	29683358	29683530	29683386	29683504	NF1	NM_001042492	2	58	52	+	29683478	29683600
241777431	chr17	29684030	29684174	29684058	29684146	NF1	NM_000267	1	57	52	+	29683978	29684108
241777431	chr17	29684030	29684174	29684058	29684146	NF1	NM_001042492	2	58	53	+	29683978	29684108
238961013	chr17	29685509	29685674	29685533	29685646	NF1	NM_000267	1	57	54	+	29685498	29685640
238961013	chr17	29685509	29685674	29685533	29685646	NF1	NM_001042492	2	58	55	+	29685498	29685640
258080174	chr17	29701003	29701177	29701029	29701152	NF1	NM_000267	1	57	57	+	29701031	29704695
258080174	chr17	29701003	29701177	29701029	29701152	NF1	NM_001042492	2	58	58	+	29701031	29704695
274623280	chr17	37618454	37618614	37618475	37618593	CDK12	NM_016507	2	14	1	+	37617739	37619370
274623280	chr17	37618454	37618614	37618475	37618593	CDK12	NM_015083	1	14	1	+	37617739	37619370
274644740	chr17	37618913	37619083	37618939	37619058	CDK12	NM_016507	2	14	1	+	37617739	37619370
274644740	chr17	37618913	37619083	37618939	37619058	CDK12	NM_015083	1	14	1	+	37617739	37619370
274385132	chr17	37627090	37627253	37627118	37627230	CDK12	NM_016507	2	14	2	+	37627132	37628016
274385132	chr17	37627090	37627253	37627118	37627230	CDK12	NM_015083	1	14	2	+	37627132	37628016
274428095	chr17	37627509	37627648	37627537	37627621	CDK12	NM_016507	2	14	2	+	37627132	37628016
274428095	chr17	37627509	37627648	37627537	37627621	CDK12	NM_015083	1	14	2	+	37627132	37628016

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273538790	chr17	37627932	37628104	37627953	37628076	CDK12	NM_016507	2	14	2	+	37627132	37628016
273538790	chr17	37627932	37628104	37627953	37628076	CDK12	NM_015083	1	14	2	+	37627132	37628016
274358298	chr17	37649009	37649158	37649035	37649131	CDK12	NM_016507	2	14	4	+	37649004	37649143
274358298	chr17	37649009	37649158	37649035	37649131	CDK12	NM_015083	1	14	4	+	37649004	37649143
274592046	chr17	37657532	37657657	37657556	37657632	CDK12	NM_016507	2	14	6	+	37657503	37657692
274592046	chr17	37657532	37657657	37657556	37657632	CDK12	NM_015083	1	14	6	+	37657503	37657692
273557530	chr17	37667780	37667953	37667803	37667924	CDK12	NM_016507	2	14	8	+	37667782	37667883
273557530	chr17	37667780	37667953	37667803	37667924	CDK12	NM_015083	1	14	8	+	37667782	37667883
274021766	chr17	37676151	37676275	37676179	37676252	CDK12	NM_016507	2	14	11	+	37676209	37676340
274021766	chr17	37676151	37676275	37676179	37676252	CDK12	NM_015083	1	14	11	+	37676209	37676340
273906826	chr17	37682075	37682245	37682103	37682224	CDK12	NM_016507	2	14	13	+	37682117	37682569
273906826	chr17	37682075	37682245	37682103	37682224	CDK12	NM_015083	1	14	13	+	37682117	37682569
274027307	chr17	37686826	37686957	37686854	37686934	CDK12	NM_016507	2	14	14	+	37686857	37690800
274027307	chr17	37686826	37686957	37686854	37686934	CDK12	NM_015083	1	14	14	+	37686884	37690800
274070974	chr17	37687217	37687390	37687238	37687368	CDK12	NM_016507	2	14	14	+	37686857	37690800
274070974	chr17	37687217	37687390	37687238	37687368	CDK12	NM_015083	1	14	14	+	37686884	37690800
298905366	chr17	37829230	37829354	37829250	37829334	PGAP3	NM_033419	1	8	7	-	37829304	37829508
299083221	chr17	37829760	37829932	37829780	37829913	PGAP3	NM_033419	1	8	6	-	37829767	37829903
299096824	chr17	37840788	37840958	37840810	37840938	PGAP3	NM_033419	1	8	3	-	37840850	37841002
299066175	chr17	37844087	37844251	37844111	37844234	PGAP3	NM_033419	1	8	1	-	37844087	37844310
230014990	chr17	37863342	37863472	37863365	37863452	ERBB2	NM_004448	2	27	2	+	37863243	37863394
230014990	chr17	37863342	37863472	37863365	37863452	ERBB2	NM_001005862	1	30	5	+	37863243	37863394
231796481	chr17	37865617	37865752	37865640	37865730	ERBB2	NM_004448	2	27	4	+	37865571	37865705
231796481	chr17	37865617	37865752	37865640	37865730	ERBB2	NM_001005862	1	30	7	+	37865571	37865705
228226906	chr17	37866641	37866779	37866661	37866755	ERBB2	NM_004448	2	27	7	+	37866593	37866734
228226906	chr17	37866641	37866779	37866661	37866755	ERBB2	NM_001005862	1	30	10	+	37866593	37866734
231722566	chr17	37868619	37868764	37868643	37868741	ERBB2	NM_004448	2	27	9	+	37868575	37868701
231722566	chr17	37868619	37868764	37868643	37868741	ERBB2	NM_001005862	1	30	12	+	37868575	37868701
228388569	chr17	37871972	37872145	37871992	37872125	ERBB2	NM_004448	2	27	12	+	37871993	37872192
228388569	chr17	37871972	37872145	37871992	37872125	ERBB2	NM_001005862	1	30	15	+	37871993	37872192
227875346	chr17	37873498	37873665	37873521	37873642	ERBB2	NM_004448	2	27	15	+	37873573	37873733
227875346	chr17	37873498	37873665	37873521	37873642	ERBB2	NM_001005862	1	30	18	+	37873573	37873733
228521634	chr17	37879659	37879823	37879680	37879805	ERBB2	NM_004448	2	27	18	+	37879791	37879913
228521634	chr17	37879659	37879823	37879680	37879805	ERBB2	NM_001005862	1	30	21	+	37879791	37879913
228521634	chr17	37879659	37879823	37879680	37879805	ERBB2	NM_004448	2	27	17	+	37879572	37879710
228521634	chr17	37879659	37879823	37879680	37879805	ERBB2	NM_001005862	1	30	20	+	37879572	37879710
232554547	chr17	37880940	37881095	37880961	37881074	ERBB2	NM_004448	2	27	20	+	37880979	37881164
232554547	chr17	37880940	37881095	37880961	37881074	ERBB2	NM_001005862	1	30	23	+	37880979	37881164
230413627	chr17	37881499	37881667	37881520	37881644	ERBB2	NM_004448	2	27	22	+	37881580	37881655
230413627	chr17	37881499	37881667	37881520	37881644	ERBB2	NM_001005862	1	30	25	+	37881580	37881655
229974672	chr17	37882069	37882204	37882095	37882180	ERBB2	NM_004448	2	27	23	+	37881960	37882106

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229974672	chr17	37882069	37882204	37882095	37882180	ERBB2	NM_001005862	1	30	26	+	37881960	37882106
229046897	chr17	37883102	37883276	37883121	37883259	ERBB2	NM_004448	2	27	25	+	37883068	37883256
229046897	chr17	37883102	37883276	37883121	37883259	ERBB2	NM_001005862	1	30	28	+	37883068	37883256
231053496	chr17	37883907	37884080	37883929	37884059	ERBB2	NM_004448	2	27	27	+	37883942	37884915
231053496	chr17	37883907	37884080	37883929	37884059	ERBB2	NM_001005862	1	30	30	+	37883942	37884915
242268366	chr17	38487534	38487696	38487554	38487678	RARA	NM_001145302	4	7	2	+	38487109	38487648
242268366	chr17	38487534	38487696	38487554	38487678	RARA	NM_001145301	3	9	2	+	38487109	38487648
242268366	chr17	38487534	38487696	38487554	38487678	RARA	NM_000964	1	9	2	+	38487109	38487648
241611325	chr17	38504636	38504762	38504657	38504738	RARA	NM_001145301	3	9	3	+	38504568	38504716
241611325	chr17	38504636	38504762	38504657	38504738	RARA	NM_000964	1	9	3	+	38504568	38504716
241611325	chr17	38504636	38504762	38504657	38504738	RARA	NM_001024809	2	8	2	+	38504568	38504716
241589297	chr17	38508251	38508422	38508272	38508401	RARA	NM_001145302	4	7	3	+	38508162	38508322
241589297	chr17	38508251	38508422	38508272	38508401	RARA	NM_001145301	3	9	5	+	38508162	38508322
241589297	chr17	38508251	38508422	38508272	38508401	RARA	NM_000964	1	9	5	+	38508162	38508322
241589297	chr17	38508251	38508422	38508272	38508401	RARA	NM_001024809	2	8	4	+	38508162	38508322
240651787	chr17	38510658	38510830	38510677	38510810	RARA	NM_001145302	4	7	5	+	38510554	38510758
240651787	chr17	38510658	38510830	38510677	38510810	RARA	NM_001145301	3	9	7	+	38510554	38510758
240651787	chr17	38510658	38510830	38510677	38510810	RARA	NM_000964	1	9	7	+	38510554	38510758
240651787	chr17	38510658	38510830	38510677	38510810	RARA	NM_001024809	2	8	6	+	38510554	38510758
262518096	chr17	38512333	38512507	38512352	38512488	RARA	NM_001145302	4	7	7	+	38512261	38513895
262518096	chr17	38512333	38512507	38512352	38512488	RARA	NM_001145301	3	9	9	+	38512261	38513895
262518096	chr17	38512333	38512507	38512352	38512488	RARA	NM_000964	1	9	9	+	38512261	38513895
262518096	chr17	38512333	38512507	38512352	38512488	RARA	NM_001024809	2	8	8	+	38512261	38513895
232843682	chr17	41606821	41606976	41606845	41606955	ETV4	NM_001986	2	13	11	-	41606872	41607044
232843682	chr17	41606821	41606976	41606845	41606955	ETV4	NM_001079675	1	13	11	-	41606872	41607044
229759257	chr17	41609927	41610085	41609948	41610063	ETV4	NM_001986	2	13	8	-	41610042	41610307
229759257	chr17	41609927	41610085	41609948	41610063	ETV4	NM_001079675	1	13	8	-	41610042	41610307
230749210	chr17	41610605	41610776	41610628	41610753	ETV4	NM_001986	2	13	7	-	41610555	41610716
230749210	chr17	41610605	41610776	41610628	41610753	ETV4	NM_001079675	1	13	7	-	41610555	41610716
228666460	chr17	41622245	41622416	41622268	41622390	ETV4	NM_001986	2	13	4	-	41622343	41622390
228666460	chr17	41622245	41622416	41622268	41622390	ETV4	NM_001079675	1	13	4	-	41622343	41622390
280395024	chr17	45331255	45331382	45331272	45331363	ITGB3	NM_000212	1	15	1	+	45331208	45331306
278076711	chr17	45361731	45361895	45361757	45361869	ITGB3	NM_000212	1	15	4	+	45361809	45362061
278737289	chr17	45363641	45363812	45363663	45363790	ITGB3	NM_000212	1	15	5	+	45363626	45363788
278973197	chr17	45367066	45367224	45367092	45367202	ITGB3	NM_000212	1	15	7	+	45367047	45367142
279340960	chr17	45369462	45369634	45369482	45369614	ITGB3	NM_000212	1	15	10	+	45369505	45369934
280534854	chr17	45376651	45376819	45376672	45376798	ITGB3	NM_000212	1	15	11	+	45376674	45376896
278742323	chr17	45380094	45380267	45380117	45380245	ITGB3	NM_000212	1	15	13	+	45380087	45380206
253699893	chr17	48262780	48262950	48262802	48262931	COL1A1	NM_000088	1	51	51	-	48261457	48263009
226708043	chr17	48263263	48263422	48263281	48263403	COL1A1	NM_000088	1	51	50	-	48263139	48263381
226582784	chr17	48264074	48264199	48264095	48264178	COL1A1	NM_000088	1	51	48	-	48264001	48264283

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225558661	chr17	48264783	48264932	48264800	48264912	COL1A1	NM_000088	1	51	46	-	48264845	48264898
226255605	chr17	48265869	48266029	48265890	48266008	COL1A1	NM_000088	1	51	43	-	48265891	48265998
226051720	chr17	48266593	48266755	48266614	48266734	COL1A1	NM_000088	1	51	40	-	48266529	48266636
225403221	chr17	48267124	48267297	48267145	48267276	COL1A1	NM_000088	1	51	37	-	48267220	48267273
225947047	chr17	48267842	48267990	48267860	48267971	COL1A1	NM_000088	1	51	34	-	48267904	48267957
225533947	chr17	48268732	48268885	48268758	48268864	COL1A1	NM_000088	1	51	32	-	48268744	48268851
225946458	chr17	48269911	48270082	48269936	48270059	COL1A1	NM_000088	1	51	28	-	48270001	48270054
225840369	chr17	48271403	48271567	48271424	48271545	COL1A1	NM_000088	1	51	24	-	48271491	48271544
226440605	chr17	48272036	48272188	48272054	48272168	COL1A1	NM_000088	1	51	21	-	48272082	48272189
225861948	chr17	48272770	48272897	48272791	48272873	COL1A1	NM_000088	1	51	18	-	48272795	48272839
226504887	chr17	48273579	48273753	48273599	48273729	COL1A1	NM_000088	1	51	14	-	48273675	48273728
225394792	chr17	48274446	48274619	48274470	48274595	COL1A1	NM_000088	1	51	10	-	48274541	48274594
226135563	chr17	48275735	48275894	48275756	48275866	COL1A1	NM_000088	1	51	6	-	48275794	48275865
253668988	chr17	48276971	48277145	48276993	48277128	COL1A1	NM_000088	1	51	2	-	48277114	48277308
227242979	chr17	53342862	53343003	53342880	53342986	HLF	NM_002126	1	4	1	+	53342321	53342960
227382888	chr17	53345357	53345514	53345376	53345492	HLF	NM_002126	1	4	2	+	53345112	53345447
230219976	chr17	53398008	53398180	53398036	53398159	HLF	NM_002126	1	4	4	+	53398025	53402426
223438756	chr17	59760738	59760876	59760767	59760850	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223436026	chr17	59761024	59761148	59761053	59761124	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223462024	chr17	59761398	59761557	59761425	59761529	BRIP1	NM_032043	1	20	20	-	59756547	59761501
222207180	chr17	59763386	59763520	59763415	59763498	BRIP1	NM_032043	1	20	19	-	59763197	59763526
223926967	chr17	59820350	59820476	59820376	59820452	BRIP1	NM_032043	1	20	16	-	59820374	59820495
222407313	chr17	59853641	59853807	59853667	59853785	BRIP1	NM_032043	1	20	14	-	59853762	59853923
222590510	chr17	59858152	59858301	59858175	59858274	BRIP1	NM_032043	1	20	12	-	59858201	59858366
222449983	chr17	59870864	59871028	59870894	59871000	BRIP1	NM_032043	1	20	10	-	59870958	59871090
223936703	chr17	59878563	59878703	59878590	59878677	BRIP1	NM_032043	1	20	8	-	59878614	59878835
223666239	chr17	59885819	59885956	59885845	59885936	BRIP1	NM_032043	1	20	7	-	59885828	59886118
224738509	chr17	59926425	59926599	59926451	59926575	BRIP1	NM_032043	1	20	5	-	59926490	59926617
224408636	chr17	59937069	59937243	59937090	59937219	BRIP1	NM_032043	1	20	3	-	59937157	59937268
226006007	chr17	62006527	62006668	62006547	62006645	CD79B	NM_000626	1	6	6	-	62006098	62006684
226006007	chr17	62006527	62006668	62006547	62006645	CD79B	NM_021602	3	5	5	-	62006098	62006684
226006007	chr17	62006527	62006668	62006547	62006645	CD79B	NM_001039933	2	6	6	-	62006098	62006684
226788499	chr17	62007169	62007314	62007190	62007293	CD79B	NM_000626	1	6	4	-	62007130	62007248
226788499	chr17	62007169	62007314	62007190	62007293	CD79B	NM_021602	3	5	3	-	62007130	62007248
226788499	chr17	62007169	62007314	62007190	62007293	CD79B	NM_001039933	2	6	4	-	62007130	62007248
227081124	chr17	62007665	62007790	62007687	62007770	CD79B	NM_000626	1	6	3	-	62007434	62007745
227081124	chr17	62007665	62007790	62007687	62007770	CD79B	NM_001039933	2	6	3	-	62007434	62007745
236769665	chr17	66511535	66511677	66511557	66511657	PRKAR1A	NM_002734	1	11	2	+	66511535	66511717
236769665	chr17	66511535	66511677	66511557	66511657	PRKAR1A	NM_212472	3	11	2	+	66511535	66511717
236769665	chr17	66511535	66511677	66511557	66511657	PRKAR1A	NM_212471	2	11	2	+	66511535	66511717
236535492	chr17	66519781	66519925	66519807	66519899	PRKAR1A	NM_002734	1	11	4	+	66519866	66519957

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236535492	chr17	66519781	66519925	66519807	66519899	PRKAR1A	NM_212472	3	11	4	+	66519866	66519957
236535492	chr17	66519781	66519925	66519807	66519899	PRKAR1A	NM_212471	2	11	4	+	66519866	66519957
235786133	chr17	66521075	66521199	66521099	66521171	PRKAR1A	NM_002734	1	11	6	+	66521053	66521099
235786133	chr17	66521075	66521199	66521099	66521171	PRKAR1A	NM_212472	3	11	6	+	66521053	66521099
235786133	chr17	66521075	66521199	66521099	66521171	PRKAR1A	NM_212471	2	11	6	+	66521053	66521099
237833750	chr17	66523986	66524111	66524008	66524084	PRKAR1A	NM_002734	1	11	8	+	66523981	66524041
237833750	chr17	66523986	66524111	66524008	66524084	PRKAR1A	NM_212472	3	11	8	+	66523981	66524041
237833750	chr17	66523986	66524111	66524008	66524084	PRKAR1A	NM_212471	2	11	8	+	66523981	66524041
236261891	chr17	66526393	66526567	66526417	66526544	PRKAR1A	NM_002734	1	11	11	+	66526418	66528910
236261891	chr17	66526393	66526567	66526417	66526544	PRKAR1A	NM_212472	3	11	11	+	66526418	66528910
236261891	chr17	66526393	66526567	66526417	66526544	PRKAR1A	NM_212471	2	11	11	+	66526418	66528910
262196327	chr17	75316379	75316512	75316398	75316488	SEPT9	NM_006640	7	11	1	+	75315597	75316430
264715987	chr17	75398260	75398421	75398281	75398401	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264715987	chr17	75398260	75398421	75398281	75398401	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264715987	chr17	75398260	75398421	75398281	75398401	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264715987	chr17	75398260	75398421	75398281	75398401	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264715987	chr17	75398260	75398421	75398281	75398401	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
264702024	chr17	75398681	75398827	75398704	75398805	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264702024	chr17	75398681	75398827	75398704	75398805	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264702024	chr17	75398681	75398827	75398704	75398805	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264702024	chr17	75398681	75398827	75398704	75398805	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264702024	chr17	75398681	75398827	75398704	75398805	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
242643780	chr17	75471848	75472007	75471865	75471988	SEPT9	NM_001113495	5	10	1	+	75471325	75471985
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_006640	7	11	4	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113496	6	10	3	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113495	5	10	3	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113494	4	11	4	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113493	3	11	4	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113492	2	12	5	+	75483506	75483634
264260707	chr17	75483507	75483639	75483524	75483621	SEPT9	NM_001113491	1	12	5	+	75483506	75483634
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_006640	7	11	6	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113496	6	10	5	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113495	5	10	5	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113494	4	11	6	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113493	3	11	6	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113492	2	12	7	+	75484809	75484946
242377525	chr17	75484812	75484975	75484836	75484957	SEPT9	NM_001113491	1	12	7	+	75484809	75484946
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_006640	7	11	9	+	75489062	75489158
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113496	6	10	8	+	75489062	75489158
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113495	5	10	8	+	75489062	75489158
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113494	4	11	9	+	75489062	75489158

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113493	3	11	9	+	75489062	75489158
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113492	2	12	10	+	75489062	75489158
240243667	chr17	75489117	75489275	75489139	75489254	SEPT9	NM_001113491	1	12	10	+	75489062	75489158
295355970	chr17	76210340	76210480	76210360	76210455	BIRC5	NM_001168	3	4	1	+	76210277	76210508
295355970	chr17	76210340	76210480	76210360	76210455	BIRC5	NM_001012271	2	5	1	+	76210277	76210508
295355970	chr17	76210340	76210480	76210360	76210455	BIRC5	NM_001012270	1	3	1	+	76210277	76210508
295410181	chr17	76212771	76212897	76212793	76212872	BIRC5	NM_001168	3	4	3	+	76212745	76212862
295410181	chr17	76212771	76212897	76212793	76212872	BIRC5	NM_001012271	2	5	4	+	76212745	76212862
242366362	chr17	78237478	78237651	78237498	78237630	RNF213	NM_020954	2	17	2	+	78237373	78237577
242366362	chr17	78237478	78237651	78237498	78237630	RNF213	NM_001256071	1	68	2	+	78237373	78237577
263744303	chr17	78261826	78261954	78261843	78261934	RNF213	NM_020954	2	17	4	+	78261614	78262162
263744303	chr17	78261826	78261954	78261843	78261934	RNF213	NM_001256071	1	68	4	+	78261614	78262162
237861943	chr17	78263425	78263554	78263446	78263532	RNF213	NM_020954	2	17	6	+	78263458	78263636
237861943	chr17	78263425	78263554	78263446	78263532	RNF213	NM_001256071	1	68	6	+	78263458	78263636
237821735	chr17	78264398	78264557	78264420	78264535	RNF213	NM_020954	2	17	7	+	78264369	78264527
237821735	chr17	78264398	78264557	78264420	78264535	RNF213	NM_001256071	1	68	7	+	78264369	78264527
241596789	chr17	78268443	78268596	78268466	78268573	RNF213	NM_020954	2	17	9	+	78268519	78268802
241596789	chr17	78268443	78268596	78268466	78268573	RNF213	NM_001256071	1	68	9	+	78268519	78268802
260403479	chr17	78269442	78269592	78269464	78269571	RNF213	NM_020954	2	17	10	+	78269357	78269613
260403479	chr17	78269442	78269592	78269464	78269571	RNF213	NM_001256071	1	68	10	+	78269357	78269613
241616453	chr17	78280017	78280183	78280038	78280155	RNF213	NM_020954	2	17	12	+	78280052	78280268
241616453	chr17	78280017	78280183	78280038	78280155	RNF213	NM_001256071	1	68	12	+	78280052	78280268
261167079	chr17	78282827	78282995	78282848	78282971	RNF213	NM_020954	2	17	14	+	78282818	78282971
261167079	chr17	78282827	78282995	78282848	78282971	RNF213	NM_001256071	1	68	14	+	78282818	78282971
238302713	chr17	78292916	78293067	78292942	78293045	RNF213	NM_001256071	1	68	17	+	78292990	78293112
238302713	chr17	78292916	78293067	78292942	78293045	RNF213	NM_020954	2	17	17	+	78292990	78295262
242068271	chr17	78298867	78299039	78298889	78299018	RNF213	NM_001256071	1	68	18	+	78298830	78298998
238168384	chr17	78302142	78302309	78302164	78302281	RNF213	NM_001256071	1	68	20	+	78302128	78302277
264003670	chr17	78306057	78306222	78306079	78306195	RNF213	NM_001256071	1	68	21	+	78305806	78306431
238611376	chr17	78307946	78308120	78307968	78308094	RNF213	NM_001256071	1	68	22	+	78307905	78308070
240823090	chr17	78311357	78311531	78311377	78311510	RNF213	NM_001256071	1	68	24	+	78311386	78311526
263863699	chr17	78312977	78313146	78312998	78313126	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263859809	chr17	78313469	78313643	78313492	78313623	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263864993	chr17	78313931	78314070	78313953	78314050	RNF213	NM_001256071	1	68	26	+	78313001	78314156
239940055	chr17	78317613	78317787	78317634	78317766	RNF213	NM_001256071	1	68	28	+	78317657	78317815
239053496	chr17	78318605	78318777	78318626	78318752	RNF213	NM_001256071	1	68	29	+	78318478	78322086
238998592	chr17	78319078	78319249	78319101	78319224	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262276465	chr17	78319495	78319666	78319521	78319645	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239032028	chr17	78319998	78320172	78320023	78320148	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262270242	chr17	78320501	78320673	78320522	78320651	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262290081	chr17	78320981	78321136	78321002	78321111	RNF213	NM_001256071	1	68	29	+	78318478	78322086

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262293123	chr17	78321413	78321586	78321435	78321565	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262438602	chr17	78321871	78322039	78321893	78322014	RNF213	NM_001256071	1	68	29	+	78318478	78322086
242671895	chr17	78324007	78324169	78324034	78324142	RNF213	NM_001256071	1	68	31	+	78324101	78324196
241244671	chr17	78327277	78327447	78327299	78327424	RNF213	NM_001256071	1	68	34	+	78327312	78327466
264666529	chr17	78328106	78328279	78328133	78328259	RNF213	NM_001256071	1	68	36	+	78328241	78328376
238007286	chr17	78333779	78333911	78333800	78333888	RNF213	NM_001256071	1	68	38	+	78333861	78334006
242633431	chr17	78336814	78336949	78336840	78336928	RNF213	NM_001256071	1	68	40	+	78336902	78337114
237876672	chr17	78337482	78337627	78337505	78337606	RNF213	NM_001256071	1	68	41	+	78337409	78337590
240917184	chr17	78341799	78341965	78341819	78341941	RNF213	NM_001256071	1	68	44	+	78341761	78341943
238569789	chr17	78343536	78343701	78343559	78343678	RNF213	NM_001256071	1	68	46	+	78343568	78343667
241807793	chr17	78346340	78346513	78346366	78346491	RNF213	NM_001256071	1	68	48	+	78346321	78346534
240520025	chr17	78348146	78348318	78348167	78348296	RNF213	NM_001256071	1	68	50	+	78348258	78348389
238818346	chr17	78350101	78350255	78350125	78350233	RNF213	NM_001256071	1	68	52	+	78350101	78350343
237899254	chr17	78353376	78353544	78353397	78353516	RNF213	NM_001256071	1	68	55	+	78353420	78353514
240241497	chr17	78355393	78355546	78355412	78355527	RNF213	NM_001256071	1	68	57	+	78355347	78355527
263521408	chr17	78357598	78357751	78357619	78357729	RNF213	NM_001256071	1	68	59	+	78357477	78357728
239456244	chr17	78360023	78360194	78360047	78360167	RNF213	NM_001256071	1	68	62	+	78360050	78360230
241971098	chr17	78360613	78360745	78360634	78360723	RNF213	NM_001256071	1	68	63	+	78360490	78360691
242479542	chr17	78363489	78363662	78363514	78363638	RNF213	NM_001256071	1	68	66	+	78363628	78363717
240942888	chr17	78367097	78367233	78367119	78367208	RNF213	NM_001256071	1	68	68	+	78367145	78372581
265810330	chr18	22642606	22642780	22642631	22642753	ZNF521	NM_015461	1	8	8	-	22641888	22642705
238449326	chr18	22671906	22672074	22671928	22672046	ZNF521	NM_015461	1	8	6	-	22671914	22672045
241253947	chr18	22804390	22804528	22804410	22804505	ZNF521	NM_015461	1	8	4	-	22804309	22807661
264989434	chr18	22804829	22804978	22804852	22804951	ZNF521	NM_015461	1	8	4	-	22804309	22807661
264984139	chr18	22805263	22805433	22805284	22805411	ZNF521	NM_015461	1	8	4	-	22804309	22807661
264968415	chr18	22805714	22805878	22805737	22805856	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265124832	chr18	22806175	22806321	22806203	22806299	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265100247	chr18	22806568	22806707	22806592	22806686	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265066688	chr18	22806996	22807169	22807017	22807146	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241270596	chr18	22807496	22807665	22807519	22807642	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241906883	chr18	22930811	22930967	22930831	22930939	ZNF521	NM_015461	1	8	2	-	22930871	22930911
271275509	chr18	25543254	25543428	25543282	25543407	CDH2	NM_001792	1	16	15	-	25543321	25543485
272096492	chr18	25562999	25563162	25563020	25563134	CDH2	NM_001792	1	16	14	-	25562908	25563047
270762726	chr18	25565499	25565670	25565528	25565649	CDH2	NM_001792	1	16	12	-	25565492	25565725
270740003	chr18	25568547	25568715	25568575	25568691	CDH2	NM_001792	1	16	11	-	25568488	25568630
271419571	chr18	25572580	25572719	25572601	25572696	CDH2	NM_001792	1	16	9	-	25572619	25572804
272174775	chr18	25582859	25583032	25582886	25583004	CDH2	NM_001792	1	16	7	-	25582961	25583133
270879938	chr18	25585814	25585958	25585835	25585933	CDH2	NM_001792	1	16	6	-	25585813	25585957
270525592	chr18	25591779	25591913	25591808	25591893	CDH2	NM_001792	1	16	4	-	25591810	25591956
271254283	chr18	25727575	25727700	25727601	25727674	CDH2	NM_001792	1	16	2	-	25727637	25727748
272421659	chr18	45368227	45368373	45368253	45368346	SMAD2	NM_005901	3	11	11	-	45359466	45368321

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272421659	chr18	45368227	45368373	45368253	45368346	SMAD2	NM_001135937	2	10	10	-	45359466	45368321
272421659	chr18	45368227	45368373	45368253	45368346	SMAD2	NM_001003652	1	11	11	-	45359466	45368321
270008618	chr18	45371973	45372137	45372001	45372113	SMAD2	NM_005901	3	11	9	-	45372034	45372171
270008618	chr18	45371973	45372137	45372001	45372113	SMAD2	NM_001135937	2	10	8	-	45372034	45372171
270008618	chr18	45371973	45372137	45372001	45372113	SMAD2	NM_001003652	1	11	9	-	45372034	45372171
271255197	chr18	45374974	45375119	45375002	45375096	SMAD2	NM_005901	3	11	8	-	45374846	45375058
271255197	chr18	45374974	45375119	45375002	45375096	SMAD2	NM_001135937	2	10	7	-	45374846	45375058
271255197	chr18	45374974	45375119	45375002	45375096	SMAD2	NM_001003652	1	11	8	-	45374846	45375058
270523442	chr18	45391429	45391555	45391456	45391530	SMAD2	NM_005901	3	11	6	-	45391430	45391504
270523442	chr18	45391429	45391555	45391456	45391530	SMAD2	NM_001135937	2	10	5	-	45391430	45391504
270523442	chr18	45391429	45391555	45391456	45391530	SMAD2	NM_001003652	1	11	6	-	45391430	45391504
272556344	chr18	45395595	45395733	45395621	45395711	SMAD2	NM_005901	3	11	4	-	45395614	45395807
272556344	chr18	45395595	45395733	45395621	45395711	SMAD2	NM_001135937	2	10	3	-	45395614	45395807
272556344	chr18	45395595	45395733	45395621	45395711	SMAD2	NM_001003652	1	11	4	-	45395614	45395807
269506531	chr18	45422983	45423149	45423008	45423127	SMAD2	NM_005901	3	11	2	-	45422892	45423180
269506531	chr18	45422983	45423149	45423008	45423127	SMAD2	NM_001135937	2	10	2	-	45422892	45423180
269506531	chr18	45422983	45423149	45423008	45423127	SMAD2	NM_001003652	1	11	2	-	45422892	45423180
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_015846	13	17	15	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204137	2	17	16	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204136	1	16	15	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_015845	12	14	13	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_015844	11	16	14	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_015847	14	16	14	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204151	9	13	12	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_002384	10	15	13	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204141	6	15	14	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204140	5	16	15	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204139	4	17	15	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204138	3	17	16	-	47799047	47799108
312365709	chr18	47798968	47799142	47798992	47799114	MBD1	NM_001204143	8	14	13	-	47799047	47799108
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204138	3	17	13	-	47799934	47800230
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_015846	13	17	12	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204137	2	17	13	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204136	1	16	12	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_015845	12	14	11	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_015844	11	16	11	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_015847	14	16	11	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204151	9	13	10	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_002384	10	15	11	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204142	7	14	12	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204141	6	15	11	-	47799934	47800233

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204140	5	16	12	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204139	4	17	12	-	47799934	47800233
312406888	chr18	47799850	47800019	47799871	47799995	MBD1	NM_001204143	8	14	11	-	47799934	47800233
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_015846	13	17	11	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204137	2	17	12	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204136	1	16	11	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_015845	12	14	10	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_015847	14	16	10	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204151	9	13	9	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204142	7	14	11	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204139	4	17	11	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204138	3	17	12	-	47800556	47800723
312177014	chr18	47800624	47800794	47800643	47800772	MBD1	NM_001204141	6	15	10	-	47800556	47800720
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_015846	13	17	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204137	2	17	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204136	1	16	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_015845	12	14	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_015844	11	16	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_015847	14	16	7	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204151	9	13	7	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_002384	10	15	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204142	7	14	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204141	6	15	7	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204140	5	16	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204139	4	17	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204138	3	17	8	-	47801970	47802098
312168705	chr18	47801936	47802098	47801956	47802080	MBD1	NM_001204143	8	14	8	-	47801970	47802098
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_015846	13	17	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204137	2	17	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204136	1	16	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_015845	12	14	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_015844	11	16	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_015847	14	16	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204151	9	13	5	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_002384	10	15	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204142	7	14	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204141	6	15	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204140	5	16	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204139	4	17	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204138	3	17	6	-	47802748	47802788
312193992	chr18	47802647	47802820	47802669	47802795	MBD1	NM_001204143	8	14	6	-	47802748	47802788

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_015846	13	17	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204137	2	17	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204136	1	16	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_015845	12	14	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_015844	11	16	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_015847	14	16	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204151	9	13	2	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_002384	10	15	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204142	7	14	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204141	6	15	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204140	5	16	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204139	4	17	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204138	3	17	3	-	47803460	47803574
312246490	chr18	47803433	47803600	47803458	47803579	MBD1	NM_001204143	8	14	3	-	47803460	47803574
260824106	chr18	48573541	48573710	48573569	48573684	SMAD4	NM_005359	1	12	2	+	48573290	48573665
263540385	chr18	48575663	48575787	48575689	48575770	SMAD4	NM_005359	1	12	4	+	48575665	48575694
238080927	chr18	48584542	48584715	48584563	48584689	SMAD4	NM_005359	1	12	6	+	48584495	48584614
326808236	chr18	48591713	48591840	48591736	48591813	SMAD4	NM_005359	1	12	9	+	48591793	48591976
239080634	chr18	48593460	48593630	48593480	48593602	SMAD4	NM_005359	1	12	10	+	48593389	48593557
261679091	chr18	48604710	48604862	48604733	48604841	SMAD4	NM_005359	1	12	12	+	48604626	48611411
287200216	chr18	50278522	50278655	50278541	50278628	DCC	NM_005215	1	29	2	+	50278424	50278744
286142091	chr18	50432579	50432722	50432600	50432698	DCC	NM_005215	1	29	3	+	50432414	50432698
288222684	chr18	50451611	50451772	50451639	50451743	DCC	NM_005215	1	29	5	+	50451604	50451740
286206233	chr18	50592410	50592562	50592432	50592540	DCC	NM_005215	1	29	7	+	50592416	50592536
286793761	chr18	50705371	50705509	50705393	50705487	DCC	NM_005215	1	29	9	+	50705332	50705486
288786430	chr18	50734142	50734296	50734165	50734270	DCC	NM_005215	1	29	11	+	50734049	50734187
287339526	chr18	50848326	50848474	50848353	50848451	DCC	NM_005215	1	29	14	+	50848417	50848527
286521196	chr18	50866241	50866376	50866265	50866351	DCC	NM_005215	1	29	15	+	50866083	50866277
286290648	chr18	50918035	50918205	50918064	50918185	DCC	NM_005215	1	29	17	+	50918025	50918257
285699181	chr18	50929113	50929287	50929138	50929263	DCC	NM_005215	1	29	19	+	50929156	50929263
285149030	chr18	50942415	50942552	50942442	50942526	DCC	NM_005215	1	29	21	+	50942494	50942526
287023544	chr18	50985548	50985722	50985573	50985694	DCC	NM_005215	1	29	24	+	50985602	50985828
286055295	chr18	51013038	51013211	51013065	51013190	DCC	NM_005215	1	29	26	+	51013167	51013328
286808758	chr18	51025667	51025834	51025689	51025811	DCC	NM_005215	1	29	27	+	51025668	51025880
287700691	chr18	51056898	51057056	51056927	51057028	DCC	NM_005215	1	29	29	+	51056934	51062273
231480141	chr18	56348325	56348499	56348349	56348477	MALT1	NM_173844	2	16	2	+	56348402	56348568
231480141	chr18	56348325	56348499	56348349	56348477	MALT1	NM_006785	1	17	2	+	56348402	56348568
231397117	chr18	56367727	56367864	56367751	56367842	MALT1	NM_173844	2	16	4	+	56367673	56367823
231397117	chr18	56367727	56367864	56367751	56367842	MALT1	NM_006785	1	17	4	+	56367673	56367823
233852334	chr18	56377155	56377285	56377183	56377257	MALT1	NM_173844	2	16	6	+	56377208	56377304
233852334	chr18	56377155	56377285	56377183	56377257	MALT1	NM_006785	1	17	6	+	56377208	56377304

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231188508	chr18	56383065	56383227	56383093	56383196	MALT1	NM_173844	2	16	8	+	56383167	56383199
231188508	chr18	56383065	56383227	56383093	56383196	MALT1	NM_006785	1	17	9	+	56383167	56383199
232175072	chr18	56390430	56390601	56390452	56390573	MALT1	NM_173844	2	16	9	+	56390280	56390483
232175072	chr18	56390430	56390601	56390452	56390573	MALT1	NM_006785	1	17	10	+	56390280	56390483
232792481	chr18	56402433	56402606	56402455	56402578	MALT1	NM_173844	2	16	12	+	56402434	56402561
232792481	chr18	56402433	56402606	56402455	56402578	MALT1	NM_006785	1	17	13	+	56402434	56402561
232289819	chr18	56411518	56411688	56411544	56411659	MALT1	NM_173844	2	16	14	+	56411570	56411727
232289819	chr18	56411518	56411688	56411544	56411659	MALT1	NM_006785	1	17	15	+	56411570	56411727
232715112	chr18	56414555	56414723	56414582	56414700	MALT1	NM_173844	2	16	16	+	56414637	56417370
232715112	chr18	56414555	56414723	56414582	56414700	MALT1	NM_006785	1	17	17	+	56414637	56417370
232758223	chr18	56414970	56415130	56414992	56415104	MALT1	NM_173844	2	16	16	+	56414637	56417370
232758223	chr18	56414970	56415130	56414992	56415104	MALT1	NM_006785	1	17	17	+	56414637	56417370
271931166	chr18	59166395	59166535	59166418	59166514	CDH20	NM_031891	1	11	2	+	59166419	59166713
271294219	chr18	59167676	59167806	59167697	59167778	CDH20	NM_031891	1	11	3	+	59167616	59167735
270183689	chr18	59174682	59174833	59174706	59174809	CDH20	NM_031891	1	11	5	+	59174606	59174793
270261792	chr18	59203635	59203788	59203661	59203760	CDH20	NM_031891	1	11	7	+	59203726	59203862
271021889	chr18	59212229	59212401	59212253	59212377	CDH20	NM_031891	1	11	9	+	59212260	59212377
272632729	chr18	59221500	59221670	59221520	59221652	CDH20	NM_031891	1	11	11	+	59221423	59222365
223158968	chr18	60795773	60795947	60795800	60795924	BCL2	NM_000633	1	3	3	-	60790579	60795992
222785067	chr18	60985414	60985570	60985434	60985551	BCL2	NM_000633	1	3	2	-	60985315	60986185
222785067	chr18	60985414	60985570	60985434	60985551	BCL2	NM_000657	2	2	2	-	60985187	60986185
224520324	chr18	60985823	60985995	60985848	60985966	BCL2	NM_000633	1	3	2	-	60985315	60986185
224520324	chr18	60985823	60985995	60985848	60985966	BCL2	NM_000657	2	2	2	-	60985187	60986185
261810639	chr19	1206821	1206994	1206846	1206972	STK11	NM_000455	1	10	1	+	1205798	1207202
238833563	chr19	1218461	1218613	1218485	1218592	STK11	NM_000455	1	10	2	+	1218416	1218499
237777336	chr19	1220368	1220522	1220391	1220504	STK11	NM_000455	1	10	4	+	1220372	1220504
238659833	chr19	1221265	1221407	1221287	1221383	STK11	NM_000455	1	10	6	+	1221212	1221339
264076303	chr19	1222993	1223166	1223015	1223144	STK11	NM_000455	1	10	8	+	1222984	1223171
240472739	chr19	1226537	1226708	1226556	1226690	STK11	NM_000455	1	10	9	+	1226453	1226662
239993724	chr19	1612267	1612416	1612285	1612395	TCF3	NM_001136139	1	19	17	-	1612206	1612432
240585439	chr19	1615390	1615564	1615411	1615544	TCF3	NM_003200	2	19	18	-	1615284	1615519
241559951	chr19	1619245	1619401	1619262	1619384	TCF3	NM_001136139	1	19	14	-	1619315	1619473
241559951	chr19	1619245	1619401	1619262	1619384	TCF3	NM_003200	2	19	15	-	1619315	1619473
262296591	chr19	1620883	1621036	1620904	1621012	TCF3	NM_001136139	1	19	12	-	1620967	1621045
262296591	chr19	1620883	1621036	1620904	1621012	TCF3	NM_003200	2	19	13	-	1620967	1621045
262587464	chr19	1621908	1622068	1621930	1622049	TCF3	NM_001136139	1	19	10	-	1621837	1621969
262587464	chr19	1621908	1622068	1621930	1622049	TCF3	NM_003200	2	19	11	-	1621837	1621969
263842989	chr19	1622304	1622467	1622326	1622449	TCF3	NM_001136139	1	19	8	-	1622312	1622414
263842989	chr19	1622304	1622467	1622326	1622449	TCF3	NM_003200	2	19	9	-	1622312	1622414
239969009	chr19	1627293	1627451	1627314	1627428	TCF3	NM_001136139	1	19	5	-	1627358	1627425
239969009	chr19	1627293	1627451	1627314	1627428	TCF3	NM_003200	2	19	6	-	1627358	1627425

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264388649	chr19	1646349	1646497	1646370	1646477	TCF3	NM_001136139	1	19	2	-	1646354	1646426
264388649	chr19	1646349	1646497	1646370	1646477	TCF3	NM_003200	2	19	3	-	1646354	1646426
274027526	chr19	3110165	3110337	3110187	3110316	GNA11	NM_002067	1	7	2	+	3110147	3110331
272792761	chr19	3114837	3114986	3114855	3114968	GNA11	NM_002067	1	7	4	+	3114942	3115070
272743168	chr19	3119172	3119334	3119193	3119314	GNA11	NM_002067	1	7	6	+	3119204	3119357
299241622	chr19	3522918	3523052	3522936	3523029	FZR1	NM_016263	3	14	2	+	3522954	3523056
299241622	chr19	3522918	3523052	3522936	3523029	FZR1	NM_001136197	1	11	1	+	3522954	3523056
299241622	chr19	3522918	3523052	3522936	3523029	FZR1	NM_001136198	2	13	1	+	3522954	3523056
299045348	chr19	3526057	3526200	3526075	3526181	FZR1	NM_016263	3	14	4	+	3526118	3526181
299045348	chr19	3526057	3526200	3526075	3526181	FZR1	NM_001136197	1	11	3	+	3526118	3526181
299045348	chr19	3526057	3526200	3526075	3526181	FZR1	NM_001136198	2	13	3	+	3526118	3526181
298959678	chr19	3527705	3527878	3527726	3527857	FZR1	NM_016263	3	14	7	+	3527629	3527812
298959678	chr19	3527705	3527878	3527726	3527857	FZR1	NM_001136198	2	13	6	+	3527629	3527812
299086650	chr19	3531920	3532069	3531940	3532051	FZR1	NM_016263	3	14	10	+	3531909	3532093
299086650	chr19	3531920	3532069	3531940	3532051	FZR1	NM_001136197	1	11	7	+	3531909	3532093
299086650	chr19	3531920	3532069	3531940	3532051	FZR1	NM_001136198	2	13	9	+	3531909	3532093
299042838	chr19	3532541	3532691	3532560	3532673	FZR1	NM_016263	3	14	11	+	3532415	3532648
299042838	chr19	3532541	3532691	3532560	3532673	FZR1	NM_001136197	1	11	8	+	3532415	3532648
299042838	chr19	3532541	3532691	3532560	3532673	FZR1	NM_001136198	2	13	10	+	3532415	3532648
269622083	chr19	4090585	4090731	4090602	4090713	MAP2K2	NM_030662	1	11	11	-	4090320	4090706
270272653	chr19	4099164	4099335	4099182	4099316	MAP2K2	NM_030662	1	11	7	-	4099199	4099412
271185540	chr19	4101124	4101265	4101145	4101246	MAP2K2	NM_030662	1	11	5	-	4101227	4101278
269769478	chr19	4110553	4110717	4110573	4110696	MAP2K2	NM_030662	1	11	3	-	4110507	4110653
270693045	chr19	4123763	4123922	4123780	4123905	MAP2K2	NM_030662	1	11	1	-	4123781	4124126
294388462	chr19	10599933	10600067	10599954	10600045	KEAP1	NM_012289	1	6	5	-	10599868	10600044
294388462	chr19	10599933	10600067	10599954	10600045	KEAP1	NM_203500	2	6	5	-	10599868	10600044
294562536	chr19	10602182	10602352	10602203	10602335	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294562536	chr19	10602182	10602352	10602203	10602335	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294568934	chr19	10602658	10602831	10602681	10602808	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294568934	chr19	10602658	10602831	10602681	10602808	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294870462	chr19	10610112	10610273	10610133	10610253	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294870462	chr19	10610112	10610273	10610133	10610253	KEAP1	NM_203500	2	6	2	-	10610071	10610756
294866475	chr19	10610599	10610744	10610620	10610723	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294866475	chr19	10610599	10610744	10610620	10610723	KEAP1	NM_203500	2	6	2	-	10610071	10610756
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128844	1	36	4	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_003072	7	35	3	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128845	2	33	2	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128849	6	36	3	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128847	4	33	2	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128846	3	33	2	+	11095949	11096081
238471614	chr19	11095897	11096021	11095916	11095999	SMARCA4	NM_001128848	5	33	2	+	11095949	11096081

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128844	1	36	5	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_003072	7	35	4	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128845	2	33	3	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128849	6	36	4	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128847	4	33	3	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128846	3	33	3	+	11096865	11097269
260488279	chr19	11097042	11097195	11097064	11097178	SMARCA4	NM_001128848	5	33	3	+	11096865	11097269
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128844	1	36	7	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_003072	7	35	6	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128845	2	33	5	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128849	6	36	6	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128847	4	33	5	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128846	3	33	5	+	11098342	11098600
240433430	chr19	11098372	11098541	11098392	11098523	SMARCA4	NM_001128848	5	33	5	+	11098342	11098600
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128844	1	36	8	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_003072	7	35	7	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128845	2	33	6	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128849	6	36	7	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128847	4	33	6	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128846	3	33	6	+	11099993	11100119
263378136	chr19	11100004	11100176	11100024	11100155	SMARCA4	NM_001128848	5	33	6	+	11099993	11100119
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128844	1	36	10	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_003072	7	35	9	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128845	2	33	8	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128849	6	36	9	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128847	4	33	8	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128846	3	33	8	+	11105504	11105677
240083789	chr19	11105545	11105713	11105569	11105692	SMARCA4	NM_001128848	5	33	8	+	11105504	11105677
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128844	1	36	13	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_003072	7	35	12	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128845	2	33	11	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128849	6	36	12	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128847	4	33	11	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128846	3	33	11	+	11113705	11113835
240332954	chr19	11113586	11113730	11113609	11113710	SMARCA4	NM_001128848	5	33	11	+	11113705	11113835
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128844	1	36	16	+	11121057	11121207
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_003072	7	35	15	+	11121057	11121207
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128845	2	33	14	+	11121057	11121207
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128849	6	36	15	+	11121057	11121207
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128847	4	33	14	+	11121057	11121207
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128846	3	33	14	+	11121057	11121207

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
260341866	chr19	11120994	11121161	11121016	11121140	SMARCA4	NM_001128848	5	33	14	+	11121057	11121207
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128844	1	36	18	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_003072	7	35	17	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128845	2	33	16	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128849	6	36	17	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128847	4	33	16	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128846	3	33	16	+	11129633	11129699
238598915	chr19	11129563	11129736	11129584	11129713	SMARCA4	NM_001128848	5	33	16	+	11129633	11129699
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128844	1	36	20	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_003072	7	35	19	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128845	2	33	18	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128849	6	36	19	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128847	4	33	18	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128846	3	33	18	+	11132401	11132643
261103039	chr19	11132568	11132723	11132589	11132704	SMARCA4	NM_001128848	5	33	18	+	11132401	11132643
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128844	1	36	23	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_003072	7	35	22	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128845	2	33	21	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128849	6	36	22	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128847	4	33	21	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128846	3	33	21	+	11136098	11136184
241272058	chr19	11136068	11136240	11136089	11136220	SMARCA4	NM_001128848	5	33	21	+	11136098	11136184
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128844	1	36	26	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_003072	7	35	25	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128845	2	33	24	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128849	6	36	25	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128847	4	33	24	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128846	3	33	24	+	11141406	11141569
238538521	chr19	11141327	11141486	11141348	11141461	SMARCA4	NM_001128848	5	33	24	+	11141406	11141569
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128844	1	36	29	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_003072	7	35	28	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128845	2	33	26	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128849	6	36	28	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128847	4	33	26	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128846	3	33	26	+	11144799	11144876
241607470	chr19	11144772	11144922	11144792	11144902	SMARCA4	NM_001128848	5	33	26	+	11144799	11144876
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128844	1	36	31	+	11151983	11152236
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_003072	7	35	30	+	11151983	11152236
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128849	6	36	31	+	11151983	11152236
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128847	4	33	28	+	11151983	11152236
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128848	5	33	28	+	11151983	11152236

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128845	2	33	28	+	11151974	11152236
238852418	chr19	11152026	11152190	11152049	11152170	SMARCA4	NM_001128846	3	33	28	+	11151974	11152236
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128844	1	36	33	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_003072	7	35	32	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128845	2	33	30	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128849	6	36	33	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128847	4	33	30	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128846	3	33	30	+	11169464	11169565
242340127	chr19	11169508	11169679	11169528	11169659	SMARCA4	NM_001128848	5	33	30	+	11169464	11169565
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128844	1	36	35	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_003072	7	35	34	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128845	2	33	32	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128849	6	36	35	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128847	4	33	32	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128846	3	33	32	+	11170721	11170863
237940525	chr19	11170738	11170872	11170758	11170854	SMARCA4	NM_001128848	5	33	32	+	11170721	11170863
234654725	chr19	17937663	17937793	17937682	17937769	JAK3	NM_000215	1	24	24	-	17935593	17937719
232649356	chr19	17942026	17942154	17942046	17942135	JAK3	NM_000215	1	24	21	-	17942037	17942209
231822479	chr19	17943253	17943411	17943275	17943391	JAK3	NM_000215	1	24	19	-	17943328	17943517
232258477	chr19	17945324	17945449	17945346	17945430	JAK3	NM_000215	1	24	17	-	17945380	17945530
233168924	chr19	17945870	17946043	17945890	17946024	JAK3	NM_000215	1	24	15	-	17945892	17946024
232670808	chr19	17948719	17948892	17948740	17948872	JAK3	NM_000215	1	24	12	-	17948741	17948872
230898405	chr19	17951018	17951190	17951038	17951169	JAK3	NM_000215	1	24	9	-	17951039	17951150
232178011	chr19	17952439	17952596	17952462	17952576	JAK3	NM_000215	1	24	7	-	17952449	17952571
233109699	chr19	17953346	17953502	17953364	17953481	JAK3	NM_000215	1	24	6	-	17953125	17953419
234208648	chr19	17954238	17954373	17954258	17954353	JAK3	NM_000215	1	24	4	-	17954189	17954300
233382101	chr19	17955157	17955304	17955176	17955283	JAK3	NM_000215	1	24	2	-	17955043	17955239
294964282	chr19	18266882	18267028	18266899	18267011	PIK3R2	NM_005027	1	16	2	+	18266267	18267011
294191398	chr19	18271767	18271930	18271785	18271908	PIK3R2	NM_005027	1	16	5	+	18271864	18271995
294032303	chr19	18273085	18273219	18273106	18273198	PIK3R2	NM_005027	1	16	8	+	18273012	18273120
293941029	chr19	18274034	18274190	18274055	18274165	PIK3R2	NM_005027	1	16	11	+	18274073	18274198
294429227	chr19	18277893	18278052	18277917	18278030	PIK3R2	NM_005027	1	16	13	+	18277940	18278116
295219107	chr19	18279869	18280043	18279887	18280026	PIK3R2	NM_005027	1	16	16	+	18279897	18281343
225460613	chr19	18854849	18854977	18854866	18854954	CRTC1	NM_001098482	1	15	3	+	18854918	18854965
253781081	chr19	18857838	18858010	18857858	18857986	CRTC1	NM_015321	2	14	4	+	18857863	18857924
253781081	chr19	18857838	18858010	18857858	18857986	CRTC1	NM_001098482	1	15	5	+	18857863	18857924
225964544	chr19	18870335	18870489	18870358	18870465	CRTC1	NM_015321	2	14	7	+	18870361	18870401
225964544	chr19	18870335	18870489	18870358	18870465	CRTC1	NM_001098482	1	15	8	+	18870361	18870401
226132778	chr19	18876311	18876470	18876328	18876444	CRTC1	NM_015321	2	14	9	+	18876214	18876338
226132778	chr19	18876311	18876470	18876328	18876444	CRTC1	NM_001098482	1	15	10	+	18876214	18876338
226136019	chr19	18882261	18882411	18882280	18882390	CRTC1	NM_015321	2	14	11	+	18882252	18882356

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226136019	chr19	18882261	18882411	18882280	18882390	CRTC1	NM_001098482	1	15	12	+	18882252	18882356
226273120	chr19	18886602	18886757	18886622	18886736	CRTC1	NM_015321	2	14	13	+	18886451	18886631
226273120	chr19	18886602	18886757	18886622	18886736	CRTC1	NM_001098482	1	15	14	+	18886451	18886631
269842266	chr19	30303476	30303634	30303493	30303617	CCNE1	NM_001238	1	12	3	+	30303596	30303683
269763311	chr19	30307954	30308126	30307980	30308104	CCNE1	NM_001238	1	12	5	+	30308044	30308189
269959599	chr19	30311617	30311760	30311644	30311733	CCNE1	NM_001238	1	12	7	+	30311609	30311755
269585806	chr19	30312913	30313058	30312935	30313037	CCNE1	NM_001238	1	12	9	+	30312903	30313037
271980735	chr19	30314494	30314618	30314518	30314593	CCNE1	NM_001238	1	12	12	+	30314562	30315215
226692613	chr19	33792347	33792502	33792365	33792484	CEBPA	NM_004364	1	1	1	-	33790840	33793430
225391692	chr19	33793107	33793281	33793124	33793263	CEBPA	NM_004364	1	1	1	-	33790840	33793430
223020999	chr19	40740973	40741124	40740995	40741104	AKT2	NM_001626	3	14	13	-	40740952	40741054
223020999	chr19	40740973	40741124	40740995	40741104	AKT2	NM_001243028	2	13	12	-	40740952	40741054
223020999	chr19	40740973	40741124	40740995	40741104	AKT2	NM_001243027	1	14	13	-	40740952	40741054
223748019	chr19	40741787	40741912	40741805	40741895	AKT2	NM_001626	3	14	11	-	40741797	40742011
223748019	chr19	40741787	40741912	40741805	40741895	AKT2	NM_001243028	2	13	10	-	40741797	40742011
223748019	chr19	40741787	40741912	40741805	40741895	AKT2	NM_001243027	1	14	11	-	40741797	40742011
222507991	chr19	40743857	40744000	40743875	40743980	AKT2	NM_001626	3	14	9	-	40743876	40743998
222507991	chr19	40743857	40744000	40743875	40743980	AKT2	NM_001243028	2	13	8	-	40743876	40743998
222507991	chr19	40743857	40744000	40743875	40743980	AKT2	NM_001243027	1	14	9	-	40743876	40743998
223559776	chr19	40747816	40747979	40747833	40747953	AKT2	NM_001626	3	14	6	-	40747845	40747976
223559776	chr19	40747816	40747979	40747833	40747953	AKT2	NM_001243028	2	13	5	-	40747845	40747976
223559776	chr19	40747816	40747979	40747833	40747953	AKT2	NM_001243027	1	14	6	-	40747845	40747976
223333005	chr19	40760979	40761105	40761002	40761084	AKT2	NM_001626	3	14	4	-	40761065	40761176
223333005	chr19	40760979	40761105	40761002	40761084	AKT2	NM_001243028	2	13	3	-	40761065	40761176
223333005	chr19	40760979	40761105	40761002	40761084	AKT2	NM_001243027	1	14	4	-	40761065	40761176
283296944	chr19	41725259	41725401	41725278	41725383	AXL	NM_021913	2	20	1	+	41725108	41725382
283296944	chr19	41725259	41725401	41725278	41725383	AXL	NM_001699	1	19	1	+	41725108	41725382
282905757	chr19	41726959	41727117	41726980	41727095	AXL	NM_021913	2	20	3	+	41727051	41727151
282905757	chr19	41726959	41727117	41726980	41727095	AXL	NM_001699	1	19	3	+	41727051	41727151
285719579	chr19	41736836	41736972	41736860	41736952	AXL	NM_021913	2	20	5	+	41736872	41736952
285719579	chr19	41736836	41736972	41736860	41736952	AXL	NM_001699	1	19	5	+	41736872	41736952
281790449	chr19	41744299	41744445	41744319	41744425	AXL	NM_021913	2	20	8	+	41744375	41744514
281790449	chr19	41744299	41744445	41744319	41744425	AXL	NM_001699	1	19	8	+	41744375	41744514
285282790	chr19	41745548	41745706	41745570	41745683	AXL	NM_021913	2	20	10	+	41745599	41745625
281576991	chr19	41749515	41749672	41749537	41749647	AXL	NM_021913	2	20	12	+	41749521	41749612
281576991	chr19	41749515	41749672	41749537	41749647	AXL	NM_001699	1	19	11	+	41749521	41749612
282036821	chr19	41758720	41758894	41758739	41758870	AXL	NM_021913	2	20	16	+	41758751	41758872
282036821	chr19	41758720	41758894	41758739	41758870	AXL	NM_001699	1	19	15	+	41758751	41758872
283332949	chr19	41762439	41762586	41762459	41762565	AXL	NM_021913	2	20	18	+	41762357	41762516
283332949	chr19	41762439	41762586	41762459	41762565	AXL	NM_001699	1	19	17	+	41762357	41762516
284496531	chr19	41765565	41765724	41765587	41765704	AXL	NM_021913	2	20	20	+	41765458	41767671

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
284496531	chr19	41765565	41765724	41765587	41765704	AXL	NM_001699	1	19	19	+	41765458	41767671
225844212	chr19	42383122	42383282	42383142	42383259	CD79A	NM_021601	2	5	2	+	42383060	42383245
225844212	chr19	42383122	42383282	42383142	42383259	CD79A	NM_001783	1	5	2	+	42383060	42383359
225633463	chr19	42384904	42385031	42384925	42385008	CD79A	NM_001783	1	5	5	+	42384934	42385439
225633463	chr19	42384904	42385031	42384925	42385008	CD79A	NM_021601	2	5	5	+	42384934	42385439
226649626	chr19	42790957	42791118	42790978	42791101	CIC	NM_015125	1	20	2	+	42790923	42791072
225730148	chr19	42791433	42791591	42791453	42791571	CIC	NM_015125	1	20	4	+	42791472	42791601
226402406	chr19	42791879	42792034	42791899	42792013	CIC	NM_015125	1	20	6	+	42791962	42792127
226133769	chr19	42793122	42793249	42793143	42793228	CIC	NM_015125	1	20	7	+	42793040	42793242
225620375	chr19	42793463	42793597	42793483	42793578	CIC	NM_015125	1	20	8	+	42793333	42793558
225867637	chr19	42794557	42794707	42794576	42794686	CIC	NM_015125	1	20	10	+	42794385	42795618
225869286	chr19	42794950	42795124	42794968	42795101	CIC	NM_015125	1	20	10	+	42794385	42795618
225869334	chr19	42795380	42795547	42795400	42795527	CIC	NM_015125	1	20	10	+	42794385	42795618
226253923	chr19	42796215	42796382	42796235	42796359	CIC	NM_015125	1	20	12	+	42796238	42796359
253710778	chr19	42796800	42796943	42796818	42796924	CIC	NM_015125	1	20	14	+	42796718	42797011
226103170	chr19	42797272	42797440	42797291	42797421	CIC	NM_015125	1	20	15	+	42797108	42797433
227047681	chr19	42797959	42798104	42797983	42798084	CIC	NM_015125	1	20	16	+	42797744	42797988
226165378	chr19	42798409	42798547	42798428	42798523	CIC	NM_015125	1	20	18	+	42798325	42798456
253756551	chr19	42799309	42799433	42799326	42799411	CIC	NM_015125	1	20	20	+	42798976	42799949
222718976	chr19	45259435	45259606	45259457	45259589	BCL3	NM_005178	1	9	3	+	45259489	45259597
223262160	chr19	45260443	45260576	45260460	45260557	BCL3	NM_005178	1	9	4	+	45260274	45260478
222727421	chr19	45261368	45261535	45261388	45261515	BCL3	NM_005178	1	9	7	+	45261503	45261670
224629092	chr19	45262660	45262801	45262682	45262783	BCL3	NM_005178	1	9	9	+	45262685	45263301
293566702	chr19	45766324	45766497	45766342	45766479	MARK4	NM_031417	2	18	3	+	45766371	45766424
293566702	chr19	45766324	45766497	45766342	45766479	MARK4	NM_001199867	1	17	3	+	45766371	45766424
290599412	chr19	45767983	45768151	45768004	45768130	MARK4	NM_031417	2	18	6	+	45768098	45768168
290599412	chr19	45767983	45768151	45768004	45768130	MARK4	NM_001199867	1	17	6	+	45768098	45768168
290599412	chr19	45767983	45768151	45768004	45768130	MARK4	NM_031417	2	18	5	+	45767942	45768007
290599412	chr19	45767983	45768151	45768004	45768130	MARK4	NM_001199867	1	17	5	+	45767942	45768007
290485882	chr19	45774666	45774827	45774687	45774806	MARK4	NM_031417	2	18	8	+	45774730	45774966
290485882	chr19	45774666	45774827	45774687	45774806	MARK4	NM_001199867	1	17	8	+	45774730	45774966
292115598	chr19	45781257	45781406	45781280	45781381	MARK4	NM_031417	2	18	9	+	45781181	45781300
292115598	chr19	45781257	45781406	45781280	45781381	MARK4	NM_001199867	1	17	9	+	45781181	45781300
293337729	chr19	45783797	45783971	45783815	45783954	MARK4	NM_031417	2	18	12	+	45783833	45783992
293337729	chr19	45783797	45783971	45783815	45783954	MARK4	NM_001199867	1	17	12	+	45783833	45783992
291015748	chr19	45797620	45797775	45797640	45797754	MARK4	NM_031417	2	18	14	+	45797607	45797710
291015748	chr19	45797620	45797775	45797640	45797754	MARK4	NM_001199867	1	17	14	+	45797607	45797710
293520808	chr19	45801286	45801440	45801307	45801420	MARK4	NM_031417	2	18	16	+	45801401	45801480
292530636	chr19	45805622	45805794	45805642	45805777	MARK4	NM_031417	2	18	18	+	45805632	45808541
292530636	chr19	45805622	45805794	45805642	45805777	MARK4	NM_001199867	1	17	17	+	45805632	45808541
228727185	chr19	45854848	45855006	45854869	45854983	ERCC2	NM_000400	1	23	23	-	45854649	45854979

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230794779	chr19	45855782	45855935	45855801	45855914	ERCC2	NM_000400	1	23	21	-	45855764	45855907
232743041	chr19	45856535	45856664	45856560	45856640	ERCC2	NM_000400	1	23	18	-	45856500	45856592
231805129	chr19	45860507	45860670	45860525	45860652	ERCC2	NM_000400	1	23	15	-	45860528	45860629
230855348	chr19	45864803	45864950	45864824	45864930	ERCC2	NM_000400	1	23	12	-	45864782	45864900
230855348	chr19	45864803	45864950	45864824	45864930	ERCC2	NM_001130867	2	12	11	-	45864782	45864900
232397272	chr19	45867355	45867523	45867375	45867504	ERCC2	NM_000400	1	23	9	-	45867493	45867589
232397272	chr19	45867355	45867523	45867375	45867504	ERCC2	NM_001130867	2	12	8	-	45867493	45867589
232397272	chr19	45867355	45867523	45867375	45867504	ERCC2	NM_000400	1	23	10	-	45867244	45867377
232397272	chr19	45867355	45867523	45867375	45867504	ERCC2	NM_001130867	2	12	9	-	45867244	45867377
230291651	chr19	45868069	45868237	45868087	45868219	ERCC2	NM_000400	1	23	7	-	45868096	45868212
230291651	chr19	45868069	45868237	45868087	45868219	ERCC2	NM_001130867	2	12	6	-	45868096	45868212
227701314	chr19	45871886	45872049	45871912	45872029	ERCC2	NM_000400	1	23	5	-	45871888	45872001
227701314	chr19	45871886	45872049	45871912	45872029	ERCC2	NM_001130867	2	12	4	-	45871888	45872001
231127677	chr19	45873407	45873575	45873427	45873556	ERCC2	NM_000400	1	23	2	-	45873391	45873490
231127677	chr19	45873407	45873575	45873427	45873556	ERCC2	NM_001130867	2	12	1	-	45873391	45873845
294285102	chr19	45917135	45917263	45917157	45917240	ERCC1	NM_202001	3	8	7	-	45917221	45917292
294285102	chr19	45917135	45917263	45917157	45917240	ERCC1	NM_001983	2	10	8	-	45917221	45917292
293773427	chr19	45922274	45922440	45922299	45922420	ERCC1	NM_202001	3	8	4	-	45922356	45922455
293773427	chr19	45922274	45922440	45922299	45922420	ERCC1	NM_001983	2	10	5	-	45922356	45922455
293773427	chr19	45922274	45922440	45922299	45922420	ERCC1	NM_001166049	1	9	5	-	45922356	45922455
294480260	chr19	45924329	45924473	45924351	45924452	ERCC1	NM_202001	3	8	2	-	45924436	45924651
294480260	chr19	45924329	45924473	45924351	45924452	ERCC1	NM_001983	2	10	3	-	45924436	45924651
294480260	chr19	45924329	45924473	45924351	45924452	ERCC1	NM_001166049	1	9	3	-	45924436	45924651
237910368	chr19	52693317	52693451	52693336	52693433	PPP2R1A	NR_033500	2	14	1	+	52693055	52693427
237910368	chr19	52693317	52693451	52693336	52693433	PPP2R1A	NM_014225	1	15	1	+	52693055	52693427
236804566	chr19	52714558	52714732	52714579	52714711	PPP2R1A	NR_033500	2	14	3	+	52714513	52714745
236804566	chr19	52714558	52714732	52714579	52714711	PPP2R1A	NM_014225	1	15	4	+	52714513	52714745
236449038	chr19	52716185	52716358	52716207	52716337	PPP2R1A	NR_033500	2	14	5	+	52716208	52716363
236449038	chr19	52716185	52716358	52716207	52716337	PPP2R1A	NM_014225	1	15	6	+	52716208	52716363
236823725	chr19	52719196	52719353	52719216	52719327	PPP2R1A	NR_033500	2	14	7	+	52719257	52719327
236823725	chr19	52719196	52719353	52719216	52719327	PPP2R1A	NM_014225	1	15	8	+	52719257	52719327
237347917	chr19	52722963	52723129	52722988	52723109	PPP2R1A	NR_033500	2	14	9	+	52722944	52723117
237347917	chr19	52722963	52723129	52722988	52723109	PPP2R1A	NM_014225	1	15	10	+	52722944	52723117
237801648	chr19	52724259	52724421	52724282	52724403	PPP2R1A	NR_033500	2	14	11	+	52724232	52724386
237801648	chr19	52724259	52724421	52724282	52724403	PPP2R1A	NM_014225	1	15	12	+	52724232	52724386
237006004	chr19	52729148	52729307	52729169	52729286	PPP2R1A	NR_033500	2	14	14	+	52729218	52729678
237006004	chr19	52729148	52729307	52729169	52729286	PPP2R1A	NM_014225	1	15	15	+	52729218	52729678
294452298	chr19	57743363	57743534	57743384	57743509	AURKC	NM_001015879	2	7	3	+	57743401	57743592
294452298	chr19	57743363	57743534	57743384	57743509	AURKC	NM_001015878	1	7	3	+	57743401	57743592
294452298	chr19	57743363	57743534	57743384	57743509	AURKC	NM_003160	3	7	3	+	57743401	57743592
293720467	chr19	57744765	57744902	57744787	57744873	AURKC	NM_001015879	2	7	5	+	57744828	57744976

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293720467	chr19	57744765	57744902	57744787	57744873	AURKC	NM_001015878	1	7	5	+	57744828	57744976
293720467	chr19	57744765	57744902	57744787	57744873	AURKC	NM_003160	3	7	5	+	57744828	57744976
294570093	chr19	57746533	57746698	57746558	57746677	AURKC	NM_001015879	2	7	7	+	57746615	57746916
294570093	chr19	57746533	57746698	57746558	57746677	AURKC	NM_001015878	1	7	7	+	57746615	57746916
294570093	chr19	57746533	57746698	57746558	57746677	AURKC	NM_003160	3	7	7	+	57746615	57746916
272636857	chr20	30253727	30253895	30253750	30253871	BCL2L1	NM_138578	2	3	3	-	30252261	30253889
272636857	chr20	30253727	30253895	30253750	30253871	BCL2L1	NM_001191	1	3	3	-	30252261	30253889
271655445	chr20	30309620	30309791	30309639	30309773	BCL2L1	NM_001191	1	3	2	-	30309647	30310151
271655445	chr20	30309620	30309791	30309639	30309773	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
224131270	chr20	30954147	30954309	30954174	30954281	ASXL1	NM_015338	2	12	2	+	30954187	30954269
224131270	chr20	30954147	30954309	30954174	30954281	ASXL1	NM_001164603	1	4	2	+	30954187	30954269
223159355	chr20	31016085	31016249	31016106	31016225	ASXL1	NM_015338	2	12	5	+	31016128	31016225
222665764	chr20	31017823	31017973	31017840	31017947	ASXL1	NM_015338	2	12	7	+	31017704	31017856
222184552	chr20	31019322	31019458	31019346	31019437	ASXL1	NM_015338	2	12	9	+	31019386	31019482
225137489	chr20	31021136	31021302	31021158	31021278	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223747788	chr20	31021542	31021673	31021563	31021649	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223993863	chr20	31022349	31022522	31022371	31022503	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225279217	chr20	31022808	31022950	31022830	31022930	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225274954	chr20	31023255	31023414	31023281	31023394	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225268126	chr20	31023730	31023887	31023751	31023864	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225265247	chr20	31024154	31024328	31024180	31024302	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225318475	chr20	31024611	31024783	31024637	31024765	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225311157	chr20	31025086	31025256	31025109	31025231	ASXL1	NM_015338	2	12	12	+	31022235	31027122
240906065	chr20	36022253	36022417	36022272	36022398	SRC	NM_198291	2	14	6	+	36022298	36022396
240906065	chr20	36022253	36022417	36022272	36022398	SRC	NM_005417	1	14	6	+	36022298	36022396
241082238	chr20	36026064	36026234	36026083	36026217	SRC	NM_198291	2	14	9	+	36026102	36026257
241082238	chr20	36026064	36026234	36026083	36026217	SRC	NM_005417	1	14	9	+	36026102	36026257
241034855	chr20	36029977	36030125	36029995	36030105	SRC	NM_198291	2	14	11	+	36030005	36030081
241034855	chr20	36029977	36030125	36029995	36030105	SRC	NM_005417	1	14	11	+	36030005	36030081
238938203	chr20	36031243	36031416	36031264	36031394	SRC	NM_198291	2	14	13	+	36031152	36031283
238938203	chr20	36031243	36031416	36031264	36031394	SRC	NM_005417	1	14	13	+	36031152	36031283
234395922	chr20	39316511	39316657	39316534	39316636	MAFB	NM_005461	1	1	1	-	39314517	39317876
234399160	chr20	39316843	39317012	39316861	39316994	MAFB	NM_005461	1	1	1	-	39314517	39317876
232729199	chr20	39317294	39317448	39317314	39317431	MAFB	NM_005461	1	1	1	-	39314517	39317876
264695053	chr20	39657578	39657737	39657596	39657716	TOP1	NM_003286	1	21	1	+	39657462	39657740
262040681	chr20	39704770	39704944	39704790	39704917	TOP1	NM_003286	1	21	4	+	39704811	39704934
241689534	chr20	39709737	39709909	39709761	39709887	TOP1	NM_003286	1	21	7	+	39709805	39709880
239222218	chr20	39725782	39725929	39725803	39725905	TOP1	NM_003286	1	21	10	+	39725860	39725981
290704438	chr20	39728634	39728797	39728663	39728773	TOP1	NM_003286	1	21	12	+	39728696	39728883
239534661	chr20	39741364	39741514	39741390	39741490	TOP1	NM_003286	1	21	14	+	39741422	39741565
240081810	chr20	39744020	39744148	39744049	39744126	TOP1	NM_003286	1	21	16	+	39744011	39744079

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264734158	chr20	39750285	39750458	39750310	39750431	TOP1	NM_003286	1	21	19	+	39750336	39750430
272249595	chr20	39766369	39766518	39766386	39766499	PLCG1	NM_002660	1	32	1	+	39766161	39766498
272249595	chr20	39766369	39766518	39766386	39766499	PLCG1	NM_182811	2	32	1	+	39766161	39766498
269666423	chr20	39788670	39788817	39788691	39788794	PLCG1	NM_002660	1	32	4	+	39788746	39788793
269666423	chr20	39788670	39788817	39788691	39788794	PLCG1	NM_182811	2	32	4	+	39788746	39788793
270916861	chr20	39791515	39791653	39791536	39791632	PLCG1	NM_002660	1	32	7	+	39791598	39791632
270916861	chr20	39791515	39791653	39791536	39791632	PLCG1	NM_182811	2	32	7	+	39791598	39791632
270162442	chr20	39792412	39792541	39792432	39792519	PLCG1	NM_002660	1	32	10	+	39792355	39792473
270162442	chr20	39792412	39792541	39792432	39792519	PLCG1	NM_182811	2	32	10	+	39792355	39792473
271042002	chr20	39793511	39793677	39793532	39793657	PLCG1	NM_002660	1	32	13	+	39793573	39793741
271042002	chr20	39793511	39793677	39793532	39793657	PLCG1	NM_182811	2	32	13	+	39793573	39793741
269575352	chr20	39794057	39794211	39794077	39794191	PLCG1	NM_002660	1	32	15	+	39794090	39794191
269575352	chr20	39794057	39794211	39794077	39794191	PLCG1	NM_182811	2	32	15	+	39794090	39794191
270266316	chr20	39794860	39795001	39794880	39794980	PLCG1	NM_002660	1	32	17	+	39794834	39795034
270266316	chr20	39794860	39795001	39794880	39794980	PLCG1	NM_182811	2	32	17	+	39794834	39795034
271245798	chr20	39795396	39795561	39795418	39795537	PLCG1	NM_002660	1	32	19	+	39795319	39795499
271245798	chr20	39795396	39795561	39795418	39795537	PLCG1	NM_182811	2	32	19	+	39795319	39795499
271206885	chr20	39797746	39797870	39797767	39797847	PLCG1	NM_002660	1	32	22	+	39797719	39797815
271206885	chr20	39797746	39797870	39797767	39797847	PLCG1	NM_182811	2	32	22	+	39797719	39797815
271442612	chr20	39800806	39800935	39800825	39800908	PLCG1	NM_002660	1	32	25	+	39800833	39800929
271442612	chr20	39800806	39800935	39800825	39800908	PLCG1	NM_182811	2	32	25	+	39800833	39800929
272240734	chr20	39801201	39801359	39801221	39801334	PLCG1	NM_002660	1	32	26	+	39801061	39801285
272240734	chr20	39801201	39801359	39801221	39801334	PLCG1	NM_182811	2	32	26	+	39801061	39801285
272562503	chr20	39802264	39802419	39802285	39802394	PLCG1	NM_002660	1	32	29	+	39802292	39802453
272562503	chr20	39802264	39802419	39802285	39802394	PLCG1	NM_182811	2	32	29	+	39802292	39802453
270150115	chr20	39802711	39802877	39802736	39802857	PLCG1	NM_182811	2	32	31	+	39802767	39802951
270150115	chr20	39802711	39802877	39802736	39802857	PLCG1	NM_002660	1	32	31	+	39802764	39802951
297077428	chr20	40710384	40710555	40710406	40710530	PTPRT	NM_007050	1	31	30	-	40710522	40710657
297077428	chr20	40710384	40710555	40710406	40710530	PTPRT	NM_133170	2	32	31	-	40710522	40710657
298205781	chr20	40714348	40714520	40714367	40714493	PTPRT	NM_007050	1	31	28	-	40714368	40714493
298205781	chr20	40714348	40714520	40714367	40714493	PTPRT	NM_133170	2	32	29	-	40714368	40714493
297065964	chr20	40730837	40730971	40730856	40730948	PTPRT	NM_007050	1	31	26	-	40730764	40730937
297065964	chr20	40730837	40730971	40730856	40730948	PTPRT	NM_133170	2	32	27	-	40730764	40730937
296943217	chr20	40735498	40735643	40735518	40735622	PTPRT	NM_007050	1	31	24	-	40735426	40735561
296943217	chr20	40735498	40735643	40735518	40735622	PTPRT	NM_133170	2	32	25	-	40735426	40735561
295546596	chr20	40743880	40744041	40743902	40744020	PTPRT	NM_007050	1	31	22	-	40743839	40743955
295546596	chr20	40743880	40744041	40743902	40744020	PTPRT	NM_133170	2	32	23	-	40743839	40743955
295750193	chr20	40770497	40770670	40770519	40770643	PTPRT	NM_007050	1	31	18	-	40770555	40770642
295750193	chr20	40770497	40770670	40770519	40770643	PTPRT	NM_133170	2	32	19	-	40770555	40770642
295765836	chr20	40827878	40828048	40827899	40828028	PTPRT	NM_007050	1	31	16	-	40827880	40828028
295765836	chr20	40827878	40828048	40827899	40828028	PTPRT	NM_133170	2	32	17	-	40827880	40828028

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
297411701	chr20	40898986	40899159	40899006	40899132	PTPRT	NM_133170	2	32	14	-	40899037	40899093
295697883	chr20	40944494	40944665	40944515	40944642	PTPRT	NM_007050	1	31	12	-	40944363	40944636
295697883	chr20	40944494	40944665	40944515	40944642	PTPRT	NM_133170	2	32	12	-	40944363	40944636
296997750	chr20	40980825	40980977	40980846	40980950	PTPRT	NM_007050	1	31	10	-	40980724	40980925
296997750	chr20	40980825	40980977	40980846	40980950	PTPRT	NM_133170	2	32	10	-	40980724	40980925
297212183	chr20	41101057	41101229	41101079	41101205	PTPRT	NM_007050	1	31	8	-	41100906	41101202
297212183	chr20	41101057	41101229	41101079	41101205	PTPRT	NM_133170	2	32	8	-	41100906	41101202
297844653	chr20	41385014	41385183	41385036	41385164	PTPRT	NM_007050	1	31	6	-	41385102	41385276
297844653	chr20	41385014	41385183	41385036	41385164	PTPRT	NM_133170	2	32	6	-	41385102	41385276
296481638	chr20	41419711	41419863	41419735	41419842	PTPRT	NM_007050	1	31	3	-	41419835	41420106
296481638	chr20	41419711	41419863	41419735	41419842	PTPRT	NM_133170	2	32	3	-	41419835	41420106
295979824	chr20	41514382	41514507	41514405	41514484	PTPRT	NM_007050	1	31	2	-	41514447	41514572
295979824	chr20	41514382	41514507	41514405	41514484	PTPRT	NM_133170	2	32	2	-	41514447	41514572
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_003600	1	9	9	-	54944445	54945396
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_198435	4	9	9	-	54944445	54945396
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_198436	5	10	10	-	54944445	54945396
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_198434	3	10	10	-	54944445	54945396
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_198433	2	11	11	-	54944445	54945396
271246397	chr20	54945362	54945505	54945386	54945478	AURKA	NM_198437	6	9	9	-	54944445	54945396
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_003600	1	9	7	-	54948464	54948612
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_198435	4	9	7	-	54948464	54948612
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_198436	5	10	8	-	54948464	54948612
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_198434	3	10	8	-	54948464	54948612
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_198433	2	11	9	-	54948464	54948612
270914187	chr20	54948521	54948695	54948549	54948671	AURKA	NM_198437	6	9	7	-	54948464	54948612
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_003600	1	9	5	-	54958041	54958232
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_198435	4	9	5	-	54958041	54958232
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_198436	5	10	6	-	54958041	54958232
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_198434	3	10	6	-	54958041	54958232
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_198433	2	11	7	-	54958041	54958232
270102225	chr20	54958095	54958236	54958123	54958217	AURKA	NM_198437	6	9	5	-	54958041	54958232
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_003600	1	9	3	-	54961313	54961589
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_198435	4	9	3	-	54961313	54961589
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_198436	5	10	4	-	54961313	54961589
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_198434	3	10	4	-	54961313	54961589
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_198433	2	11	5	-	54961313	54961589
270811124	chr20	54961335	54961494	54961360	54961469	AURKA	NM_198437	6	9	3	-	54961313	54961589
229983662	chr20	57415135	57415309	57415152	57415291	GNAS	NM_016592	5	13	1	+	57414795	57415941
228099766	chr20	57415617	57415762	57415634	57415741	GNAS	NM_016592	5	13	1	+	57414795	57415941
227533739	chr20	57428346	57428520	57428374	57428500	GNAS	NM_001077490	4	13	1	+	57428036	57430388
227533739	chr20	57428346	57428520	57428374	57428500	GNAS	NM_080425	6	13	1	+	57428036	57430388

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229445359	chr20	57428834	57429002	57428855	57428979	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229445359	chr20	57428834	57429002	57428855	57428979	GNAS	NM_080425	6	13	1	+	57428036	57430388
229438828	chr20	57429280	57429451	57429300	57429431	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229438828	chr20	57429280	57429451	57429300	57429431	GNAS	NM_080425	6	13	1	+	57428036	57430388
227514370	chr20	57429999	57430168	57430016	57430147	GNAS	NM_001077490	4	13	1	+	57428036	57430388
227514370	chr20	57429999	57430168	57430016	57430147	GNAS	NM_080425	6	13	1	+	57428036	57430388
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NM_016592	5	13	3	+	57473996	57474040
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NM_001077488	2	13	3	+	57473996	57474040
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NR_003259	8	13	3	+	57473996	57474040
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NM_001077490	4	13	3	+	57473996	57474040
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NM_080425	6	13	3	+	57473996	57474040
227784587	chr20	57473953	57474112	57473974	57474084	GNAS	NM_000516	1	13	3	+	57473996	57474040
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_016592	5	13	5	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_001077488	2	13	5	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NR_003259	8	13	5	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_001077490	4	13	5	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_080426	7	12	4	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_080425	6	13	5	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_001077489	3	12	4	+	57478727	57478846
227968922	chr20	57478790	57478964	57478814	57478943	GNAS	NM_000516	1	13	5	+	57478727	57478846
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_016592	5	13	9	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_001077488	2	13	9	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NR_003259	8	13	9	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_001077490	4	13	9	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_080426	7	12	8	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_080425	6	13	9	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_001077489	3	12	8	+	57484576	57484634
227209435	chr20	57484507	57484669	57484534	57484647	GNAS	NM_000516	1	13	9	+	57484576	57484634
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_016592	5	13	13	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_001077488	2	13	13	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_001077490	4	13	13	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_080426	7	12	12	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_080425	6	13	13	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_001077489	3	12	12	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NM_000516	1	13	13	+	57485738	57486250
230183882	chr20	57485705	57485844	57485727	57485825	GNAS	NR_003259	8	13	13	+	57485738	57486247
264588366	chr21	36164349	36164494	36164366	36164475	RUNX1	NM_001754	3	9	9	-	36160098	36164907
264588366	chr21	36164349	36164494	36164366	36164475	RUNX1	NM_001001890	1	6	6	-	36160098	36164907
242444313	chr21	36164814	36164955	36164833	36164934	RUNX1	NM_001754	3	9	9	-	36160098	36164907
242444313	chr21	36164814	36164955	36164833	36164934	RUNX1	NM_001001890	1	6	6	-	36160098	36164907
240188413	chr21	36206614	36206738	36206634	36206715	RUNX1	NM_001754	3	9	7	-	36206707	36206898

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240188413	chr21	36206614	36206738	36206634	36206715	RUNX1	NM_001122607	2	5	4	-	36206707	36206898
240188413	chr21	36206614	36206738	36206634	36206715	RUNX1	NM_001001890	1	6	4	-	36206707	36206898
241346645	chr21	36252742	36252912	36252767	36252886	RUNX1	NM_001754	3	9	5	-	36252854	36253010
241346645	chr21	36252742	36252912	36252767	36252886	RUNX1	NM_001122607	2	5	2	-	36252854	36253010
241346645	chr21	36252742	36252912	36252767	36252886	RUNX1	NM_001001890	1	6	2	-	36252854	36253010
241654701	chr21	36259323	36259448	36259342	36259427	RUNX1	NM_001122607	2	5	1	-	36259140	36260987
241654701	chr21	36259323	36259448	36259342	36259427	RUNX1	NM_001001890	1	6	1	-	36259140	36260987
241654701	chr21	36259323	36259448	36259342	36259427	RUNX1	NM_001754	3	9	4	-	36259140	36259393
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_001136154	1	12	12	-	39751950	39755845
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_001136155	2	9	9	-	39751950	39755845
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_004449	6	11	11	-	39751950	39755845
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_182918	7	10	10	-	39751950	39755845
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_001243429	4	9	9	-	39751950	39755845
230553670	chr21	39755289	39755451	39755311	39755428	ERG	NM_001243428	3	12	12	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_001136154	1	12	12	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_001136155	2	9	9	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_004449	6	11	11	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_182918	7	10	10	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_001243429	4	9	9	-	39751950	39755845
232732307	chr21	39755741	39755890	39755762	39755868	ERG	NM_001243428	3	12	12	-	39751950	39755845
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_001136154	1	12	9	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_001136155	2	9	6	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_004449	6	11	8	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_182918	7	10	7	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_001243432	5	12	9	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_001243429	4	9	6	-	39764298	39764366
229701879	chr21	39764170	39764340	39764193	39764323	ERG	NM_001243428	3	12	9	-	39764298	39764366
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_001136154	1	12	6	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_001136155	2	9	3	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_004449	6	11	6	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_182918	7	10	4	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_001243432	5	12	6	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_001243429	4	9	4	-	39775428	39775631
228220296	chr21	39775359	39775523	39775381	39775500	ERG	NM_001243428	3	12	6	-	39775428	39775631
227918663	chr21	39817286	39817454	39817308	39817434	ERG	NM_001136154	1	12	4	-	39817327	39817544
227918663	chr21	39817286	39817454	39817308	39817434	ERG	NM_004449	6	11	4	-	39817327	39817544
227918663	chr21	39817286	39817454	39817308	39817434	ERG	NM_182918	7	10	2	-	39817327	39817544
227918663	chr21	39817286	39817454	39817308	39817434	ERG	NM_001243432	5	12	4	-	39817327	39817544
227918663	chr21	39817286	39817454	39817308	39817434	ERG	NM_001243428	3	12	4	-	39817327	39817544
278598235	chr21	46306254	46306379	46306274	46306359	ITGB2	NM_000211	1	16	16	-	46305868	46306345
278598235	chr21	46306254	46306379	46306274	46306359	ITGB2	NM_001127491	2	16	16	-	46305868	46306345

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280292693	chr21	46308606	46308740	46308626	46308721	ITGB2	NM_000211	1	16	14	-	46308608	46308810
280292693	chr21	46308606	46308740	46308626	46308721	ITGB2	NM_001127491	2	16	14	-	46308608	46308810
279441199	chr21	46309286	46309441	46309306	46309423	ITGB2	NM_000211	1	16	13	-	46309191	46309410
279441199	chr21	46309286	46309441	46309306	46309423	ITGB2	NM_001127491	2	16	13	-	46309191	46309410
278402695	chr21	46311650	46311817	46311667	46311796	ITGB2	NM_000211	1	16	11	-	46311724	46311911
278402695	chr21	46311650	46311817	46311667	46311796	ITGB2	NM_001127491	2	16	11	-	46311724	46311911
279210544	chr21	46313322	46313488	46313342	46313467	ITGB2	NM_000211	1	16	10	-	46313319	46313459
279210544	chr21	46313322	46313488	46313342	46313467	ITGB2	NM_001127491	2	16	10	-	46313319	46313459
278025557	chr21	46320234	46320402	46320255	46320379	ITGB2	NM_000211	1	16	7	-	46320235	46320390
278025557	chr21	46320234	46320402	46320255	46320379	ITGB2	NM_001127491	2	16	7	-	46320235	46320390
279989777	chr21	46321599	46321754	46321617	46321732	ITGB2	NM_000211	1	16	6	-	46321407	46321648
279989777	chr21	46321599	46321754	46321617	46321732	ITGB2	NM_001127491	2	16	6	-	46321407	46321648
280498520	chr21	46326835	46326993	46326856	46326973	ITGB2	NM_000211	1	16	4	-	46326830	46327010
280498520	chr21	46326835	46326993	46326856	46326973	ITGB2	NM_001127491	2	16	4	-	46326830	46327010
278059076	chr21	46330579	46330734	46330600	46330714	ITGB2	NM_000211	1	16	2	-	46330640	46330700
278059076	chr21	46330579	46330734	46330600	46330714	ITGB2	NM_001127491	2	16	2	-	46330640	46330700
269823251	chr22	21272203	21272359	21272221	21272339	CRKL	NM_005207	1	3	1	+	21271714	21272533
271534610	chr22	21288126	21288299	21288152	21288275	CRKL	NM_005207	1	3	2	+	21288067	21288532
272262139	chr22	21303958	21304130	21303985	21304106	CRKL	NM_005207	1	3	3	+	21303999	21308037
293729618	chr22	22127139	22127302	22127161	22127275	MAPK1	NM_138957	2	8	7	-	22127162	22127271
293729618	chr22	22127139	22127302	22127161	22127275	MAPK1	NM_002745	1	9	7	-	22127162	22127271
294303058	chr22	22142972	22143145	22142995	22143117	MAPK1	NM_138957	2	8	5	-	22142983	22143097
294303058	chr22	22142972	22143145	22142995	22143117	MAPK1	NM_002745	1	9	5	-	22142983	22143097
294310102	chr22	22160140	22160311	22160163	22160283	MAPK1	NM_138957	2	8	3	-	22160139	22160328
294310102	chr22	22160140	22160311	22160163	22160283	MAPK1	NM_002745	1	9	3	-	22160139	22160328
293850788	chr22	22221493	22221660	22221512	22221639	MAPK1	NM_138957	2	8	1	-	22221612	22221970
293850788	chr22	22221493	22221660	22221512	22221639	MAPK1	NM_002745	1	9	1	-	22221612	22221970
224668442	chr22	23523353	23523527	23523370	23523509	BCR	NM_004327	1	23	1	+	23522552	23524426
224668442	chr22	23523353	23523527	23523370	23523509	BCR	NM_021574	2	22	1	+	23522552	23524426
223051911	chr22	23523671	23523827	23523694	23523810	BCR	NM_004327	1	23	1	+	23522552	23524426
223051911	chr22	23523671	23523827	23523694	23523810	BCR	NM_021574	2	22	1	+	23522552	23524426
224670152	chr22	23524136	23524291	23524156	23524272	BCR	NM_004327	1	23	1	+	23522552	23524426
224670152	chr22	23524136	23524291	23524156	23524272	BCR	NM_021574	2	22	1	+	23522552	23524426
222188987	chr22	23596054	23596193	23596075	23596174	BCR	NM_004327	1	23	2	+	23595986	23596167
222188987	chr22	23596054	23596193	23596075	23596174	BCR	NM_021574	2	22	2	+	23595986	23596167
223400109	chr22	23610558	23610724	23610579	23610702	BCR	NM_004327	1	23	5	+	23610595	23610702
223400109	chr22	23610558	23610724	23610579	23610702	BCR	NM_021574	2	22	5	+	23610595	23610702
223982831	chr22	23615877	23616005	23615898	23615986	BCR	NM_004327	1	23	8	+	23615821	23615961
223982831	chr22	23615877	23616005	23615898	23615986	BCR	NM_021574	2	22	8	+	23615821	23615961
222288194	chr22	23629296	23629424	23629315	23629402	BCR	NM_004327	1	23	11	+	23629346	23629465
222288194	chr22	23629296	23629424	23629315	23629402	BCR	NM_021574	2	22	11	+	23629346	23629465

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223709781	chr22	23632454	23632624	23632476	23632601	BCR	NM_004327	1	23	14	+	23632526	23632600
223709781	chr22	23632454	23632624	23632476	23632601	BCR	NM_021574	2	22	14	+	23632526	23632600
223642669	chr22	23653794	23653966	23653814	23653948	BCR	NM_004327	1	23	19	+	23653884	23654023
223642669	chr22	23653794	23653966	23653814	23653948	BCR	NM_021574	2	22	18	+	23653884	23654023
222700201	chr22	23656780	23656951	23656798	23656932	BCR	NM_004327	1	23	22	+	23656739	23656901
222700201	chr22	23656780	23656951	23656798	23656932	BCR	NM_021574	2	22	21	+	23656739	23656901
238301937	chr22	24133839	24133978	24133861	24133956	SMARCB1	NM_001007468	1	9	2	+	24133943	24134054
238301937	chr22	24133839	24133978	24133861	24133956	SMARCB1	NM_003073	2	9	2	+	24133943	24134081
239167801	chr22	24143208	24143374	24143230	24143353	SMARCB1	NM_001007468	1	9	4	+	24143131	24143268
239167801	chr22	24143208	24143374	24143230	24143353	SMARCB1	NM_003073	2	9	4	+	24143131	24143268
263915276	chr22	24158985	24159148	24159009	24159128	SMARCB1	NM_001007468	1	9	6	+	24158957	24159123
263915276	chr22	24158985	24159148	24159009	24159128	SMARCB1	NM_003073	2	9	6	+	24158957	24159123
261469284	chr22	24175833	24175993	24175855	24175971	SMARCB1	NM_001007468	1	9	8	+	24175759	24175890
261469284	chr22	24175833	24175993	24175855	24175971	SMARCB1	NM_003073	2	9	8	+	24175759	24175890
240615227	chr22	28146993	28147161	28147011	28147141	MN1	NM_002430	1	2	2	-	28144265	28147084
235352841	chr22	28193048	28193215	28193066	28193190	MN1	NM_002430	1	2	1	-	28192751	28197486
240190149	chr22	28193501	28193672	28193518	28193653	MN1	NM_002430	1	2	1	-	28192751	28197486
240207454	chr22	28193950	28194116	28193971	28194098	MN1	NM_002430	1	2	1	-	28192751	28197486
240206411	chr22	28194464	28194611	28194483	28194594	MN1	NM_002430	1	2	1	-	28192751	28197486
240216378	chr22	28194837	28194980	28194854	28194962	MN1	NM_002430	1	2	1	-	28192751	28197486
235389091	chr22	28195164	28195318	28195186	28195296	MN1	NM_002430	1	2	1	-	28192751	28197486
235395596	chr22	28195567	28195691	28195586	28195674	MN1	NM_002430	1	2	1	-	28192751	28197486
240243282	chr22	28195934	28196088	28195952	28196069	MN1	NM_002430	1	2	1	-	28192751	28197486
235503863	chr22	28196451	28196620	28196474	28196601	MN1	NM_002430	1	2	1	-	28192751	28197486
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_145862	3	14	11	-	29091115	29091230
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_007194	2	15	12	-	29091115	29091230
226541936	chr22	29091057	29091222	29091082	29091199	CHEK2	NM_001005735	1	16	13	-	29091115	29091230
226244636	chr22	29095773	29095947	29095801	29095925	CHEK2	NM_145862	3	14	9	-	29095826	29095925
226244636	chr22	29095773	29095947	29095801	29095925	CHEK2	NM_007194	2	15	9	-	29095826	29095925
226244636	chr22	29095773	29095947	29095801	29095925	CHEK2	NM_001005735	1	16	10	-	29095826	29095925
328645674	chr22	29107960	29108127	29107983	29108101	CHEK2	NM_145862	3	14	6	-	29107897	29108005
328645674	chr22	29107960	29108127	29107983	29108101	CHEK2	NM_007194	2	15	6	-	29107897	29108005
328645674	chr22	29107960	29108127	29107983	29108101	CHEK2	NM_001005735	1	16	7	-	29107897	29108005
253754328	chr22	29120973	29121108	29120998	29121080	CHEK2	NM_145862	3	14	4	-	29120965	29121112
253754328	chr22	29120973	29121108	29120998	29121080	CHEK2	NM_007194	2	15	4	-	29120965	29121112
253754328	chr22	29120973	29121108	29120998	29121080	CHEK2	NM_001005735	1	16	5	-	29120965	29121112
226152178	chr22	29130379	29130517	29130402	29130494	CHEK2	NM_145862	3	14	2	-	29130391	29130715
226152178	chr22	29130379	29130517	29130402	29130494	CHEK2	NM_007194	2	15	2	-	29130391	29130715
226152178	chr22	29130379	29130517	29130402	29130494	CHEK2	NM_001005735	1	16	2	-	29130391	29130715
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_016418	2	17	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_000268	1	16	1	+	29999545	30000101

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181833	9	5	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181832	8	17	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181828	4	16	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181825	3	16	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181831	7	15	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181830	6	15	1	+	29999545	30000101
238603833	chr22	30000019	30000164	30000041	30000143	NF2	NM_181829	5	16	1	+	29999545	30000101
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_016418	2	17	3	+	30035079	30035201
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_000268	1	16	3	+	30035079	30035201
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_181833	9	5	3	+	30035079	30035201
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_181832	8	17	3	+	30035079	30035201
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_181828	4	16	2	+	30035079	30035201
239086176	chr22	30035097	30035251	30035122	30035230	NF2	NM_181825	3	16	3	+	30035079	30035201
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_016418	2	17	6	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_000268	1	16	6	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181832	8	17	6	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181828	4	16	5	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181825	3	16	6	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181831	7	15	4	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181830	6	15	4	+	30051583	30051665
235101674	chr22	30051609	30051754	30051635	30051730	NF2	NM_181829	5	16	5	+	30051583	30051665
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_016418	2	17	9	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_000268	1	16	9	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181832	8	17	9	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181828	4	16	8	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181825	3	16	9	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181831	7	15	7	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181830	6	15	7	+	30060979	30061053
257971131	chr22	30060896	30061068	30060918	30061039	NF2	NM_181829	5	16	8	+	30060979	30061053
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_016418	2	17	11	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_000268	1	16	11	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181832	8	17	11	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181828	4	16	10	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181825	3	16	11	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181831	7	15	9	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181830	6	15	9	+	30067815	30067937
237096079	chr22	30067793	30067957	30067814	30067937	NF2	NM_181829	5	16	10	+	30067815	30067937
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_016418	2	17	13	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_000268	1	16	13	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181832	8	17	13	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181828	4	16	12	+	30070825	30070930

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181825	3	16	13	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181831	7	15	11	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181830	6	15	11	+	30070825	30070930
241514371	chr22	30070835	30070987	30070856	30070962	NF2	NM_181829	5	16	12	+	30070825	30070930
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_016418	2	17	15	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_000268	1	16	15	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181832	8	17	15	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181828	4	16	14	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181825	3	16	15	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181831	7	15	13	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181830	6	15	13	+	30077428	30077590
241362738	chr22	30077464	30077628	30077487	30077600	NF2	NM_181829	5	16	14	+	30077428	30077590
321650590	chr22	33245371	33245545	33245393	33245522	TIMP3	NM_000362	1	5	2	+	33245439	33245521
321710333	chr22	33255263	33255435	33255283	33255412	TIMP3	NM_000362	1	5	5	+	33255167	33259028
236010692	chr22	36680174	36680334	36680191	36680316	MYH9	NM_002473	1	41	40	-	36680139	36680311
237857533	chr22	36681242	36681400	36681262	36681380	MYH9	NM_002473	1	41	38	-	36681167	36681375
235892116	chr22	36682655	36682812	36682676	36682789	MYH9	NM_002473	1	41	35	-	36682764	36682892
237933750	chr22	36684679	36684852	36684701	36684832	MYH9	NM_002473	1	41	33	-	36684773	36684985
235697908	chr22	36685157	36685331	36685179	36685306	MYH9	NM_002473	1	41	32	-	36685131	36685343
236562974	chr22	36688244	36688410	36688267	36688389	MYH9	NM_002473	1	41	31	-	36688032	36688280
240841640	chr22	36690080	36690213	36690098	36690194	MYH9	NM_002473	1	41	28	-	36690138	36690344
242143163	chr22	36691076	36691245	36691098	36691223	MYH9	NM_002473	1	41	27	-	36690978	36691122
235729152	chr22	36692919	36693080	36692938	36693063	MYH9	NM_002473	1	41	25	-	36692889	36693060
235506419	chr22	36696189	36696343	36696211	36696322	MYH9	NM_002473	1	41	23	-	36696173	36696310
235075389	chr22	36697451	36697618	36697479	36697597	MYH9	NM_002473	1	41	21	-	36697580	36697711
238084618	chr22	36700145	36700317	36700167	36700296	MYH9	NM_002473	1	41	19	-	36700041	36700201
241134966	chr22	36702331	36702499	36702354	36702477	MYH9	NM_002473	1	41	16	-	36702460	36702653
236240960	chr22	36705337	36705505	36705359	36705485	MYH9	NM_002473	1	41	15	-	36705327	36705441
236772462	chr22	36710086	36710260	36710110	36710240	MYH9	NM_002473	1	41	13	-	36710190	36710363
235397145	chr22	36714232	36714359	36714251	36714334	MYH9	NM_002473	1	41	11	-	36714252	36714370
237169128	chr22	36716360	36716502	36716382	36716480	MYH9	NM_002473	1	41	9	-	36716265	36716408
236877524	chr22	36718460	36718596	36718477	36718579	MYH9	NM_002473	1	41	6	-	36718474	36718566
235228116	chr22	36737485	36737619	36737509	36737591	MYH9	NM_002473	1	41	3	-	36737415	36737571
236974462	chr22	36745157	36745309	36745179	36745288	MYH9	NM_002473	1	41	2	-	36744949	36745300
235461221	chr22	39627542	39627716	39627563	39627698	PDGFB	NM_033016	2	7	4	-	39627627	39627832
235461221	chr22	39627542	39627716	39627563	39627698	PDGFB	NM_002608	1	7	4	-	39627627	39627832
235243961	chr22	39631719	39631859	39631742	39631835	PDGFB	NM_033016	2	7	2	-	39631783	39631879
235243961	chr22	39631719	39631859	39631742	39631835	PDGFB	NM_002608	1	7	2	-	39631783	39631879
231448837	chr22	41488980	41489154	41489004	41489127	EP300	NM_001429	1	31	1	+	41488614	41489102
231355550	chr22	41513458	41513623	41513480	41513604	EP300	NM_001429	1	31	2	+	41513191	41513825
230173300	chr22	41521880	41522053	41521904	41522030	EP300	NM_001429	1	31	3	+	41521868	41522044

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233044505	chr22	41523683	41523809	41523703	41523783	EP300	NM_001429	1	31	4	+	41523491	41523752
229589663	chr22	41527459	41527591	41527481	41527567	EP300	NM_001429	1	31	6	+	41527392	41527637
229233334	chr22	41533697	41533821	41533718	41533794	EP300	NM_001429	1	31	8	+	41533657	41533794
230718430	chr22	41537059	41537217	41537086	41537200	EP300	NM_001429	1	31	10	+	41537052	41537226
230725276	chr22	41543915	41544070	41543936	41544042	EP300	NM_001429	1	31	12	+	41543841	41543950
229957439	chr22	41545850	41546024	41545873	41546003	EP300	NM_001429	1	31	14	+	41545765	41546202
229198434	chr22	41547794	41547965	41547815	41547941	EP300	NM_001429	1	31	15	+	41547837	41548016
228166776	chr22	41550905	41551056	41550931	41551034	EP300	NM_001429	1	31	17	+	41550999	41551117
230513883	chr22	41553336	41553508	41553357	41553480	EP300	NM_001429	1	31	18	+	41553173	41553412
228098947	chr22	41559977	41560151	41560004	41560127	EP300	NM_001429	1	31	22	+	41560057	41560134
232729013	chr22	41564614	41564776	41564640	41564754	EP300	NM_001429	1	31	25	+	41564725	41564871
232318587	chr22	41566331	41566483	41566358	41566455	EP300	NM_001429	1	31	27	+	41566410	41566575
229247294	chr22	41569552	41569695	41569578	41569667	EP300	NM_001429	1	31	29	+	41569627	41569788
227898228	chr22	41572464	41572613	41572486	41572588	EP300	NM_001429	1	31	30	+	41572251	41572532
231306028	chr22	41573000	41573159	41573018	41573141	EP300	NM_001429	1	31	31	+	41572777	41576081
227978570	chr22	41573485	41573654	41573505	41573635	EP300	NM_001429	1	31	31	+	41572777	41576081
228057279	chr22	41573955	41574129	41573976	41574107	EP300	NM_001429	1	31	31	+	41572777	41576081
228141972	chr22	41574392	41574519	41574412	41574499	EP300	NM_001429	1	31	31	+	41572777	41576081
231263944	chr22	41574819	41574986	41574844	41574961	EP300	NM_001429	1	31	31	+	41572777	41576081
285954553	chr22	42523764	42523908	42523785	42523890	CYP2D6	NM_000106	1	9	6	-	42523844	42523985
285954553	chr22	42523764	42523908	42523785	42523890	CYP2D6	NM_001025161	2	8	5	-	42523844	42523985
287207216	chr22	42524762	42524933	42524780	42524915	CYP2D6	NM_000106	1	9	4	-	42524786	42524946
287207216	chr22	42524762	42524933	42524780	42524915	CYP2D6	NM_001025161	2	8	3	-	42524786	42524946
286427537	chr22	42525766	42525928	42525785	42525909	CYP2D6	NM_000106	1	9	2	-	42525740	42525911
286427537	chr22	42525766	42525928	42525785	42525909	CYP2D6	NM_001025161	2	8	2	-	42525740	42525911
270571127	chrX	40982851	40983016	40982875	40982989	USP9X	NM_001039590	1	45	2	+	40982724	40982977
270571127	chrX	40982851	40983016	40982875	40982989	USP9X	NM_001039591	2	45	2	+	40982724	40982977
270684202	chrX	40990720	40990869	40990742	40990847	USP9X	NM_001039590	1	45	4	+	40990710	40990789
270684202	chrX	40990720	40990869	40990742	40990847	USP9X	NM_001039591	2	45	4	+	40990710	40990789
270104775	chrX	40996075	40996246	40996096	40996221	USP9X	NM_001039590	1	45	6	+	40996057	40996275
270104775	chrX	40996075	40996246	40996096	40996221	USP9X	NM_001039591	2	45	6	+	40996057	40996275
270256348	chrX	41000091	41000251	41000119	41000226	USP9X	NM_001039590	1	45	8	+	41000219	41000470
270256348	chrX	41000091	41000251	41000119	41000226	USP9X	NM_001039591	2	45	8	+	41000219	41000470
271529233	chrX	41000460	41000595	41000493	41000568	USP9X	NM_001039590	1	45	9	+	41000546	41000684
271529233	chrX	41000460	41000595	41000493	41000568	USP9X	NM_001039591	2	45	9	+	41000546	41000684
272248515	chrX	41002640	41002785	41002668	41002761	USP9X	NM_001039590	1	45	10	+	41002544	41002696
272248515	chrX	41002640	41002785	41002668	41002761	USP9X	NM_001039591	2	45	10	+	41002544	41002696
271306890	chrX	41007622	41007756	41007644	41007734	USP9X	NM_001039590	1	45	12	+	41007622	41007828
271306890	chrX	41007622	41007756	41007644	41007734	USP9X	NM_001039591	2	45	12	+	41007622	41007828
269686336	chrX	41012133	41012257	41012159	41012229	USP9X	NM_001039590	1	45	14	+	41012201	41012334
269686336	chrX	41012133	41012257	41012159	41012229	USP9X	NM_001039591	2	45	14	+	41012201	41012334

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272426933	chrX	41025062	41025236	41025090	41025210	USP9X	NM_001039590	1	45	16	+	41025125	41025467
272426933	chrX	41025062	41025236	41025090	41025210	USP9X	NM_001039591	2	45	16	+	41025125	41025467
272509377	chrX	41026714	41026878	41026742	41026850	USP9X	NM_001039590	1	45	17	+	41026735	41026830
272509377	chrX	41026714	41026878	41026742	41026850	USP9X	NM_001039591	2	45	17	+	41026735	41026830
269723131	chrX	41029201	41029360	41029228	41029332	USP9X	NM_001039590	1	45	19	+	41029248	41029488
269723131	chrX	41029201	41029360	41029228	41029332	USP9X	NM_001039591	2	45	19	+	41029248	41029488
271068758	chrX	41031006	41031168	41031034	41031146	USP9X	NM_001039590	1	45	21	+	41031091	41031211
271068758	chrX	41031006	41031168	41031034	41031146	USP9X	NM_001039591	2	45	21	+	41031091	41031211
271320055	chrX	41043354	41043490	41043381	41043461	USP9X	NM_001039590	1	45	22	+	41043251	41043381
271320055	chrX	41043354	41043490	41043381	41043461	USP9X	NM_001039591	2	45	22	+	41043251	41043381
270573714	chrX	41045686	41045816	41045710	41045796	USP9X	NM_001039590	1	45	24	+	41045770	41045895
270573714	chrX	41045686	41045816	41045710	41045796	USP9X	NM_001039591	2	45	24	+	41045770	41045895
269809920	chrX	41048573	41048700	41048595	41048677	USP9X	NM_001039590	1	45	26	+	41048562	41048728
269809920	chrX	41048573	41048700	41048595	41048677	USP9X	NM_001039591	2	45	26	+	41048562	41048728
271076552	chrX	41055793	41055965	41055817	41055937	USP9X	NM_001039590	1	45	28	+	41055845	41055991
271076552	chrX	41055793	41055965	41055817	41055937	USP9X	NM_001039591	2	45	28	+	41055845	41055991
269948403	chrX	41057821	41057947	41057850	41057925	USP9X	NM_001039590	1	45	30	+	41057781	41058003
269948403	chrX	41057821	41057947	41057850	41057925	USP9X	NM_001039591	2	45	30	+	41057781	41058003
270050691	chrX	41060511	41060660	41060532	41060639	USP9X	NM_001039590	1	45	31	+	41060313	41060533
270050691	chrX	41060511	41060660	41060532	41060639	USP9X	NM_001039591	2	45	31	+	41060313	41060533
271942876	chrX	41069658	41069803	41069682	41069784	USP9X	NM_001039590	1	45	33	+	41069762	41069935
271942876	chrX	41069658	41069803	41069682	41069784	USP9X	NM_001039591	2	45	33	+	41069762	41069935
270377443	chrX	41073917	41074050	41073945	41074025	USP9X	NM_001039590	1	45	34	+	41073821	41073962
270377443	chrX	41073917	41074050	41073945	41074025	USP9X	NM_001039591	2	45	34	+	41073821	41073962
270946113	chrX	41075366	41075531	41075390	41075504	USP9X	NM_001039590	1	45	35	+	41075152	41075905
270946113	chrX	41075366	41075531	41075390	41075504	USP9X	NM_001039591	2	45	35	+	41075152	41075905
272454736	chrX	41075823	41075978	41075851	41075952	USP9X	NM_001039590	1	45	35	+	41075152	41075905
272454736	chrX	41075823	41075978	41075851	41075952	USP9X	NM_001039591	2	45	35	+	41075152	41075905
270132124	chrX	41077628	41077765	41077653	41077746	USP9X	NM_001039590	1	45	37	+	41077625	41077850
270132124	chrX	41077628	41077765	41077653	41077746	USP9X	NM_001039591	2	45	37	+	41077625	41077850
272566989	chrX	41082490	41082657	41082517	41082630	USP9X	NM_001039590	1	45	39	+	41082470	41082655
272566989	chrX	41082490	41082657	41082517	41082630	USP9X	NM_001039591	2	45	39	+	41082470	41082655
269712342	chrX	41084204	41084332	41084232	41084308	USP9X	NM_001039590	1	45	41	+	41084302	41084390
269712342	chrX	41084204	41084332	41084232	41084308	USP9X	NM_001039591	2	45	41	+	41084302	41084390
270997796	chrX	41088718	41088885	41088750	41088859	USP9X	NM_001039591	2	45	43	+	41088820	41089032
270997796	chrX	41088718	41088885	41088750	41088859	USP9X	NM_001039590	1	45	43	+	41088820	41089080
271090201	chrX	41089641	41089792	41089669	41089768	USP9X	NM_001039590	1	45	44	+	41089754	41089849
271090201	chrX	41089641	41089792	41089669	41089768	USP9X	NM_001039591	2	45	44	+	41089754	41089849
234236334	chrX	44732761	44732896	44732778	44732879	KDM6A	NM_021140	1	29	1	+	44732423	44732958
233407041	chrX	44820574	44820745	44820603	44820717	KDM6A	NM_021140	1	29	3	+	44820529	44820637
234426021	chrX	44879852	44879987	44879877	44879959	KDM6A	NM_021140	1	29	6	+	44879855	44879975

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234678034	chrX	44910952	44911117	44910981	44911096	KDM6A	NM_021140	1	29	9	+	44910954	44911047
233653618	chrX	44918161	44918285	44918189	44918261	KDM6A	NM_021140	1	29	11	+	44918251	44918349
234518962	chrX	44918518	44918689	44918540	44918663	KDM6A	NM_021140	1	29	12	+	44918492	44918711
232629157	chrX	44920479	44920650	44920504	44920626	KDM6A	NM_021140	1	29	14	+	44920569	44920664
231275853	chrX	44922614	44922758	44922641	44922736	KDM6A	NM_021140	1	29	16	+	44922667	44923062
232781991	chrX	44928824	44928980	44928844	44928957	KDM6A	NM_021140	1	29	17	+	44928824	44929602
232907682	chrX	44929245	44929413	44929270	44929392	KDM6A	NM_021140	1	29	17	+	44928824	44929602
231536721	chrX	44935935	44936073	44935963	44936045	KDM6A	NM_021140	1	29	18	+	44935942	44936071
230940261	chrX	44938274	44938435	44938296	44938407	KDM6A	NM_021140	1	29	20	+	44938391	44938596
230878857	chrX	44941837	44941976	44941865	44941951	KDM6A	NM_021140	1	29	21	+	44941821	44941885
232215157	chrX	44945094	44945236	44945121	44945208	KDM6A	NM_021140	1	29	24	+	44945110	44945224
231832002	chrX	44949128	44949299	44949151	44949271	KDM6A	NM_021140	1	29	25	+	44948988	44949175
233083448	chrX	44966659	44966828	44966687	44966801	KDM6A	NM_021140	1	29	27	+	44966655	44966781
233520677	chrX	44970528	44970702	44970555	44970674	KDM6A	NM_021140	1	29	29	+	44970627	44971845
241097631	chrX	48121132	48121300	48121153	48121274	SSX1	NM_005635	1	8	5	+	48121201	48121250
239707192	chrX	48542312	48542485	48542330	48542462	WAS	NM_000377	1	12	1	+	48542186	48542374
242083990	chrX	48543964	48544133	48543988	48544113	WAS	NM_000377	1	12	3	+	48543936	48544022
263088536	chrX	48545137	48545309	48545160	48545285	WAS	NM_000377	1	12	7	+	48545170	48545344
242233032	chrX	48546757	48546893	48546777	48546873	WAS	NM_000377	1	12	9	+	48546689	48546842
262404898	chrX	48547326	48547477	48547343	48547458	WAS	NM_000377	1	12	10	+	48547049	48547455
228122368	chrX	48649586	48649760	48649607	48649736	GATA1	NM_002049	1	6	2	+	48649498	48649736
227560610	chrX	48650498	48650664	48650521	48650640	GATA1	NM_002049	1	6	3	+	48650251	48650628
227643534	chrX	48652087	48652253	48652113	48652230	GATA1	NM_002049	1	6	6	+	48652200	48652717
265502151	chrX	48887609	48887748	48887631	48887728	TFE3	NM_006521	1	10	10	-	48886242	48888112
265496437	chrX	48888025	48888164	48888045	48888140	TFE3	NM_006521	1	10	10	-	48886242	48888112
241585717	chrX	48891221	48891353	48891240	48891330	TFE3	NM_006521	1	10	7	-	48891241	48891297
242123593	chrX	48895686	48895810	48895705	48895791	TFE3	NM_006521	1	10	4	-	48895722	48895967
241269118	chrX	48896665	48896820	48896684	48896802	TFE3	NM_006521	1	10	3	-	48896632	48896935
241399526	chrX	48897999	48898131	48898020	48898108	TFE3	NM_006521	1	10	2	-	48897982	48898095
234382120	chrX	53221874	53222009	53221896	53221981	KDM5C	NM_004187	2	26	26	-	53220503	53222514
234382120	chrX	53221874	53222009	53221896	53221981	KDM5C	NM_001146702	1	24	24	-	53220503	53222019
232721961	chrX	53222248	53222407	53222269	53222385	KDM5C	NM_004187	2	26	26	-	53220503	53222514
231179417	chrX	53222890	53223062	53222913	53223038	KDM5C	NM_004187	2	26	24	-	53222955	53223033
231179417	chrX	53222890	53223062	53222913	53223038	KDM5C	NM_001146702	1	24	22	-	53222964	53223033
233920566	chrX	53223546	53223706	53223563	53223688	KDM5C	NM_004187	2	26	23	-	53223321	53223920
233920566	chrX	53223546	53223706	53223563	53223688	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
233470646	chrX	53224165	53224297	53224188	53224275	KDM5C	NM_004187	2	26	22	-	53224113	53224250
233470646	chrX	53224165	53224297	53224188	53224275	KDM5C	NM_001146702	1	24	20	-	53224113	53224250
234435089	chrX	53225148	53225275	53225169	53225253	KDM5C	NM_004187	2	26	20	-	53225098	53225236
234435089	chrX	53225148	53225275	53225169	53225253	KDM5C	NM_001146702	1	24	18	-	53225098	53225236
232606809	chrX	53226126	53226267	53226145	53226248	KDM5C	NM_004187	2	26	19	-	53225868	53226226

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232606809	chrX	53226126	53226267	53226145	53226248	KDM5C	NM_001146702	1	24	17	-	53225868	53226226
233073674	chrX	53227878	53228048	53227901	53228027	KDM5C	NM_004187	2	26	16	-	53227946	53228070
233073674	chrX	53227878	53228048	53227901	53228027	KDM5C	NM_001146702	1	24	14	-	53227946	53228070
232474892	chrX	53230681	53230854	53230703	53230832	KDM5C	NM_004187	2	26	14	-	53230732	53230926
232474892	chrX	53230681	53230854	53230703	53230832	KDM5C	NM_001146702	1	24	12	-	53230732	53230926
234434211	chrX	53239653	53239779	53239675	53239758	KDM5C	NM_004187	2	26	12	-	53239596	53239758
234434211	chrX	53239653	53239779	53239675	53239758	KDM5C	NM_001146702	1	24	10	-	53239596	53239758
233184086	chrX	53240744	53240869	53240769	53240845	KDM5C	NM_004187	2	26	10	-	53240679	53240837
233184086	chrX	53240744	53240869	53240769	53240845	KDM5C	NM_001146702	1	24	8	-	53240679	53240837
232497035	chrX	53244917	53245079	53244940	53245058	KDM5C	NM_004187	2	26	7	-	53244977	53245158
232497035	chrX	53244917	53245079	53244940	53245058	KDM5C	NM_001146702	1	24	5	-	53244977	53245158
234229363	chrX	53246406	53246532	53246430	53246506	KDM5C	NM_004187	2	26	5	-	53246325	53246459
234229363	chrX	53246406	53246532	53246430	53246506	KDM5C	NM_001146702	1	24	3	-	53246325	53246459
233699527	chrX	53249995	53250120	53250016	53250098	KDM5C	NM_004187	2	26	2	-	53250021	53250098
229275479	chrX	63409836	63410007	63409857	63409987	FAM123B	NM_152424	1	2	2	-	63404997	63413264
231996349	chrX	63410283	63410425	63410304	63410403	FAM123B	NM_152424	1	2	2	-	63404997	63413264
228923437	chrX	63410667	63410804	63410693	63410783	FAM123B	NM_152424	1	2	2	-	63404997	63413264
231995197	chrX	63411121	63411278	63411141	63411257	FAM123B	NM_152424	1	2	2	-	63404997	63413264
229429002	chrX	63411564	63411737	63411585	63411712	FAM123B	NM_152424	1	2	2	-	63404997	63413264
229484537	chrX	63411929	63412091	63411957	63412071	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232065940	chrX	63412389	63412541	63412416	63412524	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232041911	chrX	63412816	63412985	63412837	63412961	FAM123B	NM_152424	1	2	2	-	63404997	63413264
264338736	chrX	66764949	66765102	66764970	66765085	AR	NM_000044	1	8	1	+	66763874	66766604
264351064	chrX	66765558	66765722	66765579	66765701	AR	NM_000044	1	8	1	+	66763874	66766604
264351722	chrX	66766010	66766175	66766029	66766158	AR	NM_000044	1	8	1	+	66763874	66766604
264343357	chrX	66766518	66766687	66766538	66766666	AR	NM_000044	1	8	1	+	66763874	66766604
265878357	chrX	66905790	66905964	66905815	66905937	AR	NM_001011645	2	8	3	+	66905852	66905968
265878357	chrX	66905790	66905964	66905815	66905937	AR	NM_000044	1	8	3	+	66905852	66905968
257544121	chrX	66931418	66931566	66931438	66931544	AR	NM_001011645	2	8	4	+	66931244	66931531
257544121	chrX	66931418	66931566	66931438	66931544	AR	NM_000044	1	8	4	+	66931244	66931531
261070779	chrX	66941699	66941871	66941718	66941847	AR	NM_001011645	2	8	6	+	66941675	66941805
261070779	chrX	66941699	66941871	66941718	66941847	AR	NM_000044	1	8	6	+	66941675	66941805
264993661	chrX	66943597	66943770	66943619	66943747	AR	NM_001011645	2	8	8	+	66943528	66950461
264993661	chrX	66943597	66943770	66943619	66943747	AR	NM_000044	1	8	8	+	66943528	66950461
305048918	chrX	70587325	70587489	70587346	70587469	TAF1	NM_138923	2	38	2	+	70587349	70587463
305048918	chrX	70587325	70587489	70587346	70587469	TAF1	NM_004606	1	38	2	+	70587349	70587463
327060499	chrX	70596673	70596826	70596695	70596800	TAF1	NM_004606	1	38	5	+	70596800	70597041
302165899	chrX	70597531	70597700	70597551	70597672	TAF1	NM_138923	2	38	6	+	70597453	70597671
302165899	chrX	70597531	70597700	70597551	70597672	TAF1	NM_004606	1	38	6	+	70597453	70597671
305134203	chrX	70598743	70598909	70598766	70598889	TAF1	NM_138923	2	38	8	+	70598674	70598881
305134203	chrX	70598743	70598909	70598766	70598889	TAF1	NM_004606	1	38	8	+	70598674	70598881

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
301132412	chrX	70602420	70602549	70602440	70602525	TAF1	NM_138923	2	38	10	+	70602386	70602513
301132412	chrX	70602420	70602549	70602440	70602525	TAF1	NM_004606	1	38	10	+	70602386	70602513
301108376	chrX	70602896	70603032	70602916	70603005	TAF1	NM_138923	2	38	12	+	70602841	70603014
301108376	chrX	70602896	70603032	70602916	70603005	TAF1	NM_004606	1	38	12	+	70602841	70603014
300777167	chrX	70604721	70604892	70604750	70604870	TAF1	NM_138923	2	38	14	+	70604795	70604899
300777167	chrX	70604721	70604892	70604750	70604870	TAF1	NM_004606	1	38	14	+	70604795	70604899
300441386	chrX	70607240	70607370	70607264	70607349	TAF1	NM_138923	2	38	15	+	70607111	70607311
300441386	chrX	70607240	70607370	70607264	70607349	TAF1	NM_004606	1	38	15	+	70607111	70607311
301935249	chrX	70608577	70608743	70608599	70608719	TAF1	NM_138923	2	38	17	+	70608588	70608718
301935249	chrX	70608577	70608743	70608599	70608719	TAF1	NM_004606	1	38	17	+	70608588	70608718
303123813	chrX	70612740	70612900	70612762	70612872	TAF1	NM_138923	2	38	20	+	70612725	70612844
303123813	chrX	70612740	70612900	70612762	70612872	TAF1	NM_004606	1	38	20	+	70612725	70612844
300499196	chrX	70613858	70614013	70613886	70613985	TAF1	NM_138923	2	38	22	+	70613917	70614095
300499196	chrX	70613858	70614013	70613886	70613985	TAF1	NM_004606	1	38	22	+	70613917	70614095
301137320	chrX	70618314	70618488	70618342	70618467	TAF1	NM_138923	2	38	24	+	70618422	70618587
301137320	chrX	70618314	70618488	70618342	70618467	TAF1	NM_004606	1	38	24	+	70618422	70618587
299452569	chrX	70626455	70626624	70626482	70626599	TAF1	NM_138923	2	38	26	+	70626488	70626596
299452569	chrX	70626455	70626624	70626482	70626599	TAF1	NM_004606	1	38	26	+	70626488	70626596
302698996	chrX	70641081	70641255	70641109	70641227	TAF1	NM_138923	2	38	29	+	70641159	70641226
302698996	chrX	70641081	70641255	70641109	70641227	TAF1	NM_004606	1	38	29	+	70641159	70641226
305596595	chrX	70643829	70644000	70643857	70643975	TAF1	NM_138923	2	38	31	+	70643824	70643916
305596595	chrX	70643829	70644000	70643857	70643975	TAF1	NM_004606	1	38	31	+	70643824	70643916
301380499	chrX	70677972	70678140	70677999	70678117	TAF1	NM_138923	2	38	35	+	70678091	70678216
301380499	chrX	70677972	70678140	70677999	70678117	TAF1	NM_004606	1	38	35	+	70678091	70678216
301969926	chrX	70680433	70680591	70680459	70680564	TAF1	NM_138923	2	38	37	+	70680476	70680653
301969926	chrX	70680433	70680591	70680459	70680564	TAF1	NM_004606	1	38	37	+	70680476	70680653
300094567	chrX	70683817	70683952	70683837	70683931	TAF1	NM_138923	2	38	38	+	70683674	70685855
300094567	chrX	70683817	70683952	70683837	70683931	TAF1	NM_004606	1	38	38	+	70683674	70685855
274093861	chrX	76764022	76764156	76764048	76764131	ATRX	NM_000489	1	35	35	-	76760356	76764107
274093861	chrX	76764022	76764156	76764048	76764131	ATRX	NM_138270	2	34	34	-	76760356	76764107
273167520	chrX	76776916	76777055	76776938	76777027	ATRX	NM_000489	1	35	33	-	76776881	76776976
273167520	chrX	76776916	76777055	76776938	76777027	ATRX	NM_138270	2	34	32	-	76776881	76776976
274241245	chrX	76778658	76778822	76778685	76778794	ATRX	NM_000489	1	35	31	-	76778730	76778879
274241245	chrX	76778658	76778822	76778685	76778794	ATRX	NM_138270	2	34	30	-	76778730	76778879
273147161	chrX	76813073	76813226	76813101	76813193	ATRX	NM_000489	1	35	30	-	76812922	76813116
273147161	chrX	76813073	76813226	76813101	76813193	ATRX	NM_138270	2	34	29	-	76812922	76813116
272764071	chrX	76829610	76829774	76829639	76829750	ATRX	NM_000489	1	35	28	-	76829715	76829823
272764071	chrX	76829610	76829774	76829639	76829750	ATRX	NM_138270	2	34	27	-	76829715	76829823
273707403	chrX	76849041	76849197	76849072	76849174	ATRX	NM_000489	1	35	26	-	76849166	76849319
273707403	chrX	76849041	76849197	76849072	76849174	ATRX	NM_138270	2	34	25	-	76849166	76849319
272786317	chrX	76854858	76855023	76854886	76854995	ATRX	NM_000489	1	35	25	-	76854880	76855049

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272786317	chrX	76854858	76855023	76854886	76854995	ATRX	NM_138270	2	34	24	-	76854880	76855049
273482808	chrX	76855848	76855997	76855879	76855973	ATRX	NM_000489	1	35	23	-	76855903	76856033
273482808	chrX	76855848	76855997	76855879	76855973	ATRX	NM_138270	2	34	22	-	76855903	76856033
273184812	chrX	76874157	76874315	76874179	76874290	ATRX	NM_000489	1	35	21	-	76874274	76874449
273184812	chrX	76874157	76874315	76874179	76874290	ATRX	NM_138270	2	34	20	-	76874274	76874449
273950509	chrX	76875934	76876106	76875962	76876078	ATRX	NM_000489	1	35	20	-	76875863	76876000
273950509	chrX	76875934	76876106	76875962	76876078	ATRX	NM_138270	2	34	19	-	76875863	76876000
272999418	chrX	76888937	76889110	76888965	76889084	ATRX	NM_000489	1	35	18	-	76889054	76889200
272999418	chrX	76888937	76889110	76888965	76889084	ATRX	NM_138270	2	34	17	-	76889054	76889200
273039409	chrX	76890155	76890302	76890177	76890269	ATRX	NM_000489	1	35	17	-	76890085	76890194
273039409	chrX	76890155	76890302	76890177	76890269	ATRX	NM_138270	2	34	16	-	76890085	76890194
273630704	chrX	76907627	76907751	76907650	76907729	ATRX	NM_000489	1	35	15	-	76907604	76907843
273630704	chrX	76907627	76907751	76907650	76907729	ATRX	NM_138270	2	34	14	-	76907604	76907843
273888046	chrX	76912062	76912234	76912086	76912206	ATRX	NM_000489	1	35	13	-	76912050	76912143
273888046	chrX	76912062	76912234	76912086	76912206	ATRX	NM_138270	2	34	12	-	76912050	76912143
272934434	chrX	76920193	76920323	76920220	76920295	ATRX	NM_000489	1	35	11	-	76920134	76920267
272934434	chrX	76920193	76920323	76920220	76920295	ATRX	NM_138270	2	34	10	-	76920134	76920267
273989997	chrX	76937004	76937155	76937027	76937127	ATRX	NM_000489	1	35	9	-	76937012	76940085
273989997	chrX	76937004	76937155	76937027	76937127	ATRX	NM_138270	2	34	8	-	76937012	76940085
274016571	chrX	76937285	76937459	76937313	76937433	ATRX	NM_000489	1	35	9	-	76937012	76940085
274016571	chrX	76937285	76937459	76937313	76937433	ATRX	NM_138270	2	34	8	-	76937012	76940085
273999827	chrX	76937662	76937830	76937689	76937804	ATRX	NM_000489	1	35	9	-	76937012	76940085
273999827	chrX	76937662	76937830	76937689	76937804	ATRX	NM_138270	2	34	8	-	76937012	76940085
274001249	chrX	76938032	76938204	76938059	76938178	ATRX	NM_000489	1	35	9	-	76937012	76940085
274001249	chrX	76938032	76938204	76938059	76938178	ATRX	NM_138270	2	34	8	-	76937012	76940085
274005442	chrX	76938623	76938785	76938650	76938761	ATRX	NM_000489	1	35	9	-	76937012	76940085
274005442	chrX	76938623	76938785	76938650	76938761	ATRX	NM_138270	2	34	8	-	76937012	76940085
272771715	chrX	76939069	76939233	76939095	76939209	ATRX	NM_000489	1	35	9	-	76937012	76940085
272771715	chrX	76939069	76939233	76939095	76939209	ATRX	NM_138270	2	34	8	-	76937012	76940085
272816108	chrX	76939417	76939568	76939445	76939545	ATRX	NM_000489	1	35	9	-	76937012	76940085
272816108	chrX	76939417	76939568	76939445	76939545	ATRX	NM_138270	2	34	8	-	76937012	76940085
274024423	chrX	76939735	76939895	76939763	76939867	ATRX	NM_000489	1	35	9	-	76937012	76940085
274024423	chrX	76939735	76939895	76939763	76939867	ATRX	NM_138270	2	34	8	-	76937012	76940085
272803832	chrX	76949239	76949402	76949266	76949374	ATRX	NM_000489	1	35	6	-	76949313	76949426
273003474	chrX	76953044	76953174	76953069	76953146	ATRX	NM_000489	1	35	4	-	76953071	76953123
273003474	chrX	76953044	76953174	76953069	76953146	ATRX	NM_138270	2	34	4	-	76953071	76953123
273602546	chrX	76972654	76972809	76972679	76972781	ATRX	NM_000489	1	35	2	-	76972608	76972720
273602546	chrX	76972654	76972809	76972679	76972781	ATRX	NM_138270	2	34	2	-	76972608	76972720
269763532	chrX	79278509	79278683	79278530	79278655	TBX22	NM_016954	3	8	2	+	79278559	79278739
269763532	chrX	79278509	79278683	79278530	79278655	TBX22	NM_001109878	1	9	3	+	79278559	79278739
269763532	chrX	79278509	79278683	79278530	79278655	TBX22	NM_001109879	2	9	3	+	79278559	79278735

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270161133	chrX	79281128	79281300	79281151	79281277	TBX22	NM_016954	3	8	4	+	79281102	79281276
270161133	chrX	79281128	79281300	79281151	79281277	TBX22	NM_001109879	2	9	5	+	79281102	79281276
270161133	chrX	79281128	79281300	79281151	79281277	TBX22	NM_001109878	1	9	5	+	79281102	79281276
271294209	chrX	79283460	79283596	79283483	79283568	TBX22	NM_016954	3	8	7	+	79283490	79283575
271294209	chrX	79283460	79283596	79283483	79283568	TBX22	NM_001109879	2	9	8	+	79283490	79283575
271294209	chrX	79283460	79283596	79283483	79283568	TBX22	NM_001109878	1	9	8	+	79283490	79283575
271677659	chrX	79286178	79286350	79286203	79286322	TBX22	NM_016954	3	8	8	+	79285997	79287268
271677659	chrX	79286178	79286350	79286203	79286322	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271677659	chrX	79286178	79286350	79286203	79286322	TBX22	NM_001109878	1	9	9	+	79285997	79287268
264894959	chrX	100604827	100604990	100604848	100604962	BTK	NM_000061	1	19	19	-	100604435	100604944
254241303	chrX	100608842	100609008	100608869	100608983	BTK	NM_000061	1	19	17	-	100608858	100608976
259126143	chrX	100611687	100611844	100611710	100611822	BTK	NM_000061	1	19	14	-	100611772	100611943
263851301	chrX	100613286	100613455	100613307	100613427	BTK	NM_000061	1	19	12	-	100613298	100613425
265951022	chrX	100615411	100615583	100615433	100615562	BTK	NM_000061	1	19	8	-	100615556	100615743
254463962	chrX	100617482	100617607	100617503	100617584	BTK	NM_000061	1	19	6	-	100617549	100617677
263822180	chrX	100629482	100629652	100629505	100629623	BTK	NM_000061	1	19	3	-	100629524	100629622
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_001128172	4	15	1	+	110366305	110366506
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_001128168	3	16	1	+	110366305	110366506
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_001128173	5	15	1	+	110366305	110366506
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_001128166	1	16	3	+	110366305	110366506
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_001128167	2	15	2	+	110366305	110366506
271309755	chrX	110366367	110366527	110366388	110366506	PAK3	NM_002578	6	18	5	+	110366305	110366506
270708117	chrX	110389651	110389820	110389672	110389799	PAK3	NM_001128168	3	16	4	+	110389749	110389793
270708117	chrX	110389651	110389820	110389672	110389799	PAK3	NM_001128173	5	15	3	+	110389749	110389793
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_001128172	4	15	6	+	110406143	110406274
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_001128168	3	16	7	+	110406143	110406274
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_001128173	5	15	6	+	110406143	110406274
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_001128166	1	16	7	+	110406143	110406274
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_001128167	2	15	6	+	110406143	110406274
269560459	chrX	110406031	110406176	110406057	110406159	PAK3	NM_002578	6	18	9	+	110406143	110406274
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_001128172	4	15	7	+	110406790	110406955
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_001128168	3	16	8	+	110406790	110406955
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_001128173	5	15	7	+	110406790	110406955
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_001128166	1	16	8	+	110406790	110406955
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_001128167	2	15	7	+	110406790	110406955
271059216	chrX	110406819	110406989	110406840	110406961	PAK3	NM_002578	6	18	10	+	110406790	110406955
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_001128172	4	15	10	+	110435734	110435846
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_001128168	3	16	11	+	110435734	110435846
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_001128173	5	15	10	+	110435734	110435846
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_001128166	1	16	11	+	110435734	110435846
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_001128167	2	15	10	+	110435734	110435846

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269830478	chrX	110435645	110435778	110435671	110435756	PAK3	NM_002578	6	18	13	+	110435734	110435846
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_001128172	4	15	12	+	110439070	110439169
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_001128168	3	16	13	+	110439070	110439169
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_001128173	5	15	12	+	110439070	110439169
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_001128166	1	16	13	+	110439070	110439169
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_001128167	2	15	12	+	110439070	110439169
270032966	chrX	110438943	110439107	110438971	110439086	PAK3	NM_002578	6	18	15	+	110439070	110439169
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_001128172	4	15	14	+	110459649	110459786
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_001128168	3	16	15	+	110459649	110459786
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_001128173	5	15	14	+	110459649	110459786
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_001128166	1	16	15	+	110459649	110459786
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_001128167	2	15	14	+	110459649	110459786
270826670	chrX	110459585	110459717	110459606	110459693	PAK3	NM_002578	6	18	17	+	110459649	110459786
299281162	chrX	123480393	123480539	123480414	123480518	SH2D1A	NM_001114937	1	4	1	+	123480132	123480629
299281162	chrX	123480393	123480539	123480414	123480518	SH2D1A	NM_002351	2	4	1	+	123480132	123480629
299081217	chrX	123504067	123504211	123504094	123504188	SH2D1A	NM_002351	2	4	3	+	123504026	123504170
299081217	chrX	123504067	123504211	123504094	123504188	SH2D1A	NM_001114937	1	4	3	+	123504026	123504161
295144845	chrX	152482253	152482426	152482272	152482398	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
295157023	chrX	152482679	152482822	152482701	152482797	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
298952269	chrX	153760112	153760283	153760134	153760262	G6PD	NM_001042351	2	13	13	-	153759606	153760305
298952269	chrX	153760112	153760283	153760134	153760262	G6PD	NM_000402	1	13	13	-	153759606	153760305
299074230	chrX	153760556	153760699	153760576	153760677	G6PD	NM_001042351	2	13	11	-	153760601	153760677
299074230	chrX	153760556	153760699	153760576	153760677	G6PD	NM_000402	1	13	11	-	153760601	153760677
299079254	chrX	153761235	153761369	153761255	153761346	G6PD	NM_001042351	2	13	9	-	153761157	153761343
299079254	chrX	153761235	153761369	153761255	153761346	G6PD	NM_000402	1	13	9	-	153761157	153761343
298998844	chrX	153762295	153762467	153762315	153762446	G6PD	NM_001042351	2	13	7	-	153762250	153762375
298998844	chrX	153762295	153762467	153762315	153762446	G6PD	NM_000402	1	13	7	-	153762250	153762375
298969749	chrX	153763397	153763564	153763420	153763544	G6PD	NM_001042351	2	13	5	-	153763383	153763600
298969749	chrX	153763397	153763564	153763420	153763544	G6PD	NM_000402	1	13	5	-	153763383	153763600
298926789	chrX	153764335	153764461	153764355	153764437	G6PD	NM_001042351	2	13	3	-	153764356	153764393
298926789	chrX	153764335	153764461	153764355	153764437	G6PD	NM_000402	1	13	3	-	153764356	153764393
262048751	chr1	2489127	2489291	2489145	2489273	TNFRSF14	NM_003820	1	8	2	+	2489165	2489273
264057049	chr1	2492039	2492173	2492060	2492154	TNFRSF14	NM_003820	1	8	5	+	2492063	2492153
266253379	chr1	2494560	2494693	2494579	2494671	TNFRSF14	NM_003820	1	8	8	+	2494587	2495267
294022088	chr1	6527887	6528044	6527907	6528025	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294022088	chr1	6527887	6528044	6527907	6528025	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646
294022088	chr1	6527887	6528044	6527907	6528025	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294022088	chr1	6527887	6528044	6527907	6528025	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294022088	chr1	6527887	6528044	6527907	6528025	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
294044396	chr1	6528372	6528539	6528392	6528519	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294044396	chr1	6528372	6528539	6528392	6528519	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294044396	chr1	6528372	6528539	6528392	6528519	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294044396	chr1	6528372	6528539	6528392	6528519	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294044396	chr1	6528372	6528539	6528392	6528519	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
295414203	chr1	6529372	6529535	6529393	6529514	PLEKHG5	NM_001042664	2	21	18	-	6529395	6529510
295414203	chr1	6529372	6529535	6529393	6529514	PLEKHG5	NM_001042665	3	21	18	-	6529395	6529510
295414203	chr1	6529372	6529535	6529393	6529514	PLEKHG5	NM_020631	4	21	18	-	6529395	6529510
295414203	chr1	6529372	6529535	6529393	6529514	PLEKHG5	NM_001042663	1	22	19	-	6529395	6529510
295414203	chr1	6529372	6529535	6529393	6529514	PLEKHG5	NM_198681	5	22	19	-	6529395	6529510
293783932	chr1	6530176	6530330	6530199	6530310	PLEKHG5	NM_001042664	2	21	16	-	6530296	6530415
293783932	chr1	6530176	6530330	6530199	6530310	PLEKHG5	NM_001042665	3	21	16	-	6530296	6530415
293783932	chr1	6530176	6530330	6530199	6530310	PLEKHG5	NM_020631	4	21	16	-	6530296	6530415
293783932	chr1	6530176	6530330	6530199	6530310	PLEKHG5	NM_001042663	1	22	17	-	6530296	6530415
293783932	chr1	6530176	6530330	6530199	6530310	PLEKHG5	NM_198681	5	22	17	-	6530296	6530415
294263207	chr1	6530688	6530851	6530707	6530831	PLEKHG5	NM_001042664	2	21	14	-	6530795	6530944
294263207	chr1	6530688	6530851	6530707	6530831	PLEKHG5	NM_001042665	3	21	14	-	6530795	6530944
294263207	chr1	6530688	6530851	6530707	6530831	PLEKHG5	NM_020631	4	21	14	-	6530795	6530944
294263207	chr1	6530688	6530851	6530707	6530831	PLEKHG5	NM_001042663	1	22	15	-	6530795	6530944
294263207	chr1	6530688	6530851	6530707	6530831	PLEKHG5	NM_198681	5	22	15	-	6530795	6530944
294304450	chr1	6531040	6531188	6531057	6531171	PLEKHG5	NM_001042664	2	21	13	-	6531050	6531160
294304450	chr1	6531040	6531188	6531057	6531171	PLEKHG5	NM_001042665	3	21	13	-	6531050	6531160
294304450	chr1	6531040	6531188	6531057	6531171	PLEKHG5	NM_020631	4	21	13	-	6531050	6531160
294304450	chr1	6531040	6531188	6531057	6531171	PLEKHG5	NM_001042663	1	22	14	-	6531050	6531160
294304450	chr1	6531040	6531188	6531057	6531171	PLEKHG5	NM_198681	5	22	14	-	6531050	6531160
294791500	chr1	6531766	6531893	6531784	6531873	PLEKHG5	NM_001042664	2	21	11	-	6531818	6531868
294791500	chr1	6531766	6531893	6531784	6531873	PLEKHG5	NM_001042665	3	21	11	-	6531818	6531868
294791500	chr1	6531766	6531893	6531784	6531873	PLEKHG5	NM_020631	4	21	11	-	6531818	6531868
294791500	chr1	6531766	6531893	6531784	6531873	PLEKHG5	NM_001042663	1	22	12	-	6531818	6531868
294791500	chr1	6531766	6531893	6531784	6531873	PLEKHG5	NM_198681	5	22	12	-	6531818	6531868
294031686	chr1	6533094	6533257	6533114	6533236	PLEKHG5	NM_001042664	2	21	9	-	6533046	6533234
294031686	chr1	6533094	6533257	6533114	6533236	PLEKHG5	NM_001042665	3	21	9	-	6533046	6533234
294031686	chr1	6533094	6533257	6533114	6533236	PLEKHG5	NM_020631	4	21	9	-	6533046	6533234
294031686	chr1	6533094	6533257	6533114	6533236	PLEKHG5	NM_001042663	1	22	10	-	6533046	6533234
294031686	chr1	6533094	6533257	6533114	6533236	PLEKHG5	NM_198681	5	22	10	-	6533046	6533234
294004934	chr1	6534054	6534187	6534072	6534167	PLEKHG5	NM_001042664	2	21	7	-	6534073	6534224
294004934	chr1	6534054	6534187	6534072	6534167	PLEKHG5	NM_001042665	3	21	7	-	6534073	6534224
294004934	chr1	6534054	6534187	6534072	6534167	PLEKHG5	NM_020631	4	21	7	-	6534073	6534224
294004934	chr1	6534054	6534187	6534072	6534167	PLEKHG5	NM_001042663	1	22	8	-	6534073	6534224
294004934	chr1	6534054	6534187	6534072	6534167	PLEKHG5	NM_198681	5	22	8	-	6534073	6534224
293975925	chr1	6535082	6535242	6535100	6535223	PLEKHG5	NM_001042664	2	21	5	-	6535107	6535198
293975925	chr1	6535082	6535242	6535100	6535223	PLEKHG5	NM_001042665	3	21	5	-	6535107	6535198
293975925	chr1	6535082	6535242	6535100	6535223	PLEKHG5	NM_020631	4	21	5	-	6535107	6535198

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293975925	chr1	6535082	6535242	6535100	6535223	PLEKHG5	NM_001042663	1	22	6	-	6535107	6535198
293975925	chr1	6535082	6535242	6535100	6535223	PLEKHG5	NM_198681	5	22	6	-	6535107	6535198
294219723	chr1	6537612	6537758	6537635	6537737	PLEKHG5	NM_001042664	2	21	2	-	6537589	6537718
294219723	chr1	6537612	6537758	6537635	6537737	PLEKHG5	NM_001042665	3	21	2	-	6537589	6537718
294219723	chr1	6537612	6537758	6537635	6537737	PLEKHG5	NM_020631	4	21	2	-	6537589	6537718
294219723	chr1	6537612	6537758	6537635	6537737	PLEKHG5	NM_001042663	1	22	3	-	6537589	6537718
294219723	chr1	6537612	6537758	6537635	6537737	PLEKHG5	NM_198681	5	22	3	-	6537589	6537718
295308640	chr1	9770444	9770578	9770469	9770557	PIK3CD	NM_005026	1	24	3	+	9770482	9770654
294127306	chr1	9775777	9775936	9775797	9775915	PIK3CD	NM_005026	1	24	5	+	9775907	9776136
294127306	chr1	9775777	9775936	9775797	9775915	PIK3CD	NM_005026	1	24	4	+	9775599	9775827
294142967	chr1	9776098	9776263	9776116	9776243	PIK3CD	NM_005026	1	24	5	+	9775907	9776136
294710384	chr1	9777045	9777184	9777064	9777166	PIK3CD	NM_005026	1	24	7	+	9777017	9777166
294171402	chr1	9778891	9779058	9778909	9779039	PIK3CD	NM_005026	1	24	9	+	9778752	9778973
294153785	chr1	9780644	9780784	9780661	9780765	PIK3CD	NM_005026	1	24	12	+	9780669	9780719
294419390	chr1	9781443	9781578	9781462	9781559	PIK3CD	NM_005026	1	24	15	+	9781502	9781645
293820708	chr1	9781956	9782125	9781975	9782105	PIK3CD	NM_005026	1	24	17	+	9782033	9782211
294356489	chr1	9782532	9782698	9782556	9782679	PIK3CD	NM_005026	1	24	19	+	9782586	9782664
294858107	chr1	9784095	9784239	9784112	9784220	PIK3CD	NM_005026	1	24	21	+	9784027	9784150
295343366	chr1	9786941	9787067	9786961	9787043	PIK3CD	NM_005026	1	24	24	+	9786967	9789172
241982994	chr1	11169314	11169481	11169342	11169455	MTOR	NM_004958	1	58	56	-	11169347	11169427
236649203	chr1	11174470	11174636	11174494	11174611	MTOR	NM_004958	1	58	53	-	11174375	11174510
239287620	chr1	11177068	11177239	11177092	11177210	MTOR	NM_004958	1	58	50	-	11177061	11177143
237799313	chr1	11182053	11182221	11182078	11182196	MTOR	NM_004958	1	58	48	-	11182036	11182183
258773859	chr1	11186718	11186889	11186738	11186861	MTOR	NM_004958	1	58	46	-	11186679	11186853
237168797	chr1	11187753	11187888	11187777	11187864	MTOR	NM_004958	1	58	44	-	11187681	11187863
236005921	chr1	11188548	11188713	11188569	11188686	MTOR	NM_004958	1	58	42	-	11188511	11188609
236787506	chr1	11190470	11190614	11190492	11190597	MTOR	NM_004958	1	58	39	-	11190586	11190834
237151966	chr1	11193049	11193213	11193069	11193191	MTOR	NM_004958	1	58	38	-	11193137	11193254
235654051	chr1	11199238	11199411	11199260	11199388	MTOR	NM_004958	1	58	36	-	11199361	11199492
236637644	chr1	11204721	11204868	11204742	11204843	MTOR	NM_004958	1	58	34	-	11204705	11204812
236907273	chr1	11210216	11210343	11210237	11210314	MTOR	NM_004958	1	58	31	-	11210183	11210283
242103345	chr1	11259259	11259394	11259284	11259368	MTOR	NM_004958	1	58	28	-	11259315	11259460
236894655	chr1	11264597	11264734	11264617	11264712	MTOR	NM_004958	1	58	26	-	11264618	11264760
236380636	chr1	11270820	11270987	11270848	11270963	MTOR	NM_004958	1	58	24	-	11270871	11270963
237831689	chr1	11273425	11273597	11273448	11273571	MTOR	NM_004958	1	58	21	-	11273456	11273623
237255384	chr1	11288787	11288958	11288809	11288935	MTOR	NM_004958	1	58	19	-	11288725	11288975
242175293	chr1	11291246	11291413	11291267	11291386	MTOR	NM_004958	1	58	17	-	11291357	11291491
235121199	chr1	11293481	11293637	11293506	11293609	MTOR	NM_004958	1	58	15	-	11293455	11293544
238668874	chr1	11298392	11298566	11298415	11298545	MTOR	NM_004958	1	58	12	-	11298459	11298674
242422869	chr1	11300373	11300541	11300390	11300517	MTOR	NM_004958	1	58	11	-	11300360	11300604
238420729	chr1	11303114	11303265	11303137	11303244	MTOR	NM_004958	1	58	9	-	11303171	11303357

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235270493	chr1	11307948	11308117	11307969	11308097	MTOR	NM_004958	1	58	7	-	11307876	11308151
237286655	chr1	11316026	11316200	11316048	11316178	MTOR	NM_004958	1	58	5	-	11316049	11316249
237719798	chr1	11318420	11318580	11318443	11318557	MTOR	NM_004958	1	58	3	-	11318542	11318650
239727682	chr1	17345272	17345440	17345299	17345413	SDHB	NM_003000	1	8	8	-	17345225	17345453
242733483	chr1	17350424	17350592	17350451	17350569	SDHB	NM_003000	1	8	6	-	17350468	17350569
264243893	chr1	17355092	17355259	17355117	17355231	SDHB	NM_003000	1	8	4	-	17355095	17355231
238617532	chr1	17380422	17380584	17380442	17380566	SDHB	NM_003000	1	8	1	-	17380443	17380665
237567115	chr1	18960956	18961086	18960977	18961066	PAX7	NM_002584	2	8	2	+	18960797	18961032
237567115	chr1	18960956	18961086	18960977	18961066	PAX7	NM_001135254	1	9	2	+	18960797	18961032
237567115	chr1	18960956	18961086	18960977	18961066	PAX7	NM_013945	3	8	2	+	18960797	18961032
240337721	chr1	18962835	18962985	18962853	18962964	PAX7	NM_013945	3	8	4	+	18962737	18962865
240337721	chr1	18962835	18962985	18962853	18962964	PAX7	NM_002584	2	8	4	+	18962731	18962865
240337721	chr1	18962835	18962985	18962853	18962964	PAX7	NM_001135254	1	9	4	+	18962731	18962865
235271482	chr1	19027075	19027243	19027098	19027226	PAX7	NM_002584	2	8	6	+	19027147	19027312
235271482	chr1	19027075	19027243	19027098	19027226	PAX7	NM_001135254	1	9	6	+	19027147	19027312
235271482	chr1	19027075	19027243	19027098	19027226	PAX7	NM_013945	3	8	6	+	19027147	19027312
237301468	chr1	19062099	19062272	19062120	19062251	PAX7	NM_001135254	1	9	8	+	19062126	19062372
237301468	chr1	19062099	19062272	19062120	19062251	PAX7	NM_002584	2	8	8	+	19062126	19062632
237301468	chr1	19062099	19062272	19062120	19062251	PAX7	NM_013945	3	8	8	+	19062126	19062632
237582536	chr1	19071311	19071471	19071338	19071450	PAX7	NM_001135254	1	9	9	+	19071308	19075360
225016684	chr1	27023339	27023511	27023356	27023491	ARID1A	NM_139135	2	20	1	+	27022522	27024031
225016684	chr1	27023339	27023511	27023356	27023491	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223547417	chr1	27023777	27023903	27023797	27023885	ARID1A	NM_139135	2	20	1	+	27022522	27024031
223547417	chr1	27023777	27023903	27023797	27023885	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223467808	chr1	27056214	27056388	27056233	27056362	ARID1A	NM_139135	2	20	2	+	27056142	27056354
223467808	chr1	27056214	27056388	27056233	27056362	ARID1A	NM_006015	1	20	2	+	27056142	27056354
222726251	chr1	27057949	27058117	27057968	27058097	ARID1A	NM_139135	2	20	3	+	27057643	27058095
222726251	chr1	27057949	27058117	27057968	27058097	ARID1A	NM_006015	1	20	3	+	27057643	27058095
222488467	chr1	27087441	27087613	27087464	27087593	ARID1A	NM_139135	2	20	5	+	27087347	27087587
222488467	chr1	27087441	27087613	27087464	27087593	ARID1A	NM_006015	1	20	5	+	27087347	27087587
222881883	chr1	27088697	27088861	27088716	27088837	ARID1A	NM_139135	2	20	7	+	27088643	27088810
222881883	chr1	27088697	27088861	27088716	27088837	ARID1A	NM_006015	1	20	7	+	27088643	27088810
225164710	chr1	27092631	27092794	27092653	27092766	ARID1A	NM_139135	2	20	9	+	27092712	27092857
225164710	chr1	27092631	27092794	27092653	27092766	ARID1A	NM_006015	1	20	9	+	27092712	27092857
223443770	chr1	27094169	27094324	27094193	27094298	ARID1A	NM_139135	2	20	11	+	27094281	27094490
223443770	chr1	27094169	27094324	27094193	27094298	ARID1A	NM_006015	1	20	11	+	27094281	27094490
223289373	chr1	27097676	27097836	27097700	27097817	ARID1A	NM_139135	2	20	12	+	27097610	27097817
223289373	chr1	27097676	27097836	27097700	27097817	ARID1A	NM_006015	1	20	12	+	27097610	27097817
222906595	chr1	27099355	27099512	27099377	27099485	ARID1A	NM_139135	2	20	14	+	27099303	27099478
222906595	chr1	27099355	27099512	27099377	27099485	ARID1A	NM_006015	1	20	14	+	27099303	27099478
223591659	chr1	27100124	27100255	27100145	27100235	ARID1A	NM_139135	2	20	16	+	27100071	27100208

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223591659	chr1	27100124	27100255	27100145	27100235	ARID1A	NM_006015	1	20	16	+	27100071	27100208
225160828	chr1	27100979	27101145	27101002	27101124	ARID1A	NM_006015	1	20	18	+	27100820	27101711
222552803	chr1	27101416	27101556	27101438	27101533	ARID1A	NM_006015	1	20	18	+	27100820	27101711
222552803	chr1	27101416	27101556	27101438	27101533	ARID1A	NM_139135	2	20	18	+	27101471	27101711
223193788	chr1	27102118	27102244	27102139	27102219	ARID1A	NM_139135	2	20	19	+	27102068	27102198
223193788	chr1	27102118	27102244	27102139	27102219	ARID1A	NM_006015	1	20	19	+	27102068	27102198
223539842	chr1	27105746	27105879	27105769	27105854	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223539842	chr1	27105746	27105879	27105769	27105854	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223543832	chr1	27106152	27106305	27106173	27106284	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223543832	chr1	27106152	27106305	27106173	27106284	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224979763	chr1	27106545	27106670	27106566	27106648	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224979763	chr1	27106545	27106670	27106566	27106648	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224973534	chr1	27106937	27107087	27106957	27107069	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224973534	chr1	27106937	27107087	27106957	27107069	ARID1A	NM_006015	1	20	20	+	27105514	27108601
233536297	chr1	32739957	32740083	32739982	32740060	LCK	NM_005356	2	13	2	+	32739926	32740035
233536297	chr1	32739957	32740083	32739982	32740060	LCK	NM_001042771	1	13	2	+	32739926	32740035
231440621	chr1	32741093	32741261	32741111	32741243	LCK	NM_005356	2	13	6	+	32741170	32741273
231440621	chr1	32741093	32741261	32741111	32741243	LCK	NM_001042771	1	13	6	+	32741170	32741273
233220907	chr1	32741885	32742053	32741906	32742035	LCK	NM_005356	2	13	8	+	32741938	32742090
233220907	chr1	32741885	32742053	32741906	32742035	LCK	NM_001042771	1	13	8	+	32741938	32742090
233695721	chr1	32745238	32745400	32745258	32745379	LCK	NM_005356	2	13	10	+	32745272	32745348
233695721	chr1	32745238	32745400	32745258	32745379	LCK	NM_001042771	1	13	10	+	32745272	32745348
233076894	chr1	32745693	32745851	32745714	32745829	LCK	NM_005356	2	13	12	+	32745680	32745811
233076894	chr1	32745693	32745851	32745714	32745829	LCK	NM_001042771	1	13	12	+	32745680	32745811
241487484	chr1	40363047	40363187	40363071	40363162	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
241487484	chr1	40363047	40363187	40363071	40363162	MYCL1	NM_001033081	1	2	2	-	40361096	40363642
236541239	chr1	40363499	40363669	40363520	40363643	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
236541239	chr1	40363499	40363669	40363520	40363643	MYCL1	NM_001033081	1	2	2	-	40361096	40363642
235126969	chr1	40366697	40366858	40366714	40366838	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235126969	chr1	40366697	40366858	40366714	40366838	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235126969	chr1	40366697	40366858	40366714	40366838	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
235130386	chr1	40367064	40367194	40367092	40367177	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235130386	chr1	40367064	40367194	40367092	40367177	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235130386	chr1	40367064	40367194	40367092	40367177	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
240536873	chr1	43804269	43804414	43804291	43804392	MPL	NM_005373	1	12	3	+	43804213	43804391
236649993	chr1	43805588	43805740	43805609	43805719	MPL	NM_005373	1	12	5	+	43805635	43805797
241621238	chr1	43812077	43812234	43812099	43812208	MPL	NM_005373	1	12	7	+	43812116	43812300
239482302	chr1	43814458	43814628	43814477	43814608	MPL	NM_005373	1	12	9	+	43814514	43814673
241673388	chr1	43818154	43818321	43818175	43818299	MPL	NM_005373	1	12	12	+	43818189	43820135
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_012222	6	16	16	-	45794914	45795109
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_001048171	1	16	16	-	45794914	45795109

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_001128425	5	16	16	-	45794914	45795109
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_001048174	4	16	16	-	45794914	45795109
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_001048173	3	16	16	-	45794914	45795109
239760064	chr1	45795016	45795143	45795044	45795123	MUTYH	NM_001048172	2	16	16	-	45794914	45795109
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_012222	6	16	13	-	45797092	45797228
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_001048171	1	16	13	-	45797092	45797228
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_001128425	5	16	13	-	45797092	45797228
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_001048174	4	16	13	-	45797092	45797228
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_001048173	3	16	13	-	45797092	45797228
258584191	chr1	45797034	45797208	45797056	45797190	MUTYH	NM_001048172	2	16	13	-	45797092	45797228
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_012222	6	16	11	-	45797695	45797758
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_001048171	1	16	11	-	45797695	45797758
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_001128425	5	16	11	-	45797695	45797758
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_001048174	4	16	11	-	45797695	45797758
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_001048173	3	16	11	-	45797695	45797758
236870789	chr1	45797614	45797788	45797639	45797766	MUTYH	NM_001048172	2	16	11	-	45797695	45797758
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_012222	6	16	8	-	45798246	45798359
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_001048171	1	16	8	-	45798246	45798359
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_001128425	5	16	8	-	45798246	45798359
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_001048174	4	16	8	-	45798246	45798359
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_001048173	3	16	8	-	45798246	45798359
238611281	chr1	45798227	45798383	45798245	45798359	MUTYH	NM_001048172	2	16	8	-	45798246	45798359
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_012222	6	16	4	-	45798957	45798996
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_001048171	1	16	4	-	45798957	45798996
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_001128425	5	16	4	-	45798957	45798996
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_001048174	4	16	4	-	45798957	45798996
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_001048173	3	16	4	-	45798957	45798996
236300614	chr1	45798861	45799035	45798881	45799013	MUTYH	NM_001048172	2	16	4	-	45798957	45798996
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_012222	6	16	2	-	45800063	45800183
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_001048171	1	16	2	-	45800063	45800183
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_001128425	5	16	2	-	45800063	45800183
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_001048174	4	16	2	-	45800063	45800183
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_001048173	3	16	2	-	45800063	45800183
238676907	chr1	45800037	45800200	45800058	45800177	MUTYH	NM_001048172	2	16	2	-	45800063	45800183
265140470	chr1	47685539	47685701	47685560	47685680	TAL1	NM_003189	1	4	4	-	47681963	47685846
262508669	chr1	47689664	47689802	47689684	47689780	TAL1	NM_003189	1	4	3	-	47689676	47689770
240389174	chr1	47691329	47691474	47691348	47691457	TAL1	NM_003189	1	4	2	-	47691115	47691561
321848553	chr1	47834078	47834213	47834105	47834186	CMPK1	NM_016308	2	6	2	+	47834141	47834287
321637903	chr1	47840518	47840686	47840545	47840658	CMPK1	NM_016308	2	6	4	+	47840581	47840657
321637903	chr1	47840518	47840686	47840545	47840658	CMPK1	NM_001136140	1	5	3	+	47840581	47840657
225613002	chr1	51435964	51436138	51435985	51436110	CDKN2C	NM_001262	1	3	2	+	51436030	51436169

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225613002	chr1	51435964	51436138	51435985	51436110	CDKN2C	NM_078626	2	2	1	+	51435642	51436169
225614092	chr1	51439725	51439897	51439750	51439875	CDKN2C	NM_001262	1	3	3	+	51439565	51440306
225614092	chr1	51439725	51439897	51439750	51439875	CDKN2C	NM_078626	2	2	2	+	51439565	51440309
232169834	chr1	59247863	59248000	59247884	59247981	JUN	NM_002228	1	1	1	-	59246463	59249785
231967051	chr1	59248616	59248764	59248636	59248743	JUN	NM_002228	1	1	1	-	59246463	59249785
233347932	chr1	65300198	65300344	65300226	65300315	JAK1	NM_002227	1	25	25	-	65298906	65300340
232503885	chr1	65301799	65301926	65301823	65301899	JAK1	NM_002227	1	25	23	-	65301781	65301898
232207751	chr1	65304174	65304330	65304203	65304309	JAK1	NM_002227	1	25	21	-	65304148	65304272
233068998	chr1	65307042	65307213	65307065	65307193	JAK1	NM_002227	1	25	18	-	65307134	65307284
232234090	chr1	65310335	65310494	65310363	65310473	JAK1	NM_002227	1	25	16	-	65310437	65310572
233141675	chr1	65312306	65312457	65312330	65312435	JAK1	NM_002227	1	25	14	-	65312332	65312419
233653515	chr1	65316484	65316649	65316505	65316628	JAK1	NM_002227	1	25	12	-	65316487	65316593
232259796	chr1	65325753	65325903	65325776	65325881	JAK1	NM_002227	1	25	9	-	65325788	65325945
232890656	chr1	65332477	65332620	65332503	65332595	JAK1	NM_002227	1	25	7	-	65332549	65332891
231434090	chr1	65334881	65335054	65334904	65335030	JAK1	NM_002227	1	25	6	-	65334994	65335157
232309174	chr1	65344683	65344808	65344705	65344785	JAK1	NM_002227	1	25	4	-	65344708	65344831
233764635	chr1	65349086	65349229	65349108	65349201	JAK1	NM_002227	1	25	3	-	65348960	65349158
223199473	chr1	85733388	85733549	85733410	85733526	BCL10	NM_003921	1	3	3	-	85731460	85733665
222964581	chr1	85736332	85736468	85736360	85736441	BCL10	NM_003921	1	3	2	-	85736301	85736589
222573743	chr1	85741968	85742141	85741991	85742118	BCL10	NM_003921	1	3	1	-	85741979	85742587
298915050	chr1	97547885	97548058	97547909	97548030	DPYD	NM_000110	1	23	22	-	97547886	97548026
299068952	chr1	97658669	97658830	97658691	97658806	DPYD	NM_000110	1	23	20	-	97658625	97658804
299017958	chr1	97771689	97771860	97771716	97771839	DPYD	NM_000110	1	23	17	-	97771733	97771853
328862504	chr1	97847856	97848012	97847884	97847984	DPYD	NM_000110	1	23	15	-	97847949	97848017
329992343	chr1	97915737	97915904	97915757	97915876	DPYD	NM_000110	1	23	14	-	97915615	97915779
299235064	chr1	98015091	98015243	98015115	98015216	DPYD	NM_000110	1	23	12	-	98015116	98015300
299157917	chr1	98039436	98039562	98039463	98039531	DPYD	NM_000110	1	23	11	-	98039316	98039526
299103977	chr1	98060607	98060765	98060633	98060738	DPYD	NM_000110	1	23	9	-	98060615	98060722
299237732	chr1	98164853	98164998	98164879	98164972	DPYD	NM_000110	1	23	6	-	98164907	98165103
298944377	chr1	98187103	98187236	98187124	98187208	DPYD	NM_001160301	2	6	5	-	98187066	98187227
298944377	chr1	98187103	98187236	98187124	98187208	DPYD	NM_000110	1	23	5	-	98187066	98187227
299166900	chr1	98293583	98293756	98293607	98293728	DPYD	NM_001160301	2	6	3	-	98293670	98293752
299166900	chr1	98293583	98293756	98293607	98293728	DPYD	NM_000110	1	23	3	-	98293670	98293752
262138043	chr1	114940160	114940332	114940183	114940310	TRIM33	NM_015906	1	20	20	-	114935399	114940482
262138043	chr1	114940160	114940332	114940183	114940310	TRIM33	NM_033020	2	19	19	-	114935399	114940482
238791843	chr1	114941953	114942126	114941981	114942108	TRIM33	NM_015906	1	20	18	-	114942079	114942231
238791843	chr1	114941953	114942126	114941981	114942108	TRIM33	NM_033020	2	19	18	-	114942079	114942231
239655775	chr1	114945446	114945582	114945475	114945561	TRIM33	NM_015906	1	20	16	-	114945382	114945505
239655775	chr1	114945446	114945582	114945475	114945561	TRIM33	NM_033020	2	19	16	-	114945382	114945505
264799403	chr1	114948242	114948402	114948265	114948374	TRIM33	NM_015906	1	20	15	-	114948032	114948381
264799403	chr1	114948242	114948402	114948265	114948374	TRIM33	NM_033020	2	19	15	-	114948032	114948381

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263213093	chr1	114952786	114952943	114952812	114952922	TRIM33	NM_015906	1	20	12	-	114952806	114952938
263213093	chr1	114952786	114952943	114952812	114952922	TRIM33	NM_033020	2	19	12	-	114952806	114952938
242527953	chr1	114964150	114964304	114964170	114964276	TRIM33	NM_015906	1	20	11	-	114964058	114964258
242527953	chr1	114964150	114964304	114964170	114964276	TRIM33	NM_033020	2	19	11	-	114964058	114964258
239383830	chr1	114968096	114968229	114968120	114968209	TRIM33	NM_015906	1	20	9	-	114968071	114968345
239383830	chr1	114968096	114968229	114968120	114968209	TRIM33	NM_033020	2	19	9	-	114968071	114968345
264645373	chr1	114969798	114969923	114969826	114969895	TRIM33	NM_015906	1	20	8	-	114969799	114969916
264645373	chr1	114969798	114969923	114969826	114969895	TRIM33	NM_033020	2	19	8	-	114969799	114969916
241398926	chr1	114973463	114973597	114973487	114973570	TRIM33	NM_015906	1	20	6	-	114973420	114973534
241398926	chr1	114973463	114973597	114973487	114973570	TRIM33	NM_033020	2	19	6	-	114973420	114973534
240576731	chr1	115005738	115005865	115005765	115005844	TRIM33	NM_015906	1	20	4	-	115005726	115005858
240576731	chr1	115005738	115005865	115005765	115005844	TRIM33	NM_033020	2	19	4	-	115005726	115005858
240058818	chr1	115006145	115006280	115006167	115006247	TRIM33	NM_015906	1	20	3	-	115006034	115006178
240058818	chr1	115006145	115006280	115006167	115006247	TRIM33	NM_033020	2	19	3	-	115006034	115006178
266354582	chr1	115053177	115053345	115053194	115053328	TRIM33	NM_015906	1	20	1	-	115053172	115053781
266354582	chr1	115053177	115053345	115053194	115053328	TRIM33	NM_033020	2	19	1	-	115053172	115053781
239853329	chr1	115251163	115251333	115251185	115251310	NRAS	NM_002524	1	7	5	-	115251152	115251275
242658097	chr1	115256502	115256675	115256524	115256653	NRAS	NM_002524	1	7	3	-	115256421	115256599
242215151	chr1	120458025	120458160	120458047	120458140	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242140449	chr1	120458391	120458565	120458414	120458539	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242157302	chr1	120458828	120458998	120458854	120458978	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237463182	chr1	120460205	120460354	120460229	120460327	NOTCH2	NM_024408	2	34	33	-	120460288	120460385
238350885	chr1	120461907	120462039	120461936	120462021	NOTCH2	NM_024408	2	34	31	-	120461935	120462236
235508140	chr1	120462872	120463045	120462894	120463021	NOTCH2	NM_024408	2	34	30	-	120462852	120463020
236144827	chr1	120464919	120465091	120464941	120465069	NOTCH2	NM_024408	2	34	28	-	120464859	120465069
235126962	chr1	120466319	120466488	120466342	120466462	NOTCH2	NM_024408	2	34	26	-	120466260	120466607
242778418	chr1	120467991	120468159	120468013	120468138	NOTCH2	NM_024408	2	34	25	-	120467928	120468433
236912167	chr1	120469020	120469185	120469046	120469164	NOTCH2	NM_024408	2	34	24	-	120469122	120469234
241560220	chr1	120471690	120471862	120471712	120471836	NOTCH2	NM_024408	2	34	23	-	120471599	120471835
237748202	chr1	120479852	120480012	120479875	120479990	NOTCH2	NM_001200001	1	22	21	-	120479905	120480089
237748202	chr1	120479852	120480012	120479875	120479990	NOTCH2	NM_024408	2	34	21	-	120479905	120480089
235323189	chr1	120483149	120483287	120483172	120483262	NOTCH2	NM_001200001	1	22	19	-	120483178	120483379
235323189	chr1	120483149	120483287	120483172	120483262	NOTCH2	NM_024408	2	34	19	-	120483178	120483379
235858166	chr1	120484253	120484420	120484277	120484392	NOTCH2	NM_001200001	1	22	18	-	120484149	120484377
235858166	chr1	120484253	120484420	120484277	120484392	NOTCH2	NM_024408	2	34	18	-	120484149	120484377
238582171	chr1	120491677	120491830	120491699	120491804	NOTCH2	NM_001200001	1	22	16	-	120491630	120491749
238582171	chr1	120491677	120491830	120491699	120491804	NOTCH2	NM_024408	2	34	16	-	120491630	120491749
239960819	chr1	120496215	120496389	120496237	120496361	NOTCH2	NM_001200001	1	22	14	-	120496166	120496311
239960819	chr1	120496215	120496389	120496237	120496361	NOTCH2	NM_024408	2	34	14	-	120496166	120496311
237603917	chr1	120506115	120506287	120506138	120506264	NOTCH2	NM_001200001	1	22	11	-	120506197	120506430
237603917	chr1	120506115	120506287	120506138	120506264	NOTCH2	NM_024408	2	34	11	-	120506197	120506430

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235316396	chr1	120508915	120509052	120508937	120509029	NOTCH2	NM_001200001	1	22	9	-	120508999	120509112
235316396	chr1	120508915	120509052	120508937	120509029	NOTCH2	NM_024408	2	34	9	-	120508999	120509112
236352526	chr1	120510637	120510789	120510664	120510765	NOTCH2	NM_001200001	1	22	7	-	120510700	120510855
236352526	chr1	120510637	120510789	120510664	120510765	NOTCH2	NM_024408	2	34	7	-	120510700	120510855
236057679	chr1	120529522	120529673	120529544	120529652	NOTCH2	NM_001200001	1	22	5	-	120529583	120529705
236057679	chr1	120529522	120529673	120529544	120529652	NOTCH2	NM_024408	2	34	5	-	120529583	120529705
238073127	chr1	120539668	120539842	120539689	120539815	NOTCH2	NM_001200001	1	22	4	-	120539620	120539955
238073127	chr1	120539668	120539842	120539689	120539815	NOTCH2	NM_024408	2	34	4	-	120539620	120539955
235952365	chr1	144852275	144852419	144852295	144852393	PDE4DIP	NM_014644	8	44	44	-	144851427	144852499
235952365	chr1	144852275	144852419	144852295	144852393	PDE4DIP	NM_001198834	7	44	44	-	144851424	144852443
235952365	chr1	144852275	144852419	144852295	144852393	PDE4DIP	NM_001198832	6	46	46	-	144851424	144852499
237249120	chr1	144854532	144854703	144854555	144854683	PDE4DIP	NM_001198832	6	46	44	-	144854518	144854656
237249120	chr1	144854532	144854703	144854555	144854683	PDE4DIP	NM_001198834	7	44	42	-	144854518	144854656
237249120	chr1	144854532	144854703	144854555	144854683	PDE4DIP	NM_014644	8	44	42	-	144854518	144854656
236394283	chr1	144856976	144857140	144856997	144857113	PDE4DIP	NM_001198832	6	46	42	-	144856816	144857042
236394283	chr1	144856976	144857140	144856997	144857113	PDE4DIP	NM_001198834	7	44	40	-	144856816	144857042
236394283	chr1	144856976	144857140	144856997	144857113	PDE4DIP	NM_014644	8	44	40	-	144856816	144857042
237376025	chr1	144859797	144859941	144859820	144859922	PDE4DIP	NM_001198832	6	46	40	-	144859759	144859998
237376025	chr1	144859797	144859941	144859820	144859922	PDE4DIP	NM_001198834	7	44	38	-	144859759	144859998
237376025	chr1	144859797	144859941	144859820	144859922	PDE4DIP	NM_014644	8	44	38	-	144859759	144859998
236820759	chr1	144864049	144864223	144864075	144864200	PDE4DIP	NM_001198832	6	46	38	-	144864135	144864324
236820759	chr1	144864049	144864223	144864075	144864200	PDE4DIP	NM_001198834	7	44	36	-	144864135	144864324
236820759	chr1	144864049	144864223	144864075	144864200	PDE4DIP	NM_014644	8	44	36	-	144864135	144864324
235312777	chr1	144866530	144866670	144866554	144866647	PDE4DIP	NM_001198832	6	46	36	-	144866592	144866723
235312777	chr1	144866530	144866670	144866554	144866647	PDE4DIP	NM_001198834	7	44	34	-	144866592	144866723
235312777	chr1	144866530	144866670	144866554	144866647	PDE4DIP	NM_014644	8	44	34	-	144866592	144866723
235854962	chr1	144868053	144868215	144868074	144868190	PDE4DIP	NM_001198832	6	46	35	-	144867921	144868172
235854962	chr1	144868053	144868215	144868074	144868190	PDE4DIP	NM_001198834	7	44	33	-	144867921	144868172
235854962	chr1	144868053	144868215	144868074	144868190	PDE4DIP	NM_014644	8	44	33	-	144867921	144868172
235793748	chr1	144873831	144873985	144873856	144873962	PDE4DIP	NM_001198832	6	46	34	-	144873877	144874029
235793748	chr1	144873831	144873985	144873856	144873962	PDE4DIP	NM_001198834	7	44	31	-	144873877	144874029
235793748	chr1	144873831	144873985	144873856	144873962	PDE4DIP	NM_014644	8	44	31	-	144873877	144874029
237095395	chr1	144874775	144874944	144874793	144874922	PDE4DIP	NM_001198832	6	46	33	-	144874681	144874904
237095395	chr1	144874775	144874944	144874793	144874922	PDE4DIP	NM_001198834	7	44	30	-	144874681	144874904
237095395	chr1	144874775	144874944	144874793	144874922	PDE4DIP	NM_014644	8	44	30	-	144874681	144874904
235366141	chr1	144878967	144879124	144878987	144879102	PDE4DIP	NM_001198832	6	46	30	-	144879035	144879563
235366141	chr1	144878967	144879124	144878987	144879102	PDE4DIP	NM_001198834	7	44	27	-	144879035	144879563
235366141	chr1	144878967	144879124	144878987	144879102	PDE4DIP	NM_014644	8	44	27	-	144879035	144879563
235405311	chr1	144879363	144879516	144879390	144879498	PDE4DIP	NM_001198832	6	46	30	-	144879035	144879563
235405311	chr1	144879363	144879516	144879390	144879498	PDE4DIP	NM_001198834	7	44	27	-	144879035	144879563
235405311	chr1	144879363	144879516	144879390	144879498	PDE4DIP	NM_014644	8	44	27	-	144879035	144879563

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237704592	chr1	144882418	144882581	144882444	144882553	PDE4DIP	NM_001198834	7	44	24	-	144882446	144882881
237704592	chr1	144882418	144882581	144882444	144882553	PDE4DIP	NM_014644	8	44	24	-	144882446	144882881
237822098	chr1	144882841	144882973	144882861	144882950	PDE4DIP	NM_001198832	6	46	27	-	144882776	144882881
237822098	chr1	144882841	144882973	144882861	144882950	PDE4DIP	NM_001198834	7	44	24	-	144882446	144882881
237822098	chr1	144882841	144882973	144882861	144882950	PDE4DIP	NM_014644	8	44	24	-	144882446	144882881
238410971	chr1	144892179	144892304	144892205	144892276	PDE4DIP	NM_001002812	3	23	23	-	144890591	144892219
238410971	chr1	144892179	144892304	144892205	144892276	PDE4DIP	NM_001002811	2	19	19	-	144890591	144892219
237452245	chr1	144904606	144904768	144904631	144904742	PDE4DIP	NM_001198832	6	46	23	-	144904625	144904737
237452245	chr1	144904606	144904768	144904631	144904742	PDE4DIP	NM_001198834	7	44	20	-	144904625	144904737
237452245	chr1	144904606	144904768	144904631	144904742	PDE4DIP	NM_014644	8	44	20	-	144904625	144904737
237452245	chr1	144904606	144904768	144904631	144904742	PDE4DIP	NM_001002812	3	23	20	-	144904625	144904737
237452245	chr1	144904606	144904768	144904631	144904742	PDE4DIP	NM_001002811	2	19	16	-	144904625	144904737
238226054	chr1	144909885	144910022	144909912	144909995	PDE4DIP	NM_001198832	6	46	20	-	144909869	144909960
238226054	chr1	144909885	144910022	144909912	144909995	PDE4DIP	NM_001198834	7	44	17	-	144909869	144909960
238226054	chr1	144909885	144910022	144909912	144909995	PDE4DIP	NM_014644	8	44	17	-	144909869	144909960
238226054	chr1	144909885	144910022	144909912	144909995	PDE4DIP	NM_001002812	3	23	17	-	144909869	144909960
238226054	chr1	144909885	144910022	144909912	144909995	PDE4DIP	NM_001002811	2	19	13	-	144909869	144909960
241077756	chr1	144912138	144912274	144912160	144912246	PDE4DIP	NM_001198832	6	46	18	-	144912130	144912294
241077756	chr1	144912138	144912274	144912160	144912246	PDE4DIP	NM_001198834	7	44	15	-	144912130	144912294
241077756	chr1	144912138	144912274	144912160	144912246	PDE4DIP	NM_014644	8	44	15	-	144912130	144912294
241077756	chr1	144912138	144912274	144912160	144912246	PDE4DIP	NM_001002812	3	23	15	-	144912130	144912294
241077756	chr1	144912138	144912274	144912160	144912246	PDE4DIP	NM_001002811	2	19	11	-	144912130	144912294
236432186	chr1	144916482	144916656	144916505	144916634	PDE4DIP	NM_001198832	6	46	16	-	144916570	144916749
236432186	chr1	144916482	144916656	144916505	144916634	PDE4DIP	NM_001198834	7	44	13	-	144916570	144916749
236432186	chr1	144916482	144916656	144916505	144916634	PDE4DIP	NM_014644	8	44	13	-	144916570	144916749
236432186	chr1	144916482	144916656	144916505	144916634	PDE4DIP	NM_001002812	3	23	13	-	144916570	144916749
236432186	chr1	144916482	144916656	144916505	144916634	PDE4DIP	NM_001002811	2	19	9	-	144916570	144916749
237928974	chr1	144917820	144917952	144917847	144917923	PDE4DIP	NM_001198832	6	46	14	-	144917819	144917932
237928974	chr1	144917820	144917952	144917847	144917923	PDE4DIP	NM_001198834	7	44	11	-	144917819	144917932
237928974	chr1	144917820	144917952	144917847	144917923	PDE4DIP	NM_014644	8	44	11	-	144917819	144917932
237928974	chr1	144917820	144917952	144917847	144917923	PDE4DIP	NM_001002812	3	23	11	-	144917819	144917932
237928974	chr1	144917820	144917952	144917847	144917923	PDE4DIP	NM_001002811	2	19	7	-	144917819	144917932
236238761	chr1	144921856	144921990	144921879	144921965	PDE4DIP	NM_001198832	6	46	12	-	144921835	144922047
236238761	chr1	144921856	144921990	144921879	144921965	PDE4DIP	NM_001198834	7	44	9	-	144921835	144922047
236238761	chr1	144921856	144921990	144921879	144921965	PDE4DIP	NM_014644	8	44	9	-	144921835	144922047
236238761	chr1	144921856	144921990	144921879	144921965	PDE4DIP	NM_001002812	3	23	9	-	144921835	144922047
236238761	chr1	144921856	144921990	144921879	144921965	PDE4DIP	NM_001002811	2	19	5	-	144921835	144922047
237503920	chr1	144922525	144922695	144922548	144922666	PDE4DIP	NM_001198832	6	46	10	-	144922519	144922638
237503920	chr1	144922525	144922695	144922548	144922666	PDE4DIP	NM_001198834	7	44	7	-	144922519	144922638
237503920	chr1	144922525	144922695	144922548	144922666	PDE4DIP	NM_014644	8	44	7	-	144922519	144922638
237503920	chr1	144922525	144922695	144922548	144922666	PDE4DIP	NM_001002812	3	23	7	-	144922519	144922638

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237503920	chr1	144922525	144922695	144922548	144922666	PDE4DIP	NM_001002811	2	19	3	-	144922519	144922638
240371014	chr1	144930652	144930820	144930676	144930794	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
236895503	chr1	144931124	144931298	144931147	144931276	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
236902818	chr1	144931607	144931778	144931631	144931757	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001198834	7	44	1	-	144994591	144995033
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001002810	1	4	1	-	144994591	144995033
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001198832	6	46	4	-	144994591	144994701
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001195261	5	5	2	-	144994591	144994701
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001195260	4	5	2	-	144994591	144994701
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_022359	9	7	4	-	144994591	144994701
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_014644	8	44	1	-	144994591	144995022
235184812	chr1	144994633	144994765	144994651	144994748	PDE4DIP	NM_001002812	3	23	1	-	144994591	144995022
234953554	chr1	145015954	145016087	145015977	145016062	PDE4DIP	NM_001198832	6	46	3	-	145015860	145016011
234953554	chr1	145015954	145016087	145015977	145016062	PDE4DIP	NM_022359	9	7	3	-	145015860	145016011
240104554	chr1	145075618	145075789	145075638	145075771	PDE4DIP	NM_022359	9	7	1	-	145075630	145076186
233583480	chr1	145527618	145527784	145527638	145527761	ITGA10	NM_003637	1	30	2	+	145527613	145527724
231822894	chr1	145530176	145530306	145530204	145530280	ITGA10	NM_003637	1	30	6	+	145530267	145530394
233204277	chr1	145532068	145532201	145532093	145532178	ITGA10	NM_003637	1	30	8	+	145532115	145532265
233261722	chr1	145532708	145532875	145532729	145532847	ITGA10	NM_003637	1	30	10	+	145532757	145532830
233737295	chr1	145533485	145533649	145533507	145533627	ITGA10	NM_003637	1	30	12	+	145533412	145533560
232915385	chr1	145534152	145534311	145534174	145534286	ITGA10	NM_003637	1	30	14	+	145534083	145534286
232930759	chr1	145535880	145536037	145535900	145536016	ITGA10	NM_003637	1	30	16	+	145535735	145535901
232930759	chr1	145535880	145536037	145535900	145536016	ITGA10	NM_003637	1	30	17	+	145535998	145536140
232072297	chr1	145537381	145537513	145537403	145537485	ITGA10	NM_003637	1	30	20	+	145537423	145537564
233249726	chr1	145538196	145538358	145538216	145538334	ITGA10	NM_003637	1	30	23	+	145538218	145538307
232774700	chr1	145539651	145539823	145539677	145539796	ITGA10	NM_003637	1	30	27	+	145539683	145539796
234331446	chr1	145542139	145542308	145542163	145542281	ITGA10	NM_003637	1	30	30	+	145542213	145543868
222516765	chr1	147084838	147084975	147084860	147084954	BCL9	NM_004326	1	10	5	+	147084682	147084998
223827065	chr1	147087487	147087661	147087515	147087636	BCL9	NM_004326	1	10	7	+	147087603	147087702
224758268	chr1	147090800	147090947	147090827	147090923	BCL9	NM_004326	1	10	8	+	147090622	147092863
223211663	chr1	147091171	147091345	147091191	147091326	BCL9	NM_004326	1	10	8	+	147090622	147092863
224758836	chr1	147091648	147091784	147091671	147091760	BCL9	NM_004326	1	10	8	+	147090622	147092863
224754133	chr1	147092067	147092241	147092085	147092222	BCL9	NM_004326	1	10	8	+	147090622	147092863
223249048	chr1	147092553	147092724	147092572	147092704	BCL9	NM_004326	1	10	8	+	147090622	147092863
223346864	chr1	147094103	147094267	147094126	147094243	BCL9	NM_004326	1	10	9	+	147094072	147094332
224493871	chr1	147095768	147095942	147095786	147095922	BCL9	NM_004326	1	10	10	+	147095643	147098015
224495045	chr1	147096214	147096385	147096235	147096365	BCL9	NM_004326	1	10	10	+	147095643	147098015
222683199	chr1	147096609	147096782	147096631	147096761	BCL9	NM_004326	1	10	10	+	147095643	147098015
269787200	chr1	150550709	150550868	150550731	150550841	MCL1	NM_021960	2	3	2	-	150550720	150550967
269787200	chr1	150550709	150550868	150550731	150550841	MCL1	NM_001197320	1	4	3	-	150550720	150550967
271813834	chr1	150551438	150551583	150551455	150551565	MCL1	NM_021960	2	3	1	-	150551319	150552214

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271813834	chr1	150551438	150551583	150551455	150551565	MCL1	NM_182763	3	2	1	-	150551319	150552214
269959016	chr1	150551850	150552017	150551868	150551998	MCL1	NM_021960	2	3	1	-	150551319	150552214
269959016	chr1	150551850	150552017	150551868	150551998	MCL1	NM_182763	3	2	1	-	150551319	150552214
269959016	chr1	150551850	150552017	150551868	150551998	MCL1	NM_001197320	1	4	1	-	150551899	150552214
223632140	chr1	150785681	150785848	150785702	150785820	ARNT	NM_001668	2	22	21	-	150785648	150785814
223632140	chr1	150785681	150785848	150785702	150785820	ARNT	NM_178427	3	21	20	-	150785648	150785814
223632140	chr1	150785681	150785848	150785702	150785820	ARNT	NM_001197325	1	21	20	-	150785648	150785814
224503527	chr1	150788823	150788995	150788845	150788973	ARNT	NM_001668	2	22	19	-	150788735	150788882
224503527	chr1	150788823	150788995	150788845	150788973	ARNT	NM_178427	3	21	18	-	150788735	150788882
224503527	chr1	150788823	150788995	150788845	150788973	ARNT	NM_001197325	1	21	18	-	150788735	150788882
224120101	chr1	150789637	150789787	150789658	150789760	ARNT	NM_001668	2	22	17	-	150789558	150789678
224120101	chr1	150789637	150789787	150789658	150789760	ARNT	NM_178427	3	21	16	-	150789558	150789678
224120101	chr1	150789637	150789787	150789658	150789760	ARNT	NM_001197325	1	21	16	-	150789558	150789678
222665131	chr1	150795765	150795937	150795786	150795916	ARNT	NM_001668	2	22	14	-	150795670	150795821
222665131	chr1	150795765	150795937	150795786	150795916	ARNT	NM_178427	3	21	13	-	150795670	150795821
222665131	chr1	150795765	150795937	150795786	150795916	ARNT	NM_001197325	1	21	13	-	150795670	150795821
223946770	chr1	150802328	150802496	150802354	150802473	ARNT	NM_001668	2	22	11	-	150802380	150802456
223946770	chr1	150802328	150802496	150802354	150802473	ARNT	NM_178427	3	21	10	-	150802380	150802456
223946770	chr1	150802328	150802496	150802354	150802473	ARNT	NM_001197325	1	21	10	-	150802380	150802456
223396471	chr1	150806966	150807140	150806994	150807116	ARNT	NM_001668	2	22	8	-	150807014	150807116
223396471	chr1	150806966	150807140	150806994	150807116	ARNT	NM_178427	3	21	7	-	150807014	150807116
223396471	chr1	150806966	150807140	150806994	150807116	ARNT	NM_001197325	1	21	7	-	150807014	150807116
222870001	chr1	150811861	150812035	150811887	150812012	ARNT	NM_001668	2	22	6	-	150811917	150812130
222870001	chr1	150811861	150812035	150811887	150812012	ARNT	NM_178427	3	21	5	-	150811917	150812130
222870001	chr1	150811861	150812035	150811887	150812012	ARNT	NM_001197325	1	21	5	-	150811917	150812130
225109757	chr1	150825124	150825287	150825152	150825262	ARNT	NM_001668	2	22	3	-	150825238	150825282
225109757	chr1	150825124	150825287	150825152	150825262	ARNT	NM_178427	3	21	3	-	150825238	150825282
225109757	chr1	150825124	150825287	150825152	150825262	ARNT	NM_001197325	1	21	3	-	150825238	150825282
223039877	chr1	150848986	150849139	150849005	150849119	ARNT	NM_001668	2	22	1	-	150849019	150849244
223039877	chr1	150848986	150849139	150849005	150849119	ARNT	NM_178427	3	21	1	-	150849019	150849244
223039877	chr1	150848986	150849139	150849005	150849119	ARNT	NM_001197325	1	21	1	-	150849019	150849244
294717574	chr1	154951121	154951283	154951142	154951260	CKS1B	NM_001826	1	3	3	+	154951201	154951725
294717574	chr1	154951121	154951283	154951142	154951260	CKS1B	NR_024163	2	3	3	+	154951201	154951725
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044391	4	5	4	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044390	3	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204290	12	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204289	11	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204288	10	8	7	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_002456	20	8	7	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204286	8	9	8	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204294	16	7	6	-	155159701	155159850

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204293	15	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044392	5	5	4	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001018017	2	8	7	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044393	6	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204292	14	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204297	19	5	4	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204296	18	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204295	17	6	5	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204287	9	8	7	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204285	7	9	8	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204291	13	7	6	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001018016	1	8	7	-	155159701	155159850
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204288	10	8	6	-	155159931	155160020
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044393	6	7	5	-	155159931	155160020
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204295	17	6	4	-	155159931	155160020
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001044390	3	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204290	12	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204289	11	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_002456	20	8	6	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204286	8	9	7	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204294	16	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001018017	2	8	6	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204292	14	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204296	18	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204287	9	8	6	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204285	7	9	7	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001204291	13	7	5	-	155159931	155160052
238716325	chr1	155159789	155159958	155159810	155159935	MUC1	NM_001018016	1	8	6	-	155159931	155160052
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204290	12	7	3	-	155160484	155160530
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204289	11	7	3	-	155160484	155160530
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001044390	3	7	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204288	10	8	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_002456	20	8	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204286	8	9	5	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204293	15	7	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001018017	2	8	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001044393	6	7	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204296	18	7	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204287	9	8	4	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204285	7	9	5	-	155160484	155160539
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001204291	13	7	3	-	155160484	155160539

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235447043	chr1	155160394	155160555	155160415	155160533	MUC1	NM_001018016	1	8	4	-	155160484	155160539
237215211	chr1	155161812	155161970	155161829	155161948	MUC1	NM_001204286	8	9	2	-	155161699	155162101
237215211	chr1	155161812	155161970	155161829	155161948	MUC1	NM_001204285	7	9	2	-	155161699	155162074
235291554	chr1	156785583	156785732	156785604	156785710	NTRK1	NM_001007792	1	17	1	+	156785542	156785630
235685746	chr1	156830893	156831036	156830912	156831017	NTRK1	NM_002529	3	17	1	+	156830671	156830938
235685746	chr1	156830893	156831036	156830912	156831017	NTRK1	NM_001012331	2	16	1	+	156830671	156830938
241032033	chr1	156837830	156838002	156837852	156837980	NTRK1	NM_002529	3	17	5	+	156837896	156838041
241032033	chr1	156837830	156838002	156837852	156837980	NTRK1	NM_001012331	2	16	5	+	156837896	156838041
241032033	chr1	156837830	156838002	156837852	156837980	NTRK1	NM_001007792	1	17	6	+	156837896	156838041
235523337	chr1	156841366	156841495	156841390	156841476	NTRK1	NM_002529	3	17	7	+	156841415	156841547
235523337	chr1	156841366	156841495	156841390	156841476	NTRK1	NM_001012331	2	16	7	+	156841415	156841547
235523337	chr1	156841366	156841495	156841390	156841476	NTRK1	NM_001007792	1	17	8	+	156841415	156841547
236933520	chr1	156843604	156843778	156843621	156843760	NTRK1	NM_002529	3	17	8	+	156843425	156843751
236933520	chr1	156843604	156843778	156843621	156843760	NTRK1	NM_001012331	2	16	8	+	156843425	156843751
236933520	chr1	156843604	156843778	156843621	156843760	NTRK1	NM_001007792	1	17	9	+	156843425	156843751
235620632	chr1	156844738	156844873	156844759	156844850	NTRK1	NM_002529	3	17	11	+	156844698	156844800
235620632	chr1	156844738	156844873	156844759	156844850	NTRK1	NM_001012331	2	16	10	+	156844698	156844800
235620632	chr1	156844738	156844873	156844759	156844850	NTRK1	NM_001007792	1	17	11	+	156844698	156844800
236783252	chr1	156845928	156846076	156845950	156846054	NTRK1	NM_002529	3	17	13	+	156845872	156846002
236783252	chr1	156845928	156846076	156845950	156846054	NTRK1	NM_001012331	2	16	12	+	156845872	156846002
236783252	chr1	156845928	156846076	156845950	156846054	NTRK1	NM_001007792	1	17	13	+	156845872	156846002
238775348	chr1	156849023	156849154	156849041	156849130	NTRK1	NM_002529	3	17	15	+	156848914	156849154
238775348	chr1	156849023	156849154	156849041	156849130	NTRK1	NM_001012331	2	16	14	+	156848914	156849154
238775348	chr1	156849023	156849154	156849041	156849130	NTRK1	NM_001007792	1	17	15	+	156848914	156849154
241564195	chr1	156851244	156851378	156851263	156851359	NTRK1	NM_002529	3	17	17	+	156851249	156851642
241564195	chr1	156851244	156851378	156851263	156851359	NTRK1	NM_001012331	2	16	16	+	156851249	156851642
241564195	chr1	156851244	156851378	156851263	156851359	NTRK1	NM_001007792	1	17	17	+	156851249	156851642
237924767	chr1	161298084	161298220	161298108	161298199	SDHC	NM_003001	4	6	3	+	161298186	161298287
237924767	chr1	161298084	161298220	161298108	161298199	SDHC	NM_001035511	1	5	3	+	161298186	161298287
240472570	chr1	161326421	161326545	161326446	161326519	SDHC	NM_003001	4	6	5	+	161326467	161326630
240472570	chr1	161326421	161326545	161326446	161326519	SDHC	NM_001035512	2	5	4	+	161326467	161326630
240472570	chr1	161326421	161326545	161326446	161326519	SDHC	NM_001035513	3	4	3	+	161326467	161326630
229620102	chr1	162688804	162688975	162688826	162688947	DDR2	NM_006182	2	18	3	+	162688827	162688935
229620102	chr1	162688804	162688975	162688826	162688947	DDR2	NM_001014796	1	19	4	+	162688827	162688935
230165208	chr1	162724565	162724714	162724587	162724687	DDR2	NM_006182	2	18	5	+	162724414	162724645
230165208	chr1	162724565	162724714	162724587	162724687	DDR2	NM_001014796	1	19	6	+	162724414	162724645
228229141	chr1	162729541	162729714	162729567	162729694	DDR2	NM_006182	2	18	8	+	162729586	162729769
228229141	chr1	162729541	162729714	162729567	162729694	DDR2	NM_001014796	1	19	9	+	162729586	162729769
230494492	chr1	162731175	162731299	162731198	162731276	DDR2	NM_006182	2	18	9	+	162731001	162731244
230494492	chr1	162731175	162731299	162731198	162731276	DDR2	NM_001014796	1	19	10	+	162731001	162731244
230146744	chr1	162740067	162740225	162740091	162740201	DDR2	NM_006182	2	18	12	+	162740092	162740302

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230146744	chr1	162740067	162740225	162740091	162740201	DDR2	NM_001014796	1	19	13	+	162740092	162740302
231054993	chr1	162741979	162742116	162742003	162742088	DDR2	NM_006182	2	18	13	+	162741814	162742037
231054993	chr1	162741979	162742116	162742003	162742088	DDR2	NM_001014796	1	19	14	+	162741814	162742037
228358167	chr1	162745487	162745658	162745514	162745634	DDR2	NM_006182	2	18	15	+	162745442	162745633
228358167	chr1	162745487	162745658	162745514	162745634	DDR2	NM_001014796	1	19	16	+	162745442	162745633
232965197	chr1	162748408	162748545	162748433	162748519	DDR2	NM_006182	2	18	17	+	162748370	162748519
232965197	chr1	162748408	162748545	162748433	162748519	DDR2	NM_001014796	1	19	18	+	162748370	162748519
236983558	chr1	164529051	164529225	164529071	164529198	PBX1	NM_002585	3	9	1	+	164528597	164529250
236983558	chr1	164529051	164529225	164529071	164529198	PBX1	NM_001204963	2	9	1	+	164528597	164529250
236983558	chr1	164529051	164529225	164529071	164529198	PBX1	NM_001204961	1	8	1	+	164528597	164529250
238523441	chr1	164761765	164761933	164761784	164761908	PBX1	NM_002585	3	9	3	+	164761731	164761975
238523441	chr1	164761765	164761933	164761784	164761908	PBX1	NM_001204963	2	9	3	+	164761731	164761975
238523441	chr1	164761765	164761933	164761784	164761908	PBX1	NM_001204961	1	8	3	+	164761731	164761975
240544458	chr1	164776737	164776888	164776765	164776866	PBX1	NM_002585	3	9	5	+	164776779	164776914
240544458	chr1	164776737	164776888	164776765	164776866	PBX1	NM_001204963	2	9	5	+	164776779	164776914
240544458	chr1	164776737	164776888	164776765	164776866	PBX1	NM_001204961	1	8	5	+	164776779	164776914
237455830	chr1	164789275	164789443	164789296	164789421	PBX1	NM_002585	3	9	7	+	164789309	164789421
237455830	chr1	164789275	164789443	164789296	164789421	PBX1	NM_001204963	2	9	7	+	164789309	164789421
238840274	chr1	164818542	164818688	164818571	164818667	PBX1	NM_002585	3	9	9	+	164815821	164821060
238840274	chr1	164818542	164818688	164818571	164818667	PBX1	NM_001204961	1	8	8	+	164815821	164821060
238840274	chr1	164818542	164818688	164818571	164818667	PBX1	NM_001204963	2	9	9	+	164818577	164821060
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_001168239	6	12	12	-	179068462	179078033
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_001168238	5	12	12	-	179068462	179078033
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_001136000	1	13	13	-	179068462	179078033
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_001168237	4	13	13	-	179068462	179078033
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_005158	7	12	12	-	179068462	179078576
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_007314	8	12	12	-	179068462	179078576
224218928	chr1	179077112	179077286	179077134	179077265	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_005158	7	12	12	-	179068462	179078576
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_007314	8	12	12	-	179068462	179078576
223440315	chr1	179077577	179077740	179077599	179077715	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_005158	7	12	12	-	179068462	179078576
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_007314	8	12	12	-	179068462	179078576

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223447459	chr1	179078005	179078153	179078027	179078129	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_005158	7	12	12	-	179068462	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_007314	8	12	12	-	179068462	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_001168239	6	12	11	-	179078343	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_001168238	5	12	11	-	179078343	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_001136000	1	13	12	-	179078343	179078576
223146647	chr1	179078459	179078608	179078482	179078580	ABL2	NM_001168237	4	13	12	-	179078343	179078576
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_005158	7	12	9	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001168239	6	12	8	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001168238	5	12	8	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001136001	2	10	8	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001136000	1	13	9	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_007314	8	12	9	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001168237	4	13	9	-	179084013	179084165
223695388	chr1	179083965	179084104	179083992	179084080	ABL2	NM_001168236	3	11	8	-	179084013	179084165
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_005158	7	12	7	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001168239	6	12	6	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001168238	5	12	6	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001136001	2	10	6	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001136000	1	13	7	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_007314	8	12	7	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001168237	4	13	7	-	179087722	179087899
222348822	chr1	179087672	179087844	179087694	179087820	ABL2	NM_001168236	3	11	6	-	179087722	179087899
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_005158	7	12	5	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001168239	6	12	4	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001168238	5	12	4	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001136001	2	10	4	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001136000	1	13	5	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_007314	8	12	5	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001168237	4	13	5	-	179090730	179091002
224145182	chr1	179090760	179090934	179090784	179090914	ABL2	NM_001168236	3	11	4	-	179090730	179091002
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_005158	7	12	4	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001168239	6	12	3	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001168238	5	12	3	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001136001	2	10	3	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001136000	1	13	4	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_007314	8	12	4	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001168237	4	13	4	-	179095512	179095807
222822218	chr1	179095741	179095880	179095766	179095852	ABL2	NM_001168236	3	11	3	-	179095512	179095807
222595566	chr1	179198259	179198411	179198278	179198390	ABL2	NM_001168238	5	12	1	-	179198376	179198819

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222595566	chr1	179198259	179198411	179198278	179198390	ABL2	NM_001136001	2	10	1	-	179198376	179198819
222595566	chr1	179198259	179198411	179198278	179198390	ABL2	NM_007314	8	12	1	-	179198376	179198819
222595566	chr1	179198259	179198411	179198278	179198390	ABL2	NM_001168237	4	13	1	-	179198376	179198819
222595566	chr1	179198259	179198411	179198278	179198390	ABL2	NM_001168236	3	11	1	-	179198376	179198819
321785760	chr1	182545306	182545436	182545339	182545413	RNASEL	NM_021133	1	7	6	-	182545391	182545524
321773661	chr1	182551159	182551330	182551183	182551303	RNASEL	NM_021133	1	7	4	-	182551188	182551393
322062839	chr1	182554483	182554656	182554504	182554634	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322107939	chr1	182554937	182555061	182554959	182555039	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322048474	chr1	182555365	182555536	182555388	182555510	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322111662	chr1	182555810	182555967	182555831	182555945	RNASEL	NM_021133	1	7	2	-	182554462	182556105
312190773	chr1	185062135	185062294	185062163	185062267	RNF2	NM_007212	1	7	4	+	185062193	185062408
312477735	chr1	185067194	185067322	185067214	185067301	RNF2	NM_007212	1	7	5	+	185067204	185067476
312195371	chr1	185068939	185069086	185068960	185069062	RNF2	NM_007212	1	7	6	+	185068923	185069094
241401874	chr1	186283122	186283276	186283145	186283248	TPR	NM_003292	1	51	51	-	186280786	186283158
266281015	chr1	186286668	186286839	186286688	186286811	TPR	NM_003292	1	51	49	-	186286614	186286732
264434346	chr1	186287775	186287899	186287804	186287875	TPR	NM_003292	1	51	47	-	186287865	186287960
238996847	chr1	186291450	186291584	186291475	186291556	TPR	NM_003292	1	51	45	-	186291450	186291544
242742258	chr1	186292804	186292944	186292832	186292921	TPR	NM_003292	1	51	43	-	186292818	186293002
241942829	chr1	186296529	186296692	186296555	186296669	TPR	NM_003292	1	51	40	-	186296592	186296792
242697182	chr1	186301257	186301381	186301280	186301358	TPR	NM_003292	1	51	38	-	186301327	186301475
264809639	chr1	186302343	186302493	186302364	186302469	TPR	NM_003292	1	51	37	-	186302254	186302526
261660527	chr1	186303531	186303673	186303553	186303649	TPR	NM_003292	1	51	36	-	186303457	186303665
265779583	chr1	186304484	186304624	186304506	186304598	TPR	NM_003292	1	51	34	-	186304470	186304675
262068915	chr1	186305742	186305875	186305765	186305843	TPR	NM_003292	1	51	33	-	186305628	186305826
239500017	chr1	186307153	186307298	186307181	186307272	TPR	NM_003292	1	51	31	-	186307165	186307375
242053305	chr1	186308849	186309023	186308877	186308997	TPR	NM_003292	1	51	30	-	186308774	186308904
240146839	chr1	186310415	186310589	186310444	186310562	TPR	NM_003292	1	51	28	-	186310384	186310521
264133768	chr1	186313004	186313145	186313030	186313122	TPR	NM_003292	1	51	26	-	186313038	186313222
238628669	chr1	186314665	186314801	186314692	186314773	TPR	NM_003292	1	51	24	-	186314712	186314828
263019020	chr1	186316422	186316596	186316447	186316571	TPR	NM_003292	1	51	22	-	186316424	186316590
241006745	chr1	186319472	186319608	186319500	186319581	TPR	NM_003292	1	51	21	-	186319355	186319520
241008367	chr1	186321130	186321295	186321152	186321269	TPR	NM_003292	1	51	19	-	186321108	186321242
241227261	chr1	186324577	186324725	186324605	186324697	TPR	NM_003292	1	51	17	-	186324542	186324690
240178854	chr1	186325462	186325610	186325483	186325584	TPR	NM_003292	1	51	15	-	186325418	186325581
262616247	chr1	186327616	186327767	186327640	186327745	TPR	NM_003292	1	51	13	-	186327675	186327782
264420877	chr1	186329274	186329448	186329299	186329422	TPR	NM_003292	1	51	11	-	186329405	186329496
264981924	chr1	186330623	186330796	186330650	186330768	TPR	NM_003292	1	51	9	-	186330754	186330841
242481641	chr1	186331446	186331610	186331474	186331584	TPR	NM_003292	1	51	7	-	186331420	186331512
263321902	chr1	186336931	186337094	186336953	186337065	TPR	NM_003292	1	51	4	-	186337018	186337114
241379674	chr1	186342368	186342513	186342401	186342491	TPR	NM_003292	1	51	2	-	186342491	186342595
296644032	chr1	186643356	186643522	186643376	186643494	PTGS2	NM_000963	1	10	10	-	186640944	186643894

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
296720285	chr1	186643751	186643923	186643773	186643898	PTGS2	NM_000963	1	10	10	-	186640944	186643894
296098056	chr1	186645047	186645177	186645074	186645155	PTGS2	NM_000963	1	10	8	-	186645030	186645316
297542779	chr1	186645593	186645725	186645621	186645703	PTGS2	NM_000963	1	10	7	-	186645599	186645845
298328660	chr1	186646808	186646951	186646828	186646923	PTGS2	NM_000963	1	10	5	-	186646781	186646962
296834898	chr1	186648156	186648285	186648184	186648260	PTGS2	NM_000963	1	10	3	-	186648190	186648333
296264999	chr1	186649301	186649471	186649321	186649450	PTGS2	NM_000963	1	10	1	-	186649371	186649559
226520194	chr1	193104498	193104630	193104526	193104603	CDC73	NM_024529	1	17	4	+	193104521	193104583
226836402	chr1	193107230	193107403	193107254	193107375	CDC73	NM_024529	1	17	6	+	193107215	193107303
226252274	chr1	193117003	193117172	193117033	193117144	CDC73	NM_024529	1	17	8	+	193116997	193117095
226550378	chr1	193181145	193181292	193181176	193181265	CDC73	NM_024529	1	17	12	+	193181195	193181230
253626535	chr1	193205290	193205464	193205316	193205442	CDC73	NM_024529	1	17	15	+	193205386	193205486
226808644	chr1	193219722	193219855	193219755	193219827	CDC73	NM_024529	1	17	17	+	193219806	193223942
294748792	chr1	204394713	204394842	204394733	204394815	PIK3C2B	NM_002646	1	34	33	-	204394741	204394869
294308696	chr1	204397221	204397372	204397243	204397349	PIK3C2B	NM_002646	1	34	31	-	204397267	204397348
294661286	chr1	204400819	204400949	204400840	204400924	PIK3C2B	NM_002646	1	34	29	-	204400797	204400921
294812877	chr1	204402833	204402998	204402854	204402975	PIK3C2B	NM_002646	1	34	26	-	204402921	204403077
294083636	chr1	204407935	204408107	204407955	204408086	PIK3C2B	NM_002646	1	34	24	-	204408063	204408199
294198437	chr1	204411621	204411784	204411642	204411761	PIK3C2B	NM_002646	1	34	21	-	204411654	204411761
294271893	chr1	204413430	204413600	204413452	204413579	PIK3C2B	NM_002646	1	34	18	-	204413459	204413552
293713986	chr1	204416441	204416608	204416462	204416586	PIK3C2B	NM_002646	1	34	16	-	204416564	204416706
294431628	chr1	204419034	204419181	204419055	204419159	PIK3C2B	NM_002646	1	34	14	-	204418978	204419145
295192467	chr1	204424980	204425139	204425001	204425119	PIK3C2B	NM_002646	1	34	12	-	204424984	204425179
294767362	chr1	204426898	204427062	204426919	204427040	PIK3C2B	NM_002646	1	34	10	-	204426856	204427002
294405965	chr1	204429699	204429827	204429720	204429805	PIK3C2B	NM_002646	1	34	7	-	204429678	204429789
294280675	chr1	204438119	204438261	204438142	204438239	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
295193116	chr1	204438523	204438693	204438550	204438673	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
233292906	chr1	204494536	204494710	204494559	204494690	MDM4	NM_002393	3	11	2	+	204494612	204494724
233292906	chr1	204494536	204494710	204494559	204494690	MDM4	NR_024171	4	10	2	+	204494612	204494724
233292906	chr1	204494536	204494710	204494559	204494690	MDM4	NM_001204172	2	3	2	+	204494612	204494724
233292906	chr1	204494536	204494710	204494559	204494690	MDM4	NM_001204171	1	10	2	+	204494612	204494724
233397501	chr1	204501250	204501416	204501274	204501389	MDM4	NM_002393	3	11	5	+	204501319	204501374
233397501	chr1	204501250	204501416	204501274	204501389	MDM4	NR_024171	4	10	5	+	204501319	204501374
233397501	chr1	204501250	204501416	204501274	204501389	MDM4	NM_001204171	1	10	5	+	204501319	204501374
233105956	chr1	204511941	204512066	204511965	204512038	MDM4	NM_002393	3	11	8	+	204511912	204512072
233105956	chr1	204511941	204512066	204511965	204512038	MDM4	NR_024171	4	10	7	+	204511912	204512072
233105956	chr1	204511941	204512066	204511965	204512038	MDM4	NM_001204171	1	10	8	+	204511912	204512072
233308692	chr1	204515803	204515967	204515828	204515942	MDM4	NM_002393	3	11	10	+	204515925	204516005
233308692	chr1	204515803	204515967	204515828	204515942	MDM4	NR_024171	4	10	9	+	204515925	204516005
233308692	chr1	204515803	204515967	204515828	204515942	MDM4	NM_001204171	1	10	9	+	204515925	204516005
231964591	chr1	204518363	204518536	204518387	204518512	MDM4	NM_001204172	2	3	3	+	204518394	204527248
231964591	chr1	204518363	204518536	204518387	204518512	MDM4	NM_002393	3	11	11	+	204518241	204527248

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231964591	chr1	204518363	204518536	204518387	204518512	MDM4	NR_024171	4	10	10	+	204518241	204527248
231964591	chr1	204518363	204518536	204518387	204518512	MDM4	NM_001204171	1	10	10	+	204518241	204527248
270258662	chr1	206646522	206646676	206646545	206646657	IKBKE	NM_014002	3	22	3	+	206646539	206646657
270258662	chr1	206646522	206646676	206646545	206646657	IKBKE	NM_001193322	2	21	3	+	206646539	206646657
271544036	chr1	206648277	206648435	206648297	206648411	IKBKE	NM_014002	3	22	5	+	206648208	206648337
271544036	chr1	206648277	206648435	206648297	206648411	IKBKE	NM_001193322	2	21	5	+	206648208	206648337
271544036	chr1	206648277	206648435	206648297	206648411	IKBKE	NM_001193321	1	21	4	+	206648208	206648337
270473146	chr1	206649991	206650121	206650013	206650099	IKBKE	NM_014002	3	22	7	+	206650021	206650181
270473146	chr1	206649991	206650121	206650013	206650099	IKBKE	NM_001193322	2	21	7	+	206650021	206650181
270473146	chr1	206649991	206650121	206650013	206650099	IKBKE	NM_001193321	1	21	6	+	206650021	206650181
270208838	chr1	206651576	206651734	206651596	206651713	IKBKE	NM_014002	3	22	9	+	206651503	206651682
270208838	chr1	206651576	206651734	206651596	206651713	IKBKE	NM_001193322	2	21	9	+	206651503	206651682
270208838	chr1	206651576	206651734	206651596	206651713	IKBKE	NM_001193321	1	21	8	+	206651503	206651682
271196296	chr1	206653311	206653479	206653331	206653458	IKBKE	NM_014002	3	22	12	+	206653365	206653456
271196296	chr1	206653311	206653479	206653331	206653458	IKBKE	NM_001193322	2	21	12	+	206653365	206653456
271196296	chr1	206653311	206653479	206653331	206653458	IKBKE	NM_001193321	1	21	11	+	206653365	206653456
270062058	chr1	206658542	206658711	206658563	206658689	IKBKE	NM_014002	3	22	15	+	206658531	206658643
270062058	chr1	206658542	206658711	206658563	206658689	IKBKE	NM_001193322	2	21	15	+	206658531	206658643
270062058	chr1	206658542	206658711	206658563	206658689	IKBKE	NM_001193321	1	21	14	+	206658531	206658643
271900720	chr1	206664869	206665024	206664890	206665002	IKBKE	NM_014002	3	22	18	+	206664981	206665082
271900720	chr1	206664869	206665024	206664890	206665002	IKBKE	NM_001193322	2	21	18	+	206664981	206665082
271900720	chr1	206664869	206665024	206664890	206665002	IKBKE	NM_001193321	1	21	17	+	206664981	206665082
271310274	chr1	206667182	206667349	206667202	206667325	IKBKE	NM_014002	3	22	21	+	206667253	206667324
271310274	chr1	206667182	206667349	206667202	206667325	IKBKE	NM_001193322	2	21	20	+	206667253	206667324
271310274	chr1	206667182	206667349	206667202	206667325	IKBKE	NM_001193321	1	21	20	+	206667253	206667324
290907513	chr1	220752686	220752816	220752714	220752792	MARK1	NM_018650	1	18	2	+	220752696	220752899
290302624	chr1	220777289	220777443	220777312	220777415	MARK1	NM_018650	1	18	6	+	220777409	220777479
289852400	chr1	220791641	220791812	220791667	220791787	MARK1	NM_018650	1	18	8	+	220791652	220791888
290532421	chr1	220791991	220792165	220792014	220792139	MARK1	NM_018650	1	18	9	+	220791978	220792097
292890812	chr1	220805566	220805705	220805594	220805672	MARK1	NM_018650	1	18	11	+	220805543	220805655
290284526	chr1	220809181	220809347	220809205	220809325	MARK1	NM_018650	1	18	13	+	220809175	220809368
290300089	chr1	220825407	220825578	220825429	220825550	MARK1	NM_018650	1	18	15	+	220825328	220825492
289299495	chr1	220831019	220831178	220831045	220831158	MARK1	NM_018650	1	18	17	+	220831132	220831176
290033920	chr1	220835255	220835426	220835282	220835403	MARK1	NM_018650	1	18	18	+	220835154	220837799
291285690	chr1	226550769	226550914	226550790	226550893	PARP1	NM_001618	1	23	21	-	226550800	226550861
290555788	chr1	226553515	226553688	226553541	226553665	PARP1	NM_001618	1	23	18	-	226553655	226553753
290417349	chr1	226555931	226556065	226555953	226556044	PARP1	NM_001618	1	23	16	-	226555900	226556022
289533285	chr1	226564777	226564946	226564799	226564926	PARP1	NM_001618	1	23	13	-	226564809	226565004
292290112	chr1	226567252	226567411	226567273	226567383	PARP1	NM_001618	1	23	11	-	226567274	226567342
290434199	chr1	226567820	226567990	226567849	226567967	PARP1	NM_001618	1	23	10	-	226567623	226567865
291784752	chr1	226570721	226570885	226570742	226570858	PARP1	NM_001618	1	23	8	-	226570737	226570884

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
291411553	chr1	226573990	226574164	226574011	226574143	PARP1	NM_001618	1	23	6	-	226574027	226574143
291756906	chr1	226578227	226578393	226578249	226578373	PARP1	NM_001618	1	23	4	-	226578111	226578325
292040994	chr1	226589982	226590154	226590002	226590130	PARP1	NM_001618	1	23	2	-	226589915	226590080
291599879	chr1	236966657	236966796	236966680	236966771	MTR	NM_000254	1	33	2	+	236966728	236966942
291393059	chr1	236971943	236972116	236971971	236972094	MTR	NM_000254	1	33	4	+	236972004	236972073
293179009	chr1	236979649	236979790	236979673	236979768	MTR	NM_000254	1	33	8	+	236979749	236979843
290717217	chr1	236988507	236988673	236988534	236988648	MTR	NM_000254	1	33	10	+	236988638	236988699
291848207	chr1	236995141	236995302	236995164	236995280	MTR	NM_000254	1	33	13	+	236995266	236995378
293196050	chr1	237001673	237001804	237001695	237001777	MTR	NM_000254	1	33	15	+	237001714	237001899
290149158	chr1	237013738	237013870	237013764	237013846	MTR	NM_000254	1	33	16	+	237013644	237013823
289521631	chr1	237016304	237016468	237016327	237016440	MTR	NM_000254	1	33	18	+	237016248	237016388
289729590	chr1	237025495	237025669	237025520	237025644	MTR	NM_000254	1	33	21	+	237025536	237025643
293621578	chr1	237038045	237038182	237038067	237038155	MTR	NM_000254	1	33	24	+	237038026	237038146
292167848	chr1	237049521	237049695	237049549	237049668	MTR	NM_000254	1	33	27	+	237049592	237049667
291896426	chr1	237054449	237054573	237054471	237054551	MTR	NM_000254	1	33	29	+	237054433	237054629
290675718	chr1	237057785	237057951	237057807	237057927	MTR	NM_000254	1	33	30	+	237057657	237057857
289327400	chr1	237060281	237060445	237060302	237060418	MTR	NM_000254	1	33	32	+	237060306	237060418
228224582	chr1	241661141	241661309	241661167	241661281	FH	NM_000143	1	10	10	-	241660857	241661270
228157467	chr1	241665612	241665786	241665638	241665761	FH	NM_000143	1	10	8	-	241665743	241665870
227639267	chr1	241667498	241667637	241667523	241667608	FH	NM_000143	1	10	7	-	241667342	241667545
227953864	chr1	241671768	241671938	241671793	241671912	FH	NM_000143	1	10	5	-	241671903	241672085
227849931	chr1	241675253	241675413	241675275	241675393	FH	NM_000143	1	10	4	-	241675267	241675443
227127718	chr1	241680415	241680539	241680443	241680516	FH	NM_000143	1	10	2	-	241680482	241680616
271450024	chr1	243662964	243663098	243662992	243663076	AKT3	NM_181690	3	14	13	-	243663039	243663088
271450024	chr1	243662964	243663098	243662992	243663076	AKT3	NM_001206729	1	14	14	-	243663021	243663088
271450024	chr1	243662964	243663098	243662992	243663076	AKT3	NM_005465	2	13	13	-	243663021	243668636
271353072	chr1	243708764	243708914	243708790	243708890	AKT3	NM_005465	2	13	11	-	243708812	243708899
271353072	chr1	243708764	243708914	243708790	243708890	AKT3	NM_181690	3	14	11	-	243708812	243708899
271353072	chr1	243708764	243708914	243708790	243708890	AKT3	NM_001206729	1	14	12	-	243708812	243708899
271726671	chr1	243726993	243727136	243727019	243727112	AKT3	NM_005465	2	13	9	-	243727022	243727150
271726671	chr1	243726993	243727136	243727019	243727112	AKT3	NM_181690	3	14	9	-	243727022	243727150
271726671	chr1	243726993	243727136	243727019	243727112	AKT3	NM_001206729	1	14	10	-	243727022	243727150
270767157	chr1	243736259	243736386	243736285	243736359	AKT3	NM_005465	2	13	8	-	243736228	243736350
270767157	chr1	243736259	243736386	243736285	243736359	AKT3	NM_181690	3	14	8	-	243736228	243736350
270767157	chr1	243736259	243736386	243736285	243736359	AKT3	NM_001206729	1	14	9	-	243736228	243736350
270159115	chr1	243800855	243801022	243800877	243800994	AKT3	NM_005465	2	13	5	-	243800913	243801044
270159115	chr1	243800855	243801022	243800877	243800994	AKT3	NM_181690	3	14	5	-	243800913	243801044
270159115	chr1	243800855	243801022	243800877	243800994	AKT3	NM_001206729	1	14	6	-	243800913	243801044
272516708	chr1	243828061	243828186	243828088	243828159	AKT3	NM_005465	2	13	3	-	243828074	243828185
272516708	chr1	243828061	243828186	243828088	243828159	AKT3	NM_181690	3	14	3	-	243828074	243828185
272516708	chr1	243828061	243828186	243828088	243828159	AKT3	NM_001206729	1	14	4	-	243828074	243828185

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
297477698	chr2	5832841	5832974	5832859	5832956	SOX11	NM_003108	1	1	1	+	5832799	5841517
297490392	chr2	5833185	5833354	5833207	5833333	SOX11	NM_003108	1	1	1	+	5832799	5841517
297476478	chr2	5833510	5833680	5833532	5833663	SOX11	NM_003108	1	1	1	+	5832799	5841517
297488074	chr2	5833923	5834067	5833940	5834045	SOX11	NM_003108	1	1	1	+	5832799	5841517
241288233	chr2	16082324	16082450	16082348	16082430	MYCN	NM_005378	1	3	2	+	16082070	16082976
236529710	chr2	16082928	16083058	16082947	16083034	MYCN	NM_005378	1	3	2	+	16082070	16082976
239203333	chr2	16085893	16086033	16085913	16086012	MYCN	NM_005378	1	3	3	+	16085615	16087129
235880822	chr2	24888539	24888685	24888569	24888662	NCOA1	NM_147233	3	21	4	+	24888618	24888784
235880822	chr2	24888539	24888685	24888569	24888662	NCOA1	NM_147223	2	22	4	+	24888618	24888784
235880822	chr2	24888539	24888685	24888569	24888662	NCOA1	NM_003743	1	21	4	+	24888618	24888784
237451028	chr2	24896233	24896360	24896260	24896333	NCOA1	NM_147233	3	21	5	+	24896235	24896332
237451028	chr2	24896233	24896360	24896260	24896333	NCOA1	NM_147223	2	22	5	+	24896235	24896332
237451028	chr2	24896233	24896360	24896260	24896333	NCOA1	NM_003743	1	21	5	+	24896235	24896332
235526495	chr2	24914376	24914509	24914399	24914486	NCOA1	NM_147233	3	21	7	+	24914350	24914529
235526495	chr2	24914376	24914509	24914399	24914486	NCOA1	NM_147223	2	22	7	+	24914350	24914529
235526495	chr2	24914376	24914509	24914399	24914486	NCOA1	NM_003743	1	21	7	+	24914350	24914529
236547781	chr2	24920398	24920569	24920426	24920552	NCOA1	NM_147233	3	21	9	+	24920527	24920667
236547781	chr2	24920398	24920569	24920426	24920552	NCOA1	NM_147223	2	22	9	+	24920527	24920667
236547781	chr2	24920398	24920569	24920426	24920552	NCOA1	NM_003743	1	21	9	+	24920527	24920667
239973944	chr2	24928052	24928200	24928075	24928171	NCOA1	NM_147233	3	21	10	+	24927955	24928102
239973944	chr2	24928052	24928200	24928075	24928171	NCOA1	NM_147223	2	22	10	+	24927955	24928102
239973944	chr2	24928052	24928200	24928075	24928171	NCOA1	NM_003743	1	21	10	+	24927955	24928102
238091230	chr2	24929667	24929834	24929687	24929811	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238091230	chr2	24929667	24929834	24929687	24929811	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238091230	chr2	24929667	24929834	24929687	24929811	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238091709	chr2	24930118	24930282	24930146	24930262	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238091709	chr2	24930118	24930282	24930146	24930262	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238091709	chr2	24930118	24930282	24930146	24930262	NCOA1	NM_003743	1	21	11	+	24929437	24930757
257726201	chr2	24930575	24930707	24930602	24930684	NCOA1	NM_147233	3	21	11	+	24929437	24930757
257726201	chr2	24930575	24930707	24930602	24930684	NCOA1	NM_147223	2	22	11	+	24929437	24930757
257726201	chr2	24930575	24930707	24930602	24930684	NCOA1	NM_003743	1	21	11	+	24929437	24930757
240413144	chr2	24949413	24949551	24949441	24949523	NCOA1	NM_147233	3	21	13	+	24949458	24949575
240413144	chr2	24949413	24949551	24949441	24949523	NCOA1	NM_147223	2	22	13	+	24949458	24949575
240413144	chr2	24949413	24949551	24949441	24949523	NCOA1	NM_003743	1	21	13	+	24949458	24949575
237657285	chr2	24952307	24952464	24952333	24952443	NCOA1	NM_147233	3	21	15	+	24952370	24952684
237657285	chr2	24952307	24952464	24952333	24952443	NCOA1	NM_147223	2	22	15	+	24952370	24952684
237657285	chr2	24952307	24952464	24952333	24952443	NCOA1	NM_003743	1	21	15	+	24952370	24952684
236399890	chr2	24962302	24962431	24962326	24962404	NCOA1	NM_147233	3	21	16	+	24962301	24962402
236399890	chr2	24962302	24962431	24962326	24962404	NCOA1	NM_147223	2	22	16	+	24962301	24962402
236399890	chr2	24962302	24962431	24962326	24962404	NCOA1	NM_003743	1	21	16	+	24962301	24962402
237565508	chr2	24964895	24965028	24964916	24965004	NCOA1	NM_147233	3	21	17	+	24964653	24965055

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237565508	chr2	24964895	24965028	24964916	24965004	NCOA1	NM_147223	2	22	17	+	24964653	24965055
237565508	chr2	24964895	24965028	24964916	24965004	NCOA1	NM_003743	1	21	17	+	24964653	24965055
236236010	chr2	24980793	24980967	24980821	24980942	NCOA1	NM_147233	3	21	19	+	24980842	24981025
236236010	chr2	24980793	24980967	24980821	24980942	NCOA1	NM_147223	2	22	19	+	24980842	24981025
236236010	chr2	24980793	24980967	24980821	24980942	NCOA1	NM_003743	1	21	19	+	24980842	24981025
235667676	chr2	24990845	24991016	24990865	24990992	NCOA1	NM_147223	2	22	21	+	24990948	24991004
232880737	chr2	25457118	25457289	25457138	25457265	DNMT3A	NM_022552	1	23	23	-	25455830	25457289
232880737	chr2	25457118	25457289	25457138	25457265	DNMT3A	NM_153759	2	19	19	-	25455830	25457289
232880737	chr2	25457118	25457289	25457138	25457265	DNMT3A	NM_175629	3	23	23	-	25455830	25457289
232913830	chr2	25459773	25459900	25459793	25459875	DNMT3A	NM_022552	1	23	21	-	25459805	25459874
232913830	chr2	25459773	25459900	25459793	25459875	DNMT3A	NM_153759	2	19	17	-	25459805	25459874
232913830	chr2	25459773	25459900	25459793	25459875	DNMT3A	NM_175629	3	23	21	-	25459805	25459874
229989043	chr2	25463212	25463378	25463234	25463357	DNMT3A	NM_022552	1	23	19	-	25463171	25463319
229989043	chr2	25463212	25463378	25463234	25463357	DNMT3A	NM_153759	2	19	15	-	25463171	25463319
229989043	chr2	25463212	25463378	25463234	25463357	DNMT3A	NM_175629	3	23	19	-	25463171	25463319
228537413	chr2	25466715	25466873	25466733	25466851	DNMT3A	NM_022552	1	23	16	-	25466767	25466851
228537413	chr2	25466715	25466873	25466733	25466851	DNMT3A	NM_153759	2	19	12	-	25466767	25466851
228537413	chr2	25466715	25466873	25466733	25466851	DNMT3A	NM_175629	3	23	16	-	25466767	25466851
230720233	chr2	25467371	25467516	25467392	25467495	DNMT3A	NM_022552	1	23	14	-	25467409	25467521
230720233	chr2	25467371	25467516	25467392	25467495	DNMT3A	NM_153759	2	19	10	-	25467409	25467521
230720233	chr2	25467371	25467516	25467392	25467495	DNMT3A	NM_175629	3	23	14	-	25467409	25467521
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_022552	1	23	12	-	25468889	25468933
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_153759	2	19	8	-	25468889	25468933
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_175629	3	23	12	-	25468889	25468933
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_022552	1	23	11	-	25469029	25469178
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_153759	2	19	7	-	25469029	25469178
232214717	chr2	25468891	25469065	25468911	25469038	DNMT3A	NM_175629	3	23	11	-	25469029	25469178
230311806	chr2	25469576	25469735	25469597	25469713	DNMT3A	NM_022552	1	23	10	-	25469489	25469645
230311806	chr2	25469576	25469735	25469597	25469713	DNMT3A	NM_153759	2	19	6	-	25469489	25469645
230311806	chr2	25469576	25469735	25469597	25469713	DNMT3A	NM_175629	3	23	10	-	25469489	25469645
227736447	chr2	25470843	25470988	25470861	25470971	DNMT3A	NM_022552	1	23	7	-	25470906	25471121
227736447	chr2	25470843	25470988	25470861	25470971	DNMT3A	NM_153759	2	19	3	-	25470906	25471121
227736447	chr2	25470843	25470988	25470861	25470971	DNMT3A	NM_175629	3	23	7	-	25470906	25471121
232660462	chr2	25474986	25475138	25475003	25475117	DNMT3A	NM_153759	2	19	1	-	25475063	25475184
228721900	chr2	25505230	25505395	25505248	25505377	DNMT3A	NM_175630	4	4	4	-	25504321	25505580
228721900	chr2	25505230	25505395	25505248	25505377	DNMT3A	NM_022552	1	23	4	-	25505310	25505580
228721900	chr2	25505230	25505395	25505248	25505377	DNMT3A	NM_175629	3	23	4	-	25505310	25505580
231619460	chr2	25536769	25536925	25536786	25536902	DNMT3A	NM_022552	1	23	2	-	25536782	25537030
231619460	chr2	25536769	25536925	25536786	25536902	DNMT3A	NM_175630	4	4	2	-	25536782	25537030
231619460	chr2	25536769	25536925	25536786	25536902	DNMT3A	NM_175629	3	23	2	-	25536782	25537030
222647788	chr2	29416431	29416575	29416451	29416551	ALK	NM_004304	1	29	29	-	29415640	29416788

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223936450	chr2	29419683	29419830	29419704	29419808	ALK	NM_004304	1	29	28	-	29419636	29419726
222613231	chr2	29432630	29432802	29432651	29432776	ALK	NM_004304	1	29	25	-	29432652	29432744
222450842	chr2	29445187	29445342	29445209	29445320	ALK	NM_004304	1	29	22	-	29445210	29445274
223060065	chr2	29446287	29446459	29446309	29446439	ALK	NM_004304	1	29	20	-	29446208	29446394
223271455	chr2	29449853	29450025	29449876	29450001	ALK	NM_004304	1	29	18	-	29449788	29449940
223523988	chr2	29455065	29455219	29455085	29455194	ALK	NM_004304	1	29	15	-	29455170	29455314
223156542	chr2	29462456	29462618	29462477	29462593	ALK	NM_004304	1	29	13	-	29462546	29462696
222363548	chr2	29497896	29498057	29497921	29498030	ALK	NM_004304	1	29	11	-	29497965	29498093
225069792	chr2	29519709	29519882	29519734	29519862	ALK	NM_004304	1	29	9	-	29519754	29519923
223347388	chr2	29543635	29543800	29543655	29543775	ALK	NM_004304	1	29	7	-	29543617	29543748
223987009	chr2	29606586	29606754	29606612	29606728	ALK	NM_004304	1	29	5	-	29606598	29606725
222426227	chr2	29917617	29917771	29917640	29917750	ALK	NM_004304	1	29	3	-	29917716	29917880
222575486	chr2	29940433	29940603	29940459	29940576	ALK	NM_004304	1	29	2	-	29940444	29940563
224312925	chr2	30143093	30143261	30143112	30143243	ALK	NM_004304	1	29	1	-	30142859	30144477
222422859	chr2	30143469	30143622	30143487	30143600	ALK	NM_004304	1	29	1	-	30142859	30144477
228015527	chr2	42472763	42472910	42472785	42472878	EML4	NM_019063	2	23	2	+	42472645	42472827
228015527	chr2	42472763	42472910	42472785	42472878	EML4	NM_001145076	1	22	2	+	42472645	42472827
230510878	chr2	42490220	42490379	42490247	42490351	EML4	NM_019063	2	23	5	+	42490318	42490446
230510878	chr2	42490220	42490379	42490247	42490351	EML4	NM_001145076	1	22	4	+	42490318	42490446
233025245	chr2	42507866	42508024	42507899	42508003	EML4	NM_019063	2	23	7	+	42507990	42508113
233025245	chr2	42507866	42508024	42507899	42508003	EML4	NM_001145076	1	22	6	+	42507990	42508113
231137078	chr2	42510078	42510213	42510098	42510185	EML4	NM_019063	2	23	8	+	42509963	42510112
231137078	chr2	42510078	42510213	42510098	42510185	EML4	NM_001145076	1	22	7	+	42509963	42510112
228147507	chr2	42515257	42515415	42515288	42515392	EML4	NM_019063	2	23	11	+	42515367	42515462
228147507	chr2	42515257	42515415	42515288	42515392	EML4	NM_001145076	1	22	10	+	42515367	42515462
230706296	chr2	42522360	42522484	42522383	42522456	EML4	NM_019063	2	23	12	+	42522265	42522399
230706296	chr2	42522360	42522484	42522383	42522456	EML4	NM_001145076	1	22	11	+	42522265	42522399
227689572	chr2	42528454	42528593	42528482	42528565	EML4	NM_019063	2	23	14	+	42528381	42528532
227689572	chr2	42528454	42528593	42528482	42528565	EML4	NM_001145076	1	22	13	+	42528381	42528532
228767432	chr2	42530477	42530614	42530498	42530586	EML4	NM_019063	2	23	16	+	42530455	42530586
228767432	chr2	42530477	42530614	42530498	42530586	EML4	NM_001145076	1	22	15	+	42530455	42530586
229781040	chr2	42552475	42552643	42552495	42552624	EML4	NM_019063	2	23	20	+	42552607	42552694
229781040	chr2	42552475	42552643	42552495	42552624	EML4	NM_001145076	1	22	19	+	42552607	42552694
229606520	chr2	42555983	42556107	42556009	42556085	EML4	NM_019063	2	23	22	+	42556026	42556156
229606520	chr2	42555983	42556107	42556009	42556085	EML4	NM_001145076	1	22	21	+	42556026	42556156
228796869	chr2	42557055	42557191	42557077	42557169	EML4	NM_019063	2	23	23	+	42556874	42559688
228796869	chr2	42557055	42557191	42557077	42557169	EML4	NM_001145076	1	22	22	+	42556874	42559688
236947138	chr2	47630383	47630538	47630403	47630519	MSH2	NM_000251	1	16	1	+	47630263	47630541
237759472	chr2	47637349	47637478	47637374	47637456	MSH2	NM_000251	1	16	3	+	47637233	47637511
235692404	chr2	47639559	47639703	47639585	47639679	MSH2	NM_000251	1	16	4	+	47639553	47639699
239694657	chr2	47641420	47641559	47641445	47641535	MSH2	NM_000251	1	16	5	+	47641408	47641557

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239503262	chr2	47656792	47656958	47656819	47656930	MSH2	NM_000251	1	16	7	+	47656881	47657080
258201628	chr2	47672736	47672910	47672762	47672884	MSH2	NM_000251	1	16	8	+	47672687	47672796
238702685	chr2	47698143	47698300	47698169	47698272	MSH2	NM_000251	1	16	11	+	47698104	47698201
241375823	chr2	47703504	47703631	47703526	47703609	MSH2	NM_000251	1	16	13	+	47703506	47703710
240417352	chr2	47705490	47705618	47705518	47705595	MSH2	NM_000251	1	16	14	+	47705411	47705658
237702371	chr2	47709831	47709961	47709860	47709938	MSH2	NM_000251	1	16	16	+	47709918	47710360
238486223	chr2	48010419	48010593	48010437	48010573	MSH6	NM_000179	1	10	1	+	48010221	48010632
236246420	chr2	48023109	48023250	48023138	48023222	MSH6	NM_000179	1	10	3	+	48023033	48023202
257831625	chr2	48026031	48026204	48026053	48026182	MSH6	NM_000179	1	10	4	+	48025750	48028294
257878744	chr2	48026538	48026686	48026559	48026660	MSH6	NM_000179	1	10	4	+	48025750	48028294
238042039	chr2	48026953	48027078	48026978	48027055	MSH6	NM_000179	1	10	4	+	48025750	48028294
257758179	chr2	48027345	48027513	48027373	48027486	MSH6	NM_000179	1	10	4	+	48025750	48028294
257755837	chr2	48027703	48027867	48027732	48027847	MSH6	NM_000179	1	10	4	+	48025750	48028294
257746144	chr2	48028168	48028341	48028195	48028315	MSH6	NM_000179	1	10	4	+	48025750	48028294
235255911	chr2	48031920	48032082	48031944	48032061	MSH6	NM_000179	1	10	6	+	48032049	48032166
241839100	chr2	48033224	48033381	48033250	48033360	MSH6	NM_000179	1	10	8	+	48033343	48033497
235889826	chr2	48033625	48033754	48033653	48033726	MSH6	NM_000179	1	10	9	+	48033591	48033790
222547983	chr2	60679713	60679858	60679735	60679835	BCL11A	NM_018014	1	5	5	-	60678302	60679801
222547983	chr2	60679713	60679858	60679735	60679835	BCL11A	NM_138559	3	5	5	-	60678302	60679801
224591923	chr2	60687773	60687933	60687800	60687915	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224591923	chr2	60687773	60687933	60687800	60687915	BCL11A	NM_018014	1	5	4	-	60687817	60689559
224591330	chr2	60688234	60688402	60688255	60688385	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224591330	chr2	60688234	60688402	60688255	60688385	BCL11A	NM_018014	1	5	4	-	60687817	60689559
224601222	chr2	60688620	60688772	60688639	60688752	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224601222	chr2	60688620	60688772	60688639	60688752	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223040709	chr2	60689077	60689245	60689100	60689224	BCL11A	NM_022893	2	4	4	-	60684329	60689559
223040709	chr2	60689077	60689245	60689100	60689224	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223785700	chr2	60695879	60696011	60695900	60695983	BCL11A	NM_018014	1	5	3	-	60695867	60695968
223785700	chr2	60695879	60696011	60695900	60695983	BCL11A	NM_022893	2	4	3	-	60695867	60695968
223785700	chr2	60695879	60696011	60695900	60695983	BCL11A	NM_138559	3	5	3	-	60695867	60695968
223763257	chr2	60773323	60773488	60773344	60773465	BCL11A	NM_018014	1	5	2	-	60773106	60773435
223763257	chr2	60773323	60773488	60773344	60773465	BCL11A	NM_022893	2	4	2	-	60773106	60773435
223763257	chr2	60773323	60773488	60773344	60773465	BCL11A	NM_138559	3	5	2	-	60773106	60773435
238482716	chr2	61118864	61118990	61118892	61118965	REL	NM_002908	1	11	2	+	61118818	61118960
242266984	chr2	61144010	61144161	61144036	61144133	REL	NM_002908	1	11	5	+	61144012	61144152
239650358	chr2	61145642	61145807	61145665	61145779	REL	NM_002908	1	11	7	+	61145529	61145741
241921917	chr2	61148883	61149026	61148907	61149005	REL	NM_002908	1	11	11	+	61148898	61150178
241975315	chr2	61149324	61149497	61149350	61149469	REL	NM_002908	1	11	11	+	61148898	61150178
273389154	chr2	61705986	61706149	61706010	61706121	XPO1	NM_003400	1	25	25	-	61705069	61706101
272819653	chr2	61710113	61710284	61710141	61710258	XPO1	NM_003400	1	25	22	-	61710092	61710226
273157452	chr2	61712918	61713078	61712946	61713057	XPO1	NM_003400	1	25	20	-	61712903	61713097

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273456083	chr2	61715652	61715778	61715680	61715750	XPO1	NM_003400	1	25	18	-	61715723	61715906
273147400	chr2	61717839	61717976	61717867	61717950	XPO1	NM_003400	1	25	17	-	61717777	61717911
273398885	chr2	61719450	61719608	61719478	61719581	XPO1	NM_003400	1	25	15	-	61719460	61719616
273793030	chr2	61719967	61720121	61720000	61720093	XPO1	NM_003400	1	25	13	-	61720050	61720188
273186269	chr2	61722521	61722672	61722552	61722646	XPO1	NM_003400	1	25	11	-	61722590	61722748
274029522	chr2	61724015	61724185	61724041	61724158	XPO1	NM_003400	1	25	10	-	61724014	61724142
273465835	chr2	61726733	61726893	61726766	61726865	XPO1	NM_003400	1	25	7	-	61726848	61727029
273529969	chr2	61749621	61749767	61749646	61749747	XPO1	NM_003400	1	25	4	-	61749746	61749818
274239083	chr2	61753607	61753747	61753633	61753721	XPO1	NM_003400	1	25	3	-	61753555	61753656
298949956	chr2	85361047	85361220	85361068	85361203	TCF7L1	NM_031283	1	12	2	+	85361139	85361202
298990026	chr2	85529519	85529657	85529548	85529637	TCF7L1	NM_031283	1	12	5	+	85529607	85529739
299254899	chr2	85532278	85532417	85532298	85532396	TCF7L1	NM_031283	1	12	8	+	85532383	85532526
299111828	chr2	85533530	85533703	85533549	85533683	TCF7L1	NM_031283	1	12	10	+	85533575	85533682
299262405	chr2	85536257	85536423	85536276	85536404	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
225298935	chr2	100167819	100167993	100167841	100167973	AFF3	NM_002285	2	24	24	-	100163716	100168057
225298935	chr2	100167819	100167993	100167841	100167973	AFF3	NM_001025108	1	24	24	-	100163716	100168057
222928100	chr2	100170921	100171090	100170939	100171072	AFF3	NM_002285	2	24	23	-	100170773	100170996
222928100	chr2	100170921	100171090	100170939	100171072	AFF3	NM_001025108	1	24	23	-	100170773	100170996
224090423	chr2	100181915	100182068	100181937	100182045	AFF3	NM_002285	2	24	19	-	100181949	100182085
224090423	chr2	100181915	100182068	100181937	100182045	AFF3	NM_001025108	1	24	19	-	100181949	100182085
224342451	chr2	100194881	100195023	100194907	100194996	AFF3	NM_002285	2	24	17	-	100194789	100194913
224342451	chr2	100194881	100195023	100194907	100194996	AFF3	NM_001025108	1	24	17	-	100194789	100194913
222881666	chr2	100203600	100203773	100203621	100203745	AFF3	NM_002285	2	24	15	-	100203616	100203740
222881666	chr2	100203600	100203773	100203621	100203745	AFF3	NM_001025108	1	24	15	-	100203616	100203740
225181971	chr2	100209894	100210064	100209915	100210043	AFF3	NM_002285	2	24	14	-	100209657	100210751
225181971	chr2	100209894	100210064	100209915	100210043	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223846069	chr2	100210355	100210513	100210372	100210495	AFF3	NM_002285	2	24	14	-	100209657	100210751
223846069	chr2	100210355	100210513	100210372	100210495	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223741192	chr2	100217829	100218002	100217847	100217984	AFF3	NM_002285	2	24	13	-	100217897	100218083
223741192	chr2	100217829	100218002	100217847	100217984	AFF3	NM_001025108	1	24	13	-	100217897	100218083
224007475	chr2	100343491	100343644	100343519	100343614	AFF3	NM_002285	2	24	10	-	100343539	100343590
224007475	chr2	100343491	100343644	100343519	100343614	AFF3	NM_001025108	1	24	10	-	100343539	100343590
223059174	chr2	100623064	100623234	100623084	100623210	AFF3	NM_002285	2	24	6	-	100623094	100623479
223059174	chr2	100623064	100623234	100623084	100623210	AFF3	NM_001025108	1	24	6	-	100623094	100623479
225073259	chr2	100623569	100623735	100623593	100623714	AFF3	NM_002285	2	24	5	-	100623610	100623922
225073259	chr2	100623569	100623735	100623593	100623714	AFF3	NM_001025108	1	24	5	-	100623610	100623922
223226597	chr2	100625267	100625435	100625290	100625411	AFF3	NM_002285	2	24	4	-	100625274	100625394
223226597	chr2	100625267	100625435	100625290	100625411	AFF3	NM_001025108	1	24	4	-	100625274	100625394
237450466	chr2	113977698	113977866	113977719	113977845	PAX8	NM_003466	1	12	11	-	113977669	113977755
237450466	chr2	113977698	113977866	113977719	113977845	PAX8	NM_013992	4	9	8	-	113977669	113977755
237450466	chr2	113977698	113977866	113977719	113977845	PAX8	NM_013952	2	12	11	-	113977669	113977755

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237450466	chr2	113977698	113977866	113977719	113977845	PAX8	NM_013953	3	10	9	-	113977669	113977755
234914154	chr2	113994100	113994246	113994118	113994227	PAX8	NM_003466	1	12	8	-	113994178	113994298
234914154	chr2	113994100	113994246	113994118	113994227	PAX8	NM_013952	2	12	8	-	113994178	113994298
234932399	chr2	113999262	113999394	113999286	113999373	PAX8	NM_003466	1	12	7	-	113999128	113999303
234932399	chr2	113999262	113999394	113999286	113999373	PAX8	NM_013992	4	9	7	-	113999128	113999303
234932399	chr2	113999262	113999394	113999286	113999373	PAX8	NM_013952	2	12	7	-	113999128	113999303
234932399	chr2	113999262	113999394	113999286	113999373	PAX8	NM_013953	3	10	7	-	113999128	113999303
235035286	chr2	114001980	114002135	114002003	114002113	PAX8	NM_003466	1	12	4	-	114002004	114002201
235035286	chr2	114001980	114002135	114002003	114002113	PAX8	NM_013992	4	9	4	-	114002004	114002201
235035286	chr2	114001980	114002135	114002003	114002113	PAX8	NM_013952	2	12	4	-	114002004	114002201
235035286	chr2	114001980	114002135	114002003	114002113	PAX8	NM_013953	3	10	4	-	114002004	114002201
237337100	chr2	114035926	114036081	114035946	114036060	PAX8	NM_003466	1	12	2	-	114035947	114036046
237337100	chr2	114035926	114036081	114035946	114036060	PAX8	NM_013992	4	9	2	-	114035947	114036046
237337100	chr2	114035926	114036081	114035946	114036060	PAX8	NM_013952	2	12	2	-	114035947	114036046
237337100	chr2	114035926	114036081	114035946	114036060	PAX8	NM_013953	3	10	2	-	114035947	114036046
231939681	chr2	128016976	128017118	128016997	128017098	ERCC3	NM_000122	1	15	14	-	128016872	128017024
230528253	chr2	128028990	128029155	128029010	128029127	ERCC3	NM_000122	1	15	12	-	128028912	128029029
231129322	chr2	128037939	128038109	128037960	128038084	ERCC3	NM_000122	1	15	9	-	128038023	128038207
231036093	chr2	128044454	128044622	128044475	128044600	ERCC3	NM_000122	1	15	8	-	128044279	128044593
230508708	chr2	128046929	128047100	128046954	128047078	ERCC3	NM_000122	1	15	6	-	128046913	128047077
231611576	chr2	128050159	128050326	128050180	128050303	ERCC3	NM_000122	1	15	3	-	128050186	128050422
229961932	chr2	128051595	128051744	128051612	128051725	ERCC3	NM_000122	1	15	1	-	128051630	128051752
269957203	chr2	140995691	140995836	140995719	140995806	LRP1B	NM_018557	1	91	89	-	140995721	140995865
271729407	chr2	141027726	141027889	141027754	141027864	LRP1B	NM_018557	1	91	86	-	141027811	141027915
270955602	chr2	141032102	141032251	141032127	141032220	LRP1B	NM_018557	1	91	85	-	141031993	141032167
271815911	chr2	141072530	141072656	141072553	141072629	LRP1B	NM_018557	1	91	83	-	141072504	141072668
269976725	chr2	141081526	141081664	141081552	141081633	LRP1B	NM_018557	1	91	81	-	141081462	141081635
271096339	chr2	141093085	141093221	141093113	141093194	LRP1B	NM_018557	1	91	78	-	141093184	141093407
272188136	chr2	141108426	141108581	141108454	141108555	LRP1B	NM_018557	1	91	77	-	141108366	141108607
271325589	chr2	141113942	141114107	141113963	141114080	LRP1B	NM_018557	1	91	75	-	141113911	141114045
269693347	chr2	141116385	141116559	141116411	141116533	LRP1B	NM_018557	1	91	73	-	141116390	141116515
270393452	chr2	141128285	141128438	141128308	141128412	LRP1B	NM_018557	1	91	71	-	141128279	141128411
269685346	chr2	141135703	141135859	141135725	141135836	LRP1B	NM_018557	1	91	68	-	141135749	141135855
271033861	chr2	141200074	141200230	141200094	141200202	LRP1B	NM_018557	1	91	66	-	141200073	141200192
271272618	chr2	141202131	141202281	141202157	141202253	LRP1B	NM_018557	1	91	64	-	141202132	141202248
269949564	chr2	141214049	141214209	141214074	141214180	LRP1B	NM_018557	1	91	62	-	141214024	141214172
271054845	chr2	141232688	141232848	141232715	141232820	LRP1B	NM_018557	1	91	60	-	141232707	141232906
270768527	chr2	141243014	141243156	141243042	141243129	LRP1B	NM_018557	1	91	59	-	141242912	141243093
272116463	chr2	141250201	141250375	141250230	141250352	LRP1B	NM_018557	1	91	57	-	141250177	141250262
272602669	chr2	141259124	141259297	141259149	141259272	LRP1B	NM_018557	1	91	55	-	141259256	141259443
269953092	chr2	141260526	141260674	141260551	141260649	LRP1B	NM_018557	1	91	54	-	141260532	141260672

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271080059	chr2	141267383	141267549	141267406	141267527	LRP1B	NM_018557	1	91	52	-	141267497	141267625
271224511	chr2	141274459	141274585	141274482	141274558	LRP1B	NM_018557	1	91	50	-	141274458	141274580
270214560	chr2	141283526	141283695	141283553	141283669	LRP1B	NM_018557	1	91	49	-	141283413	141283562
270361734	chr2	141291605	141291746	141291626	141291718	LRP1B	NM_018557	1	91	47	-	141291590	141291709
270789174	chr2	141298601	141298764	141298624	141298735	LRP1B	NM_018557	1	91	45	-	141298542	141298667
270983922	chr2	141356087	141356248	141356115	141356220	LRP1B	NM_018557	1	91	43	-	141356200	141356404
272067171	chr2	141359106	141359232	141359127	141359204	LRP1B	NM_018557	1	91	42	-	141359019	141359208
270654871	chr2	141457940	141458107	141457968	141458085	LRP1B	NM_018557	1	91	41	-	141457819	141458190
271050597	chr2	141459596	141459765	141459622	141459738	LRP1B	NM_018557	1	91	39	-	141459710	141459861
270132918	chr2	141460049	141460198	141460071	141460171	LRP1B	NM_018557	1	91	38	-	141459996	141460122
269549550	chr2	141474335	141474468	141474362	141474440	LRP1B	NM_018557	1	91	36	-	141474251	141474385
272055426	chr2	141528523	141528693	141528548	141528664	LRP1B	NM_018557	1	91	34	-	141528450	141528575
270951324	chr2	141597502	141597661	141597529	141597633	LRP1B	NM_018557	1	91	31	-	141597560	141597654
270452960	chr2	141607623	141607771	141607656	141607744	LRP1B	NM_018557	1	91	29	-	141607671	141607898
271516398	chr2	141609289	141609432	141609316	141609408	LRP1B	NM_018557	1	91	28	-	141609221	141609352
269590379	chr2	141625587	141625731	141625614	141625713	LRP1B	NM_018557	1	91	26	-	141625668	141625832
270769702	chr2	141641483	141641618	141641511	141641590	LRP1B	NM_018557	1	91	25	-	141641386	141641590
270182938	chr2	141660667	141660841	141660692	141660813	LRP1B	NM_018557	1	91	23	-	141660489	141660734
272179541	chr2	141680457	141680629	141680479	141680601	LRP1B	NM_018557	1	91	21	-	141680534	141680716
269623113	chr2	141707886	141708013	141707907	141707989	LRP1B	NM_018557	1	91	20	-	141707804	141707971
272699167	chr2	141747065	141747239	141747092	141747219	LRP1B	NM_018557	1	91	17	-	141747101	141747226
271619673	chr2	141762830	141762954	141762859	141762929	LRP1B	NM_018557	1	91	15	-	141762904	141763026
270840207	chr2	141771186	141771354	141771214	141771327	LRP1B	NM_018557	1	91	14	-	141771125	141771314
271427204	chr2	141777484	141777616	141777508	141777592	LRP1B	NM_018557	1	91	12	-	141777491	141777671
271534474	chr2	141806660	141806831	141806683	141806804	LRP1B	NM_018557	1	91	11	-	141806555	141806791
271074354	chr2	141816482	141816641	141816510	141816612	LRP1B	NM_018557	1	91	9	-	141816452	141816623
270963172	chr2	141945907	141946075	141945934	141946048	LRP1B	NM_018557	1	91	7	-	141945990	141946152
269724890	chr2	141986796	141986942	141986824	141986915	LRP1B	NM_018557	1	91	6	-	141986752	141987009
269516602	chr2	142011981	142012138	142012009	142012111	LRP1B	NM_018557	1	91	4	-	142012091	142012210
272569662	chr2	142567817	142567958	142567840	142567934	LRP1B	NM_018557	1	91	2	-	142567848	142567970
284753434	chr2	148602625	148602784	148602649	148602761	ACVR2A	NM_001616	1	11	1	+	148602570	148602776
281676225	chr2	148653988	148654160	148654015	148654136	ACVR2A	NM_001616	1	11	2	+	148653870	148654077
282056971	chr2	148657393	148657540	148657417	148657512	ACVR2A	NM_001616	1	11	4	+	148657313	148657467
283570491	chr2	148674901	148675073	148674929	148675048	ACVR2A	NM_001616	1	11	6	+	148674852	148674995
283875548	chr2	148677709	148677867	148677734	148677846	ACVR2A	NM_001616	1	11	8	+	148677799	148677913
283680890	chr2	148680614	148680757	148680643	148680732	ACVR2A	NM_001616	1	11	9	+	148680542	148680680
281371173	chr2	148684603	148684750	148684624	148684724	ACVR2A	NM_001616	1	11	11	+	148684649	148688393
235210417	chr2	178095641	178095799	178095667	178095771	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235210417	chr2	178095641	178095799	178095667	178095771	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235210417	chr2	178095641	178095799	178095667	178095771	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
239701397	chr2	178096014	178096188	178096035	178096167	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239701397	chr2	178096014	178096188	178096035	178096167	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
239701397	chr2	178096014	178096188	178096035	178096167	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
239938258	chr2	178096494	178096632	178096516	178096604	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
239938258	chr2	178096494	178096632	178096516	178096604	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
239938258	chr2	178096494	178096632	178096516	178096604	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235090119	chr2	178097129	178097255	178097155	178097229	NFE2L2	NM_001145412	1	5	4	-	178097120	178097311
235090119	chr2	178097129	178097255	178097155	178097229	NFE2L2	NM_006164	3	5	4	-	178097120	178097311
235090119	chr2	178097129	178097255	178097155	178097229	NFE2L2	NM_001145413	2	5	4	-	178097120	178097290
238568546	chr2	178098691	178098827	178098717	178098799	NFE2L2	NM_001145412	1	5	2	-	178098733	178098999
238568546	chr2	178098691	178098827	178098717	178098799	NFE2L2	NM_001145413	2	5	2	-	178098733	178098999
238568546	chr2	178098691	178098827	178098717	178098799	NFE2L2	NM_006164	3	5	2	-	178098733	178098999
330063817	chr2	178129192	178129325	178129209	178129307	NFE2L2	NM_006164	3	5	1	-	178129260	178129859
235896720	chr2	190660499	190660643	190660528	190660617	PMS1	NM_001128144	3	12	3	+	190660495	190660677
235896720	chr2	190660499	190660643	190660528	190660617	PMS1	NM_000534	1	13	3	+	190660495	190660677
235896720	chr2	190660499	190660643	190660528	190660617	PMS1	NM_001128143	2	12	3	+	190660495	190660677
236651142	chr2	190670435	190670583	190670456	190670555	PMS1	NM_001128144	3	12	4	+	190670378	190670480
236651142	chr2	190670435	190670583	190670456	190670555	PMS1	NM_000534	1	13	4	+	190670378	190670480
236651142	chr2	190670435	190670583	190670456	190670555	PMS1	NM_001128143	2	12	4	+	190670378	190670480
236699373	chr2	190708691	190708861	190708717	190708833	PMS1	NM_001128144	3	12	6	+	190708690	190708806
236699373	chr2	190708691	190708861	190708717	190708833	PMS1	NM_000534	1	13	6	+	190708690	190708806
241080619	chr2	190718971	190719103	190719002	190719075	PMS1	NM_001128144	3	12	9	+	190718965	190719854
241080619	chr2	190718971	190719103	190719002	190719075	PMS1	NM_000534	1	13	9	+	190718965	190719854
241080619	chr2	190718971	190719103	190719002	190719075	PMS1	NM_001128143	2	12	8	+	190718965	190719854
237594248	chr2	190719365	190719508	190719393	190719483	PMS1	NM_001128144	3	12	9	+	190718965	190719854
237594248	chr2	190719365	190719508	190719393	190719483	PMS1	NM_000534	1	13	9	+	190718965	190719854
237594248	chr2	190719365	190719508	190719393	190719483	PMS1	NM_001128143	2	12	8	+	190718965	190719854
238258779	chr2	190728458	190728591	190728491	190728570	PMS1	NM_000534	1	13	10	+	190728469	190728954
238258779	chr2	190728458	190728591	190728491	190728570	PMS1	NM_001128143	2	12	9	+	190728469	190728954
238290218	chr2	190728872	190729038	190728898	190729010	PMS1	NM_000534	1	13	10	+	190728469	190728954
238290218	chr2	190728872	190729038	190728898	190729010	PMS1	NM_001128143	2	12	9	+	190728469	190728954
236310760	chr2	190741949	190742120	190741978	190742094	PMS1	NM_001128144	3	12	12	+	190741998	190742355
236310760	chr2	190741949	190742120	190741978	190742094	PMS1	NM_000534	1	13	13	+	190741998	190742355
236310760	chr2	190741949	190742120	190741978	190742094	PMS1	NM_001128143	2	12	12	+	190741998	190742355
273158396	chr2	198257801	198257931	198257826	198257907	SF3B1	NM_012433	2	25	24	-	198257696	198257912
272801761	chr2	198260926	198261082	198260947	198261057	SF3B1	NM_012433	2	25	23	-	198260780	198261052
274036060	chr2	198263130	198263257	198263158	198263232	SF3B1	NM_012433	2	25	21	-	198263185	198263305
273213163	chr2	198264943	198265102	198264971	198265077	SF3B1	NM_012433	2	25	19	-	198264976	198265158
273897311	chr2	198265556	198265708	198265581	198265681	SF3B1	NM_012433	2	25	18	-	198265439	198265660
273712950	chr2	198266406	198266565	198266437	198266537	SF3B1	NM_012433	2	25	16	-	198266466	198266612
272942716	chr2	198267293	198267417	198267322	198267392	SF3B1	NM_012433	2	25	14	-	198267280	198267550
272738338	chr2	198267700	198267844	198267728	198267811	SF3B1	NM_012433	2	25	13	-	198267673	198267759

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274377363	chr2	198269865	198270011	198269892	198269978	SF3B1	NM_012433	2	25	11	-	198269800	198269901
274398698	chr2	198272626	198272771	198272647	198272746	SF3B1	NM_012433	2	25	9	-	198272722	198272843
273056357	chr2	198273124	198273250	198273146	198273224	SF3B1	NM_012433	2	25	8	-	198273093	198273305
272923420	chr2	198274614	198274785	198274635	198274756	SF3B1	NM_012433	2	25	7	-	198274494	198274731
273484429	chr2	198283580	198283751	198283601	198283723	SF3B1	NM_001005526	1	5	5	-	198283521	198283675
273787572	chr2	198285681	198285824	198285708	198285800	SF3B1	NM_012433	2	25	3	-	198285753	198285857
273787572	chr2	198285681	198285824	198285708	198285800	SF3B1	NM_001005526	1	5	3	-	198285753	198285857
273848468	chr2	198288643	198288768	198288664	198288742	SF3B1	NM_012433	2	25	2	-	198288532	198288698
273848468	chr2	198288643	198288768	198288664	198288742	SF3B1	NM_001005526	1	5	2	-	198288532	198288698
226985742	chr2	208424883	208425017	208424911	208424995	CREB1	NM_134442	2	9	3	+	208424950	208425096
226985742	chr2	208424883	208425017	208424911	208424995	CREB1	NM_004379	1	8	3	+	208424950	208425096
226301845	chr2	208432197	208432359	208432222	208432331	CREB1	NM_134442	2	9	5	+	208432187	208432287
226301845	chr2	208432197	208432359	208432222	208432331	CREB1	NM_004379	1	8	4	+	208432187	208432287
225409436	chr2	208439977	208440134	208440004	208440110	CREB1	NM_134442	2	9	7	+	208439996	208440178
225409436	chr2	208439977	208440134	208440004	208440110	CREB1	NM_004379	1	8	6	+	208439996	208440178
225810007	chr2	208461614	208461747	208461637	208461718	CREB1	NM_134442	2	9	9	+	208461638	208470284
225810007	chr2	208461614	208461747	208461637	208461718	CREB1	NM_004379	1	8	8	+	208461638	208470284
228755568	chr2	209103718	209103882	209103739	209103854	IDH1	NM_005896	1	10	9	-	209103795	209103957
227414633	chr2	209106638	209106809	209106661	209106788	IDH1	NM_005896	1	10	7	-	209106718	209106869
227333543	chr2	209109928	209110083	209109961	209110060	IDH1	NM_005896	1	10	5	-	209110043	209110148
227224920	chr2	209113079	209113248	209113104	209113220	IDH1	NM_005896	1	10	4	-	209113093	209113384
228492247	chr2	209116229	209116403	209116252	209116372	IDH1	NM_005896	1	10	3	-	209116154	209116291
227767006	chr2	212248569	212248702	212248591	212248680	ERBB4	NM_001042599	1	27	27	-	212240442	212248785
227767006	chr2	212248569	212248702	212248591	212248680	ERBB4	NM_005235	2	28	28	-	212240442	212248785
229615654	chr2	212251788	212251917	212251811	212251894	ERBB4	NM_001042599	1	27	26	-	212251578	212251875
229615654	chr2	212251788	212251917	212251811	212251894	ERBB4	NM_005235	2	28	27	-	212251578	212251875
230430455	chr2	212285245	212285370	212285272	212285342	ERBB4	NM_001042599	1	27	25	-	212285166	212285336
230430455	chr2	212285245	212285370	212285272	212285342	ERBB4	NM_005235	2	28	25	-	212285166	212285336
231148393	chr2	212288925	212289095	212288953	212289067	ERBB4	NM_001042599	1	27	23	-	212288880	212289026
231148393	chr2	212288925	212289095	212288953	212289067	ERBB4	NM_005235	2	28	23	-	212288880	212289026
230760312	chr2	212426545	212426674	212426578	212426649	ERBB4	NM_001042599	1	27	20	-	212426628	212426813
230760312	chr2	212426545	212426674	212426578	212426649	ERBB4	NM_005235	2	28	20	-	212426628	212426813
229788545	chr2	212488558	212488700	212488587	212488676	ERBB4	NM_001042599	1	27	18	-	212488647	212488769
229788545	chr2	212488558	212488700	212488587	212488676	ERBB4	NM_005235	2	28	18	-	212488647	212488769
231405687	chr2	212522428	212522600	212522455	212522574	ERBB4	NM_001042599	1	27	16	-	212522479	212522553
231405687	chr2	212522428	212522600	212522455	212522574	ERBB4	NM_005235	2	28	16	-	212522479	212522553
230404087	chr2	212543745	212543903	212543767	212543881	ERBB4	NM_001042599	1	27	13	-	212543777	212543909
230404087	chr2	212543745	212543903	212543767	212543881	ERBB4	NM_005235	2	28	13	-	212543777	212543909
231192551	chr2	212566780	212566915	212566806	212566891	ERBB4	NM_001042599	1	27	12	-	212566692	212566891
231192551	chr2	212566780	212566915	212566806	212566891	ERBB4	NM_005235	2	28	12	-	212566692	212566891
230220494	chr2	212570085	212570237	212570109	212570210	ERBB4	NM_001042599	1	27	10	-	212570043	212570116

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230220494	chr2	212570085	212570237	212570109	212570210	ERBB4	NM_005235	2	28	10	-	212570043	212570116
227752479	chr2	212578277	212578440	212578305	212578414	ERBB4	NM_001042599	1	27	8	-	212578260	212578373
227752479	chr2	212578277	212578440	212578305	212578414	ERBB4	NM_005235	2	28	8	-	212578260	212578373
326739570	chr2	212589779	212589951	212589807	212589923	ERBB4	NM_001042599	1	27	6	-	212589801	212589919
326739570	chr2	212589779	212589951	212589807	212589923	ERBB4	NM_005235	2	28	6	-	212589801	212589919
229758507	chr2	212812043	212812207	212812071	212812179	ERBB4	NM_001042599	1	27	3	-	212812155	212812341
229758507	chr2	212812043	212812207	212812071	212812179	ERBB4	NM_005235	2	28	3	-	212812155	212812341
230719694	chr2	212989514	212989653	212989536	212989628	ERBB4	NM_001042599	1	27	2	-	212989477	212989628
230719694	chr2	212989514	212989653	212989536	212989628	ERBB4	NM_005235	2	28	2	-	212989477	212989628
280442508	chr2	216226286	216226455	216226310	216226428	FN1	NM_212476	4	44	44	-	216225179	216226349
280442508	chr2	216226286	216226455	216226310	216226428	FN1	NM_212478	5	46	46	-	216225179	216226349
280442508	chr2	216226286	216226455	216226310	216226428	FN1	NM_212482	6	46	46	-	216225179	216226349
280442508	chr2	216226286	216226455	216226310	216226428	FN1	NM_212474	3	44	44	-	216225179	216226349
280442508	chr2	216226286	216226455	216226310	216226428	FN1	NM_002026	1	46	46	-	216225179	216226349
277921410	chr2	216230260	216230431	216230281	216230410	FN1	NM_212476	4	44	41	-	216230228	216230353
277921410	chr2	216230260	216230431	216230281	216230410	FN1	NM_212478	5	46	43	-	216230228	216230353
277921410	chr2	216230260	216230431	216230281	216230410	FN1	NM_212482	6	46	43	-	216230228	216230353
277921410	chr2	216230260	216230431	216230281	216230410	FN1	NM_212474	3	44	41	-	216230228	216230353
277921410	chr2	216230260	216230431	216230281	216230410	FN1	NM_002026	1	46	43	-	216230228	216230353
277895199	chr2	216235018	216235180	216235038	216235155	FN1	NM_212476	4	44	39	-	216235017	216235155
277895199	chr2	216235018	216235180	216235038	216235155	FN1	NM_212478	5	46	41	-	216235017	216235155
277895199	chr2	216235018	216235180	216235038	216235155	FN1	NM_212482	6	46	41	-	216235017	216235155
277895199	chr2	216235018	216235180	216235038	216235155	FN1	NM_212474	3	44	39	-	216235017	216235155
277895199	chr2	216235018	216235180	216235038	216235155	FN1	NM_002026	1	46	41	-	216235017	216235155
278648189	chr2	216236952	216237120	216236974	216237099	FN1	NM_212478	5	46	39	-	216236832	216237023
278648189	chr2	216236952	216237120	216236974	216237099	FN1	NM_002026	1	46	39	-	216236832	216237098
278648189	chr2	216236952	216237120	216236974	216237099	FN1	NM_212476	4	44	38	-	216236632	216237098
278648189	chr2	216236952	216237120	216236974	216237099	FN1	NM_212482	6	46	40	-	216236632	216237098
278061579	chr2	216240303	216240430	216240330	216240404	FN1	NM_212476	4	44	35	-	216240352	216240441
278061579	chr2	216240303	216240430	216240330	216240404	FN1	NM_212478	5	46	36	-	216240352	216240441
278061579	chr2	216240303	216240430	216240330	216240404	FN1	NM_212482	6	46	37	-	216240352	216240441
278061579	chr2	216240303	216240430	216240330	216240404	FN1	NM_212474	3	44	35	-	216240352	216240441
278061579	chr2	216240303	216240430	216240330	216240404	FN1	NM_002026	1	46	36	-	216240352	216240441
279995709	chr2	216242820	216242955	216242846	216242930	FN1	NM_212476	4	44	33	-	216242898	216242985
279995709	chr2	216242820	216242955	216242846	216242930	FN1	NM_212478	5	46	34	-	216242898	216242985
279995709	chr2	216242820	216242955	216242846	216242930	FN1	NM_212482	6	46	35	-	216242898	216242985
279995709	chr2	216242820	216242955	216242846	216242930	FN1	NM_212474	3	44	33	-	216242898	216242985
279995709	chr2	216242820	216242955	216242846	216242930	FN1	NM_002026	1	46	34	-	216242898	216242985
278577058	chr2	216245507	216245672	216245528	216245651	FN1	NM_212478	5	46	32	-	216245534	216245803
278577058	chr2	216245507	216245672	216245528	216245651	FN1	NM_212482	6	46	33	-	216245534	216245803
278577058	chr2	216245507	216245672	216245528	216245651	FN1	NM_002026	1	46	32	-	216245534	216245803

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280838585	chr2	216246913	216247083	216246936	216247059	FN1	NM_212476	4	44	31	-	216246935	216247048
280838585	chr2	216246913	216247083	216246936	216247059	FN1	NM_212478	5	46	31	-	216246935	216247048
280838585	chr2	216246913	216247083	216246936	216247059	FN1	NM_212482	6	46	32	-	216246935	216247048
280838585	chr2	216246913	216247083	216246936	216247059	FN1	NM_212474	3	44	31	-	216246935	216247048
280838585	chr2	216246913	216247083	216246936	216247059	FN1	NM_002026	1	46	31	-	216246935	216247048
279333659	chr2	216248796	216248940	216248818	216248914	FN1	NM_212476	4	44	29	-	216248743	216248907
279333659	chr2	216248796	216248940	216248818	216248914	FN1	NM_212478	5	46	29	-	216248743	216248907
279333659	chr2	216248796	216248940	216248818	216248914	FN1	NM_212482	6	46	30	-	216248743	216248907
279333659	chr2	216248796	216248940	216248818	216248914	FN1	NM_212474	3	44	29	-	216248743	216248907
279333659	chr2	216248796	216248940	216248818	216248914	FN1	NM_002026	1	46	29	-	216248743	216248907
279064943	chr2	216251581	216251746	216251603	216251723	FN1	NM_212476	4	44	27	-	216251412	216251681
279064943	chr2	216251581	216251746	216251603	216251723	FN1	NM_212478	5	46	27	-	216251412	216251681
279064943	chr2	216251581	216251746	216251603	216251723	FN1	NM_212482	6	46	28	-	216251412	216251681
279064943	chr2	216251581	216251746	216251603	216251723	FN1	NM_212474	3	44	27	-	216251412	216251681
279064943	chr2	216251581	216251746	216251603	216251723	FN1	NM_002026	1	46	27	-	216251412	216251681
278730008	chr2	216257539	216257687	216257563	216257666	FN1	NM_212482	6	46	25	-	216257654	216257926
278926834	chr2	216259215	216259367	216259238	216259346	FN1	NM_212476	4	44	24	-	216259251	216259442
278926834	chr2	216259215	216259367	216259238	216259346	FN1	NM_212478	5	46	24	-	216259251	216259442
278926834	chr2	216259215	216259367	216259238	216259346	FN1	NM_212482	6	46	24	-	216259251	216259442
278926834	chr2	216259215	216259367	216259238	216259346	FN1	NM_212474	3	44	24	-	216259251	216259442
278926834	chr2	216259215	216259367	216259238	216259346	FN1	NM_002026	1	46	24	-	216259251	216259442
278373837	chr2	216262427	216262599	216262448	216262572	FN1	NM_212476	4	44	22	-	216262403	216262571
278373837	chr2	216262427	216262599	216262448	216262572	FN1	NM_212478	5	46	22	-	216262403	216262571
278373837	chr2	216262427	216262599	216262448	216262572	FN1	NM_212482	6	46	22	-	216262403	216262571
278373837	chr2	216262427	216262599	216262448	216262572	FN1	NM_212474	3	44	22	-	216262403	216262571
278373837	chr2	216262427	216262599	216262448	216262572	FN1	NM_002026	1	46	22	-	216262403	216262571
278519750	chr2	216269197	216269366	216269220	216269339	FN1	NM_212476	4	44	20	-	216269112	216269378
278519750	chr2	216269197	216269366	216269220	216269339	FN1	NM_212478	5	46	20	-	216269112	216269378
278519750	chr2	216269197	216269366	216269220	216269339	FN1	NM_212482	6	46	20	-	216269112	216269378
278519750	chr2	216269197	216269366	216269220	216269339	FN1	NM_212474	3	44	20	-	216269112	216269378
278519750	chr2	216269197	216269366	216269220	216269339	FN1	NM_002026	1	46	20	-	216269112	216269378
278625785	chr2	216271172	216271315	216271193	216271289	FN1	NM_212476	4	44	19	-	216270961	216271233
278625785	chr2	216271172	216271315	216271193	216271289	FN1	NM_212478	5	46	19	-	216270961	216271233
278625785	chr2	216271172	216271315	216271193	216271289	FN1	NM_212482	6	46	19	-	216270961	216271233
278625785	chr2	216271172	216271315	216271193	216271289	FN1	NM_212474	3	44	19	-	216270961	216271233
278625785	chr2	216271172	216271315	216271193	216271289	FN1	NM_002026	1	46	19	-	216270961	216271233
278004977	chr2	216272746	216272892	216272766	216272870	FN1	NM_212476	4	44	17	-	216272831	216272920
278004977	chr2	216272746	216272892	216272766	216272870	FN1	NM_212478	5	46	17	-	216272831	216272920
278004977	chr2	216272746	216272892	216272766	216272870	FN1	NM_212482	6	46	17	-	216272831	216272920
278004977	chr2	216272746	216272892	216272766	216272870	FN1	NM_212474	3	44	17	-	216272831	216272920
278004977	chr2	216272746	216272892	216272766	216272870	FN1	NM_002026	1	46	17	-	216272831	216272920

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279892369	chr2	216274253	216274419	216274275	216274397	FN1	NM_212476	4	44	15	-	216274286	216274462
279892369	chr2	216274253	216274419	216274275	216274397	FN1	NM_212478	5	46	15	-	216274286	216274462
279892369	chr2	216274253	216274419	216274275	216274397	FN1	NM_212482	6	46	15	-	216274286	216274462
279892369	chr2	216274253	216274419	216274275	216274397	FN1	NM_212474	3	44	15	-	216274286	216274462
279892369	chr2	216274253	216274419	216274275	216274397	FN1	NM_002026	1	46	15	-	216274286	216274462
278427324	chr2	216274781	216274951	216274803	216274925	FN1	NM_212476	4	44	14	-	216274657	216274837
278427324	chr2	216274781	216274951	216274803	216274925	FN1	NM_212478	5	46	14	-	216274657	216274837
278427324	chr2	216274781	216274951	216274803	216274925	FN1	NM_212482	6	46	14	-	216274657	216274837
278427324	chr2	216274781	216274951	216274803	216274925	FN1	NM_212474	3	44	14	-	216274657	216274837
278427324	chr2	216274781	216274951	216274803	216274925	FN1	NM_002026	1	46	14	-	216274657	216274837
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_054034	2	13	12	-	216283965	216284108
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_212476	4	44	12	-	216283965	216284108
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_212478	5	46	12	-	216283965	216284108
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_212482	6	46	12	-	216283965	216284108
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_212474	3	44	12	-	216283965	216284108
280795457	chr2	216283890	216284055	216283916	216284031	FN1	NM_002026	1	46	12	-	216283965	216284108
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_054034	2	13	10	-	216286814	216286966
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_212476	4	44	10	-	216286814	216286966
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_212478	5	46	10	-	216286814	216286966
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_212482	6	46	10	-	216286814	216286966
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_212474	3	44	10	-	216286814	216286966
279255889	chr2	216286761	216286914	216286785	216286892	FN1	NM_002026	1	46	10	-	216286814	216286966
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_054034	2	13	8	-	216288869	216289048
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_212476	4	44	8	-	216288869	216289048
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_212478	5	46	8	-	216288869	216289048
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_212482	6	46	8	-	216288869	216289048
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_212474	3	44	8	-	216288869	216289048
280422354	chr2	216288800	216288972	216288824	216288951	FN1	NM_002026	1	46	8	-	216288869	216289048
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_054034	2	13	6	-	216292903	216293061
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_212476	4	44	6	-	216292903	216293061
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_212478	5	46	6	-	216292903	216293061
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_212482	6	46	6	-	216292903	216293061
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_212474	3	44	6	-	216292903	216293061
279893800	chr2	216292848	216293018	216292874	216292995	FN1	NM_002026	1	46	6	-	216292903	216293061
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_054034	2	13	4	-	216296556	216296687
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_212476	4	44	4	-	216296556	216296687
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_212478	5	46	4	-	216296556	216296687
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_212482	6	46	4	-	216296556	216296687
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_212474	3	44	4	-	216296556	216296687
279961952	chr2	216296450	216296607	216296476	216296583	FN1	NM_002026	1	46	4	-	216296556	216296687
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_054034	2	13	2	-	216299419	216299547

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_212476	4	44	2	-	216299419	216299547
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_212478	5	46	2	-	216299419	216299547
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_212482	6	46	2	-	216299419	216299547
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_212474	3	44	2	-	216299419	216299547
278282065	chr2	216299401	216299549	216299422	216299527	FN1	NM_002026	1	46	2	-	216299419	216299547
240666010	chr2	219537487	219537661	219537511	219537637	STK36	NM_015690	2	27	2	+	219537464	219537636
240666010	chr2	219537487	219537661	219537511	219537637	STK36	NM_001243313	1	27	2	+	219537464	219537636
240829792	chr2	219540008	219540152	219540029	219540129	STK36	NM_015690	2	27	5	+	219540066	219540196
240829792	chr2	219540008	219540152	219540029	219540129	STK36	NM_001243313	1	27	5	+	219540066	219540196
261174156	chr2	219540904	219541064	219540925	219541036	STK36	NM_015690	2	27	6	+	219540752	219541001
261174156	chr2	219540904	219541064	219540925	219541036	STK36	NM_001243313	1	27	6	+	219540752	219541001
241137234	chr2	219544588	219544762	219544608	219544738	STK36	NM_015690	2	27	9	+	219544616	219544803
241137234	chr2	219544588	219544762	219544608	219544738	STK36	NM_001243313	1	27	9	+	219544616	219544803
262255776	chr2	219549835	219549976	219549856	219549952	STK36	NM_015690	2	27	11	+	219549808	219549951
262255776	chr2	219549835	219549976	219549856	219549952	STK36	NM_001243313	1	27	11	+	219549808	219549951
238640358	chr2	219555100	219555252	219555121	219555231	STK36	NM_015690	2	27	14	+	219555173	219555278
238640358	chr2	219555100	219555252	219555121	219555231	STK36	NM_001243313	1	27	14	+	219555173	219555278
242287217	chr2	219557201	219557371	219557223	219557350	STK36	NM_015690	2	27	16	+	219557306	219557433
242287217	chr2	219557201	219557371	219557223	219557350	STK36	NM_001243313	1	27	16	+	219557306	219557433
239936250	chr2	219558570	219558739	219558591	219558713	STK36	NM_015690	2	27	19	+	219558618	219558706
239936250	chr2	219558570	219558739	219558591	219558713	STK36	NM_001243313	1	27	19	+	219558618	219558706
239883388	chr2	219561179	219561350	219561200	219561325	STK36	NM_015690	2	27	22	+	219561250	219561324
239883388	chr2	219561179	219561350	219561200	219561325	STK36	NM_001243313	1	27	22	+	219561313	219561324
260410323	chr2	219562253	219562407	219562275	219562379	STK36	NM_015690	2	27	24	+	219562186	219562333
260410323	chr2	219562253	219562407	219562275	219562379	STK36	NM_001243313	1	27	24	+	219562186	219562333
240836543	chr2	219563419	219563578	219563440	219563552	STK36	NM_015690	2	27	26	+	219563325	219564071
240836543	chr2	219563419	219563578	219563440	219563552	STK36	NM_001243313	1	27	26	+	219563325	219564071
263763446	chr2	219563869	219563999	219563891	219563975	STK36	NM_015690	2	27	26	+	219563325	219564071
263763446	chr2	219563869	219563999	219563891	219563975	STK36	NM_001243313	1	27	26	+	219563325	219564071
238357367	chr2	223065820	223065994	223065847	223065966	PAX3	NM_181459	6	10	10	-	223064606	223065959
238357367	chr2	223065820	223065994	223065847	223065966	PAX3	NM_181460	7	9	9	-	223064606	223065959
238357367	chr2	223065820	223065994	223065847	223065966	PAX3	NM_001127366	2	9	9	-	223064606	223066161
238357367	chr2	223065820	223065994	223065847	223065966	PAX3	NM_181461	8	8	8	-	223064606	223066161
238357367	chr2	223065820	223065994	223065847	223065966	PAX3	NM_181458	5	9	9	-	223064606	223066161
235216895	chr2	223066769	223066937	223066797	223066914	PAX3	NM_001127366	2	9	8	-	223066663	223066909
235216895	chr2	223066769	223066937	223066797	223066914	PAX3	NM_181459	6	10	8	-	223066663	223066909
235216895	chr2	223066769	223066937	223066797	223066914	PAX3	NM_181458	5	9	8	-	223066663	223066909
235216895	chr2	223066769	223066937	223066797	223066914	PAX3	NM_181457	4	8	8	-	223066432	223066909
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_001127366	2	9	6	-	223085941	223086106
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_181461	8	8	6	-	223085941	223086106
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_181459	6	10	6	-	223085941	223086106

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_181460	7	9	6	-	223085941	223086106
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_181458	5	9	6	-	223085941	223086106
234925104	chr2	223085922	223086095	223085945	223086077	PAX3	NM_181457	4	8	6	-	223085941	223086106
237544405	chr2	223158332	223158502	223158360	223158476	PAX3	NM_013942	3	5	5	-	223158349	223158476
237544405	chr2	223158332	223158502	223158360	223158476	PAX3	NM_000438	1	4	4	-	223158349	223159020
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_000438	1	4	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_181461	8	8	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_181459	6	10	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_013942	3	5	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_181460	7	9	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_181458	5	9	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_181457	4	8	3	-	223160247	223160376
235248988	chr2	223160223	223160397	223160245	223160376	PAX3	NM_001127366	2	9	3	-	223160247	223160373
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_001127366	2	9	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_000438	1	4	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_181461	8	8	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_181459	6	10	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_013942	3	5	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_181460	7	9	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_181458	5	9	1	-	223163250	223163715
236713033	chr2	223163231	223163367	223163249	223163342	PAX3	NM_181457	4	8	1	-	223163250	223163715
304814675	chr2	234669253	234669392	234669281	234669372	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
304833090	chr2	234669666	234669823	234669688	234669797	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
302016854	chr2	234676461	234676604	234676487	234676582	UGT1A1	NM_000463	1	5	3	+	234676495	234676582
305731430	chr2	234680975	234681147	234680993	234681120	UGT1A1	NM_000463	1	5	5	+	234680908	234681945
295309321	chr3	3192584	3192738	3192607	3192712	CRBN	NM_016302	2	11	11	-	3191317	3192729
295309321	chr3	3192584	3192738	3192607	3192712	CRBN	NM_001173482	1	11	11	-	3191317	3192729
293865122	chr3	3195015	3195174	3195043	3195148	CRBN	NM_016302	2	11	9	-	3195108	3195172
293865122	chr3	3195015	3195174	3195043	3195148	CRBN	NM_001173482	1	11	9	-	3195108	3195172
293842240	chr3	3196401	3196555	3196422	3196530	CRBN	NM_016302	2	11	7	-	3196431	3196515
293842240	chr3	3196401	3196555	3196422	3196530	CRBN	NM_001173482	1	11	7	-	3196431	3196515
295204772	chr3	3209317	3209452	3209344	3209432	CRBN	NM_016302	2	11	5	-	3209318	3209477
295204772	chr3	3209317	3209452	3209344	3209432	CRBN	NM_001173482	1	11	5	-	3209318	3209477
294174098	chr3	3214536	3214691	3214564	3214662	CRBN	NM_016302	2	11	4	-	3214460	3214609
294174098	chr3	3214536	3214691	3214564	3214662	CRBN	NM_001173482	1	11	4	-	3214460	3214609
294663017	chr3	3216715	3216873	3216737	3216855	CRBN	NM_001173482	1	11	2	-	3216847	3216950
294663017	chr3	3216715	3216873	3216737	3216855	CRBN	NM_016302	2	11	2	-	3216847	3216953
230648785	chr3	10074417	10074589	10074443	10074561	FANCD2	NM_033084	2	43	3	+	10074516	10074656
230648785	chr3	10074417	10074589	10074443	10074561	FANCD2	NM_001018115	1	44	3	+	10074516	10074656
228247801	chr3	10076387	10076538	10076411	10076511	FANCD2	NM_033084	2	43	5	+	10076379	10076482
228247801	chr3	10076387	10076538	10076411	10076511	FANCD2	NM_001018115	1	44	5	+	10076379	10076482

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231752447	chr3	10081013	10081165	10081036	10081137	FANCD2	NM_033084	2	43	8	+	10080963	10081041
231752447	chr3	10081013	10081165	10081036	10081137	FANCD2	NM_001018115	1	44	8	+	10080963	10081041
230472820	chr3	10084131	10084288	10084156	10084259	FANCD2	NM_033084	2	43	11	+	10084243	10084347
230472820	chr3	10084131	10084288	10084156	10084259	FANCD2	NM_001018115	1	44	11	+	10084243	10084347
230709960	chr3	10085193	10085336	10085221	10085310	FANCD2	NM_033084	2	43	13	+	10085168	10085276
230709960	chr3	10085193	10085336	10085221	10085310	FANCD2	NM_001018115	1	44	13	+	10085168	10085276
227711614	chr3	10089623	10089770	10089642	10089744	FANCD2	NM_033084	2	43	16	+	10089601	10089735
227711614	chr3	10089623	10089770	10089642	10089744	FANCD2	NM_001018115	1	44	16	+	10089601	10089735
232419290	chr3	10105453	10105608	10105476	10105585	FANCD2	NM_033084	2	43	21	+	10105476	10105595
232419290	chr3	10105453	10105608	10105476	10105585	FANCD2	NM_001018115	1	44	21	+	10105476	10105595
228533196	chr3	10107023	10107193	10107050	10107167	FANCD2	NM_033084	2	43	24	+	10107078	10107178
228533196	chr3	10107023	10107193	10107050	10107167	FANCD2	NM_001018115	1	44	24	+	10107078	10107178
230818999	chr3	10108791	10108957	10108818	10108935	FANCD2	NM_033084	2	43	26	+	10108893	10109001
230818999	chr3	10108791	10108957	10108818	10108935	FANCD2	NM_001018115	1	44	26	+	10108893	10109001
233037623	chr3	10114952	10115111	10114973	10115086	FANCD2	NM_033084	2	43	28	+	10114937	10115046
233037623	chr3	10114952	10115111	10114973	10115086	FANCD2	NM_001018115	1	44	28	+	10114937	10115046
230808576	chr3	10122690	10122835	10122713	10122813	FANCD2	NM_033084	2	43	31	+	10122784	10122912
230808576	chr3	10122690	10122835	10122713	10122813	FANCD2	NM_001018115	1	44	31	+	10122784	10122912
228434291	chr3	10127467	10127641	10127491	10127613	FANCD2	NM_033084	2	43	33	+	10127496	10127606
228434291	chr3	10127467	10127641	10127491	10127613	FANCD2	NM_001018115	1	44	33	+	10127496	10127606
232778613	chr3	10130384	10130553	10130412	10130529	FANCD2	NM_033084	2	43	36	+	10130512	10130634
232778613	chr3	10130384	10130553	10130412	10130529	FANCD2	NM_001018115	1	44	36	+	10130512	10130634
228759659	chr3	10134860	10135030	10134884	10135008	FANCD2	NM_033084	2	43	39	+	10134969	10135007
228759659	chr3	10134860	10135030	10134884	10135008	FANCD2	NM_001018115	1	44	39	+	10134969	10135007
227762777	chr3	10137906	10138064	10137927	10138042	FANCD2	NM_033084	2	43	42	+	10138010	10138156
227762777	chr3	10137906	10138064	10137927	10138042	FANCD2	NM_001018115	1	44	42	+	10138010	10138156
229879988	chr3	10140524	10140667	10140545	10140639	FANCD2	NM_033084	2	43	43	+	10140404	10141344
264382687	chr3	10183717	10183875	10183734	10183854	VHL	NM_000551	1	3	1	+	10183319	10183871
264382687	chr3	10183717	10183875	10183734	10183854	VHL	NM_198156	2	2	1	+	10183319	10183871
263254464	chr3	10191388	10191562	10191410	10191542	VHL	NM_000551	1	3	3	+	10191471	10195354
263254464	chr3	10191388	10191562	10191410	10191542	VHL	NM_198156	2	2	2	+	10191471	10195354
240266787	chr3	12421243	12421368	12421264	12421340	PPARG	NM_138711	3	8	3	+	12421203	12421430
240266787	chr3	12421243	12421368	12421264	12421340	PPARG	NM_015869	2	7	2	+	12421203	12421430
240266787	chr3	12421243	12421368	12421264	12421340	PPARG	NM_138712	4	8	3	+	12421203	12421430
240266787	chr3	12421243	12421368	12421264	12421340	PPARG	NM_005037	1	7	2	+	12421203	12421430
236895167	chr3	12434057	12434221	12434084	12434192	PPARG	NM_138711	3	8	5	+	12434113	12434251
236895167	chr3	12434057	12434221	12434084	12434192	PPARG	NM_015869	2	7	4	+	12434113	12434251
236895167	chr3	12434057	12434221	12434084	12434192	PPARG	NM_138712	4	8	5	+	12434113	12434251
236895167	chr3	12434057	12434221	12434084	12434192	PPARG	NM_005037	1	7	4	+	12434113	12434251
234952730	chr3	12458171	12458341	12458195	12458322	PPARG	NM_138711	3	8	7	+	12458203	12458653
234952730	chr3	12458171	12458341	12458195	12458322	PPARG	NM_015869	2	7	6	+	12458203	12458653

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234952730	chr3	12458171	12458341	12458195	12458322	PPARG	NM_138712	4	8	7	+	12458203	12458653
234952730	chr3	12458171	12458341	12458195	12458322	PPARG	NM_005037	1	7	6	+	12458203	12458653
236594684	chr3	12475304	12475453	12475325	12475427	PPARG	NM_138711	3	8	8	+	12475397	12475855
236594684	chr3	12475304	12475453	12475325	12475427	PPARG	NM_015869	2	7	7	+	12475397	12475855
236594684	chr3	12475304	12475453	12475325	12475427	PPARG	NM_138712	4	8	8	+	12475397	12475855
236594684	chr3	12475304	12475453	12475325	12475427	PPARG	NM_005037	1	7	7	+	12475397	12475855
235233459	chr3	12626106	12626247	12626129	12626225	RAF1	NM_002880	1	17	17	-	12625100	12626156
235613485	chr3	12626653	12626791	12626672	12626763	RAF1	NM_002880	1	17	15	-	12626621	12626752
235047858	chr3	12632269	12632419	12632292	12632399	RAF1	NM_002880	1	17	12	-	12632297	12632473
236174169	chr3	12641221	12641386	12641240	12641360	RAF1	NM_002880	1	17	10	-	12641190	12641307
234916217	chr3	12645569	12645705	12645597	12645685	RAF1	NM_002880	1	17	7	-	12645635	12645788
235610924	chr3	12650158	12650324	12650184	12650302	RAF1	NM_002880	1	17	5	-	12650265	12650422
236472349	chr3	12653461	12653633	12653483	12653610	RAF1	NM_002880	1	17	3	-	12653449	12653561
241197219	chr3	14187402	14187552	14187419	14187527	XPC	NR_027299	3	15	15	-	14186648	14187659
241197219	chr3	14187402	14187552	14187419	14187527	XPC	NM_001145769	1	16	16	-	14186648	14187659
241197219	chr3	14187402	14187552	14187419	14187527	XPC	NM_004628	2	16	16	-	14186648	14187659
240301036	chr3	14189989	14190163	14190010	14190141	XPC	NR_027299	3	15	12	-	14190062	14190231
240301036	chr3	14189989	14190163	14190010	14190141	XPC	NM_001145769	1	16	13	-	14190062	14190231
240301036	chr3	14189989	14190163	14190010	14190141	XPC	NM_004628	2	16	13	-	14190062	14190231
241439744	chr3	14193737	14193861	14193758	14193840	XPC	NR_027299	3	15	10	-	14193835	14193916
241439744	chr3	14193737	14193861	14193758	14193840	XPC	NM_001145769	1	16	11	-	14193835	14193916
241439744	chr3	14193737	14193861	14193758	14193840	XPC	NM_004628	2	16	11	-	14193835	14193916
266246394	chr3	14199492	14199653	14199510	14199634	XPC	NR_027299	3	15	8	-	14199511	14200392
266246394	chr3	14199492	14199653	14199510	14199634	XPC	NM_001145769	1	16	9	-	14199511	14200392
266246394	chr3	14199492	14199653	14199510	14199634	XPC	NM_004628	2	16	9	-	14199511	14200392
262306715	chr3	14199972	14200097	14199992	14200069	XPC	NR_027299	3	15	8	-	14199511	14200392
262306715	chr3	14199972	14200097	14199992	14200069	XPC	NM_001145769	1	16	9	-	14199511	14200392
262306715	chr3	14199972	14200097	14199992	14200069	XPC	NM_004628	2	16	9	-	14199511	14200392
262345739	chr3	14200334	14200495	14200356	14200468	XPC	NR_027299	3	15	8	-	14199511	14200392
262345739	chr3	14200334	14200495	14200356	14200468	XPC	NM_001145769	1	16	9	-	14199511	14200392
262345739	chr3	14200334	14200495	14200356	14200468	XPC	NM_004628	2	16	9	-	14199511	14200392
239891166	chr3	14206863	14207023	14206887	14207002	XPC	NR_027299	3	15	5	-	14206928	14207085
239891166	chr3	14206863	14207023	14206887	14207002	XPC	NM_001145769	1	16	6	-	14206928	14207085
239891166	chr3	14206863	14207023	14206887	14207002	XPC	NM_004628	2	16	6	-	14206928	14207085
242056841	chr3	14209820	14209976	14209843	14209955	XPC	NM_004628	2	16	4	-	14209757	14209880
239065210	chr3	14214429	14214589	14214450	14214563	XPC	NR_027299	3	15	2	-	14214367	14214562
239065210	chr3	14214429	14214589	14214450	14214563	XPC	NM_001145769	1	16	2	-	14214367	14214562
239065210	chr3	14214429	14214589	14214450	14214563	XPC	NM_004628	2	16	2	-	14214367	14214562
272552201	chr3	30648429	30648556	30648447	30648539	TGFBR2	NM_001024847	1	8	1	+	30647994	30648469
272552201	chr3	30648429	30648556	30648447	30648539	TGFBR2	NM_003242	2	7	1	+	30647994	30648469
270343848	chr3	30686334	30686492	30686357	30686464	TGFBR2	NM_001024847	1	8	3	+	30686239	30686407

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270343848	chr3	30686334	30686492	30686357	30686464	TGFBR2	NM_003242	2	7	2	+	30686239	30686407
272339562	chr3	30713197	30713359	30713218	30713339	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272339562	chr3	30713197	30713359	30713218	30713339	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272298901	chr3	30713678	30713850	30713696	30713826	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272298901	chr3	30713678	30713850	30713696	30713826	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
270819491	chr3	30729797	30729964	30729818	30729942	TGFBR2	NM_001024847	1	8	7	+	30729876	30730003
270819491	chr3	30729797	30729964	30729818	30729942	TGFBR2	NM_003242	2	7	6	+	30729876	30730003
234693458	chr3	37035004	37035173	37035028	37035155	MLH1	NM_000249	1	19	1	+	37034841	37035154
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167617	2	19	3	+	37042446	37042539
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167619	4	18	3	+	37042446	37042544
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_001167618	3	19	3	+	37042446	37042544
231118321	chr3	37042476	37042600	37042504	37042574	MLH1	NM_000249	1	19	3	+	37042446	37042544
233350556	chr3	37050182	37050342	37050210	37050316	MLH1	NM_001167618	3	19	6	+	37050305	37050396
233350556	chr3	37050182	37050342	37050210	37050316	MLH1	NM_001167617	2	19	6	+	37050305	37050396
233350556	chr3	37050182	37050342	37050210	37050316	MLH1	NM_000249	1	19	6	+	37050305	37050396
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167619	4	18	7	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167618	3	19	8	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_001167617	2	19	8	+	37053502	37053590
233127617	chr3	37053538	37053676	37053561	37053646	MLH1	NM_000249	1	19	8	+	37053502	37053590
233195000	chr3	37061709	37061872	37061730	37061850	MLH1	NM_001167619	4	18	10	+	37061801	37061954
233195000	chr3	37061709	37061872	37061730	37061850	MLH1	NM_001167618	3	19	11	+	37061801	37061954
233195000	chr3	37061709	37061872	37061730	37061850	MLH1	NM_001167617	2	19	11	+	37061801	37061954
233195000	chr3	37061709	37061872	37061730	37061850	MLH1	NM_000249	1	19	11	+	37061801	37061954
233219374	chr3	37067213	37067359	37067236	37067334	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233219374	chr3	37067213	37067359	37067236	37067334	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233219374	chr3	37067213	37067359	37067236	37067334	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233219374	chr3	37067213	37067359	37067236	37067334	MLH1	NM_000249	1	19	12	+	37067128	37067498
234255953	chr3	37070304	37070474	37070328	37070454	MLH1	NM_001167619	4	18	12	+	37070275	37070423
234255953	chr3	37070304	37070474	37070328	37070454	MLH1	NM_001167618	3	19	13	+	37070275	37070423
234255953	chr3	37070304	37070474	37070328	37070454	MLH1	NM_001167617	2	19	13	+	37070275	37070423
234255953	chr3	37070304	37070474	37070328	37070454	MLH1	NM_000249	1	19	13	+	37070275	37070423
234338579	chr3	37083757	37083888	37083785	37083861	MLH1	NM_001167619	4	18	14	+	37083759	37083822
234338579	chr3	37083757	37083888	37083785	37083861	MLH1	NM_001167618	3	19	15	+	37083759	37083822
234338579	chr3	37083757	37083888	37083785	37083861	MLH1	NM_001167617	2	19	15	+	37083759	37083822
234338579	chr3	37083757	37083888	37083785	37083861	MLH1	NM_000249	1	19	15	+	37083759	37083822
234741596	chr3	37090273	37090440	37090299	37090412	MLH1	NM_001167619	4	18	17	+	37090395	37090508
234741596	chr3	37090273	37090440	37090299	37090412	MLH1	NM_001167618	3	19	18	+	37090395	37090508
234741596	chr3	37090273	37090440	37090299	37090412	MLH1	NM_001167617	2	19	18	+	37090395	37090508
234741596	chr3	37090273	37090440	37090299	37090412	MLH1	NM_000249	1	19	18	+	37090395	37090508
234220525	chr3	37494011	37494174	37494033	37494153	ITGA9	NM_002207	1	28	1	+	37493813	37494050
232987331	chr3	37514888	37515022	37514908	37514995	ITGA9	NM_002207	1	28	3	+	37514845	37514951

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233664155	chr3	37544568	37544731	37544594	37544708	ITGA9	NM_002207	1	28	6	+	37544669	37544798
233213451	chr3	37550068	37550242	37550092	37550219	ITGA9	NM_002207	1	28	8	+	37550050	37550118
233069961	chr3	37559043	37559207	37559064	37559186	ITGA9	NM_002207	1	28	10	+	37558995	37559100
232773131	chr3	37574719	37574889	37574747	37574869	ITGA9	NM_002207	1	28	14	+	37574805	37574959
232415337	chr3	37670663	37670828	37670686	37670801	ITGA9	NM_002207	1	28	16	+	37670678	37670827
230871208	chr3	37725389	37725549	37725410	37725523	ITGA9	NM_002207	1	28	18	+	37725356	37725506
231326176	chr3	37785385	37785546	37785410	37785526	ITGA9	NM_002207	1	28	22	+	37785417	37785525
232218348	chr3	37818892	37819034	37818915	37819008	ITGA9	NM_002207	1	28	24	+	37818883	37819008
232303005	chr3	37826508	37826663	37826528	37826639	ITGA9	NM_002207	1	28	26	+	37826468	37826569
274095346	chr3	38180167	38180314	38180184	38180294	MYD88	NM_002468	5	5	1	+	38179969	38180519
274095346	chr3	38180167	38180314	38180184	38180294	MYD88	NM_001172569	4	4	1	+	38179969	38180519
274095346	chr3	38180167	38180314	38180184	38180294	MYD88	NM_001172568	3	4	1	+	38179969	38180519
274095346	chr3	38180167	38180314	38180184	38180294	MYD88	NM_001172567	2	5	1	+	38179969	38180519
274095346	chr3	38180167	38180314	38180184	38180294	MYD88	NM_001172566	1	3	1	+	38179969	38180519
273160371	chr3	38181241	38181395	38181262	38181373	MYD88	NM_002468	5	5	2	+	38181355	38181489
273160371	chr3	38181241	38181395	38181262	38181373	MYD88	NM_001172569	4	4	2	+	38181355	38181489
273160371	chr3	38181241	38181395	38181262	38181373	MYD88	NM_001172567	2	5	2	+	38181355	38181489
273465317	chr3	38182021	38182194	38182046	38182173	MYD88	NM_001172567	2	5	3	+	38181879	38182083
273465317	chr3	38182021	38182194	38182046	38182173	MYD88	NM_002468	5	5	3	+	38181879	38182059
273465317	chr3	38182021	38182194	38182046	38182173	MYD88	NM_001172568	3	4	2	+	38181879	38182059
227116259	chr3	41265528	41265681	41265555	41265658	CTNNB1	NM_001904	3	15	2	+	41265512	41265572
227116259	chr3	41265528	41265681	41265555	41265658	CTNNB1	NM_001098209	1	16	2	+	41265512	41265572
227116259	chr3	41265528	41265681	41265555	41265658	CTNNB1	NM_001098210	2	16	2	+	41265512	41265572
226794852	chr3	41266393	41266521	41266421	41266498	CTNNB1	NM_001904	3	15	4	+	41266445	41266698
226794852	chr3	41266393	41266521	41266421	41266498	CTNNB1	NM_001098209	1	16	4	+	41266445	41266698
226794852	chr3	41266393	41266521	41266421	41266498	CTNNB1	NM_001098210	2	16	4	+	41266445	41266698
225697496	chr3	41266882	41267045	41266903	41267022	CTNNB1	NM_001904	3	15	5	+	41266825	41267063
225697496	chr3	41266882	41267045	41266903	41267022	CTNNB1	NM_001098209	1	16	5	+	41266825	41267063
225697496	chr3	41266882	41267045	41266903	41267022	CTNNB1	NM_001098210	2	16	5	+	41266825	41267063
226547084	chr3	41267262	41267392	41267286	41267364	CTNNB1	NM_001904	3	15	6	+	41267151	41267352
226547084	chr3	41267262	41267392	41267286	41267364	CTNNB1	NM_001098209	1	16	6	+	41267151	41267352
226547084	chr3	41267262	41267392	41267286	41267364	CTNNB1	NM_001098210	2	16	6	+	41267151	41267352
226022266	chr3	41274921	41275095	41274949	41275070	CTNNB1	NM_001904	3	15	9	+	41275020	41275358
226022266	chr3	41274921	41275095	41274949	41275070	CTNNB1	NM_001098209	1	16	9	+	41275020	41275358
226022266	chr3	41274921	41275095	41274949	41275070	CTNNB1	NM_001098210	2	16	9	+	41275020	41275358
226559633	chr3	41275598	41275738	41275623	41275717	CTNNB1	NM_001904	3	15	10	+	41275630	41275788
226559633	chr3	41275598	41275738	41275623	41275717	CTNNB1	NM_001098209	1	16	10	+	41275630	41275788
226559633	chr3	41275598	41275738	41275623	41275717	CTNNB1	NM_001098210	2	16	10	+	41275630	41275788
225798259	chr3	41277885	41278027	41277907	41278003	CTNNB1	NM_001904	3	15	12	+	41277840	41277990
225798259	chr3	41277885	41278027	41277907	41278003	CTNNB1	NM_001098209	1	16	12	+	41277840	41277990
225798259	chr3	41277885	41278027	41277907	41278003	CTNNB1	NM_001098210	2	16	12	+	41277840	41277990

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226040990	chr3	41280581	41280753	41280606	41280733	CTNNB1	NM_001098209	1	16	15	+	41280625	41280845
226040990	chr3	41280581	41280753	41280606	41280733	CTNNB1	NM_001098210	2	16	15	+	41280625	41280845
226040990	chr3	41280581	41280753	41280606	41280733	CTNNB1	NM_001904	3	15	15	+	41280625	41281939
279529079	chr3	46479406	46479567	46479427	46479540	LTF	NM_002343	2	17	16	-	46479431	46479620
279529079	chr3	46479406	46479567	46479427	46479540	LTF	NM_001199149	1	17	16	-	46479431	46479620
278217652	chr3	46482854	46483027	46482876	46482999	LTF	NM_002343	2	17	14	-	46482907	46482974
278217652	chr3	46482854	46483027	46482876	46482999	LTF	NM_001199149	1	17	14	-	46482907	46482974
279032462	chr3	46486851	46487001	46486873	46486980	LTF	NM_002343	2	17	12	-	46486772	46486927
279032462	chr3	46486851	46487001	46486873	46486980	LTF	NM_001199149	1	17	12	-	46486772	46486927
278421494	chr3	46490396	46490535	46490413	46490518	LTF	NM_002343	2	17	9	-	46490354	46490508
278421494	chr3	46490396	46490535	46490413	46490518	LTF	NM_001199149	1	17	9	-	46490354	46490508
281120020	chr3	46491963	46492125	46491984	46492103	LTF	NM_002343	2	17	7	-	46491985	46492163
281120020	chr3	46491963	46492125	46491984	46492103	LTF	NM_001199149	1	17	7	-	46491985	46492163
279857566	chr3	46496830	46496967	46496852	46496945	LTF	NM_002343	2	17	5	-	46496785	46496932
279857566	chr3	46496830	46496967	46496852	46496945	LTF	NM_001199149	1	17	5	-	46496785	46496932
280010060	chr3	46497832	46497967	46497852	46497944	LTF	NM_002343	2	17	3	-	46497780	46497888
280010060	chr3	46497832	46497967	46497852	46497944	LTF	NM_001199149	1	17	3	-	46497780	46497888
263298288	chr3	47058633	47058804	47058661	47058776	SETD2	NM_014159	1	21	21	-	47057898	47058744
241304667	chr3	47083974	47084125	47084001	47084102	SETD2	NM_014159	1	21	17	-	47084051	47084190
261162984	chr3	47098264	47098438	47098292	47098416	SETD2	NM_014159	1	21	15	-	47098311	47098980
261158262	chr3	47098743	47098909	47098765	47098886	SETD2	NM_014159	1	21	15	-	47098311	47098980
242064652	chr3	47103792	47103966	47103816	47103940	SETD2	NM_014159	1	21	14	-	47103653	47103836
264258644	chr3	47125398	47125561	47125420	47125535	SETD2	NM_014159	1	21	12	-	47125210	47125872
241485053	chr3	47127657	47127825	47127684	47127804	SETD2	NM_014159	1	21	11	-	47127685	47127804
237844563	chr3	47139464	47139602	47139489	47139576	SETD2	NM_014159	1	21	9	-	47139445	47139571
263880674	chr3	47144864	47145036	47144890	47145010	SETD2	NM_014159	1	21	7	-	47144836	47144913
262372888	chr3	47155430	47155555	47155454	47155528	SETD2	NM_014159	1	21	5	-	47155366	47155494
262467588	chr3	47161825	47161992	47161846	47161964	SETD2	NM_014159	1	21	3	-	47161672	47166038
239089045	chr3	47162189	47162363	47162214	47162337	SETD2	NM_014159	1	21	3	-	47161672	47166038
239035665	chr3	47162652	47162807	47162680	47162779	SETD2	NM_014159	1	21	3	-	47161672	47166038
239122081	chr3	47163050	47163223	47163078	47163196	SETD2	NM_014159	1	21	3	-	47161672	47166038
239186428	chr3	47163431	47163601	47163456	47163573	SETD2	NM_014159	1	21	3	-	47161672	47166038
262477106	chr3	47163813	47163985	47163841	47163957	SETD2	NM_014159	1	21	3	-	47161672	47166038
262451759	chr3	47164280	47164452	47164300	47164424	SETD2	NM_014159	1	21	3	-	47161672	47166038
238774506	chr3	47164643	47164794	47164671	47164773	SETD2	NM_014159	1	21	3	-	47161672	47166038
238830951	chr3	47165026	47165184	47165054	47165159	SETD2	NM_014159	1	21	3	-	47161672	47166038
239081546	chr3	47165289	47165451	47165317	47165425	SETD2	NM_014159	1	21	3	-	47161672	47166038
262530648	chr3	47165705	47165874	47165725	47165849	SETD2	NM_014159	1	21	3	-	47161672	47166038
238180496	chr3	47205227	47205395	47205244	47205378	SETD2	NM_014159	1	21	1	-	47205344	47205467
222938761	chr3	52436765	52436921	52436787	52436901	BAP1	NM_004656	1	17	15	-	52436795	52436887
222323192	chr3	52437519	52437687	52437541	52437667	BAP1	NM_004656	1	17	13	-	52437432	52437910

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223100270	chr3	52438479	52438644	52438500	52438624	BAP1	NM_004656	1	17	12	-	52438469	52438602
222902031	chr3	52439867	52440006	52439888	52439981	BAP1	NM_004656	1	17	10	-	52439781	52439928
222209925	chr3	52441139	52441275	52441160	52441255	BAP1	NM_004656	1	17	7	-	52441190	52441332
225221131	chr3	52441953	52442124	52441973	52442097	BAP1	NM_004656	1	17	5	-	52441974	52442093
222598226	chr3	52443617	52443791	52443638	52443771	BAP1	NM_004656	1	17	2	-	52443730	52443759
237390403	chr3	52582094	52582236	52582118	52582211	PBRM1	NM_018165	1	28	28	-	52579368	52582251
237390403	chr3	52582094	52582236	52582118	52582211	PBRM1	NM_018313	2	30	30	-	52579368	52582251
237390403	chr3	52582094	52582236	52582118	52582211	PBRM1	NM_181042	3	28	28	-	52579368	52582251
236097291	chr3	52584689	52584863	52584712	52584835	PBRM1	NM_018165	1	28	26	-	52584763	52584833
236097291	chr3	52584689	52584863	52584712	52584835	PBRM1	NM_018313	2	30	28	-	52584763	52584833
236097291	chr3	52584689	52584863	52584712	52584835	PBRM1	NM_181042	3	28	26	-	52584763	52584833
236340208	chr3	52595844	52596016	52595865	52595991	PBRM1	NM_018165	1	28	24	-	52595783	52595984
236340208	chr3	52595844	52596016	52595865	52595991	PBRM1	NM_018313	2	30	26	-	52595783	52595984
236340208	chr3	52595844	52596016	52595865	52595991	PBRM1	NM_181042	3	28	25	-	52595783	52595984
236633461	chr3	52598013	52598176	52598040	52598156	PBRM1	NM_018165	1	28	22	-	52598066	52598249
236633461	chr3	52598013	52598176	52598040	52598156	PBRM1	NM_018313	2	30	24	-	52598066	52598249
236633461	chr3	52598013	52598176	52598040	52598156	PBRM1	NM_181042	3	28	23	-	52598066	52598249
237329147	chr3	52610670	52610836	52610698	52610815	PBRM1	NM_018165	1	28	21	-	52610557	52610714
237329147	chr3	52610670	52610836	52610698	52610815	PBRM1	NM_018313	2	30	23	-	52610557	52610714
237329147	chr3	52610670	52610836	52610698	52610815	PBRM1	NM_181042	3	28	22	-	52610557	52610714
237552947	chr3	52620418	52620545	52620443	52620526	PBRM1	NM_018165	1	28	19	-	52620441	52620704
237552947	chr3	52620418	52620545	52620443	52620526	PBRM1	NM_018313	2	30	21	-	52620441	52620704
237552947	chr3	52620418	52620545	52620443	52620526	PBRM1	NM_181042	3	28	20	-	52620441	52620704
238243120	chr3	52621318	52621477	52621349	52621452	PBRM1	NM_018165	1	28	18	-	52621369	52621526
238243120	chr3	52621318	52621477	52621349	52621452	PBRM1	NM_181042	3	28	19	-	52621369	52621526
238243120	chr3	52621318	52621477	52621349	52621452	PBRM1	NM_018313	2	30	20	-	52621369	52621451
235515069	chr3	52637479	52637653	52637503	52637633	PBRM1	NM_018165	1	28	16	-	52637537	52637748
235515069	chr3	52637479	52637653	52637503	52637633	PBRM1	NM_018313	2	30	18	-	52637537	52637748
235515069	chr3	52637479	52637653	52637503	52637633	PBRM1	NM_181042	3	28	17	-	52637537	52637748
239432856	chr3	52643390	52643540	52643418	52643515	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239432856	chr3	52643390	52643540	52643418	52643515	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239432856	chr3	52643390	52643540	52643418	52643515	PBRM1	NM_181042	3	28	16	-	52643329	52643971
239419440	chr3	52643801	52643969	52643827	52643947	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239419440	chr3	52643801	52643969	52643827	52643947	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239419440	chr3	52643801	52643969	52643827	52643947	PBRM1	NM_181042	3	28	16	-	52643329	52643971
235040988	chr3	52651334	52651508	52651358	52651487	PBRM1	NM_018165	1	28	13	-	52651278	52651554
235040988	chr3	52651334	52651508	52651358	52651487	PBRM1	NM_018313	2	30	15	-	52651278	52651554
235040988	chr3	52651334	52651508	52651358	52651487	PBRM1	NM_181042	3	28	14	-	52651278	52651554
237963975	chr3	52662951	52663124	52662976	52663096	PBRM1	NM_018165	1	28	11	-	52662910	52663051
237963975	chr3	52662951	52663124	52662976	52663096	PBRM1	NM_018313	2	30	13	-	52662910	52663051
237963975	chr3	52662951	52663124	52662976	52663096	PBRM1	NM_181042	3	28	12	-	52662910	52663051

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237114548	chr3	52675927	52676100	52675950	52676073	PBRM1	NM_018165	1	28	9	-	52675970	52676061
237114548	chr3	52675927	52676100	52675950	52676073	PBRM1	NM_018313	2	30	11	-	52675970	52676061
237114548	chr3	52675927	52676100	52675950	52676073	PBRM1	NM_181042	3	28	10	-	52675970	52676061
240145155	chr3	52682376	52682507	52682402	52682479	PBRM1	NM_018165	1	28	7	-	52682360	52682458
240145155	chr3	52682376	52682507	52682402	52682479	PBRM1	NM_018313	2	30	8	-	52682360	52682458
240145155	chr3	52682376	52682507	52682402	52682479	PBRM1	NM_181042	3	28	7	-	52682360	52682458
238116712	chr3	52696106	52696253	52696127	52696225	PBRM1	NM_018165	1	28	4	-	52696149	52696292
238116712	chr3	52696106	52696253	52696127	52696225	PBRM1	NM_018313	2	30	5	-	52696149	52696292
238116712	chr3	52696106	52696253	52696127	52696225	PBRM1	NM_181042	3	28	4	-	52696149	52696292
235659832	chr3	52712503	52712672	52712523	52712646	PBRM1	NM_018165	1	28	2	-	52712516	52712613
235659832	chr3	52712503	52712672	52712523	52712646	PBRM1	NM_018313	2	30	3	-	52712516	52712613
235659832	chr3	52712503	52712672	52712523	52712646	PBRM1	NM_181042	3	28	2	-	52712516	52712613
312581491	chr3	65342167	65342335	65342187	65342318	MAGI1	NM_015520	3	25	25	-	65339906	65342807
312581491	chr3	65342167	65342335	65342187	65342318	MAGI1	NM_001033057	1	23	23	-	65339906	65342807
312476582	chr3	65344703	65344866	65344731	65344844	MAGI1	NM_015520	3	25	24	-	65344739	65344827
312469012	chr3	65349200	65349364	65349223	65349338	MAGI1	NM_004742	2	23	22	-	65349140	65349283
312469012	chr3	65349200	65349364	65349223	65349338	MAGI1	NM_015520	3	25	22	-	65349140	65349283
312469012	chr3	65349200	65349364	65349223	65349338	MAGI1	NM_001033057	1	23	21	-	65349140	65349283
312172362	chr3	65361428	65361556	65361450	65361534	MAGI1	NM_015520	3	25	19	-	65361420	65361620
312172362	chr3	65361428	65361556	65361450	65361534	MAGI1	NM_001033057	1	23	18	-	65361420	65361620
312172362	chr3	65361428	65361556	65361450	65361534	MAGI1	NM_004742	2	23	19	-	65361420	65361623
312402491	chr3	65365009	65365167	65365027	65365146	MAGI1	NM_004742	2	23	18	-	65364936	65365229
312402491	chr3	65365009	65365167	65365027	65365146	MAGI1	NM_015520	3	25	18	-	65364936	65365229
312402491	chr3	65365009	65365167	65365027	65365146	MAGI1	NM_001033057	1	23	17	-	65364936	65365229
312472905	chr3	65369137	65369264	65369158	65369235	MAGI1	NM_004742	2	23	16	-	65369207	65369298
312472905	chr3	65369137	65369264	65369158	65369235	MAGI1	NM_015520	3	25	16	-	65369207	65369298
312472905	chr3	65369137	65369264	65369158	65369235	MAGI1	NM_001033057	1	23	15	-	65369207	65369298
312545824	chr3	65376888	65377057	65376910	65377034	MAGI1	NM_004742	2	23	14	-	65376817	65377033
312545824	chr3	65376888	65377057	65376910	65377034	MAGI1	NM_015520	3	25	14	-	65376817	65377033
312545824	chr3	65376888	65377057	65376910	65377034	MAGI1	NM_001033057	1	23	14	-	65376817	65377033
312373333	chr3	65415375	65415503	65415395	65415475	MAGI1	NM_004742	2	23	12	-	65415195	65415815
312373333	chr3	65415375	65415503	65415395	65415475	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312373333	chr3	65415375	65415503	65415395	65415475	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312352559	chr3	65416326	65416477	65416348	65416457	MAGI1	NM_004742	2	23	11	-	65416374	65416556
312352559	chr3	65416326	65416477	65416348	65416457	MAGI1	NM_015520	3	25	11	-	65416374	65416556
312352559	chr3	65416326	65416477	65416348	65416457	MAGI1	NM_001033057	1	23	11	-	65416374	65416556
312170638	chr3	65425487	65425660	65425508	65425640	MAGI1	NM_004742	2	23	9	-	65425554	65425687
312170638	chr3	65425487	65425660	65425508	65425640	MAGI1	NM_015520	3	25	9	-	65425554	65425687
312170638	chr3	65425487	65425660	65425508	65425640	MAGI1	NM_001033057	1	23	9	-	65425554	65425687
312357096	chr3	65438856	65438983	65438883	65438963	MAGI1	NM_004742	2	23	6	-	65438933	65439015
312357096	chr3	65438856	65438983	65438883	65438963	MAGI1	NM_015520	3	25	6	-	65438933	65439015

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312357096	chr3	65438856	65438983	65438883	65438963	MAGI1	NM_001033057	1	23	6	-	65438933	65439015
312186287	chr3	65464232	65464383	65464253	65464363	MAGI1	NM_004742	2	23	4	-	65464267	65464473
312186287	chr3	65464232	65464383	65464253	65464363	MAGI1	NM_015520	3	25	4	-	65464267	65464473
312186287	chr3	65464232	65464383	65464253	65464363	MAGI1	NM_001033057	1	23	4	-	65464267	65464473
312186942	chr3	65607546	65607692	65607569	65607671	MAGI1	NM_004742	2	23	2	-	65607647	65607763
312186942	chr3	65607546	65607692	65607569	65607671	MAGI1	NM_015520	3	25	2	-	65607647	65607763
312186942	chr3	65607546	65607692	65607569	65607671	MAGI1	NM_001033057	1	23	2	-	65607647	65607763
312529737	chr3	66023951	66024118	66023975	66024094	MAGI1	NM_004742	2	23	1	-	66023671	66024509
312529737	chr3	66023951	66024118	66023975	66024094	MAGI1	NM_015520	3	25	1	-	66023671	66024509
312529737	chr3	66023951	66024118	66023975	66024094	MAGI1	NM_001033057	1	23	1	-	66023671	66024509
231537627	chr3	69928201	69928359	69928224	69928337	MITF	NM_001184967	2	10	2	+	69928285	69928534
231537627	chr3	69928201	69928359	69928224	69928337	MITF	NM_006722	4	10	2	+	69928285	69928534
231537627	chr3	69928201	69928359	69928224	69928337	MITF	NM_198177	7	10	2	+	69928285	69928534
231537627	chr3	69928201	69928359	69928224	69928337	MITF	NM_198159	6	10	2	+	69928285	69928534
233656552	chr3	69985854	69985999	69985879	69985966	MITF	NM_001184968	3	3	1	+	69985751	69985906
233656552	chr3	69985854	69985999	69985879	69985966	MITF	NM_000248	1	9	1	+	69985751	69985906
233656552	chr3	69985854	69985999	69985879	69985966	MITF	NM_198178	8	9	1	+	69985751	69985906
233656552	chr3	69985854	69985999	69985879	69985966	MITF	NM_198158	5	9	1	+	69985751	69985906
233658427	chr3	69987407	69987576	69987428	69987548	MITF	NM_001184968	3	3	3	+	69987503	69988216
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_001184967	2	10	6	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_006722	4	10	6	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_000248	1	9	5	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_198177	7	10	6	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_198159	6	10	6	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_198178	8	9	5	+	69998202	69998319
232178384	chr3	69998205	69998358	69998227	69998332	MITF	NM_198158	5	9	5	+	69998202	69998319
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_001184967	2	10	9	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_006722	4	10	9	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_000248	1	9	8	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_198177	7	10	9	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_198159	6	10	9	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_198178	8	9	8	+	70008424	70008571
233275023	chr3	70008399	70008533	70008423	70008505	MITF	NM_198158	5	9	8	+	70008424	70008571
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_001184967	2	10	10	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_006722	4	10	10	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_000248	1	9	9	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_198177	7	10	10	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_198159	6	10	10	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_198178	8	9	9	+	70013998	70017488
233950580	chr3	70014247	70014421	70014271	70014401	MITF	NM_198158	5	9	9	+	70013998	70017488
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244816	8	20	19	-	71015041	71015207

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244815	7	16	15	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244814	6	17	16	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244813	5	15	14	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_032682	9	21	20	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244812	4	16	15	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244808	2	21	20	-	71015041	71015207
227799111	chr3	71015135	71015259	71015158	71015233	FOXP1	NM_001244810	3	21	20	-	71015041	71015207
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244816	8	20	17	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244815	7	16	13	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244814	6	17	14	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244813	5	15	12	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_032682	9	21	18	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244812	4	16	13	-	71021706	71021827
227297776	chr3	71021660	71021801	71021683	71021777	FOXP1	NM_001244808	2	21	18	-	71021706	71021827
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244808	2	21	16	-	71026794	71026870
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244816	8	20	15	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244815	7	16	11	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244814	6	17	12	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244813	5	15	10	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_032682	9	21	16	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244812	4	16	11	-	71026794	71026873
228449482	chr3	71026691	71026863	71026717	71026835	FOXP1	NM_001244810	3	21	16	-	71026794	71026873
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244816	8	20	14	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244815	7	16	10	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244814	6	17	11	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244813	5	15	9	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_032682	9	21	15	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244812	4	16	10	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244808	2	21	15	-	71026979	71027180
229413961	chr3	71027099	71027270	71027122	71027248	FOXP1	NM_001244810	3	21	15	-	71026979	71027180
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244816	8	20	12	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244815	7	16	8	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244814	6	17	9	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244813	5	15	7	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_032682	9	21	13	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244812	4	16	8	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244808	2	21	13	-	71050123	71050210
228944033	chr3	71050129	71050298	71050153	71050270	FOXP1	NM_001244810	3	21	13	-	71050123	71050210
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244816	8	20	10	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244815	7	16	6	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244814	6	17	7	-	71090479	71090683

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244813	5	15	5	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_032682	9	21	11	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244812	4	16	6	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244808	2	21	11	-	71090479	71090683
227382601	chr3	71090568	71090741	71090589	71090713	FOXP1	NM_001244810	3	21	11	-	71090479	71090683
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244816	8	20	7	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244815	7	16	3	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244814	6	17	4	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244813	5	15	2	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_032682	9	21	8	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244808	2	21	8	-	71102787	71102924
227452948	chr3	71102763	71102923	71102785	71102903	FOXP1	NM_001244810	3	21	8	-	71102787	71102924
227451834	chr3	71179561	71179730	71179584	71179708	FOXP1	NM_001244815	7	16	1	-	71179649	71180092
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001244816	8	20	5	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001244814	6	17	2	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_032682	9	21	6	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001244812	4	16	3	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001244808	2	21	6	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001012505	1	7	6	-	71247353	71247543
228698614	chr3	71247331	71247495	71247352	71247474	FOXP1	NM_001244810	3	21	6	-	71247353	71247543
270929146	chr3	89176260	89176431	89176287	89176410	EPHA3	NM_005233	1	17	2	+	89176359	89176423
270929146	chr3	89176260	89176431	89176287	89176410	EPHA3	NM_182644	2	7	2	+	89176359	89176423
271560707	chr3	89259219	89259377	89259246	89259350	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271560707	chr3	89259219	89259377	89259246	89259350	EPHA3	NM_182644	2	7	3	+	89259010	89259670
272653591	chr3	89389925	89390099	89389953	89390075	EPHA3	NM_005233	1	17	4	+	89390066	89390221
272653591	chr3	89389925	89390099	89389953	89390075	EPHA3	NM_182644	2	7	4	+	89390066	89390221
270725593	chr3	89390950	89391102	89390974	89391081	EPHA3	NM_005233	1	17	5	+	89390905	89391240
270725593	chr3	89390950	89391102	89390974	89391081	EPHA3	NM_182644	2	7	5	+	89390905	89391240
270909250	chr3	89444975	89445142	89444999	89445119	EPHA3	NM_005233	1	17	6	+	89444987	89445111
270909250	chr3	89444975	89445142	89444999	89445119	EPHA3	NM_182644	2	7	6	+	89444987	89445111
271133912	chr3	89456341	89456488	89456370	89456464	EPHA3	NM_005233	1	17	8	+	89456419	89456521
270092967	chr3	89462324	89462473	89462351	89462446	EPHA3	NM_005233	1	17	10	+	89462291	89462416
270161468	chr3	89478252	89478380	89478279	89478351	EPHA3	NM_005233	1	17	12	+	89478256	89478317
272713661	chr3	89480440	89480607	89480467	89480584	EPHA3	NM_005233	1	17	13	+	89480300	89480509
272266382	chr3	89499271	89499444	89499298	89499421	EPHA3	NM_005233	1	17	15	+	89499327	89499520
272449599	chr3	89528462	89528635	89528490	89528607	EPHA3	NM_005233	1	17	17	+	89528547	89531284
229879088	chr3	128200045	128200215	128200066	128200193	GATA2	NM_032638	3	6	6	-	128198265	128200161
229879088	chr3	128200045	128200215	128200066	128200193	GATA2	NM_001145661	1	7	7	-	128198265	128200161
229879088	chr3	128200045	128200215	128200066	128200193	GATA2	NM_001145662	2	6	6	-	128198265	128200161
227460306	chr3	128202737	128202902	128202760	128202882	GATA2	NM_032638	3	6	4	-	128202703	128202848
227460306	chr3	128202737	128202902	128202760	128202882	GATA2	NM_001145661	1	7	5	-	128202703	128202848

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227460306	chr3	128202737	128202902	128202760	128202882	GATA2	NM_001145662	2	6	4	-	128202703	128202848
229081504	chr3	128204876	128205041	128204893	128205023	GATA2	NM_032638	3	6	3	-	128204570	128205211
229081504	chr3	128204876	128205041	128204893	128205023	GATA2	NM_001145661	1	7	4	-	128204570	128205211
229081504	chr3	128204876	128205041	128204893	128205023	GATA2	NM_001145662	2	6	3	-	128204570	128205211
227188884	chr3	128205762	128205908	128205779	128205890	GATA2	NM_032638	3	6	2	-	128205646	128205919
227188884	chr3	128205762	128205908	128205779	128205890	GATA2	NM_001145661	1	7	3	-	128205646	128205919
227188884	chr3	128205762	128205908	128205779	128205890	GATA2	NM_001145662	2	6	2	-	128205646	128205919
270974726	chr3	134670215	134670380	134670237	134670358	EPHB1	NM_004441	1	16	3	+	134670213	134670894
272490115	chr3	134670674	134670841	134670695	134670819	EPHB1	NM_004441	1	16	3	+	134670213	134670894
270581200	chr3	134851521	134851686	134851543	134851665	EPHB1	NM_004441	1	16	5	+	134851556	134851891
271255051	chr3	134873016	134873185	134873037	134873162	EPHB1	NM_004441	1	16	6	+	134872994	134873118
271088665	chr3	134885710	134885873	134885731	134885852	EPHB1	NM_004441	1	16	9	+	134885784	134885848
272373012	chr3	134911445	134911589	134911466	134911567	EPHB1	NM_004441	1	16	11	+	134911418	134911665
270334802	chr3	134959932	134960096	134959954	134960074	EPHB1	NM_004441	1	16	13	+	134959990	134960139
270115157	chr3	134968124	134968284	134968146	134968263	EPHB1	NM_004441	1	16	15	+	134968178	134968333
294552564	chr3	138374293	138374436	138374314	138374408	PIK3CB	NM_001256045	1	13	13	-	138371540	138374368
294552564	chr3	138374293	138374436	138374314	138374408	PIK3CB	NM_006219	2	22	22	-	138371540	138374368
294916433	chr3	138376562	138376724	138376590	138376696	PIK3CB	NM_001256045	1	13	11	-	138376532	138376677
294916433	chr3	138376562	138376724	138376590	138376696	PIK3CB	NM_006219	2	22	20	-	138376532	138376677
293914173	chr3	138383934	138384058	138383955	138384033	PIK3CB	NM_001256045	1	13	9	-	138383878	138384045
293914173	chr3	138383934	138384058	138383955	138384033	PIK3CB	NM_006219	2	22	18	-	138383878	138384045
294682834	chr3	138402539	138402664	138402564	138402637	PIK3CB	NM_001256045	1	13	7	-	138402520	138402629
294682834	chr3	138402539	138402664	138402564	138402637	PIK3CB	NM_006219	2	22	16	-	138402520	138402629
294050980	chr3	138407758	138407932	138407783	138407904	PIK3CB	NM_001256045	1	13	5	-	138407717	138407816
294050980	chr3	138407758	138407932	138407783	138407904	PIK3CB	NM_006219	2	22	14	-	138407717	138407816
294723591	chr3	138413638	138413787	138413658	138413759	PIK3CB	NM_001256045	1	13	3	-	138413628	138413749
294723591	chr3	138413638	138413787	138413658	138413759	PIK3CB	NM_006219	2	22	12	-	138413628	138413749
293867989	chr3	138423165	138423339	138423191	138423311	PIK3CB	NM_006219	2	22	10	-	138423285	138423335
293802393	chr3	138430980	138431135	138431009	138431111	PIK3CB	NM_006219	2	22	8	-	138431050	138431146
294674959	chr3	138433416	138433590	138433444	138433562	PIK3CB	NM_006219	2	22	7	-	138433310	138433561
294598745	chr3	138453497	138453670	138453524	138453647	PIK3CB	NM_006219	2	22	5	-	138453476	138453646
294172970	chr3	138461394	138461519	138461419	138461494	PIK3CB	NM_006219	2	22	3	-	138461400	138461623
293975493	chr3	138474693	138474819	138474719	138474792	PIK3CB	NM_006219	2	22	2	-	138474596	138474821
229746037	chr3	138664776	138664938	138664794	138664919	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229754105	chr3	138665268	138665409	138665292	138665391	FOXL2	NM_023067	1	1	1	-	138663066	138665982
282986965	chr3	142168408	142168556	142168431	142168527	ATR	NM_001184	1	47	47	-	142168077	142168444
284762169	chr3	142176467	142176595	142176487	142176567	ATR	NM_001184	1	47	45	-	142176446	142176597
281327176	chr3	142177923	142178060	142177945	142178028	ATR	NM_001184	1	47	44	-	142177800	142177953
282578321	chr3	142180722	142180852	142180754	142180826	ATR	NM_001184	1	47	42	-	142180782	142180932
282267948	chr3	142183842	142184013	142183870	142183987	ATR	NM_001184	1	47	41	-	142183939	142184082
281326039	chr3	142185143	142185294	142185176	142185266	ATR	NM_001184	1	47	40	-	142185166	142185375

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
282078140	chr3	142186784	142186910	142186813	142186887	ATR	NM_001184	1	47	39	-	142186776	142186910
283085596	chr3	142188378	142188535	142188403	142188508	ATR	NM_001184	1	47	38	-	142188179	142188411
283984885	chr3	142204039	142204164	142204062	142204136	ATR	NM_001184	1	47	36	-	142203982	142204124
283788846	chr3	142215268	142215392	142215290	142215366	ATR	NM_001184	1	47	34	-	142215203	142215362
282691778	chr3	142217481	142217650	142217503	142217622	ATR	NM_001184	1	47	32	-	142217439	142217616
283598048	chr3	142223922	142224052	142223947	142224031	ATR	NM_001184	1	47	29	-	142223981	142224145
283388314	chr3	142226771	142226931	142226799	142226905	ATR	NM_001184	1	47	28	-	142226773	142226951
283587600	chr3	142232281	142232418	142232314	142232390	ATR	NM_001184	1	47	26	-	142232343	142232480
281288089	chr3	142238520	142238667	142238547	142238639	ATR	NM_001184	1	47	24	-	142238511	142238626
281816797	chr3	142242899	142243023	142242922	142242998	ATR	NM_001184	1	47	22	-	142242835	142243041
284176671	chr3	142254884	142255057	142254911	142255030	ATR	NM_001184	1	47	20	-	142254950	142255043
282265071	chr3	142259769	142259908	142259791	142259880	ATR	NM_001184	1	47	18	-	142259746	142259876
282615988	chr3	142266678	142266850	142266705	142266823	ATR	NM_001184	1	47	16	-	142266567	142266752
283004468	chr3	142268927	142269056	142268956	142269028	ATR	NM_001184	1	47	14	-	142268974	142269144
284374831	chr3	142272208	142272341	142272233	142272314	ATR	NM_001184	1	47	13	-	142272069	142272240
283403251	chr3	142272711	142272882	142272739	142272854	ATR	NM_001184	1	47	11	-	142272667	142272857
284577335	chr3	142274913	142275080	142274941	142275053	ATR	NM_001184	1	47	10	-	142274719	142274981
284380659	chr3	142277519	142277645	142277547	142277612	ATR	NM_001184	1	47	8	-	142277466	142277618
281457107	chr3	142279051	142279214	142279077	142279186	ATR	NM_001184	1	47	6	-	142279105	142279296
282196815	chr3	142280218	142280352	142280245	142280324	ATR	NM_001184	1	47	5	-	142280085	142280263
281401671	chr3	142281350	142281486	142281378	142281460	ATR	NM_001184	1	47	4	-	142281074	142281951
283777611	chr3	142281666	142281791	142281694	142281763	ATR	NM_001184	1	47	4	-	142281074	142281951
281771074	chr3	142284911	142285063	142284939	142285040	ATR	NM_001184	1	47	3	-	142284963	142285103
237442591	chr3	178916599	178916724	178916623	178916696	PIK3CA	NM_006218	1	21	2	+	178916538	178916965
236849837	chr3	178917379	178917540	178917406	178917512	PIK3CA	NM_006218	1	21	3	+	178917478	178917687
241325709	chr3	178919091	178919223	178919119	178919195	PIK3CA	NM_006218	1	21	4	+	178919078	178919328
235942028	chr3	178921496	178921662	178921524	178921634	PIK3CA	NM_006218	1	21	5	+	178921332	178921577
236804359	chr3	178928046	178928183	178928069	178928156	PIK3CA	NM_006218	1	21	8	+	178927974	178928126
235948521	chr3	178935994	178936131	178936023	178936106	PIK3CA	NM_006218	1	21	10	+	178935998	178936122
236340778	chr3	178937690	178937835	178937709	178937811	PIK3CA	NM_006218	1	21	13	+	178937737	178937840
236986252	chr3	178942362	178942520	178942391	178942495	PIK3CA	NM_006218	1	21	16	+	178942488	178942609
235019721	chr3	178947017	178947159	178947050	178947138	PIK3CA	NM_006218	1	21	18	+	178947060	178947230
235766723	chr3	178947782	178947924	178947810	178947898	PIK3CA	NM_006218	1	21	19	+	178947792	178947909
235562527	chr3	178951809	178951969	178951835	178951940	PIK3CA	NM_006218	1	21	21	+	178951882	178952497
263669558	chr3	181430157	181430304	181430179	181430283	SOX2	NM_003106	1	1	1	+	181429712	181432223
263668375	chr3	181430620	181430761	181430640	181430744	SOX2	NM_003106	1	1	1	+	181429712	181432223
263691844	chr3	181430958	181431109	181430980	181431092	SOX2	NM_003106	1	1	1	+	181429712	181432223
224752921	chr3	187440350	187440482	187440372	187440458	BCL6	NM_001706	3	10	10	-	187439165	187440389
224752921	chr3	187440350	187440482	187440372	187440458	BCL6	NM_001134738	2	8	8	-	187439165	187440389
224752921	chr3	187440350	187440482	187440372	187440458	BCL6	NM_001130845	1	10	10	-	187439165	187440389
223601257	chr3	187443341	187443511	187443364	187443489	BCL6	NM_001706	3	10	8	-	187443287	187443417

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223601257	chr3	187443341	187443511	187443364	187443489	BCL6	NM_001134738	2	8	6	-	187443287	187443417
223601257	chr3	187443341	187443511	187443364	187443489	BCL6	NM_001130845	1	10	8	-	187443287	187443417
224049755	chr3	187446215	187446367	187446235	187446345	BCL6	NM_001706	3	10	6	-	187446148	187446332
224049755	chr3	187446215	187446367	187446235	187446345	BCL6	NM_001134738	2	8	5	-	187446148	187446332
224049755	chr3	187446215	187446367	187446235	187446345	BCL6	NM_001130845	1	10	6	-	187446148	187446332
225175818	chr3	187447140	187447309	187447161	187447289	BCL6	NM_001706	3	10	5	-	187446838	187447809
225175818	chr3	187447140	187447309	187447161	187447289	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225175818	chr3	187447140	187447309	187447161	187447289	BCL6	NM_001130845	1	10	5	-	187446838	187447809
225177314	chr3	187447585	187447742	187447605	187447720	BCL6	NM_001706	3	10	5	-	187446838	187447809
225177314	chr3	187447585	187447742	187447605	187447720	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225177314	chr3	187447585	187447742	187447605	187447720	BCL6	NM_001130845	1	10	5	-	187446838	187447809
223632022	chr3	187449605	187449773	187449629	187449745	BCL6	NM_001706	3	10	4	-	187449497	187449718
223632022	chr3	187449605	187449773	187449629	187449745	BCL6	NM_001134738	2	8	3	-	187449497	187449718
223632022	chr3	187449605	187449773	187449629	187449745	BCL6	NM_001130845	1	10	4	-	187449497	187449718
234286026	chr3	188123997	188124134	188124018	188124109	LPP	NM_001167672	2	10	2	+	188123900	188124101
234286026	chr3	188123997	188124134	188124018	188124109	LPP	NM_001167671	1	11	3	+	188123900	188124101
234286026	chr3	188123997	188124134	188124018	188124109	LPP	NM_005578	3	11	3	+	188123900	188124101
233626392	chr3	188326897	188327071	188326925	188327046	LPP	NM_001167671	1	11	6	+	188326949	188327632
233626392	chr3	188326897	188327071	188326925	188327046	LPP	NM_005578	3	11	6	+	188326949	188327632
233626392	chr3	188326897	188327071	188326925	188327046	LPP	NM_001167672	2	10	5	+	188326949	188327191
233630001	chr3	188327391	188327559	188327414	188327537	LPP	NM_001167671	1	11	6	+	188326949	188327632
233630001	chr3	188327391	188327559	188327414	188327537	LPP	NM_005578	3	11	6	+	188326949	188327632
234156180	chr3	188477837	188478000	188477860	188477974	LPP	NM_001167672	2	10	7	+	188477901	188478070
234156180	chr3	188477837	188478000	188477860	188477974	LPP	NM_001167671	1	11	8	+	188477901	188478070
234156180	chr3	188477837	188478000	188477860	188477974	LPP	NM_005578	3	11	8	+	188477901	188478070
231379709	chr3	188590396	188590570	188590423	188590551	LPP	NM_001167672	2	10	9	+	188590431	188590551
231379709	chr3	188590396	188590570	188590423	188590551	LPP	NM_001167671	1	11	10	+	188590431	188590551
231379709	chr3	188590396	188590570	188590423	188590551	LPP	NM_005578	3	11	10	+	188590431	188590551
302475390	chr3	195593673	195593845	195593691	195593826	TNK2	NM_001010938	1	15	14	-	195593760	195593887
302475390	chr3	195593673	195593845	195593691	195593826	TNK2	NM_005781	2	15	14	-	195593760	195593887
304436111	chr3	195594347	195594513	195594367	195594496	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304436111	chr3	195594347	195594513	195594367	195594496	TNK2	NM_005781	2	15	12	-	195594232	195595580
300730689	chr3	195594721	195594870	195594738	195594851	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300730689	chr3	195594721	195594870	195594738	195594851	TNK2	NM_005781	2	15	12	-	195594232	195595580
300735775	chr3	195595053	195595187	195595072	195595165	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300735775	chr3	195595053	195595187	195595072	195595165	TNK2	NM_005781	2	15	12	-	195594232	195595580
304442518	chr3	195595522	195595672	195595543	195595651	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304442518	chr3	195595522	195595672	195595543	195595651	TNK2	NM_005781	2	15	12	-	195594232	195595580
304620750	chr3	195599202	195599368	195599224	195599348	TNK2	NM_001010938	1	15	10	-	195599147	195599341
304620750	chr3	195599202	195599368	195599224	195599348	TNK2	NM_005781	2	15	10	-	195599147	195599341
305807650	chr3	195605859	195606005	195605881	195605985	TNK2	NM_001010938	1	15	7	-	195605920	195606046

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305807650	chr3	195605859	195606005	195605881	195605985	TNK2	NM_005781	2	15	7	-	195605920	195606046
301194778	chr3	195609111	195609243	195609128	195609224	TNK2	NM_001010938	1	15	6	-	195608922	195609199
301194778	chr3	195609111	195609243	195609128	195609224	TNK2	NM_005781	2	15	6	-	195608922	195609199
300547902	chr3	195611755	195611923	195611772	195611905	TNK2	NM_001010938	1	15	4	-	195611683	195611904
300547902	chr3	195611755	195611923	195611772	195611905	TNK2	NM_005781	2	15	4	-	195611683	195611904
299915521	chr3	195615355	195615515	195615372	195615495	TNK2	NM_001010938	1	15	2	-	195615297	195615477
299915521	chr3	195615355	195615515	195615372	195615495	TNK2	NM_005781	2	15	2	-	195615297	195615477
227846111	chr4	1801081	1801241	1801099	1801220	FGFR3	NM_000142	1	18	3	+	1800981	1801250
227846111	chr4	1801081	1801241	1801099	1801220	FGFR3	NM_022965	3	16	3	+	1800981	1801250
227846111	chr4	1801081	1801241	1801099	1801220	FGFR3	NM_001163213	2	18	3	+	1800981	1801250
229023268	chr4	1803189	1803326	1803208	1803309	FGFR3	NM_000142	1	18	5	+	1803094	1803263
229023268	chr4	1803189	1803326	1803208	1803309	FGFR3	NM_022965	3	16	5	+	1803094	1803263
229023268	chr4	1803189	1803326	1803208	1803309	FGFR3	NM_001163213	2	18	5	+	1803094	1803263
227442524	chr4	1803628	1803755	1803647	1803734	FGFR3	NM_000142	1	18	7	+	1803562	1803752
227442524	chr4	1803628	1803755	1803647	1803734	FGFR3	NM_022965	3	16	7	+	1803562	1803752
227442524	chr4	1803628	1803755	1803647	1803734	FGFR3	NM_001163213	2	18	7	+	1803562	1803752
227391405	chr4	1805393	1805545	1805418	1805523	FGFR3	NM_000142	1	18	8	+	1805419	1805563
227912457	chr4	1806433	1806591	1806456	1806570	FGFR3	NM_000142	1	18	10	+	1806551	1806696
227912457	chr4	1806433	1806591	1806456	1806570	FGFR3	NM_022965	3	16	8	+	1806551	1806696
227912457	chr4	1806433	1806591	1806456	1806570	FGFR3	NM_001163213	2	18	10	+	1806551	1806696
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_000142	1	18	11	+	1807082	1807203
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_022965	3	16	9	+	1807082	1807203
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_001163213	2	18	11	+	1807082	1807203
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_000142	1	18	12	+	1807286	1807396
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_022965	3	16	10	+	1807286	1807396
227877337	chr4	1807175	1807328	1807194	1807308	FGFR3	NM_001163213	2	18	12	+	1807286	1807396
228574154	chr4	1807612	1807759	1807631	1807741	FGFR3	NM_000142	1	18	13	+	1807477	1807667
228574154	chr4	1807612	1807759	1807631	1807741	FGFR3	NM_022965	3	16	11	+	1807477	1807667
228574154	chr4	1807612	1807759	1807631	1807741	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
227608571	chr4	1808245	1808409	1808264	1808391	FGFR3	NM_000142	1	18	16	+	1808273	1808410
227608571	chr4	1808245	1808409	1808264	1808391	FGFR3	NM_022965	3	16	14	+	1808273	1808410
227608571	chr4	1808245	1808409	1808264	1808391	FGFR3	NM_001163213	2	18	16	+	1808273	1808410
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_000142	1	18	18	+	1808843	1810599
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_022965	3	16	16	+	1808843	1810599
228970654	chr4	1808784	1808930	1808802	1808913	FGFR3	NM_001163213	2	18	18	+	1808843	1810599
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_007331	2	11	4	+	1902353	1902978
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_133330	3	24	4	+	1902353	1902978
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_133335	6	22	2	+	1902353	1902978
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_133334	5	9	1	+	1902353	1902978
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_133331	4	23	3	+	1902353	1902978
294607418	chr4	1902595	1902762	1902616	1902737	WHSC1	NM_001042424	1	22	2	+	1902353	1902978

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_007331	2	11	5	+	1905943	1906105
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_133330	3	24	5	+	1905943	1906105
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_133335	6	22	3	+	1905943	1906105
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_133334	5	9	2	+	1905943	1906105
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_133331	4	23	4	+	1905943	1906105
294852581	chr4	1906000	1906173	1906026	1906146	WHSC1	NM_001042424	1	22	3	+	1905943	1906105
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_007331	2	11	7	+	1919868	1920350
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_133330	3	24	7	+	1919868	1920350
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_133335	6	22	5	+	1919868	1920350
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_133334	5	9	4	+	1919868	1920350
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_133331	4	23	6	+	1919868	1920350
294401589	chr4	1919906	1920075	1919928	1920051	WHSC1	NM_001042424	1	22	5	+	1919868	1920350
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_007331	2	11	8	+	1932353	1932497
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_133330	3	24	8	+	1932353	1932497
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_133335	6	22	6	+	1932353	1932497
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_133334	5	9	5	+	1932353	1932497
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_133331	4	23	7	+	1932353	1932497
294562706	chr4	1932233	1932407	1932257	1932385	WHSC1	NM_001042424	1	22	6	+	1932353	1932497
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_007331	2	11	10	+	1940178	1940259
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_133330	3	24	10	+	1940178	1940259
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_133335	6	22	8	+	1940178	1940259
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_133334	5	9	7	+	1940178	1940259
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_133331	4	23	9	+	1940178	1940259
294303689	chr4	1940179	1940345	1940203	1940324	WHSC1	NM_001042424	1	22	8	+	1940178	1940259
295159697	chr4	1944055	1944202	1944077	1944174	WHSC1	NM_007331	2	11	11	+	1941381	1944302
295159697	chr4	1944055	1944202	1944077	1944174	WHSC1	NM_133334	5	9	9	+	1944066	1950545
293881328	chr4	1955004	1955176	1955027	1955150	WHSC1	NM_133330	3	24	14	+	1955051	1955251
293881328	chr4	1955004	1955176	1955027	1955150	WHSC1	NM_133335	6	22	12	+	1955051	1955251
293881328	chr4	1955004	1955176	1955027	1955150	WHSC1	NM_133331	4	23	13	+	1955051	1955251
293881328	chr4	1955004	1955176	1955027	1955150	WHSC1	NM_001042424	1	22	12	+	1955051	1955251
294555409	chr4	1957358	1957520	1957379	1957499	WHSC1	NM_133330	3	24	16	+	1957420	1957576
294555409	chr4	1957358	1957520	1957379	1957499	WHSC1	NM_133335	6	22	14	+	1957420	1957576
294555409	chr4	1957358	1957520	1957379	1957499	WHSC1	NM_133331	4	23	15	+	1957420	1957576
294555409	chr4	1957358	1957520	1957379	1957499	WHSC1	NM_001042424	1	22	14	+	1957420	1957576
294717847	chr4	1959596	1959734	1959620	1959713	WHSC1	NM_133330	3	24	18	+	1959660	1959763
294717847	chr4	1959596	1959734	1959620	1959713	WHSC1	NM_133335	6	22	16	+	1959660	1959763
294717847	chr4	1959596	1959734	1959620	1959713	WHSC1	NM_133331	4	23	17	+	1959660	1959763
294717847	chr4	1959596	1959734	1959620	1959713	WHSC1	NM_001042424	1	22	16	+	1959660	1959763
294333828	chr4	1961392	1961516	1961415	1961490	WHSC1	NM_133330	3	24	19	+	1961198	1961467
294333828	chr4	1961392	1961516	1961415	1961490	WHSC1	NM_133335	6	22	17	+	1961198	1961467
294333828	chr4	1961392	1961516	1961415	1961490	WHSC1	NM_133331	4	23	18	+	1961198	1961467

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294333828	chr4	1961392	1961516	1961415	1961490	WHSC1	NM_001042424	1	22	17	+	1961198	1961467
294847780	chr4	1976898	1977060	1976919	1977038	WHSC1	NM_133330	3	24	22	+	1977021	1977127
294847780	chr4	1976898	1977060	1976919	1977038	WHSC1	NM_133335	6	22	20	+	1977021	1977127
294847780	chr4	1976898	1977060	1976919	1977038	WHSC1	NM_133331	4	23	21	+	1977021	1977127
294847780	chr4	1976898	1977060	1976919	1977038	WHSC1	NM_001042424	1	22	20	+	1977021	1977127
294969432	chr4	1978289	1978462	1978309	1978444	WHSC1	NM_133330	3	24	23	+	1978202	1978406
294969432	chr4	1978289	1978462	1978309	1978444	WHSC1	NM_133335	6	22	21	+	1978202	1978406
294969432	chr4	1978289	1978462	1978309	1978444	WHSC1	NM_133331	4	23	22	+	1978202	1978406
294969432	chr4	1978289	1978462	1978309	1978444	WHSC1	NM_001042424	1	22	21	+	1978202	1978406
238601645	chr4	40244959	40245131	40244982	40245109	RHOH	NM_004310	1	3	3	+	40244798	40246281
262084495	chr4	40245398	40245555	40245421	40245533	RHOH	NM_004310	1	3	3	+	40244798	40246281
235721974	chr4	41747808	41747937	41747827	41747920	PHOX2B	NM_003924	1	3	3	-	41746099	41748339
238046811	chr4	41749402	41749574	41749422	41749547	PHOX2B	NM_003924	1	3	2	-	41749366	41749553
237548388	chr4	55124860	55125015	55124881	55124993	PDGFRA	NM_006206	1	23	2	+	55124924	55124984
235173295	chr4	55129752	55129918	55129777	55129891	PDGFRA	NM_006206	1	23	4	+	55129834	55130094
239219354	chr4	55131095	55131240	55131119	55131217	PDGFRA	NM_006206	1	23	5	+	55131086	55131216
235501145	chr4	55133763	55133935	55133784	55133908	PDGFRA	NM_006206	1	23	7	+	55133719	55133908
240237906	chr4	55138563	55138737	55138586	55138709	PDGFRA	NM_006206	1	23	9	+	55138561	55138687
235335742	chr4	55140900	55141036	55140924	55141014	PDGFRA	NM_006206	1	23	12	+	55141008	55141140
238258529	chr4	55144097	55144258	55144125	55144233	PDGFRA	NM_006206	1	23	14	+	55144063	55144173
235818276	chr4	55146548	55146677	55146573	55146649	PDGFRA	NM_006206	1	23	16	+	55146483	55146649
236757599	chr4	55152038	55152211	55152059	55152186	PDGFRA	NM_006206	1	23	18	+	55152008	55152130
235008195	chr4	55156384	55156524	55156417	55156501	PDGFRA	NM_006206	1	23	22	+	55156480	55156721
235772241	chr4	55161327	55161464	55161349	55161444	PDGFRA	NM_006206	1	23	23	+	55161292	55164412
233155382	chr4	55561808	55561971	55561834	55561949	KIT	NM_000222	1	21	2	+	55561678	55561947
233155382	chr4	55561808	55561971	55561834	55561949	KIT	NM_001093772	2	21	2	+	55561678	55561947
232351167	chr4	55565702	55565841	55565730	55565817	KIT	NM_000222	1	21	4	+	55565796	55565932
232351167	chr4	55565702	55565841	55565730	55565817	KIT	NM_001093772	2	21	4	+	55565796	55565932
233223748	chr4	55569988	55570122	55570014	55570090	KIT	NM_000222	1	21	5	+	55569890	55570058
233223748	chr4	55569988	55570122	55570014	55570090	KIT	NM_001093772	2	21	5	+	55569890	55570058
233394191	chr4	55589652	55589777	55589673	55589752	KIT	NM_000222	1	21	8	+	55589750	55589864
233394191	chr4	55589652	55589777	55589673	55589752	KIT	NM_001093772	2	21	8	+	55589750	55589864
233545312	chr4	55593347	55593521	55593375	55593493	KIT	NM_000222	1	21	10	+	55593384	55593490
233545312	chr4	55593347	55593521	55593375	55593493	KIT	NM_001093772	2	21	10	+	55593384	55593490
231846244	chr4	55594133	55594307	55594157	55594287	KIT	NM_000222	1	21	13	+	55594177	55594287
231846244	chr4	55594133	55594307	55594157	55594287	KIT	NM_001093772	2	21	13	+	55594177	55594287
233444902	chr4	55597962	55598130	55597985	55598107	KIT	NM_000222	1	21	16	+	55598037	55598164
233444902	chr4	55597962	55598130	55597985	55598107	KIT	NM_001093772	2	21	16	+	55598037	55598164
232105498	chr4	55602544	55602687	55602572	55602664	KIT	NM_000222	1	21	18	+	55602664	55602775
232105498	chr4	55602544	55602687	55602572	55602664	KIT	NM_001093772	2	21	18	+	55602664	55602775
230878131	chr4	55603221	55603371	55603246	55603350	KIT	NM_000222	1	21	20	+	55603341	55603446

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230878131	chr4	55603221	55603371	55603246	55603350	KIT	NM_001093772	2	21	20	+	55603341	55603446
234722058	chr4	55946065	55946236	55946088	55946216	KDR	NM_002253	1	30	30	-	55944426	55946330
233301996	chr4	55948597	55948769	55948621	55948741	KDR	NM_002253	1	30	28	-	55948703	55948802
230851330	chr4	55955011	55955175	55955033	55955147	KDR	NM_002253	1	30	26	-	55955035	55955140
233559313	chr4	55956045	55956212	55956067	55956189	KDR	NM_002253	1	30	23	-	55956123	55956245
326849834	chr4	55961033	55961163	55961054	55961136	KDR	NM_002253	1	30	21	-	55960969	55961122
231712764	chr4	55963710	55963883	55963732	55963857	KDR	NM_002253	1	30	18	-	55963829	55963933
233326344	chr4	55964793	55964965	55964821	55964939	KDR	NM_002253	1	30	16	-	55964864	55964970
233155477	chr4	55968488	55968645	55968511	55968620	KDR	NM_002253	1	30	14	-	55968529	55968675
232851661	chr4	55970913	55971080	55970941	55971055	KDR	NM_002253	1	30	13	-	55970810	55971151
233141604	chr4	55972927	55973097	55972951	55973072	KDR	NM_002253	1	30	11	-	55972854	55972977
230976955	chr4	55976616	55976787	55976639	55976760	KDR	NM_002253	1	30	9	-	55976570	55976733
232601951	chr4	55979524	55979680	55979546	55979653	KDR	NM_002253	1	30	7	-	55979471	55979648
233169270	chr4	55981032	55981205	55981060	55981178	KDR	NM_002253	1	30	5	-	55981041	55981209
233579446	chr4	55984728	55984884	55984752	55984859	KDR	NM_002253	1	30	3	-	55984771	55984967
294036621	chr4	62362960	62363134	62362987	62363106	LPHN3	NM_015236	1	23	1	+	62362839	62363066
294787677	chr4	62542521	62542645	62542550	62542619	LPHN3	NM_015236	1	23	3	+	62542544	62542653
294445074	chr4	62598481	62598630	62598509	62598606	LPHN3	NM_015236	1	23	5	+	62598472	62599272
295318702	chr4	62598943	62599082	62598966	62599054	LPHN3	NM_015236	1	23	5	+	62598472	62599272
294736816	chr4	62758455	62758617	62758474	62758596	LPHN3	NM_015236	1	23	7	+	62758374	62758676
294962290	chr4	62775198	62775332	62775224	62775311	LPHN3	NM_015236	1	23	9	+	62775278	62775463
294369059	chr4	62800515	62800686	62800539	62800663	LPHN3	NM_015236	1	23	11	+	62800558	62800741
294277265	chr4	62812627	62812786	62812651	62812759	LPHN3	NM_015236	1	23	13	+	62812632	62812840
294408656	chr4	62845249	62845416	62845275	62845394	LPHN3	NM_015236	1	23	15	+	62845281	62845490
294788699	chr4	62849236	62849393	62849260	62849369	LPHN3	NM_015236	1	23	16	+	62849101	62849321
294721820	chr4	62894529	62894655	62894558	62894632	LPHN3	NM_015236	1	23	19	+	62894573	62894599
294079109	chr4	62903382	62903517	62903409	62903492	LPHN3	NM_015236	1	23	21	+	62903449	62903574
294680182	chr4	62935769	62935917	62935792	62935895	LPHN3	NM_015236	1	23	23	+	62935827	62938168
294753723	chr4	62936215	62936366	62936237	62936344	LPHN3	NM_015236	1	23	23	+	62935827	62938168
222822751	chr4	87869646	87869818	87869671	87869790	AFF1	NM_001166693	1	21	2	+	87869650	87869723
223591089	chr4	87967780	87967947	87967808	87967924	AFF1	NM_005935	2	20	3	+	87967847	87968746
223591089	chr4	87967780	87967947	87967808	87967924	AFF1	NM_001166693	1	21	4	+	87967847	87968746
223656371	chr4	87968211	87968373	87968234	87968348	AFF1	NM_005935	2	20	3	+	87967847	87968746
223656371	chr4	87968211	87968373	87968234	87968348	AFF1	NM_001166693	1	21	4	+	87967847	87968746
225101720	chr4	87968684	87968810	87968706	87968786	AFF1	NM_005935	2	20	3	+	87967847	87968746
225101720	chr4	87968684	87968810	87968706	87968786	AFF1	NM_001166693	1	21	4	+	87967847	87968746
222724520	chr4	88015985	88016139	88016009	88016112	AFF1	NM_005935	2	20	7	+	88016067	88016121
222724520	chr4	88015985	88016139	88016009	88016112	AFF1	NM_001166693	1	21	8	+	88016067	88016121
222297663	chr4	88026950	88027116	88026972	88027094	AFF1	NM_005935	2	20	9	+	88026960	88026997
222297663	chr4	88026950	88027116	88026972	88027094	AFF1	NM_001166693	1	21	10	+	88026960	88026997
225149469	chr4	88035532	88035695	88035554	88035671	AFF1	NM_005935	2	20	11	+	88035519	88036451

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225149469	chr4	88035532	88035695	88035554	88035671	AFF1	NM_001166693	1	21	12	+	88035519	88036451
223715643	chr4	88036020	88036182	88036038	88036165	AFF1	NM_005935	2	20	11	+	88035519	88036451
223715643	chr4	88036020	88036182	88036038	88036165	AFF1	NM_001166693	1	21	12	+	88035519	88036451
223738570	chr4	88036424	88036584	88036447	88036563	AFF1	NM_005935	2	20	11	+	88035519	88036451
223738570	chr4	88036424	88036584	88036447	88036563	AFF1	NM_001166693	1	21	12	+	88035519	88036451
222562654	chr4	88047269	88047433	88047294	88047410	AFF1	NM_005935	2	20	13	+	88047251	88047488
222562654	chr4	88047269	88047433	88047294	88047410	AFF1	NM_001166693	1	21	14	+	88047251	88047488
223985495	chr4	88048717	88048886	88048742	88048858	AFF1	NM_005935	2	20	15	+	88048795	88048855
223985495	chr4	88048717	88048886	88048742	88048858	AFF1	NM_001166693	1	21	16	+	88048795	88048855
223664505	chr4	88052984	88053144	88053010	88053116	AFF1	NM_005935	2	20	17	+	88052945	88053016
223664505	chr4	88052984	88053144	88053010	88053116	AFF1	NM_001166693	1	21	18	+	88052945	88053016
222846773	chr4	88055646	88055809	88055667	88055786	AFF1	NM_005935	2	20	19	+	88055626	88055846
222846773	chr4	88055646	88055809	88055667	88055786	AFF1	NM_001166693	1	21	20	+	88055623	88055846
291144055	chr4	103446580	103446707	103446607	103446681	NFKB1	NM_001165412	1	24	2	+	103446669	103446714
291144055	chr4	103446580	103446707	103446607	103446681	NFKB1	NM_003998	2	24	2	+	103446669	103446714
292225639	chr4	103458982	103459143	103459010	103459115	NFKB1	NM_001165412	1	24	5	+	103459015	103459113
292225639	chr4	103458982	103459143	103459010	103459115	NFKB1	NM_003998	2	24	5	+	103459015	103459113
292540608	chr4	103498072	103498220	103498097	103498196	NFKB1	NM_001165412	1	24	7	+	103498033	103498196
292540608	chr4	103498072	103498220	103498097	103498196	NFKB1	NM_003998	2	24	7	+	103498033	103498196
299022120	chr4	103503934	103504069	103503967	103504041	NFKB1	NM_001165412	1	24	10	+	103504023	103504114
299022120	chr4	103503934	103504069	103503967	103504041	NFKB1	NM_003998	2	24	10	+	103504023	103504114
293368255	chr4	103514595	103514731	103514617	103514708	NFKB1	NM_001165412	1	24	12	+	103514582	103514725
293368255	chr4	103514595	103514731	103514617	103514708	NFKB1	NM_003998	2	24	12	+	103514582	103514725
291801994	chr4	103517304	103517471	103517331	103517445	NFKB1	NM_001165412	1	24	14	+	103517295	103517489
291801994	chr4	103517304	103517471	103517331	103517445	NFKB1	NM_003998	2	24	14	+	103517295	103517489
289879498	chr4	103521935	103522087	103521962	103522060	NFKB1	NM_001165412	1	24	16	+	103522052	103522166
289879498	chr4	103521935	103522087	103521962	103522060	NFKB1	NM_003998	2	24	16	+	103522052	103522166
290354563	chr4	103528284	103528450	103528306	103528429	NFKB1	NM_001165412	1	24	18	+	103528307	103528476
290354563	chr4	103528284	103528450	103528306	103528429	NFKB1	NM_003998	2	24	18	+	103528307	103528476
292922358	chr4	103531746	103531914	103531770	103531892	NFKB1	NM_001165412	1	24	20	+	103531732	103531856
292922358	chr4	103531746	103531914	103531770	103531892	NFKB1	NM_003998	2	24	20	+	103531732	103531856
291586253	chr4	103534532	103534661	103534554	103534638	NFKB1	NM_001165412	1	24	23	+	103534582	103534738
291586253	chr4	103534532	103534661	103534554	103534638	NFKB1	NM_003998	2	24	23	+	103534582	103534738
242095193	chr4	106155053	106155189	106155076	106155167	TET2	NM_001127208	1	11	3	+	106155054	106158508
242095193	chr4	106155053	106155189	106155076	106155167	TET2	NM_017628	2	3	3	+	106155054	106163928
265677264	chr4	106155489	106155661	106155513	106155639	TET2	NM_001127208	1	11	3	+	106155054	106158508
265677264	chr4	106155489	106155661	106155513	106155639	TET2	NM_017628	2	3	3	+	106155054	106163928
265728198	chr4	106155916	106156055	106155937	106156027	TET2	NM_001127208	1	11	3	+	106155054	106158508
265728198	chr4	106155916	106156055	106155937	106156027	TET2	NM_017628	2	3	3	+	106155054	106163928
265751107	chr4	106156339	106156513	106156361	106156489	TET2	NM_001127208	1	11	3	+	106155054	106158508
265751107	chr4	106156339	106156513	106156361	106156489	TET2	NM_017628	2	3	3	+	106155054	106163928

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242259948	chr4	106156813	106156986	106156834	106156964	TET2	NM_001127208	1	11	3	+	106155054	106158508
242259948	chr4	106156813	106156986	106156834	106156964	TET2	NM_017628	2	3	3	+	106155054	106163928
242778937	chr4	106157250	106157421	106157278	106157394	TET2	NM_001127208	1	11	3	+	106155054	106158508
242778937	chr4	106157250	106157421	106157278	106157394	TET2	NM_017628	2	3	3	+	106155054	106163928
242157897	chr4	106157640	106157769	106157666	106157744	TET2	NM_001127208	1	11	3	+	106155054	106158508
242157897	chr4	106157640	106157769	106157666	106157744	TET2	NM_017628	2	3	3	+	106155054	106163928
242132358	chr4	106158019	106158176	106158042	106158153	TET2	NM_001127208	1	11	3	+	106155054	106158508
242132358	chr4	106158019	106158176	106158042	106158153	TET2	NM_017628	2	3	3	+	106155054	106163928
242243722	chr4	106158466	106158620	106158494	106158593	TET2	NM_001127208	1	11	3	+	106155054	106158508
242243722	chr4	106158466	106158620	106158494	106158593	TET2	NM_017628	2	3	3	+	106155054	106163928
262353292	chr4	106180706	106180879	106180730	106180852	TET2	NM_001127208	1	11	7	+	106180776	106180926
262540959	chr4	106190690	106190826	106190718	106190806	TET2	NM_001127208	1	11	9	+	106190767	106190904
240666205	chr4	106193887	106194050	106193910	106194023	TET2	NM_001127208	1	11	10	+	106193721	106194075
241692652	chr4	106196319	106196480	106196341	106196456	TET2	NM_001127208	1	11	11	+	106196205	106200960
265223429	chr4	106196759	106196907	106196783	106196882	TET2	NM_001127208	1	11	11	+	106196205	106200960
265186657	chr4	106197225	106197397	106197248	106197374	TET2	NM_001127208	1	11	11	+	106196205	106200960
231674502	chr4	123372870	123373017	123372896	123372990	IL2	NM_000586	1	4	4	-	123372626	123373017
234301468	chr4	123377196	123377360	123377221	123377332	IL2	NM_000586	1	4	2	-	123377299	123377358
233257256	chr4	123377556	123377709	123377579	123377681	IL2	NM_000586	1	4	1	-	123377449	123377650
231839234	chr4	153244226	153244359	153244254	153244326	FBXW7	NM_033632	3	12	12	-	153242410	153244301
231839234	chr4	153244226	153244359	153244254	153244326	FBXW7	NM_001013415	1	11	11	-	153242410	153244301
231839234	chr4	153244226	153244359	153244254	153244326	FBXW7	NM_018315	2	11	11	-	153242410	153244301
229616947	chr4	153247106	153247265	153247133	153247238	FBXW7	NM_033632	3	12	10	-	153247158	153247383
229616947	chr4	153247106	153247265	153247133	153247238	FBXW7	NM_001013415	1	11	9	-	153247158	153247383
229616947	chr4	153247106	153247265	153247133	153247238	FBXW7	NM_018315	2	11	9	-	153247158	153247383
229697855	chr4	153249507	153249673	153249531	153249644	FBXW7	NM_033632	3	12	9	-	153249360	153249541
229697855	chr4	153249507	153249673	153249531	153249644	FBXW7	NM_001013415	1	11	8	-	153249360	153249541
229697855	chr4	153249507	153249673	153249531	153249644	FBXW7	NM_018315	2	11	8	-	153249360	153249541
230514653	chr4	153251899	153252057	153251920	153252029	FBXW7	NM_033632	3	12	7	-	153251884	153252020
230514653	chr4	153251899	153252057	153251920	153252029	FBXW7	NM_001013415	1	11	6	-	153251884	153252020
230514653	chr4	153251899	153252057	153251920	153252029	FBXW7	NM_018315	2	11	6	-	153251884	153252020
230146842	chr4	153258877	153259050	153258904	153259023	FBXW7	NM_033632	3	12	5	-	153258954	153259088
230146842	chr4	153258877	153259050	153258904	153259023	FBXW7	NM_001013415	1	11	4	-	153258954	153259088
230146842	chr4	153258877	153259050	153258904	153259023	FBXW7	NM_018315	2	11	4	-	153258954	153259088
228995997	chr4	153268180	153268344	153268204	153268313	FBXW7	NM_033632	3	12	4	-	153268082	153268223
228995997	chr4	153268180	153268344	153268204	153268313	FBXW7	NM_001013415	1	11	3	-	153268082	153268223
228995997	chr4	153268180	153268344	153268204	153268313	FBXW7	NM_018315	2	11	3	-	153268082	153268223
229430071	chr4	153273710	153273865	153273734	153273841	FBXW7	NM_018315	2	11	1	-	153273622	153274110
228107297	chr4	153332372	153332534	153332402	153332509	FBXW7	NM_033632	3	12	2	-	153332455	153333024
228206539	chr4	153332835	153332982	153332858	153332959	FBXW7	NM_033632	3	12	2	-	153332455	153333024
294490632	chr5	223620	223754	223642	223726	SDHA	NM_004168	1	15	2	+	223597	223683

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294202560	chr5	225520	225686	225542	225668	SDHA	NM_004168	1	15	4	+	225534	225677
294368868	chr5	226125	226293	226145	226273	SDHA	NM_004168	1	15	5	+	225998	226162
294546189	chr5	231046	231177	231063	231153	SDHA	NM_004168	1	15	7	+	230991	231115
294315442	chr5	235297	235460	235316	235439	SDHA	NM_004168	1	15	9	+	235259	235454
293845481	chr5	240378	240518	240400	240497	SDHA	NM_004168	1	15	11	+	240473	240591
290589068	chr5	7869208	7869363	7869229	7869345	MTRR	NM_002454	1	15	1	+	7869217	7869328
290589068	chr5	7869208	7869363	7869229	7869345	MTRR	NM_024010	2	15	1	+	7869217	7869302
289334147	chr5	7873496	7873663	7873518	7873637	MTRR	NM_002454	1	15	3	+	7873486	7873639
289334147	chr5	7873496	7873663	7873518	7873637	MTRR	NM_024010	2	15	3	+	7873486	7873639
293603325	chr5	7878099	7878273	7878122	7878246	MTRR	NM_002454	1	15	5	+	7878057	7878435
293603325	chr5	7878099	7878273	7878122	7878246	MTRR	NM_024010	2	15	5	+	7878057	7878435
293390275	chr5	7883265	7883436	7883289	7883408	MTRR	NM_002454	1	15	6	+	7883268	7883390
293390275	chr5	7883265	7883436	7883289	7883408	MTRR	NM_024010	2	15	6	+	7883268	7883390
289734803	chr5	7889153	7889303	7889181	7889283	MTRR	NM_002454	1	15	9	+	7889208	7889388
289734803	chr5	7889153	7889303	7889181	7889283	MTRR	NM_024010	2	15	9	+	7889208	7889388
290723749	chr5	7892897	7893064	7892919	7893036	MTRR	NM_002454	1	15	11	+	7892840	7893026
290723749	chr5	7892897	7893064	7892919	7893036	MTRR	NM_024010	2	15	11	+	7892840	7893026
291729352	chr5	7896968	7897106	7896995	7897078	MTRR	NM_002454	1	15	13	+	7896977	7897069
291729352	chr5	7896968	7897106	7896995	7897078	MTRR	NM_024010	2	15	13	+	7896977	7897069
291237029	chr5	7900078	7900246	7900104	7900218	MTRR	NM_002454	1	15	15	+	7900027	7901235
291237029	chr5	7900078	7900246	7900104	7900218	MTRR	NM_024010	2	15	15	+	7900027	7901235
273276935	chr5	35860956	35861116	35860980	35861092	IL7R	NM_002185	1	8	2	+	35860954	35861092
273054234	chr5	35871114	35871286	35871135	35871258	IL7R	NM_002185	1	8	4	+	35871158	35871315
273382346	chr5	35874512	35874682	35874536	35874654	IL7R	NM_002185	1	8	6	+	35874551	35874644
274651102	chr5	35876272	35876434	35876296	35876414	IL7R	NM_002185	1	8	8	+	35876085	35876923
299008308	chr5	37815802	37815934	37815829	37815906	GDNF	NM_199231	4	3	3	-	37812779	37816237
299008308	chr5	37815802	37815934	37815829	37815906	GDNF	NM_001190468	2	3	3	-	37812779	37816237
299008308	chr5	37815802	37815934	37815829	37815906	GDNF	NM_001190469	3	3	3	-	37812779	37816237
299008308	chr5	37815802	37815934	37815829	37815906	GDNF	NM_000514	1	3	3	-	37812779	37816237
299021676	chr5	37834638	37834768	37834657	37834751	GDNF	NM_001190468	2	3	2	-	37834748	37834924
299021676	chr5	37834638	37834768	37834657	37834751	GDNF	NM_000514	1	3	2	-	37834748	37834924
233015782	chr5	38481651	38481825	38481677	38481801	LIFR	NM_001127671	1	20	20	-	38475065	38482320
233015782	chr5	38481651	38481825	38481677	38481801	LIFR	NM_002310	2	20	20	-	38475065	38482320
234473379	chr5	38482125	38482298	38482149	38482269	LIFR	NM_001127671	1	20	20	-	38475065	38482320
234473379	chr5	38482125	38482298	38482149	38482269	LIFR	NM_002310	2	20	20	-	38475065	38482320
231234433	chr5	38484900	38485025	38484926	38484997	LIFR	NM_001127671	1	20	18	-	38484877	38484970
231234433	chr5	38484900	38485025	38484926	38484997	LIFR	NM_002310	2	20	18	-	38484877	38484970
231510929	chr5	38489267	38489394	38489294	38489366	LIFR	NM_001127671	1	20	16	-	38489180	38489347
231510929	chr5	38489267	38489394	38489294	38489366	LIFR	NM_002310	2	20	16	-	38489180	38489347
232849191	chr5	38493725	38493882	38493748	38493854	LIFR	NM_001127671	1	20	14	-	38493708	38493887
232849191	chr5	38493725	38493882	38493748	38493854	LIFR	NM_002310	2	20	14	-	38493708	38493887

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233145116	chr5	38499506	38499674	38499528	38499654	LIFR	NM_001127671	1	20	12	-	38499615	38499685
233145116	chr5	38499506	38499674	38499528	38499654	LIFR	NM_002310	2	20	12	-	38499615	38499685
232203142	chr5	38504066	38504226	38504093	38504198	LIFR	NM_001127671	1	20	10	-	38504078	38504223
232203142	chr5	38504066	38504226	38504093	38504198	LIFR	NM_002310	2	20	10	-	38504078	38504223
233690946	chr5	38506135	38506266	38506163	38506233	LIFR	NM_001127671	1	20	9	-	38506007	38506176
233690946	chr5	38506135	38506266	38506163	38506233	LIFR	NM_002310	2	20	9	-	38506007	38506176
230842631	chr5	38510621	38510771	38510648	38510743	LIFR	NM_001127671	1	20	7	-	38510566	38510820
230842631	chr5	38510621	38510771	38510648	38510743	LIFR	NM_002310	2	20	7	-	38510566	38510820
233529416	chr5	38523435	38523585	38523459	38523557	LIFR	NM_001127671	1	20	5	-	38523521	38523684
233529416	chr5	38523435	38523585	38523459	38523557	LIFR	NM_002310	2	20	5	-	38523521	38523684
232964706	chr5	38528847	38529021	38528869	38528993	LIFR	NM_001127671	1	20	3	-	38528828	38528942
232964706	chr5	38528847	38529021	38528869	38528993	LIFR	NM_002310	2	20	3	-	38528828	38528942
231663922	chr5	55236939	55237088	55236967	55237063	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231663922	chr5	55236939	55237088	55236967	55237063	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231663922	chr5	55236939	55237088	55236967	55237063	IL6ST	NM_002184	2	17	17	-	55230925	55237647
231738028	chr5	55237340	55237502	55237361	55237480	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231738028	chr5	55237340	55237502	55237361	55237480	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231738028	chr5	55237340	55237502	55237361	55237480	IL6ST	NM_002184	2	17	17	-	55230925	55237647
233265462	chr5	55243316	55243472	55243344	55243446	IL6ST	NM_175767	3	16	14	-	55243321	55243417
233265462	chr5	55243316	55243472	55243344	55243446	IL6ST	NM_001190981	1	16	14	-	55243321	55243417
233265462	chr5	55243316	55243472	55243344	55243446	IL6ST	NM_002184	2	17	15	-	55243321	55243417
232862973	chr5	55248053	55248181	55248080	55248157	IL6ST	NM_175767	3	16	11	-	55248078	55248179
232862973	chr5	55248053	55248181	55248080	55248157	IL6ST	NM_001190981	1	16	11	-	55248078	55248179
232862973	chr5	55248053	55248181	55248080	55248157	IL6ST	NM_002184	2	17	12	-	55248078	55248179
233693508	chr5	55250760	55250905	55250785	55250873	IL6ST	NM_175767	3	16	10	-	55250638	55250820
233693508	chr5	55250760	55250905	55250785	55250873	IL6ST	NM_002184	2	17	11	-	55250638	55250820
233713851	chr5	55256130	55256295	55256158	55256270	IL6ST	NM_175767	3	16	8	-	55256230	55256389
233713851	chr5	55256130	55256295	55256158	55256270	IL6ST	NM_001190981	1	16	8	-	55256230	55256389
233713851	chr5	55256130	55256295	55256158	55256270	IL6ST	NM_002184	2	17	8	-	55256230	55256389
233040781	chr5	55259928	55260097	55259957	55260078	IL6ST	NM_175767	3	16	6	-	55259974	55260140
233040781	chr5	55259928	55260097	55259957	55260078	IL6ST	NM_001190981	1	16	6	-	55259974	55260140
233040781	chr5	55259928	55260097	55259957	55260078	IL6ST	NM_002184	2	17	6	-	55259974	55260140
232284595	chr5	55265326	55265498	55265353	55265477	IL6ST	NM_175767	3	16	4	-	55265378	55265683
232284595	chr5	55265326	55265498	55265353	55265477	IL6ST	NM_001190981	1	16	4	-	55265378	55265683
232284595	chr5	55265326	55265498	55265353	55265477	IL6ST	NM_002184	2	17	4	-	55265378	55265683
241025997	chr5	67522710	67522878	67522738	67522852	PIK3R1	NM_181523	3	16	2	+	67522118	67522837
239346364	chr5	67575420	67575594	67575443	67575567	PIK3R1	NM_181523	3	16	5	+	67575430	67575561
235804118	chr5	67576798	67576929	67576824	67576901	PIK3R1	NM_181523	3	16	7	+	67576755	67576834
241203147	chr5	67588039	67588172	67588065	67588143	PIK3R1	NM_181523	3	16	8	+	67588087	67588189
241203147	chr5	67588039	67588172	67588065	67588143	PIK3R1	NM_181524	4	10	2	+	67588087	67588189
241203147	chr5	67588039	67588172	67588065	67588143	PIK3R1	NM_181504	2	10	2	+	67588087	67588189

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235021741	chr5	67589186	67589360	67589212	67589332	PIK3R1	NM_181523	3	16	10	+	67589131	67589311
235021741	chr5	67589186	67589360	67589212	67589332	PIK3R1	NM_001242466	1	9	3	+	67589131	67589311
235021741	chr5	67589186	67589360	67589212	67589332	PIK3R1	NM_181524	4	10	4	+	67589131	67589311
235021741	chr5	67589186	67589360	67589212	67589332	PIK3R1	NM_181504	2	10	4	+	67589131	67589311
237489917	chr5	67591025	67591150	67591054	67591124	PIK3R1	NM_181523	3	16	13	+	67590976	67591152
237489917	chr5	67591025	67591150	67591054	67591124	PIK3R1	NM_001242466	1	9	6	+	67590976	67591152
237489917	chr5	67591025	67591150	67591054	67591124	PIK3R1	NM_181524	4	10	7	+	67590976	67591152
237489917	chr5	67591025	67591150	67591054	67591124	PIK3R1	NM_181504	2	10	7	+	67590976	67591152
238555045	chr5	67592080	67592249	67592102	67592226	PIK3R1	NM_181523	3	16	15	+	67591999	67592169
238555045	chr5	67592080	67592249	67592102	67592226	PIK3R1	NM_001242466	1	9	8	+	67591999	67592169
238555045	chr5	67592080	67592249	67592102	67592226	PIK3R1	NM_181524	4	10	9	+	67591999	67592169
238555045	chr5	67592080	67592249	67592102	67592226	PIK3R1	NM_181504	2	10	9	+	67591999	67592169
222565189	chr5	112043446	112043613	112043463	112043594	APC	NM_001127511	3	14	1	+	112043202	112043579
223304441	chr5	112102040	112102194	112102069	112102170	APC	NM_000038	1	16	3	+	112102023	112102107
223304441	chr5	112102040	112102194	112102069	112102170	APC	NM_001127510	2	17	4	+	112102023	112102107
223304441	chr5	112102040	112102194	112102069	112102170	APC	NM_001127511	3	14	2	+	112102023	112102107
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_000038	1	16	5	+	112111326	112111434
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_001127510	2	17	6	+	112111326	112111434
223556481	chr5	112111218	112111383	112111245	112111355	APC	NM_001127511	3	14	4	+	112111326	112111434
222945169	chr5	112128055	112128222	112128084	112128201	APC	NM_000038	1	16	7	+	112128143	112128226
222945169	chr5	112128055	112128222	112128084	112128201	APC	NM_001127510	2	17	8	+	112128143	112128226
222619712	chr5	112151204	112151342	112151226	112151314	APC	NM_000038	1	16	9	+	112151192	112151290
222619712	chr5	112151204	112151342	112151226	112151314	APC	NM_001127510	2	17	10	+	112151192	112151290
222619712	chr5	112151204	112151342	112151226	112151314	APC	NM_001127511	3	14	7	+	112151192	112151290
222899148	chr5	112154932	112155080	112154952	112155052	APC	NM_000038	1	16	10	+	112154663	112155041
222899148	chr5	112154932	112155080	112154952	112155052	APC	NM_001127510	2	17	11	+	112154663	112155041
222899148	chr5	112154932	112155080	112154952	112155052	APC	NM_001127511	3	14	8	+	112154663	112155041
329456901	chr5	112162905	112163079	112162930	112163051	APC	NM_000038	1	16	12	+	112162805	112162944
329456901	chr5	112162905	112163079	112162930	112163051	APC	NM_001127510	2	17	13	+	112162805	112162944
329456901	chr5	112162905	112163079	112162930	112163051	APC	NM_001127511	3	14	10	+	112162805	112162944
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_000038	1	16	15	+	112170648	112170862
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_001127510	2	17	16	+	112170648	112170862
222399018	chr5	112170526	112170686	112170546	112170661	APC	NM_001127511	3	14	13	+	112170648	112170862
224523510	chr5	112173311	112173453	112173339	112173426	APC	NM_000038	1	16	16	+	112173250	112181936
224523510	chr5	112173311	112173453	112173339	112173426	APC	NM_001127510	2	17	17	+	112173250	112181936
224523510	chr5	112173311	112173453	112173339	112173426	APC	NM_001127511	3	14	14	+	112173250	112181936
224528031	chr5	112173741	112173902	112173767	112173879	APC	NM_000038	1	16	16	+	112173250	112181936
224528031	chr5	112173741	112173902	112173767	112173879	APC	NM_001127510	2	17	17	+	112173250	112181936
224528031	chr5	112173741	112173902	112173767	112173879	APC	NM_001127511	3	14	14	+	112173250	112181936
222793833	chr5	112174187	112174325	112174214	112174297	APC	NM_000038	1	16	16	+	112173250	112181936
222793833	chr5	112174187	112174325	112174214	112174297	APC	NM_001127510	2	17	17	+	112173250	112181936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222793833	chr5	112174187	112174325	112174214	112174297	APC	NM_001127511	3	14	14	+	112173250	112181936
222838061	chr5	112174627	112174763	112174655	112174735	APC	NM_000038	1	16	16	+	112173250	112181936
222838061	chr5	112174627	112174763	112174655	112174735	APC	NM_001127510	2	17	17	+	112173250	112181936
222838061	chr5	112174627	112174763	112174655	112174735	APC	NM_001127511	3	14	14	+	112173250	112181936
222782278	chr5	112174984	112175158	112175007	112175130	APC	NM_000038	1	16	16	+	112173250	112181936
222782278	chr5	112174984	112175158	112175007	112175130	APC	NM_001127510	2	17	17	+	112173250	112181936
222782278	chr5	112174984	112175158	112175007	112175130	APC	NM_001127511	3	14	14	+	112173250	112181936
222802772	chr5	112175422	112175585	112175443	112175563	APC	NM_000038	1	16	16	+	112173250	112181936
222802772	chr5	112175422	112175585	112175443	112175563	APC	NM_001127510	2	17	17	+	112173250	112181936
222802772	chr5	112175422	112175585	112175443	112175563	APC	NM_001127511	3	14	14	+	112173250	112181936
224571597	chr5	112175902	112176066	112175929	112176040	APC	NM_000038	1	16	16	+	112173250	112181936
224571597	chr5	112175902	112176066	112175929	112176040	APC	NM_001127510	2	17	17	+	112173250	112181936
224571597	chr5	112175902	112176066	112175929	112176040	APC	NM_001127511	3	14	14	+	112173250	112181936
224563669	chr5	112176351	112176519	112176375	112176497	APC	NM_000038	1	16	16	+	112173250	112181936
224563669	chr5	112176351	112176519	112176375	112176497	APC	NM_001127510	2	17	17	+	112173250	112181936
224563669	chr5	112176351	112176519	112176375	112176497	APC	NM_001127511	3	14	14	+	112173250	112181936
222814596	chr5	112176843	112177011	112176871	112176987	APC	NM_000038	1	16	16	+	112173250	112181936
222814596	chr5	112176843	112177011	112176871	112176987	APC	NM_001127510	2	17	17	+	112173250	112181936
222814596	chr5	112176843	112177011	112176871	112176987	APC	NM_001127511	3	14	14	+	112173250	112181936
224533747	chr5	112177254	112177408	112177273	112177381	APC	NM_000038	1	16	16	+	112173250	112181936
224533747	chr5	112177254	112177408	112177273	112177381	APC	NM_001127510	2	17	17	+	112173250	112181936
224533747	chr5	112177254	112177408	112177273	112177381	APC	NM_001127511	3	14	14	+	112173250	112181936
224529387	chr5	112177671	112177820	112177696	112177794	APC	NM_000038	1	16	16	+	112173250	112181936
224529387	chr5	112177671	112177820	112177696	112177794	APC	NM_001127510	2	17	17	+	112173250	112181936
224529387	chr5	112177671	112177820	112177696	112177794	APC	NM_001127511	3	14	14	+	112173250	112181936
224532942	chr5	112178169	112178338	112178193	112178309	APC	NM_000038	1	16	16	+	112173250	112181936
224532942	chr5	112178169	112178338	112178193	112178309	APC	NM_001127510	2	17	17	+	112173250	112181936
224532942	chr5	112178169	112178338	112178193	112178309	APC	NM_001127511	3	14	14	+	112173250	112181936
224587028	chr5	112178592	112178748	112178617	112178723	APC	NM_000038	1	16	16	+	112173250	112181936
224587028	chr5	112178592	112178748	112178617	112178723	APC	NM_001127510	2	17	17	+	112173250	112181936
224587028	chr5	112178592	112178748	112178617	112178723	APC	NM_001127511	3	14	14	+	112173250	112181936
222825282	chr5	112179031	112179205	112179059	112179183	APC	NM_000038	1	16	16	+	112173250	112181936
222825282	chr5	112179031	112179205	112179059	112179183	APC	NM_001127510	2	17	17	+	112173250	112181936
222825282	chr5	112179031	112179205	112179059	112179183	APC	NM_001127511	3	14	14	+	112173250	112181936
224584522	chr5	112179458	112179618	112179482	112179596	APC	NM_000038	1	16	16	+	112173250	112181936
224584522	chr5	112179458	112179618	112179482	112179596	APC	NM_001127510	2	17	17	+	112173250	112181936
224584522	chr5	112179458	112179618	112179482	112179596	APC	NM_001127511	3	14	14	+	112173250	112181936
236352716	chr5	131892948	131893105	131892968	131893077	RAD50	NM_005732	1	25	1	+	131892616	131893145
236077162	chr5	131911522	131911685	131911549	131911657	RAD50	NM_005732	1	25	3	+	131911469	131911620
237197086	chr5	131915565	131915701	131915587	131915675	RAD50	NM_005732	1	25	5	+	131915554	131915758
234914454	chr5	131923607	131923781	131923632	131923755	RAD50	NM_005732	1	25	7	+	131923616	131923781

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235124393	chr5	131924516	131924664	131924543	131924643	RAD50	NM_005732	1	25	8	+	131924379	131924572
239766808	chr5	131926909	131927045	131926934	131927024	RAD50	NM_005732	1	25	10	+	131926916	131927098
239918759	chr5	131927612	131927756	131927640	131927725	RAD50	NM_005732	1	25	11	+	131927569	131927726
235132256	chr5	131931184	131931315	131931214	131931287	RAD50	NM_005732	1	25	13	+	131931265	131931502
235552766	chr5	131938991	131939125	131939019	131939100	RAD50	NM_005732	1	25	14	+	131938992	131939181
236252383	chr5	131944236	131944360	131944261	131944334	RAD50	NM_005732	1	25	17	+	131944307	131944417
235129682	chr5	131944877	131945041	131944906	131945014	RAD50	NM_005732	1	25	19	+	131944975	131945088
235669577	chr5	131953824	131953948	131953851	131953920	RAD50	NM_005732	1	25	21	+	131953762	131953986
235916666	chr5	131973717	131973864	131973742	131973841	RAD50	NM_005732	1	25	23	+	131973773	131973915
234914319	chr5	131977772	131977943	131977797	131977915	RAD50	NM_005732	1	25	25	+	131977870	131980313
273130362	chr5	138117621	138117769	138117644	138117742	CTNNA1	NM_001903	1	18	2	+	138117612	138117718
274298971	chr5	138145682	138145848	138145711	138145825	CTNNA1	NM_001903	1	18	4	+	138145727	138145893
273786510	chr5	138160172	138160345	138160199	138160323	CTNNA1	NM_001903	1	18	6	+	138160219	138160488
272990306	chr5	138163263	138163437	138163283	138163408	CTNNA1	NM_001903	1	18	7	+	138163204	138163407
273741383	chr5	138223165	138223299	138223192	138223272	CTNNA1	NM_001903	1	18	9	+	138223179	138223331
273386619	chr5	138253327	138253484	138253352	138253463	CTNNA1	NM_001903	1	18	11	+	138253431	138253587
273133804	chr5	138260270	138260427	138260289	138260405	CTNNA1	NM_001903	1	18	12	+	138260199	138260399
273511083	chr5	138266138	138266288	138266161	138266267	CTNNA1	NM_001903	1	18	15	+	138266162	138266343
273702334	chr5	138268338	138268492	138268360	138268470	CTNNA1	NM_001903	1	18	17	+	138268267	138268401
274009735	chr5	138269743	138269907	138269762	138269886	CTNNA1	NM_001903	1	18	18	+	138269491	138270723
225884701	chr5	149434779	149434926	149434799	149434902	CSF1R	NM_005211	1	22	20	-	149434800	149434899
225627705	chr5	149435765	149435933	149435786	149435911	CSF1R	NM_005211	1	22	18	-	149435782	149435904
226109098	chr5	149439356	149439494	149439376	149439472	CSF1R	NM_005211	1	22	15	-	149439263	149439425
225398831	chr5	149441045	149441190	149441069	149441169	CSF1R	NM_005211	1	22	13	-	149441054	149441158
253770012	chr5	149447773	149447923	149447801	149447902	CSF1R	NM_005211	1	22	11	-	149447778	149447893
253702885	chr5	149449907	149450053	149449928	149450032	CSF1R	NM_005211	1	22	8	-	149450019	149450134
225824727	chr5	149456772	149456946	149456794	149456923	CSF1R	NM_005211	1	22	6	-	149456839	149456998
225563387	chr5	149459562	149459719	149459583	149459699	CSF1R	NM_005211	1	22	4	-	149459615	149459899
225389268	chr5	149460388	149460527	149460407	149460508	CSF1R	NM_005211	1	22	3	-	149460330	149460587
239111517	chr5	149495325	149495484	149495349	149495462	PDGFRB	NM_002609	1	23	23	-	149493402	149495509
240147005	chr5	149497286	149497416	149497307	149497395	PDGFRB	NM_002609	1	23	22	-	149497181	149497413
235412439	chr5	149499581	149499732	149499603	149499711	PDGFRB	NM_002609	1	23	19	-	149499575	149499686
236478867	chr5	149500755	149500908	149500776	149500886	PDGFRB	NM_002609	1	23	17	-	149500767	149500885
237301899	chr5	149502682	149502851	149502704	149502831	PDGFRB	NM_002609	1	23	15	-	149502605	149502764
235148313	chr5	149504992	149505146	149505011	149505126	PDGFRB	NM_002609	1	23	12	-	149505008	149505140
240552624	chr5	149509311	149509483	149509329	149509462	PDGFRB	NM_002609	1	23	10	-	149509320	149509531
237607361	chr5	149511454	149511591	149511472	149511569	PDGFRB	NM_002609	1	23	8	-	149511542	149511657
237873847	chr5	149513102	149513252	149513122	149513233	PDGFRB	NM_002609	1	23	6	-	149513149	149513323
236092939	chr5	149514268	149514439	149514292	149514418	PDGFRB	NM_002609	1	23	4	-	149514313	149514579
237384592	chr5	149515184	149515349	149515208	149515328	PDGFRB	NM_002609	1	23	3	-	149515118	149515441
238079289	chr5	170816977	170817120	170817001	170817093	NPM1	NM_002520	2	11	2	+	170817055	170817134

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238079289	chr5	170816977	170817120	170817001	170817093	NPM1	NM_001037738	1	10	2	+	170817055	170817134
238079289	chr5	170816977	170817120	170817001	170817093	NPM1	NM_199185	3	10	2	+	170817055	170817134
236521449	chr5	170818609	170818772	170818635	170818748	NPM1	NM_002520	2	11	4	+	170818710	170818803
236521449	chr5	170818609	170818772	170818635	170818748	NPM1	NM_001037738	1	10	4	+	170818710	170818803
236521449	chr5	170818609	170818772	170818635	170818748	NPM1	NM_199185	3	10	4	+	170818710	170818803
236009437	chr5	170827780	170827954	170827803	170827930	NPM1	NM_002520	2	11	8	+	170827843	170827929
236009437	chr5	170827780	170827954	170827803	170827930	NPM1	NM_001037738	1	10	8	+	170827843	170827929
240701448	chr5	170837476	170837642	170837502	170837614	NPM1	NM_002520	2	11	11	+	170837531	170837888
240701448	chr5	170837476	170837642	170837502	170837614	NPM1	NM_199185	3	10	10	+	170837531	170837888
270019227	chr5	176517553	176517678	176517574	176517654	FGFR4	NM_022963	2	16	2	+	176517391	176517654
270019227	chr5	176517553	176517678	176517574	176517654	FGFR4	NM_002011	1	18	3	+	176517391	176517654
270019227	chr5	176517553	176517678	176517574	176517654	FGFR4	NM_213647	3	18	3	+	176517391	176517654
272007653	chr5	176518597	176518764	176518618	176518742	FGFR4	NM_022963	2	16	5	+	176518686	176518809
272007653	chr5	176518597	176518764	176518618	176518742	FGFR4	NM_002011	1	18	6	+	176518686	176518809
272007653	chr5	176518597	176518764	176518618	176518742	FGFR4	NM_213647	3	18	6	+	176518686	176518809
270995475	chr5	176519506	176519680	176519529	176519658	FGFR4	NM_022963	2	16	7	+	176519647	176519785
270995475	chr5	176519506	176519680	176519529	176519658	FGFR4	NM_002011	1	18	8	+	176519647	176519785
270995475	chr5	176519506	176519680	176519529	176519658	FGFR4	NM_213647	3	18	8	+	176519647	176519785
269928748	chr5	176520291	176520455	176520311	176520433	FGFR4	NM_002011	1	18	10	+	176520407	176520552
269928748	chr5	176520291	176520455	176520311	176520433	FGFR4	NM_213647	3	18	10	+	176520407	176520552
269928748	chr5	176520291	176520455	176520311	176520433	FGFR4	NM_022963	2	16	8	+	176520333	176520552
269928748	chr5	176520291	176520455	176520311	176520433	FGFR4	NM_002011	1	18	9	+	176520139	176520332
269928748	chr5	176520291	176520455	176520311	176520433	FGFR4	NM_213647	3	18	9	+	176520139	176520332
272535051	chr5	176522312	176522479	176522330	176522462	FGFR4	NM_022963	2	16	10	+	176522331	176522441
272535051	chr5	176522312	176522479	176522330	176522462	FGFR4	NM_002011	1	18	12	+	176522331	176522441
272535051	chr5	176522312	176522479	176522330	176522462	FGFR4	NM_213647	3	18	12	+	176522331	176522441
271192643	chr5	176522997	176523122	176523017	176523096	FGFR4	NM_022963	2	16	12	+	176523058	176523180
271192643	chr5	176522997	176523122	176523017	176523096	FGFR4	NM_002011	1	18	14	+	176523058	176523180
271192643	chr5	176522997	176523122	176523017	176523096	FGFR4	NM_213647	3	18	14	+	176523058	176523180
269961478	chr5	176523616	176523787	176523640	176523767	FGFR4	NM_022963	2	16	14	+	176523605	176523742
269961478	chr5	176523616	176523787	176523640	176523767	FGFR4	NM_002011	1	18	16	+	176523605	176523742
269961478	chr5	176523616	176523787	176523640	176523767	FGFR4	NM_213647	3	18	16	+	176523605	176523742
271567273	chr5	176524602	176524767	176524623	176524746	FGFR4	NM_022963	2	16	16	+	176524528	176525126
271567273	chr5	176524602	176524767	176524623	176524746	FGFR4	NM_002011	1	18	18	+	176524528	176525126
271567273	chr5	176524602	176524767	176524623	176524746	FGFR4	NM_213647	3	18	18	+	176524528	176525126
240586717	chr5	176562415	176562558	176562437	176562531	NSD1	NM_022455	1	23	2	+	176562088	176563031
235823180	chr5	176562844	176563003	176562867	176562975	NSD1	NM_172349	2	24	3	+	176562942	176563031
235823180	chr5	176562844	176563003	176562867	176562975	NSD1	NM_022455	1	23	2	+	176562088	176563031
236768945	chr5	176631093	176631234	176631119	176631210	NSD1	NM_022455	1	23	4	+	176631121	176631293
236768945	chr5	176631093	176631234	176631119	176631210	NSD1	NM_172349	2	24	5	+	176631121	176631293
257572069	chr5	176636793	176636959	176636818	176636932	NSD1	NM_022455	1	23	5	+	176636637	176639196

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
257572069	chr5	176636793	176636959	176636818	176636932	NSD1	NM_172349	2	24	6	+	176636637	176639196
237621847	chr5	176637245	176637373	176637269	176637350	NSD1	NM_022455	1	23	5	+	176636637	176639196
237621847	chr5	176637245	176637373	176637269	176637350	NSD1	NM_172349	2	24	6	+	176636637	176639196
242569747	chr5	176637644	176637805	176637670	176637778	NSD1	NM_022455	1	23	5	+	176636637	176639196
242569747	chr5	176637644	176637805	176637670	176637778	NSD1	NM_172349	2	24	6	+	176636637	176639196
257509184	chr5	176638074	176638222	176638101	176638202	NSD1	NM_022455	1	23	5	+	176636637	176639196
257509184	chr5	176638074	176638222	176638101	176638202	NSD1	NM_172349	2	24	6	+	176636637	176639196
257655352	chr5	176638491	176638619	176638513	176638599	NSD1	NM_022455	1	23	5	+	176636637	176639196
257655352	chr5	176638491	176638619	176638513	176638599	NSD1	NM_172349	2	24	6	+	176636637	176639196
242621354	chr5	176638884	176639044	176638906	176639019	NSD1	NM_022455	1	23	5	+	176636637	176639196
242621354	chr5	176638884	176639044	176638906	176639019	NSD1	NM_172349	2	24	6	+	176636637	176639196
238527794	chr5	176662810	176662982	176662833	176662957	NSD1	NM_022455	1	23	6	+	176662822	176662946
238527794	chr5	176662810	176662982	176662833	176662957	NSD1	NM_172349	2	24	7	+	176662822	176662946
235404766	chr5	176666707	176666854	176666733	176666837	NSD1	NM_022455	1	23	8	+	176666757	176666866
235404766	chr5	176666707	176666854	176666733	176666837	NSD1	NM_172349	2	24	9	+	176666757	176666866
258615367	chr5	176673662	176673828	176673688	176673800	NSD1	NM_022455	1	23	10	+	176673679	176673797
258615367	chr5	176673662	176673828	176673688	176673800	NSD1	NM_172349	2	24	11	+	176673679	176673797
240319482	chr5	176683826	176683985	176683847	176683959	NSD1	NM_022455	1	23	13	+	176683952	176684152
240319482	chr5	176683826	176683985	176683847	176683959	NSD1	NM_172349	2	24	14	+	176683952	176684152
238549363	chr5	176687052	176687185	176687074	176687157	NSD1	NM_022455	1	23	14	+	176686990	176687169
238549363	chr5	176687052	176687185	176687074	176687157	NSD1	NM_172349	2	24	15	+	176686990	176687169
236716112	chr5	176696546	176696674	176696567	176696646	NSD1	NM_022455	1	23	16	+	176696603	176696808
236716112	chr5	176696546	176696674	176696567	176696646	NSD1	NM_172349	2	24	17	+	176696603	176696808
235819686	chr5	176707525	176707686	176707550	176707665	NSD1	NM_022455	1	23	18	+	176707566	176707835
235819686	chr5	176707525	176707686	176707550	176707665	NSD1	NM_172349	2	24	19	+	176707566	176707835
235160819	chr5	176709475	176709611	176709503	176709584	NSD1	NM_022455	1	23	19	+	176709466	176709582
235160819	chr5	176709475	176709611	176709503	176709584	NSD1	NM_172349	2	24	20	+	176709466	176709582
258749617	chr5	176715807	176715951	176715831	176715927	NSD1	NM_022455	1	23	21	+	176715820	176715926
258749617	chr5	176715807	176715951	176715831	176715927	NSD1	NM_172349	2	24	22	+	176715820	176715926
239778898	chr5	176720881	176721017	176720902	176720997	NSD1	NM_022455	1	23	23	+	176720833	176727214
239778898	chr5	176720881	176721017	176720902	176720997	NSD1	NM_172349	2	24	24	+	176720833	176727214
235273751	chr5	176721271	176721405	176721293	176721385	NSD1	NM_022455	1	23	23	+	176720833	176727214
235273751	chr5	176721271	176721405	176721293	176721385	NSD1	NM_172349	2	24	24	+	176720833	176727214
235326041	chr5	176721691	176721836	176721717	176721814	NSD1	NM_022455	1	23	23	+	176720833	176727214
235326041	chr5	176721691	176721836	176721717	176721814	NSD1	NM_172349	2	24	24	+	176720833	176727214
239839152	chr5	176722126	176722300	176722146	176722280	NSD1	NM_022455	1	23	23	+	176720833	176727214
239839152	chr5	176722126	176722300	176722146	176722280	NSD1	NM_172349	2	24	24	+	176720833	176727214
272470023	chr5	180030176	180030304	180030199	180030283	FLT4	NM_182925	2	30	30	-	180028506	180030390
271118143	chr5	180038251	180038425	180038271	180038407	FLT4	NM_182925	2	30	27	-	180038331	180038479
271118143	chr5	180038251	180038425	180038271	180038407	FLT4	NM_002020	1	30	27	-	180038331	180038479
269606807	chr5	180041022	180041174	180041041	180041156	FLT4	NM_182925	2	30	24	-	180041068	180041179

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269606807	chr5	180041022	180041174	180041041	180041156	FLT4	NM_002020	1	30	24	-	180041068	180041179
269647802	chr5	180045670	180045843	180045688	180045825	FLT4	NM_182925	2	30	21	-	180045770	180045920
269647802	chr5	180045670	180045843	180045688	180045825	FLT4	NM_002020	1	30	21	-	180045770	180045920
269585357	chr5	180046532	180046690	180046553	180046671	FLT4	NM_182925	2	30	18	-	180046665	180046769
269585357	chr5	180046532	180046690	180046553	180046671	FLT4	NM_002020	1	30	18	-	180046665	180046769
271439294	chr5	180047523	180047663	180047549	180047642	FLT4	NM_182925	2	30	16	-	180047609	180047715
271439294	chr5	180047523	180047663	180047549	180047642	FLT4	NM_002020	1	30	16	-	180047609	180047715
270117422	chr5	180047967	180048140	180047988	180048119	FLT4	NM_182925	2	30	15	-	180047876	180048007
270117422	chr5	180047967	180048140	180047988	180048119	FLT4	NM_002020	1	30	15	-	180047876	180048007
270117422	chr5	180047967	180048140	180047988	180048119	FLT4	NM_182925	2	30	14	-	180048106	180048252
270117422	chr5	180047967	180048140	180047988	180048119	FLT4	NM_002020	1	30	14	-	180048106	180048252
271354454	chr5	180048596	180048748	180048616	180048729	FLT4	NM_182925	2	30	13	-	180048542	180048904
271354454	chr5	180048596	180048748	180048616	180048729	FLT4	NM_002020	1	30	13	-	180048542	180048904
269974005	chr5	180049767	180049919	180049788	180049898	FLT4	NM_182925	2	30	12	-	180049731	180049839
269974005	chr5	180049767	180049919	180049788	180049898	FLT4	NM_002020	1	30	12	-	180049731	180049839
269952998	chr5	180052971	180053119	180052988	180053098	FLT4	NM_182925	2	30	10	-	180052869	180053031
269952998	chr5	180052971	180053119	180052988	180053098	FLT4	NM_002020	1	30	10	-	180052869	180053031
270928424	chr5	180055872	180056043	180055893	180056022	FLT4	NM_182925	2	30	8	-	180055882	180055999
270928424	chr5	180055872	180056043	180055893	180056022	FLT4	NM_002020	1	30	8	-	180055882	180055999
271339664	chr5	180056714	180056856	180056736	180056836	FLT4	NM_182925	2	30	6	-	180056696	180056835
271339664	chr5	180056714	180056856	180056736	180056836	FLT4	NM_002020	1	30	6	-	180056696	180056835
270888256	chr5	180057537	180057688	180057554	180057670	FLT4	NM_182925	2	30	3	-	180057555	180057799
270888256	chr5	180057537	180057688	180057554	180057670	FLT4	NM_002020	1	30	3	-	180057555	180057799
233364559	chr6	393178	393303	393196	393281	IRF4	NM_001195286	1	9	2	+	393098	393368
233364559	chr6	393178	393303	393196	393281	IRF4	NR_046000	4	10	2	+	393098	393368
233364559	chr6	393178	393303	393196	393281	IRF4	NM_002460	2	9	2	+	393098	393368
232236793	chr6	395794	395923	395819	395902	IRF4	NM_001195286	1	9	4	+	395847	395935
232236793	chr6	395794	395923	395819	395902	IRF4	NR_046000	4	10	4	+	395847	395935
232236793	chr6	395794	395923	395819	395902	IRF4	NM_002460	2	9	4	+	395847	395935
232236793	chr6	395794	395923	395819	395902	IRF4	NR_036585	3	8	3	+	395847	395935
233718102	chr6	398777	398951	398797	398931	IRF4	NM_001195286	1	9	6	+	398828	398935
233718102	chr6	398777	398951	398797	398931	IRF4	NR_046000	4	10	6	+	398828	398935
233718102	chr6	398777	398951	398797	398931	IRF4	NM_002460	2	9	6	+	398828	398935
233718102	chr6	398777	398951	398797	398931	IRF4	NR_036585	3	8	5	+	398828	398935
234182429	chr6	401552	401684	401573	401663	IRF4	NM_001195286	1	9	7	+	401424	401777
234182429	chr6	401552	401684	401573	401663	IRF4	NR_046000	4	10	7	+	401424	401777
234182429	chr6	401552	401684	401573	401663	IRF4	NM_002460	2	9	7	+	401424	401777
234182429	chr6	401552	401684	401573	401663	IRF4	NR_036585	3	8	6	+	401424	401777
233847028	chr6	407460	407596	407486	407569	IRF4	NM_001195286	1	9	9	+	407455	411443
233847028	chr6	407460	407596	407486	407569	IRF4	NR_046000	4	10	10	+	407455	411443
233847028	chr6	407460	407596	407486	407569	IRF4	NM_002460	2	9	9	+	407455	411443

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233847028	chr6	407460	407596	407486	407569	IRF4	NR_036585	3	8	8	+	407455	411443
227687912	chr6	18237631	18237805	18237652	18237780	DEK	NM_003472	2	11	8	-	18237612	18237747
227687912	chr6	18237631	18237805	18237652	18237780	DEK	NM_001134709	1	10	7	-	18237612	18237747
230690925	chr6	18255864	18256038	18255888	18256010	DEK	NM_003472	2	11	6	-	18255962	18256082
230690925	chr6	18255864	18256038	18255888	18256010	DEK	NM_001134709	1	10	5	-	18255962	18256082
230026174	chr6	18258482	18258642	18258508	18258617	DEK	NM_003472	2	11	3	-	18258535	18258636
235181399	chr6	31132884	31133015	31132904	31132992	POU5F1	NM_002701	2	5	4	-	31132905	31133063
235181399	chr6	31132884	31133015	31132904	31132992	POU5F1	NM_203289	3	4	3	-	31132905	31133063
235181399	chr6	31132884	31133015	31132904	31132992	POU5F1	NM_001173531	1	5	4	-	31132905	31133063
239939613	chr6	31133603	31133766	31133626	31133745	POU5F1	NM_002701	2	5	2	-	31133704	31133824
239939613	chr6	31133603	31133766	31133626	31133745	POU5F1	NM_001173531	1	5	2	-	31133704	31133824
239939613	chr6	31133603	31133766	31133626	31133745	POU5F1	NM_203289	3	4	1	-	31133704	31134615
237538795	chr6	31138272	31138446	31138292	31138426	POU5F1	NM_002701	2	5	1	-	31137993	31138451
290134531	chr6	32163528	32163699	32163549	32163682	NOTCH4	NM_004557	1	30	30	-	32162620	32163927
291189570	chr6	32164668	32164839	32164694	32164817	NOTCH4	NM_004557	1	30	28	-	32164702	32164849
290771444	chr6	32165260	32165411	32165280	32165384	NOTCH4	NM_004557	1	30	27	-	32165076	32165371
291221756	chr6	32166677	32166846	32166699	32166825	NOTCH4	NM_004557	1	30	24	-	32166703	32166922
293589786	chr6	32168831	32168994	32168853	32168969	NOTCH4	NM_004557	1	30	22	-	32168894	32169277
292901226	chr6	32169790	32169955	32169810	32169936	NOTCH4	NM_004557	1	30	21	-	32169853	32170376
292893765	chr6	32170273	32170439	32170292	32170419	NOTCH4	NM_004557	1	30	21	-	32169853	32170376
291452387	chr6	32172055	32172197	32172076	32172172	NOTCH4	NM_004557	1	30	19	-	32171914	32172166
291685287	chr6	32180241	32180414	32180262	32180393	NOTCH4	NM_004557	1	30	17	-	32180251	32180404
290139697	chr6	32181395	32181548	32181420	32181527	NOTCH4	NM_004557	1	30	14	-	32181465	32181617
289750628	chr6	32182981	32183122	32183002	32183099	NOTCH4	NM_004557	1	30	12	-	32183003	32183162
291494900	chr6	32184900	32185073	32184918	32185054	NOTCH4	NM_004557	1	30	10	-	32184930	32185043
292323364	chr6	32187828	32187987	32187851	32187967	NOTCH4	NM_004557	1	30	7	-	32187906	32188061
293015876	chr6	32188377	32188519	32188398	32188499	NOTCH4	NM_004557	1	30	6	-	32188182	32188418
290062379	chr6	32188950	32189092	32188969	32189071	NOTCH4	NM_004557	1	30	4	-	32188755	32189102
291668852	chr6	32190430	32190576	32190450	32190558	NOTCH4	NM_004557	1	30	3	-	32190288	32190583
273602316	chr6	33286754	33286928	33286773	33286909	DAXX	NM_001254717	3	7	6	-	33286774	33286996
273602316	chr6	33286754	33286928	33286773	33286909	DAXX	NM_001350	4	8	7	-	33286774	33286996
273602316	chr6	33286754	33286928	33286773	33286909	DAXX	NM_001141969	1	8	7	-	33286774	33286996
273602316	chr6	33286754	33286928	33286773	33286909	DAXX	NM_001141970	2	8	7	-	33286774	33286996
273083855	chr6	33287336	33287509	33287357	33287485	DAXX	NM_001254717	3	7	5	-	33287157	33287631
273083855	chr6	33287336	33287509	33287357	33287485	DAXX	NM_001350	4	8	6	-	33287157	33287631
273083855	chr6	33287336	33287509	33287357	33287485	DAXX	NM_001141969	1	8	6	-	33287157	33287631
273083855	chr6	33287336	33287509	33287357	33287485	DAXX	NM_001141970	2	8	6	-	33287157	33287631
273089728	chr6	33287782	33287955	33287803	33287933	DAXX	NM_001254717	3	7	4	-	33287788	33288001
273089728	chr6	33287782	33287955	33287803	33287933	DAXX	NM_001350	4	8	5	-	33287788	33288001
273089728	chr6	33287782	33287955	33287803	33287933	DAXX	NM_001141969	1	8	5	-	33287788	33288001
273089728	chr6	33287782	33287955	33287803	33287933	DAXX	NM_001141970	2	8	5	-	33287788	33288001

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274311050	chr6	33288455	33288611	33288476	33288591	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274311050	chr6	33288455	33288611	33288476	33288591	DAXX	NM_001350	4	8	3	-	33288513	33289344
274311050	chr6	33288455	33288611	33288476	33288591	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274311050	chr6	33288455	33288611	33288476	33288591	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274371701	chr6	33288895	33289061	33288919	33289040	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274371701	chr6	33288895	33289061	33288919	33289040	DAXX	NM_001350	4	8	3	-	33288513	33289344
274371701	chr6	33288895	33289061	33288919	33289040	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274371701	chr6	33288895	33289061	33288919	33289040	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274349754	chr6	33289315	33289454	33289340	33289434	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274349754	chr6	33289315	33289454	33289340	33289434	DAXX	NM_001350	4	8	3	-	33288513	33289344
274349754	chr6	33289315	33289454	33289340	33289434	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274349754	chr6	33289315	33289454	33289340	33289434	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274235752	chr6	33290565	33290721	33290583	33290702	DAXX	NM_001254717	3	7	1	-	33290639	33290793
274235752	chr6	33290565	33290721	33290583	33290702	DAXX	NM_001350	4	8	1	-	33290639	33290793
274235752	chr6	33290565	33290721	33290583	33290702	DAXX	NM_001141969	1	8	1	-	33290639	33290793
274235752	chr6	33290565	33290721	33290583	33290702	DAXX	NM_001141970	2	8	1	-	33290639	33290793
235090322	chr6	37138610	37138748	37138630	37138729	PIM1	NM_002648	2	6	2	+	37138549	37138655
235090322	chr6	37138610	37138748	37138630	37138729	PIM1	NM_001243186	1	6	2	+	37138549	37138655
238253203	chr6	37139030	37139192	37139050	37139167	PIM1	NM_002648	2	6	4	+	37138901	37139267
238253203	chr6	37139030	37139192	37139050	37139167	PIM1	NM_001243186	1	6	4	+	37138901	37139267
237430981	chr6	37141643	37141788	37141665	37141763	PIM1	NM_002648	2	6	6	+	37141710	37143204
237430981	chr6	37141643	37141788	37141665	37141763	PIM1	NM_001243186	1	6	6	+	37141710	37143204
271316527	chr6	41545690	41545832	41545709	41545812	FOXP4	NM_138457	3	17	3	+	41545724	41545819
271316527	chr6	41545690	41545832	41545709	41545812	FOXP4	NM_001012427	2	17	3	+	41545724	41545819
271316527	chr6	41545690	41545832	41545709	41545812	FOXP4	NM_001012426	1	17	3	+	41545724	41545819
271229686	chr6	41553123	41553275	41553143	41553256	FOXP4	NM_001012427	2	17	5	+	41553175	41553255
271229686	chr6	41553123	41553275	41553143	41553256	FOXP4	NM_138457	3	17	5	+	41553169	41553255
271229686	chr6	41553123	41553275	41553143	41553256	FOXP4	NM_001012426	1	17	5	+	41553169	41553255
269969607	chr6	41555059	41555216	41555076	41555198	FOXP4	NM_138457	3	17	7	+	41555040	41555250
269969607	chr6	41555059	41555216	41555076	41555198	FOXP4	NM_001012427	2	17	7	+	41555037	41555250
269969607	chr6	41555059	41555216	41555076	41555198	FOXP4	NM_001012426	1	17	7	+	41555037	41555250
271552092	chr6	41556340	41556498	41556361	41556479	FOXP4	NM_138457	3	17	9	+	41556382	41556469
271552092	chr6	41556340	41556498	41556361	41556479	FOXP4	NM_001012427	2	17	9	+	41556382	41556469
271552092	chr6	41556340	41556498	41556361	41556479	FOXP4	NM_001012426	1	17	9	+	41556382	41556469
270275877	chr6	41557837	41558003	41557854	41557981	FOXP4	NM_138457	3	17	11	+	41557737	41557908
270275877	chr6	41557837	41558003	41557854	41557981	FOXP4	NM_001012427	2	17	11	+	41557701	41557908
270275877	chr6	41557837	41558003	41557854	41557981	FOXP4	NM_001012426	1	17	11	+	41557701	41557908
272561181	chr6	41562577	41562750	41562597	41562730	FOXP4	NM_138457	3	17	14	+	41562608	41562729
272561181	chr6	41562577	41562750	41562597	41562730	FOXP4	NM_001012427	2	17	14	+	41562608	41562729
272561181	chr6	41562577	41562750	41562597	41562730	FOXP4	NM_001012426	1	17	14	+	41562608	41562729
270527437	chr6	41565537	41565707	41565556	41565690	FOXP4	NM_138457	3	17	16	+	41565519	41565688

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270527437	chr6	41565537	41565707	41565556	41565690	FOXP4	NM_001012427	2	17	16	+	41565519	41565688
270527437	chr6	41565537	41565707	41565556	41565690	FOXP4	NM_001012426	1	17	16	+	41565519	41565688
227394252	chr6	44216391	44216537	44216413	44216514	HSP90AB1	NM_007355	1	12	2	+	44216367	44216513
228811161	chr6	44217444	44217603	44217467	44217575	HSP90AB1	NM_007355	1	12	4	+	44217412	44217571
227467698	chr6	44218740	44218901	44218767	44218874	HSP90AB1	NM_007355	1	12	7	+	44218785	44218950
228024756	chr6	44219449	44219583	44219472	44219556	HSP90AB1	NM_007355	1	12	9	+	44219474	44219621
228586085	chr6	44219848	44220017	44219872	44219992	HSP90AB1	NM_007355	1	12	10	+	44219736	44220004
227207264	chr6	44220926	44221098	44220947	44221078	HSP90AB1	NM_007355	1	12	11	+	44220782	44221115
272221835	chr6	51483945	51484097	51483968	51484074	PKHD1	NM_138694	1	67	67	-	51480145	51484318
271271720	chr6	51491689	51491851	51491714	51491830	PKHD1	NM_138694	1	67	66	-	51491795	51491914
271523537	chr6	51497373	51497531	51497396	51497512	PKHD1	NM_138694	1	67	65	-	51497363	51497521
269727664	chr6	51513805	51513958	51513833	51513936	PKHD1	NM_138694	1	67	62	-	51513883	51514018
271103840	chr6	51523884	51524057	51523909	51524031	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271078663	chr6	51524324	51524496	51524351	51524472	PKHD1	NM_138694	1	67	61	-	51523750	51524767
272478632	chr6	51586688	51586857	51586711	51586828	PKHD1	NM_170724	2	61	61	-	51585647	51586818
270383156	chr6	51611580	51611749	51611602	51611721	PKHD1	NM_138694	1	67	59	-	51611519	51611687
270383156	chr6	51611580	51611749	51611602	51611721	PKHD1	NM_170724	2	61	59	-	51611519	51611687
272316150	chr6	51612871	51613041	51612899	51613013	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272316150	chr6	51612871	51613041	51612899	51613013	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270554034	chr6	51613349	51613503	51613375	51613480	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270554034	chr6	51613349	51613503	51613375	51613480	PKHD1	NM_170724	2	61	58	-	51612585	51613463
271919872	chr6	51619625	51619762	51619649	51619737	PKHD1	NM_138694	1	67	56	-	51619582	51619736
271919872	chr6	51619625	51619762	51619649	51619737	PKHD1	NM_170724	2	61	56	-	51619582	51619736
272526015	chr6	51655940	51656111	51655963	51656088	PKHD1	NM_138694	1	67	53	-	51656034	51656171
272526015	chr6	51655940	51656111	51655963	51656088	PKHD1	NM_170724	2	61	53	-	51656034	51656171
272697665	chr6	51701124	51701294	51701152	51701269	PKHD1	NM_138694	1	67	51	-	51701202	51701267
272697665	chr6	51701124	51701294	51701152	51701269	PKHD1	NM_170724	2	61	51	-	51701202	51701267
271521218	chr6	51720766	51720939	51720787	51720911	PKHD1	NM_138694	1	67	49	-	51720691	51720868
271521218	chr6	51720766	51720939	51720787	51720911	PKHD1	NM_170724	2	61	49	-	51720691	51720868
269750958	chr6	51735261	51735388	51735288	51735362	PKHD1	NM_138694	1	67	47	-	51735302	51735437
269750958	chr6	51735261	51735388	51735288	51735362	PKHD1	NM_170724	2	61	47	-	51735302	51735437
271041254	chr6	51750593	51750758	51750617	51750731	PKHD1	NM_138694	1	67	45	-	51750665	51750770
271041254	chr6	51750593	51750758	51750617	51750731	PKHD1	NM_170724	2	61	45	-	51750665	51750770
272626428	chr6	51768331	51768456	51768359	51768430	PKHD1	NM_138694	1	67	43	-	51768395	51768525
272626428	chr6	51768331	51768456	51768359	51768430	PKHD1	NM_170724	2	61	43	-	51768395	51768525
269699487	chr6	51770967	51771137	51770994	51771115	PKHD1	NM_138694	1	67	41	-	51771013	51771138
269699487	chr6	51770967	51771137	51770994	51771115	PKHD1	NM_170724	2	61	41	-	51771013	51771138
269935463	chr6	51776513	51776680	51776535	51776652	PKHD1	NM_138694	1	67	39	-	51776597	51776754
269935463	chr6	51776513	51776680	51776535	51776652	PKHD1	NM_170724	2	61	39	-	51776597	51776754
269974491	chr6	51798866	51799034	51798892	51799013	PKHD1	NM_138694	1	67	37	-	51798908	51799120
269974491	chr6	51798866	51799034	51798892	51799013	PKHD1	NM_170724	2	61	37	-	51798908	51799120

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271398107	chr6	51875010	51875163	51875033	51875137	PKHD1	NM_138694	1	67	35	-	51875107	51875257
271398107	chr6	51875010	51875163	51875033	51875137	PKHD1	NM_170724	2	61	35	-	51875107	51875257
269750797	chr6	51882330	51882458	51882351	51882431	PKHD1	NM_138694	1	67	34	-	51882208	51882427
269750797	chr6	51882330	51882458	51882351	51882431	PKHD1	NM_170724	2	61	34	-	51882208	51882427
271881208	chr6	51889304	51889473	51889327	51889454	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271881208	chr6	51889304	51889473	51889327	51889454	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271936584	chr6	51889768	51889942	51889790	51889915	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271936584	chr6	51889768	51889942	51889790	51889915	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271917247	chr6	51890187	51890313	51890207	51890289	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271917247	chr6	51890187	51890313	51890207	51890289	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271936779	chr6	51890611	51890781	51890633	51890763	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271936779	chr6	51890611	51890781	51890633	51890763	PKHD1	NM_170724	2	61	32	-	51889372	51890979
270738083	chr6	51892600	51892756	51892626	51892727	PKHD1	NM_138694	1	67	31	-	51892627	51892694
270738083	chr6	51892600	51892756	51892626	51892727	PKHD1	NM_170724	2	61	31	-	51892627	51892694
272123659	chr6	51897749	51897902	51897773	51897874	PKHD1	NM_138694	1	67	29	-	51897828	51897963
272123659	chr6	51897749	51897902	51897773	51897874	PKHD1	NM_170724	2	61	29	-	51897828	51897963
272507692	chr6	51900416	51900554	51900439	51900526	PKHD1	NM_138694	1	67	28	-	51900389	51900519
272507692	chr6	51900416	51900554	51900439	51900526	PKHD1	NM_170724	2	61	28	-	51900389	51900519
270809686	chr6	51908343	51908484	51908364	51908461	PKHD1	NM_138694	1	67	26	-	51908423	51908528
270809686	chr6	51908343	51908484	51908364	51908461	PKHD1	NM_170724	2	61	26	-	51908423	51908528
270910957	chr6	51910763	51910932	51910783	51910911	PKHD1	NM_138694	1	67	24	-	51910802	51910986
270910957	chr6	51910763	51910932	51910783	51910911	PKHD1	NM_170724	2	61	24	-	51910802	51910986
270371129	chr6	51914997	51915168	51915018	51915145	PKHD1	NM_138694	1	67	22	-	51914955	51915093
270371129	chr6	51914997	51915168	51915018	51915145	PKHD1	NM_170724	2	61	22	-	51914955	51915093
271851227	chr6	51918857	51918991	51918878	51918963	PKHD1	NM_138694	1	67	20	-	51918836	51918963
271851227	chr6	51918857	51918991	51918878	51918963	PKHD1	NM_170724	2	61	20	-	51918836	51918963
269656673	chr6	51921487	51921641	51921508	51921613	PKHD1	NM_138694	1	67	18	-	51921496	51921586
269656673	chr6	51921487	51921641	51921508	51921613	PKHD1	NM_170724	2	61	18	-	51921496	51921586
271470841	chr6	51923274	51923447	51923296	51923423	PKHD1	NM_138694	1	67	16	-	51923121	51923399
271470841	chr6	51923274	51923447	51923296	51923423	PKHD1	NM_170724	2	61	16	-	51923121	51923399
271837703	chr6	51927320	51927494	51927342	51927469	PKHD1	NM_138694	1	67	14	-	51927317	51927458
271837703	chr6	51927320	51927494	51927342	51927469	PKHD1	NM_170724	2	61	14	-	51927317	51927458
271374667	chr6	51934146	51934298	51934167	51934270	PKHD1	NM_138694	1	67	11	-	51934255	51934325
271374667	chr6	51934146	51934298	51934167	51934270	PKHD1	NM_170724	2	61	11	-	51934255	51934325
270491520	chr6	51936877	51937043	51936899	51937015	PKHD1	NM_138694	1	67	8	-	51936913	51936987
270491520	chr6	51936877	51937043	51936899	51937015	PKHD1	NM_170724	2	61	8	-	51936913	51936987
269490178	chr6	51944668	51944833	51944692	51944806	PKHD1	NM_138694	1	67	5	-	51944698	51944806
269490178	chr6	51944668	51944833	51944692	51944806	PKHD1	NM_170724	2	61	5	-	51944698	51944806
270221195	chr6	51949653	51949801	51949682	51949774	PKHD1	NM_138694	1	67	2	-	51949680	51949815
270221195	chr6	51949653	51949801	51949682	51949774	PKHD1	NM_170724	2	61	2	-	51949680	51949815
280907855	chr6	52874178	52874342	52874200	52874319	ICK	NM_016513	2	15	13	-	52874237	52874365

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280907855	chr6	52874178	52874342	52874200	52874319	ICK	NM_014920	1	14	12	-	52874237	52874365
280383576	chr6	52876797	52876961	52876825	52876933	ICK	NM_016513	2	15	11	-	52876835	52877025
280383576	chr6	52876797	52876961	52876825	52876933	ICK	NM_014920	1	14	10	-	52876835	52877025
279496552	chr6	52878646	52878819	52878671	52878791	ICK	NM_016513	2	15	10	-	52878460	52878780
279496552	chr6	52878646	52878819	52878671	52878791	ICK	NM_014920	1	14	9	-	52878460	52878780
279533294	chr6	52883203	52883354	52883227	52883329	ICK	NM_016513	2	15	8	-	52883128	52883299
279533294	chr6	52883203	52883354	52883227	52883329	ICK	NM_014920	1	14	7	-	52883128	52883299
280208780	chr6	52897314	52897445	52897343	52897422	ICK	NM_016513	2	15	5	-	52897331	52897452
280208780	chr6	52897314	52897445	52897343	52897422	ICK	NM_014920	1	14	4	-	52897331	52897452
286489720	chr6	56323684	56323847	56323709	56323826	DST	NM_015548	2	84	84	-	56322785	56324065
287427733	chr6	56324988	56325115	56325009	56325089	DST	NM_015548	2	84	83	-	56324929	56325052
286793941	chr6	56328453	56328627	56328473	56328606	DST	NM_015548	2	84	81	-	56328363	56328562
285188270	chr6	56334593	56334753	56334618	56334728	DST	NM_015548	2	84	78	-	56334681	56334755
288171458	chr6	56335814	56335971	56335839	56335943	DST	NM_015548	2	84	76	-	56335904	56336066
287708908	chr6	56336928	56337056	56336953	56337033	DST	NM_015548	2	84	75	-	56336857	56337020
287906348	chr6	56340867	56341006	56340895	56340982	DST	NM_015548	2	84	73	-	56340947	56341135
287143223	chr6	56342155	56342328	56342176	56342302	DST	NM_015548	2	84	72	-	56342143	56342286
287822869	chr6	56347579	56347737	56347599	56347709	DST	NM_015548	2	84	70	-	56347481	56347675
288263135	chr6	56351859	56352018	56351885	56351996	DST	NM_015548	2	84	68	-	56351902	56352071
287542684	chr6	56354359	56354484	56354385	56354455	DST	NM_015548	2	84	67	-	56354288	56354407
287382813	chr6	56357681	56357812	56357705	56357787	DST	NM_015548	2	84	65	-	56357732	56357887
285881099	chr6	56358918	56359061	56358941	56359035	DST	NM_015548	2	84	64	-	56358808	56358978
285709961	chr6	56362675	56362839	56362698	56362814	DST	NM_015548	2	84	62	-	56362654	56362851
288699047	chr6	56365991	56366156	56366012	56366132	DST	NM_015548	2	84	61	-	56365878	56366033
285245790	chr6	56366432	56366606	56366461	56366583	DST	NM_015548	2	84	60	-	56366318	56366491
286090884	chr6	56371437	56371561	56371463	56371532	DST	NM_015548	2	84	57	-	56371465	56371587
289175087	chr6	56373441	56373581	56373465	56373553	DST	NM_015548	2	84	56	-	56373327	56373553
286587073	chr6	56374636	56374794	56374662	56374761	DST	NM_015548	2	84	55	-	56374440	56374671
285176915	chr6	56380126	56380297	56380152	56380273	DST	NM_015548	2	84	53	-	56380248	56380466
286972332	chr6	56382042	56382210	56382068	56382182	DST	NM_015548	2	84	52	-	56381996	56382103
286971747	chr6	56391187	56391314	56391210	56391293	DST	NM_015548	2	84	50	-	56391159	56391365
289076789	chr6	56392449	56392606	56392475	56392578	DST	NM_015548	2	84	49	-	56392291	56392532
287512495	chr6	56394340	56394497	56394365	56394474	DST	NM_015548	2	84	47	-	56394246	56394572
287652183	chr6	56394796	56394961	56394822	56394936	DST	NM_015548	2	84	46	-	56394772	56394931
286184025	chr6	56399888	56400050	56399916	56400030	DST	NM_015548	2	84	44	-	56399920	56400090
285329817	chr6	56401661	56401826	56401685	56401799	DST	NM_015548	2	84	43	-	56401577	56401738
285871715	chr6	56417220	56417386	56417244	56417362	DST	NM_015548	2	84	42	-	56416982	56418453
288168338	chr6	56417678	56417831	56417699	56417810	DST	NM_015548	2	84	42	-	56416982	56418453
288133625	chr6	56418129	56418273	56418158	56418247	DST	NM_015548	2	84	42	-	56416982	56418453
287228163	chr6	56420057	56420231	56420082	56420203	DST	NM_015548	2	84	41	-	56420143	56420638
287311681	chr6	56420510	56420664	56420530	56420638	DST	NM_015548	2	84	41	-	56420143	56420638

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
286638933	chr6	56425059	56425226	56425086	56425202	DST	NM_015548	2	84	39	-	56425092	56425221
285187700	chr6	56426246	56426396	56426273	56426368	DST	NM_015548	2	84	38	-	56426106	56426347
286431505	chr6	56433337	56433511	56433365	56433483	DST	NM_015548	2	84	36	-	56433267	56433393
286293208	chr6	56436779	56436940	56436807	56436912	DST	NM_015548	2	84	34	-	56436898	56437064
285846611	chr6	56437717	56437861	56437739	56437837	DST	NM_015548	2	84	33	-	56437545	56437862
287244225	chr6	56438607	56438758	56438631	56438730	DST	NM_015548	2	84	32	-	56438477	56438685
286299183	chr6	56456920	56457091	56456947	56457069	DST	NM_015548	2	84	30	-	56456980	56457156
288833731	chr6	56458620	56458791	56458647	56458763	DST	NM_015548	2	84	29	-	56458461	56458991
287000072	chr6	56462610	56462757	56462638	56462731	DST	NM_015548	2	84	28	-	56462538	56462804
286393781	chr6	56463446	56463606	56463471	56463579	DST	NM_015548	2	84	27	-	56463274	56463507
286252927	chr6	56475152	56475287	56475176	56475259	DST	NM_015548	2	84	25	-	56475225	56475360
287062457	chr6	56479071	56479198	56479097	56479175	DST	NM_015548	2	84	23	-	56479154	56479282
287161929	chr6	56480487	56480652	56480513	56480625	DST	NM_001723	1	24	24	-	56479375	56482216
289067982	chr6	56480947	56481107	56480967	56481079	DST	NM_001723	1	24	24	-	56479375	56482216
289053354	chr6	56481370	56481543	56481398	56481516	DST	NM_001723	1	24	24	-	56479375	56482216
287462660	chr6	56481825	56481994	56481850	56481974	DST	NM_001723	1	24	24	-	56479375	56482216
288254810	chr6	56482746	56482884	56482774	56482860	DST	NM_001723	1	24	23	-	56482784	56485513
288319928	chr6	56483170	56483344	56483198	56483320	DST	NM_001723	1	24	23	-	56482784	56485513
288291244	chr6	56483602	56483776	56483630	56483755	DST	NM_001723	1	24	23	-	56482784	56485513
286212555	chr6	56484043	56484167	56484070	56484143	DST	NM_001723	1	24	23	-	56482784	56485513
288268313	chr6	56484449	56484575	56484472	56484552	DST	NM_001723	1	24	23	-	56482784	56485513
286154531	chr6	56484871	56484997	56484898	56484969	DST	NM_001723	1	24	23	-	56482784	56485513
286111400	chr6	56485318	56485447	56485340	56485420	DST	NM_001723	1	24	23	-	56482784	56485513
287223135	chr6	56489900	56490034	56489928	56490012	DST	NM_015548	2	84	21	-	56489955	56490062
287223135	chr6	56489900	56490034	56489928	56490012	DST	NM_001723	1	24	21	-	56489955	56490062
289120065	chr6	56492720	56492881	56492746	56492852	DST	NM_015548	2	84	19	-	56492797	56492959
289120065	chr6	56492720	56492881	56492746	56492852	DST	NM_001723	1	24	19	-	56492797	56492959
288070076	chr6	56495075	56495224	56495103	56495196	DST	NM_015548	2	84	17	-	56495043	56495181
288070076	chr6	56495075	56495224	56495103	56495196	DST	NM_001723	1	24	17	-	56495043	56495181
287393325	chr6	56496658	56496795	56496686	56496767	DST	NM_015548	2	84	15	-	56496681	56496838
287393325	chr6	56496658	56496795	56496686	56496767	DST	NM_001723	1	24	15	-	56496681	56496838
287528613	chr6	56498866	56499022	56498891	56498996	DST	NM_015548	2	84	13	-	56498930	56499056
287528613	chr6	56498866	56499022	56498891	56498996	DST	NM_001723	1	24	13	-	56498930	56499056
286845967	chr6	56499570	56499743	56499597	56499717	DST	NM_015548	2	84	11	-	56499599	56499751
286845967	chr6	56499570	56499743	56499597	56499717	DST	NM_001723	1	24	11	-	56499599	56499751
286488097	chr6	56501370	56501498	56501393	56501473	DST	NM_015548	2	84	9	-	56501355	56501450
286488097	chr6	56501370	56501498	56501393	56501473	DST	NM_001723	1	24	9	-	56501355	56501450
287930540	chr6	56504285	56504411	56504310	56504385	DST	NM_015548	2	84	7	-	56504248	56504409
287930540	chr6	56504285	56504411	56504310	56504385	DST	NM_001723	1	24	7	-	56504248	56504409
287183045	chr6	56504726	56504855	56504754	56504835	DST	NM_015548	2	84	5	-	56504727	56504855
287183045	chr6	56504726	56504855	56504754	56504835	DST	NM_001723	1	24	5	-	56504727	56504855

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287001473	chr6	56505037	56505161	56505060	56505140	DST	NM_015548	2	84	4	-	56504941	56505403
287001473	chr6	56505037	56505161	56505060	56505140	DST	NM_001723	1	24	4	-	56504941	56505403
285067867	chr6	56506822	56506996	56506851	56506975	DST	NM_015548	2	84	3	-	56506745	56506899
285067867	chr6	56506822	56506996	56506851	56506975	DST	NM_001723	1	24	3	-	56506745	56506899
288442599	chr6	56507514	56507674	56507535	56507648	DST	NM_015548	2	84	1	-	56507420	56507694
288442599	chr6	56507514	56507674	56507535	56507648	DST	NM_001723	1	24	1	-	56507420	56507694
284140582	chr6	69348788	69348916	69348812	69348888	BAI3	NM_001704	1	32	3	+	69348553	69349324
284125592	chr6	69349084	69349250	69349109	69349229	BAI3	NM_001704	1	32	3	+	69348553	69349324
283306387	chr6	69646321	69646475	69646349	69646453	BAI3	NM_001704	1	32	5	+	69646411	69646572
281287631	chr6	69665821	69665992	69665843	69665970	BAI3	NM_001704	1	32	7	+	69665916	69666080
282583961	chr6	69684616	69684779	69684642	69684757	BAI3	NM_001704	1	32	9	+	69684655	69684756
284499726	chr6	69723849	69724022	69723873	69723994	BAI3	NM_001704	1	32	12	+	69723930	69723998
283864245	chr6	69759052	69759213	69759078	69759189	BAI3	NM_001704	1	32	15	+	69759163	69759238
283662325	chr6	69785781	69785943	69785809	69785917	BAI3	NM_001704	1	32	17	+	69785887	69785930
283710748	chr6	69944832	69944974	69944859	69944949	BAI3	NM_001704	1	32	19	+	69944924	69945027
282577439	chr6	69949076	69949222	69949102	69949191	BAI3	NM_001704	1	32	20	+	69949016	69949118
282681423	chr6	70040323	70040482	70040351	70040454	BAI3	NM_001704	1	32	23	+	70040398	70040464
283220045	chr6	70048823	70048968	70048844	70048940	BAI3	NM_001704	1	32	25	+	70048808	70048906
285683794	chr6	70064168	70064336	70064193	70064307	BAI3	NM_001704	1	32	27	+	70064125	70064220
284258261	chr6	70070867	70071039	70070892	70071012	BAI3	NM_001704	1	32	29	+	70070761	70071404
282157061	chr6	70071272	70071411	70071296	70071384	BAI3	NM_001704	1	32	29	+	70070761	70071404
281791083	chr6	70092692	70092853	70092718	70092827	BAI3	NM_001704	1	32	31	+	70092723	70092827
294782855	chr6	91226282	91226445	91226310	91226412	MAP3K7	NM_145333	4	15	15	-	91225353	91226400
294782855	chr6	91226282	91226445	91226310	91226412	MAP3K7	NM_145332	3	16	16	-	91225353	91226400
294782855	chr6	91226282	91226445	91226310	91226412	MAP3K7	NM_145331	2	17	17	-	91225353	91226400
294782855	chr6	91226282	91226445	91226310	91226412	MAP3K7	NM_003188	1	16	16	-	91225353	91226400
293923134	chr6	91228961	91229111	91228989	91229084	MAP3K7	NM_145333	4	15	14	-	91228977	91229038
293923134	chr6	91228961	91229111	91228989	91229084	MAP3K7	NM_145332	3	16	15	-	91228977	91229038
293923134	chr6	91228961	91229111	91228989	91229084	MAP3K7	NM_145331	2	17	15	-	91228977	91229038
293923134	chr6	91228961	91229111	91228989	91229084	MAP3K7	NM_003188	1	16	14	-	91228977	91229038
294185961	chr6	91254222	91254396	91254249	91254368	MAP3K7	NM_145332	3	16	12	-	91254271	91254351
294185961	chr6	91254222	91254396	91254249	91254368	MAP3K7	NM_145331	2	17	12	-	91254271	91254351
294199341	chr6	91257761	91257931	91257783	91257903	MAP3K7	NM_145333	4	15	10	-	91257766	91257896
294199341	chr6	91257761	91257931	91257783	91257903	MAP3K7	NM_145332	3	16	10	-	91257766	91257896
294199341	chr6	91257761	91257931	91257783	91257903	MAP3K7	NM_145331	2	17	10	-	91257766	91257896
294199341	chr6	91257761	91257931	91257783	91257903	MAP3K7	NM_003188	1	16	10	-	91257766	91257896
294983156	chr6	91263207	91263371	91263228	91263343	MAP3K7	NM_145333	4	15	7	-	91263177	91263305
294983156	chr6	91263207	91263371	91263228	91263343	MAP3K7	NM_145332	3	16	7	-	91263177	91263305
294983156	chr6	91263207	91263371	91263228	91263343	MAP3K7	NM_145331	2	17	7	-	91263177	91263305
294983156	chr6	91263207	91263371	91263228	91263343	MAP3K7	NM_003188	1	16	7	-	91263177	91263305
293829085	chr6	91269830	91270003	91269853	91269975	MAP3K7	NM_145333	4	15	5	-	91269795	91269933

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293829085	chr6	91269830	91270003	91269853	91269975	MAP3K7	NM_145332	3	16	5	-	91269795	91269933
293829085	chr6	91269830	91270003	91269853	91269975	MAP3K7	NM_145331	2	17	5	-	91269795	91269933
293829085	chr6	91269830	91270003	91269853	91269975	MAP3K7	NM_003188	1	16	5	-	91269795	91269933
293834090	chr6	91281362	91281518	91281391	91281495	MAP3K7	NM_145333	4	15	2	-	91281416	91281526
293834090	chr6	91281362	91281518	91281391	91281495	MAP3K7	NM_145332	3	16	2	-	91281416	91281526
293834090	chr6	91281362	91281518	91281391	91281495	MAP3K7	NM_145331	2	17	2	-	91281416	91281526
293834090	chr6	91281362	91281518	91281391	91281495	MAP3K7	NM_003188	1	16	2	-	91281416	91281526
272306952	chr6	93953036	93953203	93953058	93953178	EPHA7	NM_004440	1	17	17	-	93949740	93953258
271547975	chr6	93956480	93956652	93956504	93956634	EPHA7	NM_004440	1	17	15	-	93956510	93956703
270975979	chr6	93964460	93964631	93964482	93964609	EPHA7	NM_004440	1	17	14	-	93964365	93964514
270810451	chr6	93967084	93967215	93967112	93967190	EPHA7	NM_004440	1	17	12	-	93967180	93967241
270474946	chr6	93968935	93969107	93968956	93969079	EPHA7	NM_004440	1	17	10	-	93969072	93969197
271365023	chr6	93974370	93974494	93974398	93974461	EPHA7	NM_004440	1	17	8	-	93974312	93974420
271201209	chr6	93982091	93982244	93982111	93982220	EPHA7	NM_004440	1	17	6	-	93982016	93982140
270935536	chr6	94066716	94066857	94066743	94066836	EPHA7	NM_004440	1	17	5	-	94066435	94066770
270603600	chr6	94120228	94120397	94120250	94120371	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270660716	chr6	94120597	94120736	94120624	94120711	EPHA7	NM_004440	1	17	3	-	94120219	94120888
271206101	chr6	94124436	94124568	94124462	94124535	EPHA7	NM_004440	1	17	2	-	94124421	94124485
273426398	chr6	106536053	106536227	106536075	106536202	PRDM1	NM_001198	1	7	2	+	106536076	106536324
273829964	chr6	106543552	106543682	106543579	106543661	PRDM1	NM_001198	1	7	3	+	106543490	106543609
274614174	chr6	106547337	106547479	106547358	106547454	PRDM1	NM_182907	2	5	2	+	106547175	106547427
274614174	chr6	106547337	106547479	106547358	106547454	PRDM1	NM_001198	1	7	4	+	106547175	106547427
272812611	chr6	106552979	106553152	106552998	106553133	PRDM1	NM_182907	2	5	3	+	106552700	106553808
272812611	chr6	106552979	106553152	106552998	106553133	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273923662	chr6	106553412	106553568	106553433	106553547	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273923662	chr6	106553412	106553568	106553433	106553547	PRDM1	NM_001198	1	7	5	+	106552700	106553808
272738457	chr6	106554160	106554305	106554183	106554284	PRDM1	NM_182907	2	5	4	+	106554246	106554374
272738457	chr6	106554160	106554305	106554183	106554284	PRDM1	NM_001198	1	7	6	+	106554246	106554374
273008982	chr6	106554956	106555091	106554980	106555063	PRDM1	NM_182907	2	5	5	+	106554786	106557814
273008982	chr6	106554956	106555091	106554980	106555063	PRDM1	NM_001198	1	7	7	+	106554786	106557814
228907146	chr6	108882890	108883044	108882908	108883026	FOXO3	NM_201559	2	4	2	+	108882289	108883032
228907146	chr6	108882890	108883044	108882908	108883026	FOXO3	NM_001455	1	3	1	+	108882069	108883032
227529268	chr6	108985136	108985291	108985156	108985268	FOXO3	NM_001455	1	3	2	+	108984658	108986092
227529268	chr6	108985136	108985291	108985156	108985268	FOXO3	NM_201559	2	4	3	+	108984658	108986092
227554000	chr6	108985928	108986102	108985950	108986084	FOXO3	NM_001455	1	3	2	+	108984658	108986092
227554000	chr6	108985928	108986102	108985950	108986084	FOXO3	NM_201559	2	4	3	+	108984658	108986092
241725482	chr6	117622041	117622197	117622063	117622168	ROS1	NM_002944	1	43	42	-	117622137	117622300
238488115	chr6	117629988	117630156	117630009	117630129	ROS1	NM_002944	1	43	41	-	117629957	117630091
238644032	chr6	117632139	117632284	117632165	117632256	ROS1	NM_002944	1	43	39	-	117632183	117632280
239797121	chr6	117641001	117641171	117641026	117641147	ROS1	NM_002944	1	43	36	-	117641031	117641193
237794475	chr6	117645390	117645534	117645418	117645505	ROS1	NM_002944	1	43	34	-	117645495	117645578

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264121766	chr6	117647502	117647664	117647529	117647636	ROS1	NM_002944	1	43	33	-	117647387	117647577
240773269	chr6	117658349	117658483	117658376	117658459	ROS1	NM_002944	1	43	31	-	117658335	117658503
240307429	chr6	117662463	117662630	117662485	117662605	ROS1	NM_002944	1	43	29	-	117662563	117662795
260669812	chr6	117665182	117665329	117665210	117665306	ROS1	NM_002944	1	43	27	-	117665223	117665425
239588213	chr6	117674164	117674334	117674192	117674310	ROS1	NM_002944	1	43	26	-	117674153	117674332
238542166	chr6	117678001	117678157	117678023	117678128	ROS1	NM_002944	1	43	25	-	117677792	117678078
242338282	chr6	117681035	117681159	117681062	117681131	ROS1	NM_002944	1	43	23	-	117680972	117681174
262204318	chr6	117683782	117683955	117683803	117683930	ROS1	NM_002944	1	43	21	-	117683766	117684028
240975931	chr6	117686655	117686829	117686680	117686803	ROS1	NM_002944	1	43	19	-	117686744	117686904
262585531	chr6	117687276	117687410	117687303	117687385	ROS1	NM_002944	1	43	18	-	117687239	117687453
238457845	chr6	117704376	117704550	117704404	117704527	ROS1	NM_002944	1	43	16	-	117704480	117704671
261942226	chr6	117706940	117707112	117706963	117707088	ROS1	NM_002944	1	43	15	-	117706846	117707024
241784484	chr6	117709096	117709222	117709117	117709200	ROS1	NM_002944	1	43	13	-	117708943	117709197
260390550	chr6	117710740	117710911	117710768	117710886	ROS1	NM_002944	1	43	12	-	117710513	117711009
260537218	chr6	117715294	117715441	117715322	117715417	ROS1	NM_002944	1	43	10	-	117715325	117715509
237914369	chr6	117718035	117718205	117718058	117718182	ROS1	NM_002944	1	43	7	-	117718078	117718279
239081306	chr6	117725408	117725551	117725430	117725525	ROS1	NM_002944	1	43	5	-	117725443	117725591
241639949	chr6	117739558	117739698	117739586	117739670	ROS1	NM_002944	1	43	2	-	117739625	117739669
294208716	chr6	134491430	134491595	134491453	134491574	SGK1	NM_001143676	1	14	14	-	134490384	134491573
294208716	chr6	134491430	134491595	134491453	134491574	SGK1	NM_001143677	2	12	12	-	134490384	134491573
294208716	chr6	134491430	134491595	134491453	134491574	SGK1	NM_005627	4	12	12	-	134490384	134491573
294208716	chr6	134491430	134491595	134491453	134491574	SGK1	NM_001143678	3	12	12	-	134490384	134491573
294411379	chr6	134492723	134492894	134492745	134492870	SGK1	NM_001143676	1	14	11	-	134492775	134492870
294411379	chr6	134492723	134492894	134492745	134492870	SGK1	NM_001143677	2	12	9	-	134492775	134492870
294411379	chr6	134492723	134492894	134492745	134492870	SGK1	NM_005627	4	12	9	-	134492775	134492870
294411379	chr6	134492723	134492894	134492745	134492870	SGK1	NM_001143678	3	12	9	-	134492775	134492870
293947596	chr6	134494053	134494215	134494075	134494189	SGK1	NM_001143676	1	14	8	-	134494161	134494292
293947596	chr6	134494053	134494215	134494075	134494189	SGK1	NM_001143677	2	12	6	-	134494161	134494292
293947596	chr6	134494053	134494215	134494075	134494189	SGK1	NM_005627	4	12	6	-	134494161	134494292
293947596	chr6	134494053	134494215	134494075	134494189	SGK1	NM_001143678	3	12	6	-	134494161	134494292
294654436	chr6	134494607	134494760	134494629	134494732	SGK1	NM_001143676	1	14	6	-	134494600	134494704
294654436	chr6	134494607	134494760	134494629	134494732	SGK1	NM_001143677	2	12	4	-	134494600	134494704
294654436	chr6	134494607	134494760	134494629	134494732	SGK1	NM_005627	4	12	4	-	134494600	134494704
294654436	chr6	134494607	134494760	134494629	134494732	SGK1	NM_001143678	3	12	4	-	134494600	134494704
294789478	chr6	134496683	134496841	134496701	134496824	SGK1	NM_001143678	3	12	1	-	134496682	134497070
293897225	chr6	134528513	134528663	134528534	134528635	SGK1	NM_001143676	1	14	3	-	134528494	134528569
294499863	chr6	134638447	134638618	134638469	134638598	SGK1	NM_001143676	1	14	1	-	134638530	134639196
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001130173	2	16	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001130172	1	15	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001161657	4	14	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001161656	3	16	3	+	135508972	135509043

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_005375	8	15	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001161658	5	16	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001161660	7	14	3	+	135508972	135509043
235078160	chr6	135508999	135509173	135509025	135509147	MYB	NM_001161659	6	14	3	+	135508972	135509043
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001130173	2	16	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001130172	1	15	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001161657	4	14	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001161656	3	16	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_005375	8	15	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001161658	5	16	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001161660	7	14	5	+	135511265	135511485
238992936	chr6	135511251	135511405	135511279	135511378	MYB	NM_001161659	6	14	5	+	135511265	135511485
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001130173	2	16	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001130172	1	15	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001161657	4	14	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001161656	3	16	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_005375	8	15	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001161658	5	16	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001161660	7	14	6	+	135513462	135513696
235789742	chr6	135513587	135513752	135513611	135513728	MYB	NM_001161659	6	14	6	+	135513462	135513696
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001130173	2	16	9	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001130172	1	15	9	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001161656	3	16	9	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_005375	8	15	9	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001161660	7	14	8	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001161659	6	14	9	+	135516886	135517140
237135601	chr6	135516833	135516993	135516860	135516972	MYB	NM_001161658	5	16	9	+	135516886	135517092
239287296	chr6	135518209	135518382	135518231	135518360	MYB	NM_001130173	2	16	10	+	135518099	135518461
239287296	chr6	135518209	135518382	135518231	135518360	MYB	NM_001161656	3	16	10	+	135518099	135518461
239287296	chr6	135518209	135518382	135518231	135518360	MYB	NM_001161658	5	16	10	+	135518099	135518461
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001130173	2	16	12	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001130172	1	15	11	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001161657	4	14	10	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001161656	3	16	12	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_005375	8	15	11	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001161658	5	16	12	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001161660	7	14	10	+	135521223	135521337
236628343	chr6	135521158	135521294	135521180	135521269	MYB	NM_001161659	6	14	11	+	135521223	135521337
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001130173	2	16	14	+	135522777	135522887
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001130172	1	15	13	+	135522777	135522887
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001161657	4	14	12	+	135522777	135522887

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001161656	3	16	14	+	135522777	135522887
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_005375	8	15	13	+	135522777	135522887
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001161658	5	16	14	+	135522777	135522887
238012538	chr6	135522734	135522908	135522761	135522888	MYB	NM_001161660	7	14	12	+	135522777	135522887
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001130173	2	16	16	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001130172	1	15	15	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001161657	4	14	14	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001161656	3	16	16	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001161658	5	16	16	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001161660	7	14	14	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_001161659	6	14	14	+	135539002	135540311
235581910	chr6	135539010	135539165	135539031	135539138	MYB	NM_005375	8	15	15	+	135539002	135540310
264621182	chr6	138195933	138196107	138195961	138196080	TNFAIP3	NM_006290	1	9	3	+	138195982	138196172
264841781	chr6	138197087	138197260	138197109	138197237	TNFAIP3	NM_006290	1	9	5	+	138197133	138197303
241410487	chr6	138198331	138198496	138198354	138198470	TNFAIP3	NM_006290	1	9	6	+	138198213	138198393
263788163	chr6	138199831	138200002	138199854	138199979	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
263795758	chr6	138200260	138200411	138200281	138200390	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
240190110	chr6	138202147	138202318	138202170	138202300	TNFAIP3	NM_006290	1	9	9	+	138202172	138204449
272093240	chr6	152129064	152129191	152129085	152129171	ESR1	NM_000125	1	8	1	+	152128814	152129499
272093240	chr6	152129064	152129191	152129085	152129171	ESR1	NM_001122740	2	9	2	+	152128978	152129499
272093240	chr6	152129064	152129191	152129085	152129171	ESR1	NM_001122742	4	10	3	+	152128978	152129499
272093240	chr6	152129064	152129191	152129085	152129171	ESR1	NM_001122741	3	9	2	+	152128978	152129499
270291053	chr6	152129431	152129597	152129452	152129580	ESR1	NM_000125	1	8	1	+	152128814	152129499
270291053	chr6	152129431	152129597	152129452	152129580	ESR1	NM_001122740	2	9	2	+	152128978	152129499
270291053	chr6	152129431	152129597	152129452	152129580	ESR1	NM_001122742	4	10	3	+	152128978	152129499
270291053	chr6	152129431	152129597	152129452	152129580	ESR1	NM_001122741	3	9	2	+	152128978	152129499
270160140	chr6	152201671	152201841	152201695	152201816	ESR1	NM_000125	1	8	3	+	152201790	152201906
270160140	chr6	152201671	152201841	152201695	152201816	ESR1	NM_001122740	2	9	4	+	152201790	152201906
270160140	chr6	152201671	152201841	152201695	152201816	ESR1	NM_001122742	4	10	5	+	152201790	152201906
270160140	chr6	152201671	152201841	152201695	152201816	ESR1	NM_001122741	3	9	4	+	152201790	152201906
269919979	chr6	152265424	152265559	152265444	152265534	ESR1	NM_000125	1	8	4	+	152265308	152265643
269919979	chr6	152265424	152265559	152265444	152265534	ESR1	NM_001122740	2	9	5	+	152265308	152265643
269919979	chr6	152265424	152265559	152265444	152265534	ESR1	NM_001122742	4	10	6	+	152265308	152265643
269919979	chr6	152265424	152265559	152265444	152265534	ESR1	NM_001122741	3	9	5	+	152265308	152265643
272238289	chr6	152382039	152382178	152382065	152382156	ESR1	NM_000125	1	8	6	+	152382126	152382259
272238289	chr6	152382039	152382178	152382065	152382156	ESR1	NM_001122740	2	9	7	+	152382126	152382259
272238289	chr6	152382039	152382178	152382065	152382156	ESR1	NM_001122742	4	10	8	+	152382126	152382259
272238289	chr6	152382039	152382178	152382065	152382156	ESR1	NM_001122741	3	9	7	+	152382126	152382259
272070863	chr6	152419818	152419975	152419837	152419956	ESR1	NM_000125	1	8	8	+	152419867	152424408
272070863	chr6	152419818	152419975	152419837	152419956	ESR1	NM_001122740	2	9	9	+	152419867	152424408
272070863	chr6	152419818	152419975	152419837	152419956	ESR1	NM_001122742	4	10	10	+	152419867	152424408

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272070863	chr6	152419818	152419975	152419837	152419956	ESR1	NM_001122741	3	9	9	+	152419867	152424408
305017555	chr6	152443642	152443814	152443664	152443794	SYNE1	NM_033071	1	146	146	-	152442819	152443811
305017555	chr6	152443642	152443814	152443664	152443794	SYNE1	NM_182961	2	146	146	-	152442819	152443811
302848298	chr6	152454294	152454461	152454318	152454433	SYNE1	NM_033071	1	146	143	-	152454411	152454623
302848298	chr6	152454294	152454461	152454318	152454433	SYNE1	NM_182961	2	146	143	-	152454411	152454623
301223483	chr6	152456294	152456447	152456322	152456421	SYNE1	NM_033071	1	146	142	-	152456239	152456367
301223483	chr6	152456294	152456447	152456322	152456421	SYNE1	NM_182961	2	146	142	-	152456239	152456367
299283776	chr6	152460972	152461132	152460995	152461111	SYNE1	NM_033071	1	146	140	-	152461085	152461296
299283776	chr6	152460972	152461132	152460995	152461111	SYNE1	NM_182961	2	146	140	-	152461085	152461296
300128035	chr6	152464681	152464841	152464702	152464816	SYNE1	NM_033071	1	146	138	-	152464758	152464900
300128035	chr6	152464681	152464841	152464702	152464816	SYNE1	NM_182961	2	146	138	-	152464758	152464900
302561541	chr6	152469271	152469424	152469292	152469404	SYNE1	NM_033071	1	146	136	-	152469180	152469513
302561541	chr6	152469271	152469424	152469292	152469404	SYNE1	NM_182961	2	146	137	-	152469180	152469513
300977858	chr6	152472613	152472778	152472638	152472757	SYNE1	NM_033071	1	146	134	-	152472688	152472825
300977858	chr6	152472613	152472778	152472638	152472757	SYNE1	NM_182961	2	146	135	-	152472688	152472825
302521900	chr6	152475961	152476129	152475982	152476104	SYNE1	NM_033071	1	146	132	-	152476027	152476177
302521900	chr6	152475961	152476129	152475982	152476104	SYNE1	NM_182961	2	146	133	-	152476027	152476177
302541298	chr6	152485242	152485371	152485264	152485351	SYNE1	NM_033071	1	146	130	-	152485298	152485460
302541298	chr6	152485242	152485371	152485264	152485351	SYNE1	NM_182961	2	146	131	-	152485298	152485460
299708733	chr6	152501187	152501360	152501211	152501336	SYNE1	NM_033071	1	146	128	-	152501271	152501429
299708733	chr6	152501187	152501360	152501211	152501336	SYNE1	NM_182961	2	146	129	-	152501271	152501429
302365729	chr6	152522881	152523050	152522903	152523025	SYNE1	NM_033071	1	146	126	-	152522959	152523084
302365729	chr6	152522881	152523050	152522903	152523025	SYNE1	NM_182961	2	146	127	-	152522959	152523084
301955516	chr6	152527421	152527559	152527442	152527533	SYNE1	NM_033071	1	146	125	-	152527303	152527497
301955516	chr6	152527421	152527559	152527442	152527533	SYNE1	NM_182961	2	146	126	-	152527303	152527497
301767193	chr6	152532505	152532670	152532525	152532647	SYNE1	NM_033071	1	146	123	-	152532629	152532723
301767193	chr6	152532505	152532670	152532525	152532647	SYNE1	NM_182961	2	146	124	-	152532629	152532723
303068272	chr6	152536009	152536177	152536032	152536155	SYNE1	NM_033071	1	146	121	-	152536041	152536195
303068272	chr6	152536009	152536177	152536032	152536155	SYNE1	NM_182961	2	146	122	-	152536041	152536195
303163413	chr6	152540050	152540223	152540076	152540195	SYNE1	NM_033071	1	146	119	-	152540138	152540320
303163413	chr6	152540050	152540223	152540076	152540195	SYNE1	NM_182961	2	146	120	-	152540138	152540320
299936193	chr6	152542514	152542670	152542546	152542644	SYNE1	NM_033071	1	146	117	-	152542561	152542694
299936193	chr6	152542514	152542670	152542546	152542644	SYNE1	NM_182961	2	146	118	-	152542561	152542694
305435223	chr6	152545737	152545909	152545758	152545881	SYNE1	NM_033071	1	146	116	-	152545629	152545799
305435223	chr6	152545737	152545909	152545758	152545881	SYNE1	NM_182961	2	146	117	-	152545629	152545799
303970879	chr6	152551680	152551850	152551705	152551827	SYNE1	NM_033071	1	146	114	-	152551682	152551837
303970879	chr6	152551680	152551850	152551705	152551827	SYNE1	NM_182961	2	146	115	-	152551682	152551837
305913690	chr6	152553269	152553441	152553295	152553415	SYNE1	NM_033071	1	146	112	-	152553251	152553400
305913690	chr6	152553269	152553441	152553295	152553415	SYNE1	NM_182961	2	146	113	-	152553251	152553400
303822861	chr6	152555826	152555995	152555847	152555966	SYNE1	NM_033071	1	146	110	-	152555803	152555935
303822861	chr6	152555826	152555995	152555847	152555966	SYNE1	NM_182961	2	146	111	-	152555803	152555935

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
302084272	chr6	152557927	152558100	152557947	152558076	SYNE1	NM_033071	1	146	108	-	152557952	152558083
302084272	chr6	152557927	152558100	152557947	152558076	SYNE1	NM_182961	2	146	109	-	152557952	152558083
302574579	chr6	152563316	152563487	152563339	152563466	SYNE1	NM_033071	1	146	106	-	152563375	152563575
302574579	chr6	152563316	152563487	152563339	152563466	SYNE1	NM_182961	2	146	107	-	152563375	152563575
300412769	chr6	152570180	152570344	152570204	152570320	SYNE1	NM_033071	1	146	104	-	152570296	152570397
300412769	chr6	152570180	152570344	152570204	152570320	SYNE1	NM_182961	2	146	105	-	152570296	152570397
305978709	chr6	152576085	152576253	152576109	152576225	SYNE1	NM_033071	1	146	103	-	152576015	152576224
305978709	chr6	152576085	152576253	152576109	152576225	SYNE1	NM_182961	2	146	104	-	152576015	152576224
300642948	chr6	152577752	152577921	152577775	152577900	SYNE1	NM_033071	1	146	101	-	152577769	152577900
300642948	chr6	152577752	152577921	152577775	152577900	SYNE1	NM_182961	2	146	102	-	152577769	152577900
299295816	chr6	152589150	152589322	152589178	152589300	SYNE1	NM_033071	1	146	99	-	152589191	152589300
299295816	chr6	152589150	152589322	152589178	152589300	SYNE1	NM_182961	2	146	100	-	152589191	152589300
305418697	chr6	152599214	152599384	152599235	152599360	SYNE1	NM_033071	1	146	97	-	152599224	152599415
305418697	chr6	152599214	152599384	152599235	152599360	SYNE1	NM_182961	2	146	98	-	152599224	152599415
301709388	chr6	152605082	152605238	152605104	152605216	SYNE1	NM_033071	1	146	95	-	152605113	152605307
301709388	chr6	152605082	152605238	152605104	152605216	SYNE1	NM_182961	2	146	96	-	152605113	152605307
299961287	chr6	152615030	152615192	152615057	152615172	SYNE1	NM_033071	1	146	93	-	152615095	152615262
299961287	chr6	152615030	152615192	152615057	152615172	SYNE1	NM_182961	2	146	94	-	152615095	152615262
300100284	chr6	152622879	152623022	152622901	152623004	SYNE1	NM_033071	1	146	91	-	152623004	152623198
300100284	chr6	152622879	152623022	152622901	152623004	SYNE1	NM_182961	2	146	92	-	152623004	152623198
299349059	chr6	152629643	152629775	152629665	152629747	SYNE1	NM_182961	2	146	91	-	152629624	152629767
299349059	chr6	152629643	152629775	152629665	152629747	SYNE1	NM_033071	1	146	90	-	152629624	152629763
304300912	chr6	152631539	152631711	152631560	152631684	SYNE1	NM_033071	1	146	88	-	152631531	152631653
304300912	chr6	152631539	152631711	152631560	152631684	SYNE1	NM_182961	2	146	89	-	152631531	152631653
304569401	chr6	152637886	152638057	152637914	152638030	SYNE1	NM_033071	1	146	86	-	152637984	152638121
304569401	chr6	152637886	152638057	152637914	152638030	SYNE1	NM_182961	2	146	87	-	152637984	152638121
300375462	chr6	152639922	152640084	152639950	152640057	SYNE1	NM_033071	1	146	84	-	152639998	152640150
300375462	chr6	152639922	152640084	152639950	152640057	SYNE1	NM_182961	2	146	85	-	152639998	152640150
300568670	chr6	152642821	152642962	152642848	152642935	SYNE1	NM_033071	1	146	82	-	152642856	152643021
300568670	chr6	152642821	152642962	152642848	152642935	SYNE1	NM_182961	2	146	83	-	152642856	152643021
305547036	chr6	152644823	152644949	152644848	152644923	SYNE1	NM_033071	1	146	81	-	152644613	152644872
305547036	chr6	152644823	152644949	152644848	152644923	SYNE1	NM_182961	2	146	82	-	152644613	152644872
302977205	chr6	152647181	152647305	152647208	152647280	SYNE1	NM_033071	1	146	79	-	152647093	152647237
302977205	chr6	152647181	152647305	152647208	152647280	SYNE1	NM_182961	2	146	80	-	152647093	152647237
303837026	chr6	152647638	152647804	152647657	152647777	SYNE1	NM_033071	1	146	78	-	152647431	152647768
303837026	chr6	152647638	152647804	152647657	152647777	SYNE1	NM_182961	2	146	79	-	152647431	152647768
305453226	chr6	152651131	152651287	152651152	152651266	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305453226	chr6	152651131	152651287	152651152	152651266	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305443255	chr6	152651590	152651757	152651612	152651732	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305443255	chr6	152651590	152651757	152651612	152651732	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305414115	chr6	152651995	152652163	152652023	152652134	SYNE1	NM_033071	1	146	77	-	152650865	152653025

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305414115	chr6	152651995	152652163	152652023	152652134	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305425390	chr6	152652430	152652576	152652452	152652555	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305425390	chr6	152652430	152652576	152652452	152652555	SYNE1	NM_182961	2	146	78	-	152650865	152653025
302235143	chr6	152652851	152653023	152652877	152653000	SYNE1	NM_033071	1	146	77	-	152650865	152653025
302235143	chr6	152652851	152653023	152652877	152653000	SYNE1	NM_182961	2	146	78	-	152650865	152653025
304392555	chr6	152657864	152658006	152657889	152657982	SYNE1	NM_033071	1	146	75	-	152657976	152658152
304392555	chr6	152657864	152658006	152657889	152657982	SYNE1	NM_182961	2	146	76	-	152657976	152658152
300336630	chr6	152660375	152660528	152660399	152660502	SYNE1	NM_033071	1	146	74	-	152660376	152660501
300336630	chr6	152660375	152660528	152660399	152660502	SYNE1	NM_182961	2	146	75	-	152660376	152660501
300464263	chr6	152668252	152668387	152668277	152668364	SYNE1	NM_033071	1	146	72	-	152668194	152668370
300464263	chr6	152668252	152668387	152668277	152668364	SYNE1	NM_182961	2	146	73	-	152668194	152668370
300006074	chr6	152671808	152671966	152671830	152671939	SYNE1	NM_033071	1	146	71	-	152671753	152671905
300006074	chr6	152671808	152671966	152671830	152671939	SYNE1	NM_182961	2	146	71	-	152671753	152671905
305770045	chr6	152674348	152674504	152674369	152674475	SYNE1	NM_033071	1	146	69	-	152674398	152674568
305770045	chr6	152674348	152674504	152674369	152674475	SYNE1	NM_182961	2	146	69	-	152674398	152674568
302426491	chr6	152675753	152675926	152675781	152675900	SYNE1	NM_033071	1	146	67	-	152675860	152676111
302426491	chr6	152675753	152675926	152675781	152675900	SYNE1	NM_182961	2	146	67	-	152675794	152676111
302181318	chr6	152679482	152679628	152679509	152679600	SYNE1	NM_033071	1	146	66	-	152679508	152679672
302181318	chr6	152679482	152679628	152679509	152679600	SYNE1	NM_182961	2	146	66	-	152679508	152679672
302812515	chr6	152683217	152683389	152683243	152683364	SYNE1	NM_033071	1	146	64	-	152683305	152683458
302812515	chr6	152683217	152683389	152683243	152683364	SYNE1	NM_182961	2	146	64	-	152683305	152683458
303419578	chr6	152688280	152688433	152688303	152688411	SYNE1	NM_033071	1	146	62	-	152688353	152688517
303419578	chr6	152688280	152688433	152688303	152688411	SYNE1	NM_182961	2	146	62	-	152688353	152688517
300211626	chr6	152690503	152690667	152690525	152690645	SYNE1	NM_033071	1	146	60	-	152690606	152690749
300211626	chr6	152690503	152690667	152690525	152690645	SYNE1	NM_182961	2	146	60	-	152690606	152690749
300283861	chr6	152697462	152697608	152697490	152697582	SYNE1	NM_033071	1	146	58	-	152697516	152697693
300283861	chr6	152697462	152697608	152697490	152697582	SYNE1	NM_182961	2	146	58	-	152697516	152697693
302029871	chr6	152698006	152698177	152698030	152698150	SYNE1	NM_033071	1	146	57	-	152697911	152698047
302029871	chr6	152698006	152698177	152698030	152698150	SYNE1	NM_182961	2	146	57	-	152697911	152698047
304684577	chr6	152702404	152702530	152702424	152702503	SYNE1	NM_033071	1	146	56	-	152702141	152702497
304684577	chr6	152702404	152702530	152702424	152702503	SYNE1	NM_182961	2	146	56	-	152702141	152702497
304602434	chr6	152708226	152708368	152708254	152708347	SYNE1	NM_033071	1	146	54	-	152708207	152708516
304602434	chr6	152708226	152708368	152708254	152708347	SYNE1	NM_182961	2	146	54	-	152708207	152708516
305967513	chr6	152711446	152711620	152711468	152711592	SYNE1	NM_033071	1	146	53	-	152711415	152711587
305967513	chr6	152711446	152711620	152711468	152711592	SYNE1	NM_182961	2	146	53	-	152711415	152711587
300507683	chr6	152712648	152712818	152712669	152712796	SYNE1	NM_033071	1	146	52	-	152712412	152712703
300507683	chr6	152712648	152712818	152712669	152712796	SYNE1	NM_182961	2	146	52	-	152712412	152712703
305269294	chr6	152717939	152718087	152717964	152718064	SYNE1	NM_033071	1	146	50	-	152717910	152718115
305269294	chr6	152717939	152718087	152717964	152718064	SYNE1	NM_182961	2	146	50	-	152717910	152718115
303392503	chr6	152720727	152720900	152720747	152720878	SYNE1	NM_033071	1	146	48	-	152720751	152720958
303392503	chr6	152720727	152720900	152720747	152720878	SYNE1	NM_182961	2	146	48	-	152720751	152720958

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305787949	chr6	152722380	152722552	152722403	152722524	SYNE1	NM_033071	1	146	47	-	152722273	152722476
305787949	chr6	152722380	152722552	152722403	152722524	SYNE1	NM_182961	2	146	47	-	152722273	152722476
304604328	chr6	152730117	152730244	152730143	152730221	SYNE1	NM_033071	1	146	44	-	152730203	152730361
304604328	chr6	152730117	152730244	152730143	152730221	SYNE1	NM_182961	2	146	44	-	152730203	152730361
305937676	chr6	152730718	152730842	152730746	152730821	SYNE1	NM_033071	1	146	43	-	152730694	152730844
305937676	chr6	152730718	152730842	152730746	152730821	SYNE1	NM_182961	2	146	43	-	152730694	152730844
302648489	chr6	152734606	152734771	152734630	152734744	SYNE1	NM_033071	1	146	42	-	152734487	152734666
302648489	chr6	152734606	152734771	152734630	152734744	SYNE1	NM_182961	2	146	42	-	152734487	152734666
305300367	chr6	152737801	152737961	152737822	152737940	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305300367	chr6	152737801	152737961	152737822	152737940	SYNE1	NM_182961	2	146	41	-	152737522	152738150
304005966	chr6	152740806	152740948	152740830	152740925	SYNE1	NM_033071	1	146	40	-	152740704	152740857
304005966	chr6	152740806	152740948	152740830	152740925	SYNE1	NM_182961	2	146	40	-	152740704	152740857
305030597	chr6	152748802	152748976	152748825	152748953	SYNE1	NM_033071	1	146	38	-	152748828	152748951
305030597	chr6	152748802	152748976	152748825	152748953	SYNE1	NM_182961	2	146	38	-	152748828	152748951
304723723	chr6	152751554	152751691	152751580	152751669	SYNE1	NM_033071	1	146	35	-	152751617	152751844
304723723	chr6	152751554	152751691	152751580	152751669	SYNE1	NM_182961	2	146	35	-	152751617	152751844
304001624	chr6	152754920	152755049	152754942	152755021	SYNE1	NM_033071	1	146	34	-	152754930	152755080
304001624	chr6	152754920	152755049	152754942	152755021	SYNE1	NM_182961	2	146	34	-	152754930	152755080
303769400	chr6	152762233	152762403	152762259	152762375	SYNE1	NM_033071	1	146	32	-	152762265	152762405
303769400	chr6	152762233	152762403	152762259	152762375	SYNE1	NM_182961	2	146	32	-	152762265	152762405
302709889	chr6	152765450	152765611	152765471	152765583	SYNE1	NM_033071	1	146	30	-	152765546	152765713
302709889	chr6	152765450	152765611	152765471	152765583	SYNE1	NM_182961	2	146	30	-	152765546	152765713
305651691	chr6	152770637	152770780	152770664	152770752	SYNE1	NM_033071	1	146	28	-	152770668	152770776
305651691	chr6	152770637	152770780	152770664	152770752	SYNE1	NM_182961	2	146	28	-	152770668	152770776
300662235	chr6	152771884	152772011	152771905	152771984	SYNE1	NM_033071	1	146	27	-	152771760	152771968
300662235	chr6	152771884	152772011	152771905	152771984	SYNE1	NM_182961	2	146	27	-	152771760	152771968
300535651	chr6	152774707	152774878	152774729	152774857	SYNE1	NM_033071	1	146	25	-	152774721	152774855
300535651	chr6	152774707	152774878	152774729	152774857	SYNE1	NM_182961	2	146	25	-	152774721	152774855
302580064	chr6	152777084	152777242	152777106	152777213	SYNE1	NM_033071	1	146	23	-	152777021	152777179
302580064	chr6	152777084	152777242	152777106	152777213	SYNE1	NM_182961	2	146	23	-	152777021	152777179
300461320	chr6	152782688	152782853	152782710	152782824	SYNE1	NM_033071	1	146	21	-	152782732	152782875
300461320	chr6	152782688	152782853	152782710	152782824	SYNE1	NM_182961	2	146	21	-	152782732	152782875
304013849	chr6	152784379	152784553	152784402	152784529	SYNE1	NM_033071	1	146	19	-	152784488	152784652
304013849	chr6	152784379	152784553	152784402	152784529	SYNE1	NM_182961	2	146	19	-	152784488	152784652
299681189	chr6	152786445	152786593	152786465	152786565	SYNE1	NM_033071	1	146	18	-	152786393	152786595
299681189	chr6	152786445	152786593	152786465	152786565	SYNE1	NM_182961	2	146	18	-	152786393	152786595
302914469	chr6	152792796	152792970	152792818	152792943	SYNE1	NM_033071	1	146	16	-	152792732	152792900
302914469	chr6	152792796	152792970	152792818	152792943	SYNE1	NM_182961	2	146	16	-	152792732	152792900
302702495	chr6	152804238	152804385	152804262	152804360	SYNE1	NM_033071	1	146	14	-	152804220	152804384
302702495	chr6	152804238	152804385	152804262	152804360	SYNE1	NM_182961	2	146	14	-	152804220	152804384
305053853	chr6	152819898	152820023	152819920	152819997	SYNE1	NM_033071	1	146	11	-	152819877	152819927

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305053853	chr6	152819898	152820023	152819920	152819997	SYNE1	NM_182961	2	146	11	-	152819877	152819927
305430502	chr6	152826349	152826480	152826370	152826455	SYNE1	NM_033071	1	146	9	-	152826336	152826532
305430502	chr6	152826349	152826480	152826370	152826455	SYNE1	NM_182961	2	146	9	-	152826336	152826532
305527336	chr6	152832086	152832228	152832107	152832201	SYNE1	NM_033071	1	146	7	-	152832146	152832238
305527336	chr6	152832086	152832228	152832107	152832201	SYNE1	NM_182961	2	146	7	-	152832146	152832238
302833975	chr6	152841535	152841690	152841561	152841665	SYNE1	NM_033071	1	146	5	-	152841594	152841677
302833975	chr6	152841535	152841690	152841561	152841665	SYNE1	NM_182961	2	146	6	-	152841594	152841677
305919165	chr6	152861081	152861254	152861105	152861229	SYNE1	NM_033071	1	146	3	-	152861095	152861156
305919165	chr6	152861081	152861254	152861105	152861229	SYNE1	NM_182961	2	146	4	-	152861095	152861156
270426962	chr6	160430013	160430187	160430038	160430167	IGF2R	NM_000876	1	48	3	+	160430042	160430166
271938809	chr6	160445597	160445760	160445618	160445738	IGF2R	NM_000876	1	48	5	+	160445604	160445736
269745170	chr6	160453520	160453694	160453547	160453667	IGF2R	NM_000876	1	48	8	+	160453583	160453745
269552602	chr6	160455404	160455575	160455429	160455555	IGF2R	NM_000876	1	48	10	+	160455451	160455554
270356841	chr6	160464183	160464356	160464205	160464332	IGF2R	NM_000876	1	48	12	+	160464180	160464320
272011244	chr6	160466789	160466961	160466811	160466936	IGF2R	NM_000876	1	48	14	+	160466777	160466914
272216685	chr6	160468152	160468310	160468175	160468289	IGF2R	NM_000876	1	48	16	+	160468191	160468368
270120342	chr6	160469298	160469472	160469324	160469451	IGF2R	NM_000876	1	48	18	+	160469407	160469575
270161129	chr6	160477396	160477566	160477425	160477544	IGF2R	NM_000876	1	48	20	+	160477456	160477557
271581805	chr6	160480025	160480175	160480047	160480154	IGF2R	NM_000876	1	48	22	+	160479938	160480130
271136222	chr6	160482551	160482717	160482572	160482693	IGF2R	NM_000876	1	48	24	+	160482535	160482678
270819854	chr6	160484417	160484578	160484440	160484557	IGF2R	NM_000876	1	48	27	+	160484447	160484662
271638675	chr6	160485493	160485630	160485519	160485606	IGF2R	NM_000876	1	48	28	+	160485433	160485563
271165808	chr6	160490857	160491009	160490878	160490983	IGF2R	NM_000876	1	48	31	+	160490900	160491090
269627245	chr6	160493718	160493880	160493737	160493857	IGF2R	NM_000876	1	48	33	+	160493797	160493916
270573664	chr6	160494416	160494582	160494438	160494562	IGF2R	NM_000876	1	48	34	+	160494245	160494501
270884091	chr6	160496952	160497089	160496973	160497067	IGF2R	NM_000876	1	48	36	+	160496879	160497028
270092252	chr6	160500666	160500796	160500688	160500772	IGF2R	NM_000876	1	48	38	+	160500612	160500819
272005881	chr6	160504968	160505141	160504988	160505119	IGF2R	NM_000876	1	48	40	+	160504982	160505216
271125328	chr6	160509000	160509130	160509021	160509108	IGF2R	NM_000876	1	48	42	+	160509065	160509179
269842026	chr6	160510858	160511029	160510879	160511006	IGF2R	NM_000876	1	48	44	+	160510948	160511135
272052089	chr6	160523446	160523613	160523467	160523593	IGF2R	NM_000876	1	48	46	+	160523551	160523703
272088823	chr6	160525799	160525973	160525822	160525953	IGF2R	NM_000876	1	48	48	+	160525706	160527583
240238809	chr6	166826327	166826490	166826349	166826470	RPS6KA2	NM_001006932	1	22	22	-	166822854	166826375
240238809	chr6	166826327	166826490	166826349	166826470	RPS6KA2	NM_021135	2	21	21	-	166822854	166826375
238836233	chr6	166831772	166831943	166831791	166831920	RPS6KA2	NM_001006932	1	22	20	-	166831713	166831830
238836233	chr6	166831772	166831943	166831791	166831920	RPS6KA2	NM_021135	2	21	19	-	166831713	166831830
237981490	chr6	166836879	166837021	166836899	166837001	RPS6KA2	NM_001006932	1	22	18	-	166836744	166836905
237981490	chr6	166836879	166837021	166836899	166837001	RPS6KA2	NM_021135	2	21	17	-	166836744	166836905
242031500	chr6	166845831	166846000	166845857	166845978	RPS6KA2	NM_001006932	1	22	16	-	166845889	166845978
242031500	chr6	166845831	166846000	166845857	166845978	RPS6KA2	NM_021135	2	21	15	-	166845889	166845978
238038895	chr6	166864578	166864750	166864600	166864729	RPS6KA2	NM_001006932	1	22	14	-	166864591	166864721

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238038895	chr6	166864578	166864750	166864600	166864729	RPS6KA2	NM_021135	2	21	13	-	166864591	166864721
261797677	chr6	166902311	166902474	166902331	166902451	RPS6KA2	NM_001006932	1	22	11	-	166902321	166902409
261797677	chr6	166902311	166902474	166902331	166902451	RPS6KA2	NM_021135	2	21	10	-	166902321	166902409
237823848	chr6	166914279	166914442	166914301	166914416	RPS6KA2	NM_001006932	1	22	8	-	166914375	166914412
237823848	chr6	166914279	166914442	166914301	166914416	RPS6KA2	NM_021135	2	21	7	-	166914375	166914412
239993600	chr6	166923721	166923881	166923741	166923854	RPS6KA2	NM_001006932	1	22	5	-	166923765	166923845
239993600	chr6	166923721	166923881	166923741	166923854	RPS6KA2	NM_021135	2	21	4	-	166923765	166923845
237899918	chr6	167040299	167040451	167040318	167040433	RPS6KA2	NM_021135	2	21	1	-	167040409	167040726
225218200	chr7	2946338	2946494	2946355	2946477	CARD11	NM_032415	1	25	25	-	2945710	2946476
225189402	chr7	2951871	2952041	2951893	2952017	CARD11	NM_032415	1	25	23	-	2951806	2951930
222686000	chr7	2956836	2956963	2956859	2956944	CARD11	NM_032415	1	25	20	-	2956924	2957019
224134424	chr7	2959084	2959220	2959105	2959200	CARD11	NM_032415	1	25	18	-	2959006	2959246
223242481	chr7	2962795	2962958	2962812	2962940	CARD11	NM_032415	1	25	16	-	2962766	2962967
222856780	chr7	2966321	2966468	2966340	2966447	CARD11	NM_032415	1	25	14	-	2966373	2966425
224608239	chr7	2972111	2972268	2972134	2972239	CARD11	NM_032415	1	25	11	-	2972169	2972220
225191933	chr7	2976672	2976842	2976692	2976821	CARD11	NM_032415	1	25	9	-	2976671	2976868
222461291	chr7	2978342	2978498	2978364	2978477	CARD11	NM_032415	1	25	7	-	2978313	2978465
222273966	chr7	2983774	2983946	2983795	2983923	CARD11	NM_032415	1	25	5	-	2983846	2984171
222335589	chr7	2985408	2985532	2985431	2985503	CARD11	NM_032415	1	25	4	-	2985453	2985590
222216727	chr7	2998113	2998270	2998135	2998249	CARD11	NM_032415	1	25	2	-	2998134	2998265
240542777	chr7	6026587	6026735	6026609	6026708	PMS2	NM_000535	1	15	11	-	6026390	6027251
240542777	chr7	6026587	6026735	6026609	6026708	PMS2	NR_003085	2	15	11	-	6026390	6027251
240518057	chr7	6026999	6027160	6027020	6027136	PMS2	NM_000535	1	15	11	-	6026390	6027251
240518057	chr7	6026999	6027160	6027020	6027136	PMS2	NR_003085	2	15	11	-	6026390	6027251
236859715	chr7	6031569	6031739	6031596	6031712	PMS2	NM_000535	1	15	9	-	6031604	6031688
236859715	chr7	6031569	6031739	6031596	6031712	PMS2	NR_003085	2	15	9	-	6031604	6031688
235345048	chr7	6037000	6037158	6037022	6037131	PMS2	NM_000535	1	15	7	-	6036957	6037054
235345048	chr7	6037000	6037158	6037022	6037131	PMS2	NR_003085	2	15	7	-	6036957	6037054
235531311	chr7	6042107	6042235	6042128	6042214	PMS2	NM_000535	1	15	5	-	6042084	6042267
235531311	chr7	6042107	6042235	6042128	6042214	PMS2	NR_003085	2	15	5	-	6042084	6042267
237924233	chr7	6043621	6043747	6043646	6043724	PMS2	NM_000535	1	15	3	-	6043603	6043689
237924233	chr7	6043621	6043747	6043646	6043724	PMS2	NR_003085	2	15	3	-	6043603	6043689
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163151	5	9	8	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163150	4	10	9	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163149	3	12	11	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163148	2	13	12	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163147	1	12	11	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_004956	7	14	13	-	13940363	13940464
229159917	chr7	13940266	13940440	13940290	13940412	ETV1	NM_001163152	6	9	8	-	13940363	13940464
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163151	5	9	6	-	13949257	13949325
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163150	4	10	7	-	13949257	13949325

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163149	3	12	9	-	13949257	13949325
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163148	2	13	10	-	13949257	13949325
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163147	1	12	9	-	13949257	13949325
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_004956	7	14	11	-	13949257	13949325
230451474	chr7	13949181	13949348	13949205	13949322	ETV1	NM_001163152	6	9	6	-	13949257	13949325
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163151	5	9	4	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163150	4	10	5	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163149	3	12	7	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163148	2	13	8	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163147	1	12	8	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_004956	7	14	9	-	13971127	13971374
230191972	chr7	13971315	13971459	13971334	13971431	ETV1	NM_001163152	6	9	4	-	13971127	13971374
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163151	5	9	2	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163150	4	10	3	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163149	3	12	5	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163148	2	13	6	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163147	1	12	6	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_004956	7	14	7	-	13978742	13978871
231661458	chr7	13978797	13978937	13978817	13978906	ETV1	NM_001163152	6	9	3	-	13978742	13978871
229051666	chr7	14025725	14025886	14025752	14025861	ETV1	NM_001163151	5	9	1	-	14025741	14026139
229051666	chr7	14025725	14025886	14025752	14025861	ETV1	NM_001163150	4	10	1	-	14025741	14026139
229051666	chr7	14025725	14025886	14025752	14025861	ETV1	NM_001163152	6	9	1	-	14025741	14026139
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_006060	13	8	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220771	7	5	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220770	6	6	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220774	10	5	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220773	9	5	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220772	8	3	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220769	5	6	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220768	4	6	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220767	3	7	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220766	2	7	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220765	1	7	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220776	12	4	2	+	50358644	50358697
228760046	chr7	50358565	50358724	50358592	50358698	IKZF1	NM_001220775	11	4	2	+	50358644	50358697
227712152	chr7	50444389	50444513	50444411	50444491	IKZF1	NM_006060	13	8	4	+	50444231	50444491
227712152	chr7	50444389	50444513	50444411	50444491	IKZF1	NM_001220771	7	5	4	+	50444231	50444491
227712152	chr7	50444389	50444513	50444411	50444491	IKZF1	NM_001220768	4	6	4	+	50444231	50444491
227712152	chr7	50444389	50444513	50444411	50444491	IKZF1	NM_001220765	1	7	4	+	50444231	50444491
227469012	chr7	50455087	50455260	50455110	50455240	IKZF1	NM_006060	13	8	6	+	50455043	50455168
227469012	chr7	50455087	50455260	50455110	50455240	IKZF1	NM_001220774	10	5	3	+	50455043	50455168

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227469012	chr7	50455087	50455260	50455110	50455240	IKZF1	NM_001220773	9	5	3	+	50455043	50455168
227469012	chr7	50455087	50455260	50455110	50455240	IKZF1	NM_001220767	3	7	5	+	50455043	50455168
227469012	chr7	50455087	50455260	50455110	50455240	IKZF1	NM_001220766	2	7	5	+	50455043	50455168
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_006060	13	8	8	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
228275541	chr7	50467674	50467823	50467697	50467803	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_006060	13	8	8	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
230036634	chr7	50468088	50468262	50468107	50468244	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
229919273	chr7	55210020	55210190	55210046	55210162	EGFR	NM_005228	1	28	2	+	55209979	55210130
229919273	chr7	55210020	55210190	55210046	55210162	EGFR	NM_201284	4	16	2	+	55209979	55210130
229919273	chr7	55210020	55210190	55210046	55210162	EGFR	NM_201283	3	10	2	+	55209979	55210130
229919273	chr7	55210020	55210190	55210046	55210162	EGFR	NM_201282	2	16	2	+	55209979	55210130
227816834	chr7	55214357	55214491	55214377	55214470	EGFR	NM_005228	1	28	4	+	55214299	55214433
227816834	chr7	55214357	55214491	55214377	55214470	EGFR	NM_201284	4	16	4	+	55214299	55214433
227816834	chr7	55214357	55214491	55214377	55214470	EGFR	NM_201283	3	10	4	+	55214299	55214433
227816834	chr7	55214357	55214491	55214377	55214470	EGFR	NM_201282	2	16	4	+	55214299	55214433
228030652	chr7	55221648	55221793	55221669	55221772	EGFR	NM_005228	1	28	7	+	55221704	55221845
228030652	chr7	55221648	55221793	55221669	55221772	EGFR	NM_201284	4	16	7	+	55221704	55221845
228030652	chr7	55221648	55221793	55221669	55221772	EGFR	NM_201283	3	10	7	+	55221704	55221845
228030652	chr7	55221648	55221793	55221669	55221772	EGFR	NM_201282	2	16	7	+	55221704	55221845

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230679876	chr7	55224155	55224281	55224176	55224252	EGFR	NM_005228	1	28	9	+	55224226	55224352
230679876	chr7	55224155	55224281	55224176	55224252	EGFR	NM_201284	4	16	9	+	55224226	55224352
230679876	chr7	55224155	55224281	55224176	55224252	EGFR	NM_201283	3	10	9	+	55224226	55224352
230679876	chr7	55224155	55224281	55224176	55224252	EGFR	NM_201282	2	16	9	+	55224226	55224352
229747025	chr7	55225305	55225469	55225329	55225447	EGFR	NM_005228	1	28	11	+	55225356	55225446
229747025	chr7	55225305	55225469	55225329	55225447	EGFR	NM_201284	4	16	11	+	55225356	55225446
229747025	chr7	55225305	55225469	55225329	55225447	EGFR	NM_201282	2	16	11	+	55225356	55225446
228741519	chr7	55229161	55229312	55229181	55229292	EGFR	NM_005228	1	28	13	+	55229192	55229324
228741519	chr7	55229161	55229312	55229181	55229292	EGFR	NM_201284	4	16	13	+	55229192	55229324
228741519	chr7	55229161	55229312	55229181	55229292	EGFR	NM_201282	2	16	13	+	55229192	55229324
228636601	chr7	55233038	55233162	55233060	55233135	EGFR	NM_005228	1	28	15	+	55232973	55233130
228636601	chr7	55233038	55233162	55233060	55233135	EGFR	NM_201284	4	16	15	+	55232973	55233130
228636601	chr7	55233038	55233162	55233060	55233135	EGFR	NM_201282	2	16	15	+	55232973	55233130
230635054	chr7	55238113	55238260	55238137	55238239	EGFR	NM_201284	4	16	16	+	55238000	55238738
230738160	chr7	55241576	55241707	55241597	55241679	EGFR	NM_005228	1	28	18	+	55241614	55241736
232984355	chr7	55249062	55249226	55249081	55249204	EGFR	NM_005228	1	28	20	+	55248986	55249171
228941652	chr7	55266331	55266464	55266359	55266442	EGFR	NM_005228	1	28	23	+	55266410	55266556
230495367	chr7	55268919	55269092	55268940	55269067	EGFR	NM_005228	1	28	25	+	55268881	55269048
231212482	chr7	55272981	55273134	55273001	55273112	EGFR	NM_005228	1	28	28	+	55272949	55275031
241382681	chr7	66453391	66453532	66453420	66453507	SBDS	NM_016038	1	5	5	-	66452690	66453486
261498793	chr7	66458213	66458363	66458237	66458341	SBDS	NM_016038	1	5	3	-	66458204	66458404
260590774	chr7	66460289	66460450	66460308	66460433	SBDS	NM_016038	1	5	1	-	66460277	66460588
224095560	chr7	91603100	91603264	91603125	91603236	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224095560	chr7	91603100	91603264	91603125	91603236	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224460601	chr7	91621366	91621517	91621394	91621490	AKAP9	NM_005751	1	50	4	+	91621472	91621525
224460601	chr7	91621366	91621517	91621394	91621490	AKAP9	NM_147185	2	50	4	+	91621472	91621525
223420452	chr7	91623827	91623986	91623858	91623960	AKAP9	NM_005751	1	50	6	+	91623935	91624090
223420452	chr7	91623827	91623986	91623858	91623960	AKAP9	NM_147185	2	50	6	+	91623935	91624090
224414266	chr7	91624979	91625153	91625002	91625126	AKAP9	NM_005751	1	50	7	+	91624917	91625114
224414266	chr7	91624979	91625153	91625002	91625126	AKAP9	NM_147185	2	50	7	+	91624917	91625114
224468057	chr7	91630636	91630783	91630664	91630756	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224468057	chr7	91630636	91630783	91630664	91630756	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224487753	chr7	91630963	91631136	91630991	91631108	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224487753	chr7	91630963	91631136	91630991	91631108	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224470869	chr7	91631439	91631604	91631466	91631576	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224470869	chr7	91631439	91631604	91631466	91631576	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224486223	chr7	91632006	91632146	91632030	91632118	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224486223	chr7	91632006	91632146	91632030	91632118	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222663987	chr7	91632319	91632492	91632347	91632465	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222663987	chr7	91632319	91632492	91632347	91632465	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222266855	chr7	91641807	91641958	91641836	91641930	AKAP9	NM_005751	1	50	9	+	91641743	91641956

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222266855	chr7	91641807	91641958	91641836	91641930	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222535245	chr7	91646271	91646432	91646299	91646407	AKAP9	NM_005751	1	50	12	+	91646331	91646416
222535245	chr7	91646271	91646432	91646299	91646407	AKAP9	NM_147185	2	50	12	+	91646331	91646416
223252821	chr7	91652210	91652335	91652234	91652313	AKAP9	NM_005751	1	50	14	+	91652128	91652323
223252821	chr7	91652210	91652335	91652234	91652313	AKAP9	NM_147185	2	50	14	+	91652128	91652323
222540515	chr7	91667619	91667793	91667637	91667766	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222540515	chr7	91667619	91667793	91667637	91667766	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222555831	chr7	91668011	91668179	91668034	91668151	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222555831	chr7	91668011	91668179	91668034	91668151	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222166455	chr7	91671254	91671427	91671272	91671405	AKAP9	NM_005751	1	50	19	+	91671360	91671500
222166455	chr7	91671254	91671427	91671272	91671405	AKAP9	NM_147185	2	50	19	+	91671360	91671500
223883139	chr7	91674319	91674460	91674342	91674435	AKAP9	NM_005751	1	50	21	+	91674322	91674527
223883139	chr7	91674319	91674460	91674342	91674435	AKAP9	NM_147185	2	50	21	+	91674322	91674527
222681021	chr7	91682152	91682278	91682176	91682254	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222681021	chr7	91682152	91682278	91682176	91682254	AKAP9	NM_147185	2	50	22	+	91682040	91682272
224116042	chr7	91691578	91691712	91691606	91691686	AKAP9	NM_005751	1	50	24	+	91691588	91691800
224116042	chr7	91691578	91691712	91691606	91691686	AKAP9	NM_147185	2	50	24	+	91691588	91691800
224494459	chr7	91694669	91694837	91694698	91694809	AKAP9	NM_005751	1	50	25	+	91694545	91694777
224494459	chr7	91694669	91694837	91694698	91694809	AKAP9	NM_147185	2	50	25	+	91694545	91694777
222451061	chr7	91699413	91699556	91699441	91699524	AKAP9	NM_005751	1	50	27	+	91699344	91699520
222451061	chr7	91699413	91699556	91699441	91699524	AKAP9	NM_147185	2	50	27	+	91699344	91699496
224425371	chr7	91707001	91707132	91707027	91707104	AKAP9	NM_005751	1	50	30	+	91707010	91707189
224425371	chr7	91707001	91707132	91707027	91707104	AKAP9	NM_147185	2	50	30	+	91707010	91707189
223491540	chr7	91708515	91708671	91708543	91708645	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223491540	chr7	91708515	91708671	91708543	91708645	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223510004	chr7	91708902	91709034	91708929	91709006	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223510004	chr7	91708902	91709034	91708929	91709006	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223524897	chr7	91709239	91709389	91709267	91709360	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223524897	chr7	91709239	91709389	91709267	91709360	AKAP9	NM_147185	2	50	31	+	91708393	91709466
224036656	chr7	91712393	91712564	91712418	91712541	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224036656	chr7	91712393	91712564	91712418	91712541	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224071437	chr7	91712816	91712957	91712841	91712934	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224071437	chr7	91712816	91712957	91712841	91712934	AKAP9	NM_147185	2	50	33	+	91712484	91712969
222164895	chr7	91713998	91714170	91714024	91714144	AKAP9	NM_005751	1	50	35	+	91714133	91714254
222164895	chr7	91713998	91714170	91714024	91714144	AKAP9	NM_147185	2	50	35	+	91714133	91714254
222608818	chr7	91715428	91715598	91715452	91715578	AKAP9	NM_005751	1	50	37	+	91715542	91715730
222608818	chr7	91715428	91715598	91715452	91715578	AKAP9	NM_147185	2	50	37	+	91715542	91715730
224709057	chr7	91718722	91718874	91718746	91718846	AKAP9	NM_005751	1	50	38	+	91718699	91718843
224709057	chr7	91718722	91718874	91718746	91718846	AKAP9	NM_147185	2	50	38	+	91718699	91718843
222474653	chr7	91724416	91724572	91724436	91724544	AKAP9	NM_005751	1	50	40	+	91724337	91724487
222474653	chr7	91724416	91724572	91724436	91724544	AKAP9	NM_147185	2	50	40	+	91724337	91724487

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224263135	chr7	91726300	91726449	91726323	91726427	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224263135	chr7	91726300	91726449	91726323	91726427	AKAP9	NM_147185	2	50	41	+	91726003	91726671
225147999	chr7	91726817	91726988	91726849	91726960	AKAP9	NM_005751	1	50	42	+	91726900	91727108
225147999	chr7	91726817	91726988	91726849	91726960	AKAP9	NM_147185	2	50	42	+	91726900	91727108
223648833	chr7	91728964	91729138	91728990	91729113	AKAP9	NM_005751	1	50	44	+	91729001	91729183
223648833	chr7	91728964	91729138	91728990	91729113	AKAP9	NM_147185	2	50	44	+	91729001	91729183
223656496	chr7	91731845	91731989	91731866	91731965	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223656496	chr7	91731845	91731989	91731866	91731965	AKAP9	NM_147185	2	50	46	+	91731908	91732140
223234899	chr7	91736517	91736648	91736549	91736621	AKAP9	NM_005751	1	50	48	+	91736607	91736736
223234899	chr7	91736517	91736648	91736549	91736621	AKAP9	NM_147185	2	50	48	+	91736607	91736736
224431844	chr7	91739372	91739544	91739394	91739515	AKAP9	NM_005751	1	50	50	+	91739436	91739987
224431844	chr7	91739372	91739544	91739394	91739515	AKAP9	NM_147185	2	50	50	+	91739436	91739987
226066464	chr7	92247390	92247549	92247417	92247521	CDK6	NM_001145306	1	8	7	-	92247386	92247521
226066464	chr7	92247390	92247549	92247417	92247521	CDK6	NM_001259	2	8	7	-	92247386	92247521
226220622	chr7	92354874	92355048	92354900	92355023	CDK6	NM_001145306	1	8	4	-	92354940	92355107
226220622	chr7	92354874	92355048	92354900	92355023	CDK6	NM_001259	2	8	4	-	92354940	92355107
227038387	chr7	92462321	92462479	92462341	92462461	CDK6	NM_001145306	1	8	2	-	92462405	92463004
227038387	chr7	92462321	92462479	92462341	92462461	CDK6	NM_001259	2	8	2	-	92462405	92463004
294133690	chr7	92730714	92730885	92730739	92730864	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294133690	chr7	92730714	92730885	92730739	92730864	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294131241	chr7	92731154	92731287	92731182	92731261	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294131241	chr7	92731154	92731287	92731182	92731261	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294042653	chr7	92731534	92731692	92731562	92731663	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294042653	chr7	92731534	92731692	92731562	92731663	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294098980	chr7	92731995	92732153	92732023	92732127	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294098980	chr7	92731995	92732153	92732023	92732127	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295056881	chr7	92732406	92732532	92732434	92732506	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295056881	chr7	92732406	92732532	92732434	92732506	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295083065	chr7	92732696	92732858	92732723	92732835	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295083065	chr7	92732696	92732858	92732723	92732835	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295061193	chr7	92733121	92733247	92733145	92733219	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295061193	chr7	92733121	92733247	92733145	92733219	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294140466	chr7	92733455	92733613	92733483	92733585	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294140466	chr7	92733455	92733613	92733483	92733585	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294077423	chr7	92733872	92734030	92733897	92734007	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294077423	chr7	92733872	92734030	92733897	92734007	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294095425	chr7	92734266	92734394	92734293	92734371	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294095425	chr7	92734266	92734394	92734293	92734371	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295068814	chr7	92734555	92734701	92734578	92734678	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295068814	chr7	92734555	92734701	92734578	92734678	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294143104	chr7	92734985	92735128	92735013	92735103	SAMD9	NM_001193307	1	2	2	-	92728826	92735418

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294143104	chr7	92734985	92735128	92735013	92735103	SAMD9	NM_017654	2	3	3	-	92728826	92735418
300151336	chr7	98478714	98478888	98478736	98478862	TRRAP	NM_003496	2	71	2	+	98478713	98478873
300151336	chr7	98478714	98478888	98478736	98478862	TRRAP	NM_001244580	1	72	2	+	98478713	98478873
299702761	chr7	98489931	98490104	98489954	98490075	TRRAP	NM_003496	2	71	5	+	98490047	98490151
299702761	chr7	98489931	98490104	98489954	98490075	TRRAP	NM_001244580	1	72	5	+	98490047	98490151
300339261	chr7	98493354	98493524	98493383	98493498	TRRAP	NM_003496	2	71	7	+	98493387	98493443
300339261	chr7	98493354	98493524	98493383	98493498	TRRAP	NM_001244580	1	72	7	+	98493387	98493443
304006421	chr7	98497220	98497360	98497245	98497338	TRRAP	NM_003496	2	71	10	+	98497302	98497390
304006421	chr7	98497220	98497360	98497245	98497338	TRRAP	NM_001244580	1	72	10	+	98497302	98497390
305615618	chr7	98500948	98501076	98500977	98501050	TRRAP	NM_003496	2	71	12	+	98501002	98501140
305615618	chr7	98500948	98501076	98500977	98501050	TRRAP	NM_001244580	1	72	12	+	98501002	98501140
302902285	chr7	98506446	98506620	98506468	98506596	TRRAP	NM_003496	2	71	14	+	98506351	98506585
302902285	chr7	98506446	98506620	98506468	98506596	TRRAP	NM_001244580	1	72	14	+	98506351	98506585
301108934	chr7	98507896	98508023	98507913	98508002	TRRAP	NM_003496	2	71	15	+	98507679	98508042
301108934	chr7	98507896	98508023	98507913	98508002	TRRAP	NM_001244580	1	72	15	+	98507679	98508042
299892714	chr7	98508599	98508745	98508628	98508724	TRRAP	NM_003496	2	71	17	+	98508700	98508894
299892714	chr7	98508599	98508745	98508628	98508724	TRRAP	NM_001244580	1	72	17	+	98508700	98508894
302204466	chr7	98509730	98509880	98509750	98509855	TRRAP	NM_003496	2	71	18	+	98509645	98509836
302204466	chr7	98509730	98509880	98509750	98509855	TRRAP	NM_001244580	1	72	18	+	98509645	98509836
305216725	chr7	98515040	98515214	98515060	98515192	TRRAP	NM_003496	2	71	20	+	98515046	98515302
305216725	chr7	98515040	98515214	98515060	98515192	TRRAP	NM_001244580	1	72	20	+	98515046	98515302
304984106	chr7	98522706	98522851	98522733	98522830	TRRAP	NM_003496	2	71	22	+	98522735	98522886
304984106	chr7	98522706	98522851	98522733	98522830	TRRAP	NM_001244580	1	72	22	+	98522735	98522886
305993159	chr7	98524934	98525108	98524954	98525082	TRRAP	NM_003496	2	71	23	+	98524790	98524989
305993159	chr7	98524934	98525108	98524954	98525082	TRRAP	NM_001244580	1	72	23	+	98524790	98524989
302468535	chr7	98528341	98528512	98528369	98528485	TRRAP	NM_003496	2	71	25	+	98528256	98528453
302468535	chr7	98528341	98528512	98528369	98528485	TRRAP	NM_001244580	1	72	25	+	98528256	98528453
302083778	chr7	98530834	98531006	98530853	98530986	TRRAP	NM_003496	2	71	27	+	98530864	98531025
302083778	chr7	98530834	98531006	98530853	98530986	TRRAP	NM_001244580	1	72	27	+	98530864	98531025
304778792	chr7	98534751	98534903	98534778	98534879	TRRAP	NM_003496	2	71	29	+	98534779	98534900
304778792	chr7	98534751	98534903	98534778	98534879	TRRAP	NM_001244580	1	72	29	+	98534779	98534900
302491233	chr7	98540515	98540668	98540535	98540643	TRRAP	NM_003496	2	71	31	+	98540572	98540640
302491233	chr7	98540515	98540668	98540535	98540643	TRRAP	NM_001244580	1	72	31	+	98540572	98540640
302005074	chr7	98545841	98545985	98545867	98545964	TRRAP	NM_003496	2	71	32	+	98545844	98545963
302005074	chr7	98545841	98545985	98545867	98545964	TRRAP	NM_001244580	1	72	33	+	98545844	98545963
301468309	chr7	98547089	98547260	98547110	98547237	TRRAP	NM_003496	2	71	34	+	98547040	98547204
301468309	chr7	98547089	98547260	98547110	98547237	TRRAP	NM_001244580	1	72	35	+	98547040	98547204
300800048	chr7	98547782	98547949	98547810	98547923	TRRAP	NM_003496	2	71	36	+	98547687	98547885
300800048	chr7	98547782	98547949	98547810	98547923	TRRAP	NM_001244580	1	72	37	+	98547687	98547885
301003750	chr7	98550879	98551038	98550902	98551014	TRRAP	NM_003496	2	71	38	+	98550790	98551056
301003750	chr7	98550879	98551038	98550902	98551014	TRRAP	NM_001244580	1	72	39	+	98550790	98551056

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299835976	chr7	98552829	98552990	98552849	98552964	TRRAP	NM_003496	2	71	39	+	98552721	98552927
299835976	chr7	98552829	98552990	98552849	98552964	TRRAP	NM_001244580	1	72	40	+	98552721	98552927
299830836	chr7	98554009	98554181	98554034	98554158	TRRAP	NM_003496	2	71	41	+	98554022	98554156
299830836	chr7	98554009	98554181	98554034	98554158	TRRAP	NM_001244580	1	72	42	+	98554022	98554156
302883186	chr7	98558859	98559020	98558879	98559001	TRRAP	NM_003496	2	71	44	+	98558884	98559097
302883186	chr7	98558859	98559020	98558879	98559001	TRRAP	NM_001244580	1	72	45	+	98558884	98559097
299830397	chr7	98562182	98562326	98562207	98562304	TRRAP	NM_003496	2	71	46	+	98562252	98562398
299830397	chr7	98562182	98562326	98562207	98562304	TRRAP	NM_001244580	1	72	47	+	98562252	98562398
300106693	chr7	98564541	98564710	98564568	98564683	TRRAP	NM_003496	2	71	48	+	98564664	98564785
300106693	chr7	98564541	98564710	98564568	98564683	TRRAP	NM_001244580	1	72	49	+	98564664	98564785
300280832	chr7	98567667	98567833	98567689	98567812	TRRAP	NM_003496	2	71	50	+	98567735	98567914
300280832	chr7	98567667	98567833	98567689	98567812	TRRAP	NM_001244580	1	72	51	+	98567735	98567914
302275121	chr7	98573740	98573884	98573762	98573860	TRRAP	NM_003496	2	71	52	+	98573772	98573891
302275121	chr7	98573740	98573884	98573762	98573860	TRRAP	NM_001244580	1	72	53	+	98573772	98573891
301236900	chr7	98574306	98574432	98574330	98574404	TRRAP	NM_003496	2	71	53	+	98574106	98574393
301236900	chr7	98574306	98574432	98574330	98574404	TRRAP	NM_001244580	1	72	54	+	98574106	98574393
305465942	chr7	98576346	98576514	98576368	98576493	TRRAP	NM_003496	2	71	56	+	98576392	98576527
305465942	chr7	98576346	98576514	98576368	98576493	TRRAP	NM_001244580	1	72	57	+	98576392	98576527
299830842	chr7	98579551	98579702	98579570	98579677	TRRAP	NM_003496	2	71	57	+	98579392	98579583
299830842	chr7	98579551	98579702	98579570	98579677	TRRAP	NM_001244580	1	72	58	+	98579392	98579583
300942983	chr7	98581651	98581792	98581676	98581771	TRRAP	NM_003496	2	71	59	+	98581716	98581981
300942983	chr7	98581651	98581792	98581676	98581771	TRRAP	NM_001244580	1	72	60	+	98581716	98581981
302225843	chr7	98582604	98582751	98582629	98582722	TRRAP	NM_003496	2	71	60	+	98582567	98582667
302225843	chr7	98582604	98582751	98582629	98582722	TRRAP	NM_001244580	1	72	61	+	98582567	98582667
301646621	chr7	98588120	98588282	98588138	98588260	TRRAP	NM_003496	2	71	62	+	98588078	98588242
301646621	chr7	98588120	98588282	98588138	98588260	TRRAP	NM_001244580	1	72	63	+	98588078	98588242
301486880	chr7	98591308	98591455	98591328	98591431	TRRAP	NM_003496	2	71	64	+	98591215	98591360
301486880	chr7	98591308	98591455	98591328	98591431	TRRAP	NM_001244580	1	72	65	+	98591215	98591360
300485344	chr7	98601755	98601893	98601777	98601865	TRRAP	NM_003496	2	71	66	+	98601813	98602038
300485344	chr7	98601755	98601893	98601777	98601865	TRRAP	NM_001244580	1	72	67	+	98601813	98602038
303186548	chr7	98602817	98602955	98602839	98602934	TRRAP	NM_003496	2	71	67	+	98602754	98602971
303186548	chr7	98602817	98602955	98602839	98602934	TRRAP	NM_001244580	1	72	68	+	98602754	98602971
304193632	chr7	98608635	98608801	98608657	98608778	TRRAP	NM_003496	2	71	69	+	98608675	98608878
304193632	chr7	98608635	98608801	98608657	98608778	TRRAP	NM_001244580	1	72	70	+	98608675	98608878
305998645	chr7	98609640	98609814	98609662	98609793	TRRAP	NM_003496	2	71	71	+	98609694	98610866
305998645	chr7	98609640	98609814	98609662	98609793	TRRAP	NM_001244580	1	72	72	+	98609694	98610866
271872516	chr7	100401150	100401322	100401172	100401297	EPHB4	NM_004444	1	17	17	-	100400187	100401212
271423764	chr7	100403220	100403383	100403242	100403362	EPHB4	NM_004444	1	17	15	-	100403123	100403316
271014702	chr7	100405050	100405222	100405071	100405202	EPHB4	NM_004444	1	17	13	-	100404987	100405202
271684748	chr7	100410602	100410758	100410624	100410734	EPHB4	NM_004444	1	17	11	-	100410717	100410830
270908397	chr7	100414798	100414961	100414815	100414944	EPHB4	NM_004444	1	17	8	-	100414814	100414979

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271317562	chr7	100417161	100417312	100417178	100417295	EPHB4	NM_004444	1	17	6	-	100417179	100417511
270016113	chr7	100417823	100417950	100417843	100417923	EPHB4	NM_004444	1	17	5	-	100417763	100417918
270691045	chr7	100420201	100420370	100420218	100420350	EPHB4	NM_004444	1	17	4	-	100419893	100420289
271722677	chr7	100421770	100421920	100421790	100421896	EPHB4	NM_004444	1	17	2	-	100421825	100421895
294975421	chr7	106508199	106508368	106508219	106508348	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294980827	chr7	106508632	106508806	106508655	106508784	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294006760	chr7	106509130	106509279	106509153	106509252	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294020044	chr7	106509537	106509704	106509563	106509681	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
293749338	chr7	106512924	106513097	106512950	106513070	PIK3CG	NM_002649	1	11	3	+	106512982	106513047
293943973	chr7	106515104	106515275	106515131	106515249	PIK3CG	NM_002649	1	11	5	+	106515145	106515248
294563847	chr7	106522544	106522701	106522563	106522675	PIK3CG	NM_002649	1	11	7	+	106522562	106522652
293862648	chr7	106524607	106524732	106524634	106524704	PIK3CG	NM_002649	1	11	9	+	106524600	106524711
294608980	chr7	106545530	106545680	106545558	106545652	PIK3CG	NM_002649	1	11	11	+	106545554	106547592
234546229	chr7	116339223	116339382	116339247	116339356	MET	NM_001127500	2	21	2	+	116339125	116340338
234546229	chr7	116339223	116339382	116339247	116339356	MET	NM_000245	1	21	2	+	116339125	116340338
234549355	chr7	116339675	116339804	116339696	116339779	MET	NM_001127500	2	21	2	+	116339125	116340338
234549355	chr7	116339675	116339804	116339696	116339779	MET	NM_000245	1	21	2	+	116339125	116340338
233157068	chr7	116340025	116340174	116340051	116340151	MET	NM_001127500	2	21	2	+	116339125	116340338
233157068	chr7	116340025	116340174	116340051	116340151	MET	NM_000245	1	21	2	+	116339125	116340338
231577696	chr7	116371789	116371938	116371809	116371913	MET	NM_001127500	2	21	3	+	116371722	116371913
231577696	chr7	116371789	116371938	116371809	116371913	MET	NM_000245	1	21	3	+	116371722	116371913
232354611	chr7	116380979	116381112	116381000	116381086	MET	NM_001127500	2	21	5	+	116380906	116381079
232354611	chr7	116380979	116381112	116381000	116381086	MET	NM_000245	1	21	5	+	116380906	116381079
231228936	chr7	116397569	116397740	116397596	116397717	MET	NM_001127500	2	21	8	+	116397692	116397828
231228936	chr7	116397569	116397740	116397596	116397717	MET	NM_000245	1	21	8	+	116397692	116397828
231825456	chr7	116398598	116398768	116398621	116398740	MET	NM_001127500	2	21	9	+	116398513	116398674
231825456	chr7	116398598	116398768	116398621	116398740	MET	NM_000245	1	21	9	+	116398513	116398674
234440329	chr7	116403105	116403278	116403133	116403250	MET	NM_001127500	2	21	11	+	116403104	116403322
234440329	chr7	116403105	116403278	116403133	116403250	MET	NM_000245	1	21	11	+	116403104	116403322
233288663	chr7	116411475	116411619	116411497	116411590	MET	NM_001127500	2	21	13	+	116411552	116411708
233288663	chr7	116411475	116411619	116411497	116411590	MET	NM_000245	1	21	13	+	116411552	116411708
233167176	chr7	116411932	116412101	116411957	116412073	MET	NM_001127500	2	21	14	+	116411903	116412043
233167176	chr7	116411932	116412101	116411957	116412073	MET	NM_000245	1	21	14	+	116411903	116412043
233063076	chr7	116417405	116417569	116417428	116417542	MET	NM_001127500	2	21	16	+	116417443	116417523
233063076	chr7	116417405	116417569	116417428	116417542	MET	NM_000245	1	21	16	+	116417443	116417523
231126210	chr7	116423325	116423483	116423351	116423461	MET	NM_001127500	2	21	19	+	116423358	116423523
231126210	chr7	116423325	116423483	116423351	116423461	MET	NM_000245	1	21	19	+	116423358	116423523
234543880	chr7	116435849	116436019	116435877	116435997	MET	NM_001127500	2	21	21	+	116435941	116438440
234543880	chr7	116435849	116436019	116435877	116435997	MET	NM_000245	1	21	21	+	116435941	116438440
295296277	chr7	124464071	124464220	124464099	124464193	POT1	NR_003103	4	18	18	-	124462440	124464128
295296277	chr7	124464071	124464220	124464099	124464193	POT1	NR_003104	5	20	20	-	124462440	124464128

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295296277	chr7	124464071	124464220	124464099	124464193	POT1	NR_003102	3	20	20	-	124462440	124464128
295296277	chr7	124464071	124464220	124464099	124464193	POT1	NM_001042594	1	18	18	-	124462440	124464128
295296277	chr7	124464071	124464220	124464099	124464193	POT1	NM_015450	2	19	19	-	124462440	124464128
294340048	chr7	124475346	124475472	124475374	124475446	POT1	NR_003103	4	18	15	-	124475333	124475468
294340048	chr7	124475346	124475472	124475374	124475446	POT1	NR_003104	5	20	16	-	124475333	124475468
294340048	chr7	124475346	124475472	124475374	124475446	POT1	NR_003102	3	20	16	-	124475333	124475468
294340048	chr7	124475346	124475472	124475374	124475446	POT1	NM_001042594	1	18	14	-	124475333	124475468
294340048	chr7	124475346	124475472	124475374	124475446	POT1	NM_015450	2	19	15	-	124475333	124475468
293936336	chr7	124481172	124481306	124481196	124481276	POT1	NR_003103	4	18	14	-	124481027	124481232
293936336	chr7	124481172	124481306	124481196	124481276	POT1	NR_003104	5	20	14	-	124481027	124481232
293936336	chr7	124481172	124481306	124481196	124481276	POT1	NR_003102	3	20	15	-	124481027	124481232
293936336	chr7	124481172	124481306	124481196	124481276	POT1	NM_001042594	1	18	13	-	124481027	124481232
293936336	chr7	124481172	124481306	124481196	124481276	POT1	NM_015450	2	19	14	-	124481027	124481232
293924695	chr7	124491914	124492086	124491941	124492058	POT1	NR_003103	4	18	11	-	124491926	124492005
293924695	chr7	124491914	124492086	124491941	124492058	POT1	NR_003104	5	20	11	-	124491926	124492005
293924695	chr7	124491914	124492086	124491941	124492058	POT1	NR_003102	3	20	11	-	124491926	124492005
293924695	chr7	124491914	124492086	124491941	124492058	POT1	NM_001042594	1	18	10	-	124491926	124492005
293924695	chr7	124491914	124492086	124491941	124492058	POT1	NM_015450	2	19	11	-	124491926	124492005
294636034	chr7	124499065	124499189	124499089	124499161	POT1	NR_003103	4	18	9	-	124499011	124499166
294636034	chr7	124499065	124499189	124499089	124499161	POT1	NR_003104	5	20	9	-	124499011	124499166
294636034	chr7	124499065	124499189	124499089	124499161	POT1	NR_003102	3	20	9	-	124499011	124499166
294636034	chr7	124499065	124499189	124499089	124499161	POT1	NM_001042594	1	18	8	-	124499011	124499166
294636034	chr7	124499065	124499189	124499089	124499161	POT1	NM_015450	2	19	9	-	124499011	124499166
293896609	chr7	124503586	124503759	124503606	124503731	POT1	NR_003103	4	18	8	-	124503404	124503694
293896609	chr7	124503586	124503759	124503606	124503731	POT1	NR_003104	5	20	8	-	124503404	124503694
293896609	chr7	124503586	124503759	124503606	124503731	POT1	NR_003102	3	20	8	-	124503404	124503694
293896609	chr7	124503586	124503759	124503606	124503731	POT1	NM_001042594	1	18	7	-	124503404	124503694
293896609	chr7	124503586	124503759	124503606	124503731	POT1	NM_015450	2	19	8	-	124503404	124503694
294107928	chr7	124532185	124532345	124532209	124532323	POT1	NR_003103	4	18	6	-	124532320	124532434
294107928	chr7	124532185	124532345	124532209	124532323	POT1	NR_003104	5	20	6	-	124532320	124532434
294107928	chr7	124532185	124532345	124532209	124532323	POT1	NR_003102	3	20	6	-	124532320	124532434
294107928	chr7	124532185	124532345	124532209	124532323	POT1	NM_001042594	1	18	6	-	124532320	124532434
294107928	chr7	124532185	124532345	124532209	124532323	POT1	NM_015450	2	19	6	-	124532320	124532434
294013987	chr7	126079096	126079242	126079121	126079214	GRM8	NR_028041	3	11	11	-	126078652	126079222
294013987	chr7	126079096	126079242	126079121	126079214	GRM8	NM_001127323	2	11	11	-	126078652	126079222
294013987	chr7	126079096	126079242	126079121	126079214	GRM8	NM_000845	1	10	10	-	126078652	126079222
294606386	chr7	126086364	126086525	126086388	126086497	GRM8	NR_028041	3	11	10	-	126086180	126086426
294606386	chr7	126086364	126086525	126086388	126086497	GRM8	NM_000845	1	10	9	-	126086180	126086426
294606386	chr7	126086364	126086525	126086388	126086497	GRM8	NM_001127323	2	11	10	-	126086125	126086426
293789702	chr7	126173237	126173382	126173257	126173361	GRM8	NR_028041	3	11	9	-	126173006	126173941
293789702	chr7	126173237	126173382	126173257	126173361	GRM8	NM_001127323	2	11	9	-	126173006	126173941

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293789702	chr7	126173237	126173382	126173257	126173361	GRM8	NM_000845	1	10	8	-	126173006	126173941
293828094	chr7	126173689	126173815	126173711	126173791	GRM8	NR_028041	3	11	9	-	126173006	126173941
293828094	chr7	126173689	126173815	126173711	126173791	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293828094	chr7	126173689	126173815	126173711	126173791	GRM8	NM_000845	1	10	8	-	126173006	126173941
294815286	chr7	126249439	126249607	126249461	126249581	GRM8	NR_028041	3	11	8	-	126249416	126249552
294815286	chr7	126249439	126249607	126249461	126249581	GRM8	NM_001127323	2	11	8	-	126249416	126249552
294815286	chr7	126249439	126249607	126249461	126249581	GRM8	NM_000845	1	10	7	-	126249416	126249552
295197735	chr7	126542697	126542868	126542717	126542839	GRM8	NR_028041	3	11	5	-	126542596	126542733
295197735	chr7	126542697	126542868	126542717	126542839	GRM8	NM_001127323	2	11	6	-	126542596	126542733
295197735	chr7	126542697	126542868	126542717	126542839	GRM8	NM_000845	1	10	5	-	126542596	126542733
293886550	chr7	126746464	126746634	126746491	126746610	GRM8	NR_028041	3	11	2	-	126746550	126746766
293886550	chr7	126746464	126746634	126746491	126746610	GRM8	NM_001127323	2	11	3	-	126746550	126746766
293886550	chr7	126746464	126746634	126746491	126746610	GRM8	NM_000845	1	10	2	-	126746550	126746766
295229718	chr7	126882821	126882945	126882843	126882924	GRM8	NR_028041	3	11	1	-	126882749	126883569
295229718	chr7	126882821	126882945	126882843	126882924	GRM8	NM_001127323	2	11	2	-	126882749	126883569
295229718	chr7	126882821	126882945	126882843	126882924	GRM8	NM_000845	1	10	1	-	126882749	126883569
260961762	chr7	128829208	128829339	128829225	128829322	SMO	NM_005631	1	12	1	+	128828713	128829323
262553226	chr7	128844956	128845085	128844978	128845064	SMO	NM_005631	1	12	3	+	128845044	128845253
238071583	chr7	128845471	128845643	128845491	128845624	SMO	NM_005631	1	12	4	+	128845451	128845623
238691315	chr7	128846313	128846476	128846335	128846451	SMO	NM_005631	1	12	6	+	128846305	128846428
262126135	chr7	128850316	128850470	128850335	128850446	SMO	NM_005631	1	12	9	+	128850204	128850389
263585145	chr7	128851572	128851743	128851594	128851722	SMO	NM_005631	1	12	11	+	128851477	128851611
241173339	chr7	128852113	128852282	128852130	128852259	SMO	NM_005631	1	12	12	+	128851865	128853385
274231949	chr7	138188938	138189076	138188966	138189055	TRIM24	NM_015905	2	19	2	+	138189035	138189153
274231949	chr7	138188938	138189076	138188966	138189055	TRIM24	NM_003852	1	19	2	+	138189035	138189153
273470034	chr7	138203904	138204036	138203931	138204012	TRIM24	NM_015905	2	19	4	+	138203934	138204066
273470034	chr7	138203904	138204036	138203931	138204012	TRIM24	NM_003852	1	19	4	+	138203934	138204066
273074756	chr7	138223445	138223605	138223466	138223577	TRIM24	NM_015905	2	19	7	+	138223402	138223548
273074756	chr7	138223445	138223605	138223466	138223577	TRIM24	NM_003852	1	19	7	+	138223402	138223548
274260245	chr7	138239469	138239618	138239489	138239596	TRIM24	NM_003852	1	19	9	+	138239443	138239609
274260245	chr7	138239469	138239618	138239489	138239596	TRIM24	NM_015905	2	19	9	+	138239443	138239711
273672522	chr7	138252343	138252500	138252365	138252472	TRIM24	NM_015905	2	19	10	+	138252226	138252399
273672522	chr7	138252343	138252500	138252365	138252472	TRIM24	NM_003852	1	19	10	+	138252226	138252399
273211066	chr7	138258255	138258403	138258283	138258381	TRIM24	NM_015905	2	19	12	+	138258252	138258387
273211066	chr7	138258255	138258403	138258283	138258381	TRIM24	NM_003852	1	19	12	+	138258252	138258387
273581620	chr7	138263829	138263993	138263853	138263969	TRIM24	NM_015905	2	19	15	+	138263949	138264277
273581620	chr7	138263829	138263993	138263853	138263969	TRIM24	NM_003852	1	19	15	+	138263949	138264277
274478288	chr7	138265240	138265378	138265266	138265352	TRIM24	NM_015905	2	19	16	+	138265307	138265439
274478288	chr7	138265240	138265378	138265266	138265352	TRIM24	NM_003852	1	19	16	+	138265307	138265439
273229747	chr7	138268482	138268656	138268508	138268628	TRIM24	NM_015905	2	19	18	+	138268595	138268744
273229747	chr7	138268482	138268656	138268508	138268628	TRIM24	NM_003852	1	19	18	+	138268595	138268744

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273279806	chr7	138269576	138269717	138269604	138269697	TRIM24	NM_015905	2	19	19	+	138269487	138270332
273279806	chr7	138269576	138269717	138269604	138269697	TRIM24	NM_003852	1	19	19	+	138269487	138270332
223519358	chr7	140439578	140439749	140439605	140439721	BRAF	NM_004333	1	18	17	-	140439612	140439746
223465859	chr7	140453078	140453249	140453103	140453221	BRAF	NM_004333	1	18	15	-	140453075	140453193
223971374	chr7	140476840	140476971	140476866	140476944	BRAF	NM_004333	1	18	13	-	140476712	140476888
222680486	chr7	140482758	140482912	140482786	140482885	BRAF	NM_004333	1	18	10	-	140482821	140482957
223741661	chr7	140494173	140494319	140494199	140494286	BRAF	NM_004333	1	18	8	-	140494108	140494267
223950351	chr7	140501226	140501353	140501253	140501327	BRAF	NM_004333	1	18	6	-	140501212	140501360
224410546	chr7	140508747	140508916	140508771	140508888	BRAF	NM_004333	1	18	4	-	140508692	140508795
222935598	chr7	140534597	140534723	140534621	140534698	BRAF	NM_004333	1	18	3	-	140534409	140534672
224119999	chr7	140624359	140624524	140624379	140624505	BRAF	NM_004333	1	18	1	-	140624366	140624564
271202204	chr7	142561739	142561890	142561757	142561867	EPHB6	NM_004445	1	20	7	+	142561724	142562504
272590527	chr7	142562124	142562297	142562144	142562277	EPHB6	NM_004445	1	20	7	+	142561724	142562504
270782300	chr7	142563330	142563495	142563349	142563469	EPHB6	NM_004445	1	20	8	+	142563230	142563385
271804530	chr7	142563980	142564152	142564001	142564130	EPHB6	NM_004445	1	20	9	+	142563715	142564071
272734182	chr7	142564731	142564889	142564753	142564869	EPHB6	NM_004445	1	20	11	+	142564661	142564823
271134217	chr7	142565954	142566112	142565974	142566086	EPHB6	NM_004445	1	20	14	+	142565996	142566115
272728231	chr7	142566649	142566823	142566670	142566803	EPHB6	NM_004445	1	20	16	+	142566727	142566900
272240988	chr7	142567891	142568054	142567913	142568026	EPHB6	NM_004445	1	20	18	+	142567967	142568160
269989120	chr7	142568349	142568513	142568370	142568491	EPHB6	NM_004445	1	20	19	+	142568283	142568438
229361991	chr7	148506347	148506515	148506371	148506493	EZH2	NM_001203248	2	20	18	-	148506402	148506482
229361991	chr7	148506347	148506515	148506371	148506493	EZH2	NM_152998	5	19	17	-	148506402	148506482
229361991	chr7	148506347	148506515	148506371	148506493	EZH2	NM_001203247	1	20	18	-	148506402	148506482
229361991	chr7	148506347	148506515	148506371	148506493	EZH2	NM_001203249	3	19	17	-	148506402	148506482
229361991	chr7	148506347	148506515	148506371	148506493	EZH2	NM_004456	4	20	18	-	148506402	148506482
228064692	chr7	148510977	148511151	148511002	148511131	EZH2	NM_001203248	2	20	15	-	148511051	148511229
228064692	chr7	148510977	148511151	148511002	148511131	EZH2	NM_152998	5	19	14	-	148511051	148511229
228064692	chr7	148510977	148511151	148511002	148511131	EZH2	NM_001203247	1	20	15	-	148511051	148511229
228064692	chr7	148510977	148511151	148511002	148511131	EZH2	NM_001203249	3	19	14	-	148511051	148511229
228064692	chr7	148510977	148511151	148511002	148511131	EZH2	NM_004456	4	20	15	-	148511051	148511229
232947863	chr7	148512566	148512691	148512595	148512668	EZH2	NM_001203248	2	20	13	-	148512598	148512638
232947863	chr7	148512566	148512691	148512595	148512668	EZH2	NM_152998	5	19	12	-	148512598	148512638
232947863	chr7	148512566	148512691	148512595	148512668	EZH2	NM_001203247	1	20	13	-	148512598	148512638
232947863	chr7	148512566	148512691	148512595	148512668	EZH2	NM_001203249	3	19	13	-	148512598	148512638
232947863	chr7	148512566	148512691	148512595	148512668	EZH2	NM_004456	4	20	13	-	148512598	148512638
228973959	chr7	148514902	148515027	148514928	148514999	EZH2	NM_001203248	2	20	10	-	148514969	148515209
228973959	chr7	148514902	148515027	148514928	148514999	EZH2	NM_152998	5	19	9	-	148514969	148515209
228973959	chr7	148514902	148515027	148514928	148514999	EZH2	NM_001203247	1	20	10	-	148514969	148515209
228973959	chr7	148514902	148515027	148514928	148514999	EZH2	NM_001203249	3	19	10	-	148514969	148515209
228973959	chr7	148514902	148515027	148514928	148514999	EZH2	NM_004456	4	20	10	-	148514969	148515209
229726822	chr7	148516687	148516851	148516709	148516823	EZH2	NM_001203248	2	20	9	-	148516688	148516779

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229726822	chr7	148516687	148516851	148516709	148516823	EZH2	NM_152998	5	19	8	-	148516688	148516779
229726822	chr7	148516687	148516851	148516709	148516823	EZH2	NM_001203247	1	20	9	-	148516688	148516779
229726822	chr7	148516687	148516851	148516709	148516823	EZH2	NM_001203249	3	19	9	-	148516688	148516779
229726822	chr7	148516687	148516851	148516709	148516823	EZH2	NM_004456	4	20	9	-	148516688	148516779
230185926	chr7	148524204	148524348	148524230	148524330	EZH2	NM_001203248	2	20	7	-	148524256	148524358
230185926	chr7	148524204	148524348	148524230	148524330	EZH2	NM_152998	5	19	6	-	148524256	148524358
230185926	chr7	148524204	148524348	148524230	148524330	EZH2	NM_001203247	1	20	7	-	148524256	148524358
230185926	chr7	148524204	148524348	148524230	148524330	EZH2	NM_001203249	3	19	7	-	148524256	148524358
230185926	chr7	148524204	148524348	148524230	148524330	EZH2	NM_004456	4	20	7	-	148524256	148524358
230654547	chr7	148526877	148527047	148526904	148527021	EZH2	NM_001203248	2	20	5	-	148526820	148526940
230654547	chr7	148526877	148527047	148526904	148527021	EZH2	NM_152998	5	19	4	-	148526820	148526940
230654547	chr7	148526877	148527047	148526904	148527021	EZH2	NM_001203247	1	20	5	-	148526820	148526940
230654547	chr7	148526877	148527047	148526904	148527021	EZH2	NM_001203249	3	19	5	-	148526820	148526940
230654547	chr7	148526877	148527047	148526904	148527021	EZH2	NM_004456	4	20	5	-	148526820	148526940
227701875	chr7	148543576	148543734	148543598	148543706	EZH2	NM_152998	5	19	3	-	148543562	148543690
227701875	chr7	148543576	148543734	148543598	148543706	EZH2	NM_001203247	1	20	3	-	148543562	148543690
227701875	chr7	148543576	148543734	148543598	148543706	EZH2	NM_004456	4	20	3	-	148543562	148543690
227701875	chr7	148543576	148543734	148543598	148543706	EZH2	NM_001203248	2	20	3	-	148543589	148543690
227701875	chr7	148543576	148543734	148543598	148543706	EZH2	NM_001203249	3	19	3	-	148543589	148543690
273392299	chr7	151835843	151836016	151835865	151835994	MLL3	NM_170606	1	59	58	-	151835881	151835989
274312505	chr7	151841742	151841904	151841764	151841876	MLL3	NM_170606	1	59	55	-	151841798	151841966
273139449	chr7	151843623	151843797	151843647	151843775	MLL3	NM_170606	1	59	53	-	151843684	151843820
273099170	chr7	151845300	151845456	151845322	151845434	MLL3	NM_170606	1	59	52	-	151845118	151846237
274166332	chr7	151845764	151845938	151845787	151845910	MLL3	NM_170606	1	59	52	-	151845118	151846237
273684389	chr7	151847932	151848073	151847957	151848048	MLL3	NM_170606	1	59	51	-	151847985	151848092
274024613	chr7	151849673	151849830	151849695	151849806	MLL3	NM_170606	1	59	49	-	151849790	151850039
273420212	chr7	151851099	151851231	151851121	151851202	MLL3	NM_170606	1	59	48	-	151851095	151851231
274362058	chr7	151852900	151853040	151852929	151853022	MLL3	NM_170606	1	59	46	-	151852995	151853142
273210112	chr7	151853311	151853484	151853333	151853458	MLL3	NM_170606	1	59	45	-	151853290	151853431
274528239	chr7	151859213	151859365	151859242	151859345	MLL3	NM_170606	1	59	43	-	151859202	151860911
274529213	chr7	151859644	151859783	151859665	151859761	MLL3	NM_170606	1	59	43	-	151859202	151860911
274569972	chr7	151860032	151860186	151860054	151860160	MLL3	NM_170606	1	59	43	-	151859202	151860911
274605373	chr7	151860480	151860619	151860508	151860596	MLL3	NM_170606	1	59	43	-	151859202	151860911
273645219	chr7	151860853	151861015	151860881	151860995	MLL3	NM_170606	1	59	43	-	151859202	151860911
273827029	chr7	151866166	151866336	151866187	151866308	MLL3	NM_170606	1	59	41	-	151866271	151866334
274252120	chr7	151873212	151873385	151873236	151873359	MLL3	NM_170606	1	59	38	-	151873276	151875095
274314509	chr7	151873658	151873794	151873680	151873766	MLL3	NM_170606	1	59	38	-	151873276	151875095
273363028	chr7	151873976	151874126	151874004	151874098	MLL3	NM_170606	1	59	38	-	151873276	151875095
273282012	chr7	151874302	151874473	151874330	151874448	MLL3	NM_170606	1	59	38	-	151873276	151875095
274254905	chr7	151874753	151874879	151874778	151874854	MLL3	NM_170606	1	59	38	-	151873276	151875095
272972218	chr7	151876858	151877006	151876881	151876979	MLL3	NM_170606	1	59	37	-	151876919	151877211

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273822238	chr7	151877852	151878022	151877874	151877996	MLL3	NM_170606	1	59	36	-	151877796	151879679
273835307	chr7	151878293	151878449	151878317	151878430	MLL3	NM_170606	1	59	36	-	151877796	151879679
273819567	chr7	151878718	151878875	151878739	151878853	MLL3	NM_170606	1	59	36	-	151877796	151879679
273914282	chr7	151879150	151879315	151879177	151879294	MLL3	NM_170606	1	59	36	-	151877796	151879679
273893468	chr7	151879604	151879741	151879628	151879713	MLL3	NM_170606	1	59	36	-	151877796	151879679
273693989	chr7	151884291	151884423	151884317	151884401	MLL3	NM_170606	1	59	33	-	151884347	151884561
273234329	chr7	151884683	151884831	151884713	151884807	MLL3	NM_170606	1	59	32	-	151884800	151884932
274328501	chr7	151891139	151891265	151891160	151891236	MLL3	NM_170606	1	59	31	-	151891094	151891213
273852533	chr7	151893060	151893193	151893089	151893170	MLL3	NM_170606	1	59	28	-	151892992	151893096
272913001	chr7	151896462	151896633	151896490	151896608	MLL3	NM_170606	1	59	27	-	151896364	151896544
273586077	chr7	151902200	151902372	151902222	151902343	MLL3	NM_170606	1	59	25	-	151902191	151902310
273456006	chr7	151918999	151919149	151919023	151919129	MLL3	NM_170606	1	59	22	-	151919086	151919151
272780231	chr7	151935720	151935873	151935747	151935852	MLL3	NM_170606	1	59	15	-	151935792	151935911
273471824	chr7	151945247	151945421	151945272	151945398	MLL3	NM_170606	1	59	14	-	151944987	151945705
273233547	chr7	151946948	151947099	151946976	151947071	MLL3	NM_170606	1	59	13	-	151946961	151947038
274438115	chr7	151949077	151949250	151949101	151949222	MLL3	NM_170606	1	59	11	-	151949024	151949175
273949165	chr7	151959996	151960146	151960021	151960118	MLL3	NM_170606	1	59	9	-	151960101	151960215
273500221	chr7	152006943	152007089	152006971	152007067	MLL3	NM_170606	1	59	6	-	152007051	152007160
273317968	chr7	152012196	152012352	152012224	152012327	MLL3	NM_170606	1	59	4	-	152012223	152012423
273256305	chr7	152055710	152055858	152055731	152055828	MLL3	NM_170606	1	59	2	-	152055672	152055760
293887128	chr7	152345929	152346092	152345951	152346067	XRCC2	NM_005431	1	3	3	-	152343587	152346448
294983490	chr7	152346351	152346489	152346373	152346461	XRCC2	NM_005431	1	3	3	-	152343587	152346448
239999847	chr8	30916620	30916769	30916648	30916745	WRN	NM_000553	1	35	3	+	30916669	30916781
239080321	chr8	30922368	30922500	30922399	30922475	WRN	NM_000553	1	35	5	+	30922431	30922579
262080378	chr8	30924572	30924700	30924599	30924678	WRN	NM_000553	1	35	6	+	30924549	30924698
239961657	chr8	30933625	30933796	30933653	30933768	WRN	NM_000553	1	35	8	+	30933689	30933803
240019775	chr8	30938521	30938686	30938550	30938658	WRN	NM_000553	1	35	9	+	30938383	30938812
262248491	chr8	30945317	30945483	30945345	30945459	WRN	NM_000553	1	35	12	+	30945292	30945436
262969364	chr8	30948344	30948496	30948371	30948468	WRN	NM_000553	1	35	15	+	30948350	30948458
264146108	chr8	30958358	30958495	30958382	30958471	WRN	NM_000553	1	35	18	+	30958365	30958471
262964260	chr8	30973806	30973972	30973827	30973944	WRN	NM_000553	1	35	20	+	30973870	30974044
262315530	chr8	30977858	30978030	30977880	30978002	WRN	NM_000553	1	35	21	+	30977759	30977940
238378845	chr8	30982413	30982568	30982441	30982537	WRN	NM_000553	1	35	23	+	30982424	30982516
240547892	chr8	30998950	30999074	30998969	30999047	WRN	NM_000553	1	35	25	+	30998946	30999116
242598516	chr8	31000055	31000193	31000086	31000163	WRN	NM_000553	1	35	27	+	31000142	31000217
238709495	chr8	31004598	31004728	31004623	31004700	WRN	NM_000553	1	35	29	+	31004569	31004644
264763371	chr8	31007855	31007997	31007879	31007973	WRN	NM_000553	1	35	31	+	31007857	31007971
239402777	chr8	31024432	31024606	31024457	31024583	WRN	NM_000553	1	35	34	+	31024538	31024746
239377327	chr8	31030503	31030643	31030527	31030616	WRN	NM_000553	1	35	35	+	31030511	31031277
228357335	chr8	37655023	37655176	37655041	37655154	GPR124	NM_032777	1	19	1	+	37654401	37655052
227441502	chr8	37686702	37686873	37686724	37686851	GPR124	NM_032777	1	19	4	+	37686779	37686850

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227391271	chr8	37688201	37688362	37688218	37688342	GPR124	NM_032777	1	19	7	+	37688228	37688441
227668395	chr8	37690450	37690595	37690472	37690573	GPR124	NM_032777	1	19	9	+	37690528	37690726
228747837	chr8	37691268	37691418	37691289	37691397	GPR124	NM_032777	1	19	10	+	37691206	37691355
227892781	chr8	37692748	37692921	37692766	37692901	GPR124	NM_032777	1	19	12	+	37692692	37692916
227133842	chr8	37693261	37693415	37693278	37693395	GPR124	NM_032777	1	19	13	+	37693072	37693288
228102396	chr8	37696432	37696596	37696453	37696572	GPR124	NM_032777	1	19	15	+	37696474	37696601
229021753	chr8	37697651	37697825	37697673	37697804	GPR124	NM_032777	1	19	17	+	37697639	37697784
227507796	chr8	37698804	37698957	37698822	37698938	GPR124	NM_032777	1	19	19	+	37698604	37701504
229575668	chr8	37699282	37699420	37699300	37699403	GPR124	NM_032777	1	19	19	+	37698604	37701504
227561996	chr8	37699830	37699961	37699850	37699940	GPR124	NM_032777	1	19	19	+	37698604	37701504
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_001174066	4	17	15	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_001174065	3	18	16	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_001174063	1	18	16	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_023110	9	18	16	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_023106	8	17	15	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_023105	7	17	15	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_015850	6	18	16	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_001174067	5	19	17	-	38271670	38271807
229652521	chr8	38271562	38271734	38271582	38271711	FGFR1	NM_001174064	2	19	17	-	38271670	38271807
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_001174066	4	17	13	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_001174065	3	18	14	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_001174063	1	18	14	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_023110	9	18	14	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_023106	8	17	13	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_023105	7	17	13	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_015850	6	18	14	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_001174067	5	19	15	-	38272297	38272419
227948164	chr8	38272239	38272385	38272260	38272362	FGFR1	NM_001174064	2	19	15	-	38272297	38272419
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_001174066	4	17	11	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_001174065	3	18	12	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_001174063	1	18	12	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_023110	9	18	12	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_023106	8	17	11	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_023105	7	17	11	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_015850	6	18	12	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_001174067	5	19	13	-	38274824	38274934
228562186	chr8	38274714	38274886	38274736	38274860	FGFR1	NM_001174064	2	19	13	-	38274824	38274934
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_001174066	4	17	9	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_001174065	3	18	10	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_001174063	1	18	10	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_023110	9	18	10	-	38275746	38275891

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_023106	8	17	9	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_023105	7	17	9	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_015850	6	18	10	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_001174067	5	19	11	-	38275746	38275891
228878666	chr8	38275713	38275879	38275740	38275857	FGFR1	NM_001174064	2	19	11	-	38275746	38275891
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_001174066	4	17	7	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_001174065	3	18	8	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_001174063	1	18	8	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_023110	9	18	8	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_023106	8	17	7	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_023105	7	17	7	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_015850	6	18	8	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_001174067	5	19	9	-	38279315	38279459
232409801	chr8	38279240	38279365	38279261	38279340	FGFR1	NM_001174064	2	19	9	-	38279315	38279459
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_001174066	4	17	5	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_001174065	3	18	6	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_001174063	1	18	6	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_023110	9	18	6	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_023106	8	17	5	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_023105	7	17	5	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_015850	6	18	6	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_001174067	5	19	7	-	38283640	38283763
229749627	chr8	38283536	38283674	38283558	38283652	FGFR1	NM_001174064	2	19	7	-	38283640	38283763
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_001174065	3	18	4	-	38285870	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_023106	8	17	3	-	38285870	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_015850	6	18	4	-	38285870	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_001174067	5	19	5	-	38285870	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_001174066	4	17	3	-	38285864	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_001174063	1	18	4	-	38285864	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_023110	9	18	4	-	38285864	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_023105	7	17	3	-	38285864	38285953
228001452	chr8	38285807	38285975	38285829	38285953	FGFR1	NM_001174064	2	19	5	-	38285864	38285953
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_023110	9	18	3	-	38287200	38287466
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_015850	6	18	3	-	38287200	38287466
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
227983074	chr8	38287422	38287566	38287443	38287547	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_001174066	4	17	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_001174065	3	18	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_001174063	1	18	2	-	38314874	38315052

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_023110	9	18	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_023106	8	17	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_023105	7	17	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_015850	6	18	2	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_001174067	5	19	3	-	38314874	38315052
329445076	chr8	38314996	38315169	38315019	38315143	FGFR1	NM_001174064	2	19	2	-	38314874	38315052
312183949	chr8	41789797	41789952	41789819	41789931	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312183949	chr8	41789797	41789952	41789819	41789931	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312183949	chr8	41789797	41789952	41789819	41789931	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312221077	chr8	41790226	41790398	41790248	41790376	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312221077	chr8	41790226	41790398	41790248	41790376	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312221077	chr8	41790226	41790398	41790248	41790376	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312328294	chr8	41790911	41791065	41790932	41791040	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312328294	chr8	41790911	41791065	41790932	41791040	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312328294	chr8	41790911	41791065	41790932	41791040	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312390434	chr8	41791308	41791465	41791329	41791443	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312390434	chr8	41791308	41791465	41791329	41791443	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312390434	chr8	41791308	41791465	41791329	41791443	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312653412	chr8	41791789	41791963	41791807	41791939	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312653412	chr8	41791789	41791963	41791807	41791939	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312653412	chr8	41791789	41791963	41791807	41791939	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312355592	chr8	41792116	41792252	41792140	41792229	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312355592	chr8	41792116	41792252	41792140	41792229	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312355592	chr8	41792116	41792252	41792140	41792229	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312352120	chr8	41794824	41794952	41794848	41794929	KAT6A	NM_001099412	1	18	17	-	41794774	41795086
312352120	chr8	41794824	41794952	41794848	41794929	KAT6A	NM_006766	3	17	16	-	41794774	41795086
312352120	chr8	41794824	41794952	41794848	41794929	KAT6A	NM_001099413	2	18	17	-	41794774	41795086
312392053	chr8	41798348	41798518	41798371	41798492	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312392053	chr8	41798348	41798518	41798371	41798492	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312392053	chr8	41798348	41798518	41798371	41798492	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312389295	chr8	41798806	41798963	41798827	41798941	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312389295	chr8	41798806	41798963	41798827	41798941	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312389295	chr8	41798806	41798963	41798827	41798941	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312353734	chr8	41801240	41801373	41801270	41801346	KAT6A	NM_001099412	1	18	14	-	41801266	41801497
312353734	chr8	41801240	41801373	41801270	41801346	KAT6A	NM_006766	3	17	13	-	41801266	41801497
312353734	chr8	41801240	41801373	41801270	41801346	KAT6A	NM_001099413	2	18	14	-	41801266	41801497
312299006	chr8	41805181	41805354	41805202	41805326	KAT6A	NM_001099412	1	18	12	-	41805269	41805430
312299006	chr8	41805181	41805354	41805202	41805326	KAT6A	NM_006766	3	17	11	-	41805269	41805430
312299006	chr8	41805181	41805354	41805202	41805326	KAT6A	NM_001099413	2	18	12	-	41805269	41805430
312347822	chr8	41812780	41812904	41812804	41812885	KAT6A	NM_001099412	1	18	10	-	41812814	41812929
312347822	chr8	41812780	41812904	41812804	41812885	KAT6A	NM_006766	3	17	9	-	41812814	41812929

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312347822	chr8	41812780	41812904	41812804	41812885	KAT6A	NM_001099413	2	18	10	-	41812814	41812929
312417932	chr8	41834456	41834597	41834489	41834570	KAT6A	NM_001099412	1	18	8	-	41834526	41834845
312417932	chr8	41834456	41834597	41834489	41834570	KAT6A	NM_006766	3	17	7	-	41834526	41834845
312417932	chr8	41834456	41834597	41834489	41834570	KAT6A	NM_001099413	2	18	8	-	41834526	41834845
312262188	chr8	41836118	41836290	41836142	41836262	KAT6A	NM_001099412	1	18	7	-	41836160	41836295
312262188	chr8	41836118	41836290	41836142	41836262	KAT6A	NM_006766	3	17	6	-	41836160	41836295
312262188	chr8	41836118	41836290	41836142	41836262	KAT6A	NM_001099413	2	18	7	-	41836160	41836295
312212885	chr8	41839324	41839490	41839350	41839467	KAT6A	NM_001099412	1	18	5	-	41839357	41839472
312212885	chr8	41839324	41839490	41839350	41839467	KAT6A	NM_006766	3	17	4	-	41839357	41839472
312212885	chr8	41839324	41839490	41839350	41839467	KAT6A	NM_001099413	2	18	5	-	41839357	41839472
312527471	chr8	41906099	41906267	41906125	41906247	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312527471	chr8	41906099	41906267	41906125	41906247	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312527471	chr8	41906099	41906267	41906125	41906247	KAT6A	NM_001099413	2	18	3	-	41905896	41906820
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NM_001242778	2	21	1	+	42128820	42128987
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NR_033819	5	21	1	+	42128820	42128987
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NR_033818	4	22	1	+	42128820	42128987
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NM_001556	3	22	1	+	42128820	42128987
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NM_001190720	1	21	1	+	42128820	42128987
278432780	chr8	42128819	42128991	42128838	42128974	IKBKB	NR_040009	6	22	1	+	42128820	42128987
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NM_001242778	2	21	3	+	42147674	42147791
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NR_033819	5	21	4	+	42147674	42147791
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NR_033818	4	22	4	+	42147674	42147791
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NM_001556	3	22	4	+	42147674	42147791
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NM_001190720	1	21	3	+	42147674	42147791
278644364	chr8	42147642	42147779	42147663	42147758	IKBKB	NR_040009	6	22	4	+	42147674	42147791
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NM_001242778	2	21	5	+	42162705	42162793
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NR_033819	5	21	6	+	42162705	42162793
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NR_033818	4	22	6	+	42162705	42162793
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NM_001556	3	22	6	+	42162705	42162793
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NM_001190720	1	21	5	+	42162705	42162793
278817606	chr8	42162700	42162872	42162722	42162851	IKBKB	NR_040009	6	22	6	+	42162705	42162793
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NM_001242778	2	21	8	+	42171840	42171947
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NR_033819	5	21	9	+	42171840	42171947
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NR_033818	4	22	9	+	42171840	42171947
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NM_001556	3	22	9	+	42171840	42171947
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NM_001190720	1	21	8	+	42171840	42171947
278446241	chr8	42171807	42171975	42171834	42171953	IKBKB	NR_040009	6	22	9	+	42171840	42171947
279020701	chr8	42175090	42175247	42175111	42175218	IKBKB	NM_001242778	2	21	11	+	42175175	42175289
279020701	chr8	42175090	42175247	42175111	42175218	IKBKB	NR_033819	5	21	12	+	42175175	42175289
279020701	chr8	42175090	42175247	42175111	42175218	IKBKB	NR_033818	4	22	12	+	42175175	42175289
279020701	chr8	42175090	42175247	42175111	42175218	IKBKB	NM_001556	3	22	12	+	42175175	42175289

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279020701	chr8	42175090	42175247	42175111	42175218	IKBKB	NM_001190720	1	21	11	+	42175175	42175289
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NM_001242778	2	21	13	+	42176788	42176939
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NR_033819	5	21	14	+	42176788	42176939
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NR_033818	4	22	14	+	42176788	42176939
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NM_001556	3	22	14	+	42176788	42176939
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NM_001190720	1	21	13	+	42176788	42176939
281248390	chr8	42176713	42176849	42176739	42176825	IKBKB	NR_040009	6	22	14	+	42176788	42176939
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NM_001242778	2	21	16	+	42179414	42179463
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NR_033819	5	21	16	+	42179414	42179463
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NR_033818	4	22	17	+	42179414	42179463
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NM_001556	3	22	17	+	42179414	42179463
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NM_001190720	1	21	16	+	42179414	42179463
279836374	chr8	42179367	42179513	42179393	42179485	IKBKB	NR_040009	6	22	17	+	42179414	42179463
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NM_001242778	2	21	19	+	42183488	42183615
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NR_033819	5	21	19	+	42183488	42183615
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NR_033818	4	22	20	+	42183488	42183615
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NM_001556	3	22	20	+	42183488	42183615
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NM_001190720	1	21	19	+	42183488	42183615
280350475	chr8	42183395	42183550	42183416	42183529	IKBKB	NR_040009	6	22	20	+	42183488	42183615
227207996	chr8	42752269	42752393	42752291	42752376	HOOK3	NM_032410	1	22	1	+	42752033	42752331
228710892	chr8	42780696	42780869	42780724	42780845	HOOK3	NM_032410	1	22	3	+	42780700	42780772
228165872	chr8	42798549	42798702	42798572	42798677	HOOK3	NM_032410	1	22	5	+	42798456	42798588
227631354	chr8	42814258	42814414	42814279	42814388	HOOK3	NM_032410	1	22	8	+	42814374	42814457
229944271	chr8	42821554	42821712	42821579	42821685	HOOK3	NM_032410	1	22	10	+	42821616	42821756
229798736	chr8	42823279	42823427	42823307	42823397	HOOK3	NM_032410	1	22	11	+	42823156	42823357
228752557	chr8	42837712	42837870	42837738	42837845	HOOK3	NM_032410	1	22	14	+	42837770	42837839
227418661	chr8	42862955	42863122	42862981	42863096	HOOK3	NM_032410	1	22	18	+	42862990	42863072
227339244	chr8	42868481	42868647	42868509	42868617	HOOK3	NM_032410	1	22	21	+	42868472	42868543
270870435	chr8	48686801	48686975	48686824	48686948	PRKDC	NM_001081640	1	85	85	-	48685669	48686938
270870435	chr8	48686801	48686975	48686824	48686948	PRKDC	NM_006904	2	86	86	-	48685669	48686938
270368803	chr8	48690328	48690502	48690349	48690478	PRKDC	NM_001081640	1	85	83	-	48690247	48690435
270368803	chr8	48690328	48690502	48690349	48690478	PRKDC	NM_006904	2	86	84	-	48690247	48690435
269471541	chr8	48691315	48691487	48691342	48691459	PRKDC	NM_001081640	1	85	81	-	48691289	48691360
269471541	chr8	48691315	48691487	48691342	48691459	PRKDC	NM_006904	2	86	82	-	48691289	48691360
269600827	chr8	48694737	48694861	48694759	48694835	PRKDC	NM_006904	2	86	80	-	48694723	48694815
270786175	chr8	48697583	48697716	48697609	48697691	PRKDC	NM_001081640	1	85	77	-	48697674	48697878
270786175	chr8	48697583	48697716	48697609	48697691	PRKDC	NM_006904	2	86	77	-	48697674	48697878
269638656	chr8	48701571	48701698	48701594	48701670	PRKDC	NM_001081640	1	85	76	-	48701467	48701610
269638656	chr8	48701571	48701698	48701594	48701670	PRKDC	NM_006904	2	86	76	-	48701467	48701610
270004280	chr8	48706847	48706975	48706875	48706948	PRKDC	NM_001081640	1	85	74	-	48706851	48707062
270004280	chr8	48706847	48706975	48706875	48706948	PRKDC	NM_006904	2	86	74	-	48706851	48707062

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271949406	chr8	48711729	48711876	48711755	48711858	PRKDC	NM_001081640	1	85	72	-	48711771	48711951
271949406	chr8	48711729	48711876	48711755	48711858	PRKDC	NM_006904	2	86	72	-	48711771	48711951
269834686	chr8	48715759	48715893	48715787	48715868	PRKDC	NM_001081640	1	85	70	-	48715867	48716041
269834686	chr8	48715759	48715893	48715787	48715868	PRKDC	NM_006904	2	86	70	-	48715867	48716041
270831079	chr8	48719763	48719936	48719788	48719912	PRKDC	NM_001081640	1	85	69	-	48719698	48719887
270831079	chr8	48719763	48719936	48719788	48719912	PRKDC	NM_006904	2	86	69	-	48719698	48719887
271996184	chr8	48733273	48733444	48733301	48733420	PRKDC	NM_001081640	1	85	66	-	48733280	48733504
271996184	chr8	48733273	48733444	48733301	48733420	PRKDC	NM_006904	2	86	66	-	48733280	48733504
270326104	chr8	48734263	48734415	48734287	48734387	PRKDC	NM_001081640	1	85	65	-	48734165	48734353
270326104	chr8	48734263	48734415	48734287	48734387	PRKDC	NM_006904	2	86	65	-	48734165	48734353
270780839	chr8	48739314	48739487	48739333	48739464	PRKDC	NM_001081640	1	85	63	-	48739217	48739422
270780839	chr8	48739314	48739487	48739333	48739464	PRKDC	NM_006904	2	86	63	-	48739217	48739422
269797825	chr8	48743078	48743234	48743100	48743213	PRKDC	NM_001081640	1	85	61	-	48743166	48743297
269797825	chr8	48743078	48743234	48743100	48743213	PRKDC	NM_006904	2	86	61	-	48743166	48743297
270605492	chr8	48746693	48746866	48746718	48746841	PRKDC	NM_001081640	1	85	59	-	48746757	48746957
270605492	chr8	48746693	48746866	48746718	48746841	PRKDC	NM_006904	2	86	59	-	48746757	48746957
271211783	chr8	48749051	48749225	48749073	48749197	PRKDC	NM_001081640	1	85	58	-	48748899	48749088
271211783	chr8	48749051	48749225	48749073	48749197	PRKDC	NM_006904	2	86	58	-	48748899	48749088
270039550	chr8	48751675	48751833	48751698	48751808	PRKDC	NM_001081640	1	85	56	-	48751709	48751807
270039550	chr8	48751675	48751833	48751698	48751808	PRKDC	NM_006904	2	86	56	-	48751709	48751807
269675595	chr8	48761841	48762001	48761867	48761974	PRKDC	NM_001081640	1	85	53	-	48761940	48762064
269675595	chr8	48761841	48762001	48761867	48761974	PRKDC	NM_006904	2	86	53	-	48761940	48762064
269640072	chr8	48766523	48766688	48766546	48766668	PRKDC	NM_001081640	1	85	51	-	48766644	48766775
269640072	chr8	48766523	48766688	48766546	48766668	PRKDC	NM_006904	2	86	51	-	48766644	48766775
270045915	chr8	48767847	48767983	48767875	48767961	PRKDC	NM_001081640	1	85	50	-	48767783	48767934
270045915	chr8	48767847	48767983	48767875	48767961	PRKDC	NM_006904	2	86	50	-	48767783	48767934
272042474	chr8	48771135	48771286	48771157	48771257	PRKDC	NM_001081640	1	85	48	-	48771077	48771196
272042474	chr8	48771135	48771286	48771157	48771257	PRKDC	NM_006904	2	86	48	-	48771077	48771196
270242562	chr8	48772169	48772322	48772188	48772296	PRKDC	NM_001081640	1	85	46	-	48772172	48772320
270242562	chr8	48772169	48772322	48772188	48772296	PRKDC	NM_006904	2	86	46	-	48772172	48772320
270085914	chr8	48774568	48774738	48774595	48774710	PRKDC	NM_001081640	1	85	44	-	48774623	48774688
270085914	chr8	48774568	48774738	48774595	48774710	PRKDC	NM_006904	2	86	44	-	48774623	48774688
271078902	chr8	48775999	48776149	48776027	48776118	PRKDC	NM_001081640	1	85	42	-	48775960	48776138
271078902	chr8	48775999	48776149	48776027	48776118	PRKDC	NM_006904	2	86	42	-	48775960	48776138
270592738	chr8	48777259	48777385	48777283	48777358	PRKDC	NM_001081640	1	85	41	-	48777117	48777324
270592738	chr8	48777259	48777385	48777283	48777358	PRKDC	NM_006904	2	86	41	-	48777117	48777324
269704377	chr8	48792132	48792264	48792153	48792237	PRKDC	NM_001081640	1	85	39	-	48792052	48792219
269704377	chr8	48792132	48792264	48792153	48792237	PRKDC	NM_006904	2	86	39	-	48792052	48792219
270534371	chr8	48798506	48798639	48798535	48798619	PRKDC	NM_001081640	1	85	36	-	48798505	48798708
270534371	chr8	48798506	48798639	48798535	48798619	PRKDC	NM_006904	2	86	36	-	48798505	48798708
270948891	chr8	48800967	48801136	48800991	48801114	PRKDC	NM_001081640	1	85	34	-	48801079	48801211

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270948891	chr8	48800967	48801136	48800991	48801114	PRKDC	NM_006904	2	86	34	-	48801079	48801211
269942705	chr8	48802735	48802884	48802759	48802865	PRKDC	NM_001081640	1	85	32	-	48802818	48803041
269942705	chr8	48802735	48802884	48802759	48802865	PRKDC	NM_006904	2	86	32	-	48802818	48803041
271168104	chr8	48805801	48805951	48805820	48805926	PRKDC	NM_001081640	1	85	31	-	48805700	48805947
271168104	chr8	48805801	48805951	48805820	48805926	PRKDC	NM_006904	2	86	31	-	48805700	48805947
271330469	chr8	48810950	48811121	48810973	48811097	PRKDC	NM_001081640	1	85	29	-	48811030	48811129
271330469	chr8	48810950	48811121	48810973	48811097	PRKDC	NM_006904	2	86	29	-	48811030	48811129
271559960	chr8	48815198	48815343	48815222	48815316	PRKDC	NM_001081640	1	85	27	-	48815129	48815355
271559960	chr8	48815198	48815343	48815222	48815316	PRKDC	NM_006904	2	86	27	-	48815129	48815355
271906494	chr8	48824896	48825039	48824920	48825018	PRKDC	NM_001081640	1	85	25	-	48824970	48825122
271906494	chr8	48824896	48825039	48824920	48825018	PRKDC	NM_006904	2	86	25	-	48824970	48825122
271155646	chr8	48826584	48826716	48826606	48826688	PRKDC	NM_001081640	1	85	24	-	48826461	48826624
271155646	chr8	48826584	48826716	48826606	48826688	PRKDC	NM_006904	2	86	24	-	48826461	48826624
269732920	chr8	48830902	48831036	48830924	48831003	PRKDC	NM_001081640	1	85	22	-	48830837	48830943
269732920	chr8	48830902	48831036	48830924	48831003	PRKDC	NM_006904	2	86	22	-	48830837	48830943
272025776	chr8	48840281	48840452	48840302	48840428	PRKDC	NM_001081640	1	85	20	-	48840331	48840450
272025776	chr8	48840281	48840452	48840302	48840428	PRKDC	NM_006904	2	86	20	-	48840331	48840450
270100595	chr8	48842396	48842566	48842422	48842540	PRKDC	NM_001081640	1	85	18	-	48842413	48842572
270100595	chr8	48842396	48842566	48842422	48842540	PRKDC	NM_006904	2	86	18	-	48842413	48842572
271546691	chr8	48845472	48845644	48845500	48845616	PRKDC	NM_001081640	1	85	16	-	48845580	48845732
271546691	chr8	48845472	48845644	48845500	48845616	PRKDC	NM_006904	2	86	16	-	48845580	48845732
270642164	chr8	48846598	48846764	48846619	48846741	PRKDC	NM_001081640	1	85	15	-	48846525	48846650
270642164	chr8	48846598	48846764	48846619	48846741	PRKDC	NM_006904	2	86	15	-	48846525	48846650
270600037	chr8	48848286	48848414	48848313	48848388	PRKDC	NM_001081640	1	85	13	-	48848292	48848460
270600037	chr8	48848286	48848414	48848313	48848388	PRKDC	NM_006904	2	86	13	-	48848292	48848460
272427871	chr8	48849022	48849159	48849047	48849131	PRKDC	NM_001081640	1	85	12	-	48848913	48849077
272427871	chr8	48849022	48849159	48849047	48849131	PRKDC	NM_006904	2	86	12	-	48848913	48849077
269590690	chr8	48855701	48855874	48855728	48855847	PRKDC	NM_001081640	1	85	10	-	48855769	48855926
269590690	chr8	48855701	48855874	48855728	48855847	PRKDC	NM_006904	2	86	10	-	48855769	48855926
271449773	chr8	48856466	48856622	48856492	48856594	PRKDC	NM_001081640	1	85	8	-	48856534	48856589
271449773	chr8	48856466	48856622	48856492	48856594	PRKDC	NM_006904	2	86	8	-	48856534	48856589
270253904	chr8	48866394	48866519	48866418	48866494	PRKDC	NM_001081640	1	85	6	-	48866367	48866479
270253904	chr8	48866394	48866519	48866418	48866494	PRKDC	NM_006904	2	86	6	-	48866367	48866479
269459408	chr8	48869599	48869771	48869625	48869751	PRKDC	NM_001081640	1	85	3	-	48869731	48869823
269459408	chr8	48869599	48869771	48869625	48869751	PRKDC	NM_006904	2	86	3	-	48869731	48869823
237033733	chr8	57078748	57078902	57078770	57078879	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237033733	chr8	57078748	57078902	57078770	57078879	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237033733	chr8	57078748	57078902	57078770	57078879	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
240860912	chr8	57079157	57079329	57079181	57079307	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240860912	chr8	57079157	57079329	57079181	57079307	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
240860912	chr8	57079157	57079329	57079181	57079307	PLAG1	NM_001114635	2	3	3	-	57073468	57080062

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237168083	chr8	57079648	57079817	57079672	57079796	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237168083	chr8	57079648	57079817	57079672	57079796	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237168083	chr8	57079648	57079817	57079672	57079796	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
238258736	chr8	57080524	57080649	57080547	57080625	PLAG1	NM_002655	3	5	4	-	57080587	57080945
238258736	chr8	57080524	57080649	57080547	57080625	PLAG1	NM_001114634	1	4	3	-	57080587	57080945
237139050	chr8	71033445	71033583	71033475	71033557	NCOA2	NM_006540	1	23	22	-	71033537	71033626
236250927	chr8	71036867	71037033	71036888	71037011	NCOA2	NM_006540	1	23	20	-	71036923	71037100
237379635	chr8	71039133	71039304	71039157	71039284	NCOA2	NM_006540	1	23	19	-	71039048	71039282
235661448	chr8	71041043	71041210	71041063	71041185	NCOA2	NM_006540	1	23	17	-	71040937	71041215
239977787	chr8	71050414	71050577	71050435	71050551	NCOA2	NM_006540	1	23	15	-	71050438	71050567
236809345	chr8	71056841	71056970	71056867	71056944	NCOA2	NM_006540	1	23	13	-	71056877	71057083
236283564	chr8	71060569	71060694	71060590	71060667	NCOA2	NM_006540	1	23	12	-	71060508	71060718
240191283	chr8	71068391	71068552	71068411	71068524	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240161497	chr8	71068758	71068902	71068783	71068876	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240187068	chr8	71069191	71069355	71069214	71069326	NCOA2	NM_006540	1	23	11	-	71068206	71069475
238176328	chr8	71071832	71072006	71071857	71071979	NCOA2	NM_006540	1	23	10	-	71071740	71071887
235447984	chr8	71075705	71075879	71075731	71075852	NCOA2	NM_006540	1	23	8	-	71075700	71075801
235550790	chr8	71082420	71082594	71082447	71082572	NCOA2	NM_006540	1	23	6	-	71082437	71082614
240422418	chr8	71126148	71126309	71126173	71126284	NCOA2	NM_006540	1	23	4	-	71126138	71126310
240605573	chr8	90947767	90947941	90947795	90947914	NBN	NM_002485	1	16	16	-	90945564	90947840
241229935	chr8	90958334	90958507	90958359	90958480	NBN	NM_002485	1	16	13	-	90958368	90958523
258687897	chr8	90965482	90965612	90965508	90965583	NBN	NM_002485	1	16	11	-	90965472	90965919
258761299	chr8	90965829	90965989	90965856	90965961	NBN	NM_002485	1	16	11	-	90965472	90965919
235657431	chr8	90967707	90967855	90967734	90967824	NBN	NM_002485	1	16	10	-	90967511	90967783
238364889	chr8	90976692	90976821	90976713	90976790	NBN	NM_002485	1	16	8	-	90976638	90976735
236201712	chr8	90983444	90983598	90983465	90983570	NBN	NM_002485	1	16	6	-	90983401	90983518
239099062	chr8	90993031	90993179	90993059	90993156	NBN	NM_002485	1	16	4	-	90992962	90993121
236152793	chr8	90994899	90995057	90994922	90995032	NBN	NM_002485	1	16	2	-	90994950	90995083
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_004349	12	11	11	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198625	1	15	15	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198626	2	13	13	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198627	3	14	14	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198679	11	12	12	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_175636	15	10	10	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198630	6	13	13	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_175635	14	11	11	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_175634	13	12	12	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198633	9	11	11	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198632	8	12	12	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198631	7	12	12	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198634	10	11	11	-	92967195	92972745

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198629	5	12	12	-	92967195	92972745
240166378	chr8	92972530	92972691	92972549	92972669	RUNX1T1	NM_001198628	4	12	12	-	92967195	92972745
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_004349	12	11	9	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198625	1	15	13	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198626	2	13	11	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198627	3	14	12	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198679	11	12	10	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_175636	15	10	8	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198630	6	13	11	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_175635	14	11	9	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_175634	13	12	10	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198633	9	11	9	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198632	8	12	10	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198631	7	12	10	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198634	10	11	9	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198629	5	12	10	-	92988133	92988201
241404270	chr8	92988063	92988225	92988090	92988202	RUNX1T1	NM_001198628	4	12	10	-	92988133	92988201
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_004349	12	11	7	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198625	1	15	11	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198626	2	13	9	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198627	3	14	10	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198679	11	12	8	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_175636	15	10	6	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198630	6	13	9	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_175635	14	11	7	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_175634	13	12	8	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198633	9	11	7	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198632	8	12	8	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198631	7	12	8	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198634	10	11	7	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198629	5	12	8	-	92999115	92999200
264446807	chr8	92999108	92999235	92999135	92999207	RUNX1T1	NM_001198628	4	12	8	-	92999115	92999200
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_004349	12	11	5	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198625	1	15	9	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198626	2	13	7	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198627	3	14	8	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198679	11	12	6	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_175636	15	10	4	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198630	6	13	7	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_175635	14	11	5	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_175634	13	12	6	-	93017344	93017525

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198633	9	11	5	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198632	8	12	6	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198631	7	12	6	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198634	10	11	5	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198629	5	12	6	-	93017344	93017525
241679670	chr8	93017245	93017419	93017268	93017399	RUNX1T1	NM_001198628	4	12	6	-	93017344	93017525
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_004349	12	11	3	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198625	1	15	7	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198626	2	13	5	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198627	3	14	6	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198679	11	12	4	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_175636	15	10	2	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198630	6	13	5	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_175635	14	11	3	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_175634	13	12	4	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198633	9	11	3	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198632	8	12	4	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198631	7	12	4	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198634	10	11	3	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198629	5	12	4	-	93026807	93027048
240921248	chr8	93026713	93026861	93026736	93026836	RUNX1T1	NM_001198628	4	12	4	-	93026807	93027048
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_175636	15	10	1	-	93029454	93029908
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_004349	12	11	2	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198625	1	15	6	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198626	2	13	4	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198627	3	14	5	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198679	11	12	3	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198630	6	13	4	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_175635	14	11	2	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_175634	13	12	3	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198633	9	11	2	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198632	8	12	3	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198631	7	12	3	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198634	10	11	2	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198629	5	12	3	-	93029454	93029591
238575716	chr8	93029509	93029647	93029530	93029619	RUNX1T1	NM_001198628	4	12	3	-	93029454	93029591
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198630	6	13	1	-	93107256	93107490
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_175635	14	11	1	-	93107256	93107490
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198632	8	12	1	-	93107256	93107490
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198629	5	12	1	-	93107256	93107490
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198625	1	15	2	-	93107256	93107399

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198626	2	13	2	-	93107256	93107399
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198627	3	14	2	-	93107256	93107399
239381201	chr8	93107257	93107425	93107277	93107399	RUNX1T1	NM_001198679	11	12	2	-	93107256	93107399
303497222	chr8	103266429	103266600	103266453	103266571	UBR5	NM_015902	1	59	59	-	103264502	103266742
302814485	chr8	103271113	103271269	103271139	103271248	UBR5	NM_015902	1	59	57	-	103271213	103271357
302527710	chr8	103273396	103273529	103273421	103273501	UBR5	NM_015902	1	59	56	-	103273374	103273487
304017398	chr8	103277318	103277445	103277346	103277422	UBR5	NM_015902	1	59	53	-	103277328	103277506
299488471	chr8	103281125	103281280	103281153	103281255	UBR5	NM_015902	1	59	51	-	103281206	103281336
300936102	chr8	103283441	103283599	103283466	103283571	UBR5	NM_015902	1	59	49	-	103283362	103283473
300123039	chr8	103287741	103287913	103287770	103287888	UBR5	NM_015902	1	59	47	-	103287749	103287847
302476702	chr8	103289289	103289421	103289311	103289393	UBR5	NM_015902	1	59	45	-	103289200	103289420
303845083	chr8	103291146	103291320	103291170	103291299	UBR5	NM_015902	1	59	43	-	103291264	103291436
299284128	chr8	103293423	103293558	103293451	103293534	UBR5	NM_015902	1	59	41	-	103293517	103293747
302265511	chr8	103297455	103297627	103297476	103297598	UBR5	NM_015902	1	59	40	-	103297355	103297566
301346189	chr8	103298566	103298730	103298593	103298704	UBR5	NM_015902	1	59	38	-	103298588	103298845
303129296	chr8	103300362	103300502	103300389	103300479	UBR5	NM_015902	1	59	36	-	103300383	103300494
302119660	chr8	103305733	103305904	103305756	103305879	UBR5	NM_015902	1	59	34	-	103305833	103306072
300345575	chr8	103306058	103306220	103306086	103306196	UBR5	NM_015902	1	59	33	-	103306183	103306343
300233954	chr8	103307238	103307366	103307261	103307339	UBR5	NM_015902	1	59	32	-	103307210	103307339
300659642	chr8	103307646	103307788	103307668	103307763	UBR5	NM_015902	1	59	30	-	103307642	103307760
330045616	chr8	103309002	103309176	103309029	103309152	UBR5	NM_015902	1	59	28	-	103309121	103309212
304430875	chr8	103310673	103310798	103310695	103310765	UBR5	NM_015902	1	59	26	-	103310620	103310717
305703288	chr8	103311679	103311852	103311701	103311824	UBR5	NM_015902	1	59	24	-	103311680	103311775
303256754	chr8	103316263	103316391	103316289	103316364	UBR5	NM_015902	1	59	22	-	103316271	103316397
301660074	chr8	103317405	103317549	103317431	103317524	UBR5	NM_015902	1	59	21	-	103317313	103317523
299438638	chr8	103323872	103324009	103323898	103323987	UBR5	NM_015902	1	59	19	-	103323963	103324117
300628403	chr8	103324446	103324609	103324467	103324581	UBR5	NM_015902	1	59	18	-	103324362	103324473
300628403	chr8	103324446	103324609	103324467	103324581	UBR5	NM_015902	1	59	17	-	103324570	103324713
300596884	chr8	103325933	103326076	103325956	103326049	UBR5	NM_015902	1	59	16	-	103326032	103326144
300462231	chr8	103335609	103335751	103335636	103335725	UBR5	NM_015902	1	59	14	-	103335539	103335723
300912867	chr8	103340031	103340184	103340055	103340156	UBR5	NM_015902	1	59	12	-	103339970	103340124
303516246	chr8	103341574	103341709	103341599	103341680	UBR5	NM_015902	1	59	10	-	103341511	103341627
300316983	chr8	103357568	103357710	103357591	103357682	UBR5	NM_015902	1	59	8	-	103357624	103357773
300196634	chr8	103359101	103359267	103359129	103359245	UBR5	NM_015902	1	59	6	-	103359131	103359320
302194718	chr8	103372713	103372886	103372741	103372861	UBR5	NM_015902	1	59	4	-	103372817	103372893
306013774	chr8	103424382	103424555	103424399	103424538	UBR5	NM_015902	1	59	1	-	103424401	103424917
286218273	chr8	113243723	113243850	113243751	113243822	CSMD3	NM_052900	1	69	67	-	113243774	113243861
286218273	chr8	113243723	113243850	113243751	113243822	CSMD3	NM_198123	2	71	69	-	113243774	113243861
286218273	chr8	113243723	113243850	113243751	113243822	CSMD3	NM_198124	3	72	70	-	113243774	113243861
287663353	chr8	113249377	113249509	113249403	113249481	CSMD3	NM_052900	1	69	65	-	113249419	113249577
287663353	chr8	113249377	113249509	113249403	113249481	CSMD3	NM_198123	2	71	67	-	113249419	113249577

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287663353	chr8	113249377	113249509	113249403	113249481	CSMD3	NM_198124	3	72	68	-	113249419	113249577
286208090	chr8	113256658	113256819	113256685	113256790	CSMD3	NM_052900	1	69	63	-	113256623	113256802
286208090	chr8	113256658	113256819	113256685	113256790	CSMD3	NM_198123	2	71	65	-	113256623	113256802
286208090	chr8	113256658	113256819	113256685	113256790	CSMD3	NM_198124	3	72	66	-	113256623	113256802
285930418	chr8	113266485	113266659	113266513	113266635	CSMD3	NM_052900	1	69	61	-	113266482	113266555
285930418	chr8	113266485	113266659	113266513	113266635	CSMD3	NM_198123	2	71	63	-	113266482	113266555
285930418	chr8	113266485	113266659	113266513	113266635	CSMD3	NM_198124	3	72	64	-	113266482	113266555
285265290	chr8	113275866	113276006	113275887	113275982	CSMD3	NM_052900	1	69	59	-	113275868	113276041
285265290	chr8	113275866	113276006	113275887	113275982	CSMD3	NM_198123	2	71	61	-	113275868	113276041
285265290	chr8	113275866	113276006	113275887	113275982	CSMD3	NM_198124	3	72	62	-	113275868	113276041
289035237	chr8	113293278	113293451	113293305	113293431	CSMD3	NM_052900	1	69	57	-	113293403	113293579
289035237	chr8	113293278	113293451	113293305	113293431	CSMD3	NM_198123	2	71	59	-	113293403	113293579
289035237	chr8	113293278	113293451	113293305	113293431	CSMD3	NM_198124	3	72	60	-	113293403	113293579
286707314	chr8	113299280	113299430	113299304	113299403	CSMD3	NM_052900	1	69	56	-	113299293	113299475
286707314	chr8	113299280	113299430	113299304	113299403	CSMD3	NM_198123	2	71	58	-	113299293	113299475
286707314	chr8	113299280	113299430	113299304	113299403	CSMD3	NM_198124	3	72	59	-	113299293	113299475
286335906	chr8	113303675	113303840	113303705	113303812	CSMD3	NM_052900	1	69	54	-	113303739	113303924
286335906	chr8	113303675	113303840	113303705	113303812	CSMD3	NM_198123	2	71	56	-	113303739	113303924
286335906	chr8	113303675	113303840	113303705	113303812	CSMD3	NM_198124	3	72	57	-	113303739	113303924
287749970	chr8	113304730	113304867	113304758	113304839	CSMD3	NM_052900	1	69	53	-	113304766	113304939
287749970	chr8	113304730	113304867	113304758	113304839	CSMD3	NM_198123	2	71	55	-	113304766	113304939
287749970	chr8	113304730	113304867	113304758	113304839	CSMD3	NM_198124	3	72	56	-	113304766	113304939
287205821	chr8	113308194	113308326	113308219	113308299	CSMD3	NM_052900	1	69	52	-	113308062	113308235
287205821	chr8	113308194	113308326	113308219	113308299	CSMD3	NM_198123	2	71	54	-	113308062	113308235
287205821	chr8	113308194	113308326	113308219	113308299	CSMD3	NM_198124	3	72	55	-	113308062	113308235
286328580	chr8	113316881	113317013	113316910	113316988	CSMD3	NM_198123	2	71	52	-	113316950	113317144
286328580	chr8	113316881	113317013	113316910	113316988	CSMD3	NM_198124	3	72	53	-	113316950	113317144
288591171	chr8	113318293	113318451	113318320	113318423	CSMD3	NM_052900	1	69	50	-	113318236	113318421
288591171	chr8	113318293	113318451	113318320	113318423	CSMD3	NM_198123	2	71	51	-	113318236	113318421
288591171	chr8	113318293	113318451	113318320	113318423	CSMD3	NM_198124	3	72	52	-	113318236	113318421
287630566	chr8	113326091	113326265	113326119	113326242	CSMD3	NM_052900	1	69	48	-	113326135	113326281
287630566	chr8	113326091	113326265	113326119	113326242	CSMD3	NM_198123	2	71	49	-	113326135	113326281
287630566	chr8	113326091	113326265	113326119	113326242	CSMD3	NM_198124	3	72	50	-	113326135	113326281
287435934	chr8	113330941	113331105	113330972	113331084	CSMD3	NM_052900	1	69	46	-	113331066	113331179
287435934	chr8	113330941	113331105	113330972	113331084	CSMD3	NM_198123	2	71	47	-	113331066	113331179
287435934	chr8	113330941	113331105	113330972	113331084	CSMD3	NM_198124	3	72	48	-	113331066	113331179
288763888	chr8	113347632	113347767	113347658	113347739	CSMD3	NM_052900	1	69	44	-	113347558	113347703
288763888	chr8	113347632	113347767	113347658	113347739	CSMD3	NM_198123	2	71	45	-	113347558	113347703
288763888	chr8	113347632	113347767	113347658	113347739	CSMD3	NM_198124	3	72	46	-	113347558	113347703
288727667	chr8	113349766	113349934	113349789	113349915	CSMD3	NM_052900	1	69	42	-	113349772	113349960
288727667	chr8	113349766	113349934	113349789	113349915	CSMD3	NM_198123	2	71	43	-	113349772	113349960

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288727667	chr8	113349766	113349934	113349789	113349915	CSMD3	NM_198124	3	72	44	-	113349772	113349960
287949252	chr8	113353843	113354002	113353870	113353975	CSMD3	NM_052900	1	69	41	-	113353706	113353915
287949252	chr8	113353843	113354002	113353870	113353975	CSMD3	NM_198123	2	71	42	-	113353706	113353915
287949252	chr8	113353843	113354002	113353870	113353975	CSMD3	NM_198124	3	72	43	-	113353706	113353915
287151024	chr8	113363430	113363583	113363454	113363552	CSMD3	NM_052900	1	69	39	-	113363404	113363473
287151024	chr8	113363430	113363583	113363454	113363552	CSMD3	NM_198123	2	71	40	-	113363404	113363473
287151024	chr8	113363430	113363583	113363454	113363552	CSMD3	NM_198124	3	72	41	-	113363404	113363473
287583814	chr8	113392604	113392730	113392627	113392702	CSMD3	NM_052900	1	69	37	-	113392581	113392685
287583814	chr8	113392604	113392730	113392627	113392702	CSMD3	NM_198123	2	71	38	-	113392581	113392685
287583814	chr8	113392604	113392730	113392627	113392702	CSMD3	NM_198124	3	72	39	-	113392581	113392685
286753007	chr8	113402907	113403047	113402928	113403023	CSMD3	NM_052900	1	69	35	-	113402893	113403017
286753007	chr8	113402907	113403047	113402928	113403023	CSMD3	NM_198123	2	71	36	-	113402893	113403017
286753007	chr8	113402907	113403047	113402928	113403023	CSMD3	NM_198124	3	72	37	-	113402893	113403017
287116268	chr8	113420519	113420657	113420544	113420629	CSMD3	NM_052900	1	69	33	-	113420547	113420642
287116268	chr8	113420519	113420657	113420544	113420629	CSMD3	NM_198123	2	71	34	-	113420547	113420642
287116268	chr8	113420519	113420657	113420544	113420629	CSMD3	NM_198124	3	72	35	-	113420547	113420642
285177464	chr8	113484802	113484944	113484830	113484926	CSMD3	NM_052900	1	69	31	-	113484820	113484936
285177464	chr8	113484802	113484944	113484830	113484926	CSMD3	NM_198123	2	71	32	-	113484820	113484936
285177464	chr8	113484802	113484944	113484830	113484926	CSMD3	NM_198124	3	72	33	-	113484820	113484936
284758652	chr8	113515938	113516112	113515964	113516084	CSMD3	NM_052900	1	69	29	-	113516019	113516206
284758652	chr8	113515938	113516112	113515964	113516084	CSMD3	NM_198123	2	71	30	-	113516019	113516206
284758652	chr8	113515938	113516112	113515964	113516084	CSMD3	NM_198124	3	72	31	-	113516019	113516206
288895357	chr8	113518929	113519053	113518954	113519027	CSMD3	NM_052900	1	69	28	-	113518920	113519058
288895357	chr8	113518929	113519053	113518954	113519027	CSMD3	NM_198123	2	71	29	-	113518920	113519058
288895357	chr8	113518929	113519053	113518954	113519027	CSMD3	NM_198124	3	72	30	-	113518920	113519058
288870147	chr8	113562852	113562992	113562880	113562964	CSMD3	NM_052900	1	69	26	-	113562900	113563102
288870147	chr8	113562852	113562992	113562880	113562964	CSMD3	NM_198123	2	71	27	-	113562900	113563102
288870147	chr8	113562852	113562992	113562880	113562964	CSMD3	NM_198124	3	72	28	-	113562900	113563102
286433787	chr8	113564854	113565000	113564874	113564972	CSMD3	NM_052900	1	69	25	-	113564823	113564949
286433787	chr8	113564854	113565000	113564874	113564972	CSMD3	NM_198123	2	71	26	-	113564823	113564949
286433787	chr8	113564854	113565000	113564874	113564972	CSMD3	NM_198124	3	72	27	-	113564823	113564949
286262556	chr8	113569147	113569311	113569169	113569282	CSMD3	NM_052900	1	69	24	-	113568992	113569183
286262556	chr8	113569147	113569311	113569169	113569282	CSMD3	NM_198123	2	71	25	-	113568992	113569183
286262556	chr8	113569147	113569311	113569169	113569282	CSMD3	NM_198124	3	72	26	-	113568992	113569183
286419140	chr8	113599261	113599409	113599292	113599381	CSMD3	NM_052900	1	69	22	-	113599295	113599464
286419140	chr8	113599261	113599409	113599292	113599381	CSMD3	NM_198123	2	71	23	-	113599295	113599464
286419140	chr8	113599261	113599409	113599292	113599381	CSMD3	NM_198124	3	72	24	-	113599295	113599464
288909724	chr8	113649085	113649221	113649108	113649198	CSMD3	NM_052900	1	69	21	-	113649046	113649234
288909724	chr8	113649085	113649221	113649108	113649198	CSMD3	NM_198123	2	71	22	-	113649046	113649234
288909724	chr8	113649085	113649221	113649108	113649198	CSMD3	NM_198124	3	72	23	-	113649046	113649234
288134928	chr8	113651060	113651197	113651084	113651168	CSMD3	NM_052900	1	69	20	-	113650925	113651140

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288134928	chr8	113651060	113651197	113651084	113651168	CSMD3	NM_198123	2	71	21	-	113650925	113651140
288134928	chr8	113651060	113651197	113651084	113651168	CSMD3	NM_198124	3	72	22	-	113650925	113651140
286823090	chr8	113662450	113662619	113662476	113662591	CSMD3	NM_052900	1	69	18	-	113662390	113662578
286823090	chr8	113662450	113662619	113662476	113662591	CSMD3	NM_198123	2	71	19	-	113662390	113662578
286823090	chr8	113662450	113662619	113662476	113662591	CSMD3	NM_198124	3	72	20	-	113662390	113662578
286456495	chr8	113678380	113678553	113678403	113678531	CSMD3	NM_052900	1	69	16	-	113678506	113678644
286456495	chr8	113678380	113678553	113678403	113678531	CSMD3	NM_198123	2	71	17	-	113678506	113678644
286456495	chr8	113678380	113678553	113678403	113678531	CSMD3	NM_198124	3	72	18	-	113678506	113678644
286414130	chr8	113694663	113694829	113694690	113694809	CSMD3	NM_052900	1	69	15	-	113694671	113694865
286414130	chr8	113694663	113694829	113694690	113694809	CSMD3	NM_198123	2	71	16	-	113694671	113694865
286414130	chr8	113694663	113694829	113694690	113694809	CSMD3	NM_198124	3	72	17	-	113694671	113694865
285081564	chr8	113697642	113697809	113697665	113697783	CSMD3	NM_052900	1	69	14	-	113697635	113697961
285081564	chr8	113697642	113697809	113697665	113697783	CSMD3	NM_198123	2	71	15	-	113697635	113697961
285081564	chr8	113697642	113697809	113697665	113697783	CSMD3	NM_198124	3	72	16	-	113697635	113697961
288682907	chr8	113702173	113702333	113702195	113702310	CSMD3	NM_052900	1	69	13	-	113702097	113702279
288682907	chr8	113702173	113702333	113702195	113702310	CSMD3	NM_198123	2	71	14	-	113702097	113702279
288682907	chr8	113702173	113702333	113702195	113702310	CSMD3	NM_198124	3	72	15	-	113702097	113702279
289055422	chr8	113871249	113871421	113871274	113871400	CSMD3	NM_052900	1	69	10	-	113871374	113871495
289055422	chr8	113871249	113871421	113871274	113871400	CSMD3	NM_198123	2	71	11	-	113871374	113871495
289055422	chr8	113871249	113871421	113871274	113871400	CSMD3	NM_198124	3	72	12	-	113871374	113871495
288712389	chr8	113959909	113960083	113959935	113960059	CSMD3	NM_052900	1	69	8	-	113960019	113960106
288712389	chr8	113959909	113960083	113959935	113960059	CSMD3	NM_198123	2	71	9	-	113960019	113960106
288712389	chr8	113959909	113960083	113959935	113960059	CSMD3	NM_198124	3	72	10	-	113960019	113960106
287602592	chr8	113988102	113988269	113988128	113988248	CSMD3	NM_198123	2	71	7	-	113988066	113988377
287602592	chr8	113988102	113988269	113988128	113988248	CSMD3	NM_198124	3	72	8	-	113988066	113988377
285112533	chr8	114110939	114111108	114110963	114111084	CSMD3	NM_052900	1	69	5	-	114110985	114111192
285112533	chr8	114110939	114111108	114110963	114111084	CSMD3	NM_198123	2	71	5	-	114110985	114111192
285112533	chr8	114110939	114111108	114110963	114111084	CSMD3	NM_198124	3	72	6	-	114110985	114111192
286371633	chr8	114186019	114186145	114186040	114186121	CSMD3	NM_052900	1	69	4	-	114185951	114186145
286371633	chr8	114186019	114186145	114186040	114186121	CSMD3	NM_198123	2	71	4	-	114185951	114186145
286371633	chr8	114186019	114186145	114186040	114186121	CSMD3	NM_198124	3	72	5	-	114185951	114186145
288175566	chr8	114326811	114326979	114326837	114326954	CSMD3	NM_052900	1	69	2	-	114326800	114327022
288175566	chr8	114326811	114326979	114326837	114326954	CSMD3	NM_198123	2	71	2	-	114326800	114327022
288175566	chr8	114326811	114326979	114326837	114326954	CSMD3	NM_198124	3	72	3	-	114326800	114327022
287781817	chr8	114388969	114389107	114388989	114389083	CSMD3	NM_198124	3	72	2	-	114388967	114389114
232634104	chr8	118812017	118812187	118812038	118812163	EXT1	NM_000127	1	11	11	-	118811602	118812136
229568209	chr8	118819472	118819645	118819493	118819623	EXT1	NM_000127	1	11	9	-	118819456	118819616
228004057	chr8	118834636	118834780	118834662	118834756	EXT1	NM_000127	1	11	5	-	118834704	118834836
232762629	chr8	118849301	118849470	118849321	118849442	EXT1	NM_000127	1	11	2	-	118849347	118849440
231402468	chr8	119122654	119122799	119122674	119122777	EXT1	NM_000127	1	11	1	-	119122324	119124058
231410283	chr8	119123052	119123226	119123073	119123203	EXT1	NM_000127	1	11	1	-	119122324	119124058

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240725334	chr8	128750536	128750677	128750559	128750656	MYC	NM_002467	1	3	2	+	128750494	128751265
240719158	chr8	128750932	128751080	128750952	128751061	MYC	NM_002467	1	3	2	+	128750494	128751265
242581871	chr8	128752643	128752809	128752671	128752787	MYC	NM_002467	1	3	3	+	128752642	128753680
237590480	chr8	128753079	128753218	128753100	128753192	MYC	NM_002467	1	3	3	+	128752642	128753680
240785971	chr8	145737061	145737208	145737080	145737187	RECQL4	NM_004260	1	22	21	-	145737064	145737172
242698868	chr8	145737599	145737733	145737624	145737712	RECQL4	NM_004260	1	22	19	-	145737527	145737707
239191013	chr8	145738121	145738264	145738139	145738243	RECQL4	NM_004260	1	22	17	-	145738025	145738154
239191013	chr8	145738121	145738264	145738139	145738243	RECQL4	NM_004260	1	22	16	-	145738230	145738521
240942348	chr8	145738564	145738731	145738582	145738714	RECQL4	NM_004260	1	22	15	-	145738601	145738767
262835372	chr8	145738980	145739108	145738997	145739089	RECQL4	NM_004260	1	22	13	-	145738955	145739096
238167004	chr8	145739546	145739717	145739565	145739698	RECQL4	NM_004260	1	22	11	-	145739573	145739746
264210570	chr8	145740273	145740442	145740292	145740424	RECQL4	NM_004260	1	22	9	-	145740320	145740456
264233808	chr8	145740632	145740801	145740657	145740780	RECQL4	NM_004260	1	22	7	-	145740710	145740841
264055210	chr8	145741297	145741451	145741317	145741429	RECQL4	NM_004260	1	22	5	-	145741372	145742148
264089017	chr8	145741705	145741872	145741726	145741847	RECQL4	NM_004260	1	22	5	-	145741372	145742148
240782358	chr8	145742397	145742547	145742417	145742528	RECQL4	NM_004260	1	22	4	-	145742434	145742574
240873483	chr8	145742868	145743039	145742888	145743019	RECQL4	NM_004260	1	22	2	-	145742986	145743019
240873483	chr8	145742868	145743039	145742888	145743019	RECQL4	NM_004260	1	22	3	-	145742798	145742892
233789894	chr9	5022064	5022214	5022092	5022189	JAK2	NM_004972	1	25	3	+	5021963	5022213
234416067	chr9	5044354	5044516	5044382	5044489	JAK2	NM_004972	1	25	5	+	5044403	5044520
233545013	chr9	5054442	5054612	5054464	5054584	JAK2	NM_004972	1	25	7	+	5054563	5054884
233555182	chr9	5054832	5054992	5054857	5054967	JAK2	NM_004972	1	25	7	+	5054563	5054884
233184457	chr9	5064991	5065123	5065015	5065092	JAK2	NM_004972	1	25	9	+	5064883	5065040
232754257	chr9	5069092	5069263	5069116	5069235	JAK2	NM_004972	1	25	11	+	5069022	5069208
231998053	chr9	5072520	5072687	5072548	5072659	JAK2	NM_004972	1	25	13	+	5072492	5072626
233378246	chr9	5077539	5077704	5077564	5077676	JAK2	NM_004972	1	25	15	+	5077453	5077580
232463812	chr9	5080329	5080493	5080351	5080465	JAK2	NM_004972	1	25	17	+	5080229	5080380
234400110	chr9	5089565	5089714	5089590	5089695	JAK2	NM_004972	1	25	20	+	5089674	5089863
233441306	chr9	5090533	5090684	5090561	5090651	JAK2	NM_004972	1	25	21	+	5090446	5090570
233003442	chr9	5123004	5123128	5123028	5123111	JAK2	NM_004972	1	25	23	+	5123004	5123121
234770646	chr9	5126742	5126914	5126764	5126887	JAK2	NM_004972	1	25	25	+	5126684	5128183
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_001040712	1	30	28	-	8331582	8331736
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_001171025	2	29	27	-	8331582	8331736
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_130393	6	29	27	-	8331582	8331736
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_130392	5	31	29	-	8331582	8331736
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_130391	4	31	29	-	8331582	8331736
271430708	chr9	8331537	8331661	8331560	8331635	PTPRD	NM_002839	3	46	44	-	8331582	8331736
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_001040712	1	30	26	-	8340343	8340469
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_001171025	2	29	25	-	8340343	8340469
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_130393	6	29	25	-	8340343	8340469
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_130392	5	31	27	-	8340343	8340469

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_130391	4	31	27	-	8340343	8340469
269727960	chr9	8340273	8340402	8340301	8340378	PTPRD	NM_002839	3	46	42	-	8340343	8340469
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_001040712	1	30	25	-	8341090	8341268
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_001171025	2	29	24	-	8341090	8341268
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_130393	6	29	24	-	8341090	8341268
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_130392	5	31	26	-	8341090	8341268
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_130391	4	31	26	-	8341090	8341268
271895412	chr9	8341217	8341344	8341243	8341322	PTPRD	NM_002839	3	46	41	-	8341090	8341268
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_001040712	1	30	23	-	8375936	8376090
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_001171025	2	29	22	-	8375936	8376090
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_130393	6	29	22	-	8375936	8376090
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_130392	5	31	24	-	8375936	8376090
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_130391	4	31	24	-	8375936	8376090
270134507	chr9	8375844	8376009	8375871	8375981	PTPRD	NM_002839	3	46	39	-	8375936	8376090
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_001040712	1	30	21	-	8389232	8389407
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_001171025	2	29	20	-	8389232	8389407
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_130393	6	29	20	-	8389232	8389407
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_130392	5	31	22	-	8389232	8389407
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_130391	4	31	22	-	8389232	8389407
269460282	chr9	8389134	8389308	8389161	8389281	PTPRD	NM_002839	3	46	37	-	8389232	8389407
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_001040712	1	30	19	-	8436592	8436689
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_001171025	2	29	18	-	8436592	8436689
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_130393	6	29	18	-	8436592	8436689
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_130392	5	31	20	-	8436592	8436689
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_130391	4	31	20	-	8436592	8436689
270229852	chr9	8436657	8436828	8436680	8436802	PTPRD	NM_002839	3	46	35	-	8436592	8436689
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_001040712	1	30	18	-	8449725	8449837
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_001171025	2	29	16	-	8449725	8449837
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_130393	6	29	17	-	8449725	8449837
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_130392	5	31	19	-	8449725	8449837
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_130391	4	31	19	-	8449725	8449837
270400693	chr9	8449748	8449913	8449771	8449887	PTPRD	NM_002839	3	46	34	-	8449725	8449837
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_001040712	1	30	16	-	8460411	8460571
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_001171025	2	29	15	-	8460411	8460571
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_130393	6	29	16	-	8460411	8460571
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_130392	5	31	17	-	8460411	8460571
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_130391	4	31	17	-	8460411	8460571
271215238	chr9	8460546	8460706	8460568	8460678	PTPRD	NM_002839	3	46	33	-	8460411	8460571
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_001040712	1	30	14	-	8470995	8471085
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_001171025	2	29	13	-	8470995	8471085
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_130393	6	29	14	-	8470995	8471085

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_130392	5	31	15	-	8470995	8471085
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_130391	4	31	15	-	8470995	8471085
269894332	chr9	8470968	8471136	8470990	8471107	PTPRD	NM_002839	3	46	31	-	8470995	8471085
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_130393	6	29	12	-	8485227	8485327
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_001040712	1	30	12	-	8485227	8485324
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_001171025	2	29	11	-	8485227	8485324
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_130392	5	31	13	-	8485227	8485324
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_130391	4	31	13	-	8485227	8485324
270703969	chr9	8485140	8485274	8485164	8485248	PTPRD	NM_002839	3	46	29	-	8485227	8485324
272581653	chr9	8485987	8486154	8486008	8486132	PTPRD	NM_002839	3	46	28	-	8485762	8486349
271958187	chr9	8492897	8493033	8492918	8493006	PTPRD	NM_002839	3	46	27	-	8492862	8492979
270815091	chr9	8500686	8500859	8500712	8500835	PTPRD	NM_002839	3	46	24	-	8500754	8501059
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_001040712	1	30	11	-	8504261	8504405
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_001171025	2	29	10	-	8504261	8504405
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_130393	6	29	11	-	8504261	8504405
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_130392	5	31	12	-	8504261	8504405
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_130391	4	31	12	-	8504261	8504405
271991845	chr9	8504260	8504432	8504283	8504406	PTPRD	NM_002839	3	46	23	-	8504261	8504405
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_130393	6	29	9	-	8517848	8518429
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_130392	5	31	10	-	8517848	8518429
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_130391	4	31	10	-	8517848	8518429
269869408	chr9	8517939	8518112	8517962	8518089	PTPRD	NM_002839	3	46	21	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_130393	6	29	9	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_130392	5	31	10	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_130391	4	31	10	-	8517848	8518429
271717115	chr9	8518390	8518538	8518412	8518505	PTPRD	NM_002839	3	46	21	-	8517848	8518429
269567412	chr9	8523375	8523545	8523396	8523524	PTPRD	NM_001040712	1	30	7	-	8523513	8523524
269567412	chr9	8523375	8523545	8523396	8523524	PTPRD	NM_130393	6	29	7	-	8523513	8523524
269567412	chr9	8523375	8523545	8523396	8523524	PTPRD	NM_130392	5	31	8	-	8523513	8523524
269567412	chr9	8523375	8523545	8523396	8523524	PTPRD	NM_130391	4	31	8	-	8523513	8523524
269567412	chr9	8523375	8523545	8523396	8523524	PTPRD	NM_002839	3	46	19	-	8523513	8523524
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_001040712	1	30	4	-	8528591	8528779
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_001171025	2	29	4	-	8528591	8528779
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_130393	6	29	4	-	8528591	8528779
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_130392	5	31	4	-	8528591	8528779
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_130391	4	31	4	-	8528591	8528779
270384137	chr9	8528567	8528696	8528594	8528675	PTPRD	NM_002839	3	46	15	-	8528591	8528779

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_001040712	1	30	3	-	8633317	8633458
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_001171025	2	29	3	-	8633317	8633458
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_130393	6	29	3	-	8633317	8633458
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_130392	5	31	3	-	8633317	8633458
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_130391	4	31	3	-	8633317	8633458
270191077	chr9	8633320	8633487	8633343	8633459	PTPRD	NM_002839	3	46	14	-	8633317	8633458
237862032	chr9	15465465	15465603	15465493	15465578	PSIP1	NM_001128217	1	16	16	-	15464065	15465578
237862032	chr9	15465465	15465603	15465493	15465578	PSIP1	NM_033222	3	16	16	-	15464065	15465578
240146408	chr9	15468829	15469002	15468852	15468979	PSIP1	NM_001128217	1	16	13	-	15468955	15469056
240146408	chr9	15468829	15469002	15468852	15468979	PSIP1	NM_033222	3	16	13	-	15468955	15469056
236255845	chr9	15472578	15472722	15472603	15472698	PSIP1	NM_001128217	1	16	10	-	15472630	15472748
236255845	chr9	15472578	15472722	15472603	15472698	PSIP1	NM_033222	3	16	10	-	15472630	15472748
236255845	chr9	15472578	15472722	15472603	15472698	PSIP1	NM_021144	2	10	9	-	15472630	15472748
235300136	chr9	15478404	15478568	15478432	15478536	PSIP1	NM_001128217	1	16	8	-	15478475	15478550
235300136	chr9	15478404	15478568	15478432	15478536	PSIP1	NM_033222	3	16	8	-	15478475	15478550
235300136	chr9	15478404	15478568	15478432	15478536	PSIP1	NM_021144	2	10	7	-	15478475	15478550
238731741	chr9	15486004	15486167	15486027	15486140	PSIP1	NM_001128217	1	16	6	-	15486004	15486066
238731741	chr9	15486004	15486167	15486027	15486140	PSIP1	NM_033222	3	16	6	-	15486004	15486066
238731741	chr9	15486004	15486167	15486027	15486140	PSIP1	NM_021144	2	10	5	-	15486004	15486066
235102726	chr9	15506464	15506630	15506492	15506607	PSIP1	NM_001128217	1	16	3	-	15506559	15506635
235102726	chr9	15506464	15506630	15506492	15506607	PSIP1	NM_033222	3	16	3	-	15506559	15506635
235102726	chr9	15506464	15506630	15506492	15506607	PSIP1	NM_021144	2	10	2	-	15506559	15506635
226574550	chr9	21968655	21968806	21968674	21968779	CDKN2A	NM_001195132	2	4	3	-	21968574	21968770
225528190	chr9	21974427	21974592	21974448	21974570	CDKN2A	NM_058197	4	3	1	-	21974403	21974826
226643556	chr9	21994246	21994395	21994264	21994376	CDKN2A	NM_058195	3	3	1	-	21994138	21994490
226281763	chr9	22006137	22006305	22006154	22006287	CDKN2B	NM_004936	1	2	2	-	22002902	22006246
226281763	chr9	22006137	22006305	22006154	22006287	CDKN2B	NM_078487	2	2	2	-	22002902	22006246
261242926	chr9	32630008	32630169	32630029	32630145	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261203560	chr9	32630399	32630537	32630425	32630509	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261402290	chr9	32630784	32630958	32630812	32630933	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237849574	chr9	32631121	32631256	32631146	32631235	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237980419	chr9	32631503	32631664	32631525	32631644	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237773299	chr9	32631858	32632017	32631879	32631994	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237914002	chr9	32632277	32632418	32632301	32632396	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261293407	chr9	32632632	32632791	32632653	32632763	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261271903	chr9	32633005	32633141	32633030	32633117	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237778242	chr9	32633387	32633552	32633411	32633529	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237882402	chr9	32633847	32634021	32633869	32633997	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237932822	chr9	32634263	32634418	32634285	32634393	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261407053	chr9	32634657	32634826	32634682	32634801	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261422429	chr9	32635127	32635291	32635155	32635265	TAF1L	NM_153809	1	1	1	-	32629452	32635667

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261354776	chr9	32635503	32635668	32635524	32635648	TAF1L	NM_153809	1	1	1	-	32629452	32635667
229514242	chr9	35074836	35075004	35074860	35074983	FANCG	NM_004629	1	14	12	-	35074924	35075079
228783762	chr9	35075551	35075715	35075573	35075694	FANCG	NM_004629	1	14	10	-	35075462	35075751
228475831	chr9	35076505	35076633	35076526	35076605	FANCG	NM_004629	1	14	8	-	35076429	35076580
229663297	chr9	35077055	35077215	35077075	35077193	FANCG	NM_004629	1	14	6	-	35076968	35077098
230958611	chr9	35078184	35078349	35078204	35078327	FANCG	NM_004629	1	14	4	-	35078138	35078340
230557479	chr9	35079089	35079263	35079111	35079243	FANCG	NM_004629	1	14	2	-	35079148	35079238
235491997	chr9	36881964	36882136	36881982	36882114	PAX5	NM_016734	1	10	8	-	36882001	36882102
237373093	chr9	36966573	36966746	36966597	36966723	PAX5	NM_016734	1	10	6	-	36966546	36966721
238857483	chr9	37006469	37006631	37006491	37006605	PAX5	NM_016734	1	10	4	-	37006470	37006534
241264293	chr9	37020694	37020848	37020715	37020824	PAX5	NM_016734	1	10	2	-	37020633	37020798
228764124	chr9	80343375	80343530	80343402	80343506	GNAQ	NM_002072	1	7	6	-	80343430	80343583
227444016	chr9	80412327	80412477	80412353	80412449	GNAQ	NM_002072	1	7	4	-	80412436	80412564
228905439	chr9	80537038	80537210	80537059	80537185	GNAQ	NM_002072	1	7	2	-	80537077	80537261
237989195	chr9	93606103	93606268	93606125	93606246	SYK	NM_001135052	1	13	2	+	93606140	93606597
237989195	chr9	93606103	93606268	93606125	93606246	SYK	NM_001174167	2	14	2	+	93606140	93606597
237989195	chr9	93606103	93606268	93606125	93606246	SYK	NM_001174168	3	13	2	+	93606140	93606597
237989195	chr9	93606103	93606268	93606125	93606246	SYK	NM_003177	4	14	2	+	93606140	93606597
238013374	chr9	93606450	93606595	93606472	93606574	SYK	NM_001135052	1	13	2	+	93606140	93606597
238013374	chr9	93606450	93606595	93606472	93606574	SYK	NM_001174167	2	14	2	+	93606140	93606597
238013374	chr9	93606450	93606595	93606472	93606574	SYK	NM_001174168	3	13	2	+	93606140	93606597
238013374	chr9	93606450	93606595	93606472	93606574	SYK	NM_003177	4	14	2	+	93606140	93606597
241572645	chr9	93624460	93624586	93624483	93624563	SYK	NM_001135052	1	13	4	+	93624488	93624626
241572645	chr9	93624460	93624586	93624483	93624563	SYK	NM_001174167	2	14	4	+	93624488	93624626
241572645	chr9	93624460	93624586	93624483	93624563	SYK	NM_001174168	3	13	4	+	93624488	93624626
241572645	chr9	93624460	93624586	93624483	93624563	SYK	NM_003177	4	14	4	+	93624488	93624626
241576957	chr9	93629344	93629518	93629367	93629496	SYK	NM_001174167	2	14	7	+	93629413	93629481
241576957	chr9	93629344	93629518	93629367	93629496	SYK	NM_003177	4	14	7	+	93629413	93629481
237780168	chr9	93639806	93639944	93639832	93639917	SYK	NM_001135052	1	13	9	+	93639853	93640062
237780168	chr9	93639806	93639944	93639832	93639917	SYK	NM_001174167	2	14	10	+	93639853	93640062
237780168	chr9	93639806	93639944	93639832	93639917	SYK	NM_001174168	3	13	9	+	93639853	93640062
237780168	chr9	93639806	93639944	93639832	93639917	SYK	NM_003177	4	14	10	+	93639853	93640062
262143870	chr9	93641095	93641269	93641118	93641241	SYK	NM_001135052	1	13	10	+	93641046	93641235
262143870	chr9	93641095	93641269	93641118	93641241	SYK	NM_001174167	2	14	11	+	93641046	93641235
262143870	chr9	93641095	93641269	93641118	93641241	SYK	NM_001174168	3	13	10	+	93641046	93641235
262143870	chr9	93641095	93641269	93641118	93641241	SYK	NM_003177	4	14	11	+	93641046	93641235
238035113	chr9	93650802	93650933	93650825	93650910	SYK	NM_001135052	1	13	12	+	93650797	93650909
238035113	chr9	93650802	93650933	93650825	93650910	SYK	NM_001174167	2	14	13	+	93650797	93650909
238035113	chr9	93650802	93650933	93650825	93650910	SYK	NM_001174168	3	13	12	+	93650797	93650909
238035113	chr9	93650802	93650933	93650825	93650910	SYK	NM_003177	4	14	13	+	93650797	93650909
230196615	chr9	97869299	97869454	97869322	97869434	FANCC	NM_001243743	2	15	14	-	97869348	97869551

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230196615	chr9	97869299	97869454	97869322	97869434	FANCC	NM_000136	1	15	14	-	97869348	97869551
232649231	chr9	97873712	97873875	97873731	97873856	FANCC	NM_001243744	3	14	13	-	97873745	97873919
232649231	chr9	97873712	97873875	97873731	97873856	FANCC	NM_001243743	2	15	13	-	97873745	97873919
232649231	chr9	97873712	97873875	97873731	97873856	FANCC	NM_000136	1	15	13	-	97873745	97873919
227935487	chr9	97887320	97887494	97887345	97887467	FANCC	NM_001243744	3	14	10	-	97887368	97887467
227935487	chr9	97887320	97887494	97887345	97887467	FANCC	NM_001243743	2	15	10	-	97887368	97887467
227935487	chr9	97887320	97887494	97887345	97887467	FANCC	NM_000136	1	15	10	-	97887368	97887467
228770787	chr9	97897742	97897901	97897763	97897874	FANCC	NM_001243744	3	14	8	-	97897628	97897784
228770787	chr9	97897742	97897901	97897763	97897874	FANCC	NM_001243743	2	15	8	-	97897628	97897784
228770787	chr9	97897742	97897901	97897763	97897874	FANCC	NM_000136	1	15	8	-	97897628	97897784
229975242	chr9	97934249	97934405	97934276	97934377	FANCC	NM_001243744	3	14	5	-	97934319	97934429
229975242	chr9	97934249	97934405	97934276	97934377	FANCC	NM_001243743	2	15	5	-	97934319	97934429
229975242	chr9	97934249	97934405	97934276	97934377	FANCC	NM_000136	1	15	5	-	97934319	97934429
232563459	chr9	98011336	98011510	98011363	98011489	FANCC	NM_001243744	3	14	2	-	98011409	98011651
232563459	chr9	98011336	98011510	98011363	98011489	FANCC	NM_001243743	2	15	2	-	98011409	98011651
232563459	chr9	98011336	98011510	98011363	98011489	FANCC	NM_000136	1	15	2	-	98011409	98011651
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237371289	chr9	98209333	98209503	98209351	98209483	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083605	5	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083602	2	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_000264	1	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083604	4	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083606	6	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083607	7	24	22	-	98211351	98211605
235186235	chr9	98211328	98211493	98211349	98211471	PTCH1	NM_001083603	3	24	22	-	98211351	98211605
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083605	5	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083602	2	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_000264	1	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083604	4	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083606	6	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083607	7	24	20	-	98215760	98215902
239395452	chr9	98215706	98215843	98215728	98215824	PTCH1	NM_001083603	3	24	20	-	98215760	98215902
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083605	5	24	18	-	98220295	98220575
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083602	2	24	18	-	98220295	98220575
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_000264	1	24	18	-	98220295	98220575
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083604	4	24	18	-	98220295	98220575

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083606	6	24	18	-	98220295	98220575
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083607	7	24	18	-	98220295	98220575
234948002	chr9	98220244	98220415	98220271	98220394	PTCH1	NM_001083603	3	24	18	-	98220295	98220575
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083605	5	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083602	2	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_000264	1	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083604	4	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083606	6	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083607	7	24	17	-	98221882	98222065
236333256	chr9	98221987	98222111	98222006	98222090	PTCH1	NM_001083603	3	24	17	-	98221882	98222065
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083602	2	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_000264	1	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
235691810	chr9	98229453	98229625	98229480	98229604	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235331991	chr9	98231169	98231342	98231187	98231323	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083605	5	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083602	2	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_000264	1	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083604	4	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083606	6	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083607	7	24	12	-	98238316	98238441
237662469	chr9	98238225	98238387	98238247	98238365	PTCH1	NM_001083603	3	24	12	-	98238316	98238441
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083605	5	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083602	2	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_000264	1	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083604	4	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083606	6	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083607	7	24	10	-	98239829	98239984
235845407	chr9	98239839	98240013	98239862	98239993	PTCH1	NM_001083603	3	24	10	-	98239829	98239984
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083605	5	24	8	-	98241282	98241429
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083602	2	24	8	-	98241282	98241429
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_000264	1	24	8	-	98241282	98241429

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083604	4	24	8	-	98241282	98241429
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083606	6	24	8	-	98241282	98241429
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083607	7	24	8	-	98241282	98241429
237021950	chr9	98241322	98241464	98241343	98241442	PTCH1	NM_001083603	3	24	8	-	98241282	98241429
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083605	5	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083602	2	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_000264	1	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083604	4	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083606	6	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083607	7	24	6	-	98242672	98242870
237563902	chr9	98242735	98242906	98242755	98242878	PTCH1	NM_001083603	3	24	6	-	98242672	98242870
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083605	5	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083602	2	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_000264	1	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083604	4	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083606	6	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083607	7	24	3	-	98247967	98248156
237023515	chr9	98248036	98248209	98248058	98248180	PTCH1	NM_001083603	3	24	3	-	98247967	98248156
235586242	chr9	98270429	98270594	98270454	98270577	PTCH1	NM_000264	1	24	1	-	98270443	98270831
264389311	chr9	100437607	100437766	100437636	100437742	XPA	NR_027302	2	7	7	-	100437191	100437869
264389311	chr9	100437607	100437766	100437636	100437742	XPA	NM_000380	1	6	6	-	100437191	100437869
239477450	chr9	100447244	100447411	100447265	100447382	XPA	NR_027302	2	7	5	-	100447205	100447322
239477450	chr9	100447244	100447411	100447265	100447382	XPA	NM_000380	1	6	5	-	100447205	100447322
241028486	chr9	100451752	100451890	100451777	100451862	XPA	NR_027302	2	7	3	-	100451816	100451921
241028486	chr9	100451752	100451890	100451777	100451862	XPA	NM_000380	1	6	3	-	100451816	100451921
262322666	chr9	100455930	100456089	100455958	100456062	XPA	NR_027302	2	7	2	-	100455931	100456041
262322666	chr9	100455930	100456089	100455958	100456062	XPA	NM_000380	1	6	2	-	100455931	100456041
293900375	chr9	120470789	120470941	120470812	120470918	TLR4	NR_024168	4	4	3	+	120470841	120471007
293900375	chr9	120470789	120470941	120470812	120470918	TLR4	NM_003266	1	4	3	+	120470841	120471007
293900375	chr9	120470789	120470941	120470812	120470918	TLR4	NM_138554	2	3	2	+	120470841	120471007
295070142	chr9	120474760	120474887	120474780	120474859	TLR4	NM_003266	1	4	4	+	120474667	120479769
295070142	chr9	120474760	120474887	120474780	120474859	TLR4	NM_138554	2	3	3	+	120474667	120479769
295070142	chr9	120474760	120474887	120474780	120474859	TLR4	NM_138557	3	2	2	+	120474667	120479769
295070142	chr9	120474760	120474887	120474780	120474859	TLR4	NR_024169	5	2	2	+	120474667	120479766
295070142	chr9	120474760	120474887	120474780	120474859	TLR4	NR_024168	4	4	4	+	120474667	120479766
294044688	chr9	120475140	120475279	120475166	120475252	TLR4	NM_003266	1	4	4	+	120474667	120479769
294044688	chr9	120475140	120475279	120475166	120475252	TLR4	NM_138554	2	3	3	+	120474667	120479769
294044688	chr9	120475140	120475279	120475166	120475252	TLR4	NM_138557	3	2	2	+	120474667	120479769
294044688	chr9	120475140	120475279	120475166	120475252	TLR4	NR_024169	5	2	2	+	120474667	120479766
294044688	chr9	120475140	120475279	120475166	120475252	TLR4	NR_024168	4	4	4	+	120474667	120479766
294076807	chr9	120475558	120475701	120475584	120475674	TLR4	NM_003266	1	4	4	+	120474667	120479769

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294076807	chr9	120475558	120475701	120475584	120475674	TLR4	NM_138554	2	3	3	+	120474667	120479769
294076807	chr9	120475558	120475701	120475584	120475674	TLR4	NM_138557	3	2	2	+	120474667	120479769
294076807	chr9	120475558	120475701	120475584	120475674	TLR4	NR_024169	5	2	2	+	120474667	120479766
294076807	chr9	120475558	120475701	120475584	120475674	TLR4	NR_024168	4	4	4	+	120474667	120479766
295122172	chr9	120475989	120476159	120476014	120476130	TLR4	NM_003266	1	4	4	+	120474667	120479769
295122172	chr9	120475989	120476159	120476014	120476130	TLR4	NM_138554	2	3	3	+	120474667	120479769
295122172	chr9	120475989	120476159	120476014	120476130	TLR4	NM_138557	3	2	2	+	120474667	120479769
295122172	chr9	120475989	120476159	120476014	120476130	TLR4	NR_024169	5	2	2	+	120474667	120479766
295122172	chr9	120475989	120476159	120476014	120476130	TLR4	NR_024168	4	4	4	+	120474667	120479766
294169854	chr9	120476433	120476602	120476458	120476577	TLR4	NM_003266	1	4	4	+	120474667	120479769
294169854	chr9	120476433	120476602	120476458	120476577	TLR4	NM_138554	2	3	3	+	120474667	120479769
294169854	chr9	120476433	120476602	120476458	120476577	TLR4	NM_138557	3	2	2	+	120474667	120479769
294169854	chr9	120476433	120476602	120476458	120476577	TLR4	NR_024169	5	2	2	+	120474667	120479766
294169854	chr9	120476433	120476602	120476458	120476577	TLR4	NR_024168	4	4	4	+	120474667	120479766
224778157	chr9	133589648	133589798	133589671	133589775	ABL1	NM_007313	2	11	1	+	133589268	133589842
222694630	chr9	133729558	133729688	133729579	133729662	ABL1	NM_005157	1	11	2	+	133729451	133729624
222694630	chr9	133729558	133729688	133729579	133729662	ABL1	NM_007313	2	11	2	+	133729451	133729624
224057205	chr9	133738048	133738220	133738074	133738201	ABL1	NM_005157	1	11	4	+	133738150	133738422
224057205	chr9	133738048	133738220	133738074	133738201	ABL1	NM_007313	2	11	4	+	133738150	133738422
222723538	chr9	133747409	133747581	133747429	133747555	ABL1	NM_005157	1	11	5	+	133747516	133747600
222723538	chr9	133747409	133747581	133747429	133747555	ABL1	NM_007313	2	11	5	+	133747516	133747600
223948714	chr9	133748387	133748542	133748409	133748520	ABL1	NM_005157	1	11	6	+	133748247	133748424
223948714	chr9	133748387	133748542	133748409	133748520	ABL1	NM_007313	2	11	6	+	133748247	133748424
223751577	chr9	133753801	133753975	133753825	133753954	ABL1	NM_005157	1	11	8	+	133753802	133753954
223751577	chr9	133753801	133753975	133753825	133753954	ABL1	NM_007313	2	11	8	+	133753802	133753954
224375399	chr9	133759326	133759482	133759347	133759462	ABL1	NM_005157	1	11	11	+	133759356	133763062
224375399	chr9	133759326	133759482	133759347	133759462	ABL1	NM_007313	2	11	11	+	133759356	133763062
224385829	chr9	133759724	133759880	133759744	133759861	ABL1	NM_005157	1	11	11	+	133759356	133763062
224385829	chr9	133759724	133759880	133759744	133759861	ABL1	NM_007313	2	11	11	+	133759356	133763062
224380899	chr9	133760106	133760254	133760126	133760236	ABL1	NM_005157	1	11	11	+	133759356	133763062
224380899	chr9	133760106	133760254	133760126	133760236	ABL1	NM_007313	2	11	11	+	133759356	133763062
224375522	chr9	133760473	133760644	133760495	133760625	ABL1	NM_005157	1	11	11	+	133759356	133763062
224375522	chr9	133760473	133760644	133760495	133760625	ABL1	NM_007313	2	11	11	+	133759356	133763062
224384637	chr9	133760903	133761074	133760928	133761052	ABL1	NM_005157	1	11	11	+	133759356	133763062
224384637	chr9	133760903	133761074	133760928	133761052	ABL1	NM_007313	2	11	11	+	133759356	133763062
235077668	chr9	134002792	134002946	134002818	134002922	NUP214	NM_005085	1	36	2	+	134002911	134003106
235003725	chr9	134003778	134003925	134003802	134003900	NUP214	NM_005085	1	36	3	+	134003719	134003870
237483254	chr9	134006084	134006231	134006112	134006205	NUP214	NM_005085	1	36	5	+	134006153	134006223
236895448	chr9	134008483	134008624	134008506	134008596	NUP214	NM_005085	1	36	7	+	134008493	134008596
238489534	chr9	134014546	134014717	134014572	134014693	NUP214	NM_005085	1	36	10	+	134014668	134014794
237079459	chr9	134019600	134019759	134019628	134019738	NUP214	NM_005085	1	36	12	+	134019667	134020141

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237118247	chr9	134020035	134020184	134020055	134020157	NUP214	NM_005085	1	36	12	+	134019667	134020141
235999342	chr9	134022801	134022928	134022828	134022904	NUP214	NM_005085	1	36	14	+	134022877	134022971
239973885	chr9	134026023	134026190	134026047	134026162	NUP214	NM_005085	1	36	16	+	134026003	134026152
235145869	chr9	134038318	134038459	134038344	134038436	NUP214	NM_005085	1	36	19	+	134038378	134038560
235409404	chr9	134039447	134039582	134039468	134039560	NUP214	NM_005085	1	36	21	+	134039448	134039531
236988768	chr9	134050788	134050938	134050816	134050918	NUP214	NM_005085	1	36	23	+	134050847	134051008
239191641	chr9	134064385	134064515	134064418	134064489	NUP214	NM_005085	1	36	26	+	134064440	134064518
235203593	chr9	134070563	134070710	134070584	134070682	NUP214	NM_005085	1	36	28	+	134070620	134070681
238085432	chr9	134072849	134072974	134072872	134072950	NUP214	NM_005085	1	36	29	+	134072603	134074402
234939106	chr9	134073270	134073408	134073294	134073387	NUP214	NM_005085	1	36	29	+	134072603	134074402
237994613	chr9	134073703	134073871	134073724	134073850	NUP214	NM_005085	1	36	29	+	134072603	134074402
238000818	chr9	134074159	134074333	134074179	134074314	NUP214	NM_005085	1	36	29	+	134072603	134074402
236908758	chr9	134090653	134090819	134090675	134090792	NUP214	NM_005085	1	36	31	+	134090599	134090755
235025130	chr9	134103636	134103808	134103656	134103781	NUP214	NM_005085	1	36	33	+	134103547	134103718
240505270	chr9	134108744	134108911	134108765	134108890	NUP214	NM_005085	1	36	36	+	134108841	134109091
265437079	chr9	135771927	135772100	135771946	135772079	TSC1	NM_000368	1	23	23	-	135766735	135772141
265437079	chr9	135771927	135772100	135771946	135772079	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265437079	chr9	135771927	135772100	135771946	135772079	TSC1	NM_001162426	2	23	23	-	135766735	135772141
261802015	chr9	135772720	135772869	135772743	135772844	TSC1	NM_000368	1	23	21	-	135772810	135772997
261802015	chr9	135772720	135772869	135772743	135772844	TSC1	NM_001162427	3	22	20	-	135772810	135772997
261802015	chr9	135772720	135772869	135772743	135772844	TSC1	NM_001162426	2	23	21	-	135772810	135772997
241503590	chr9	135776091	135776259	135776112	135776231	TSC1	NM_000368	1	23	20	-	135776102	135776224
241503590	chr9	135776091	135776259	135776112	135776231	TSC1	NM_001162427	3	22	19	-	135776102	135776224
241503590	chr9	135776091	135776259	135776112	135776231	TSC1	NM_001162426	2	23	20	-	135776102	135776224
262410295	chr9	135778973	135779146	135778996	135779118	TSC1	NM_000368	1	23	17	-	135779038	135779204
262410295	chr9	135778973	135779146	135778996	135779118	TSC1	NM_001162427	3	22	16	-	135779038	135779204
262410295	chr9	135778973	135779146	135778996	135779118	TSC1	NM_001162426	2	23	17	-	135779038	135779204
240525377	chr9	135781071	135781233	135781096	135781210	TSC1	NM_000368	1	23	15	-	135780968	135781526
240525377	chr9	135781071	135781233	135781096	135781210	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240525377	chr9	135781071	135781233	135781096	135781210	TSC1	NM_001162426	2	23	15	-	135780968	135781526
239945240	chr9	135782076	135782250	135782102	135782222	TSC1	NM_000368	1	23	14	-	135782118	135782222
239945240	chr9	135782076	135782250	135782102	135782222	TSC1	NM_001162427	3	22	13	-	135782118	135782222
239945240	chr9	135782076	135782250	135782102	135782222	TSC1	NM_001162426	2	23	14	-	135782118	135782222
266406814	chr9	135786369	135786531	135786396	135786503	TSC1	NM_000368	1	23	11	-	135786389	135786500
266406814	chr9	135786369	135786531	135786396	135786503	TSC1	NM_001162427	3	22	10	-	135786389	135786500
266406814	chr9	135786369	135786531	135786396	135786503	TSC1	NM_001162426	2	23	11	-	135786389	135786500
241038032	chr9	135796619	135796784	135796644	135796762	TSC1	NM_000368	1	23	8	-	135796750	135796823
241038032	chr9	135796619	135796784	135796644	135796762	TSC1	NM_001162427	3	22	7	-	135796750	135796823
241038032	chr9	135796619	135796784	135796644	135796762	TSC1	NM_001162426	2	23	8	-	135796750	135796823
239625181	chr9	135798640	135798777	135798666	135798756	TSC1	NM_000368	1	23	6	-	135798735	135798879
239625181	chr9	135798640	135798777	135798666	135798756	TSC1	NM_001162427	3	22	5	-	135798735	135798879

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239625181	chr9	135798640	135798777	135798666	135798756	TSC1	NM_001162426	2	23	6	-	135798735	135798879
239564394	chr9	135802457	135802620	135802478	135802599	TSC1	NM_000368	1	23	4	-	135802588	135802691
239564394	chr9	135802457	135802620	135802478	135802599	TSC1	NM_001162427	3	22	4	-	135802588	135802691
239564394	chr9	135802457	135802620	135802478	135802599	TSC1	NM_001162426	2	23	4	-	135802588	135802691
273828274	chr9	135973918	135974084	135973940	135974064	RALGDS	NM_001042368	1	18	18	-	135973107	135974149
273828274	chr9	135973918	135974084	135973940	135974064	RALGDS	NM_006266	2	18	18	-	135973107	135974149
273034737	chr9	135976971	135977145	135976991	135977124	RALGDS	NM_001042368	1	18	16	-	135976907	135977149
273034737	chr9	135976971	135977145	135976991	135977124	RALGDS	NM_006266	2	18	16	-	135976907	135977149
273262578	chr9	135977431	135977580	135977448	135977561	RALGDS	NM_001042368	1	18	15	-	135977325	135977526
273262578	chr9	135977431	135977580	135977448	135977561	RALGDS	NM_006266	2	18	15	-	135977325	135977526
274592761	chr9	135978511	135978683	135978535	135978663	RALGDS	NM_001042368	1	18	12	-	135978617	135978649
274592761	chr9	135978511	135978683	135978535	135978663	RALGDS	NM_006266	2	18	12	-	135978617	135978649
274046587	chr9	135982007	135982133	135982026	135982112	RALGDS	NM_001042368	1	18	8	-	135982032	135982135
274046587	chr9	135982007	135982133	135982026	135982112	RALGDS	NM_006266	2	18	8	-	135982032	135982135
273157706	chr9	135983281	135983410	135983303	135983388	RALGDS	NM_001042368	1	18	6	-	135983375	135983793
273157706	chr9	135983281	135983410	135983303	135983388	RALGDS	NM_006266	2	18	6	-	135983375	135983793
273412275	chr9	135984141	135984290	135984160	135984271	RALGDS	NM_001042368	1	18	5	-	135984060	135984253
273412275	chr9	135984141	135984290	135984160	135984271	RALGDS	NM_006266	2	18	5	-	135984060	135984253
273707150	chr9	135987366	135987524	135987388	135987503	RALGDS	NM_001042368	1	18	2	-	135987429	135987539
273707150	chr9	135987366	135987524	135987388	135987503	RALGDS	NM_006266	2	18	2	-	135987429	135987539
330040169	chr9	136024221	136024382	136024238	136024364	RALGDS	NM_001042368	1	18	1	-	136024350	136024588
223022307	chr9	136901134	136901258	136901153	136901230	BRD3	NM_007371	1	12	10	-	136901154	136901446
224456272	chr9	136905185	136905358	136905205	136905336	BRD3	NM_007371	1	12	9	-	136905156	136905391
223289199	chr9	136907037	136907200	136907058	136907180	BRD3	NM_007371	1	12	8	-	136906882	136907073
222642629	chr9	136913222	136913383	136913243	136913364	BRD3	NM_007371	1	12	6	-	136913205	136913576
224443588	chr9	136915579	136915738	136915597	136915713	BRD3	NM_007371	1	12	5	-	136915496	136915710
222184498	chr9	136917453	136917602	136917477	136917574	BRD3	NM_007371	1	12	3	-	136917428	136917565
240911940	chr9	139390514	139390641	139390532	139390622	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236037082	chr9	139390971	139391144	139390992	139391125	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240922854	chr9	139391379	139391521	139391398	139391504	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240926801	chr9	139391708	139391882	139391726	139391863	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
238433664	chr9	139393447	139393613	139393468	139393591	NOTCH1	NM_017617	1	34	32	-	139393564	139393711
236198019	chr9	139395158	139395329	139395177	139395311	NOTCH1	NM_017617	1	34	31	-	139395004	139395299
241777763	chr9	139396445	139396587	139396466	139396568	NOTCH1	NM_017617	1	34	29	-	139396453	139396540
237193438	chr9	139397635	139397808	139397653	139397788	NOTCH1	NM_017617	1	34	27	-	139397634	139397782
235674308	chr9	139399706	139399872	139399727	139399852	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
235688709	chr9	139400141	139400314	139400160	139400293	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
239234799	chr9	139401165	139401291	139401182	139401274	NOTCH1	NM_017617	1	34	23	-	139401168	139401425
236015033	chr9	139401747	139401917	139401765	139401900	NOTCH1	NM_017617	1	34	22	-	139401757	139401889
236752686	chr9	139402717	139402862	139402735	139402842	NOTCH1	NM_017617	1	34	20	-	139402684	139402837
236507235	chr9	139404180	139404338	139404200	139404315	NOTCH1	NM_017617	1	34	18	-	139404185	139404413

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238240250	chr9	139405181	139405353	139405200	139405334	NOTCH1	NM_017617	1	34	17	-	139405105	139405257
236471982	chr9	139407550	139407707	139407571	139407685	NOTCH1	NM_017617	1	34	15	-	139407473	139407586
236462274	chr9	139409012	139409165	139409033	139409147	NOTCH1	NM_017617	1	34	13	-	139408962	139409154
235381427	chr9	139409938	139410084	139409957	139410066	NOTCH1	NM_017617	1	34	11	-	139409935	139410168
241247830	chr9	139411765	139411933	139411782	139411914	NOTCH1	NM_017617	1	34	9	-	139411724	139411837
237717598	chr9	139412673	139412806	139412692	139412789	NOTCH1	NM_017617	1	34	7	-	139412589	139412744
241565599	chr9	139413952	139414104	139413973	139414083	NOTCH1	NM_017617	1	34	5	-	139413895	139414017
238632111	chr9	139417438	139417573	139417457	139417552	NOTCH1	NM_017617	1	34	4	-	139417302	139417640
237664764	chr9	139418316	139418461	139418336	139418441	NOTCH1	NM_017617	1	34	3	-	139418169	139418431
233988415	chr10	3822277	3822446	3822297	3822426	KLF6	NM_001300	3	4	3	-	3822298	3822421
233988415	chr10	3822277	3822446	3822297	3822426	KLF6	NR_027653	4	4	3	-	3822298	3822421
233988415	chr10	3822277	3822446	3822297	3822426	KLF6	NM_001160124	1	4	3	-	3822298	3822421
233079030	chr10	3824045	3824206	3824067	3824183	KLF6	NM_001160124	1	4	2	-	3823959	3824406
233079030	chr10	3824045	3824206	3824067	3824183	KLF6	NR_027653	4	4	2	-	3823987	3824406
233079030	chr10	3824045	3824206	3824067	3824183	KLF6	NM_001300	3	4	2	-	3823833	3824406
233079030	chr10	3824045	3824206	3824067	3824183	KLF6	NM_001160125	2	3	2	-	3823833	3824406
232700194	chr10	3827162	3827322	3827184	3827301	KLF6	NM_001300	3	4	1	-	3827105	3827473
232700194	chr10	3827162	3827322	3827184	3827301	KLF6	NR_027653	4	4	1	-	3827105	3827473
232700194	chr10	3827162	3827322	3827184	3827301	KLF6	NM_001160125	2	3	1	-	3827105	3827473
232700194	chr10	3827162	3827322	3827184	3827301	KLF6	NM_001160124	1	4	1	-	3827105	3827473
229533655	chr10	8100225	8100399	8100246	8100379	GATA3	NM_002051	2	6	3	+	8100268	8100804
229533655	chr10	8100225	8100399	8100246	8100379	GATA3	NM_001002295	1	6	3	+	8100268	8100804
229540899	chr10	8100674	8100824	8100693	8100805	GATA3	NM_002051	2	6	3	+	8100268	8100804
229540899	chr10	8100674	8100824	8100693	8100805	GATA3	NM_001002295	1	6	3	+	8100268	8100804
228746318	chr10	8111493	8111617	8111515	8111596	GATA3	NM_002051	2	6	5	+	8111436	8111561
228746318	chr10	8111493	8111617	8111515	8111596	GATA3	NM_001002295	1	6	5	+	8111436	8111561
228237968	chr10	8115935	8116084	8115955	8116060	GATA3	NM_002051	2	6	6	+	8115702	8117164
228237968	chr10	8115935	8116084	8115955	8116060	GATA3	NM_001002295	1	6	6	+	8115702	8117164
232320233	chr10	21827744	21827913	21827772	21827889	MLLT10	NM_004641	5	24	3	+	21827762	21827841
232320233	chr10	21827744	21827913	21827772	21827889	MLLT10	NM_001195627	2	5	3	+	21827762	21827841
232320233	chr10	21827744	21827913	21827772	21827889	MLLT10	NM_001195626	1	22	2	+	21827762	21827841
232320233	chr10	21827744	21827913	21827772	21827889	MLLT10	NM_001195628	3	4	3	+	21827762	21827841
232320233	chr10	21827744	21827913	21827772	21827889	MLLT10	NM_001195630	4	4	3	+	21827762	21827841
231661973	chr10	21884263	21884435	21884281	21884408	MLLT10	NM_004641	5	24	5	+	21884260	21884369
231661973	chr10	21884263	21884435	21884281	21884408	MLLT10	NM_001195626	1	22	4	+	21884260	21884369
231136341	chr10	21903794	21903964	21903819	21903936	MLLT10	NM_004641	5	24	7	+	21903760	21903853
231136341	chr10	21903794	21903964	21903819	21903936	MLLT10	NM_001195626	1	22	6	+	21903760	21903853
232490486	chr10	21959289	21959441	21959316	21959416	MLLT10	NM_004641	5	24	10	+	21959378	21959633
232490486	chr10	21959289	21959441	21959316	21959416	MLLT10	NM_001195626	1	22	9	+	21959378	21959633
234529427	chr10	21962180	21962333	21962208	21962309	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234529427	chr10	21962180	21962333	21962208	21962309	MLLT10	NM_001195626	1	22	10	+	21962279	21962848

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234557749	chr10	21962594	21962764	21962622	21962742	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234557749	chr10	21962594	21962764	21962622	21962742	MLLT10	NM_001195626	1	22	10	+	21962279	21962848
234690261	chr10	21977318	21977492	21977345	21977469	MLLT10	NM_004641	5	24	14	+	21977420	21977467
231844881	chr10	22015191	22015330	22015213	22015301	MLLT10	NM_004641	5	24	16	+	22015173	22015284
231844881	chr10	22015191	22015330	22015213	22015301	MLLT10	NM_001195626	1	22	14	+	22015173	22015284
232696641	chr10	22021752	22021918	22021773	22021890	MLLT10	NM_004641	5	24	19	+	22021828	22022016
232696641	chr10	22021752	22021918	22021773	22021890	MLLT10	NM_001195626	1	22	17	+	22021828	22022016
234668502	chr10	22022651	22022816	22022677	22022795	MLLT10	NM_004641	5	24	21	+	22022697	22023058
234668502	chr10	22022651	22022816	22022677	22022795	MLLT10	NM_001195626	1	22	19	+	22022697	22023058
231639116	chr10	22024005	22024135	22024036	22024109	MLLT10	NM_004641	5	24	22	+	22024068	22024164
231639116	chr10	22024005	22024135	22024036	22024109	MLLT10	NM_001195626	1	22	20	+	22024068	22024164
232271814	chr10	22029115	22029240	22029137	22029213	MLLT10	NM_001195626	1	22	21	+	22028959	22029165
232271814	chr10	22029115	22029240	22029137	22029213	MLLT10	NM_004641	5	24	23	+	22029083	22029165
240747929	chr10	43596068	43596239	43596088	43596219	RET	NM_020630	1	19	2	+	43595907	43596170
240747929	chr10	43596068	43596239	43596088	43596219	RET	NM_020975	2	20	2	+	43595907	43596170
242042504	chr10	43600377	43600545	43600394	43600527	RET	NM_020630	1	19	4	+	43600400	43600641
242042504	chr10	43600377	43600545	43600394	43600527	RET	NM_020975	2	20	4	+	43600400	43600641
261518628	chr10	43601935	43602080	43601954	43602058	RET	NM_020630	1	19	5	+	43601824	43602019
261518628	chr10	43601935	43602080	43601954	43602058	RET	NM_020975	2	20	5	+	43601824	43602019
238701795	chr10	43606672	43606842	43606693	43606819	RET	NM_020630	1	19	7	+	43606655	43606913
238701795	chr10	43606672	43606842	43606693	43606819	RET	NM_020975	2	20	7	+	43606655	43606913
240757346	chr10	43608260	43608434	43608278	43608411	RET	NM_020630	1	19	9	+	43608301	43608411
240757346	chr10	43608260	43608434	43608278	43608411	RET	NM_020975	2	20	9	+	43608301	43608411
264076697	chr10	43610015	43610188	43610036	43610166	RET	NM_020630	1	19	11	+	43609928	43610184
264076697	chr10	43610015	43610188	43610036	43610166	RET	NM_020975	2	20	11	+	43609928	43610184
239650035	chr10	43612124	43612297	43612146	43612277	RET	NM_020630	1	19	12	+	43612032	43612179
239650035	chr10	43612124	43612297	43612146	43612277	RET	NM_020975	2	20	12	+	43612032	43612179
241506126	chr10	43614979	43615103	43614996	43615085	RET	NM_020630	1	19	14	+	43614979	43615193
241506126	chr10	43614979	43615103	43614996	43615085	RET	NM_020975	2	20	14	+	43614979	43615193
240381740	chr10	43617328	43617502	43617352	43617481	RET	NM_020630	1	19	16	+	43617394	43617464
240381740	chr10	43617328	43617502	43617352	43617481	RET	NM_020975	2	20	16	+	43617394	43617464
238905395	chr10	43621964	43622122	43621990	43622100	RET	NM_020630	1	19	19	+	43622023	43622952
238905395	chr10	43621964	43622122	43621990	43622100	RET	NM_020975	2	20	19	+	43622023	43622170
294673757	chr10	49609635	49609769	49609658	49609741	MAPK8	NM_002750	1	11	1	+	49609687	49609825
294673757	chr10	49609635	49609769	49609658	49609741	MAPK8	NM_139049	4	11	1	+	49609687	49609825
294673757	chr10	49609635	49609769	49609658	49609741	MAPK8	NM_139046	2	11	1	+	49609687	49609825
294673757	chr10	49609635	49609769	49609658	49609741	MAPK8	NM_139047	3	11	1	+	49609687	49609825
295398349	chr10	49612946	49613071	49612971	49613039	MAPK8	NM_002750	1	11	2	+	49612895	49613024
295398349	chr10	49612946	49613071	49612971	49613039	MAPK8	NM_139049	4	11	2	+	49612895	49613024
295398349	chr10	49612946	49613071	49612971	49613039	MAPK8	NM_139046	2	11	2	+	49612895	49613024
295398349	chr10	49612946	49613071	49612971	49613039	MAPK8	NM_139047	3	11	2	+	49612895	49613024

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294209663	chr10	49628091	49628255	49628120	49628227	MAPK8	NM_002750	1	11	5	+	49628198	49628363
294209663	chr10	49628091	49628255	49628120	49628227	MAPK8	NM_139049	4	11	5	+	49628198	49628363
294209663	chr10	49628091	49628255	49628120	49628227	MAPK8	NM_139046	2	11	5	+	49628198	49628363
294209663	chr10	49628091	49628255	49628120	49628227	MAPK8	NM_139047	3	11	5	+	49628198	49628363
295372071	chr10	49632422	49632583	49632453	49632561	MAPK8	NM_139046	2	11	6	+	49632557	49632628
295372071	chr10	49632422	49632583	49632453	49632561	MAPK8	NM_139047	3	11	6	+	49632557	49632628
294684548	chr10	49634020	49634166	49634048	49634143	MAPK8	NM_002750	1	11	7	+	49633931	49634113
294684548	chr10	49634020	49634166	49634048	49634143	MAPK8	NM_139049	4	11	7	+	49633931	49634113
294684548	chr10	49634020	49634166	49634048	49634143	MAPK8	NM_139046	2	11	7	+	49633931	49634113
294684548	chr10	49634020	49634166	49634048	49634143	MAPK8	NM_139047	3	11	7	+	49633931	49634113
293923272	chr10	49639159	49639298	49639184	49639275	MAPK8	NM_002750	1	11	10	+	49639236	49639313
293923272	chr10	49639159	49639298	49639184	49639275	MAPK8	NM_139049	4	11	10	+	49639236	49639313
293923272	chr10	49639159	49639298	49639184	49639275	MAPK8	NM_139046	2	11	10	+	49639236	49639313
293923272	chr10	49639159	49639298	49639184	49639275	MAPK8	NM_139047	3	11	10	+	49639236	49639313
236488329	chr10	51568256	51568429	51568284	51568401	NCOA4	NM_001145261	2	11	2	+	51568294	51568390
236488329	chr10	51568256	51568429	51568284	51568401	NCOA4	NM_001145260	1	12	2	+	51568294	51568390
239103139	chr10	51580587	51580720	51580611	51580696	NCOA4	NM_001145261	2	11	4	+	51580556	51580696
239103139	chr10	51580587	51580720	51580611	51580696	NCOA4	NM_005437	5	10	3	+	51580556	51580696
239103139	chr10	51580587	51580720	51580611	51580696	NCOA4	NM_001145262	3	10	3	+	51580556	51580696
239103139	chr10	51580587	51580720	51580611	51580696	NCOA4	NM_001145263	4	10	3	+	51580556	51580696
239103139	chr10	51580587	51580720	51580611	51580696	NCOA4	NM_001145260	1	12	4	+	51580556	51580696
237236540	chr10	51581265	51581406	51581285	51581380	NCOA4	NM_001145261	2	11	6	+	51581270	51581378
237236540	chr10	51581265	51581406	51581285	51581380	NCOA4	NM_005437	5	10	5	+	51581270	51581378
237236540	chr10	51581265	51581406	51581285	51581380	NCOA4	NM_001145262	3	10	5	+	51581270	51581378
237236540	chr10	51581265	51581406	51581285	51581380	NCOA4	NM_001145263	4	10	5	+	51581270	51581378
237236540	chr10	51581265	51581406	51581285	51581380	NCOA4	NM_001145260	1	12	6	+	51581270	51581378
241398159	chr10	51584564	51584730	51584591	51584702	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
241398159	chr10	51584564	51584730	51584591	51584702	NCOA4	NM_005437	5	10	8	+	51584616	51585599
241398159	chr10	51584564	51584730	51584591	51584702	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
241398159	chr10	51584564	51584730	51584591	51584702	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
241398159	chr10	51584564	51584730	51584591	51584702	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
241449553	chr10	51584961	51585118	51584982	51585098	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
241449553	chr10	51584961	51585118	51584982	51585098	NCOA4	NM_005437	5	10	8	+	51584616	51585599
241449553	chr10	51584961	51585118	51584982	51585098	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
241449553	chr10	51584961	51585118	51584982	51585098	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
241449553	chr10	51584961	51585118	51584982	51585098	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
236632063	chr10	51585371	51585519	51585389	51585496	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
236632063	chr10	51585371	51585519	51585389	51585496	NCOA4	NM_005437	5	10	8	+	51584616	51585599
236632063	chr10	51585371	51585519	51585389	51585496	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
236632063	chr10	51585371	51585519	51585389	51585496	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
236632063	chr10	51585371	51585519	51585389	51585496	NCOA4	NM_001145260	1	12	9	+	51584616	51585599

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236093811	chr10	51586494	51586662	51586519	51586639	NCOA4	NM_001145260	1	12	11	+	51586610	51586698
262791917	chr10	70332193	70332333	70332216	70332312	TET1	NM_030625	1	12	2	+	70331974	70334009
262781003	chr10	70332548	70332718	70332573	70332692	TET1	NM_030625	1	12	2	+	70331974	70334009
262854137	chr10	70333030	70333203	70333051	70333181	TET1	NM_030625	1	12	2	+	70331974	70334009
262790432	chr10	70333473	70333630	70333495	70333607	TET1	NM_030625	1	12	2	+	70331974	70334009
262836600	chr10	70333896	70334030	70333917	70334009	TET1	NM_030625	1	12	2	+	70331974	70334009
262678224	chr10	70404613	70404774	70404639	70404745	TET1	NM_030625	1	12	4	+	70404455	70406762
262690411	chr10	70405000	70405159	70405028	70405131	TET1	NM_030625	1	12	4	+	70404455	70406762
262859166	chr10	70405419	70405554	70405447	70405526	TET1	NM_030625	1	12	4	+	70404455	70406762
262755540	chr10	70405724	70405876	70405751	70405849	TET1	NM_030625	1	12	4	+	70404455	70406762
262785569	chr10	70406163	70406310	70406186	70406286	TET1	NM_030625	1	12	4	+	70404455	70406762
262803246	chr10	70406613	70406787	70406641	70406763	TET1	NM_030625	1	12	4	+	70404455	70406762
240761684	chr10	70426743	70426906	70426770	70426886	TET1	NM_030625	1	12	7	+	70426802	70427013
262661399	chr10	70432680	70432804	70432701	70432783	TET1	NM_030625	1	12	8	+	70432652	70432802
238839772	chr10	70445982	70446142	70446009	70446118	TET1	NM_030625	1	12	11	+	70446113	70446464
239064543	chr10	70450441	70450611	70450464	70450584	TET1	NM_030625	1	12	12	+	70450565	70454239
239159964	chr10	70450907	70451051	70450928	70451026	TET1	NM_030625	1	12	12	+	70450565	70454239
239234199	chr10	70451327	70451467	70451350	70451438	TET1	NM_030625	1	12	12	+	70450565	70454239
312553419	chr10	76602595	76602760	76602623	76602735	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312553419	chr10	76602595	76602760	76602623	76602735	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312553419	chr10	76602595	76602760	76602623	76602735	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312581000	chr10	76603089	76603261	76603112	76603237	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312581000	chr10	76603089	76603261	76603112	76603237	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312581000	chr10	76603089	76603261	76603112	76603237	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312218273	chr10	76729423	76729593	76729451	76729568	KAT6B	NM_012330	3	18	5	+	76729418	76729533
312218273	chr10	76729423	76729593	76729451	76729568	KAT6B	NM_001256468	1	18	5	+	76729418	76729533
312218273	chr10	76729423	76729593	76729451	76729568	KAT6B	NM_001256469	2	18	5	+	76729418	76729533
312304035	chr10	76732265	76732408	76732287	76732384	KAT6B	NM_012330	3	18	7	+	76732265	76732397
312304035	chr10	76732265	76732408	76732287	76732384	KAT6B	NM_001256468	1	18	7	+	76732265	76732397
312304035	chr10	76732265	76732408	76732287	76732384	KAT6B	NM_001256469	2	18	7	+	76732265	76732397
312406640	chr10	76735264	76735401	76735286	76735374	KAT6B	NM_001256468	1	18	8	+	76735157	76735539
312406640	chr10	76735264	76735401	76735286	76735374	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312401463	chr10	76735609	76735767	76735631	76735743	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312463282	chr10	76736986	76737149	76737010	76737123	KAT6B	NM_012330	3	18	9	+	76737074	76737195
312463282	chr10	76736986	76737149	76737010	76737123	KAT6B	NM_001256468	1	18	9	+	76737074	76737195
312463282	chr10	76736986	76737149	76737010	76737123	KAT6B	NM_001256469	2	18	9	+	76737074	76737195
312396222	chr10	76741541	76741693	76741567	76741666	KAT6B	NM_012330	3	18	11	+	76741545	76741686
312396222	chr10	76741541	76741693	76741567	76741666	KAT6B	NM_001256468	1	18	11	+	76741545	76741686
312396222	chr10	76741541	76741693	76741567	76741666	KAT6B	NM_001256469	2	18	11	+	76741545	76741686
312398603	chr10	76744914	76745074	76744942	76745051	KAT6B	NM_012330	3	18	12	+	76744838	76744999
312398603	chr10	76744914	76745074	76744942	76745051	KAT6B	NM_001256468	1	18	12	+	76744838	76744999

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312398603	chr10	76744914	76745074	76744942	76745051	KAT6B	NM_001256469	2	18	12	+	76744838	76744999
312622068	chr10	76780515	76780680	76780536	76780653	KAT6B	NM_012330	3	18	14	+	76780340	76780571
312622068	chr10	76780515	76780680	76780536	76780653	KAT6B	NM_001256468	1	18	14	+	76780340	76780571
312622068	chr10	76780515	76780680	76780536	76780653	KAT6B	NM_001256469	2	18	14	+	76780340	76780571
312513069	chr10	76781674	76781828	76781699	76781803	KAT6B	NM_012330	3	18	16	+	76781639	76781989
312513069	chr10	76781674	76781828	76781699	76781803	KAT6B	NM_001256468	1	18	16	+	76781639	76781989
312513069	chr10	76781674	76781828	76781699	76781803	KAT6B	NM_001256469	2	18	16	+	76781639	76781989
312245072	chr10	76784799	76784948	76784823	76784925	KAT6B	NM_012330	3	18	17	+	76784716	76785007
312245072	chr10	76784799	76784948	76784823	76784925	KAT6B	NM_001256468	1	18	17	+	76784716	76785007
312245072	chr10	76784799	76784948	76784823	76784925	KAT6B	NM_001256469	2	18	17	+	76784716	76785007
312627403	chr10	76788440	76788614	76788464	76788590	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312627403	chr10	76788440	76788614	76788464	76788590	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312627403	chr10	76788440	76788614	76788464	76788590	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312590687	chr10	76788847	76789016	76788867	76788994	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312590687	chr10	76788847	76789016	76788867	76788994	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312590687	chr10	76788847	76789016	76788867	76788994	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312603764	chr10	76789318	76789487	76789339	76789465	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312603764	chr10	76789318	76789487	76789339	76789465	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312603764	chr10	76789318	76789487	76789339	76789465	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312593063	chr10	76789819	76789984	76789840	76789964	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312593063	chr10	76789819	76789984	76789840	76789964	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312593063	chr10	76789819	76789984	76789840	76789964	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312597015	chr10	76790262	76790427	76790284	76790408	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312597015	chr10	76790262	76790427	76790284	76790408	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312597015	chr10	76790262	76790427	76790284	76790408	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312269727	chr10	76790737	76790871	76790759	76790844	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312269727	chr10	76790737	76790871	76790759	76790844	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312269727	chr10	76790737	76790871	76790759	76790844	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
223129514	chr10	88649853	88650016	88649877	88649988	BMPR1A	NM_004329	1	13	4	+	88649819	88649981
223980312	chr10	88659565	88659691	88659584	88659666	BMPR1A	NM_004329	1	13	6	+	88659551	88659647
222393516	chr10	88672011	88672175	88672033	88672148	BMPR1A	NM_004329	1	13	8	+	88671997	88672141
223047037	chr10	88678911	88679085	88678938	88679063	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
222658484	chr10	88681229	88681388	88681256	88681366	BMPR1A	NM_004329	1	13	11	+	88681277	88681452
223026331	chr10	88683246	88683389	88683268	88683362	BMPR1A	NM_004329	1	13	13	+	88683351	88684945
237680230	chr10	89685231	89685402	89685259	89685374	PTEN	NM_000314	1	9	3	+	89685270	89685314
235014277	chr10	89692806	89692946	89692834	89692920	PTEN	NM_000314	1	9	5	+	89692770	89693008
326922661	chr10	89717476	89717643	89717503	89717622	PTEN	NM_000314	1	9	7	+	89717610	89717776
236875490	chr10	89720760	89720918	89720785	89720895	PTEN	NM_000314	1	9	8	+	89720651	89720875
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NM_152872	3	8	2	+	90762786	90762951
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NM_152871	2	8	2	+	90762786	90762951
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NR_028036	7	8	2	+	90762786	90762951

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NR_028035	6	7	2	+	90762786	90762951
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NR_028034	5	6	2	+	90762786	90762951
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NR_028033	4	7	2	+	90762786	90762951
228652178	chr10	90762688	90762859	90762710	90762835	FAS	NM_000043	1	9	2	+	90762786	90762951
231867504	chr10	90768578	90768752	90768602	90768733	FAS	NM_152872	3	8	4	+	90768646	90768754
231867504	chr10	90768578	90768752	90768602	90768733	FAS	NM_152871	2	8	4	+	90768646	90768754
231867504	chr10	90768578	90768752	90768602	90768733	FAS	NM_000043	1	9	4	+	90768646	90768754
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NM_152872	3	8	7	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NM_152871	2	8	6	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NR_028036	7	8	6	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NR_028035	6	7	5	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NR_028034	5	6	4	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NR_028033	4	7	5	+	90771756	90771838
230965802	chr10	90771716	90771867	90771744	90771837	FAS	NM_000043	1	9	7	+	90771756	90771838
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NM_152872	3	8	8	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NM_152871	2	8	8	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NR_028036	7	8	8	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NR_028035	6	7	7	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NR_028034	5	6	6	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NR_028033	4	7	7	+	90773876	90775542
231218729	chr10	90774056	90774202	90774084	90774174	FAS	NM_000043	1	9	9	+	90773876	90775542
286776765	chr10	96522569	96522726	96522597	96522698	CYP2C19	NM_000769	1	9	1	+	96522463	96522630
287042962	chr10	96535147	96535310	96535174	96535288	CYP2C19	NM_000769	1	9	3	+	96535147	96535296
286698250	chr10	96540299	96540455	96540327	96540430	CYP2C19	NM_000769	1	9	4	+	96540256	96540416
286940249	chr10	96580345	96580514	96580369	96580494	CYP2C19	NM_000769	1	9	6	+	96580253	96580394
285388456	chr10	96609754	96609894	96609782	96609870	CYP2C19	NM_000769	1	9	8	+	96609674	96609815
294679145	chr10	97951780	97951912	97951807	97951885	BLNK	NM_013314	2	17	17	-	97951455	97951848
294679145	chr10	97951780	97951912	97951807	97951885	BLNK	NM_001114094	1	16	16	-	97951455	97951848
293993809	chr10	97959751	97959877	97959775	97959856	BLNK	NM_013314	2	17	15	-	97959831	97959914
293993809	chr10	97959751	97959877	97959775	97959856	BLNK	NM_001114094	1	16	14	-	97959831	97959914
294771469	chr10	97964175	97964345	97964201	97964321	BLNK	NM_013314	2	17	12	-	97964288	97964372
294771469	chr10	97964175	97964345	97964201	97964321	BLNK	NM_001114094	1	16	11	-	97964288	97964372
294404714	chr10	97969544	97969691	97969566	97969663	BLNK	NM_013314	2	17	9	-	97969594	97969663
294404714	chr10	97969544	97969691	97969566	97969663	BLNK	NM_001114094	1	16	8	-	97969594	97969663
293825407	chr10	97983553	97983709	97983576	97983687	BLNK	NM_013314	2	17	6	-	97983582	97983745
293825407	chr10	97983553	97983709	97983576	97983687	BLNK	NM_001114094	1	16	6	-	97983582	97983745
294099307	chr10	97990457	97990626	97990478	97990604	BLNK	NM_013314	2	17	4	-	97990550	97990590
294099307	chr10	97990457	97990626	97990478	97990604	BLNK	NM_001114094	1	16	4	-	97990550	97990590
264714311	chr10	102891810	102891978	102891829	102891961	TLX1	NM_005521	2	3	1	+	102891061	102891866
264714311	chr10	102891810	102891978	102891829	102891961	TLX1	NM_001195517	1	3	1	+	102891061	102891866
266221729	chr10	102896346	102896502	102896368	102896484	TLX1	NM_001195517	1	3	3	+	102896425	102897546

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266221729	chr10	102896346	102896502	102896368	102896484	TLX1	NM_005521	2	3	3	+	102896448	102897546
235648879	chr10	104155703	104155840	104155725	104155817	NFKB2	NM_002502	3	23	2	+	104155645	104155737
235648879	chr10	104155703	104155840	104155725	104155817	NFKB2	NM_001077494	2	23	2	+	104155645	104155737
235648879	chr10	104155703	104155840	104155725	104155817	NFKB2	NM_001077493	1	23	2	+	104155645	104155737
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_002502	3	23	6	+	104156661	104156812
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_001077494	2	23	6	+	104156661	104156812
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_001077493	1	23	6	+	104156661	104156812
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_002502	3	23	5	+	104156482	104156580
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_001077494	2	23	5	+	104156482	104156580
235545543	chr10	104156556	104156703	104156577	104156683	NFKB2	NM_001077493	1	23	5	+	104156482	104156580
236868846	chr10	104157215	104157356	104157235	104157334	NFKB2	NM_002502	3	23	8	+	104157284	104157442
236868846	chr10	104157215	104157356	104157235	104157334	NFKB2	NM_001077494	2	23	8	+	104157284	104157442
236868846	chr10	104157215	104157356	104157235	104157334	NFKB2	NM_001077493	1	23	8	+	104157284	104157442
240586409	chr10	104158087	104158232	104158111	104158213	NFKB2	NM_002502	3	23	11	+	104158142	104158280
240586409	chr10	104158087	104158232	104158111	104158213	NFKB2	NM_001077494	2	23	11	+	104158142	104158280
240586409	chr10	104158087	104158232	104158111	104158213	NFKB2	NM_001077493	1	23	11	+	104158142	104158280
237225205	chr10	104159021	104159187	104159040	104159170	NFKB2	NM_002502	3	23	13	+	104159045	104159254
237225205	chr10	104159021	104159187	104159040	104159170	NFKB2	NM_001077494	2	23	13	+	104159045	104159254
237225205	chr10	104159021	104159187	104159040	104159170	NFKB2	NM_001077493	1	23	13	+	104159045	104159254
235072234	chr10	104159748	104159907	104159768	104159882	NFKB2	NM_002502	3	23	15	+	104159837	104159951
235072234	chr10	104159748	104159907	104159768	104159882	NFKB2	NM_001077494	2	23	15	+	104159837	104159951
235072234	chr10	104159748	104159907	104159768	104159882	NFKB2	NM_001077493	1	23	15	+	104159837	104159951
237346051	chr10	104160389	104160534	104160410	104160513	NFKB2	NM_002502	3	23	17	+	104160412	104160581
237346051	chr10	104160389	104160534	104160410	104160513	NFKB2	NM_001077494	2	23	17	+	104160412	104160581
237346051	chr10	104160389	104160534	104160410	104160513	NFKB2	NM_001077493	1	23	17	+	104160412	104160581
237305760	chr10	104160988	104161160	104161010	104161134	NFKB2	NM_002502	3	23	19	+	104160937	104161088
237305760	chr10	104160988	104161160	104161010	104161134	NFKB2	NM_001077494	2	23	19	+	104160937	104161088
237305760	chr10	104160988	104161160	104161010	104161134	NFKB2	NM_001077493	1	23	19	+	104160937	104161088
239792247	chr10	104161780	104161954	104161804	104161934	NFKB2	NM_002502	3	23	22	+	104161805	104161916
239792247	chr10	104161780	104161954	104161804	104161934	NFKB2	NM_001077494	2	23	22	+	104161805	104161916
239792247	chr10	104161780	104161954	104161804	104161934	NFKB2	NM_001077493	1	23	22	+	104161805	104161916
237856977	chr10	104268822	104268967	104268844	104268941	SUFU	NM_016169	2	12	2	+	104268926	104269060
237856977	chr10	104268822	104268967	104268844	104268941	SUFU	NM_001178133	1	11	2	+	104268926	104269060
240703072	chr10	104352264	104352418	104352285	104352394	SUFU	NM_016169	2	12	4	+	104352339	104352481
240703072	chr10	104352264	104352418	104352285	104352394	SUFU	NM_001178133	1	11	4	+	104352339	104352481
240128237	chr10	104356789	104356949	104356810	104356928	SUFU	NM_016169	2	12	7	+	104356897	104357050
240128237	chr10	104356789	104356949	104356810	104356928	SUFU	NM_001178133	1	11	7	+	104356897	104357050
241850726	chr10	104375002	104375161	104375024	104375138	SUFU	NM_016169	2	12	9	+	104375025	104375159
241850726	chr10	104375002	104375161	104375024	104375138	SUFU	NM_001178133	1	11	9	+	104375025	104375159
240276098	chr10	104378730	104378881	104378755	104378861	SUFU	NM_001178133	1	11	11	+	104378823	104379220
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001146283	2	13	1	+	114710009	114710704

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198526	7	13	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_030756	13	14	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001146286	5	12	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001146285	4	13	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198530	11	11	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198529	10	13	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198525	6	15	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198531	12	13	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001146274	1	14	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198528	9	15	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001198527	8	15	1	+	114710009	114710704
274196119	chr10	114710456	114710621	114710484	114710599	TCF7L2	NM_001146284	3	13	1	+	114710009	114710704
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001146283	2	13	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198526	7	13	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_030756	13	14	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001146286	5	12	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001146285	4	13	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198530	11	11	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198529	10	13	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198525	6	15	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198531	12	13	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001146274	1	14	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198528	9	15	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001198527	8	15	3	+	114711242	114711366
273159693	chr10	114711232	114711380	114711251	114711362	TCF7L2	NM_001146284	3	13	3	+	114711242	114711366
273002351	chr10	114849123	114849260	114849144	114849237	TCF7L2	NM_001146283	2	13	5	+	114849159	114849299
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001146283	2	13	7	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198526	7	13	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_030756	13	14	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001146286	5	12	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001146285	4	13	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198530	11	11	5	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198529	10	13	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198525	6	15	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198531	12	13	7	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001146274	1	14	7	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198528	9	15	6	+	114903682	114903784
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001198527	8	15	6	+	114903682	114903772
273588361	chr10	114903607	114903741	114903630	114903722	TCF7L2	NM_001146284	3	13	6	+	114903682	114903772
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001146283	2	13	9	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198526	7	13	8	+	114910757	114910882

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_030756	13	14	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001146286	5	12	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001146285	4	13	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198530	11	11	7	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198529	10	13	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198531	12	13	9	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001146274	1	14	9	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198528	9	15	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198527	8	15	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001146284	3	13	8	+	114910757	114910882
272810408	chr10	114910748	114910909	114910770	114910884	TCF7L2	NM_001198525	6	15	8	+	114910742	114910882
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001146283	2	13	12	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198526	7	13	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_030756	13	14	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001146286	5	12	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001146285	4	13	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198530	11	11	10	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198529	10	13	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198525	6	15	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198531	12	13	12	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001146274	1	14	12	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198528	9	15	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001198527	8	15	11	+	114917780	114917828
273899463	chr10	114917716	114917857	114917737	114917828	TCF7L2	NM_001146284	3	13	11	+	114917780	114917828
273009973	chr10	114920300	114920474	114920326	114920450	TCF7L2	NM_001198526	7	13	12	+	114920378	114920450
273009973	chr10	114920300	114920474	114920326	114920450	TCF7L2	NM_001198525	6	15	14	+	114920378	114920450
273009973	chr10	114920300	114920474	114920326	114920450	TCF7L2	NM_001146274	1	14	13	+	114920378	114920450
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001146283	2	13	13	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198526	7	13	13	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_030756	13	14	14	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001146286	5	12	12	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001146285	4	13	13	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198530	11	11	11	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198529	10	13	13	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198525	6	15	15	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198531	12	13	13	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001146274	1	14	14	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198528	9	15	15	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001198527	8	15	15	+	114925314	114927436
274215023	chr10	114925405	114925561	114925423	114925544	TCF7L2	NM_001146284	3	13	13	+	114925314	114927436
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_001144918	7	16	16	-	123237844	123239535

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_000141	1	18	18	-	123237844	123239535
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_001144917	6	16	16	-	123237844	123239535
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_001144916	5	15	15	-	123237844	123239535
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_022970	9	18	18	-	123237844	123239535
228301321	chr10	123239303	123239472	123239323	123239443	FGFR2	NM_001144914	3	15	15	-	123237844	123239535
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144913	2	17	16	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144918	7	16	15	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_000141	1	18	17	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144917	6	16	15	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144916	5	15	14	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_022970	9	18	17	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144914	3	15	14	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144915	4	17	16	-	123243212	123243317
231684536	chr10	123243199	123243368	123243225	123243341	FGFR2	NM_001144919	8	17	16	-	123243212	123243317
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144913	2	17	14	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144918	7	16	13	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_000141	1	18	15	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144917	6	16	13	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144916	5	15	12	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_022970	9	18	15	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144914	3	15	12	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144915	4	17	14	-	123246868	123246938
228314166	chr10	123246880	123247010	123246908	123246986	FGFR2	NM_001144919	8	17	14	-	123246868	123246938
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144913	2	17	12	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144918	7	16	11	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_000141	1	18	13	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144917	6	16	11	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144916	5	15	10	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_022970	9	18	13	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144914	3	15	10	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144915	4	17	12	-	123256046	123256236
230746948	chr10	123256090	123256260	123256111	123256236	FGFR2	NM_001144919	8	17	12	-	123256046	123256236
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144913	2	17	9	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144918	7	16	8	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_000141	1	18	10	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144917	6	16	8	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144916	5	15	7	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_022970	9	18	10	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144914	3	15	7	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144915	4	17	9	-	123263304	123263455
228448200	chr10	123263243	123263415	123263271	123263394	FGFR2	NM_001144919	8	17	9	-	123263304	123263455

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228070439	chr10	123276763	123276895	123276792	123276872	FGFR2	NM_001144918	7	16	6	-	123276833	123276977
228070439	chr10	123276763	123276895	123276792	123276872	FGFR2	NM_000141	1	18	8	-	123276833	123276977
228070439	chr10	123276763	123276895	123276792	123276872	FGFR2	NM_001144916	5	15	5	-	123276833	123276977
228070439	chr10	123276763	123276895	123276792	123276872	FGFR2	NM_001144915	4	17	7	-	123276833	123276977
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144913	2	17	6	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144918	7	16	5	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_000141	1	18	7	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144917	6	16	7	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144916	5	15	4	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_022970	9	18	7	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144915	4	17	6	-	123279493	123279683
228034759	chr10	123279453	123279625	123279475	123279604	FGFR2	NM_001144919	8	17	6	-	123279493	123279683
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144913	2	17	4	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144918	7	16	3	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_000141	1	18	5	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144917	6	16	5	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144916	5	15	2	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_022970	9	18	5	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144914	3	15	4	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144915	4	17	4	-	123310804	123310973
229686118	chr10	123310792	123310916	123310819	123310895	FGFR2	NM_001144919	8	17	4	-	123310804	123310973
231595865	chr10	123324963	123325137	123324988	123325118	FGFR2	NM_001144913	2	17	2	-	123324952	123325218
231595865	chr10	123324963	123325137	123324988	123325118	FGFR2	NM_000141	1	18	3	-	123324952	123325218
231595865	chr10	123324963	123325137	123324988	123325118	FGFR2	NM_001144917	6	16	3	-	123324952	123325218
231595865	chr10	123324963	123325137	123324988	123325118	FGFR2	NM_022970	9	18	3	-	123324952	123325218
231595865	chr10	123324963	123325137	123324988	123325118	FGFR2	NM_001144914	3	15	2	-	123324952	123325218
227881193	chr11	533258	533382	533276	533362	HRAS	NM_176795	3	6	5	-	533277	533358
227465584	chr11	533765	533935	533787	533914	HRAS	NM_001130442	1	5	3	-	533766	533944
227465584	chr11	533765	533935	533787	533914	HRAS	NM_176795	3	6	3	-	533766	533944
227465584	chr11	533765	533935	533787	533914	HRAS	NM_005343	2	6	3	-	533766	533944
330090766	chr11	2154196	2154326	2154214	2154309	IGF2	NM_000612	1	4	4	-	2150347	2154453
330090766	chr11	2154196	2154326	2154214	2154309	IGF2	NM_001127598	3	5	5	-	2150347	2154453
330090766	chr11	2154196	2154326	2154214	2154309	IGF2	NM_001007139	2	5	5	-	2150347	2154453
330105985	chr11	2154794	2154933	2154815	2154913	IGF2	NM_000612	1	4	3	-	2154747	2154895
330105985	chr11	2154794	2154933	2154815	2154913	IGF2	NM_001127598	3	5	4	-	2154747	2154895
330105985	chr11	2154794	2154933	2154815	2154913	IGF2	NM_001007139	2	5	4	-	2154747	2154895
330145473	chr11	2161430	2161560	2161452	2161533	IGF2	NM_001127598	3	5	2	-	2161365	2161529
236794681	chr11	3697707	3697879	3697730	3697852	NUP98	NM_016320	2	33	32	-	3697739	3697850
236794681	chr11	3697707	3697879	3697730	3697852	NUP98	NM_139132	4	32	31	-	3697739	3697850
235829250	chr11	3704466	3704609	3704486	3704581	NUP98	NM_016320	2	33	30	-	3704430	3704671
235829250	chr11	3704466	3704609	3704486	3704581	NUP98	NM_139132	4	32	29	-	3704430	3704671

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235044412	chr11	3712533	3712668	3712555	3712646	NUP98	NM_016320	2	33	28	-	3712577	3712719
235044412	chr11	3712533	3712668	3712555	3712646	NUP98	NM_139132	4	32	28	-	3712577	3712719
235019026	chr11	3716592	3716766	3716616	3716747	NUP98	NM_016320	2	33	26	-	3716679	3716836
235019026	chr11	3716592	3716766	3716616	3716747	NUP98	NM_139132	4	32	26	-	3716679	3716836
236100338	chr11	3720460	3720632	3720486	3720604	NUP98	NM_016320	2	33	25	-	3720312	3720578
236100338	chr11	3720460	3720632	3720486	3720604	NUP98	NM_139132	4	32	25	-	3720312	3720578
237316341	chr11	3723617	3723786	3723641	3723764	NUP98	NM_016320	2	33	23	-	3723693	3724122
237316341	chr11	3723617	3723786	3723641	3723764	NUP98	NM_139132	4	32	23	-	3723693	3724122
235452841	chr11	3726350	3726518	3726378	3726494	NUP98	NM_016320	2	33	22	-	3726430	3726586
235452841	chr11	3726350	3726518	3726378	3726494	NUP98	NM_139132	4	32	22	-	3726430	3726586
237062840	chr11	3733739	3733908	3733764	3733882	NUP98	NM_016320	2	33	20	-	3733794	3733958
237062840	chr11	3733739	3733908	3733764	3733882	NUP98	NM_139132	4	32	20	-	3733794	3733958
237062840	chr11	3733739	3733908	3733764	3733882	NUP98	NM_005387	1	20	20	-	3733059	3733958
237062840	chr11	3733739	3733908	3733764	3733882	NUP98	NM_139131	3	20	20	-	3733059	3733958
238874601	chr11	3735146	3735291	3735170	3735262	NUP98	NM_005387	1	20	19	-	3735048	3735225
238874601	chr11	3735146	3735291	3735170	3735262	NUP98	NM_139131	3	20	19	-	3735048	3735225
238874601	chr11	3735146	3735291	3735170	3735262	NUP98	NM_016320	2	33	19	-	3735048	3735225
238874601	chr11	3735146	3735291	3735170	3735262	NUP98	NM_139132	4	32	19	-	3735048	3735225
235458671	chr11	3744417	3744588	3744444	3744563	NUP98	NM_005387	1	20	16	-	3744387	3744685
235458671	chr11	3744417	3744588	3744444	3744563	NUP98	NM_139131	3	20	16	-	3744387	3744685
235458671	chr11	3744417	3744588	3744444	3744563	NUP98	NM_016320	2	33	16	-	3744387	3744685
235458671	chr11	3744417	3744588	3744444	3744563	NUP98	NM_139132	4	32	16	-	3744387	3744685
237927525	chr11	3752615	3752780	3752636	3752751	NUP98	NM_005387	1	20	14	-	3752621	3752808
237927525	chr11	3752615	3752780	3752636	3752751	NUP98	NM_139131	3	20	14	-	3752621	3752808
237927525	chr11	3752615	3752780	3752636	3752751	NUP98	NM_016320	2	33	14	-	3752621	3752808
237927525	chr11	3752615	3752780	3752636	3752751	NUP98	NM_139132	4	32	14	-	3752621	3752808
236364596	chr11	3765710	3765870	3765738	3765848	NUP98	NM_005387	1	20	12	-	3765739	3765879
236364596	chr11	3765710	3765870	3765738	3765848	NUP98	NM_139131	3	20	12	-	3765739	3765879
236364596	chr11	3765710	3765870	3765738	3765848	NUP98	NM_016320	2	33	12	-	3765739	3765879
236364596	chr11	3765710	3765870	3765738	3765848	NUP98	NM_139132	4	32	12	-	3765739	3765879
236791255	chr11	3781777	3781944	3781797	3781920	NUP98	NM_139131	3	20	10	-	3781769	3781856
236791255	chr11	3781777	3781944	3781797	3781920	NUP98	NM_016320	2	33	10	-	3781769	3781856
236791255	chr11	3781777	3781944	3781797	3781920	NUP98	NM_139132	4	32	10	-	3781769	3781856
236791255	chr11	3781777	3781944	3781797	3781920	NUP98	NM_005387	1	20	10	-	3781718	3781856
235637041	chr11	3789897	3790065	3789919	3790038	NUP98	NM_005387	1	20	8	-	3789811	3789974
235637041	chr11	3789897	3790065	3789919	3790038	NUP98	NM_139131	3	20	8	-	3789811	3789974
235637041	chr11	3789897	3790065	3789919	3790038	NUP98	NM_016320	2	33	8	-	3789811	3789974
235637041	chr11	3789897	3790065	3789919	3790038	NUP98	NM_139132	4	32	8	-	3789811	3789974
235607483	chr11	3794856	3795025	3794883	3794997	NUP98	NM_005387	1	20	6	-	3794862	3794969
235607483	chr11	3794856	3795025	3794883	3794997	NUP98	NM_139131	3	20	6	-	3794862	3794969
235607483	chr11	3794856	3795025	3794883	3794997	NUP98	NM_016320	2	33	6	-	3794862	3794969

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235607483	chr11	3794856	3795025	3794883	3794997	NUP98	NM_139132	4	32	6	-	3794862	3794969
238403461	chr11	3800169	3800333	3800190	3800305	NUP98	NM_005387	1	20	4	-	3800103	3800279
238403461	chr11	3800169	3800333	3800190	3800305	NUP98	NM_139131	3	20	4	-	3800103	3800279
238403461	chr11	3800169	3800333	3800190	3800305	NUP98	NM_016320	2	33	4	-	3800103	3800279
238403461	chr11	3800169	3800333	3800190	3800305	NUP98	NM_139132	4	32	4	-	3800103	3800279
235775595	chr11	3803304	3803471	3803321	3803443	NUP98	NM_005387	1	20	2	-	3803272	3803375
235775595	chr11	3803304	3803471	3803321	3803443	NUP98	NM_139131	3	20	2	-	3803272	3803375
235775595	chr11	3803304	3803471	3803321	3803443	NUP98	NM_016320	2	33	2	-	3803272	3803375
235775595	chr11	3803304	3803471	3803321	3803443	NUP98	NM_139132	4	32	2	-	3803272	3803375
294636526	chr11	4127186	4127358	4127210	4127335	RRM1	NM_001033	1	19	3	+	4127276	4127453
294102499	chr11	4130876	4131050	4130904	4131026	RRM1	NM_001033	1	19	5	+	4130874	4130933
294713882	chr11	4139460	4139619	4139487	4139591	RRM1	NM_001033	1	19	8	+	4139550	4139691
294266209	chr11	4142863	4143025	4142890	4142996	RRM1	NM_001033	1	19	10	+	4142834	4142995
293714743	chr11	4144435	4144605	4144458	4144581	RRM1	NM_001033	1	19	12	+	4144413	4144614
293937775	chr11	4148187	4148325	4148213	4148304	RRM1	NM_001033	1	19	14	+	4148265	4148486
294897620	chr11	4153440	4153576	4153466	4153554	RRM1	NM_001033	1	19	16	+	4153516	4153651
295389686	chr11	4156184	4156344	4156211	4156319	RRM1	NM_001033	1	19	18	+	4156312	4156500
293728308	chr11	4159456	4159609	4159476	4159582	RRM1	NM_001033	1	19	19	+	4159425	4160106
232951195	chr11	22646365	22646539	22646387	22646515	FANCF	NM_022725	1	1	1	-	22644079	22647387
230653886	chr11	22646859	22647028	22646882	22647008	FANCF	NM_022725	1	1	1	-	22644079	22647387
230573582	chr11	22647288	22647459	22647310	22647436	FANCF	NM_022725	1	1	1	-	22644079	22647387
239746111	chr11	32413495	32413635	32413523	32413610	WT1	NM_000378	1	9	8	-	32413527	32413610
239746111	chr11	32413495	32413635	32413523	32413610	WT1	NM_001198551	2	10	9	-	32413527	32413610
239746111	chr11	32413495	32413635	32413523	32413610	WT1	NM_024424	4	10	9	-	32413527	32413610
239746111	chr11	32413495	32413635	32413523	32413610	WT1	NM_001198552	3	9	8	-	32413518	32413610
239746111	chr11	32413495	32413635	32413523	32413610	WT1	NM_024426	5	10	9	-	32413518	32413610
240948996	chr11	32421399	32421528	32421421	32421508	WT1	NM_000378	1	9	5	-	32421494	32421590
240948996	chr11	32421399	32421528	32421421	32421508	WT1	NM_001198552	3	9	5	-	32421494	32421590
240948996	chr11	32421399	32421528	32421421	32421508	WT1	NM_001198551	2	10	6	-	32421494	32421590
240948996	chr11	32421399	32421528	32421421	32421508	WT1	NM_024426	5	10	6	-	32421494	32421590
240948996	chr11	32421399	32421528	32421421	32421508	WT1	NM_024424	4	10	6	-	32421494	32421590
242611032	chr11	32439121	32439274	32439142	32439247	WT1	NM_000378	1	9	4	-	32439123	32439200
242611032	chr11	32439121	32439274	32439142	32439247	WT1	NM_001198552	3	9	4	-	32439123	32439200
242611032	chr11	32439121	32439274	32439142	32439247	WT1	NM_001198551	2	10	4	-	32439123	32439200
242611032	chr11	32439121	32439274	32439142	32439247	WT1	NM_024426	5	10	4	-	32439123	32439200
242611032	chr11	32439121	32439274	32439142	32439247	WT1	NM_024424	4	10	4	-	32439123	32439200
238603145	chr11	32450060	32450200	32450079	32450179	WT1	NM_000378	1	9	2	-	32450043	32450165
238603145	chr11	32450060	32450200	32450079	32450179	WT1	NM_001198552	3	9	2	-	32450043	32450165
238603145	chr11	32450060	32450200	32450079	32450179	WT1	NM_001198551	2	10	2	-	32450043	32450165
238603145	chr11	32450060	32450200	32450079	32450179	WT1	NM_024426	5	10	2	-	32450043	32450165
238603145	chr11	32450060	32450200	32450079	32450179	WT1	NM_024424	4	10	2	-	32450043	32450165

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_000378	1	9	1	-	32456246	32457081
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_024426	5	10	1	-	32456246	32457081
262325189	chr11	32456385	32456551	32456405	32456533	WT1	NM_024424	4	10	1	-	32456246	32457081
229913773	chr11	44117699	44117870	44117719	44117853	EXT2	NM_000401	1	14	1	+	44117747	44117871
230558335	chr11	44129429	44129581	44129451	44129555	EXT2	NM_000401	1	14	2	+	44129233	44129798
230558335	chr11	44129429	44129581	44129451	44129555	EXT2	NM_001178083	2	15	2	+	44129233	44129798
230558335	chr11	44129429	44129581	44129451	44129555	EXT2	NM_207122	3	14	2	+	44129233	44129798
230118761	chr11	44130731	44130867	44130755	44130845	EXT2	NM_000401	1	14	3	+	44130744	44130833
230118761	chr11	44130731	44130867	44130755	44130845	EXT2	NM_001178083	2	15	3	+	44130744	44130833
230118761	chr11	44130731	44130867	44130755	44130845	EXT2	NM_207122	3	14	3	+	44130744	44130833
230707368	chr11	44146394	44146562	44146414	44146537	EXT2	NM_000401	1	14	5	+	44146339	44146534
230707368	chr11	44146394	44146562	44146414	44146537	EXT2	NM_001178083	2	15	5	+	44146339	44146534
230707368	chr11	44146394	44146562	44146414	44146537	EXT2	NM_207122	3	14	5	+	44146339	44146534
229134027	chr11	44165695	44165864	44165717	44165839	EXT2	NM_001178083	2	15	8	+	44165797	44165889
230132147	chr11	44219296	44219470	44219319	44219450	EXT2	NM_000401	1	14	9	+	44219379	44219568
230132147	chr11	44219296	44219470	44219319	44219450	EXT2	NM_001178083	2	15	10	+	44219379	44219568
230132147	chr11	44219296	44219470	44219319	44219450	EXT2	NM_207122	3	14	9	+	44219379	44219568
231619521	chr11	44228485	44228635	44228509	44228606	EXT2	NM_000401	1	14	10	+	44228343	44228509
231619521	chr11	44228485	44228635	44228509	44228606	EXT2	NM_001178083	2	15	11	+	44228343	44228509
231619521	chr11	44228485	44228635	44228509	44228606	EXT2	NM_207122	3	14	10	+	44228343	44228509
231188807	chr11	44257775	44257949	44257802	44257925	EXT2	NM_000401	1	14	13	+	44257843	44257925
231188807	chr11	44257775	44257949	44257802	44257925	EXT2	NM_001178083	2	15	14	+	44257843	44257925
231188807	chr11	44257775	44257949	44257802	44257925	EXT2	NM_207122	3	14	13	+	44257843	44257925
229070337	chr11	47236727	47236856	47236749	47236831	DDB2	NM_000107	1	10	1	+	47236493	47236814
230314844	chr11	47238419	47238556	47238442	47238533	DDB2	NM_000107	1	10	3	+	47238409	47238600
229947003	chr11	47255986	47256151	47256007	47256128	DDB2	NM_000107	1	10	5	+	47256124	47256223
228725988	chr11	47256382	47256512	47256404	47256488	DDB2	NM_000107	1	10	6	+	47256308	47256485
228831085	chr11	47259433	47259594	47259461	47259571	DDB2	NM_000107	1	10	8	+	47259388	47259552
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130800	3	10	10	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130803	6	10	10	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130802	5	10	10	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130801	4	10	10	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130804	7	11	11	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_000244	1	10	10	-	64570986	64572288
233337573	chr11	64571825	64571994	64571848	64571973	MEN1	NM_130799	2	10	10	-	64570986	64572288
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130800	3	10	9	-	64572506	64572670
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130803	6	10	9	-	64572506	64572670
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130802	5	10	9	-	64572506	64572670
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130801	4	10	9	-	64572506	64572670
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130804	7	11	10	-	64572506	64572670
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_000244	1	10	9	-	64572506	64572670

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233522057	chr11	64572456	64572622	64572476	64572602	MEN1	NM_130799	2	10	9	-	64572506	64572670
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130800	3	10	7	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130803	6	10	7	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130802	5	10	7	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130801	4	10	7	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130804	7	11	8	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_000244	1	10	7	-	64573704	64573840
233055760	chr11	64573638	64573812	64573659	64573788	MEN1	NM_130799	2	10	7	-	64573704	64573840
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130800	3	10	4	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130803	6	10	4	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130802	5	10	4	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130801	4	10	4	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130804	7	11	5	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_000244	1	10	4	-	64575024	64575152
232458215	chr11	64575033	64575194	64575051	64575171	MEN1	NM_130799	2	10	4	-	64575024	64575152
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130800	3	10	2	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130803	6	10	2	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130802	5	10	2	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130801	4	10	2	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130804	7	11	3	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_000244	1	10	2	-	64577122	64577604
231191963	chr11	64577191	64577344	64577213	64577323	MEN1	NM_130799	2	10	2	-	64577137	64577604
253634967	chr11	69455928	69456101	69455945	69456082	CCND1	NM_053056	1	5	1	+	69455873	69456279
226296151	chr11	69457871	69457999	69457891	69457981	CCND1	NM_053056	1	5	2	+	69457799	69458014
226678230	chr11	69462734	69462904	69462756	69462880	CCND1	NM_053056	1	5	4	+	69462762	69462910
226973939	chr11	69466004	69466169	69466022	69466143	CCND1	NM_053056	1	5	5	+	69465886	69469242
238769513	chr11	71715239	71715412	71715259	71715387	NUMA1	NM_006185	1	27	25	-	71715271	71715387
237462153	chr11	71716291	71716457	71716313	71716435	NUMA1	NM_006185	1	27	23	-	71716279	71716415
235528206	chr11	71718246	71718404	71718268	71718381	NUMA1	NM_006185	1	27	21	-	71718235	71718481
238707579	chr11	71719971	71720140	71719994	71720119	NUMA1	NM_006185	1	27	19	-	71720013	71720231
237543586	chr11	71720319	71720458	71720340	71720435	NUMA1	NM_006185	1	27	18	-	71720314	71720433
258168828	chr11	71723996	71724161	71724017	71724138	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238431698	chr11	71724397	71724558	71724414	71724538	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238464412	chr11	71724829	71724967	71724849	71724946	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258182700	chr11	71725250	71725420	71725275	71725400	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238413411	chr11	71725667	71725840	71725686	71725818	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258215667	chr11	71726088	71726247	71726109	71726226	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258199336	chr11	71726504	71726670	71726521	71726651	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238116451	chr11	71726984	71727157	71727006	71727135	NUMA1	NM_006185	1	27	15	-	71723941	71727306
237022187	chr11	71728696	71728860	71728716	71728839	NUMA1	NM_006185	1	27	13	-	71728733	71728873
239147154	chr11	71729420	71729555	71729441	71729533	NUMA1	NM_006185	1	27	11	-	71729442	71729559

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241998221	chr11	71730440	71730600	71730461	71730579	NUMA1	NM_006185	1	27	9	-	71730540	71730663
236362649	chr11	71734047	71734219	71734067	71734193	NUMA1	NM_006185	1	27	6	-	71734111	71734193
242776336	chr11	94153247	94153390	94153276	94153362	MRE11A	NM_005591	2	20	20	-	94150469	94153347
242776336	chr11	94153247	94153390	94153276	94153362	MRE11A	NM_005590	1	19	19	-	94150469	94153347
237439377	chr11	94170359	94170513	94170381	94170486	MRE11A	NM_005591	2	20	17	-	94170343	94170401
237439377	chr11	94170359	94170513	94170381	94170486	MRE11A	NM_005590	1	19	16	-	94170343	94170401
238318029	chr11	94180458	94180632	94180480	94180606	MRE11A	NM_005591	2	20	15	-	94180385	94180604
238318029	chr11	94180458	94180632	94180480	94180606	MRE11A	NM_005590	1	19	15	-	94180385	94180604
239788707	chr11	94194102	94194275	94194126	94194248	MRE11A	NM_005591	2	20	12	-	94194102	94194202
239788707	chr11	94194102	94194275	94194126	94194248	MRE11A	NM_005590	1	19	12	-	94194102	94194202
236175521	chr11	94200974	94201123	94200997	94201096	MRE11A	NM_005591	2	20	10	-	94200979	94201059
236175521	chr11	94200974	94201123	94200997	94201096	MRE11A	NM_005590	1	19	10	-	94200979	94201059
239327716	chr11	94204637	94204782	94204657	94204758	MRE11A	NM_005591	2	20	8	-	94204740	94204925
239327716	chr11	94204637	94204782	94204657	94204758	MRE11A	NM_005590	1	19	8	-	94204740	94204925
237368063	chr11	94211892	94212022	94211919	94211994	MRE11A	NM_005591	2	20	6	-	94211901	94212042
237368063	chr11	94211892	94212022	94211919	94211994	MRE11A	NM_005590	1	19	6	-	94211901	94212042
235432260	chr11	94219046	94219196	94219074	94219168	MRE11A	NM_005591	2	20	4	-	94219090	94219250
235432260	chr11	94219046	94219196	94219074	94219168	MRE11A	NM_005590	1	19	4	-	94219090	94219250
235243982	chr11	94225883	94226008	94225904	94225987	MRE11A	NM_005591	2	20	2	-	94225948	94226072
235243982	chr11	94225883	94226008	94225904	94225987	MRE11A	NM_005590	1	19	2	-	94225948	94226072
234476864	chr11	95712359	95712512	95712380	95712489	MAML2	NM_032427	1	5	5	-	95711440	95713127
234503186	chr11	95712790	95712930	95712813	95712904	MAML2	NM_032427	1	5	5	-	95711440	95713127
232880655	chr11	95724640	95724794	95724664	95724768	MAML2	NM_032427	1	5	3	-	95724684	95724887
234508902	chr11	95825552	95825682	95825573	95825661	MAML2	NM_032427	1	5	2	-	95825056	95826681
234504857	chr11	95825961	95826131	95825981	95826104	MAML2	NM_032427	1	5	2	-	95825056	95826681
234538724	chr11	95826440	95826614	95826463	95826586	MAML2	NM_032427	1	5	2	-	95825056	95826681
233185762	chr11	96074779	96074908	96074800	96074885	MAML2	NM_032427	1	5	1	-	96074547	96076344
223915026	chr11	102195288	102195437	102195309	102195412	BIRC3	NM_182962	2	10	3	+	102195192	102196093
223915026	chr11	102195288	102195437	102195309	102195412	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222440440	chr11	102195723	102195895	102195750	102195874	BIRC3	NM_182962	2	10	3	+	102195192	102196093
222440440	chr11	102195723	102195895	102195750	102195874	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222486589	chr11	102196088	102196248	102196117	102196227	BIRC3	NM_182962	2	10	4	+	102196197	102196296
222486589	chr11	102196088	102196248	102196117	102196227	BIRC3	NM_001165	1	9	3	+	102196197	102196296
223744517	chr11	102199493	102199665	102199515	102199643	BIRC3	NM_182962	2	10	6	+	102199628	102199676
223744517	chr11	102199493	102199665	102199515	102199643	BIRC3	NM_001165	1	9	5	+	102199628	102199676
222716012	chr11	102206638	102206769	102206662	102206741	BIRC3	NM_182962	2	10	8	+	102206697	102206951
222716012	chr11	102206638	102206769	102206662	102206741	BIRC3	NM_001165	1	9	7	+	102206697	102206951
224614189	chr11	102207482	102207652	102207511	102207624	BIRC3	NM_182962	2	10	9	+	102207491	102207532
224614189	chr11	102207482	102207652	102207511	102207624	BIRC3	NM_001165	1	9	8	+	102207491	102207532
295141266	chr11	102220568	102220694	102220592	102220669	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294238331	chr11	102220930	102221082	102220952	102221055	BIRC2	NM_001166	1	9	2	+	102219329	102221480

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295159952	chr11	102221316	102221456	102221340	102221437	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294611653	chr11	102238913	102239087	102238941	102239060	BIRC2	NM_001166	1	9	6	+	102239037	102239279
294109366	chr11	102248247	102248421	102248273	102248396	BIRC2	NM_001166	1	9	7	+	102248227	102248481
293816706	chr11	102248713	102248884	102248740	102248859	BIRC2	NM_001166	1	9	9	+	102248721	102249401
270813802	chr11	106579133	106579292	106579161	106579271	GUCY1A2	NM_000855	1	8	7	-	106579238	106579392
270813802	chr11	106579133	106579292	106579161	106579271	GUCY1A2	NM_001256424	2	9	8	-	106579238	106579392
272123278	chr11	106680731	106680874	106680754	106680850	GUCY1A2	NM_000855	1	8	5	-	106680719	106681204
272123278	chr11	106680731	106680874	106680754	106680850	GUCY1A2	NM_001256424	2	9	5	-	106680719	106681204
272156608	chr11	106681130	106681257	106681156	106681229	GUCY1A2	NM_000855	1	8	5	-	106680719	106681204
272156608	chr11	106681130	106681257	106681156	106681229	GUCY1A2	NM_001256424	2	9	5	-	106680719	106681204
272675604	chr11	106810407	106810577	106810429	106810549	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
272675604	chr11	106810407	106810577	106810429	106810549	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
271399064	chr11	106849240	106849410	106849266	106849381	GUCY1A2	NM_000855	1	8	3	-	106849345	106849466
271399064	chr11	106849240	106849410	106849266	106849381	GUCY1A2	NM_001256424	2	9	3	-	106849345	106849466
270720590	chr11	106888511	106888684	106888529	106888666	GUCY1A2	NM_000855	1	8	1	-	106888479	106889171
270720590	chr11	106888511	106888684	106888529	106888666	GUCY1A2	NM_001256424	2	9	1	-	106888479	106889171
223701627	chr11	108098393	108098566	108098421	108098538	ATM	NM_000051	1	63	2	+	108098322	108098423
223701627	chr11	108098393	108098566	108098421	108098538	ATM	NM_000051	1	63	3	+	108098503	108098615
222448053	chr11	108106399	108106553	108106426	108106525	ATM	NM_000051	1	63	5	+	108106397	108106561
222538062	chr11	108114701	108114861	108114727	108114834	ATM	NM_000051	1	63	6	+	108114680	108114845
222998755	chr11	108115705	108115866	108115734	108115838	ATM	NM_000051	1	63	7	+	108115515	108115753
225122942	chr11	108119668	108119809	108119696	108119781	ATM	NM_000051	1	63	9	+	108119660	108119829
223543451	chr11	108121579	108121741	108121603	108121714	ATM	NM_000051	1	63	10	+	108121428	108121799
223273342	chr11	108122712	108122836	108122738	108122810	ATM	NM_000051	1	63	11	+	108122564	108122758
223079261	chr11	108124533	108124704	108124561	108124680	ATM	NM_000051	1	63	13	+	108124541	108124766
222204633	chr11	108127014	108127174	108127042	108127143	ATM	NM_000051	1	63	14	+	108126942	108127067
326938567	chr11	108137864	108138038	108137891	108138010	ATM	NM_000051	1	63	17	+	108137898	108138069
223396098	chr11	108141819	108141992	108141841	108141965	ATM	NM_000051	1	63	19	+	108141791	108141873
223582489	chr11	108143188	108143336	108143213	108143309	ATM	NM_000051	1	63	21	+	108143259	108143334
223784312	chr11	108143518	108143661	108143545	108143633	ATM	NM_000051	1	63	22	+	108143449	108143579
222174650	chr11	108151721	108151888	108151742	108151861	ATM	NM_000051	1	63	24	+	108151722	108151895
224367525	chr11	108155057	108155213	108155085	108155189	ATM	NM_000051	1	63	26	+	108154954	108155200
224114665	chr11	108159714	108159847	108159737	108159819	ATM	NM_000051	1	63	28	+	108159704	108159830
222319815	chr11	108163244	108163393	108163273	108163367	ATM	NM_000051	1	63	30	+	108163346	108163520
224737023	chr11	108165679	108165826	108165706	108165799	ATM	NM_000051	1	63	32	+	108165654	108165786
223706191	chr11	108172335	108172481	108172362	108172453	ATM	NM_000051	1	63	35	+	108172375	108172516
224429561	chr11	108173709	108173852	108173737	108173824	ATM	NM_000051	1	63	36	+	108173580	108173756
222213434	chr11	108178571	108178745	108178593	108178718	ATM	NM_000051	1	63	38	+	108178624	108178711
223586299	chr11	108183141	108183311	108183165	108183284	ATM	NM_000051	1	63	40	+	108183138	108183225
329445161	chr11	108186742	108186907	108186768	108186879	ATM	NM_000051	1	63	42	+	108186738	108186840
223104068	chr11	108191922	108192088	108191948	108192064	ATM	NM_000051	1	63	45	+	108192028	108192147

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223495661	chr11	108196200	108196354	108196228	108196330	ATM	NM_000051	1	63	46	+	108196037	108196271
223676910	chr11	108198379	108198508	108198407	108198483	ATM	NM_000051	1	63	48	+	108198372	108198485
222167249	chr11	108200888	108201017	108200916	108200993	ATM	NM_000051	1	63	50	+	108200941	108201148
222587210	chr11	108202488	108202662	108202508	108202634	ATM	NM_000051	1	63	52	+	108202606	108202764
222306820	chr11	108203430	108203565	108203459	108203542	ATM	NM_000051	1	63	53	+	108203489	108203627
326938015	chr11	108205630	108205771	108205663	108205748	ATM	NM_000051	1	63	55	+	108205696	108205836
224104146	chr11	108213888	108214056	108213916	108214028	ATM	NM_000051	1	63	57	+	108213949	108214098
329888112	chr11	108217860	108218034	108217886	108218006	ATM	NM_000051	1	63	59	+	108218006	108218092
223107326	chr11	108225489	108225663	108225515	108225635	ATM	NM_000051	1	63	61	+	108225538	108225601
224478109	chr11	108236141	108236313	108236164	108236285	ATM	NM_000051	1	63	63	+	108236052	108239826
242160928	chr11	111959509	111959681	111959533	111959658	SDHD	NM_003002	1	4	3	+	111959591	111959735
233663665	chr11	118307510	118307678	118307531	118307660	MLL	NM_005933	2	36	1	+	118307205	118307659
233663665	chr11	118307510	118307678	118307531	118307660	MLL	NM_001197104	1	36	1	+	118307205	118307659
234018335	chr11	118342448	118342604	118342476	118342578	MLL	NM_005933	2	36	3	+	118342377	118345030
234018335	chr11	118342448	118342604	118342476	118342578	MLL	NM_001197104	1	36	3	+	118342377	118345030
231610074	chr11	118342880	118343014	118342908	118342991	MLL	NM_005933	2	36	3	+	118342377	118345030
231610074	chr11	118342880	118343014	118342908	118342991	MLL	NM_001197104	1	36	3	+	118342377	118345030
231664256	chr11	118343268	118343422	118343292	118343401	MLL	NM_005933	2	36	3	+	118342377	118345030
231664256	chr11	118343268	118343422	118343292	118343401	MLL	NM_001197104	1	36	3	+	118342377	118345030
231728889	chr11	118343715	118343859	118343740	118343839	MLL	NM_005933	2	36	3	+	118342377	118345030
231728889	chr11	118343715	118343859	118343740	118343839	MLL	NM_001197104	1	36	3	+	118342377	118345030
234034521	chr11	118344110	118344246	118344135	118344225	MLL	NM_005933	2	36	3	+	118342377	118345030
234034521	chr11	118344110	118344246	118344135	118344225	MLL	NM_001197104	1	36	3	+	118342377	118345030
234030483	chr11	118344458	118344631	118344478	118344607	MLL	NM_005933	2	36	3	+	118342377	118345030
234030483	chr11	118344458	118344631	118344478	118344607	MLL	NM_001197104	1	36	3	+	118342377	118345030
234035121	chr11	118344909	118345066	118344930	118345037	MLL	NM_005933	2	36	3	+	118342377	118345030
234035121	chr11	118344909	118345066	118344930	118345037	MLL	NM_001197104	1	36	3	+	118342377	118345030
233594021	chr11	118348768	118348942	118348789	118348917	MLL	NM_005933	2	36	5	+	118348682	118348916
233594021	chr11	118348768	118348942	118348789	118348917	MLL	NM_001197104	1	36	5	+	118348682	118348916
233124610	chr11	118352504	118352657	118352529	118352636	MLL	NM_005933	2	36	7	+	118352430	118352807
233124610	chr11	118352504	118352657	118352529	118352636	MLL	NM_001197104	1	36	7	+	118352430	118352807
233950770	chr11	118354835	118354983	118354860	118354957	MLL	NM_005933	2	36	9	+	118354898	118355029
233950770	chr11	118354835	118354983	118354860	118354957	MLL	NM_001197104	1	36	9	+	118354898	118355029
233480155	chr11	118359347	118359506	118359368	118359478	MLL	NM_005933	2	36	11	+	118359329	118359475
233480155	chr11	118359347	118359506	118359368	118359478	MLL	NM_001197104	1	36	11	+	118359329	118359475
232709227	chr11	118360832	118360999	118360861	118360978	MLL	NM_005933	2	36	13	+	118360844	118360964
232709227	chr11	118360832	118360999	118360861	118360978	MLL	NM_001197104	1	36	13	+	118360844	118360964
231614756	chr11	118362551	118362691	118362573	118362664	MLL	NM_005933	2	36	15	+	118362459	118362643
231614756	chr11	118362551	118362691	118362573	118362664	MLL	NM_001197104	1	36	15	+	118362459	118362643
231033272	chr11	118365087	118365229	118365111	118365200	MLL	NM_005933	2	36	17	+	118365003	118365113
231033272	chr11	118365087	118365229	118365111	118365200	MLL	NM_001197104	1	36	17	+	118365003	118365113

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233267819	chr11	118366398	118366542	118366426	118366517	MLL	NM_005933	2	36	19	+	118366415	118366608
233267819	chr11	118366398	118366542	118366426	118366517	MLL	NM_001197104	1	36	19	+	118366415	118366608
231649909	chr11	118368674	118368837	118368695	118368809	MLL	NM_005933	2	36	21	+	118368651	118368788
231649909	chr11	118368674	118368837	118368695	118368809	MLL	NM_001197104	1	36	21	+	118368651	118368788
234388695	chr11	118369992	118370160	118370020	118370136	MLL	NM_005933	2	36	23	+	118370018	118370135
234388695	chr11	118369992	118370160	118370020	118370136	MLL	NM_001197104	1	36	23	+	118370018	118370135
233066561	chr11	118372264	118372418	118372290	118372391	MLL	NM_005933	2	36	26	+	118372387	118372572
233066561	chr11	118372264	118372418	118372290	118372391	MLL	NM_001197104	1	36	26	+	118372387	118372572
231232550	chr11	118373174	118373344	118373195	118373317	MLL	NM_005933	2	36	27	+	118373113	118377361
231232550	chr11	118373174	118373344	118373195	118373317	MLL	NM_001197104	1	36	27	+	118373113	118377361
233870196	chr11	118373614	118373765	118373642	118373742	MLL	NM_005933	2	36	27	+	118373113	118377361
233870196	chr11	118373614	118373765	118373642	118373742	MLL	NM_001197104	1	36	27	+	118373113	118377361
233890515	chr11	118374040	118374212	118374063	118374184	MLL	NM_005933	2	36	27	+	118373113	118377361
233890515	chr11	118374040	118374212	118374063	118374184	MLL	NM_001197104	1	36	27	+	118373113	118377361
231360276	chr11	118374479	118374631	118374503	118374610	MLL	NM_005933	2	36	27	+	118373113	118377361
231360276	chr11	118374479	118374631	118374503	118374610	MLL	NM_001197104	1	36	27	+	118373113	118377361
233878468	chr11	118374829	118374998	118374857	118374974	MLL	NM_005933	2	36	27	+	118373113	118377361
233878468	chr11	118374829	118374998	118374857	118374974	MLL	NM_001197104	1	36	27	+	118373113	118377361
233880699	chr11	118375241	118375407	118375266	118375383	MLL	NM_005933	2	36	27	+	118373113	118377361
233880699	chr11	118375241	118375407	118375266	118375383	MLL	NM_001197104	1	36	27	+	118373113	118377361
233892308	chr11	118375740	118375914	118375763	118375892	MLL	NM_005933	2	36	27	+	118373113	118377361
233892308	chr11	118375740	118375914	118375763	118375892	MLL	NM_001197104	1	36	27	+	118373113	118377361
233911429	chr11	118376231	118376396	118376253	118376369	MLL	NM_005933	2	36	27	+	118373113	118377361
233911429	chr11	118376231	118376396	118376253	118376369	MLL	NM_001197104	1	36	27	+	118373113	118377361
233903660	chr11	118376654	118376780	118376678	118376752	MLL	NM_005933	2	36	27	+	118373113	118377361
233903660	chr11	118376654	118376780	118376678	118376752	MLL	NM_001197104	1	36	27	+	118373113	118377361
233899352	chr11	118377046	118377179	118377068	118377155	MLL	NM_005933	2	36	27	+	118373113	118377361
233899352	chr11	118377046	118377179	118377068	118377155	MLL	NM_001197104	1	36	27	+	118373113	118377361
232641935	chr11	118379767	118379939	118379794	118379914	MLL	NM_005933	2	36	29	+	118379851	118379915
232641935	chr11	118379767	118379939	118379794	118379914	MLL	NM_001197104	1	36	29	+	118379851	118379915
233102862	chr11	118390272	118390444	118390294	118390421	MLL	NM_005933	2	36	32	+	118390333	118390507
233102862	chr11	118390272	118390444	118390294	118390421	MLL	NM_001197104	1	36	32	+	118390333	118390507
233087040	chr11	118391397	118391546	118391420	118391525	MLL	NM_005933	2	36	34	+	118391517	118391600
233087040	chr11	118391397	118391546	118391420	118391525	MLL	NM_001197104	1	36	34	+	118391517	118391600
232526302	chr11	118392584	118392757	118392608	118392732	MLL	NM_005933	2	36	36	+	118392612	118397539
232526302	chr11	118392584	118392757	118392608	118392732	MLL	NM_001197104	1	36	36	+	118392612	118397539
253777424	chr11	119077136	119077305	119077157	119077282	CBL	NM_005188	1	16	1	+	119076990	119077322
226478350	chr11	119103277	119103450	119103306	119103423	CBL	NM_005188	1	16	2	+	119103158	119103405
225867746	chr11	119144535	119144700	119144563	119144672	CBL	NM_005188	1	16	4	+	119144578	119144734
226122844	chr11	119146635	119146770	119146657	119146745	CBL	NM_005188	1	16	6	+	119146707	119146844
226426486	chr11	119148885	119149017	119148911	119148997	CBL	NM_005188	1	16	8	+	119148876	119149007

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253641636	chr11	119155609	119155782	119155636	119155760	CBL	NM_005188	1	16	10	+	119155679	119155810
225902236	chr11	119156048	119156195	119156070	119156174	CBL	NM_005188	1	16	11	+	119155899	119156276
227080104	chr11	119167507	119167680	119167533	119167658	CBL	NM_005188	1	16	13	+	119167628	119167744
226196214	chr11	119168987	119169145	119169007	119169121	CBL	NM_005188	1	16	15	+	119169068	119169250
226365721	chr11	119170385	119170518	119170407	119170497	CBL	NM_005188	1	16	16	+	119170205	119178859
226465757	chr11	125497569	125497725	125497597	125497699	CHEK1	NM_001244846	3	12	3	+	125497502	125497725
226465757	chr11	125497569	125497725	125497597	125497699	CHEK1	NR_045205	6	13	3	+	125497502	125497725
226465757	chr11	125497569	125497725	125497597	125497699	CHEK1	NM_001114121	1	14	3	+	125497502	125497725
226465757	chr11	125497569	125497725	125497597	125497699	CHEK1	NM_001114122	2	13	3	+	125497502	125497725
226465757	chr11	125497569	125497725	125497597	125497699	CHEK1	NM_001274	4	13	3	+	125497502	125497725
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NM_001244846	3	12	5	+	125499286	125499355
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NR_045205	6	13	5	+	125499286	125499355
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NM_001114121	1	14	5	+	125499286	125499355
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NM_001114122	2	13	5	+	125499286	125499355
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NM_001274	4	13	5	+	125499286	125499355
226159122	chr11	125499187	125499357	125499214	125499331	CHEK1	NR_045204	5	12	4	+	125499286	125499355
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NM_001244846	3	12	6	+	125503058	125503246
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NR_045205	6	13	6	+	125503058	125503246
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NM_001114121	1	14	6	+	125503058	125503246
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NM_001114122	2	13	6	+	125503058	125503246
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NM_001274	4	13	6	+	125503058	125503246
225727031	chr11	125503123	125503253	125503151	125503232	CHEK1	NR_045204	5	12	5	+	125503058	125503246
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NM_001244846	3	12	8	+	125507344	125507439
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NR_045205	6	13	8	+	125507344	125507439
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NM_001114121	1	14	8	+	125507344	125507439
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NM_001114122	2	13	8	+	125507344	125507439
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NM_001274	4	13	8	+	125507344	125507439
226572534	chr11	125507327	125507499	125507355	125507472	CHEK1	NR_045204	5	12	7	+	125507344	125507439
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NM_001244846	3	12	10	+	125513986	125514163
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NR_045205	6	13	10	+	125513986	125514163
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NM_001114121	1	14	10	+	125513986	125514163
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NM_001114122	2	13	10	+	125513986	125514163
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NM_001274	4	13	10	+	125513986	125514163
225533394	chr11	125514054	125514182	125514082	125514154	CHEK1	NR_045204	5	12	9	+	125513986	125514163
225439977	chr11	125523710	125523848	125523738	125523820	CHEK1	NR_045205	6	13	12	+	125523641	125523742
225439977	chr11	125523710	125523848	125523738	125523820	CHEK1	NM_001114121	1	14	12	+	125523641	125523742
225439977	chr11	125523710	125523848	125523738	125523820	CHEK1	NM_001114122	2	13	12	+	125523641	125523742
225439977	chr11	125523710	125523848	125523738	125523820	CHEK1	NM_001274	4	13	12	+	125523641	125523742
225439977	chr11	125523710	125523848	125523738	125523820	CHEK1	NR_045204	5	12	11	+	125523641	125523742
294569290	chr11	128332253	128332412	128332273	128332393	ETS1	NM_005238	3	8	8	-	128328656	128332471
294569290	chr11	128332253	128332412	128332273	128332393	ETS1	NM_001143820	1	10	10	-	128328656	128332471

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294569290	chr11	128332253	128332412	128332273	128332393	ETS1	NM_001162422	2	4	4	-	128328656	128332471
294038881	chr11	128350036	128350174	128350057	128350152	ETS1	NM_005238	3	8	6	-	128350086	128350346
294038881	chr11	128350036	128350174	128350057	128350152	ETS1	NM_001143820	1	10	8	-	128350086	128350346
294038881	chr11	128350036	128350174	128350057	128350152	ETS1	NM_001162422	2	4	2	-	128350086	128350346
293786210	chr11	128354751	128354916	128354773	128354893	ETS1	NM_005238	3	8	5	-	128354718	128354966
293786210	chr11	128354751	128354916	128354773	128354893	ETS1	NM_001143820	1	10	7	-	128354718	128354966
293819156	chr11	128359274	128359413	128359295	128359386	ETS1	NM_005238	3	8	3	-	128359185	128359385
293819156	chr11	128359274	128359413	128359295	128359386	ETS1	NM_001143820	1	10	5	-	128359185	128359385
293927735	chr11	128391816	128391983	128391839	128391962	ETS1	NM_005238	3	8	1	-	128391808	128392205
293927735	chr11	128391816	128391983	128391839	128391962	ETS1	NM_001162422	2	4	1	-	128391808	128392205
227207279	chr11	128564103	128564276	128564124	128564257	FLI1	NM_001167681	1	10	1	+	128563811	128564171
227207279	chr11	128564103	128564276	128564124	128564257	FLI1	NM_002017	2	9	1	+	128563813	128564171
229380425	chr11	128637936	128638106	128637957	128638079	FLI1	NM_002017	2	9	3	+	128638013	128638167
229380425	chr11	128637936	128638106	128637957	128638079	FLI1	NM_001167681	1	10	4	+	128638013	128638167
229788733	chr11	128651727	128651880	128651748	128651856	FLI1	NM_002017	2	9	5	+	128651853	128651918
229788733	chr11	128651727	128651880	128651748	128651856	FLI1	NM_001167681	1	10	6	+	128651853	128651918
227622284	chr11	128678969	128679121	128678996	128679100	FLI1	NM_002017	2	9	8	+	128679052	128679099
227622284	chr11	128678969	128679121	128678996	128679100	FLI1	NM_001167681	1	10	9	+	128679052	128679099
229122311	chr11	128680642	128680791	128680661	128680771	FLI1	NM_002017	2	9	9	+	128680354	128683162
229122311	chr11	128680642	128680791	128680661	128680771	FLI1	NM_001167681	1	10	10	+	128680354	128683162
226083642	chr12	4383213	4383373	4383230	4383353	CCND2	NM_001759	1	5	1	+	4382902	4383401
226195659	chr12	4385300	4385473	4385322	4385452	CCND2	NM_001759	1	5	2	+	4385171	4385386
226707678	chr12	4398020	4398194	4398039	4398170	CCND2	NM_001759	1	5	4	+	4398008	4398156
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_001127584	3	8	7	-	6760490	6760551
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_001127583	2	8	7	-	6760490	6760551
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_016162	6	8	7	-	6760490	6760551
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_001127582	1	8	7	-	6760490	6760551
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_001127586	5	7	6	-	6760490	6760551
277835991	chr12	6760415	6760578	6760438	6760551	ING4	NM_001127585	4	7	6	-	6760490	6760551
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_016162	6	8	4	-	6762102	6762216
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_001127582	1	8	4	-	6762102	6762216
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_001127586	5	7	4	-	6762102	6762216
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_001127585	4	7	3	-	6762102	6762216
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_001127584	3	8	4	-	6762111	6762216
278237463	chr12	6762004	6762142	6762025	6762117	ING4	NM_001127583	2	8	4	-	6762111	6762216
278293774	chr12	6765785	6765936	6765810	6765912	ING4	NM_001127584	3	8	2	-	6765893	6765964
278293774	chr12	6765785	6765936	6765810	6765912	ING4	NM_001127583	2	8	2	-	6765893	6765964
278293774	chr12	6765785	6765936	6765810	6765912	ING4	NM_016162	6	8	2	-	6765893	6765964
278293774	chr12	6765785	6765936	6765810	6765912	ING4	NM_001127582	1	8	2	-	6765893	6765964
278293774	chr12	6765785	6765936	6765810	6765912	ING4	NM_001127586	5	7	2	-	6765893	6765964
264679607	chr12	6776921	6777064	6776944	6777043	ZNF384	NM_133476	3	10	10	-	6775643	6777281

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264679607	chr12	6776921	6777064	6776944	6777043	ZNF384	NM_001135734	2	11	11	-	6775643	6777281
264679607	chr12	6776921	6777064	6776944	6777043	ZNF384	NM_001039920	1	9	9	-	6775643	6777281
240885974	chr12	6778248	6778408	6778268	6778385	ZNF384	NM_133476	3	10	9	-	6778197	6778355
240885974	chr12	6778248	6778408	6778268	6778385	ZNF384	NM_001135734	2	11	10	-	6778197	6778355
240885974	chr12	6778248	6778408	6778268	6778385	ZNF384	NM_001039920	1	9	8	-	6778197	6778355
262016396	chr12	6781663	6781794	6781683	6781772	ZNF384	NM_001135734	2	11	8	-	6781516	6781698
239035173	chr12	6787219	6787392	6787242	6787371	ZNF384	NM_133476	3	10	6	-	6787293	6787626
239035173	chr12	6787219	6787392	6787242	6787371	ZNF384	NM_001135734	2	11	6	-	6787293	6787626
239035173	chr12	6787219	6787392	6787242	6787371	ZNF384	NM_001039920	1	9	5	-	6787293	6787509
262349949	chr12	6787741	6787889	6787763	6787864	ZNF384	NM_133476	3	10	5	-	6787829	6787876
262349949	chr12	6787741	6787889	6787763	6787864	ZNF384	NM_001135734	2	11	5	-	6787829	6787876
239530810	chr12	6788569	6788726	6788597	6788702	ZNF384	NM_133476	3	10	3	-	6788621	6788691
239530810	chr12	6788569	6788726	6788597	6788702	ZNF384	NM_001135734	2	11	3	-	6788621	6788691
239530810	chr12	6788569	6788726	6788597	6788702	ZNF384	NM_001039920	1	9	3	-	6788621	6788691
233466735	chr12	25378518	25378685	25378550	25378658	KRAS	NM_004985	1	5	4	-	25378548	25378707
233466735	chr12	25378518	25378685	25378550	25378658	KRAS	NM_033360	2	6	4	-	25378548	25378707
231132733	chr12	25398161	25398331	25398184	25398304	KRAS	NM_004985	1	5	2	-	25398208	25398329
231132733	chr12	25398161	25398331	25398184	25398304	KRAS	NM_033360	2	6	2	-	25398208	25398329
282747174	chr12	43750239	43750379	43750266	43750351	ADAMTS20	NM_025003	1	39	38	-	43750287	43750391
283124538	chr12	43769094	43769268	43769122	43769244	ADAMTS20	NM_025003	1	39	36	-	43769182	43769315
282553706	chr12	43769923	43770097	43769947	43770070	ADAMTS20	NM_025003	1	39	35	-	43769860	43769951
282553706	chr12	43769923	43770097	43769947	43770070	ADAMTS20	NM_025003	1	39	34	-	43770039	43770133
282533077	chr12	43770416	43770549	43770444	43770521	ADAMTS20	NM_025003	1	39	33	-	43770327	43770456
282863158	chr12	43777354	43777516	43777377	43777488	ADAMTS20	NM_025003	1	39	31	-	43777361	43777531
328491585	chr12	43792765	43792909	43792794	43792886	ADAMTS20	NM_025003	1	39	29	-	43792869	43793036
282550522	chr12	43819285	43819454	43819313	43819426	ADAMTS20	NM_025003	1	39	28	-	43819317	43819493
283405313	chr12	43821190	43821315	43821213	43821290	ADAMTS20	NM_025003	1	39	27	-	43821111	43821272
282275217	chr12	43822318	43822480	43822340	43822458	ADAMTS20	NM_025003	1	39	25	-	43822438	43822602
281752450	chr12	43823427	43823553	43823449	43823526	ADAMTS20	NM_025003	1	39	24	-	43823420	43823527
282467247	chr12	43825024	43825198	43825048	43825172	ADAMTS20	NM_025003	1	39	22	-	43825135	43825299
284455842	chr12	43826096	43826225	43826123	43826198	ADAMTS20	NM_025003	1	39	21	-	43826107	43826271
282539053	chr12	43826484	43826618	43826507	43826595	ADAMTS20	NM_025003	1	39	20	-	43826404	43826614
283914250	chr12	43828144	43828270	43828171	43828242	ADAMTS20	NM_025003	1	39	19	-	43828048	43828174
282761708	chr12	43833680	43833805	43833708	43833779	ADAMTS20	NM_025003	1	39	17	-	43833700	43833872
283057285	chr12	43840324	43840450	43840351	43840423	ADAMTS20	NM_025003	1	39	15	-	43840398	43840515
282068065	chr12	43846157	43846321	43846183	43846293	ADAMTS20	NM_025003	1	39	14	-	43846077	43846213
283488456	chr12	43847614	43847788	43847637	43847762	ADAMTS20	NM_025003	1	39	12	-	43847710	43847855
281977947	chr12	43858422	43858595	43858442	43858568	ADAMTS20	NM_025003	1	39	10	-	43858394	43858535
281835796	chr12	43862465	43862627	43862492	43862597	ADAMTS20	NM_025003	1	39	8	-	43862403	43862508
284891501	chr12	43886896	43887058	43886926	43887032	ADAMTS20	NM_025003	1	39	5	-	43886973	43887056
284552138	chr12	43925893	43926052	43925921	43926027	ADAMTS20	NM_025003	1	39	3	-	43925839	43925998

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
283617205	chr12	43944968	43945142	43944987	43945114	ADAMTS20	NM_025003	1	39	2	-	43944712	43945073
273049324	chr12	46123858	46123985	46123879	46123963	ARID2	NM_152641	1	21	2	+	46123827	46123920
272834131	chr12	46205253	46205381	46205274	46205354	ARID2	NM_152641	1	21	4	+	46205201	46205334
272861654	chr12	46215104	46215253	46215132	46215226	ARID2	NM_152641	1	21	6	+	46215203	46215270
273643059	chr12	46230399	46230571	46230424	46230545	ARID2	NM_152641	1	21	7	+	46230372	46230438
273643059	chr12	46230399	46230571	46230424	46230545	ARID2	NM_152641	1	21	8	+	46230524	46230774
273577360	chr12	46231193	46231360	46231221	46231332	ARID2	NM_152641	1	21	10	+	46231281	46231490
272963226	chr12	46233033	46233201	46233058	46233176	ARID2	NM_152641	1	21	11	+	46233112	46233279
274564223	chr12	46242534	46242708	46242556	46242681	ARID2	NM_152641	1	21	13	+	46242619	46242753
273520201	chr12	46243424	46243557	46243452	46243535	ARID2	NM_152641	1	21	14	+	46243363	46243559
274459612	chr12	46243995	46244166	46244019	46244144	ARID2	NM_152641	1	21	15	+	46243819	46246679
274473703	chr12	46244446	46244582	46244468	46244562	ARID2	NM_152641	1	21	15	+	46243819	46246679
274457301	chr12	46244877	46245047	46244899	46245025	ARID2	NM_152641	1	21	15	+	46243819	46246679
273523428	chr12	46245331	46245501	46245355	46245480	ARID2	NM_152641	1	21	15	+	46243819	46246679
273572534	chr12	46245815	46245984	46245839	46245956	ARID2	NM_152641	1	21	15	+	46243819	46246679
273599358	chr12	46246176	46246313	46246198	46246292	ARID2	NM_152641	1	21	15	+	46243819	46246679
274471919	chr12	46246602	46246771	46246630	46246746	ARID2	NM_152641	1	21	15	+	46243819	46246679
273970301	chr12	46285458	46285606	46285484	46285583	ARID2	NM_152641	1	21	17	+	46285563	46285701
273715941	chr12	46285779	46285950	46285806	46285922	ARID2	NM_152641	1	21	18	+	46285794	46285879
273975205	chr12	46298673	46298803	46298694	46298780	ARID2	NM_152641	1	21	21	+	46298717	46301819
272902800	chr12	49415992	49416160	49416014	49416137	MLL2	NM_003482	1	54	52	-	49416063	49416136
273218346	chr12	49418249	49418395	49418270	49418371	MLL2	NM_003482	1	54	50	-	49418361	49418491
273618551	chr12	49419933	49420083	49419959	49420063	MLL2	NM_003482	1	54	48	-	49419965	49421105
273657147	chr12	49420390	49420555	49420411	49420535	MLL2	NM_003482	1	54	48	-	49419965	49421105
274630055	chr12	49420793	49420963	49420816	49420940	MLL2	NM_003482	1	54	48	-	49419965	49421105
274393388	chr12	49421742	49421886	49421763	49421864	MLL2	NM_003482	1	54	46	-	49421792	49421924
273156222	chr12	49422821	49422969	49422843	49422948	MLL2	NM_003482	1	54	44	-	49422844	49423019
273033088	chr12	49424111	49424269	49424131	49424248	MLL2	NM_003482	1	54	42	-	49424063	49424222
273484614	chr12	49424676	49424841	49424699	49424817	MLL2	NM_003482	1	54	40	-	49424676	49424816
274248347	chr12	49425230	49425358	49425251	49425338	MLL2	NM_003482	1	54	39	-	49424958	49427747
274233230	chr12	49425674	49425827	49425694	49425807	MLL2	NM_003482	1	54	39	-	49424958	49427747
273256005	chr12	49426055	49426205	49426077	49426185	MLL2	NM_003482	1	54	39	-	49424958	49427747
273240676	chr12	49426446	49426571	49426466	49426549	MLL2	NM_003482	1	54	39	-	49424958	49427747
273256516	chr12	49426995	49427167	49427016	49427149	MLL2	NM_003482	1	54	39	-	49424958	49427747
273195987	chr12	49427362	49427532	49427382	49427514	MLL2	NM_003482	1	54	39	-	49424958	49427747
273546003	chr12	49427870	49428041	49427892	49428021	MLL2	NM_003482	1	54	38	-	49427850	49428082
274041543	chr12	49428573	49428739	49428594	49428718	MLL2	NM_003482	1	54	35	-	49428595	49428718
274299635	chr12	49431232	49431398	49431252	49431376	MLL2	NM_003482	1	54	34	-	49430908	49432772
273275824	chr12	49431657	49431802	49431680	49431782	MLL2	NM_003482	1	54	34	-	49430908	49432772
273344246	chr12	49432133	49432304	49432153	49432283	MLL2	NM_003482	1	54	34	-	49430908	49432772
274274633	chr12	49432602	49432765	49432623	49432744	MLL2	NM_003482	1	54	34	-	49430908	49432772

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273584325	chr12	49433126	49433266	49433148	49433246	MLL2	NM_003482	1	54	32	-	49433218	49433400
274194055	chr12	49433581	49433748	49433602	49433729	MLL2	NM_003482	1	54	31	-	49433507	49435318
273169371	chr12	49433970	49434134	49433988	49434113	MLL2	NM_003482	1	54	31	-	49433507	49435318
273144105	chr12	49434414	49434549	49434437	49434528	MLL2	NM_003482	1	54	31	-	49433507	49435318
273153844	chr12	49434705	49434873	49434724	49434855	MLL2	NM_003482	1	54	31	-	49433507	49435318
274188037	chr12	49435132	49435274	49435151	49435255	MLL2	NM_003482	1	54	31	-	49433507	49435318
273359285	chr12	49435842	49436005	49435861	49435987	MLL2	NM_003482	1	54	28	-	49435872	49436113
273067549	chr12	49436474	49436616	49436496	49436595	MLL2	NM_003482	1	54	26	-	49436524	49436661
272894878	chr12	49437142	49437270	49437163	49437248	MLL2	NM_003482	1	54	24	-	49437146	49437211
273959429	chr12	49437703	49437853	49437726	49437831	MLL2	NM_003482	1	54	22	-	49437651	49437781
274260207	chr12	49438494	49438620	49438514	49438599	MLL2	NM_003482	1	54	19	-	49438527	49438748
273871689	chr12	49439826	49439986	49439846	49439960	MLL2	NM_003482	1	54	17	-	49439848	49439957
273290509	chr12	49440436	49440604	49440458	49440582	MLL2	NM_003482	1	54	15	-	49440392	49440573
273724365	chr12	49443411	49443584	49443432	49443562	MLL2	NM_003482	1	54	11	-	49443465	49444573
273779730	chr12	49443844	49444003	49443863	49443982	MLL2	NM_003482	1	54	11	-	49443465	49444573
273756816	chr12	49444272	49444444	49444293	49444423	MLL2	NM_003482	1	54	11	-	49443465	49444573
273080859	chr12	49444750	49444875	49444768	49444855	MLL2	NM_003482	1	54	10	-	49444669	49446207
273130214	chr12	49445113	49445279	49445131	49445261	MLL2	NM_003482	1	54	10	-	49444669	49446207
273136495	chr12	49445560	49445685	49445580	49445665	MLL2	NM_003482	1	54	10	-	49444669	49446207
273099345	chr12	49445854	49445996	49445874	49445978	MLL2	NM_003482	1	54	10	-	49444669	49446207
274416260	chr12	49446313	49446471	49446336	49446452	MLL2	NM_003482	1	54	9	-	49446347	49446492
273343431	chr12	49446966	49447139	49446987	49447114	MLL2	NM_003482	1	54	7	-	49446990	49447104
273566340	chr12	49447804	49447957	49447830	49447936	MLL2	NM_003482	1	54	5	-	49447761	49447923
273194684	chr12	49448435	49448561	49448455	49448539	MLL2	NM_003482	1	54	3	-	49448311	49448534
222373936	chr12	51173796	51173968	51173824	51173949	ATF1	NM_005171	1	7	2	+	51173923	51174021
224769124	chr12	51207720	51207890	51207741	51207864	ATF1	NM_005171	1	7	5	+	51207793	51207975
223285061	chr12	51208135	51208307	51208159	51208279	ATF1	NM_005171	1	7	6	+	51208063	51208222
321681470	chr12	54575946	54576117	54575966	54576097	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321681470	chr12	54575946	54576117	54575966	54576097	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321681470	chr12	54575946	54576117	54575966	54576097	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_014311	6	4	3	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NR_045039	7	5	3	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_001243791	5	4	2	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_001243790	4	5	3	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_001243789	3	6	4	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_001243788	2	3	2	-	54577440	54577743
321752584	chr12	54577381	54577549	54577402	54577528	SMUG1	NM_001243787	1	4	3	-	54577440	54577743
272509301	chr12	56477475	56477612	56477496	56477589	ERBB3	NM_001005915	1	3	2	+	56477535	56477686
272509301	chr12	56477475	56477612	56477496	56477589	ERBB3	NM_001982	2	28	2	+	56477535	56477686
269991153	chr12	56478886	56479050	56478910	56479029	ERBB3	NM_001005915	1	3	3	+	56478779	56479401
269991153	chr12	56478886	56479050	56478910	56479029	ERBB3	NM_001982	2	28	3	+	56478779	56478965

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270471828	chr12	56481547	56481721	56481568	56481698	ERBB3	NM_001982	2	28	6	+	56481579	56481697
270361863	chr12	56482504	56482674	56482528	56482652	ERBB3	NM_001982	2	28	9	+	56482532	56482652
272734148	chr12	56487193	56487355	56487216	56487334	ERBB3	NM_001982	2	28	12	+	56487129	56487334
272012432	chr12	56488141	56488315	56488165	56488291	ERBB3	NM_001982	2	28	15	+	56488186	56488340
269630298	chr12	56489485	56489651	56489512	56489627	ERBB3	NM_001982	2	28	17	+	56489449	56489590
270991928	chr12	56490905	56491038	56490930	56491015	ERBB3	NM_001982	2	28	20	+	56490829	56491014
271320502	chr12	56492454	56492626	56492480	56492602	ERBB3	NM_001982	2	28	23	+	56492543	56492689
270570880	chr12	56493691	56493848	56493714	56493822	ERBB3	NM_001982	2	28	25	+	56493622	56493813
270324312	chr12	56495026	56495181	56495047	56495154	ERBB3	NM_001982	2	28	27	+	56494845	56495145
269774413	chr12	56495567	56495702	56495589	56495680	ERBB3	NM_001982	2	28	28	+	56495313	56497291
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_001195055	3	4	4	-	57910371	57910963
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_001195054	2	4	4	-	57910371	57910963
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_001195053	1	4	4	-	57910371	57910963
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_001195057	5	4	4	-	57910371	57910963
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_001195056	4	3	3	-	57910371	57910963
231113397	chr12	57910585	57910758	57910608	57910738	DDIT3	NM_004083	6	4	4	-	57910371	57910963
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_001195053	1	4	3	-	57911052	57911378
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_001195056	4	3	2	-	57911052	57911536
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_001195057	5	4	3	-	57911052	57911207
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_001195054	2	4	3	-	57911052	57911325
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_001195055	3	4	3	-	57911052	57911302
228176804	chr12	57911067	57911193	57911090	57911171	DDIT3	NM_004083	6	4	3	-	57911052	57911221
226189682	chr12	58143056	58143205	58143079	58143178	CDK4	NM_000075	1	8	7	-	58142965	58143100
226066486	chr12	58144770	58144899	58144791	58144874	CDK4	NM_000075	1	8	4	-	58144706	58144873
226599064	chr12	58145308	58145475	58145329	58145455	CDK4	NM_000075	1	8	2	-	58145283	58145519
231426392	chr12	69202988	69203161	69203012	69203133	MDM2	NM_002392	1	11	2	+	69202988	69203072
231190470	chr12	69214018	69214179	69214044	69214151	MDM2	NM_002392	1	11	5	+	69214105	69214154
234462822	chr12	69222473	69222643	69222502	69222621	MDM2	NM_002392	1	11	8	+	69222551	69222711
233172919	chr12	69229643	69229769	69229669	69229740	MDM2	NM_002392	1	11	9	+	69229609	69229764
234787278	chr12	69233218	69233392	69233245	69233365	MDM2	NM_002392	1	11	11	+	69233054	69239212
236437547	chr12	112883979	112884125	112884007	112884103	PTPN11	NM_002834	1	16	2	+	112884080	112884202
235141580	chr12	112890936	112891108	112890963	112891087	PTPN11	NM_002834	1	16	4	+	112890999	112891191
241329778	chr12	112893763	112893934	112893786	112893907	PTPN11	NM_002834	1	16	6	+	112893754	112893867
235523599	chr12	112915595	112915768	112915623	112915749	PTPN11	NM_002834	1	16	9	+	112915661	112915819
237939245	chr12	112924248	112924416	112924275	112924398	PTPN11	NM_002834	1	16	11	+	112924279	112924433
238297245	chr12	112926896	112927024	112926920	112926999	PTPN11	NM_002834	1	16	13	+	112926828	112926979
227190318	chr12	121416561	121416721	121416578	121416703	HNF1A	NM_000545	1	10	1	+	121416549	121416897
227536267	chr12	121426605	121426774	121426625	121426753	HNF1A	NM_000545	1	10	2	+	121426636	121426835
227417568	chr12	121431351	121431518	121431373	121431495	HNF1A	NM_000545	1	10	3	+	121431323	121431509
227614542	chr12	121432087	121432231	121432105	121432208	HNF1A	NM_000545	1	10	4	+	121431967	121432208
227979609	chr12	121434439	121434612	121434461	121434592	HNF1A	NM_000545	1	10	6	+	121434344	121434545

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227541265	chr12	121437181	121437342	121437201	121437325	HNF1A	NM_000545	1	10	9	+	121437286	121437430
280145337	chr12	123213779	123213944	123213799	123213925	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280124403	chr12	123214183	123214344	123214205	123214323	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280124478	chr12	123214634	123214765	123214655	123214744	HCAR1	NM_032554	1	1	1	-	123212153	123215129
288138334	chr12	132445377	132445540	132445397	132445519	EP400	NM_015409	1	53	2	+	132445130	132446499
287851706	chr12	132464185	132464356	132464211	132464339	EP400	NM_015409	1	53	3	+	132464239	132464338
287508294	chr12	132466808	132466979	132466826	132466961	EP400	NM_015409	1	53	5	+	132466638	132467023
287566653	chr12	132471177	132471350	132471202	132471323	EP400	NM_015409	1	53	6	+	132471059	132471352
288796354	chr12	132474454	132474587	132474482	132474564	EP400	NM_015409	1	53	8	+	132474509	132474649
287931186	chr12	132476649	132476816	132476671	132476792	EP400	NM_015409	1	53	11	+	132476718	132476775
287783105	chr12	132490615	132490744	132490636	132490721	EP400	NM_015409	1	53	14	+	132490657	132490847
285917060	chr12	132495990	132496164	132496014	132496140	EP400	NM_015409	1	53	16	+	132496043	132496179
288316871	chr12	132497928	132498087	132497952	132498065	EP400	NM_015409	1	53	18	+	132498035	132498209
285043149	chr12	132498391	132498560	132498416	132498539	EP400	NM_015409	1	53	19	+	132498322	132498458
287268958	chr12	132502714	132502879	132502734	132502857	EP400	NM_015409	1	53	21	+	132502755	132502921
288759366	chr12	132505580	132505731	132505604	132505713	EP400	NM_015409	1	53	23	+	132505624	132505866
284835791	chr12	132508287	132508439	132508315	132508418	EP400	NM_015409	1	53	24	+	132508322	132508486
287234185	chr12	132511928	132512098	132511951	132512076	EP400	NM_015409	1	53	26	+	132511982	132512076
288244301	chr12	132512776	132512936	132512798	132512912	EP400	NM_015409	1	53	27	+	132512562	132512833
286420935	chr12	132514588	132514760	132514616	132514738	EP400	NM_015409	1	53	29	+	132514534	132514703
286847949	chr12	132522387	132522547	132522408	132522523	EP400	NM_015409	1	53	32	+	132522498	132522641
288970731	chr12	132527970	132528137	132527994	132528109	EP400	NM_015409	1	53	33	+	132527849	132528007
288741447	chr12	132529150	132529323	132529178	132529299	EP400	NM_015409	1	53	36	+	132529216	132529260
289030728	chr12	132529932	132530091	132529957	132530070	EP400	NM_015409	1	53	38	+	132529864	132530105
287072844	chr12	132534777	132534908	132534798	132534886	EP400	NM_015409	1	53	40	+	132534868	132535004
289104357	chr12	132537635	132537809	132537661	132537785	EP400	NM_015409	1	53	42	+	132537691	132537769
288934392	chr12	132539599	132539773	132539619	132539754	EP400	NM_015409	1	53	45	+	132539644	132539753
286321229	chr12	132547027	132547198	132547049	132547177	EP400	NM_015409	1	53	47	+	132547011	132547246
288811789	chr12	132549298	132549469	132549318	132549444	EP400	NM_015409	1	53	48	+	132549213	132549431
289062154	chr12	132551903	132552073	132551921	132552051	EP400	NM_015409	1	53	50	+	132551907	132552031
286151315	chr12	132561898	132562069	132561919	132562049	EP400	NM_015409	1	53	53	+	132561946	132565011
269675746	chr13	26828855	26828983	26828873	26828966	CDK8	NM_001260	1	13	1	+	26828756	26828906
271157588	chr13	26927884	26928016	26927910	26927994	CDK8	NM_001260	1	13	4	+	26927877	26928017
270250897	chr13	26959351	26959479	26959371	26959453	CDK8	NM_001260	1	13	6	+	26959348	26959479
271175991	chr13	26971214	26971363	26971241	26971335	CDK8	NM_001260	1	13	9	+	26971290	26971362
270892434	chr13	26975558	26975729	26975581	26975705	CDK8	NM_001260	1	13	12	+	26975603	26975761
228481137	chr13	28578118	28578290	28578145	28578269	FLT3	NM_004119	1	24	24	-	28577411	28578311
227323489	chr13	28589263	28589420	28589289	28589394	FLT3	NM_004119	1	24	22	-	28589294	28589393
227350132	chr13	28597376	28597530	28597402	28597502	FLT3	NM_004119	1	24	19	-	28597487	28597614
228709192	chr13	28601288	28601432	28601316	28601404	FLT3	NM_004119	1	24	17	-	28601225	28601378
227211972	chr13	28608170	28608335	28608195	28608314	FLT3	NM_004119	1	24	14	-	28608219	28608351

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228511354	chr13	28609596	28609743	28609622	28609717	FLT3	NM_004119	1	24	12	-	28609632	28609810
229764158	chr13	28611215	28611376	28611243	28611352	FLT3	NM_004119	1	24	10	-	28611322	28611425
227335232	chr13	28623596	28623762	28623622	28623733	FLT3	NM_004119	1	24	8	-	28623521	28623674
227654708	chr13	28624263	28624432	28624284	28624404	FLT3	NM_004119	1	24	6	-	28624232	28624359
228773031	chr13	28635932	28636056	28635962	28636032	FLT3	NM_004119	1	24	3	-	28636004	28636206
227396590	chr13	28644647	28644809	28644675	28644781	FLT3	NM_004119	1	24	2	-	28644628	28644749
228827336	chr13	28877470	28877597	28877493	28877569	FLT1	NM_002019	4	30	30	-	28874483	28877505
227145522	chr13	28885798	28885922	28885822	28885895	FLT1	NM_002019	4	30	27	-	28885727	28885869
228714798	chr13	28893464	28893605	28893491	28893583	FLT1	NM_002019	4	30	24	-	28893560	28893671
227236164	chr13	28896273	28896423	28896300	28896400	FLT1	NM_002019	4	30	22	-	28896399	28896496
228401508	chr13	28901510	28901682	28901539	28901654	FLT1	NM_002019	4	30	20	-	28901599	28901687
227742364	chr13	28913344	28913516	28913364	28913488	FLT1	NM_002019	4	30	17	-	28913305	28913437
228023540	chr13	28931734	28931861	28931756	28931836	FLT1	NM_002019	4	30	15	-	28931691	28931822
227285226	chr13	28963859	28964021	28963884	28963998	FLT1	NM_001159920	1	13	13	-	28959688	28964241
227285226	chr13	28963859	28964021	28963884	28963998	FLT1	NM_002019	4	30	13	-	28963933	28964241
227285226	chr13	28963859	28964021	28963884	28963998	FLT1	NM_001160030	2	15	13	-	28963933	28964241
227617379	chr13	28971065	28971239	28971089	28971211	FLT1	NM_002019	4	30	12	-	28971097	28971205
227617379	chr13	28971065	28971239	28971089	28971211	FLT1	NM_001159920	1	13	12	-	28971097	28971205
227617379	chr13	28971065	28971239	28971089	28971211	FLT1	NM_001160030	2	15	12	-	28971097	28971205
228565229	chr13	29001201	29001367	29001222	29001343	FLT1	NM_002019	4	30	10	-	29001296	29001455
228565229	chr13	29001201	29001367	29001222	29001343	FLT1	NM_001159920	1	13	10	-	29001296	29001455
228565229	chr13	29001201	29001367	29001222	29001343	FLT1	NM_001160031	3	12	10	-	29001296	29001455
228565229	chr13	29001201	29001367	29001222	29001343	FLT1	NM_001160030	2	15	10	-	29001296	29001455
229948530	chr13	29004075	29004242	29004097	29004221	FLT1	NM_002019	4	30	8	-	29004187	29004304
229948530	chr13	29004075	29004242	29004097	29004221	FLT1	NM_001159920	1	13	8	-	29004187	29004304
229948530	chr13	29004075	29004242	29004097	29004221	FLT1	NM_001160031	3	12	8	-	29004187	29004304
229948530	chr13	29004075	29004242	29004097	29004221	FLT1	NM_001160030	2	15	8	-	29004187	29004304
227344833	chr13	29007892	29008036	29007912	29008011	FLT1	NM_002019	4	30	6	-	29007956	29008092
227344833	chr13	29007892	29008036	29007912	29008011	FLT1	NM_001159920	1	13	6	-	29007956	29008092
227344833	chr13	29007892	29008036	29007912	29008011	FLT1	NM_001160031	3	12	6	-	29007956	29008092
227344833	chr13	29007892	29008036	29007912	29008011	FLT1	NM_001160030	2	15	6	-	29007956	29008092
227249221	chr13	29012311	29012446	29012338	29012419	FLT1	NM_002019	4	30	4	-	29012358	29012482
227249221	chr13	29012311	29012446	29012338	29012419	FLT1	NM_001159920	1	13	4	-	29012358	29012482
227249221	chr13	29012311	29012446	29012338	29012419	FLT1	NM_001160031	3	12	4	-	29012358	29012482
227249221	chr13	29012311	29012446	29012338	29012419	FLT1	NM_001160030	2	15	4	-	29012358	29012482
227425169	chr13	29041140	29041310	29041166	29041285	FLT1	NM_002019	4	30	3	-	29041040	29041266
227425169	chr13	29041140	29041310	29041166	29041285	FLT1	NM_001159920	1	13	3	-	29041040	29041266
227425169	chr13	29041140	29041310	29041166	29041285	FLT1	NM_001160031	3	12	3	-	29041040	29041266
227425169	chr13	29041140	29041310	29041166	29041285	FLT1	NM_001160030	2	15	3	-	29041040	29041266
229045535	chr13	29068955	29069126	29068972	29069106	FLT1	NM_002019	4	30	1	-	29068917	29069265
229045535	chr13	29068955	29069126	29068972	29069106	FLT1	NM_001159920	1	13	1	-	29068917	29069265

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229045535	chr13	29068955	29069126	29068972	29069106	FLT1	NM_001160031	3	12	1	-	29068917	29069265
229045535	chr13	29068955	29069126	29068972	29069106	FLT1	NM_001160030	2	15	1	-	29068917	29069265
230298214	chr13	41133934	41134101	41133956	41134073	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230295723	chr13	41134334	41134495	41134363	41134470	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230263596	chr13	41134683	41134846	41134707	41134822	FOXO1	NM_002015	1	3	2	-	41133646	41134997
229109703	chr13	41239733	41239902	41239754	41239885	FOXO1	NM_002015	1	3	1	-	41239720	41240734
242692069	chr13	48878045	48878202	48878062	48878185	RB1	NM_000321	1	27	1	+	48877883	48878185
260627711	chr13	48916727	48916896	48916755	48916873	RB1	NM_000321	1	27	3	+	48916735	48916850
242583475	chr13	48934086	48934259	48934114	48934237	RB1	NM_000321	1	27	7	+	48934153	48934263
241479159	chr13	48951004	48951178	48951032	48951152	RB1	NM_000321	1	27	13	+	48951054	48951170
242315995	chr13	48955498	48955667	48955526	48955639	RB1	NM_000321	1	27	17	+	48955383	48955579
242180376	chr13	49033810	49033959	49033835	49033934	RB1	NM_000321	1	27	20	+	49033824	49033969
241675149	chr13	49039120	49039247	49039145	49039221	RB1	NM_000321	1	27	22	+	49039134	49039247
242609458	chr13	49047367	49047540	49047392	49047513	RB1	NM_000321	1	27	24	+	49047496	49047526
240875639	chr13	49051488	49051654	49051512	49051630	RB1	NM_000321	1	27	26	+	49051491	49051540
230805461	chr13	103504513	103504662	103504539	103504632	ERCC5	NM_000123	1	15	2	+	103504468	103504643
229225984	chr13	103506625	103506787	103506652	103506758	ERCC5	NM_000123	1	15	4	+	103506638	103506724
227920004	chr13	103513845	103513970	103513872	103513945	ERCC5	NM_000123	1	15	7	+	103513857	103514064
227761566	chr13	103514459	103514595	103514486	103514572	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230962597	chr13	103514899	103515044	103514924	103515024	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230942108	chr13	103515326	103515483	103515353	103515457	ERCC5	NM_000123	1	15	8	+	103514380	103515453
232974821	chr13	103518496	103518661	103518523	103518637	ERCC5	NM_000123	1	15	10	+	103518612	103518731
230538184	chr13	103519115	103519288	103519140	103519261	ERCC5	NM_000123	1	15	11	+	103518982	103519195
227780579	chr13	103524507	103524641	103524536	103524616	ERCC5	NM_000123	1	15	13	+	103524548	103524748
229742508	chr13	103525601	103525735	103525624	103525710	ERCC5	NM_000123	1	15	14	+	103525609	103525693
231493565	chr13	103527935	103528097	103527959	103528074	ERCC5	NM_000123	1	15	15	+	103527657	103528351
272379822	chr13	110434299	110434426	110434321	110434405	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383555	chr13	110434773	110434914	110434790	110434897	IRS2	NM_003749	1	2	1	-	110434389	110438914
272382473	chr13	110435201	110435375	110435218	110435357	IRS2	NM_003749	1	2	1	-	110434389	110438914
272382521	chr13	110435677	110435822	110435696	110435804	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383311	chr13	110436039	110436192	110436058	110436173	IRS2	NM_003749	1	2	1	-	110434389	110438914
272384768	chr13	110436458	110436628	110436476	110436610	IRS2	NM_003749	1	2	1	-	110434389	110438914
270670335	chr13	110436890	110437063	110436910	110437046	IRS2	NM_003749	1	2	1	-	110434389	110438914
272384572	chr13	110437499	110437655	110437519	110437637	IRS2	NM_003749	1	2	1	-	110434389	110438914
272385094	chr13	110437969	110438113	110437987	110438091	IRS2	NM_003749	1	2	1	-	110434389	110438914
280702370	chr13	113963958	113964091	113963979	113964064	LAMP1	NM_005561	1	9	3	+	113963958	113964177
280866059	chr13	113973850	113973982	113973867	113973965	LAMP1	NM_005561	1	9	5	+	113973784	113973971
279022258	chr13	113975669	113975808	113975696	113975787	LAMP1	NM_005561	1	9	7	+	113975719	113975785
280903287	chr13	113976670	113976809	113976691	113976789	LAMP1	NM_005561	1	9	9	+	113976597	113977741
269581181	chr14	23777010	23777172	23777031	23777152	BCL2L2	NM_004050	2	4	3	+	23776969	23777408
269581181	chr14	23777010	23777172	23777031	23777152	BCL2L2	NM_001199839	1	4	3	+	23776969	23777408

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272046961	chr14	23777970	23778121	23777996	23778104	BCL2L2	NM_004050	2	4	4	+	23778025	23780968
272046961	chr14	23777970	23778121	23777996	23778104	BCL2L2	NM_001199839	1	4	4	+	23778025	23780968
258651309	chr14	36986674	36986819	36986691	36986801	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
258651309	chr14	36986674	36986819	36986691	36986801	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
237517874	chr14	36988119	36988266	36988137	36988245	NKX2-1	NM_003317	2	2	1	-	36988190	36988903
237517874	chr14	36988119	36988266	36988137	36988245	NKX2-1	NM_001079668	1	3	2	-	36988190	36988575
235707658	chr14	36989203	36989377	36989222	36989357	NKX2-1	NM_001079668	1	3	1	-	36989258	36989430
237132072	chr14	51192585	51192715	51192613	51192688	NIN	NM_020921	2	31	30	-	51192671	51192784
237132072	chr14	51192585	51192715	51192613	51192688	NIN	NM_016350	1	29	29	-	51192546	51192784
237132072	chr14	51192585	51192715	51192613	51192688	NIN	NM_182946	4	30	30	-	51192546	51192784
242365080	chr14	51196259	51196427	51196282	51196410	NIN	NM_016350	1	29	28	-	51196241	51196441
242365080	chr14	51196259	51196427	51196282	51196410	NIN	NM_182946	4	30	29	-	51196241	51196441
242365080	chr14	51196259	51196427	51196282	51196410	NIN	NM_182944	3	30	29	-	51196241	51196441
242365080	chr14	51196259	51196427	51196282	51196410	NIN	NM_020921	2	31	29	-	51196241	51196441
236533874	chr14	51204770	51204934	51204798	51204907	NIN	NM_016350	1	29	26	-	51204858	51205004
236533874	chr14	51204770	51204934	51204798	51204907	NIN	NM_182946	4	30	27	-	51204858	51205004
236533874	chr14	51204770	51204934	51204798	51204907	NIN	NM_182944	3	30	27	-	51204858	51205004
236533874	chr14	51204770	51204934	51204798	51204907	NIN	NM_020921	2	31	27	-	51204858	51205004
236797775	chr14	51208288	51208442	51208310	51208416	NIN	NM_016350	1	29	24	-	51208300	51208446
236797775	chr14	51208288	51208442	51208310	51208416	NIN	NM_182946	4	30	25	-	51208300	51208446
236797775	chr14	51208288	51208442	51208310	51208416	NIN	NM_182944	3	30	25	-	51208300	51208446
236797775	chr14	51208288	51208442	51208310	51208416	NIN	NM_020921	2	31	25	-	51208300	51208446
235423712	chr14	51210950	51211111	51210979	51211083	NIN	NM_016350	1	29	22	-	51210961	51211083
235423712	chr14	51210950	51211111	51210979	51211083	NIN	NM_182946	4	30	23	-	51210961	51211083
235423712	chr14	51210950	51211111	51210979	51211083	NIN	NM_182944	3	30	23	-	51210961	51211083
235423712	chr14	51210950	51211111	51210979	51211083	NIN	NM_020921	2	31	23	-	51210961	51211083
237344220	chr14	51219328	51219499	51219354	51219471	NIN	NM_016350	1	29	20	-	51219236	51219451
237344220	chr14	51219328	51219499	51219354	51219471	NIN	NM_182946	4	30	21	-	51219236	51219451
237344220	chr14	51219328	51219499	51219354	51219471	NIN	NM_182944	3	30	21	-	51219236	51219451
237344220	chr14	51219328	51219499	51219354	51219471	NIN	NM_020921	2	31	21	-	51219236	51219451
235979011	chr14	51223814	51223979	51223837	51223955	NIN	NM_182946	4	30	18	-	51223210	51225348
235979011	chr14	51223814	51223979	51223837	51223955	NIN	NM_182944	3	30	18	-	51223210	51225348
235979011	chr14	51223814	51223979	51223837	51223955	NIN	NM_020921	2	31	18	-	51223210	51225348
240823447	chr14	51224234	51224400	51224262	51224376	NIN	NM_182946	4	30	18	-	51223210	51225348
240823447	chr14	51224234	51224400	51224262	51224376	NIN	NM_182944	3	30	18	-	51223210	51225348
240823447	chr14	51224234	51224400	51224262	51224376	NIN	NM_020921	2	31	18	-	51223210	51225348
236103901	chr14	51224674	51224842	51224701	51224815	NIN	NM_182946	4	30	18	-	51223210	51225348
236103901	chr14	51224674	51224842	51224701	51224815	NIN	NM_182944	3	30	18	-	51223210	51225348
236103901	chr14	51224674	51224842	51224701	51224815	NIN	NM_020921	2	31	18	-	51223210	51225348
236163715	chr14	51225152	51225302	51225175	51225279	NIN	NM_182946	4	30	18	-	51223210	51225348
236163715	chr14	51225152	51225302	51225175	51225279	NIN	NM_182944	3	30	18	-	51223210	51225348

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236163715	chr14	51225152	51225302	51225175	51225279	NIN	NM_020921	2	31	18	-	51223210	51225348
235482505	chr14	51226767	51226919	51226788	51226897	NIN	NM_016350	1	29	17	-	51226575	51227077
235482505	chr14	51226767	51226919	51226788	51226897	NIN	NM_182946	4	30	17	-	51226575	51227077
235482505	chr14	51226767	51226919	51226788	51226897	NIN	NM_182944	3	30	17	-	51226575	51227077
235482505	chr14	51226767	51226919	51226788	51226897	NIN	NM_020921	2	31	17	-	51226575	51227077
237300703	chr14	51230512	51230639	51230534	51230617	NIN	NM_016350	1	29	15	-	51230544	51230682
237300703	chr14	51230512	51230639	51230534	51230617	NIN	NM_182946	4	30	15	-	51230544	51230682
237300703	chr14	51230512	51230639	51230534	51230617	NIN	NM_182944	3	30	15	-	51230544	51230682
237300703	chr14	51230512	51230639	51230534	51230617	NIN	NM_020921	2	31	15	-	51230544	51230682
235561468	chr14	51233489	51233638	51233517	51233609	NIN	NM_016350	1	29	13	-	51233498	51233608
235561468	chr14	51233489	51233638	51233517	51233609	NIN	NM_182946	4	30	13	-	51233498	51233608
235561468	chr14	51233489	51233638	51233517	51233609	NIN	NM_182944	3	30	13	-	51233498	51233608
235561468	chr14	51233489	51233638	51233517	51233609	NIN	NM_020921	2	31	13	-	51233498	51233608
237480904	chr14	51237582	51237756	51237601	51237728	NIN	NM_016350	1	29	11	-	51237570	51237710
237480904	chr14	51237582	51237756	51237601	51237728	NIN	NM_182946	4	30	11	-	51237570	51237710
237480904	chr14	51237582	51237756	51237601	51237728	NIN	NM_182944	3	30	11	-	51237570	51237710
237480904	chr14	51237582	51237756	51237601	51237728	NIN	NM_020921	2	31	11	-	51237570	51237710
242676343	chr14	51239062	51239230	51239087	51239207	NIN	NM_016350	1	29	9	-	51239019	51239186
242676343	chr14	51239062	51239230	51239087	51239207	NIN	NM_182946	4	30	9	-	51239019	51239186
242676343	chr14	51239062	51239230	51239087	51239207	NIN	NM_182944	3	30	9	-	51239019	51239186
242676343	chr14	51239062	51239230	51239087	51239207	NIN	NM_020921	2	31	9	-	51239019	51239186
257669324	chr14	51243639	51243788	51243666	51243760	NIN	NM_016350	1	29	7	-	51243667	51243857
257669324	chr14	51243639	51243788	51243666	51243760	NIN	NM_182946	4	30	7	-	51243667	51243857
257669324	chr14	51243639	51243788	51243666	51243760	NIN	NM_182944	3	30	7	-	51243667	51243857
257669324	chr14	51243639	51243788	51243666	51243760	NIN	NM_020921	2	31	7	-	51243667	51243857
235657283	chr14	51259467	51259624	51259489	51259600	NIN	NM_016350	1	29	5	-	51259430	51259599
235657283	chr14	51259467	51259624	51259489	51259600	NIN	NM_182946	4	30	5	-	51259430	51259599
235657283	chr14	51259467	51259624	51259489	51259600	NIN	NM_182944	3	30	5	-	51259430	51259599
235657283	chr14	51259467	51259624	51259489	51259600	NIN	NM_020921	2	31	5	-	51259430	51259599
278929044	chr14	62162409	62162576	62162430	62162557	HIF1A	NM_001530	2	15	1	+	62162119	62162557
278929044	chr14	62162409	62162576	62162430	62162557	HIF1A	NM_181054	3	14	1	+	62162119	62162557
279367698	chr14	62187096	62187263	62187124	62187238	HIF1A	NM_001530	2	15	2	+	62187100	62187290
279367698	chr14	62187096	62187263	62187124	62187238	HIF1A	NM_181054	3	14	2	+	62187100	62187290
279367698	chr14	62187096	62187263	62187124	62187238	HIF1A	NM_001243084	1	15	2	+	62187097	62187290
280412270	chr14	62188360	62188518	62188387	62188493	HIF1A	NM_001243084	1	15	4	+	62188457	62188541
280412270	chr14	62188360	62188518	62188387	62188493	HIF1A	NM_001530	2	15	4	+	62188457	62188541
280412270	chr14	62188360	62188518	62188387	62188493	HIF1A	NM_181054	3	14	4	+	62188457	62188541
279354186	chr14	62193488	62193636	62193515	62193611	HIF1A	NM_001243084	1	15	5	+	62193424	62193536
279354186	chr14	62193488	62193636	62193515	62193611	HIF1A	NM_001530	2	15	5	+	62193424	62193536
279354186	chr14	62193488	62193636	62193515	62193611	HIF1A	NM_181054	3	14	5	+	62193424	62193536
279574945	chr14	62199051	62199192	62199077	62199165	HIF1A	NM_001243084	1	15	7	+	62199136	62199242

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279574945	chr14	62199051	62199192	62199077	62199165	HIF1A	NM_001530	2	15	7	+	62199136	62199242
279574945	chr14	62199051	62199192	62199077	62199165	HIF1A	NM_181054	3	14	7	+	62199136	62199242
280851197	chr14	62200963	62201131	62200987	62201098	HIF1A	NM_001243084	1	15	8	+	62200856	62201003
280851197	chr14	62200963	62201131	62200987	62201098	HIF1A	NM_001530	2	15	8	+	62200856	62201003
280851197	chr14	62200963	62201131	62200987	62201098	HIF1A	NM_181054	3	14	8	+	62200856	62201003
280343608	chr14	62204799	62204928	62204823	62204907	HIF1A	NM_001243084	1	15	10	+	62204805	62205091
280343608	chr14	62204799	62204928	62204823	62204907	HIF1A	NM_001530	2	15	10	+	62204805	62205091
280343608	chr14	62204799	62204928	62204823	62204907	HIF1A	NM_181054	3	14	10	+	62204805	62205091
280785989	chr14	62207213	62207346	62207240	62207319	HIF1A	NM_001243084	1	15	11	+	62207223	62207345
280785989	chr14	62207213	62207346	62207240	62207319	HIF1A	NM_001530	2	15	11	+	62207223	62207345
280785989	chr14	62207213	62207346	62207240	62207319	HIF1A	NM_181054	3	14	11	+	62207223	62207345
278414054	chr14	62207618	62207785	62207643	62207757	HIF1A	NM_001243084	1	15	12	+	62207473	62207906
278414054	chr14	62207618	62207785	62207643	62207757	HIF1A	NM_001530	2	15	12	+	62207473	62207906
278414054	chr14	62207618	62207785	62207643	62207757	HIF1A	NM_181054	3	14	12	+	62207473	62207906
278852788	chr14	62211430	62211571	62211458	62211543	HIF1A	NM_001243084	1	15	13	+	62211423	62211531
278852788	chr14	62211430	62211571	62211458	62211543	HIF1A	NM_001530	2	15	13	+	62211423	62211531
278852788	chr14	62211430	62211571	62211458	62211543	HIF1A	NM_181054	3	14	13	+	62211423	62211531
280859434	chr14	62213751	62213910	62213775	62213884	HIF1A	NM_001243084	1	15	15	+	62213652	62214977
280859434	chr14	62213751	62213910	62213775	62213884	HIF1A	NM_001530	2	15	15	+	62213652	62214977
280859434	chr14	62213751	62213910	62213775	62213884	HIF1A	NM_181054	3	14	14	+	62213652	62214977
266318770	chr14	81528511	81528672	81528539	81528641	TSHR	NM_001142626	3	9	2	+	81528492	81528563
266318770	chr14	81528511	81528672	81528539	81528641	TSHR	NM_000369	1	10	2	+	81528492	81528563
266318770	chr14	81528511	81528672	81528539	81528641	TSHR	NM_001018036	2	9	2	+	81528492	81528563
241442042	chr14	81557411	81557561	81557434	81557533	TSHR	NM_001142626	3	9	5	+	81557413	81557487
241442042	chr14	81557411	81557561	81557434	81557533	TSHR	NM_000369	1	10	5	+	81557413	81557487
241442042	chr14	81557411	81557561	81557434	81557533	TSHR	NM_001018036	2	9	5	+	81557413	81557487
242701781	chr14	81574788	81574961	81574813	81574937	TSHR	NM_001142626	3	9	9	+	81574893	81575294
262604122	chr14	81609261	81609426	81609284	81609402	TSHR	NM_000369	1	10	10	+	81609284	81612646
262814177	chr14	81609692	81609856	81609713	81609832	TSHR	NM_000369	1	10	10	+	81609284	81612646
262608447	chr14	81610184	81610351	81610206	81610325	TSHR	NM_000369	1	10	10	+	81609284	81612646
262878343	chr14	81610625	81610773	81610651	81610745	TSHR	NM_000369	1	10	10	+	81609284	81612646
241038413	chr14	92439126	92439282	92439150	92439254	TRIP11	NM_004239	1	21	20	-	92439061	92439205
241378032	chr14	92454532	92454706	92454557	92454685	TRIP11	NM_004239	1	21	16	-	92454628	92454727
239009272	chr14	92461669	92461835	92461694	92461807	TRIP11	NM_004239	1	21	14	-	92461696	92461859
264830407	chr14	92466227	92466362	92466254	92466338	TRIP11	NM_004239	1	21	12	-	92466312	92466452
266120212	chr14	92469783	92469952	92469804	92469924	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266143461	chr14	92470188	92470362	92470213	92470341	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266152301	chr14	92470599	92470765	92470620	92470739	TRIP11	NM_004239	1	21	11	-	92469763	92472792
261992674	chr14	92470980	92471135	92471008	92471108	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266132462	chr14	92471346	92471494	92471374	92471466	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266154838	chr14	92471681	92471842	92471701	92471814	TRIP11	NM_004239	1	21	11	-	92469763	92472792

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266161373	chr14	92471985	92472155	92472013	92472134	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266165492	chr14	92472328	92472490	92472357	92472463	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266166160	chr14	92472724	92472853	92472752	92472820	TRIP11	NM_004239	1	21	11	-	92469763	92472792
242082040	chr14	92477269	92477410	92477291	92477382	TRIP11	NM_004239	1	21	9	-	92477330	92477416
264667248	chr14	92480596	92480744	92480618	92480715	TRIP11	NM_004239	1	21	7	-	92480559	92480921
240208742	chr14	92487895	92488064	92487918	92488036	TRIP11	NM_004239	1	21	4	-	92487900	92488175
265039724	chr14	92491673	92491844	92491698	92491816	TRIP11	NM_004239	1	21	3	-	92491654	92491764
266231828	chr14	92505904	92506057	92505924	92506035	TRIP11	NM_004239	1	21	1	-	92505891	92506403
231481010	chr14	95557258	95557415	95557286	95557392	DICER1	NM_177438	3	27	26	-	95557371	95557446
231481010	chr14	95557258	95557415	95557286	95557392	DICER1	NM_001195573	1	25	24	-	95557371	95557446
231481010	chr14	95557258	95557415	95557286	95557392	DICER1	NM_030621	2	28	27	-	95557371	95557446
230821754	chr14	95557617	95557772	95557641	95557749	DICER1	NM_177438	3	27	25	-	95557540	95557702
230821754	chr14	95557617	95557772	95557641	95557749	DICER1	NM_030621	2	28	26	-	95557540	95557702
232972592	chr14	95562073	95562215	95562099	95562190	DICER1	NM_177438	3	27	23	-	95562162	95563050
232972592	chr14	95562073	95562215	95562099	95562190	DICER1	NM_001195573	1	25	22	-	95562162	95563050
232972592	chr14	95562073	95562215	95562099	95562190	DICER1	NM_030621	2	28	24	-	95562162	95563050
233021779	chr14	95562472	95562644	95562496	95562624	DICER1	NM_177438	3	27	23	-	95562162	95563050
233021779	chr14	95562472	95562644	95562496	95562624	DICER1	NM_001195573	1	25	22	-	95562162	95563050
233021779	chr14	95562472	95562644	95562496	95562624	DICER1	NM_030621	2	28	24	-	95562162	95563050
230668181	chr14	95562915	95563089	95562943	95563068	DICER1	NM_177438	3	27	23	-	95562162	95563050
230668181	chr14	95562915	95563089	95562943	95563068	DICER1	NM_001195573	1	25	22	-	95562162	95563050
230668181	chr14	95562915	95563089	95562943	95563068	DICER1	NM_030621	2	28	24	-	95562162	95563050
228112207	chr14	95569615	95569788	95569638	95569766	DICER1	NM_177438	3	27	21	-	95569683	95570463
228112207	chr14	95569615	95569788	95569638	95569766	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228112207	chr14	95569615	95569788	95569638	95569766	DICER1	NM_030621	2	28	22	-	95569683	95570463
228106314	chr14	95570101	95570250	95570130	95570228	DICER1	NM_177438	3	27	21	-	95569683	95570463
228106314	chr14	95570101	95570250	95570130	95570228	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228106314	chr14	95570101	95570250	95570130	95570228	DICER1	NM_030621	2	28	22	-	95569683	95570463
230549511	chr14	95571348	95571506	95571375	95571483	DICER1	NM_177438	3	27	20	-	95571408	95571583
230549511	chr14	95571348	95571506	95571375	95571483	DICER1	NM_001195573	1	25	19	-	95571408	95571583
230549511	chr14	95571348	95571506	95571375	95571483	DICER1	NM_030621	2	28	21	-	95571408	95571583
227785418	chr14	95572306	95572480	95572330	95572452	DICER1	NM_177438	3	27	18	-	95572378	95572560
227785418	chr14	95572306	95572480	95572330	95572452	DICER1	NM_001195573	1	25	17	-	95572378	95572560
227785418	chr14	95572306	95572480	95572330	95572452	DICER1	NM_030621	2	28	19	-	95572378	95572560
228399064	chr14	95574035	95574189	95574063	95574157	DICER1	NM_177438	3	27	17	-	95573945	95574098
228399064	chr14	95574035	95574189	95574063	95574157	DICER1	NM_001195573	1	25	16	-	95573945	95574098
228399064	chr14	95574035	95574189	95574063	95574157	DICER1	NM_030621	2	28	18	-	95573945	95574098
228816570	chr14	95574393	95574549	95574413	95574524	DICER1	NM_177438	3	27	16	-	95574217	95574430
228816570	chr14	95574393	95574549	95574413	95574524	DICER1	NM_001195573	1	25	15	-	95574217	95574430
228816570	chr14	95574393	95574549	95574413	95574524	DICER1	NM_030621	2	28	17	-	95574217	95574430
227764512	chr14	95577693	95577835	95577715	95577806	DICER1	NM_177438	3	27	14	-	95577654	95577793

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227764512	chr14	95577693	95577835	95577715	95577806	DICER1	NM_001195573	1	25	13	-	95577654	95577793
227764512	chr14	95577693	95577835	95577715	95577806	DICER1	NM_030621	2	28	15	-	95577654	95577793
230408003	chr14	95579422	95579590	95579446	95579562	DICER1	NM_177438	3	27	12	-	95579429	95579561
230408003	chr14	95579422	95579590	95579446	95579562	DICER1	NM_001195573	1	25	11	-	95579429	95579561
230408003	chr14	95579422	95579590	95579446	95579562	DICER1	NM_030621	2	28	13	-	95579429	95579561
230700935	chr14	95582875	95583001	95582897	95582973	DICER1	NM_177438	3	27	10	-	95582790	95583032
230700935	chr14	95582875	95583001	95582897	95582973	DICER1	NM_001195573	1	25	9	-	95582790	95583032
230700935	chr14	95582875	95583001	95582897	95582973	DICER1	NM_030621	2	28	11	-	95582790	95583032
232489617	chr14	95590492	95590666	95590515	95590639	DICER1	NM_177438	3	27	8	-	95590533	95591005
232489617	chr14	95590492	95590666	95590515	95590639	DICER1	NM_001195573	1	25	7	-	95590533	95591005
232489617	chr14	95590492	95590666	95590515	95590639	DICER1	NM_030621	2	28	9	-	95590533	95591005
232542263	chr14	95590958	95591104	95590978	95591078	DICER1	NM_177438	3	27	8	-	95590533	95591005
232542263	chr14	95590958	95591104	95590978	95591078	DICER1	NM_001195573	1	25	7	-	95590533	95591005
232542263	chr14	95590958	95591104	95590978	95591078	DICER1	NM_030621	2	28	9	-	95590533	95591005
232993252	chr14	95596276	95596447	95596297	95596422	DICER1	NM_177438	3	27	5	-	95596395	95596529
232993252	chr14	95596276	95596447	95596297	95596422	DICER1	NM_001195573	1	25	4	-	95596395	95596529
232993252	chr14	95596276	95596447	95596297	95596422	DICER1	NM_030621	2	28	6	-	95596395	95596529
230020038	chr14	95598809	95598938	95598831	95598910	DICER1	NM_177438	3	27	3	-	95598852	95599014
230020038	chr14	95598809	95598938	95598831	95598910	DICER1	NM_001195573	1	25	2	-	95598852	95599014
230020038	chr14	95598809	95598938	95598831	95598910	DICER1	NM_030621	2	28	4	-	95598852	95599014
231603173	chr14	95599705	95599855	95599728	95599828	DICER1	NM_177438	3	27	2	-	95599652	95599840
231603173	chr14	95599705	95599855	95599728	95599828	DICER1	NM_001195573	1	25	1	-	95599652	95599840
231603173	chr14	95599705	95599855	95599728	95599828	DICER1	NM_030621	2	28	3	-	95599652	95599840
238516790	chr14	96180183	96180333	96180204	96180310	TCL1A	NM_021966	2	4	1	-	96180284	96180533
238516790	chr14	96180183	96180333	96180204	96180310	TCL1A	NM_001098725	1	4	1	-	96180284	96180533
225213992	chr14	99640631	99640791	99640649	99640773	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225213992	chr14	99640631	99640791	99640649	99640773	BCL11B	NM_022898	1	3	3	-	99635625	99642532
223927896	chr14	99641358	99641521	99641375	99641504	BCL11B	NM_138576	2	4	4	-	99635625	99642532
223927896	chr14	99641358	99641521	99641375	99641504	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225213060	chr14	99641850	99642022	99641874	99642005	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225213060	chr14	99641850	99642022	99641874	99642005	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225211487	chr14	99642290	99642439	99642308	99642420	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225211487	chr14	99642290	99642439	99642308	99642420	BCL11B	NM_022898	1	3	3	-	99635625	99642532
222197754	chr14	99697673	99697847	99697697	99697827	BCL11B	NM_138576	2	4	3	-	99697682	99697894
222972175	chr14	99723988	99724145	99724008	99724124	BCL11B	NM_138576	2	4	2	-	99723808	99724176
222972175	chr14	99723988	99724145	99724008	99724124	BCL11B	NM_022898	1	3	2	-	99723808	99724176
229822631	chr14	102548116	102548260	102548137	102548232	HSP90AA1	NM_005348	2	11	11	-	102547075	102548158
229822631	chr14	102548116	102548260	102548137	102548232	HSP90AA1	NM_001017963	1	12	12	-	102547075	102548158
227285149	chr14	102548677	102548803	102548703	102548775	HSP90AA1	NM_005348	2	11	10	-	102548448	102548781
227285149	chr14	102548677	102548803	102548703	102548775	HSP90AA1	NM_001017963	1	12	11	-	102548448	102548781
228140361	chr14	102549540	102549713	102549569	102549686	HSP90AA1	NM_005348	2	11	9	-	102549371	102549639

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228140361	chr14	102549540	102549713	102549569	102549686	HSP90AA1	NM_001017963	1	12	10	-	102549371	102549639
227288562	chr14	102550166	102550298	102550191	102550273	HSP90AA1	NM_005348	2	11	7	-	102550130	102550320
227288562	chr14	102550166	102550298	102550191	102550273	HSP90AA1	NM_001017963	1	12	8	-	102550130	102550320
227302248	chr14	102550988	102551155	102551009	102551127	HSP90AA1	NM_005348	2	11	5	-	102551018	102551335
227302248	chr14	102550988	102551155	102551009	102551127	HSP90AA1	NM_001017963	1	12	6	-	102551018	102551335
228644290	chr14	102551577	102551729	102551599	102551702	HSP90AA1	NM_005348	2	11	4	-	102551635	102551768
228644290	chr14	102551577	102551729	102551599	102551702	HSP90AA1	NM_001017963	1	12	5	-	102551635	102551768
227768245	chr14	102552305	102552471	102552330	102552445	HSP90AA1	NM_005348	2	11	3	-	102552095	102552461
227768245	chr14	102552305	102552471	102552330	102552445	HSP90AA1	NM_001017963	1	12	4	-	102552095	102552461
227403991	chr14	102568099	102568263	102568127	102568242	HSP90AA1	NM_001017963	1	12	2	-	102568212	102568422
229414721	chr14	102605574	102605744	102605598	102605727	HSP90AA1	NM_001017963	1	12	1	-	102605587	102606086
223723826	chr14	105238603	105238760	105238624	105238738	AKT1	NM_005163	3	14	12	-	105238702	105238789
223723826	chr14	105238603	105238760	105238624	105238738	AKT1	NM_001014432	2	15	13	-	105238702	105238789
223723826	chr14	105238603	105238760	105238624	105238738	AKT1	NM_001014431	1	14	12	-	105238702	105238789
223650918	chr14	105239553	105239711	105239571	105239690	AKT1	NM_005163	3	14	10	-	105239588	105239716
223650918	chr14	105239553	105239711	105239571	105239690	AKT1	NM_001014432	2	15	11	-	105239588	105239716
223650918	chr14	105239553	105239711	105239571	105239690	AKT1	NM_001014431	1	14	10	-	105239588	105239716
222517767	chr14	105241191	105241360	105241212	105241341	AKT1	NM_005163	3	14	7	-	105241275	105241340
222517767	chr14	105241191	105241360	105241212	105241341	AKT1	NM_001014432	2	15	8	-	105241275	105241340
222517767	chr14	105241191	105241360	105241212	105241341	AKT1	NM_001014431	1	14	7	-	105241275	105241340
224106159	chr14	105241931	105242104	105241950	105242085	AKT1	NM_005163	3	14	5	-	105241989	105242136
224106159	chr14	105241931	105242104	105241950	105242085	AKT1	NM_001014432	2	15	6	-	105241989	105242136
224106159	chr14	105241931	105242104	105241950	105242085	AKT1	NM_001014431	1	14	5	-	105241989	105242136
223793811	chr14	105243053	105243215	105243074	105243195	AKT1	NM_005163	3	14	4	-	105242996	105243107
223793811	chr14	105243053	105243215	105243074	105243195	AKT1	NM_001014432	2	15	5	-	105242996	105243107
223793811	chr14	105243053	105243215	105243074	105243195	AKT1	NM_001014431	1	14	4	-	105242996	105243107
304166021	chr15	39874292	39874442	39874313	39874421	THBS1	NM_003246	1	22	3	+	39874394	39874953
304204634	chr15	39874718	39874867	39874738	39874845	THBS1	NM_003246	1	22	3	+	39874394	39874953
300847123	chr15	39876178	39876320	39876199	39876298	THBS1	NM_003246	1	22	5	+	39876189	39876388
303327969	chr15	39879486	39879659	39879510	39879638	THBS1	NM_003246	1	22	8	+	39879548	39879721
299938571	chr15	39880688	39880861	39880714	39880839	THBS1	NM_003246	1	22	10	+	39880727	39880900
300826738	chr15	39881422	39881583	39881443	39881556	THBS1	NM_003246	1	22	12	+	39881403	39881555
304981287	chr15	39882736	39882867	39882758	39882840	THBS1	NM_003246	1	22	14	+	39882717	39882824
304307934	chr15	39884734	39884902	39884762	39884880	THBS1	NM_003246	1	22	17	+	39884769	39885003
299929083	chr15	39885339	39885473	39885364	39885445	THBS1	NM_003246	1	22	18	+	39885201	39885428
303481725	chr15	39886261	39886434	39886283	39886407	THBS1	NM_003246	1	22	20	+	39886300	39886397
224666269	chr15	40453312	40453478	40453333	40453457	BUB1B	NM_001211	1	23	1	+	40453210	40453456
225141771	chr15	40462610	40462781	40462634	40462758	BUB1B	NM_001211	1	23	4	+	40462738	40462882
222265348	chr15	40475815	40475989	40475843	40475962	BUB1B	NM_001211	1	23	6	+	40475915	40476084
223702142	chr15	40477359	40477486	40477379	40477463	BUB1B	NM_001211	1	23	7	+	40477366	40477580
224127854	chr15	40488634	40488790	40488661	40488762	BUB1B	NM_001211	1	23	9	+	40488746	40488975

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222930507	chr15	40491737	40491909	40491759	40491880	BUB1B	NM_001211	1	23	10	+	40491816	40491928
223005482	chr15	40493080	40493208	40493105	40493182	BUB1B	NM_001211	1	23	12	+	40493132	40493181
222373002	chr15	40498288	40498456	40498310	40498428	BUB1B	NM_001211	1	23	15	+	40498385	40498659
224044664	chr15	40500838	40501008	40500864	40500980	BUB1B	NM_001211	1	23	16	+	40500838	40500971
223138926	chr15	40502366	40502497	40502383	40502469	BUB1B	NM_001211	1	23	18	+	40502311	40502411
222952376	chr15	40505591	40505722	40505618	40505694	BUB1B	NM_001211	1	23	20	+	40505533	40505675
224956096	chr15	40512675	40512815	40512700	40512789	BUB1B	NM_001211	1	23	23	+	40512765	40513337
225929764	chr15	40895137	40895273	40895159	40895245	CASC5	NM_144508	1	26	2	+	40895113	40895164
225929764	chr15	40895137	40895273	40895159	40895245	CASC5	NM_170589	2	27	2	+	40895113	40895164
226139089	chr15	40898587	40898760	40898613	40898734	CASC5	NM_144508	1	26	4	+	40898591	40898650
226139089	chr15	40898587	40898760	40898613	40898734	CASC5	NM_170589	2	27	4	+	40898591	40898650
226511546	chr15	40911084	40911208	40911112	40911185	CASC5	NM_144508	1	26	9	+	40911157	40911209
226511546	chr15	40911084	40911208	40911112	40911185	CASC5	NM_170589	2	27	10	+	40911157	40911209
225336880	chr15	40912950	40913087	40912978	40913059	CASC5	NM_144508	1	26	10	+	40912838	40917838
225336880	chr15	40912950	40913087	40912978	40913059	CASC5	NM_170589	2	27	11	+	40912838	40917838
225351033	chr15	40913213	40913385	40913241	40913362	CASC5	NM_144508	1	26	10	+	40912838	40917838
225351033	chr15	40913213	40913385	40913241	40913362	CASC5	NM_170589	2	27	11	+	40912838	40917838
226629446	chr15	40913637	40913782	40913659	40913754	CASC5	NM_144508	1	26	10	+	40912838	40917838
226629446	chr15	40913637	40913782	40913659	40913754	CASC5	NM_170589	2	27	11	+	40912838	40917838
226625343	chr15	40913912	40914057	40913940	40914029	CASC5	NM_144508	1	26	10	+	40912838	40917838
226625343	chr15	40913912	40914057	40913940	40914029	CASC5	NM_170589	2	27	11	+	40912838	40917838
226622376	chr15	40914316	40914470	40914341	40914445	CASC5	NM_144508	1	26	10	+	40912838	40917838
226622376	chr15	40914316	40914470	40914341	40914445	CASC5	NM_170589	2	27	11	+	40912838	40917838
226635312	chr15	40914669	40914798	40914695	40914772	CASC5	NM_144508	1	26	10	+	40912838	40917838
226635312	chr15	40914669	40914798	40914695	40914772	CASC5	NM_170589	2	27	11	+	40912838	40917838
226630568	chr15	40915133	40915275	40915155	40915247	CASC5	NM_144508	1	26	10	+	40912838	40917838
226630568	chr15	40915133	40915275	40915155	40915247	CASC5	NM_170589	2	27	11	+	40912838	40917838
225352137	chr15	40915505	40915653	40915526	40915625	CASC5	NM_144508	1	26	10	+	40912838	40917838
225352137	chr15	40915505	40915653	40915526	40915625	CASC5	NM_170589	2	27	11	+	40912838	40917838
225375365	chr15	40915856	40915998	40915884	40915974	CASC5	NM_144508	1	26	10	+	40912838	40917838
225375365	chr15	40915856	40915998	40915884	40915974	CASC5	NM_170589	2	27	11	+	40912838	40917838
225394704	chr15	40916271	40916416	40916299	40916387	CASC5	NM_144508	1	26	10	+	40912838	40917838
225394704	chr15	40916271	40916416	40916299	40916387	CASC5	NM_170589	2	27	11	+	40912838	40917838
226635566	chr15	40916645	40916817	40916674	40916796	CASC5	NM_144508	1	26	10	+	40912838	40917838
226635566	chr15	40916645	40916817	40916674	40916796	CASC5	NM_170589	2	27	11	+	40912838	40917838
226630701	chr15	40917029	40917202	40917055	40917174	CASC5	NM_144508	1	26	10	+	40912838	40917838
226630701	chr15	40917029	40917202	40917055	40917174	CASC5	NM_170589	2	27	11	+	40912838	40917838
226638502	chr15	40917361	40917499	40917385	40917475	CASC5	NM_144508	1	26	10	+	40912838	40917838
226638502	chr15	40917361	40917499	40917385	40917475	CASC5	NM_170589	2	27	11	+	40912838	40917838
226643258	chr15	40917718	40917857	40917744	40917836	CASC5	NM_144508	1	26	10	+	40912838	40917838
226643258	chr15	40917718	40917857	40917744	40917836	CASC5	NM_170589	2	27	11	+	40912838	40917838

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226418538	chr15	40920353	40920514	40920374	40920486	CASC5	NM_144508	1	26	11	+	40920268	40920406
226418538	chr15	40920353	40920514	40920374	40920486	CASC5	NM_170589	2	27	12	+	40920268	40920406
226109796	chr15	40933060	40933208	40933085	40933179	CASC5	NM_144508	1	26	14	+	40933110	40933225
226109796	chr15	40933060	40933208	40933085	40933179	CASC5	NM_170589	2	27	15	+	40933110	40933225
226275264	chr15	40937906	40938080	40937932	40938052	CASC5	NM_144508	1	26	16	+	40937854	40937970
226275264	chr15	40937906	40938080	40937932	40938052	CASC5	NM_170589	2	27	17	+	40937854	40937970
226385797	chr15	40942613	40942785	40942635	40942761	CASC5	NM_144508	1	26	19	+	40942742	40942781
226385797	chr15	40942613	40942785	40942635	40942761	CASC5	NM_170589	2	27	20	+	40942742	40942781
225405071	chr15	40944201	40944359	40944222	40944332	CASC5	NM_144508	1	26	21	+	40944203	40944303
225405071	chr15	40944201	40944359	40944222	40944332	CASC5	NM_170589	2	27	22	+	40944203	40944303
272482804	chr15	41796160	41796329	41796180	41796307	LTK	NM_001135685	1	18	18	-	41795840	41796442
272482804	chr15	41796160	41796329	41796180	41796307	LTK	NM_002344	2	20	20	-	41795840	41796442
272482804	chr15	41796160	41796329	41796180	41796307	LTK	NM_206961	3	19	19	-	41795840	41796442
271683660	chr15	41796662	41796817	41796682	41796793	LTK	NM_001135685	1	18	16	-	41796704	41796838
271683660	chr15	41796662	41796817	41796682	41796793	LTK	NM_002344	2	20	18	-	41796704	41796838
271683660	chr15	41796662	41796817	41796682	41796793	LTK	NM_206961	3	19	17	-	41796704	41796838
270238026	chr15	41797056	41797198	41797077	41797176	LTK	NM_001135685	1	18	14	-	41797170	41797262
270238026	chr15	41797056	41797198	41797077	41797176	LTK	NM_002344	2	20	16	-	41797170	41797262
270238026	chr15	41797056	41797198	41797077	41797176	LTK	NM_206961	3	19	15	-	41797170	41797262
271978395	chr15	41797623	41797765	41797645	41797743	LTK	NM_001135685	1	18	12	-	41797599	41797728
271978395	chr15	41797623	41797765	41797645	41797743	LTK	NM_002344	2	20	14	-	41797599	41797728
271978395	chr15	41797623	41797765	41797645	41797743	LTK	NM_206961	3	19	13	-	41797599	41797728
270479650	chr15	41799368	41799521	41799391	41799501	LTK	NM_002344	2	20	11	-	41799293	41799488
270479650	chr15	41799368	41799521	41799391	41799501	LTK	NM_206961	3	19	10	-	41799293	41799488
272108412	chr15	41801172	41801309	41801192	41801289	LTK	NM_001135685	1	18	7	-	41801229	41801327
272108412	chr15	41801172	41801309	41801192	41801289	LTK	NM_002344	2	20	8	-	41801229	41801327
272108412	chr15	41801172	41801309	41801192	41801289	LTK	NM_206961	3	19	7	-	41801229	41801327
270279692	chr15	41804108	41804245	41804128	41804228	LTK	NM_001135685	1	18	5	-	41804015	41804161
270279692	chr15	41804108	41804245	41804128	41804228	LTK	NM_002344	2	20	5	-	41804015	41804161
270279692	chr15	41804108	41804245	41804128	41804228	LTK	NM_206961	3	19	5	-	41804015	41804161
272205726	chr15	41804849	41805023	41804870	41805002	LTK	NM_001135685	1	18	3	-	41804905	41805076
272205726	chr15	41804849	41805023	41804870	41805002	LTK	NM_002344	2	20	3	-	41804905	41805076
272205726	chr15	41804849	41805023	41804870	41805002	LTK	NM_206961	3	19	3	-	41804905	41805076
269618428	chr15	41805191	41805340	41805213	41805319	LTK	NM_001135685	1	18	2	-	41805175	41805318
269618428	chr15	41805191	41805340	41805213	41805319	LTK	NM_002344	2	20	2	-	41805175	41805318
269618428	chr15	41805191	41805340	41805213	41805319	LTK	NM_206961	3	19	2	-	41805175	41805318
294805639	chr15	43569012	43569161	43569032	43569140	TGM7	NM_052955	1	13	12	-	43569060	43569193
294896033	chr15	43571803	43571970	43571820	43571952	TGM7	NM_052955	1	13	10	-	43571823	43572149
294702434	chr15	43574089	43574213	43574111	43574192	TGM7	NM_052955	1	13	9	-	43574042	43574284
294871817	chr15	43577020	43577191	43577043	43577163	TGM7	NM_052955	1	13	7	-	43577012	43577150
294924087	chr15	43579788	43579956	43579810	43579932	TGM7	NM_052955	1	13	5	-	43579739	43579867

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295311625	chr15	43585043	43585217	43585066	43585190	TGM7	NM_052955	1	13	3	-	43584907	43585152
238888294	chr15	57212079	57212210	57212099	57212186	TCF12	NM_207038	4	20	2	+	57212100	57212186
238888294	chr15	57212079	57212210	57212099	57212186	TCF12	NM_207036	2	21	2	+	57212100	57212186
238888294	chr15	57212079	57212210	57212099	57212186	TCF12	NM_003205	1	20	2	+	57212090	57212186
238888294	chr15	57212079	57212210	57212099	57212186	TCF12	NM_207037	3	21	2	+	57212090	57212186
239317698	chr15	57383874	57384014	57383900	57383989	TCF12	NM_207038	4	20	5	+	57383987	57384089
239317698	chr15	57383874	57384014	57383900	57383989	TCF12	NM_207036	2	21	5	+	57383987	57384089
239317698	chr15	57383874	57384014	57383900	57383989	TCF12	NM_003205	1	20	5	+	57383987	57384089
239317698	chr15	57383874	57384014	57383900	57383989	TCF12	NM_207037	3	21	5	+	57383987	57384089
264294442	chr15	57484392	57484518	57484415	57484492	TCF12	NM_207038	4	20	7	+	57484356	57484491
264294442	chr15	57484392	57484518	57484415	57484492	TCF12	NM_207036	2	21	7	+	57484356	57484491
264294442	chr15	57484392	57484518	57484415	57484492	TCF12	NM_003205	1	20	7	+	57484356	57484491
264294442	chr15	57484392	57484518	57484415	57484492	TCF12	NM_207037	3	21	7	+	57484356	57484491
242128641	chr15	57511727	57511856	57511749	57511828	TCF12	NM_207040	5	13	1	+	57511655	57511788
242155874	chr15	57524480	57524653	57524505	57524628	TCF12	NM_207038	4	20	10	+	57524489	57524628
242155874	chr15	57524480	57524653	57524505	57524628	TCF12	NM_207036	2	21	10	+	57524489	57524628
242155874	chr15	57524480	57524653	57524505	57524628	TCF12	NM_003205	1	20	10	+	57524489	57524628
242155874	chr15	57524480	57524653	57524505	57524628	TCF12	NM_207037	3	21	10	+	57524489	57524628
242155874	chr15	57524480	57524653	57524505	57524628	TCF12	NM_207040	5	13	3	+	57524489	57524628
240576606	chr15	57526144	57526315	57526170	57526292	TCF12	NM_207038	4	20	12	+	57526241	57526305
240576606	chr15	57526144	57526315	57526170	57526292	TCF12	NM_207036	2	21	12	+	57526241	57526305
240576606	chr15	57526144	57526315	57526170	57526292	TCF12	NM_003205	1	20	12	+	57526241	57526305
240576606	chr15	57526144	57526315	57526170	57526292	TCF12	NM_207037	3	21	12	+	57526241	57526305
240576606	chr15	57526144	57526315	57526170	57526292	TCF12	NM_207040	5	13	5	+	57526241	57526305
261867178	chr15	57544633	57544784	57544653	57544756	TCF12	NM_207036	2	21	15	+	57544619	57544690
261867178	chr15	57544633	57544784	57544653	57544756	TCF12	NM_207037	3	21	15	+	57544619	57544690
242175178	chr15	57554161	57554319	57554187	57554297	TCF12	NM_207038	4	20	16	+	57554292	57554406
242175178	chr15	57554161	57554319	57554187	57554297	TCF12	NM_207036	2	21	17	+	57554292	57554406
242175178	chr15	57554161	57554319	57554187	57554297	TCF12	NM_003205	1	20	16	+	57554292	57554406
242175178	chr15	57554161	57554319	57554187	57554297	TCF12	NM_207037	3	21	17	+	57554292	57554406
242175178	chr15	57554161	57554319	57554187	57554297	TCF12	NM_207040	5	13	9	+	57554292	57554406
238699336	chr15	57555413	57555538	57555440	57555510	TCF12	NM_207038	4	20	17	+	57555310	57555472
238699336	chr15	57555413	57555538	57555440	57555510	TCF12	NM_207036	2	21	18	+	57555310	57555472
238699336	chr15	57555413	57555538	57555440	57555510	TCF12	NM_003205	1	20	17	+	57555310	57555472
238699336	chr15	57555413	57555538	57555440	57555510	TCF12	NM_207037	3	21	18	+	57555310	57555472
238699336	chr15	57555413	57555538	57555440	57555510	TCF12	NM_207040	5	13	10	+	57555310	57555472
238858612	chr15	57574546	57574682	57574574	57574661	TCF12	NM_207038	4	20	19	+	57574643	57574796
238858612	chr15	57574546	57574682	57574574	57574661	TCF12	NM_207036	2	21	20	+	57574643	57574796
238858612	chr15	57574546	57574682	57574574	57574661	TCF12	NM_003205	1	20	19	+	57574643	57574796
238858612	chr15	57574546	57574682	57574574	57574661	TCF12	NM_207037	3	21	20	+	57574643	57574796
238858612	chr15	57574546	57574682	57574574	57574661	TCF12	NM_207040	5	13	12	+	57574643	57574796

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233524764	chr15	66727432	66727604	66727454	66727576	MAP2K1	NM_002755	1	11	2	+	66727365	66727575
233671933	chr15	66735621	66735778	66735644	66735750	MAP2K1	NM_002755	1	11	4	+	66735618	66735695
233374474	chr15	66774102	66774258	66774125	66774237	MAP2K1	NM_002755	1	11	6	+	66774093	66774217
231106070	chr15	66781511	66781648	66781533	66781623	MAP2K1	NM_002755	1	11	9	+	66781553	66781614
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033250	9	7	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033249	8	7	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033247	7	5	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033246	6	6	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033244	5	8	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033240	4	7	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033239	3	8	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_033238	2	9	1	+	74287014	74287282
237005879	chr15	74287149	74287315	74287167	74287292	PML	NM_002675	1	8	1	+	74287014	74287282
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033250	9	7	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033249	8	7	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033247	7	5	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033246	6	6	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033244	5	8	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033240	4	7	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033239	3	8	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_033238	2	9	2	+	74290345	74290817
237957004	chr15	74290628	74290785	74290647	74290761	PML	NM_002675	1	8	2	+	74290345	74290817
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033250	9	7	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033249	8	7	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033247	7	5	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033246	6	6	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033244	5	8	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033240	4	7	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033239	3	8	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_033238	2	9	3	+	74315169	74315749
239374666	chr15	74315308	74315472	74315329	74315454	PML	NM_002675	1	8	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033250	9	7	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033249	8	7	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033247	7	5	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033246	6	6	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033244	5	8	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033240	4	7	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033239	3	8	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_033238	2	9	3	+	74315169	74315749
239371364	chr15	74315690	74315851	74315710	74315823	PML	NM_002675	1	8	3	+	74315169	74315749
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033250	9	7	5	+	74325497	74325755

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033249	8	7	5	+	74325497	74325755
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033240	4	7	6	+	74325497	74325755
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033239	3	8	6	+	74325497	74325755
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033238	2	9	6	+	74325497	74325755
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_002675	1	8	6	+	74325497	74325755
235477606	chr15	74325414	74325587	74325433	74325567	PML	NM_033244	5	8	6	+	74325497	74325763
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033240	4	7	7	+	74326819	74328735
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033250	9	7	6	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033249	8	7	6	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033246	6	6	5	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033244	5	8	7	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033239	3	8	7	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_033238	2	9	7	+	74326819	74326871
235904102	chr15	74326847	74327019	74326870	74327000	PML	NM_002675	1	8	7	+	74326819	74326871
238146745	chr15	74327860	74327991	74327879	74327973	PML	NM_033250	9	7	7	+	74327513	74328735
238146745	chr15	74327860	74327991	74327879	74327973	PML	NM_033244	5	8	8	+	74327513	74328735
238146745	chr15	74327860	74327991	74327879	74327973	PML	NM_033239	3	8	8	+	74327513	74328735
238146745	chr15	74327860	74327991	74327879	74327973	PML	NM_033240	4	7	7	+	74326819	74328735
235002827	chr15	74328285	74328441	74328306	74328413	PML	NM_033247	7	5	5	+	74328348	74328735
235002827	chr15	74328285	74328441	74328306	74328413	PML	NM_033250	9	7	7	+	74327513	74328735
235002827	chr15	74328285	74328441	74328306	74328413	PML	NM_033244	5	8	8	+	74327513	74328735
235002827	chr15	74328285	74328441	74328306	74328413	PML	NM_033239	3	8	8	+	74327513	74328735
235002827	chr15	74328285	74328441	74328306	74328413	PML	NM_033240	4	7	7	+	74326819	74328735
239450815	chr15	74336641	74336801	74336662	74336777	PML	NM_033238	2	9	9	+	74336562	74340155
239451635	chr15	74337096	74337255	74337118	74337233	PML	NM_033238	2	9	9	+	74336562	74340155
236384813	chr15	88423392	88423561	88423414	88423538	NTRK3	NM_002530	4	19	18	-	88423501	88423659
236384813	chr15	88423392	88423561	88423414	88423538	NTRK3	NM_001012338	2	20	19	-	88423501	88423659
236384813	chr15	88423392	88423561	88423414	88423538	NTRK3	NM_001243101	3	18	17	-	88423501	88423659
235956752	chr15	88472538	88472690	88472558	88472668	NTRK3	NM_002530	4	19	17	-	88472422	88472665
235956752	chr15	88472538	88472690	88472558	88472668	NTRK3	NM_001012338	2	20	17	-	88472422	88472665
235956752	chr15	88472538	88472690	88472558	88472668	NTRK3	NM_001243101	3	18	16	-	88472422	88472665
257450849	chr15	88483862	88484009	88483884	88483987	NTRK3	NM_002530	4	19	15	-	88483854	88483984
257450849	chr15	88483862	88484009	88483884	88483987	NTRK3	NM_001012338	2	20	15	-	88483854	88483984
257450849	chr15	88483862	88484009	88483884	88483987	NTRK3	NM_001243101	3	18	14	-	88483854	88483984
235162257	chr15	88576134	88576306	88576156	88576286	NTRK3	NM_002530	4	19	14	-	88576088	88576276
235162257	chr15	88576134	88576306	88576156	88576286	NTRK3	NM_001007156	1	16	14	-	88576088	88576276
235162257	chr15	88576134	88576306	88576156	88576286	NTRK3	NM_001012338	2	20	14	-	88576088	88576276
235162257	chr15	88576134	88576306	88576156	88576286	NTRK3	NM_001243101	3	18	13	-	88576088	88576276
239293657	chr15	88678271	88678428	88678292	88678402	NTRK3	NM_002530	4	19	10	-	88678332	88678628
239293657	chr15	88678271	88678428	88678292	88678402	NTRK3	NM_001007156	1	16	10	-	88678332	88678628
239293657	chr15	88678271	88678428	88678292	88678402	NTRK3	NM_001012338	2	20	10	-	88678332	88678628

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239293657	chr15	88678271	88678428	88678292	88678402	NTRK3	NM_001243101	3	18	10	-	88678332	88678628
239059191	chr15	88679198	88679322	88679219	88679296	NTRK3	NM_002530	4	19	9	-	88679130	88679271
239059191	chr15	88679198	88679322	88679219	88679296	NTRK3	NM_001007156	1	16	9	-	88679130	88679271
239059191	chr15	88679198	88679322	88679219	88679296	NTRK3	NM_001012338	2	20	9	-	88679130	88679271
239059191	chr15	88679198	88679322	88679219	88679296	NTRK3	NM_001243101	3	18	9	-	88679130	88679271
242011113	chr15	88680675	88680839	88680696	88680818	NTRK3	NM_002530	4	19	7	-	88680635	88680792
242011113	chr15	88680675	88680839	88680696	88680818	NTRK3	NM_001007156	1	16	7	-	88680635	88680792
242011113	chr15	88680675	88680839	88680696	88680818	NTRK3	NM_001012338	2	20	7	-	88680635	88680792
242011113	chr15	88680675	88680839	88680696	88680818	NTRK3	NM_001243101	3	18	7	-	88680635	88680792
237359819	chr15	88799120	88799285	88799137	88799263	NTRK3	NM_002530	4	19	3	-	88799137	88799399
237359819	chr15	88799120	88799285	88799137	88799263	NTRK3	NM_001007156	1	16	3	-	88799137	88799399
237359819	chr15	88799120	88799285	88799137	88799263	NTRK3	NM_001012338	2	20	3	-	88799137	88799399
237359819	chr15	88799120	88799285	88799137	88799263	NTRK3	NM_001243101	3	18	3	-	88799137	88799399
227492323	chr15	90628015	90628161	90628033	90628140	IDH2	NM_002168	1	11	10	-	90628048	90628140
227347287	chr15	90630234	90630397	90630255	90630376	IDH2	NM_002168	1	11	7	-	90630344	90630495
227882867	chr15	90631576	90631738	90631594	90631716	IDH2	NM_002168	1	11	5	-	90631591	90631734
227257853	chr15	90633611	90633777	90633633	90633757	IDH2	NM_002168	1	11	3	-	90633711	90633876
227441552	chr15	90634815	90634980	90634838	90634959	IDH2	NM_002168	1	11	2	-	90634785	90634876
222687006	chr15	91292721	91292873	91292742	91292848	BLM	NM_000057	1	22	3	+	91292597	91293297
224508908	chr15	91293130	91293268	91293154	91293240	BLM	NM_000057	1	22	3	+	91292597	91293297
222359413	chr15	91297993	91298133	91298021	91298105	BLM	NM_000057	1	22	5	+	91298041	91298168
224453627	chr15	91303471	91303604	91303492	91303582	BLM	NM_000057	1	22	6	+	91303377	91303509
225090238	chr15	91304118	91304252	91304144	91304224	BLM	NM_000057	1	22	7	+	91303824	91304485
222168809	chr15	91306095	91306252	91306117	91306228	BLM	NM_000057	1	22	8	+	91306196	91306387
222984915	chr15	91308606	91308769	91308634	91308741	BLM	NM_000057	1	22	9	+	91308526	91308644
223789639	chr15	91312587	91312721	91312614	91312695	BLM	NM_000057	1	22	12	+	91312668	91312816
225111789	chr15	91328250	91328388	91328271	91328364	BLM	NM_000057	1	22	14	+	91328151	91328311
223299251	chr15	91337408	91337576	91337436	91337549	BLM	NM_000057	1	22	16	+	91337397	91337587
222443847	chr15	91341434	91341607	91341462	91341577	BLM	NM_000057	1	22	17	+	91341420	91341567
223276627	chr15	91347349	91347515	91347374	91347487	BLM	NM_000057	1	22	19	+	91347397	91347589
223620023	chr15	91354405	91354578	91354433	91354550	BLM	NM_000057	1	22	21	+	91354435	91354636
271090650	chr15	99192663	99192833	99192686	99192816	IGF1R	NM_000875	1	21	1	+	99192761	99192904
269840156	chr15	99250924	99251055	99250945	99251034	IGF1R	NM_000875	1	21	2	+	99250791	99251336
270048462	chr15	99434520	99434693	99434541	99434670	IGF1R	NM_000875	1	21	3	+	99434554	99434866
270846660	chr15	99440051	99440207	99440079	99440185	IGF1R	NM_000875	1	21	4	+	99439986	99440134
271024295	chr15	99451992	99452154	99452015	99452133	IGF1R	NM_000875	1	21	6	+	99451914	99452128
270102696	chr15	99456367	99456500	99456385	99456474	IGF1R	NM_000875	1	21	8	+	99456273	99456511
272063787	chr15	99459836	99459985	99459862	99459964	IGF1R	NM_000875	1	21	10	+	99459901	99460105
271296364	chr15	99465452	99465590	99465473	99465569	IGF1R	NM_000875	1	21	11	+	99465377	99465660
272235319	chr15	99467712	99467886	99467739	99467865	IGF1R	NM_000875	1	21	13	+	99467754	99467913
269469898	chr15	99473349	99473522	99473373	99473500	IGF1R	NM_000875	1	21	15	+	99473464	99473534

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269763727	chr15	99478506	99478655	99478530	99478633	IGF1R	NM_000875	1	21	17	+	99478545	99478655
272643368	chr15	99486021	99486180	99486042	99486152	IGF1R	NM_000875	1	21	19	+	99486152	99486281
272133116	chr15	99500189	99500347	99500210	99500325	IGF1R	NM_000875	1	21	21	+	99500290	99507759
272144118	chr15	99500601	99500768	99500620	99500745	IGF1R	NM_000875	1	21	21	+	99500290	99507759
262489980	chr16	2098626	2098778	2098649	2098755	TSC2	NM_000548	1	42	2	+	2098588	2098754
262489980	chr16	2098626	2098778	2098649	2098755	TSC2	NM_001077183	2	40	2	+	2098588	2098754
262489980	chr16	2098626	2098778	2098649	2098755	TSC2	NM_001114382	3	41	2	+	2098588	2098754
238430074	chr16	2104322	2104486	2104347	2104464	TSC2	NM_000548	1	42	5	+	2104297	2104441
238430074	chr16	2104322	2104486	2104347	2104464	TSC2	NM_001077183	2	40	5	+	2104297	2104441
238430074	chr16	2104322	2104486	2104347	2104464	TSC2	NM_001114382	3	41	5	+	2104297	2104441
242731871	chr16	2106626	2106797	2106644	2106774	TSC2	NM_000548	1	42	8	+	2106645	2106770
242731871	chr16	2106626	2106797	2106644	2106774	TSC2	NM_001077183	2	40	8	+	2106645	2106770
242731871	chr16	2106626	2106797	2106644	2106774	TSC2	NM_001114382	3	41	8	+	2106645	2106770
240810403	chr16	2110580	2110721	2110599	2110697	TSC2	NM_000548	1	42	11	+	2110671	2110814
240810403	chr16	2110580	2110721	2110599	2110697	TSC2	NM_001077183	2	40	11	+	2110671	2110814
240810403	chr16	2110580	2110721	2110599	2110697	TSC2	NM_001114382	3	41	11	+	2110671	2110814
239056689	chr16	2112474	2112621	2112495	2112601	TSC2	NM_000548	1	42	13	+	2112498	2112601
239056689	chr16	2112474	2112621	2112495	2112601	TSC2	NM_001077183	2	40	13	+	2112498	2112601
239056689	chr16	2112474	2112621	2112495	2112601	TSC2	NM_001114382	3	41	13	+	2112498	2112601
241966660	chr16	2115490	2115658	2115511	2115640	TSC2	NM_000548	1	42	16	+	2115520	2115636
241966660	chr16	2115490	2115658	2115511	2115640	TSC2	NM_001077183	2	40	16	+	2115520	2115636
241966660	chr16	2115490	2115658	2115511	2115640	TSC2	NM_001114382	3	41	16	+	2115520	2115636
265944117	chr16	2121565	2121712	2121586	2121691	TSC2	NM_000548	1	42	18	+	2121511	2121617
265944117	chr16	2121565	2121712	2121586	2121691	TSC2	NM_001077183	2	40	18	+	2121511	2121617
265944117	chr16	2121565	2121712	2121586	2121691	TSC2	NM_001114382	3	41	18	+	2121511	2121617
241056948	chr16	2122179	2122341	2122198	2122322	TSC2	NM_000548	1	42	20	+	2122242	2122364
241056948	chr16	2122179	2122341	2122198	2122322	TSC2	NM_001077183	2	40	20	+	2122242	2122364
241056948	chr16	2122179	2122341	2122198	2122322	TSC2	NM_001114382	3	41	20	+	2122242	2122364
240322255	chr16	2124176	2124347	2124195	2124327	TSC2	NM_000548	1	42	22	+	2124201	2124390
240322255	chr16	2124176	2124347	2124195	2124327	TSC2	NM_001077183	2	40	22	+	2124201	2124390
240322255	chr16	2124176	2124347	2124195	2124327	TSC2	NM_001114382	3	41	22	+	2124201	2124390
241103511	chr16	2126048	2126214	2126068	2126195	TSC2	NM_000548	1	42	24	+	2126069	2126171
241103511	chr16	2126048	2126214	2126068	2126195	TSC2	NM_001077183	2	40	24	+	2126069	2126171
241103511	chr16	2126048	2126214	2126068	2126195	TSC2	NM_001114382	3	41	24	+	2126069	2126171
239212134	chr16	2127694	2127827	2127717	2127806	TSC2	NM_000548	1	42	26	+	2127599	2127727
239212134	chr16	2127694	2127827	2127717	2127806	TSC2	NM_001114382	3	41	26	+	2127599	2127727
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_000548	1	42	28	+	2129277	2129429
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_001077183	2	40	27	+	2129277	2129429
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_001114382	3	41	28	+	2129277	2129429
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_001077183	2	40	26	+	2129036	2129197
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_000548	1	42	27	+	2129033	2129197

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239506153	chr16	2129156	2129325	2129177	2129306	TSC2	NM_001114382	3	41	27	+	2129033	2129197
265785073	chr16	2130142	2130310	2130163	2130289	TSC2	NM_000548	1	42	30	+	2130166	2130378
265785073	chr16	2130142	2130310	2130163	2130289	TSC2	NM_001077183	2	40	29	+	2130166	2130378
265785073	chr16	2130142	2130310	2130163	2130289	TSC2	NM_001114382	3	41	30	+	2130166	2130378
241060589	chr16	2131725	2131872	2131746	2131855	TSC2	NM_000548	1	42	31	+	2131596	2131799
241060589	chr16	2131725	2131872	2131746	2131855	TSC2	NM_001077183	2	40	30	+	2131596	2131799
241060589	chr16	2131725	2131872	2131746	2131855	TSC2	NM_001114382	3	41	31	+	2131596	2131799
262605694	chr16	2134218	2134387	2134242	2134367	TSC2	NM_000548	1	42	34	+	2134229	2134716
262605694	chr16	2134218	2134387	2134242	2134367	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262605694	chr16	2134218	2134387	2134242	2134367	TSC2	NM_001114382	3	41	33	+	2134229	2134716
264924043	chr16	2134864	2135019	2134883	2134999	TSC2	NM_000548	1	42	35	+	2134952	2135027
264924043	chr16	2134864	2135019	2134883	2134999	TSC2	NM_001077183	2	40	33	+	2134952	2135027
264924043	chr16	2134864	2135019	2134883	2134999	TSC2	NM_001114382	3	41	34	+	2134952	2135027
242596342	chr16	2136207	2136338	2136227	2136319	TSC2	NM_000548	1	42	37	+	2136194	2136380
242596342	chr16	2136207	2136338	2136227	2136319	TSC2	NM_001077183	2	40	35	+	2136194	2136380
242596342	chr16	2136207	2136338	2136227	2136319	TSC2	NM_001114382	3	41	36	+	2136194	2136380
262386513	chr16	2137763	2137920	2137784	2137899	TSC2	NM_000548	1	42	39	+	2137864	2137942
262386513	chr16	2137763	2137920	2137784	2137899	TSC2	NM_001077183	2	40	37	+	2137864	2137942
262386513	chr16	2137763	2137920	2137784	2137899	TSC2	NM_001114382	3	41	38	+	2137864	2137942
239347884	chr16	2138404	2138537	2138422	2138519	TSC2	NM_000548	1	42	42	+	2138447	2138713
239347884	chr16	2138404	2138537	2138422	2138519	TSC2	NM_001077183	2	40	40	+	2138447	2138713
239347884	chr16	2138404	2138537	2138422	2138519	TSC2	NM_001114382	3	41	41	+	2138447	2138713
225471220	chr16	3777874	3778045	3777893	3778024	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225471220	chr16	3777874	3778045	3777893	3778024	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225491370	chr16	3778327	3778497	3778344	3778469	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225491370	chr16	3778327	3778497	3778344	3778469	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226719808	chr16	3778731	3778855	3778752	3778837	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226719808	chr16	3778731	3778855	3778752	3778837	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226718354	chr16	3779150	3779317	3779168	3779300	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226718354	chr16	3779150	3779317	3779168	3779300	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226720781	chr16	3779641	3779809	3779660	3779791	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226720781	chr16	3779641	3779809	3779660	3779791	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225895126	chr16	3781328	3781499	3781349	3781478	CREBBP	NM_001079846	1	30	29	-	3781193	3781474
225895126	chr16	3781328	3781499	3781349	3781478	CREBBP	NM_004380	2	31	30	-	3781193	3781474
226614803	chr16	3786090	3786236	3786119	3786213	CREBBP	NM_001079846	1	30	27	-	3786037	3786204
226614803	chr16	3786090	3786236	3786119	3786213	CREBBP	NM_004380	2	31	28	-	3786037	3786204
225399885	chr16	3788550	3788704	3788579	3788680	CREBBP	NM_001079846	1	30	25	-	3788560	3788673
225399885	chr16	3788550	3788704	3788579	3788680	CREBBP	NM_004380	2	31	26	-	3788560	3788673
225749631	chr16	3790417	3790573	3790437	3790551	CREBBP	NM_001079846	1	30	23	-	3790400	3790550
225749631	chr16	3790417	3790573	3790437	3790551	CREBBP	NM_004380	2	31	24	-	3790400	3790550
226513775	chr16	3801674	3801830	3801697	3801808	CREBBP	NM_001079846	1	30	19	-	3801727	3801807

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226513775	chr16	3801674	3801830	3801697	3801808	CREBBP	NM_004380	2	31	20	-	3801727	3801807
226500750	chr16	3807923	3808087	3807945	3808064	CREBBP	NM_001079846	1	30	17	-	3807810	3808049
226500750	chr16	3807923	3808087	3807945	3808064	CREBBP	NM_004380	2	31	18	-	3807810	3808049
226204935	chr16	3817737	3817887	3817760	3817860	CREBBP	NM_001079846	1	30	15	-	3817721	3817910
226204935	chr16	3817737	3817887	3817760	3817860	CREBBP	NM_004380	2	31	16	-	3817721	3817910
226568220	chr16	3820493	3820665	3820517	3820645	CREBBP	NM_001079846	1	30	13	-	3820571	3820987
226568220	chr16	3820493	3820665	3820517	3820645	CREBBP	NM_004380	2	31	14	-	3820571	3820987
226570881	chr16	3820888	3821012	3820907	3820988	CREBBP	NM_001079846	1	30	13	-	3820571	3820987
226570881	chr16	3820888	3821012	3820907	3820988	CREBBP	NM_004380	2	31	14	-	3820571	3820987
225609948	chr16	3824557	3824719	3824578	3824694	CREBBP	NM_001079846	1	30	11	-	3824570	3824694
225609948	chr16	3824557	3824719	3824578	3824694	CREBBP	NM_004380	2	31	12	-	3824570	3824694
225403465	chr16	3828081	3828247	3828102	3828219	CREBBP	NM_001079846	1	30	9	-	3828012	3828183
225403465	chr16	3828081	3828247	3828102	3828219	CREBBP	NM_004380	2	31	10	-	3828012	3828183
225919091	chr16	3830786	3830928	3830809	3830901	CREBBP	NM_001079846	1	30	7	-	3830733	3830879
225919091	chr16	3830786	3830928	3830809	3830901	CREBBP	NM_004380	2	31	8	-	3830733	3830879
226169376	chr16	3832786	3832956	3832806	3832932	CREBBP	NM_001079846	1	30	5	-	3832685	3832927
226169376	chr16	3832786	3832956	3832806	3832932	CREBBP	NM_004380	2	31	6	-	3832685	3832927
225708863	chr16	3843407	3843567	3843433	3843544	CREBBP	NM_001079846	1	30	4	-	3843387	3843627
225708863	chr16	3843407	3843567	3843433	3843544	CREBBP	NM_004380	2	31	4	-	3843387	3843627
225996869	chr16	3900254	3900428	3900276	3900407	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
225996869	chr16	3900254	3900428	3900276	3900407	CREBBP	NM_004380	2	31	2	-	3900298	3901010
226012585	chr16	3900709	3900868	3900731	3900848	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
226012585	chr16	3900709	3900868	3900731	3900848	CREBBP	NM_004380	2	31	2	-	3900298	3901010
264754199	chr16	11348623	11348772	11348644	11348753	SOCS1	NM_003745	1	2	2	-	11348274	11349385
264724490	chr16	11348988	11349161	11349009	11349144	SOCS1	NM_003745	1	2	2	-	11348274	11349385
229991948	chr16	14013935	14014059	14013954	14014041	ERCC4	NM_005236	1	11	1	+	14014014	14014229
231875454	chr16	14015903	14016047	14015929	14016019	ERCC4	NM_005236	1	11	2	+	14015888	14016068
228020040	chr16	14020531	14020692	14020556	14020664	ERCC4	NM_005236	1	11	3	+	14020418	14020613
233003616	chr16	14024538	14024662	14024570	14024634	ERCC4	NM_005236	1	11	5	+	14024567	14024747
229984849	chr16	14026032	14026173	14026058	14026145	ERCC4	NM_005236	1	11	6	+	14026014	14026142
232140954	chr16	14029034	14029204	14029056	14029179	ERCC4	NM_005236	1	11	8	+	14029003	14029600
229721082	chr16	14029476	14029634	14029499	14029606	ERCC4	NM_005236	1	11	8	+	14029003	14029600
232481141	chr16	14041428	14041555	14041450	14041532	ERCC4	NM_005236	1	11	11	+	14041471	14046205
232564406	chr16	14041820	14041980	14041845	14041959	ERCC4	NM_005236	1	11	11	+	14041471	14046205
237731334	chr16	15797888	15798033	15797910	15798006	MYH11	NM_022844	4	42	42	-	15796992	15797980
237731334	chr16	15797888	15798033	15797910	15798006	MYH11	NM_002474	3	41	41	-	15796992	15797980
237731334	chr16	15797888	15798033	15797910	15798006	MYH11	NM_001040113	1	43	43	-	15796992	15797980
237731334	chr16	15797888	15798033	15797910	15798006	MYH11	NM_001040114	2	42	42	-	15796992	15797980
236868194	chr16	15808937	15809108	15808955	15809086	MYH11	NM_022844	4	42	39	-	15809021	15809129
236868194	chr16	15808937	15809108	15808955	15809086	MYH11	NM_002474	3	41	39	-	15809021	15809129
236868194	chr16	15808937	15809108	15808955	15809086	MYH11	NM_001040113	1	43	40	-	15809021	15809129

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236868194	chr16	15808937	15809108	15808955	15809086	MYH11	NM_001040114	2	42	40	-	15809021	15809129
240652682	chr16	15811105	15811268	15811125	15811248	MYH11	NM_022844	4	42	38	-	15810997	15811205
240652682	chr16	15811105	15811268	15811125	15811248	MYH11	NM_002474	3	41	38	-	15810997	15811205
240652682	chr16	15811105	15811268	15811125	15811248	MYH11	NM_001040113	1	43	39	-	15810997	15811205
240652682	chr16	15811105	15811268	15811125	15811248	MYH11	NM_001040114	2	42	39	-	15810997	15811205
258676704	chr16	15813421	15813591	15813440	15813570	MYH11	NM_022844	4	42	35	-	15813442	15813570
258676704	chr16	15813421	15813591	15813440	15813570	MYH11	NM_002474	3	41	35	-	15813442	15813570
258676704	chr16	15813421	15813591	15813440	15813570	MYH11	NM_001040113	1	43	36	-	15813442	15813570
258676704	chr16	15813421	15813591	15813440	15813570	MYH11	NM_001040114	2	42	36	-	15813442	15813570
242158020	chr16	15814742	15814907	15814764	15814886	MYH11	NM_022844	4	42	33	-	15814696	15814908
242158020	chr16	15814742	15814907	15814764	15814886	MYH11	NM_002474	3	41	33	-	15814696	15814908
242158020	chr16	15814742	15814907	15814764	15814886	MYH11	NM_001040113	1	43	34	-	15814696	15814908
242158020	chr16	15814742	15814907	15814764	15814886	MYH11	NM_001040114	2	42	34	-	15814696	15814908
235074018	chr16	15817934	15818092	15817953	15818069	MYH11	NM_022844	4	42	31	-	15818018	15818266
235074018	chr16	15817934	15818092	15817953	15818069	MYH11	NM_002474	3	41	31	-	15818018	15818266
235074018	chr16	15817934	15818092	15817953	15818069	MYH11	NM_001040113	1	43	32	-	15818018	15818266
235074018	chr16	15817934	15818092	15817953	15818069	MYH11	NM_001040114	2	42	32	-	15818018	15818266
236866863	chr16	15818568	15818740	15818587	15818720	MYH11	NM_022844	4	42	30	-	15818504	15818656
236866863	chr16	15818568	15818740	15818587	15818720	MYH11	NM_002474	3	41	30	-	15818504	15818656
236866863	chr16	15818568	15818740	15818587	15818720	MYH11	NM_001040113	1	43	31	-	15818504	15818656
236866863	chr16	15818568	15818740	15818587	15818720	MYH11	NM_001040114	2	42	31	-	15818504	15818656
237078653	chr16	15820785	15820941	15820805	15820920	MYH11	NM_022844	4	42	28	-	15820705	15820911
237078653	chr16	15820785	15820941	15820805	15820920	MYH11	NM_002474	3	41	28	-	15820705	15820911
237078653	chr16	15820785	15820941	15820805	15820920	MYH11	NM_001040113	1	43	29	-	15820705	15820911
237078653	chr16	15820785	15820941	15820805	15820920	MYH11	NM_001040114	2	42	29	-	15820705	15820911
235999363	chr16	15829242	15829415	15829263	15829390	MYH11	NM_022844	4	42	26	-	15829223	15829435
235999363	chr16	15829242	15829415	15829263	15829390	MYH11	NM_002474	3	41	26	-	15829223	15829435
235999363	chr16	15829242	15829415	15829263	15829390	MYH11	NM_001040113	1	43	27	-	15829223	15829435
235999363	chr16	15829242	15829415	15829263	15829390	MYH11	NM_001040114	2	42	27	-	15829223	15829435
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_022844	4	42	24	-	15832422	15832545
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_002474	3	41	24	-	15832422	15832545
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_001040113	1	43	25	-	15832422	15832545
235717531	chr16	15832399	15832528	15832426	15832500	MYH11	NM_001040114	2	42	25	-	15832422	15832545
241751419	chr16	15834022	15834159	15834044	15834135	MYH11	NM_022844	4	42	23	-	15833908	15834045
241751419	chr16	15834022	15834159	15834044	15834135	MYH11	NM_002474	3	41	23	-	15833908	15834045
241751419	chr16	15834022	15834159	15834044	15834135	MYH11	NM_001040113	1	43	24	-	15833908	15834045
241751419	chr16	15834022	15834159	15834044	15834135	MYH11	NM_001040114	2	42	24	-	15833908	15834045
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_022844	4	42	21	-	15835617	15835748
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_002474	3	41	21	-	15835617	15835748
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_001040113	1	43	22	-	15835617	15835748
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_001040114	2	42	22	-	15835617	15835748

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_022844	4	42	22	-	15835320	15835526
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_002474	3	41	22	-	15835320	15835526
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_001040113	1	43	23	-	15835320	15835526
236981632	chr16	15835493	15835662	15835515	15835637	MYH11	NM_001040114	2	42	23	-	15835320	15835526
235664071	chr16	15841367	15841501	15841389	15841478	MYH11	NM_022844	4	42	19	-	15841427	15841587
235664071	chr16	15841367	15841501	15841389	15841478	MYH11	NM_002474	3	41	19	-	15841427	15841587
235664071	chr16	15841367	15841501	15841389	15841478	MYH11	NM_001040113	1	43	20	-	15841427	15841587
235664071	chr16	15841367	15841501	15841389	15841478	MYH11	NM_001040114	2	42	20	-	15841427	15841587
238053321	chr16	15843866	15844031	15843887	15844012	MYH11	NM_022844	4	42	16	-	15843995	15844188
238053321	chr16	15843866	15844031	15843887	15844012	MYH11	NM_002474	3	41	16	-	15843995	15844188
238053321	chr16	15843866	15844031	15843887	15844012	MYH11	NM_001040113	1	43	17	-	15843995	15844188
238053321	chr16	15843866	15844031	15843887	15844012	MYH11	NM_001040114	2	42	17	-	15843995	15844188
235096903	chr16	15847294	15847425	15847314	15847398	MYH11	NM_022844	4	42	15	-	15847251	15847365
235096903	chr16	15847294	15847425	15847314	15847398	MYH11	NM_002474	3	41	15	-	15847251	15847365
235096903	chr16	15847294	15847425	15847314	15847398	MYH11	NM_001040113	1	43	16	-	15847251	15847365
235096903	chr16	15847294	15847425	15847314	15847398	MYH11	NM_001040114	2	42	16	-	15847251	15847365
237032468	chr16	15851630	15851792	15851650	15851771	MYH11	NM_022844	4	42	13	-	15851684	15851857
237032468	chr16	15851630	15851792	15851650	15851771	MYH11	NM_002474	3	41	13	-	15851684	15851857
237032468	chr16	15851630	15851792	15851650	15851771	MYH11	NM_001040113	1	43	14	-	15851684	15851857
237032468	chr16	15851630	15851792	15851650	15851771	MYH11	NM_001040114	2	42	14	-	15851684	15851857
235190667	chr16	15854390	15854541	15854417	15854515	MYH11	NM_022844	4	42	11	-	15854397	15854515
235190667	chr16	15854390	15854541	15854417	15854515	MYH11	NM_002474	3	41	11	-	15854397	15854515
235190667	chr16	15854390	15854541	15854417	15854515	MYH11	NM_001040113	1	43	12	-	15854397	15854515
235190667	chr16	15854390	15854541	15854417	15854515	MYH11	NM_001040114	2	42	12	-	15854397	15854515
239893201	chr16	15869890	15870058	15869911	15870035	MYH11	NM_022844	4	42	8	-	15869935	15870033
239893201	chr16	15869890	15870058	15869911	15870035	MYH11	NM_002474	3	41	8	-	15869935	15870033
239893201	chr16	15869890	15870058	15869911	15870035	MYH11	NM_001040113	1	43	9	-	15869935	15870033
239893201	chr16	15869890	15870058	15869911	15870035	MYH11	NM_001040114	2	42	9	-	15869935	15870033
236245499	chr16	15880440	15880613	15880462	15880589	MYH11	NM_022844	4	42	5	-	15880487	15880589
236245499	chr16	15880440	15880613	15880462	15880589	MYH11	NM_002474	3	41	5	-	15880487	15880589
236245499	chr16	15880440	15880613	15880462	15880589	MYH11	NM_001040113	1	43	5	-	15880487	15880589
236245499	chr16	15880440	15880613	15880462	15880589	MYH11	NM_001040114	2	42	5	-	15880487	15880589
235083434	chr16	15931687	15931818	15931708	15931798	MYH11	NM_022844	4	42	2	-	15931765	15932126
235083434	chr16	15931687	15931818	15931708	15931798	MYH11	NM_002474	3	41	2	-	15931765	15932126
235083434	chr16	15931687	15931818	15931708	15931798	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235083434	chr16	15931687	15931818	15931708	15931798	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235972250	chr16	23614734	23614861	23614762	23614837	PALB2	NM_024675	1	13	13	-	23614483	23614990
235367443	chr16	23619225	23619386	23619244	23619358	PALB2	NM_024675	1	13	12	-	23619185	23619333
235292994	chr16	23634321	23634494	23634344	23634471	PALB2	NM_024675	1	13	9	-	23634290	23634451
238192268	chr16	23637580	23637742	23637601	23637719	PALB2	NM_024675	1	13	7	-	23637557	23637718
236544450	chr16	23641105	23641262	23641126	23641238	PALB2	NM_024675	1	13	5	-	23640961	23641790

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239971549	chr16	23641558	23641720	23641579	23641700	PALB2	NM_024675	1	13	5	-	23640961	23641790
238241292	chr16	23646331	23646505	23646354	23646479	PALB2	NM_024675	1	13	4	-	23646183	23647655
235062367	chr16	23646780	23646922	23646808	23646894	PALB2	NM_024675	1	13	4	-	23646183	23647655
235068956	chr16	23647097	23647247	23647125	23647219	PALB2	NM_024675	1	13	4	-	23646183	23647655
238276216	chr16	23647480	23647630	23647503	23647603	PALB2	NM_024675	1	13	4	-	23646183	23647655
235661489	chr16	23652366	23652509	23652386	23652488	PALB2	NM_024675	1	13	1	-	23652431	23652678
229395272	chr16	27445643	27445789	27445661	27445770	IL21R	NM_181079	3	10	4	+	27445668	27445770
229395272	chr16	27445643	27445789	27445661	27445770	IL21R	NM_181078	2	9	3	+	27445668	27445770
229395272	chr16	27445643	27445789	27445661	27445770	IL21R	NM_021798	1	9	3	+	27445668	27445770
227799714	chr16	27454326	27454463	27454351	27454443	IL21R	NM_181079	3	10	6	+	27454283	27454437
227799714	chr16	27454326	27454463	27454351	27454443	IL21R	NM_181078	2	9	5	+	27454283	27454437
227799714	chr16	27454326	27454463	27454351	27454443	IL21R	NM_021798	1	9	5	+	27454283	27454437
228369840	chr16	27456529	27456679	27456552	27456653	IL21R	NM_181079	3	10	8	+	27456498	27456597
228369840	chr16	27456529	27456679	27456552	27456653	IL21R	NM_181078	2	9	7	+	27456498	27456597
228369840	chr16	27456529	27456679	27456552	27456653	IL21R	NM_021798	1	9	7	+	27456498	27456597
228961855	chr16	27459978	27460138	27459999	27460116	IL21R	NM_181079	3	10	10	+	27459855	27463363
228961855	chr16	27459978	27460138	27459999	27460116	IL21R	NM_181078	2	9	9	+	27459855	27463363
228961855	chr16	27459978	27460138	27459999	27460116	IL21R	NM_021798	1	9	9	+	27459855	27463363
228957137	chr16	27460431	27460591	27460448	27460572	IL21R	NM_181079	3	10	10	+	27459855	27463363
228957137	chr16	27460431	27460591	27460448	27460572	IL21R	NM_181078	2	9	9	+	27459855	27463363
228957137	chr16	27460431	27460591	27460448	27460572	IL21R	NM_021798	1	9	9	+	27459855	27463363
225426052	chr16	50783685	50783851	50783709	50783823	CYLD	NM_015247	3	20	4	+	50783487	50784113
225426052	chr16	50783685	50783851	50783709	50783823	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225426052	chr16	50783685	50783851	50783709	50783823	CYLD	NM_001042412	2	18	3	+	50783487	50784113
225421529	chr16	50784056	50784181	50784077	50784154	CYLD	NM_015247	3	20	4	+	50783487	50784113
225421529	chr16	50784056	50784181	50784077	50784154	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225421529	chr16	50784056	50784181	50784077	50784154	CYLD	NM_001042412	2	18	3	+	50783487	50784113
226491965	chr16	50810071	50810241	50810097	50810214	CYLD	NM_015247	3	20	8	+	50810086	50810188
226491965	chr16	50810071	50810241	50810097	50810214	CYLD	NM_001042355	1	18	6	+	50810090	50810188
226491965	chr16	50810071	50810241	50810097	50810214	CYLD	NM_001042412	2	18	6	+	50810090	50810188
226578267	chr16	50813748	50813882	50813770	50813859	CYLD	NM_015247	3	20	10	+	50813576	50813955
226578267	chr16	50813748	50813882	50813770	50813859	CYLD	NM_001042355	1	18	8	+	50813576	50813955
226578267	chr16	50813748	50813882	50813770	50813859	CYLD	NM_001042412	2	18	8	+	50813576	50813955
225899532	chr16	50815257	50815410	50815278	50815381	CYLD	NM_015247	3	20	11	+	50815157	50815322
225899532	chr16	50815257	50815410	50815278	50815381	CYLD	NM_001042355	1	18	9	+	50815157	50815322
225899532	chr16	50815257	50815410	50815278	50815381	CYLD	NM_001042412	2	18	9	+	50815157	50815322
225735454	chr16	50818223	50818347	50818250	50818321	CYLD	NM_015247	3	20	13	+	50818240	50818362
225735454	chr16	50818223	50818347	50818250	50818321	CYLD	NM_001042355	1	18	11	+	50818240	50818362
225735454	chr16	50818223	50818347	50818250	50818321	CYLD	NM_001042412	2	18	11	+	50818240	50818362
225685124	chr16	50825378	50825544	50825402	50825520	CYLD	NM_015247	3	20	16	+	50825469	50825601
225685124	chr16	50825378	50825544	50825402	50825520	CYLD	NM_001042355	1	18	14	+	50825469	50825601

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225685124	chr16	50825378	50825544	50825402	50825520	CYLD	NM_001042412	2	18	14	+	50825469	50825601
226385016	chr16	50827434	50827602	50827456	50827575	CYLD	NM_015247	3	20	18	+	50827457	50827575
226385016	chr16	50827434	50827602	50827456	50827575	CYLD	NM_001042355	1	18	16	+	50827457	50827575
226385016	chr16	50827434	50827602	50827456	50827575	CYLD	NM_001042412	2	18	16	+	50827457	50827575
226733872	chr16	50830305	50830466	50830327	50830444	CYLD	NM_015247	3	20	20	+	50830235	50835846
226733872	chr16	50830305	50830466	50830327	50830444	CYLD	NM_001042355	1	18	18	+	50830235	50835846
226733872	chr16	50830305	50830466	50830327	50830444	CYLD	NM_001042412	2	18	18	+	50830235	50835846
289225820	chr16	55516867	55517040	55516891	55517017	MMP2	NM_001127891	1	13	2	+	55516821	55517047
289225820	chr16	55516867	55517040	55516891	55517017	MMP2	NM_004530	2	13	2	+	55516821	55517047
290278382	chr16	55519172	55519330	55519192	55519308	MMP2	NM_001127891	1	13	4	+	55519211	55519339
290278382	chr16	55519172	55519330	55519192	55519308	MMP2	NM_004530	2	13	4	+	55519211	55519339
292505619	chr16	55522403	55522531	55522425	55522509	MMP2	NM_001127891	1	13	6	+	55522455	55522628
292505619	chr16	55522403	55522531	55522425	55522509	MMP2	NM_004530	2	13	6	+	55522455	55522628
289620690	chr16	55523611	55523773	55523633	55523752	MMP2	NM_001127891	1	13	7	+	55523563	55523736
289620690	chr16	55523611	55523773	55523633	55523752	MMP2	NM_004530	2	13	7	+	55523563	55523736
289612943	chr16	55527121	55527286	55527143	55527259	MMP2	NM_001127891	1	13	9	+	55527070	55527205
289612943	chr16	55527121	55527286	55527143	55527259	MMP2	NM_004530	2	13	9	+	55527070	55527205
289931679	chr16	55532300	55532466	55532323	55532447	MMP2	NM_001127891	1	13	11	+	55532201	55532360
289931679	chr16	55532300	55532466	55532323	55532447	MMP2	NM_004530	2	13	11	+	55532201	55532360
226963440	chr16	64981450	64981612	64981474	64981585	CDH11	NM_001797	1	13	13	-	64980683	64982002
226984041	chr16	64981891	64982044	64981918	64982018	CDH11	NM_001797	1	13	13	-	64980683	64982002
226454444	chr16	65005345	65005519	65005373	65005491	CDH11	NM_001797	1	13	11	-	65005482	65005599
225326057	chr16	65006783	65006943	65006810	65006919	CDH11	NM_001797	1	13	9	-	65006807	65006943
225513496	chr16	65016091	65016231	65016112	65016205	CDH11	NM_001797	1	13	8	-	65015951	65016204
225905543	chr16	65025581	65025744	65025608	65025724	CDH11	NM_001797	1	13	6	-	65025671	65025838
253660947	chr16	65032370	65032535	65032395	65032512	CDH11	NM_001797	1	13	4	-	65032465	65032759
225408912	chr16	65038505	65038672	65038527	65038652	CDH11	NM_001797	1	13	3	-	65038545	65038944
270798884	chr16	66420687	66420861	66420711	66420840	CDH5	NM_001795	1	12	3	+	66420712	66421000
270053942	chr16	66423228	66423398	66423251	66423376	CDH5	NM_001795	1	12	5	+	66423261	66423425
270127286	chr16	66426011	66426149	66426035	66426128	CDH5	NM_001795	1	12	7	+	66426039	66426286
271263841	chr16	66430037	66430167	66430061	66430140	CDH5	NM_001795	1	12	8	+	66429962	66430104
271413078	chr16	66434635	66434775	66434655	66434753	CDH5	NM_001795	1	12	11	+	66434674	66434919
271652708	chr16	66436637	66436796	66436655	66436778	CDH5	NM_001795	1	12	12	+	66436555	66438689
225530287	chr16	68771224	68771398	68771244	68771380	CDH1	NM_004360	1	16	1	+	68771195	68771366
226327144	chr16	68835564	68835698	68835586	68835675	CDH1	NM_004360	1	16	3	+	68835573	68835796
227045676	chr16	68842535	68842708	68842557	68842680	CDH1	NM_004360	1	16	5	+	68842596	68842751
225346010	chr16	68845538	68845702	68845560	68845676	CDH1	NM_004360	1	16	7	+	68845587	68845762
226224197	chr16	68847167	68847318	68847192	68847298	CDH1	NM_004360	1	16	9	+	68847216	68847398
225858736	chr16	68849556	68849699	68849578	68849674	CDH1	NM_004360	1	16	10	+	68849418	68849662
225499340	chr16	68855890	68856045	68855918	68856018	CDH1	NM_004360	1	16	12	+	68855904	68856128
226281541	chr16	68861955	68862115	68861975	68862094	CDH1	NM_004360	1	16	14	+	68862077	68862207

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225379651	chr16	68867166	68867323	68867191	68867300	CDH1	NM_004360	1	16	16	+	68867193	68869444
232454985	chr16	79632637	79632771	79632658	79632744	MAF	NM_001031804	1	1	1	-	79627745	79634622
232454985	chr16	79632637	79632771	79632658	79632744	MAF	NM_005360	2	2	1	-	79632682	79634622
233796702	chr16	79633402	79633544	79633419	79633523	MAF	NM_001031804	1	1	1	-	79627745	79634622
233796702	chr16	79633402	79633544	79633419	79633523	MAF	NM_005360	2	2	1	-	79632682	79634622
233802271	chr16	79633693	79633855	79633721	79633837	MAF	NM_001031804	1	1	1	-	79627745	79634622
233802271	chr16	79633693	79633855	79633721	79633837	MAF	NM_005360	2	2	1	-	79632682	79634622
230576805	chr16	89805459	89805625	89805480	89805604	FANCA	NM_000135	1	43	41	-	89805541	89805697
230679559	chr16	89807179	89807339	89807200	89807310	FANCA	NM_000135	1	43	38	-	89807212	89807274
231473939	chr16	89812883	89813050	89812904	89813028	FANCA	NM_000135	1	43	35	-	89812992	89813096
230129759	chr16	89816115	89816248	89816136	89816227	FANCA	NM_000135	1	43	32	-	89816138	89816310
230494883	chr16	89825070	89825234	89825092	89825213	FANCA	NM_000135	1	43	30	-	89824985	89825113
228987188	chr16	89831436	89831568	89831456	89831546	FANCA	NM_000135	1	43	28	-	89831298	89831474
227865869	chr16	89836338	89836504	89836357	89836485	FANCA	NM_000135	1	43	26	-	89836245	89836432
230069833	chr16	89837991	89838157	89838016	89838133	FANCA	NM_000135	1	43	23	-	89838086	89838222
228351347	chr16	89845154	89845327	89845178	89845303	FANCA	NM_000135	1	43	20	-	89845209	89845258
228336517	chr16	89849366	89849534	89849386	89849513	FANCA	NM_000135	1	43	16	-	89849415	89849510
230585581	chr16	89858286	89858449	89858307	89858427	FANCA	NM_000135	1	43	13	-	89858335	89858476
230809211	chr16	89862365	89862504	89862388	89862483	FANCA	NM_000135	1	43	11	-	89862314	89862426
229068919	chr16	89869625	89869799	89869645	89869771	FANCA	NM_000135	1	43	8	-	89869667	89869749
229068919	chr16	89869625	89869799	89869645	89869771	FANCA	NM_001018112	2	11	8	-	89869667	89869749
230334334	chr16	89877034	89877200	89877055	89877172	FANCA	NM_000135	1	43	5	-	89877115	89877210
230334334	chr16	89877034	89877200	89877055	89877172	FANCA	NM_001018112	2	11	5	-	89877115	89877210
328565829	chr16	89880817	89880987	89880838	89880962	FANCA	NM_000135	1	43	3	-	89880928	89881021
328565829	chr16	89880817	89880987	89880838	89880962	FANCA	NM_001018112	2	11	3	-	89880928	89881021
240312479	chr17	5418038	5418188	5418058	5418168	NLRP1	NM_014922	2	16	16	-	5417438	5418393
240312479	chr17	5418038	5418188	5418058	5418168	NLRP1	NM_033007	5	15	15	-	5417438	5418393
240312479	chr17	5418038	5418188	5418058	5418168	NLRP1	NM_033006	4	16	16	-	5417438	5418393
240312479	chr17	5418038	5418188	5418058	5418168	NLRP1	NM_033004	3	17	17	-	5417438	5418393
241279252	chr17	5420998	5421172	5421022	5421150	NLRP1	NM_014922	2	16	14	-	5421066	5421207
241279252	chr17	5420998	5421172	5421022	5421150	NLRP1	NM_001033053	1	16	15	-	5421066	5421207
241279252	chr17	5420998	5421172	5421022	5421150	NLRP1	NM_033007	5	15	13	-	5421066	5421207
241279252	chr17	5420998	5421172	5421022	5421150	NLRP1	NM_033006	4	16	14	-	5421066	5421207
241279252	chr17	5420998	5421172	5421022	5421150	NLRP1	NM_033004	3	17	15	-	5421066	5421207
236741237	chr17	5424749	5424886	5424771	5424864	NLRP1	NM_014922	2	16	13	-	5424844	5425106
236741237	chr17	5424749	5424886	5424771	5424864	NLRP1	NM_001033053	1	16	13	-	5424844	5425106
236741237	chr17	5424749	5424886	5424771	5424864	NLRP1	NM_033007	5	15	12	-	5424844	5425106
236741237	chr17	5424749	5424886	5424771	5424864	NLRP1	NM_033006	4	16	12	-	5424844	5425106
236741237	chr17	5424749	5424886	5424771	5424864	NLRP1	NM_033004	3	17	13	-	5424844	5425106
236167611	chr17	5433904	5434050	5433925	5434029	NLRP1	NM_014922	2	16	12	-	5433801	5434024
236167611	chr17	5433904	5434050	5433925	5434029	NLRP1	NM_001033053	1	16	12	-	5433801	5434024

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236167611	chr17	5433904	5434050	5433925	5434029	NLRP1	NM_033007	5	15	11	-	5433801	5434024
236167611	chr17	5433904	5434050	5433925	5434029	NLRP1	NM_033006	4	16	11	-	5433801	5434024
236167611	chr17	5433904	5434050	5433925	5434029	NLRP1	NM_033004	3	17	12	-	5433801	5434024
238117364	chr17	5437195	5437345	5437216	5437317	NLRP1	NM_014922	2	16	9	-	5437217	5437308
238117364	chr17	5437195	5437345	5437216	5437317	NLRP1	NM_001033053	1	16	9	-	5437217	5437308
238117364	chr17	5437195	5437345	5437216	5437317	NLRP1	NM_033007	5	15	8	-	5437217	5437308
238117364	chr17	5437195	5437345	5437216	5437317	NLRP1	NM_033006	4	16	8	-	5437217	5437308
238117364	chr17	5437195	5437345	5437216	5437317	NLRP1	NM_033004	3	17	9	-	5437217	5437308
237949576	chr17	5445087	5445254	5445110	5445234	NLRP1	NM_014922	2	16	6	-	5445177	5445347
237949576	chr17	5445087	5445254	5445110	5445234	NLRP1	NM_001033053	1	16	6	-	5445177	5445347
237949576	chr17	5445087	5445254	5445110	5445234	NLRP1	NM_033007	5	15	6	-	5445177	5445347
237949576	chr17	5445087	5445254	5445110	5445234	NLRP1	NM_033006	4	16	6	-	5445177	5445347
237949576	chr17	5445087	5445254	5445110	5445234	NLRP1	NM_033004	3	17	6	-	5445177	5445347
242578052	chr17	5461595	5461766	5461614	5461742	NLRP1	NM_014922	2	16	4	-	5461659	5463363
242578052	chr17	5461595	5461766	5461614	5461742	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
242578052	chr17	5461595	5461766	5461614	5461742	NLRP1	NM_033007	5	15	4	-	5461659	5463363
242578052	chr17	5461595	5461766	5461614	5461742	NLRP1	NM_033006	4	16	4	-	5461659	5463363
242578052	chr17	5461595	5461766	5461614	5461742	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237462561	chr17	5462092	5462265	5462117	5462243	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237462561	chr17	5462092	5462265	5462117	5462243	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237462561	chr17	5462092	5462265	5462117	5462243	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237462561	chr17	5462092	5462265	5462117	5462243	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237462561	chr17	5462092	5462265	5462117	5462243	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237521999	chr17	5462555	5462680	5462577	5462656	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237521999	chr17	5462555	5462680	5462577	5462656	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237521999	chr17	5462555	5462680	5462577	5462656	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237521999	chr17	5462555	5462680	5462577	5462656	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237521999	chr17	5462555	5462680	5462577	5462656	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237741017	chr17	5462991	5463143	5463013	5463122	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237741017	chr17	5462991	5463143	5463013	5463122	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237741017	chr17	5462991	5463143	5463013	5463122	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237741017	chr17	5462991	5463143	5463013	5463122	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237741017	chr17	5462991	5463143	5463013	5463122	NLRP1	NM_033004	3	17	4	-	5461659	5463363
235645150	chr17	5485236	5485384	5485255	5485360	NLRP1	NM_014922	2	16	3	-	5485179	5485382
235645150	chr17	5485236	5485384	5485255	5485360	NLRP1	NM_001033053	1	16	3	-	5485179	5485382
235645150	chr17	5485236	5485384	5485255	5485360	NLRP1	NM_033007	5	15	3	-	5485179	5485382
235645150	chr17	5485236	5485384	5485255	5485360	NLRP1	NM_033006	4	16	3	-	5485179	5485382
235645150	chr17	5485236	5485384	5485255	5485360	NLRP1	NM_033004	3	17	3	-	5485179	5485382
235918954	chr17	5487092	5487250	5487113	5487226	NLRP1	NM_014922	2	16	1	-	5487007	5487832
235918954	chr17	5487092	5487250	5487113	5487226	NLRP1	NM_001033053	1	16	1	-	5487007	5487832
235918954	chr17	5487092	5487250	5487113	5487226	NLRP1	NM_033007	5	15	1	-	5487007	5487832

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235918954	chr17	5487092	5487250	5487113	5487226	NLRP1	NM_033006	4	16	1	-	5487007	5487832
235918954	chr17	5487092	5487250	5487113	5487226	NLRP1	NM_033004	3	17	1	-	5487007	5487832
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126117	7	8	7	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126116	6	8	7	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126113	3	12	11	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_000546	1	11	10	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126118	8	10	9	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126114	4	12	11	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126112	2	11	10	-	7573927	7574033
326843856	chr17	7573864	7574036	7573887	7574019	TP53	NM_001126115	5	7	6	-	7573927	7574033
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126117	7	8	4	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126116	6	8	4	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126113	3	12	8	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_000546	1	11	8	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126118	8	10	7	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126114	4	12	8	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126112	2	11	8	-	7577019	7577155
261669586	chr17	7577067	7577218	7577089	7577196	TP53	NM_001126115	5	7	4	-	7577019	7577155
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126117	7	8	2	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126116	6	8	2	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126113	3	12	6	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_000546	1	11	6	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126118	8	10	5	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126114	4	12	6	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126112	2	11	6	-	7578177	7578289
262347540	chr17	7578196	7578320	7578220	7578298	TP53	NM_001126115	5	7	2	-	7578177	7578289
263769320	chr17	7579366	7579535	7579386	7579512	TP53	NM_001126113	3	12	4	-	7579312	7579590
263769320	chr17	7579366	7579535	7579386	7579512	TP53	NM_000546	1	11	4	-	7579312	7579590
263769320	chr17	7579366	7579535	7579386	7579512	TP53	NM_001126118	8	10	3	-	7579312	7579590
263769320	chr17	7579366	7579535	7579386	7579512	TP53	NM_001126114	4	12	4	-	7579312	7579590
263769320	chr17	7579366	7579535	7579386	7579512	TP53	NM_001126112	2	11	4	-	7579312	7579590
239251433	chr17	8044310	8044484	8044336	8044463	PER1	NM_002616	1	23	23	-	8043788	8044658
236321132	chr17	8045191	8045365	8045211	8045342	PER1	NM_002616	1	23	22	-	8045123	8045273
236751142	chr17	8046067	8046226	8046085	8046204	PER1	NM_002616	1	23	20	-	8045967	8046153
237932183	chr17	8046835	8047009	8046857	8046988	PER1	NM_002616	1	23	19	-	8046584	8047194
237540516	chr17	8047977	8048121	8047999	8048103	PER1	NM_002616	1	23	18	-	8048069	8048311
234920036	chr17	8049315	8049483	8049337	8049461	PER1	NM_002616	1	23	17	-	8049276	8049455
237296461	chr17	8049979	8050131	8049999	8050108	PER1	NM_002616	1	23	15	-	8049912	8050083
238160464	chr17	8050766	8050922	8050786	8050898	PER1	NM_002616	1	23	12	-	8050788	8050896
239396320	chr17	8051201	8051340	8051221	8051319	PER1	NM_002616	1	23	10	-	8051315	8051421
235248469	chr17	8052020	8052146	8052041	8052121	PER1	NM_002616	1	23	8	-	8051962	8052104

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237445936	chr17	8052921	8053093	8052944	8053069	PER1	NM_002616	1	23	6	-	8052780	8052981
237012448	chr17	8053373	8053497	8053394	8053476	PER1	NM_002616	1	23	4	-	8053289	8053443
236703185	chr17	8053855	8054026	8053879	8054006	PER1	NM_002616	1	23	2	-	8053750	8054163
272109048	chr17	8108403	8108575	8108425	8108553	AURKB	NM_004217	1	9	8	-	8108534	8108708
272538217	chr17	8109843	8110001	8109864	8109978	AURKB	NM_004217	1	9	7	-	8109809	8109957
269866011	chr17	8110481	8110617	8110502	8110595	AURKB	NM_004217	1	9	5	-	8110494	8110685
270875825	chr17	8113365	8113538	8113385	8113516	AURKB	NM_004217	1	9	2	-	8113495	8113567
233289315	chr17	11958211	11958349	11958236	11958322	MAP2K4	NM_003010	1	11	2	+	11958206	11958308
231237397	chr17	11998794	11998960	11998819	11998932	MAP2K4	NM_003010	1	11	4	+	11998892	11999011
233415381	chr17	12013593	12013749	12013615	12013721	MAP2K4	NM_003010	1	11	6	+	12013692	12013743
233356106	chr17	12028541	12028715	12028565	12028688	MAP2K4	NM_003010	1	11	8	+	12028611	12028688
232637182	chr17	12043156	12043283	12043181	12043261	MAP2K4	NM_003010	1	11	10	+	12043156	12043201
228487585	chr17	17117042	17117201	17117065	17117173	FLCN	NM_144997	2	14	14	-	17115527	17117170
227624711	chr17	17118498	17118653	17118516	17118633	FLCN	NM_144997	2	14	12	-	17118499	17118630
229332805	chr17	17122291	17122462	17122312	17122439	FLCN	NM_144997	2	14	9	-	17122333	17122523
227429471	chr17	17124779	17124953	17124799	17124933	FLCN	NM_144606	1	8	8	-	17124485	17124942
227429471	chr17	17124779	17124953	17124799	17124933	FLCN	NM_144997	2	14	8	-	17124851	17124942
227304677	chr17	17127303	17127429	17127326	17127409	FLCN	NM_144997	2	14	6	-	17127236	17127457
227304677	chr17	17127303	17127429	17127326	17127409	FLCN	NM_144606	1	8	6	-	17127236	17127457
227937469	chr17	17131157	17131315	17131178	17131292	FLCN	NM_144997	2	14	4	-	17131203	17131475
227937469	chr17	17131157	17131315	17131178	17131292	FLCN	NM_144606	1	8	4	-	17131203	17131475
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_000267	1	57	1	+	29421945	29422387
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_001128147	3	15	1	+	29421945	29422387
258121305	chr17	29422337	29422461	29422354	29422441	NF1	NM_001042492	2	58	1	+	29421945	29422387
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_000267	1	57	4	+	29490204	29490394
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_001128147	3	15	4	+	29490204	29490394
236474471	chr17	29490204	29490354	29490232	29490328	NF1	NM_001042492	2	58	4	+	29490204	29490394
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_000267	1	57	6	+	29508440	29508507
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_001128147	3	15	6	+	29508440	29508507
240266483	chr17	29508477	29508623	29508505	29508593	NF1	NM_001042492	2	58	6	+	29508440	29508507
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_000267	1	57	9	+	29527440	29527613
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_001128147	3	15	9	+	29527440	29527613
235100920	chr17	29527340	29527500	29527370	29527479	NF1	NM_001042492	2	58	9	+	29527440	29527613
258489720	chr17	29527941	29528103	29527963	29528084	NF1	NM_000267	1	57	10	+	29528055	29528177
258489720	chr17	29527941	29528103	29527963	29528084	NF1	NM_001128147	3	15	10	+	29528055	29528177
258489720	chr17	29527941	29528103	29527963	29528084	NF1	NM_001042492	2	58	10	+	29528055	29528177
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_000267	1	57	11	+	29528429	29528503
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_001128147	3	15	11	+	29528429	29528503
236499063	chr17	29528436	29528604	29528462	29528578	NF1	NM_001042492	2	58	11	+	29528429	29528503
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_000267	1	57	14	+	29546023	29546136
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_001128147	3	15	14	+	29546023	29546136

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237167296	chr17	29546015	29546150	29546039	29546126	NF1	NM_001042492	2	58	14	+	29546023	29546136
237215886	chr17	29552023	29552172	29552049	29552145	NF1	NM_000267	1	57	17	+	29552113	29552268
237215886	chr17	29552023	29552172	29552049	29552145	NF1	NM_001042492	2	58	17	+	29552113	29552268
236072083	chr17	29553623	29553752	29553648	29553731	NF1	NM_000267	1	57	18	+	29553453	29553702
236072083	chr17	29553623	29553752	29553648	29553731	NF1	NM_001042492	2	58	18	+	29553453	29553702
236363213	chr17	29556046	29556214	29556069	29556193	NF1	NM_000267	1	57	21	+	29556043	29556483
236363213	chr17	29556046	29556214	29556069	29556193	NF1	NM_001042492	2	58	21	+	29556043	29556483
236397974	chr17	29556411	29556546	29556439	29556516	NF1	NM_000267	1	57	21	+	29556043	29556483
236397974	chr17	29556411	29556546	29556439	29556516	NF1	NM_001042492	2	58	21	+	29556043	29556483
239102154	chr17	29557800	29557937	29557823	29557910	NF1	NM_000267	1	57	24	+	29557860	29557943
239102154	chr17	29557800	29557937	29557823	29557910	NF1	NM_001042492	2	58	24	+	29557860	29557943
236227630	chr17	29559739	29559881	29559764	29559857	NF1	NM_000267	1	57	26	+	29559718	29559899
236227630	chr17	29559739	29559881	29559764	29559857	NF1	NM_001042492	2	58	26	+	29559718	29559899
239144275	chr17	29562585	29562733	29562611	29562705	NF1	NM_000267	1	57	28	+	29562629	29562790
239144275	chr17	29562585	29562733	29562611	29562705	NF1	NM_001042492	2	58	28	+	29562629	29562790
242686025	chr17	29575883	29576048	29575906	29576028	NF1	NM_000267	1	57	30	+	29576002	29576137
242686025	chr17	29575883	29576048	29575906	29576028	NF1	NM_001042492	2	58	30	+	29576002	29576137
235370584	chr17	29585286	29585431	29585314	29585404	NF1	NM_000267	1	57	31	+	29585362	29585520
235370584	chr17	29585286	29585431	29585314	29585404	NF1	NM_001042492	2	58	32	+	29585362	29585520
237203200	chr17	29586052	29586176	29586080	29586152	NF1	NM_000267	1	57	32	+	29586050	29586147
237203200	chr17	29586052	29586176	29586080	29586152	NF1	NM_001042492	2	58	33	+	29586050	29586147
236401388	chr17	29588750	29588924	29588775	29588896	NF1	NM_000267	1	57	34	+	29588729	29588875
236401388	chr17	29588750	29588924	29588775	29588896	NF1	NM_001042492	2	58	35	+	29588729	29588875
239268489	chr17	29652823	29652960	29652851	29652940	NF1	NM_000267	1	57	36	+	29652838	29653270
239268489	chr17	29652823	29652960	29652851	29652940	NF1	NM_001042492	2	58	37	+	29652838	29653270
239712250	chr17	29654484	29654654	29654503	29654629	NF1	NM_000267	1	57	37	+	29654517	29654857
239712250	chr17	29654484	29654654	29654503	29654629	NF1	NM_001042492	2	58	38	+	29654517	29654857
242446520	chr17	29657203	29657353	29657236	29657325	NF1	NM_000267	1	57	38	+	29657314	29657516
242446520	chr17	29657203	29657353	29657236	29657325	NF1	NM_001042492	2	58	39	+	29657314	29657516
258370730	chr17	29661816	29661940	29661844	29661913	NF1	NM_000267	1	57	39	+	29661856	29662049
258370730	chr17	29661816	29661940	29661844	29661913	NF1	NM_001042492	2	58	40	+	29661856	29662049
238336948	chr17	29663441	29663615	29663465	29663589	NF1	NM_000267	1	57	40	+	29663351	29663491
238336948	chr17	29663441	29663615	29663465	29663589	NF1	NM_001042492	2	58	41	+	29663351	29663491
239206598	chr17	29664348	29664479	29664381	29664455	NF1	NM_000267	1	57	42	+	29664386	29664600
239206598	chr17	29664348	29664479	29664381	29664455	NF1	NM_001042492	2	58	43	+	29664386	29664600
239663045	chr17	29664869	29665028	29664891	29665000	NF1	NM_000267	1	57	43	+	29664837	29664898
239663045	chr17	29664869	29665028	29664891	29665000	NF1	NM_001042492	2	58	44	+	29664837	29664898
237659175	chr17	29667567	29667697	29667588	29667671	NF1	NM_000267	1	57	46	+	29667523	29667663
237659175	chr17	29667567	29667697	29667588	29667671	NF1	NM_001042492	2	58	47	+	29667523	29667663
235996736	chr17	29676144	29676269	29676167	29676250	NF1	NM_000267	1	57	48	+	29676138	29676269
235996736	chr17	29676144	29676269	29676167	29676250	NF1	NM_001042492	2	58	49	+	29676138	29676269

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237980984	chr17	29679170	29679344	29679198	29679323	NF1	NM_000267	1	57	50	+	29679275	29679432
237980984	chr17	29679170	29679344	29679198	29679323	NF1	NM_001042492	2	58	51	+	29679275	29679432
235938569	chr17	29683477	29683602	29683505	29683574	NF1	NM_000267	1	57	51	+	29683478	29683600
235938569	chr17	29683477	29683602	29683505	29683574	NF1	NM_001042492	2	58	52	+	29683478	29683600
241695176	chr17	29684188	29684330	29684220	29684302	NF1	NM_000267	1	57	53	+	29684287	29684387
241695176	chr17	29684188	29684330	29684220	29684302	NF1	NM_001042492	2	58	54	+	29684287	29684387
236222301	chr17	29685975	29686114	29686003	29686086	NF1	NM_000267	1	57	55	+	29685987	29686033
236222301	chr17	29685975	29686114	29686003	29686086	NF1	NM_001042492	2	58	56	+	29685987	29686033
258106547	chr17	29701131	29701294	29701153	29701267	NF1	NM_000267	1	57	57	+	29701031	29704695
258106547	chr17	29701131	29701294	29701153	29701267	NF1	NM_001042492	2	58	58	+	29701031	29704695
274635715	chr17	37618573	37618739	37618593	37618717	CDK12	NM_016507	2	14	1	+	37617739	37619370
274635715	chr17	37618573	37618739	37618593	37618717	CDK12	NM_015083	1	14	1	+	37617739	37619370
274648232	chr17	37619038	37619187	37619059	37619168	CDK12	NM_016507	2	14	1	+	37617739	37619370
274648232	chr17	37619038	37619187	37619059	37619168	CDK12	NM_015083	1	14	1	+	37617739	37619370
274397103	chr17	37627209	37627366	37627230	37627341	CDK12	NM_016507	2	14	2	+	37627132	37628016
274397103	chr17	37627209	37627366	37627230	37627341	CDK12	NM_015083	1	14	2	+	37627132	37628016
273498592	chr17	37627598	37627764	37627622	37627742	CDK12	NM_016507	2	14	2	+	37627132	37628016
273498592	chr17	37627598	37627764	37627622	37627742	CDK12	NM_015083	1	14	2	+	37627132	37628016
273618289	chr17	37646719	37646893	37646746	37646872	CDK12	NM_016507	2	14	3	+	37646810	37646986
273618289	chr17	37646719	37646893	37646746	37646872	CDK12	NM_015083	1	14	3	+	37646810	37646986
274447625	chr17	37650689	37650859	37650711	37650833	CDK12	NM_016507	2	14	5	+	37650777	37650947
274447625	chr17	37650689	37650859	37650711	37650833	CDK12	NM_015083	1	14	5	+	37650777	37650947
274594084	chr17	37657606	37657750	37657633	37657723	CDK12	NM_016507	2	14	6	+	37657503	37657692
274594084	chr17	37657606	37657750	37657633	37657723	CDK12	NM_015083	1	14	6	+	37657503	37657692
273220086	chr17	37671872	37672042	37671898	37672017	CDK12	NM_016507	2	14	9	+	37671984	37672061
273220086	chr17	37671872	37672042	37671898	37672017	CDK12	NM_015083	1	14	9	+	37671984	37672061
274042172	chr17	37676228	37676394	37676253	37676374	CDK12	NM_016507	2	14	11	+	37676209	37676340
274042172	chr17	37676228	37676394	37676253	37676374	CDK12	NM_015083	1	14	11	+	37676209	37676340
273926655	chr17	37682204	37682354	37682225	37682331	CDK12	NM_016507	2	14	13	+	37682117	37682569
273926655	chr17	37682204	37682354	37682225	37682331	CDK12	NM_015083	1	14	13	+	37682117	37682569
274031774	chr17	37686865	37687017	37686889	37686994	CDK12	NM_016507	2	14	14	+	37686857	37690800
274031774	chr17	37686865	37687017	37686889	37686994	CDK12	NM_015083	1	14	14	+	37686884	37690800
274035281	chr17	37687347	37687520	37687368	37687500	CDK12	NM_016507	2	14	14	+	37686857	37690800
274035281	chr17	37687347	37687520	37687368	37687500	CDK12	NM_015083	1	14	14	+	37686884	37690800
298907602	chr17	37829303	37829435	37829325	37829417	PGAP3	NM_033419	1	8	7	-	37829304	37829508
299092715	chr17	37830199	37830352	37830218	37830333	PGAP3	NM_033419	1	8	5	-	37830246	37830307
299102593	chr17	37840906	37841031	37840925	37841007	PGAP3	NM_033419	1	8	3	-	37840850	37841002
299067593	chr17	37844168	37844329	37844186	37844307	PGAP3	NM_033419	1	8	1	-	37844087	37844310
229715479	chr17	37864541	37864714	37864563	37864693	ERBB2	NM_004448	2	27	3	+	37864574	37864787
229715479	chr17	37864541	37864714	37864563	37864693	ERBB2	NM_001005862	1	30	6	+	37864574	37864787
229114711	chr17	37866035	37866206	37866056	37866183	ERBB2	NM_004448	2	27	5	+	37866066	37866134

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229114711	chr17	37866035	37866206	37866056	37866183	ERBB2	NM_001005862	1	30	8	+	37866066	37866134
230699580	chr17	37868145	37868279	37868167	37868258	ERBB2	NM_004448	2	27	8	+	37868181	37868300
230699580	chr17	37868145	37868279	37868167	37868258	ERBB2	NM_001005862	1	30	11	+	37868181	37868300
228406832	chr17	37871486	37871614	37871507	37871591	ERBB2	NM_004448	2	27	10	+	37871539	37871612
228406832	chr17	37871486	37871614	37871507	37871591	ERBB2	NM_001005862	1	30	13	+	37871539	37871612
228394314	chr17	37872086	37872212	37872107	37872192	ERBB2	NM_004448	2	27	12	+	37871993	37872192
228394314	chr17	37872086	37872212	37872107	37872192	ERBB2	NM_001005862	1	30	15	+	37871993	37872192
227880055	chr17	37873599	37873757	37873622	37873735	ERBB2	NM_004448	2	27	15	+	37873573	37873733
227880055	chr17	37873599	37873757	37873622	37873735	ERBB2	NM_001005862	1	30	18	+	37873573	37873733
229249824	chr17	37879687	37879858	37879707	37879836	ERBB2	NM_004448	2	27	18	+	37879791	37879913
229249824	chr17	37879687	37879858	37879707	37879836	ERBB2	NM_001005862	1	30	21	+	37879791	37879913
229249824	chr17	37879687	37879858	37879707	37879836	ERBB2	NM_004448	2	27	17	+	37879572	37879710
229249824	chr17	37879687	37879858	37879707	37879836	ERBB2	NM_001005862	1	30	20	+	37879572	37879710
232572207	chr17	37881054	37881227	37881075	37881206	ERBB2	NM_004448	2	27	20	+	37880979	37881164
232572207	chr17	37881054	37881227	37881075	37881206	ERBB2	NM_001005862	1	30	23	+	37880979	37881164
230419342	chr17	37881624	37881765	37881645	37881745	ERBB2	NM_004448	2	27	22	+	37881580	37881655
230419342	chr17	37881624	37881765	37881645	37881745	ERBB2	NM_001005862	1	30	25	+	37881580	37881655
232152124	chr17	37882709	37882879	37882730	37882858	ERBB2	NM_004448	2	27	24	+	37882815	37882912
232152124	chr17	37882709	37882879	37882730	37882858	ERBB2	NM_001005862	1	30	27	+	37882815	37882912
230192486	chr17	37883496	37883665	37883516	37883644	ERBB2	NM_004448	2	27	26	+	37883548	37883800
230192486	chr17	37883496	37883665	37883516	37883644	ERBB2	NM_001005862	1	30	29	+	37883548	37883800
231061093	chr17	37884039	37884211	37884060	37884192	ERBB2	NM_004448	2	27	27	+	37883942	37884915
231061093	chr17	37884039	37884211	37884060	37884192	ERBB2	NM_001005862	1	30	30	+	37883942	37884915
260756130	chr17	38498866	38499036	38498884	38499013	RARA	NM_001024809	2	8	1	+	38498271	38499119
260967304	chr17	38505956	38506118	38505976	38506097	RARA	NM_001145301	3	9	4	+	38506036	38506177
260967304	chr17	38505956	38506118	38505976	38506097	RARA	NM_000964	1	9	4	+	38506036	38506177
260967304	chr17	38505956	38506118	38505976	38506097	RARA	NM_001024809	2	8	3	+	38506036	38506177
242277756	chr17	38508545	38508684	38508565	38508661	RARA	NM_001145302	4	7	4	+	38508583	38508759
242277756	chr17	38508545	38508684	38508565	38508661	RARA	NM_001145301	3	9	6	+	38508583	38508759
242277756	chr17	38508545	38508684	38508565	38508661	RARA	NM_000964	1	9	6	+	38508583	38508759
242277756	chr17	38508545	38508684	38508565	38508661	RARA	NM_001024809	2	8	5	+	38508583	38508759
263442726	chr17	38511495	38511662	38511514	38511639	RARA	NM_001145302	4	7	6	+	38511515	38511673
263442726	chr17	38511495	38511662	38511514	38511639	RARA	NM_001145301	3	9	8	+	38511515	38511673
263442726	chr17	38511495	38511662	38511514	38511639	RARA	NM_000964	1	9	8	+	38511515	38511673
263442726	chr17	38511495	38511662	38511514	38511639	RARA	NM_001024809	2	8	7	+	38511515	38511673
232335912	chr17	41605827	41606001	41605854	41605980	ETV4	NM_001986	2	13	13	-	41605211	41606111
232335912	chr17	41605827	41606001	41605854	41605980	ETV4	NM_001079675	1	13	13	-	41605211	41606111
232850013	chr17	41606931	41607080	41606954	41607057	ETV4	NM_001986	2	13	11	-	41606872	41607044
232850013	chr17	41606931	41607080	41606954	41607057	ETV4	NM_001079675	1	13	11	-	41606872	41607044
229771536	chr17	41610046	41610208	41610064	41610191	ETV4	NM_001986	2	13	8	-	41610042	41610307
229771536	chr17	41610046	41610208	41610064	41610191	ETV4	NM_001079675	1	13	8	-	41610042	41610307

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228704890	chr17	41611194	41611362	41611214	41611343	ETV4	NM_001986	2	13	6	-	41611227	41611353
228704890	chr17	41611194	41611362	41611214	41611343	ETV4	NM_001079675	1	13	6	-	41611227	41611353
229736596	chr17	41622613	41622785	41622633	41622766	ETV4	NM_001986	2	13	3	-	41622642	41622735
229736596	chr17	41622613	41622785	41622633	41622766	ETV4	NM_001079675	1	13	3	-	41622642	41622735
279995917	chr17	45351724	45351894	45351744	45351870	ITGB3	NM_000212	1	15	2	+	45351785	45351870
278085044	chr17	45361846	45362010	45361870	45361988	ITGB3	NM_000212	1	15	4	+	45361809	45362061
279878940	chr17	45364368	45364493	45364391	45364471	ITGB3	NM_000212	1	15	6	+	45364436	45364597
278381703	chr17	45367497	45367666	45367518	45367642	ITGB3	NM_000212	1	15	8	+	45367551	45367640
279357238	chr17	45369595	45369765	45369615	45369745	ITGB3	NM_000212	1	15	10	+	45369505	45369934
280546358	chr17	45376749	45376919	45376770	45376897	ITGB3	NM_000212	1	15	11	+	45376674	45376896
278007644	chr17	45384781	45384955	45384805	45384934	ITGB3	NM_000212	1	15	14	+	45384837	45385003
253693017	chr17	48262889	48263062	48262910	48263042	COL1A1	NM_000088	1	51	51	-	48261457	48263009
225526158	chr17	48263639	48263811	48263662	48263789	COL1A1	NM_000088	1	51	49	-	48263678	48263868
226587281	chr17	48264153	48264318	48264174	48264297	COL1A1	NM_000088	1	51	48	-	48264001	48264283
253629987	chr17	48265187	48265328	48265207	48265307	COL1A1	NM_000088	1	51	45	-	48265237	48265344
226531309	chr17	48266079	48266237	48266102	48266217	COL1A1	NM_000088	1	51	42	-	48266103	48266156
253964048	chr17	48266656	48266819	48266675	48266799	COL1A1	NM_000088	1	51	39	-	48266738	48266899
226608394	chr17	48267288	48267448	48267307	48267427	COL1A1	NM_000088	1	51	36	-	48267362	48267469
225776907	chr17	48268134	48268301	48268156	48268275	COL1A1	NM_000088	1	51	33	-	48268178	48268285
226591604	chr17	48269110	48269268	48269127	48269248	COL1A1	NM_000088	1	51	31	-	48269149	48269247
226498107	chr17	48270105	48270247	48270126	48270225	COL1A1	NM_000088	1	51	27	-	48270158	48270211
225660664	chr17	48271651	48271803	48271670	48271784	COL1A1	NM_000088	1	51	23	-	48271710	48271808
226440780	chr17	48272125	48272288	48272143	48272269	COL1A1	NM_000088	1	51	21	-	48272082	48272189
226021347	chr17	48272877	48273050	48272902	48273023	COL1A1	NM_000088	1	51	17	-	48272928	48273026
226205360	chr17	48273823	48273964	48273843	48273941	COL1A1	NM_000088	1	51	13	-	48273845	48273889
253715312	chr17	48275058	48275218	48275081	48275197	COL1A1	NM_000088	1	51	9	-	48275093	48275146
225643957	chr17	48276641	48276782	48276659	48276762	COL1A1	NM_000088	1	51	5	-	48276587	48276688
253669697	chr17	48277167	48277341	48277186	48277320	COL1A1	NM_000088	1	51	2	-	48277114	48277308
227372478	chr17	53345081	53345235	53345108	53345212	HLF	NM_002126	1	4	2	+	53345112	53345447
229404451	chr17	53392553	53392724	53392580	53392703	HLF	NM_002126	1	4	3	+	53392588	53392808
230225633	chr17	53398124	53398292	53398146	53398265	HLF	NM_002126	1	4	4	+	53398025	53402426
223438771	chr17	59760823	59760966	59760851	59760938	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223437149	chr17	59761104	59761265	59761125	59761237	BRIP1	NM_032043	1	20	20	-	59756547	59761501
222191725	chr17	59763069	59763228	59763102	59763201	BRIP1	NM_032043	1	20	19	-	59763197	59763526
223441179	chr17	59770767	59770941	59770791	59770915	BRIP1	NM_032043	1	20	18	-	59770791	59770873
223930973	chr17	59820373	59820506	59820401	59820481	BRIP1	NM_032043	1	20	16	-	59820374	59820495
222414936	chr17	59853760	59853885	59853786	59853858	BRIP1	NM_032043	1	20	14	-	59853762	59853923
222595304	chr17	59858242	59858396	59858271	59858368	BRIP1	NM_032043	1	20	12	-	59858201	59858366
222454752	chr17	59870977	59871140	59871001	59871114	BRIP1	NM_032043	1	20	10	-	59870958	59871090
223941064	chr17	59878647	59878795	59878675	59878769	BRIP1	NM_032043	1	20	8	-	59878614	59878835
223680961	chr17	59885911	59886074	59885937	59886046	BRIP1	NM_032043	1	20	7	-	59885828	59886118

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224744628	chr17	59926549	59926703	59926576	59926676	BRIP1	NM_032043	1	20	5	-	59926490	59926617
224415366	chr17	59937197	59937368	59937220	59937340	BRIP1	NM_032043	1	20	3	-	59937157	59937268
227030577	chr17	62006604	62006745	62006627	62006723	CD79B	NM_000626	1	6	6	-	62006098	62006684
227030577	chr17	62006604	62006745	62006627	62006723	CD79B	NM_021602	3	5	5	-	62006098	62006684
227030577	chr17	62006604	62006745	62006627	62006723	CD79B	NM_001039933	2	6	6	-	62006098	62006684
227070807	chr17	62007352	62007516	62007373	62007492	CD79B	NM_000626	1	6	3	-	62007434	62007745
227070807	chr17	62007352	62007516	62007373	62007492	CD79B	NM_001039933	2	6	3	-	62007434	62007745
225662516	chr17	62008677	62008830	62008694	62008809	CD79B	NM_001039933	2	6	2	-	62008695	62008748
225662516	chr17	62008677	62008830	62008694	62008809	CD79B	NM_000626	1	6	2	-	62008695	62008745
225662516	chr17	62008677	62008830	62008694	62008809	CD79B	NM_021602	3	5	2	-	62008695	62008745
236776767	chr17	66511630	66511761	66511656	66511735	PRKAR1A	NM_002734	1	11	2	+	66511535	66511717
236776767	chr17	66511630	66511761	66511656	66511735	PRKAR1A	NM_212472	3	11	2	+	66511535	66511717
236776767	chr17	66511630	66511761	66511656	66511735	PRKAR1A	NM_212471	2	11	2	+	66511535	66511717
236543106	chr17	66519877	66520007	66519900	66519979	PRKAR1A	NM_002734	1	11	4	+	66519866	66519957
236543106	chr17	66519877	66520007	66519900	66519979	PRKAR1A	NM_212472	3	11	4	+	66519866	66519957
236543106	chr17	66519877	66520007	66519900	66519979	PRKAR1A	NM_212471	2	11	4	+	66519866	66519957
235356758	chr17	66524964	66525092	66524992	66525069	PRKAR1A	NM_002734	1	11	9	+	66525011	66525132
235356758	chr17	66524964	66525092	66524992	66525069	PRKAR1A	NM_212472	3	11	9	+	66525011	66525132
235356758	chr17	66524964	66525092	66524992	66525069	PRKAR1A	NM_212471	2	11	9	+	66525011	66525132
236287132	chr17	66526524	66526650	66526545	66526627	PRKAR1A	NM_002734	1	11	11	+	66526418	66528910
236287132	chr17	66526524	66526650	66526545	66526627	PRKAR1A	NM_212472	3	11	11	+	66526418	66528910
236287132	chr17	66526524	66526650	66526545	66526627	PRKAR1A	NM_212471	2	11	11	+	66526418	66528910
238949359	chr17	75369458	75369630	75369475	75369607	SEPT9	NM_001113493	3	11	1	+	75369272	75369634
264720895	chr17	75398383	75398552	75398402	75398535	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264720895	chr17	75398383	75398552	75398402	75398535	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264720895	chr17	75398383	75398552	75398402	75398535	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264720895	chr17	75398383	75398552	75398402	75398535	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264720895	chr17	75398383	75398552	75398402	75398535	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
242658095	chr17	75471491	75471626	75471512	75471605	SEPT9	NM_001113495	5	10	1	+	75471325	75471985
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_006640	7	11	3	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113496	6	10	2	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113495	5	10	2	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113494	4	11	3	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113493	3	11	3	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113492	2	12	4	+	75478226	75478417
240845699	chr17	75478196	75478342	75478219	75478323	SEPT9	NM_001113491	1	12	4	+	75478226	75478417
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_006640	7	11	5	+	75484322	75484403
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113496	6	10	4	+	75484322	75484403
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113495	5	10	4	+	75484322	75484403
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113494	4	11	5	+	75484322	75484403
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113493	3	11	5	+	75484322	75484403

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113492	2	12	6	+	75484322	75484403
239435289	chr17	75484203	75484373	75484224	75484351	SEPT9	NM_001113491	1	12	6	+	75484322	75484403
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_006640	7	11	7	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113496	6	10	6	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113495	5	10	6	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113494	4	11	7	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113493	3	11	7	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113492	2	12	8	+	75486824	75486941
261929876	chr17	75486791	75486965	75486811	75486942	SEPT9	NM_001113491	1	12	8	+	75486824	75486941
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_006640	7	11	10	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113496	6	10	9	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113495	5	10	9	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113494	4	11	10	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113493	3	11	10	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113492	2	12	11	+	75493397	75493448
241654465	chr17	75493348	75493509	75493369	75493490	SEPT9	NM_001113491	1	12	11	+	75493397	75493448
295357206	chr17	76210437	76210577	76210456	76210559	BIRC5	NM_001168	3	4	1	+	76210277	76210508
295357206	chr17	76210437	76210577	76210456	76210559	BIRC5	NM_001012271	2	5	1	+	76210277	76210508
295357206	chr17	76210437	76210577	76210456	76210559	BIRC5	NM_001012270	1	3	1	+	76210277	76210508
293724669	chr17	76219507	76219681	76219531	76219662	BIRC5	NM_001168	3	4	4	+	76219546	76221716
293724669	chr17	76219507	76219681	76219531	76219662	BIRC5	NM_001012271	2	5	5	+	76219546	76221716
293724669	chr17	76219507	76219681	76219531	76219662	BIRC5	NM_001012270	1	3	3	+	76219546	76221716
241003926	chr17	78247016	78247184	78247037	78247164	RNF213	NM_020954	2	17	3	+	78247040	78247203
241003926	chr17	78247016	78247184	78247037	78247164	RNF213	NM_001256071	1	68	3	+	78247040	78247203
263722695	chr17	78261501	78261670	78261520	78261649	RNF213	NM_020954	2	17	4	+	78261614	78262162
263722695	chr17	78261501	78261670	78261520	78261649	RNF213	NM_001256071	1	68	4	+	78261614	78262162
263745509	chr17	78261906	78262072	78261926	78262053	RNF213	NM_020954	2	17	4	+	78261614	78262162
263745509	chr17	78261906	78262072	78261926	78262053	RNF213	NM_001256071	1	68	4	+	78261614	78262162
237882152	chr17	78263500	78263645	78263527	78263623	RNF213	NM_020954	2	17	6	+	78263458	78263636
237882152	chr17	78263500	78263645	78263527	78263623	RNF213	NM_001256071	1	68	6	+	78263458	78263636
238502596	chr17	78265316	78265475	78265339	78265453	RNF213	NM_020954	2	17	8	+	78265427	78265626
238502596	chr17	78265316	78265475	78265339	78265453	RNF213	NM_001256071	1	68	8	+	78265427	78265626
241622028	chr17	78268553	78268724	78268574	78268703	RNF213	NM_020954	2	17	9	+	78268519	78268802
241622028	chr17	78268553	78268724	78268574	78268703	RNF213	NM_001256071	1	68	9	+	78268519	78268802
242478303	chr17	78269552	78269705	78269572	78269677	RNF213	NM_020954	2	17	10	+	78269357	78269613
242478303	chr17	78269552	78269705	78269572	78269677	RNF213	NM_001256071	1	68	10	+	78269357	78269613
241653498	chr17	78280133	78280294	78280156	78280274	RNF213	NM_020954	2	17	12	+	78280052	78280268
241653498	chr17	78280133	78280294	78280156	78280274	RNF213	NM_001256071	1	68	12	+	78280052	78280268
241743680	chr17	78286780	78286935	78286801	78286907	RNF213	NM_020954	2	17	15	+	78286812	78286967
241743680	chr17	78286780	78286935	78286801	78286907	RNF213	NM_001256071	1	68	15	+	78286812	78286967
238324782	chr17	78293022	78293188	78293045	78293166	RNF213	NM_001256071	1	68	17	+	78292990	78293112

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238324782	chr17	78293022	78293188	78293045	78293166	RNF213	NM_020954	2	17	17	+	78292990	78295262
239852045	chr17	78301533	78301705	78301557	78301681	RNF213	NM_001256071	1	68	19	+	78301616	78301789
263910382	chr17	78305688	78305849	78305709	78305827	RNF213	NM_001256071	1	68	21	+	78305806	78306431
264042734	chr17	78306176	78306338	78306196	78306314	RNF213	NM_001256071	1	68	21	+	78305806	78306431
264481507	chr17	78309919	78310081	78309940	78310061	RNF213	NM_001256071	1	68	23	+	78309961	78310178
240840772	chr17	78311481	78311633	78311506	78311606	RNF213	NM_001256071	1	68	24	+	78311386	78311526
263879861	chr17	78313107	78313269	78313127	78313246	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263862448	chr17	78313586	78313758	78313603	78313737	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263868042	chr17	78314031	78314175	78314049	78314157	RNF213	NM_001256071	1	68	26	+	78313001	78314156
239996493	chr17	78317743	78317884	78317767	78317858	RNF213	NM_001256071	1	68	28	+	78317657	78317815
239094877	chr17	78318727	78318896	78318750	78318873	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239045841	chr17	78319204	78319361	78319224	78319337	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262337816	chr17	78319621	78319791	78319646	78319766	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239084111	chr17	78320127	78320296	78320148	78320277	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262283259	chr17	78320627	78320799	78320646	78320781	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262331865	chr17	78321089	78321220	78321111	78321197	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262331143	chr17	78321545	78321676	78321565	78321655	RNF213	NM_001256071	1	68	29	+	78318478	78322086
238968319	chr17	78321991	78322151	78322014	78322128	RNF213	NM_001256071	1	68	29	+	78318478	78322086
242673416	chr17	78324111	78324257	78324139	78324232	RNF213	NM_001256071	1	68	31	+	78324101	78324196
241252046	chr17	78327402	78327532	78327425	78327507	RNF213	NM_001256071	1	68	34	+	78327312	78327466
264692816	chr17	78328239	78328402	78328260	78328377	RNF213	NM_001256071	1	68	36	+	78328241	78328376
238069400	chr17	78333868	78334042	78333889	78334019	RNF213	NM_001256071	1	68	38	+	78333861	78334006
260644344	chr17	78336899	78337065	78336921	78337043	RNF213	NM_001256071	1	68	40	+	78336902	78337114
264125420	chr17	78338209	78338374	78338227	78338355	RNF213	NM_001256071	1	68	42	+	78338233	78338353
240923315	chr17	78341914	78342075	78341937	78342047	RNF213	NM_001256071	1	68	44	+	78341761	78341943
240037800	chr17	78345631	78345798	78345654	78345776	RNF213	NM_001256071	1	68	47	+	78345674	78345785
241812122	chr17	78346445	78346619	78346467	78346592	RNF213	NM_001256071	1	68	48	+	78346321	78346534
240566819	chr17	78348275	78348436	78348296	78348416	RNF213	NM_001256071	1	68	50	+	78348258	78348389
238835142	chr17	78350213	78350368	78350234	78350344	RNF213	NM_001256071	1	68	52	+	78350101	78350343
264524057	chr17	78354595	78354758	78354617	78354737	RNF213	NM_001256071	1	68	56	+	78354631	78354787
239445608	chr17	78356721	78356894	78356743	78356871	RNF213	NM_001256071	1	68	58	+	78356779	78356870
239612485	chr17	78358762	78358913	78358787	78358890	RNF213	NM_001256071	1	68	60	+	78358839	78358971
239489141	chr17	78360148	78360289	78360168	78360269	RNF213	NM_001256071	1	68	62	+	78360050	78360230
241500160	chr17	78362341	78362514	78362366	78362490	RNF213	NM_001256071	1	68	64	+	78362412	78362489
242509307	chr17	78363617	78363788	78363639	78363767	RNF213	NM_001256071	1	68	66	+	78363628	78363717
240951845	chr17	78367182	78367330	78367209	78367302	RNF213	NM_001256071	1	68	68	+	78367145	78372581
263144145	chr18	22669303	22669473	22669327	22669445	ZNF521	NM_015461	1	8	7	-	22669429	22669544
266318680	chr18	22775011	22775185	22775035	22775157	ZNF521	NM_015461	1	8	5	-	22775124	22775208
241268471	chr18	22804485	22804655	22804506	22804630	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265049388	chr18	22804925	22805077	22804952	22805056	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265053900	chr18	22805384	22805553	22805412	22805527	ZNF521	NM_015461	1	8	4	-	22804309	22807661

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
265020783	chr18	22805831	22806001	22805856	22805978	ZNF521	NM_015461	1	8	4	-	22804309	22807661
264994341	chr18	22806272	22806434	22806300	22806413	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265130523	chr18	22806661	22806815	22806687	22806792	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265116526	chr18	22807125	22807297	22807147	22807276	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241286496	chr18	22807623	22807748	22807643	22807727	ZNF521	NM_015461	1	8	4	-	22804309	22807661
271812029	chr18	25532004	25532162	25532026	25532139	CDH2	NM_001792	1	16	16	-	25530930	25532323
271278610	chr18	25543387	25543545	25543407	25543516	CDH2	NM_001792	1	16	15	-	25543321	25543485
271592904	chr18	25564907	25565075	25564930	25565054	CDH2	NM_001792	1	16	13	-	25564964	25565197
270770124	chr18	25565629	25565770	25565650	25565745	CDH2	NM_001792	1	16	12	-	25565492	25565725
270530972	chr18	25570007	25570178	25570035	25570156	CDH2	NM_001792	1	16	10	-	25570061	25570314
271435109	chr18	25572677	25572833	25572697	25572808	CDH2	NM_001792	1	16	9	-	25572619	25572804
272180150	chr18	25582982	25583109	25583005	25583085	CDH2	NM_001792	1	16	7	-	25582961	25583133
270887014	chr18	25585911	25586067	25585934	25586039	CDH2	NM_001792	1	16	6	-	25585813	25585957
270529504	chr18	25591871	25591998	25591893	25591970	CDH2	NM_001792	1	16	4	-	25591810	25591956
271266554	chr18	25727652	25727795	25727675	25727769	CDH2	NM_001792	1	16	2	-	25727637	25727748
271187749	chr18	45371637	45371762	45371665	45371734	SMAD2	NM_005901	3	11	10	-	45371711	45371855
271187749	chr18	45371637	45371762	45371665	45371734	SMAD2	NM_001135937	2	10	9	-	45371711	45371855
271187749	chr18	45371637	45371762	45371665	45371734	SMAD2	NM_001003652	1	11	10	-	45371711	45371855
270014379	chr18	45372092	45372236	45372114	45372208	SMAD2	NM_005901	3	11	9	-	45372034	45372171
270014379	chr18	45372092	45372236	45372114	45372208	SMAD2	NM_001135937	2	10	8	-	45372034	45372171
270014379	chr18	45372092	45372236	45372114	45372208	SMAD2	NM_001003652	1	11	9	-	45372034	45372171
272646005	chr18	45377529	45377693	45377556	45377665	SMAD2	NM_005901	3	11	7	-	45377645	45377698
272646005	chr18	45377529	45377693	45377556	45377665	SMAD2	NM_001135937	2	10	6	-	45377645	45377698
272646005	chr18	45377529	45377693	45377556	45377665	SMAD2	NM_001003652	1	11	7	-	45377645	45377698
269819757	chr18	45394661	45394790	45394689	45394768	SMAD2	NM_005901	3	11	5	-	45394694	45394828
269819757	chr18	45394661	45394790	45394689	45394768	SMAD2	NM_001135937	2	10	4	-	45394694	45394828
269819757	chr18	45394661	45394790	45394689	45394768	SMAD2	NM_001003652	1	11	5	-	45394694	45394828
272575545	chr18	45395687	45395830	45395712	45395809	SMAD2	NM_005901	3	11	4	-	45395614	45395807
272575545	chr18	45395687	45395830	45395712	45395809	SMAD2	NM_001135937	2	10	3	-	45395614	45395807
272575545	chr18	45395687	45395830	45395712	45395809	SMAD2	NM_001003652	1	11	4	-	45395614	45395807
312522652	chr18	47793905	47794078	47793931	47794050	MBD1	NM_001204141	6	15	15	-	47793252	47794033
312522652	chr18	47793905	47794078	47793931	47794050	MBD1	NM_001204139	4	17	17	-	47793252	47794033
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_015846	13	17	14	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204137	2	17	15	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204136	1	16	14	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_015845	12	14	12	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_015844	11	16	13	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_015847	14	16	13	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204151	9	13	11	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_002384	10	15	12	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204142	7	14	13	-	47799194	47799325

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204141	6	15	13	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204140	5	16	14	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204139	4	17	14	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204138	3	17	15	-	47799194	47799325
312330096	chr18	47799176	47799348	47799193	47799326	MBD1	NM_001204143	8	14	12	-	47799194	47799325
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204138	3	17	13	-	47799934	47800230
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_015846	13	17	12	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204137	2	17	13	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204136	1	16	12	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_015845	12	14	11	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_015844	11	16	11	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_015847	14	16	11	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204151	9	13	10	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_002384	10	15	11	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204142	7	14	12	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204141	6	15	11	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204140	5	16	12	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204139	4	17	12	-	47799934	47800233
312412678	chr18	47799974	47800145	47799993	47800128	MBD1	NM_001204143	8	14	11	-	47799934	47800233
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_015846	13	17	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204137	2	17	11	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204136	1	16	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_015844	11	16	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_015847	14	16	9	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_002384	10	15	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204142	7	14	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204141	6	15	9	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204140	5	16	11	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204139	4	17	10	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204138	3	17	11	-	47801347	47801415
312383656	chr18	47801265	47801436	47801288	47801415	MBD1	NM_001204143	8	14	10	-	47801347	47801415
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_015846	13	17	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204137	2	17	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204136	1	16	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_015845	12	14	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_015844	11	16	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_015847	14	16	7	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204151	9	13	7	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_002384	10	15	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204142	7	14	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204141	6	15	7	-	47801970	47802098

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204140	5	16	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204139	4	17	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204138	3	17	8	-	47801970	47802098
312176088	chr18	47802050	47802203	47802072	47802182	MBD1	NM_001204143	8	14	8	-	47801970	47802098
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_015846	13	17	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204137	2	17	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204136	1	16	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_015845	12	14	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_015844	11	16	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_015847	14	16	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204151	9	13	4	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_002384	10	15	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204142	7	14	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204141	6	15	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204140	5	16	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204139	4	17	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204138	3	17	5	-	47803032	47803114
312377733	chr18	47802979	47803138	47802999	47803118	MBD1	NM_001204143	8	14	5	-	47803032	47803114
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_015846	13	17	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204137	2	17	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204136	1	16	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_015845	12	14	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_015844	11	16	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_015847	14	16	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204151	9	13	1	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_002384	10	15	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204142	7	14	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204141	6	15	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204140	5	16	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204139	4	17	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204138	3	17	2	-	47806253	47806387
312323690	chr18	47806221	47806395	47806241	47806374	MBD1	NM_001204143	8	14	2	-	47806253	47806387
261778873	chr18	48575051	48575223	48575069	48575196	SMAD4	NM_005359	1	12	3	+	48575056	48575230
240139242	chr18	48581162	48581331	48581189	48581308	SMAD4	NM_005359	1	12	5	+	48581151	48581363
264297447	chr18	48584679	48584853	48584703	48584826	SMAD4	NM_005359	1	12	7	+	48584710	48584826
239634238	chr18	48591792	48591931	48591814	48591909	SMAD4	NM_005359	1	12	9	+	48591793	48591976
238601985	chr18	48603006	48603138	48603029	48603114	SMAD4	NM_005359	1	12	11	+	48603008	48603146
286440423	chr18	49867137	49867261	49867157	49867238	DCC	NM_005215	1	29	1	+	49866542	49867248
287216686	chr18	50278604	50278760	50278629	50278737	DCC	NM_005215	1	29	2	+	50278424	50278744
288728137	chr18	50450048	50450178	50450075	50450153	DCC	NM_005215	1	29	4	+	50450077	50450227
286987007	chr18	50589581	50589715	50589606	50589690	DCC	NM_005215	1	29	6	+	50589675	50589829

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287231080	chr18	50683636	50683801	50683660	50683781	DCC	NM_005215	1	29	8	+	50683726	50683882
287778555	chr18	50731587	50731758	50731606	50731737	DCC	NM_005215	1	29	10	+	50731586	50731734
285501519	chr18	50741836	50741997	50741864	50741969	DCC	NM_005215	1	29	12	+	50741918	50741967
287349982	chr18	50848428	50848590	50848452	50848562	DCC	NM_005215	1	29	14	+	50848417	50848527
287842150	chr18	50912330	50912469	50912357	50912445	DCC	NM_005215	1	29	16	+	50912413	50912508
286301720	chr18	50918162	50918334	50918185	50918306	DCC	NM_005215	1	29	17	+	50918025	50918257
287040549	chr18	50936753	50936899	50936774	50936874	DCC	NM_005215	1	29	20	+	50936822	50937016
288691869	chr18	50961477	50961649	50961502	50961621	DCC	NM_005215	1	29	22	+	50961514	50961579
287046438	chr18	50985667	50985809	50985695	50985788	DCC	NM_005215	1	29	24	+	50985602	50985828
286059899	chr18	51013152	51013324	51013176	51013303	DCC	NM_005215	1	29	26	+	51013167	51013328
286828429	chr18	51025791	51025946	51025812	51025918	DCC	NM_005215	1	29	27	+	51025668	51025880
232263203	chr18	56338749	56338901	56338768	56338884	MALT1	NM_173844	2	16	1	+	56338618	56339084
232263203	chr18	56338749	56338901	56338768	56338884	MALT1	NM_006785	1	17	1	+	56338618	56339084
231499556	chr18	56348456	56348608	56348478	56348580	MALT1	NM_173844	2	16	2	+	56348402	56348568
231499556	chr18	56348456	56348608	56348478	56348580	MALT1	NM_006785	1	17	2	+	56348402	56348568
233261881	chr18	56376526	56376652	56376556	56376626	MALT1	NM_173844	2	16	5	+	56376610	56376788
233261881	chr18	56376526	56376652	56376556	56376626	MALT1	NM_006785	1	17	5	+	56376610	56376788
233852564	chr18	56377231	56377385	56377258	56377357	MALT1	NM_173844	2	16	6	+	56377208	56377304
233852564	chr18	56377231	56377385	56377258	56377357	MALT1	NM_006785	1	17	6	+	56377208	56377304
231188521	chr18	56383177	56383317	56383198	56383288	MALT1	NM_173844	2	16	8	+	56383167	56383199
231188521	chr18	56383177	56383317	56383198	56383288	MALT1	NM_006785	1	17	9	+	56383167	56383199
233956237	chr18	56400562	56400716	56400587	56400689	MALT1	NM_173844	2	16	10	+	56400629	56400806
233956237	chr18	56400562	56400716	56400587	56400689	MALT1	NM_006785	1	17	11	+	56400629	56400806
233149581	chr18	56408995	56409151	56409027	56409124	MALT1	NM_173844	2	16	13	+	56409097	56409246
233149581	chr18	56408995	56409151	56409027	56409124	MALT1	NM_006785	1	17	14	+	56409097	56409246
232296708	chr18	56411630	56411759	56411655	56411726	MALT1	NM_173844	2	16	14	+	56411570	56411727
232296708	chr18	56411630	56411759	56411655	56411726	MALT1	NM_006785	1	17	15	+	56411570	56411727
232717900	chr18	56414674	56414814	56414701	56414786	MALT1	NM_173844	2	16	16	+	56414637	56417370
232717900	chr18	56414674	56414814	56414701	56414786	MALT1	NM_006785	1	17	17	+	56414637	56417370
271372351	chr18	59157656	59157810	59157682	59157787	CDH20	NM_031891	1	11	1	+	59157775	59158032
271940283	chr18	59166496	59166660	59166515	59166632	CDH20	NM_031891	1	11	2	+	59166419	59166713
271260107	chr18	59170105	59170256	59170129	59170227	CDH20	NM_031891	1	11	4	+	59170186	59170353
271399185	chr18	59195123	59195294	59195145	59195272	CDH20	NM_031891	1	11	6	+	59195200	59195453
270277406	chr18	59203740	59203888	59203761	59203862	CDH20	NM_031891	1	11	7	+	59203726	59203862
269686489	chr18	59217187	59217359	59217208	59217338	CDH20	NM_031891	1	11	10	+	59217211	59217462
272633725	chr18	59221625	59221783	59221643	59221766	CDH20	NM_031891	1	11	11	+	59221423	59222365
223169258	chr18	60795905	60796054	60795925	60796027	BCL2	NM_000633	1	3	3	-	60790579	60795992
222786889	chr18	60985471	60985637	60985489	60985620	BCL2	NM_000633	1	3	2	-	60985315	60986185
222786889	chr18	60985471	60985637	60985489	60985620	BCL2	NM_000657	2	2	2	-	60985187	60986185
261814797	chr19	1206951	1207118	1206969	1207098	STK11	NM_000455	1	10	1	+	1205798	1207202
260221995	chr19	1219236	1219401	1219255	1219381	STK11	NM_000455	1	10	3	+	1219323	1219412

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238616212	chr19	1220501	1220675	1220519	1220657	STK11	NM_000455	1	10	5	+	1220580	1220716
240505284	chr19	1221829	1221975	1221850	1221956	STK11	NM_000455	1	10	7	+	1221948	1222005
326727288	chr19	1223122	1223265	1223145	1223244	STK11	NM_000455	1	10	8	+	1222984	1223171
240648438	chr19	1611634	1611802	1611652	1611780	TCF3	NM_003200	2	19	19	-	1609289	1611848
240648438	chr19	1611634	1611802	1611652	1611780	TCF3	NM_001136139	1	19	18	-	1611703	1611848
240003822	chr19	1612353	1612526	1612370	1612503	TCF3	NM_001136139	1	19	17	-	1612206	1612432
238564925	chr19	1615701	1615842	1615719	1615823	TCF3	NM_001136139	1	19	16	-	1615685	1615820
238564925	chr19	1615701	1615842	1615719	1615823	TCF3	NM_003200	2	19	17	-	1615685	1615820
241560861	chr19	1619346	1619484	1619364	1619466	TCF3	NM_001136139	1	19	14	-	1619315	1619473
241560861	chr19	1619346	1619484	1619364	1619466	TCF3	NM_003200	2	19	15	-	1619315	1619473
262299624	chr19	1620994	1621160	1621013	1621143	TCF3	NM_001136139	1	19	12	-	1620967	1621045
262299624	chr19	1620994	1621160	1621013	1621143	TCF3	NM_003200	2	19	13	-	1620967	1621045
262299624	chr19	1620994	1621160	1621013	1621143	TCF3	NM_001136139	1	19	11	-	1621132	1621190
262299624	chr19	1620994	1621160	1621013	1621143	TCF3	NM_003200	2	19	12	-	1621132	1621190
242042980	chr19	1622035	1622204	1622052	1622186	TCF3	NM_001136139	1	19	9	-	1622053	1622222
242042980	chr19	1622035	1622204	1622052	1622186	TCF3	NM_003200	2	19	10	-	1622053	1622222
238749069	chr19	1623862	1624025	1623883	1624001	TCF3	NM_001136139	1	19	7	-	1623950	1623999
238749069	chr19	1623862	1624025	1623883	1624001	TCF3	NM_003200	2	19	8	-	1623950	1623999
238594455	chr19	1631982	1632141	1632001	1632121	TCF3	NM_001136139	1	19	4	-	1632037	1632115
238594455	chr19	1631982	1632141	1632001	1632121	TCF3	NM_003200	2	19	5	-	1632037	1632115
239705756	chr19	1650071	1650215	1650091	1650193	TCF3	NM_001136139	1	19	1	-	1650176	1650286
239705756	chr19	1650071	1650215	1650091	1650193	TCF3	NM_003200	2	19	2	-	1650176	1650286
274029194	chr19	3110265	3110397	3110283	3110378	GNA11	NM_002067	1	7	2	+	3110147	3110331
272800257	chr19	3114950	3115124	3114967	3115104	GNA11	NM_002067	1	7	4	+	3114942	3115070
272751753	chr19	3119284	3119442	3119305	3119419	GNA11	NM_002067	1	7	6	+	3119204	3119357
299242970	chr19	3523011	3523136	3523029	3523119	FZR1	NM_016263	3	14	2	+	3522954	3523056
299242970	chr19	3523011	3523136	3523029	3523119	FZR1	NM_001136197	1	11	1	+	3522954	3523056
299242970	chr19	3523011	3523136	3523029	3523119	FZR1	NM_001136198	2	13	1	+	3522954	3523056
299006781	chr19	3526231	3526396	3526249	3526378	FZR1	NM_016263	3	14	5	+	3526257	3526384
299006781	chr19	3526231	3526396	3526249	3526378	FZR1	NM_001136197	1	11	4	+	3526257	3526384
299006781	chr19	3526231	3526396	3526249	3526378	FZR1	NM_001136198	2	13	4	+	3526257	3526384
299086156	chr19	3530760	3530910	3530779	3530889	FZR1	NM_016263	3	14	8	+	3530790	3530855
299086156	chr19	3530760	3530910	3530779	3530889	FZR1	NM_001136197	1	11	5	+	3530790	3530855
299086156	chr19	3530760	3530910	3530779	3530889	FZR1	NM_001136198	2	13	7	+	3530790	3530855
299087102	chr19	3532029	3532165	3532046	3532146	FZR1	NM_016263	3	14	10	+	3531909	3532093
299087102	chr19	3532029	3532165	3532046	3532146	FZR1	NM_001136197	1	11	7	+	3531909	3532093
299087102	chr19	3532029	3532165	3532046	3532146	FZR1	NM_001136198	2	13	9	+	3531909	3532093
299125255	chr19	3533248	3533416	3533265	3533398	FZR1	NM_016263	3	14	12	+	3533292	3533396
299125255	chr19	3533248	3533416	3533265	3533398	FZR1	NM_001136197	1	11	9	+	3533292	3533396
299125255	chr19	3533248	3533416	3533265	3533398	FZR1	NM_001136198	2	13	11	+	3533292	3533396
270360662	chr19	4094372	4094520	4094391	4094501	MAP2K2	NM_030662	1	11	10	-	4094451	4094496

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270276355	chr19	4099282	4099444	4099303	4099425	MAP2K2	NM_030662	1	11	7	-	4099199	4099412
271186259	chr19	4101220	4101367	4101240	4101346	MAP2K2	NM_030662	1	11	5	-	4101227	4101278
269994217	chr19	4117300	4117464	4117320	4117443	MAP2K2	NM_030662	1	11	2	-	4117417	4117627
294186460	chr19	10597291	10597458	10597316	10597434	KEAP1	NM_012289	1	6	6	-	10596796	10597494
294186460	chr19	10597291	10597458	10597316	10597434	KEAP1	NM_203500	2	6	6	-	10596796	10597494
293867760	chr19	10600207	10600372	10600227	10600351	KEAP1	NM_012289	1	6	4	-	10600324	10600529
293867760	chr19	10600207	10600372	10600227	10600351	KEAP1	NM_203500	2	6	4	-	10600324	10600529
294564161	chr19	10602298	10602470	10602320	10602453	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294564161	chr19	10602298	10602470	10602320	10602453	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294671485	chr19	10602786	10602924	10602806	10602903	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294671485	chr19	10602786	10602924	10602806	10602903	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294874537	chr19	10610235	10610407	10610254	10610386	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294874537	chr19	10610235	10610407	10610254	10610386	KEAP1	NM_203500	2	6	2	-	10610071	10610756
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128845	2	33	1	+	11094828	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128847	4	33	1	+	11094828	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128846	3	33	1	+	11094828	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128848	5	33	1	+	11094828	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128844	1	36	3	+	11094797	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_003072	7	35	2	+	11094797	11095049
262123737	chr19	11094809	11094962	11094827	11094945	SMARCA4	NM_001128849	6	36	2	+	11094797	11095049
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128844	1	36	4	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_003072	7	35	3	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128845	2	33	2	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128849	6	36	3	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128847	4	33	2	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128846	3	33	2	+	11095949	11096081
238479961	chr19	11095960	11096131	11095981	11096107	SMARCA4	NM_001128848	5	33	2	+	11095949	11096081
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128844	1	36	5	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_003072	7	35	4	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128845	2	33	3	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128849	6	36	4	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128847	4	33	3	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128846	3	33	3	+	11096865	11097269
260496390	chr19	11097154	11097316	11097173	11097296	SMARCA4	NM_001128848	5	33	3	+	11096865	11097269
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128844	1	36	7	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_003072	7	35	6	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128845	2	33	5	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128849	6	36	6	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128847	4	33	5	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128846	3	33	5	+	11098342	11098600
240433532	chr19	11098454	11098611	11098471	11098593	SMARCA4	NM_001128848	5	33	5	+	11098342	11098600

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128844	1	36	9	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_003072	7	35	8	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128845	2	33	7	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128849	6	36	8	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128847	4	33	7	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128846	3	33	7	+	11101826	11101999
238380979	chr19	11101802	11101975	11101823	11101954	SMARCA4	NM_001128848	5	33	7	+	11101826	11101999
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128844	1	36	11	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_003072	7	35	10	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128845	2	33	9	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128849	6	36	10	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128847	4	33	9	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128846	3	33	9	+	11106889	11107056
242406478	chr19	11106852	11106987	11106873	11106966	SMARCA4	NM_001128848	5	33	9	+	11106889	11107056
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128844	1	36	13	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_003072	7	35	12	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128845	2	33	11	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128849	6	36	12	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128847	4	33	11	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128846	3	33	11	+	11113705	11113835
240350430	chr19	11113686	11113856	11113710	11113836	SMARCA4	NM_001128848	5	33	11	+	11113705	11113835
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128844	1	36	16	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_003072	7	35	15	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128845	2	33	14	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128849	6	36	15	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128847	4	33	14	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128846	3	33	14	+	11121057	11121207
260397183	chr19	11121110	11121272	11121131	11121253	SMARCA4	NM_001128848	5	33	14	+	11121057	11121207
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128844	1	36	19	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_003072	7	35	18	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128845	2	33	17	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128849	6	36	18	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128847	4	33	17	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128846	3	33	17	+	11130267	11130377
260772398	chr19	11130232	11130399	11130252	11130379	SMARCA4	NM_001128848	5	33	17	+	11130267	11130377
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128844	1	36	21	+	11134194	11134307
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_003072	7	35	20	+	11134194	11134307
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128845	2	33	19	+	11134194	11134307
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128849	6	36	20	+	11134194	11134307
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128847	4	33	19	+	11134194	11134307
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128846	3	33	19	+	11134194	11134307

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238803728	chr19	11134158	11134329	11134179	11134308	SMARCA4	NM_001128848	5	33	19	+	11134194	11134307
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128844	1	36	24	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_003072	7	35	23	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128845	2	33	22	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128849	6	36	23	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128847	4	33	22	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128846	3	33	22	+	11136976	11137022
263408977	chr19	11136880	11137046	11136900	11137025	SMARCA4	NM_001128848	5	33	22	+	11136976	11137022
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128844	1	36	26	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_003072	7	35	25	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128845	2	33	24	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128849	6	36	25	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128847	4	33	24	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128846	3	33	24	+	11141406	11141569
238551717	chr19	11141434	11141608	11141455	11141588	SMARCA4	NM_001128848	5	33	24	+	11141406	11141569
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128844	1	36	30	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_003072	7	35	29	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128845	2	33	27	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128849	6	36	29	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128847	4	33	27	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128846	3	33	27	+	11145590	11145808
238625175	chr19	11145543	11145696	11145561	11145678	SMARCA4	NM_001128848	5	33	27	+	11145590	11145808
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128844	1	36	31	+	11151983	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_003072	7	35	30	+	11151983	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128849	6	36	31	+	11151983	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128847	4	33	28	+	11151983	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128848	5	33	28	+	11151983	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128845	2	33	28	+	11151974	11152236
238853072	chr19	11152149	11152316	11152166	11152295	SMARCA4	NM_001128846	3	33	28	+	11151974	11152236
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128844	1	36	34	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_003072	7	35	33	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128845	2	33	31	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128849	6	36	34	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128847	4	33	31	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128846	3	33	31	+	11170429	11170561
240215350	chr19	11170391	11170563	11170408	11170542	SMARCA4	NM_001128848	5	33	31	+	11170429	11170561
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128844	1	36	36	+	11172460	11172958
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_003072	7	35	35	+	11172460	11172958
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128845	2	33	33	+	11172460	11172958
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128849	6	36	36	+	11172460	11172958
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128847	4	33	33	+	11172460	11172958

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128846	3	33	33	+	11172460	11172958
261803704	chr19	11172425	11172557	11172445	11172536	SMARCA4	NM_001128848	5	33	33	+	11172460	11172958
233078915	chr19	17940879	17941053	17940901	17941035	JAK3	NM_000215	1	24	23	-	17940917	17941027
232652544	chr19	17942108	17942267	17942128	17942246	JAK3	NM_000215	1	24	21	-	17942037	17942209
231834658	chr19	17943370	17943541	17943391	17943521	JAK3	NM_000215	1	24	19	-	17943328	17943517
232263042	chr19	17945407	17945559	17945426	17945537	JAK3	NM_000215	1	24	17	-	17945380	17945530
234522816	chr19	17946664	17946826	17946687	17946800	JAK3	NM_000215	1	24	14	-	17946733	17946860
230840345	chr19	17949050	17949221	17949071	17949199	JAK3	NM_000215	1	24	11	-	17949072	17949199
232413753	chr19	17952113	17952272	17952134	17952251	JAK3	NM_000215	1	24	8	-	17952198	17952355
233107506	chr19	17953041	17953204	17953059	17953187	JAK3	NM_000215	1	24	6	-	17953125	17953419
233220494	chr19	17953786	17953949	17953805	17953930	JAK3	NM_000215	1	24	5	-	17953836	17953981
232606438	chr19	17954523	17954696	17954546	17954674	JAK3	NM_000215	1	24	3	-	17954586	17954709
293915262	chr19	18266609	18266767	18266628	18266749	PIK3R2	NM_005027	1	16	2	+	18266267	18267011
293762842	chr19	18271199	18271372	18271220	18271351	PIK3R2	NM_005027	1	16	3	+	18271281	18271373
294192972	chr19	18271878	18272048	18271897	18272031	PIK3R2	NM_005027	1	16	5	+	18271864	18271995
295315984	chr19	18273189	18273353	18273211	18273333	PIK3R2	NM_005027	1	16	9	+	18273218	18273316
293954419	chr19	18274146	18274305	18274166	18274279	PIK3R2	NM_005027	1	16	11	+	18274073	18274198
294432287	chr19	18277970	18278138	18277988	18278118	PIK3R2	NM_005027	1	16	13	+	18277940	18278116
226262330	chr19	18794499	18794626	18794516	18794608	CRTC1	NM_015321	2	14	1	+	18794425	18794638
226262330	chr19	18794499	18794626	18794516	18794608	CRTC1	NM_001098482	1	15	1	+	18794425	18794638
225460620	chr19	18854912	18855057	18854932	18855039	CRTC1	NM_001098482	1	15	3	+	18854918	18854965
225855433	chr19	18860531	18860705	18860552	18860686	CRTC1	NM_015321	2	14	5	+	18860591	18860685
225855433	chr19	18860531	18860705	18860552	18860686	CRTC1	NM_001098482	1	15	6	+	18860591	18860685
226305670	chr19	18870796	18870961	18870814	18870944	CRTC1	NM_015321	2	14	8	+	18870818	18871038
226305670	chr19	18870796	18870961	18870814	18870944	CRTC1	NM_001098482	1	15	9	+	18870818	18871038
226064057	chr19	18879201	18879358	18879218	18879340	CRTC1	NM_015321	2	14	10	+	18879295	18879603
226064057	chr19	18879201	18879358	18879218	18879340	CRTC1	NM_001098482	1	15	11	+	18879295	18879603
225531129	chr19	18885683	18885855	18885703	18885836	CRTC1	NM_015321	2	14	12	+	18885710	18885796
225531129	chr19	18885683	18885855	18885703	18885836	CRTC1	NM_001098482	1	15	13	+	18885710	18885796
253986811	chr19	18887941	18888097	18887961	18888075	CRTC1	NM_015321	2	14	14	+	18887981	18893143
253986811	chr19	18887941	18888097	18887961	18888075	CRTC1	NM_001098482	1	15	15	+	18887981	18893143
269842916	chr19	30303587	30303711	30303606	30303688	CCNE1	NM_001238	1	12	3	+	30303596	30303683
269781602	chr19	30308084	30308229	30308105	30308206	CCNE1	NM_001238	1	12	5	+	30308044	30308189
269963235	chr19	30311678	30311832	30311706	30311812	CCNE1	NM_001238	1	12	7	+	30311609	30311755
270447389	chr19	30313113	30313281	30313134	30313258	CCNE1	NM_001238	1	12	10	+	30313147	30313258
271984964	chr19	30314571	30314715	30314594	30314691	CCNE1	NM_001238	1	12	12	+	30314562	30315215
226693517	chr19	33792656	33792793	33792673	33792774	CEBPA	NM_004364	1	1	1	-	33790840	33793430
223873840	chr19	40741097	40741240	40741116	40741221	AKT2	NM_001626	3	14	12	-	40741170	40741257
223873840	chr19	40741097	40741240	40741116	40741221	AKT2	NM_001243028	2	13	11	-	40741170	40741257
223873840	chr19	40741097	40741240	40741116	40741221	AKT2	NM_001243027	1	14	12	-	40741170	40741257
223751049	chr19	40741869	40742034	40741891	40742011	AKT2	NM_001626	3	14	11	-	40741797	40742011

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223751049	chr19	40741869	40742034	40741891	40742011	AKT2	NM_001243028	2	13	10	-	40741797	40742011
223751049	chr19	40741869	40742034	40741891	40742011	AKT2	NM_001243027	1	14	11	-	40741797	40742011
222517254	chr19	40743957	40744125	40743977	40744104	AKT2	NM_001626	3	14	9	-	40743876	40743998
222517254	chr19	40743957	40744125	40743977	40744104	AKT2	NM_001243028	2	13	8	-	40743876	40743998
222517254	chr19	40743957	40744125	40743977	40744104	AKT2	NM_001243027	1	14	9	-	40743876	40743998
223574253	chr19	40747933	40748073	40747954	40748045	AKT2	NM_001626	3	14	6	-	40747845	40747976
223574253	chr19	40747933	40748073	40747954	40748045	AKT2	NM_001243028	2	13	5	-	40747845	40747976
223574253	chr19	40747933	40748073	40747954	40748045	AKT2	NM_001243027	1	14	6	-	40747845	40747976
223340972	chr19	40761059	40761232	40761082	40761213	AKT2	NM_001626	3	14	4	-	40761065	40761176
223340972	chr19	40761059	40761232	40761082	40761213	AKT2	NM_001243028	2	13	3	-	40761065	40761176
223340972	chr19	40761059	40761232	40761082	40761213	AKT2	NM_001243027	1	14	4	-	40761065	40761176
281435992	chr19	41726506	41726671	41726532	41726650	AXL	NM_021913	2	20	2	+	41726541	41726763
281435992	chr19	41726506	41726671	41726532	41726650	AXL	NM_001699	1	19	2	+	41726541	41726763
282925364	chr19	41727075	41727205	41727096	41727185	AXL	NM_021913	2	20	3	+	41727051	41727151
282925364	chr19	41727075	41727205	41727096	41727185	AXL	NM_001699	1	19	3	+	41727051	41727151
282426334	chr19	41737059	41737229	41737079	41737204	AXL	NM_021913	2	20	6	+	41737088	41737203
282426334	chr19	41737059	41737229	41737079	41737204	AXL	NM_001699	1	19	6	+	41737088	41737203
281794666	chr19	41744394	41744552	41744417	41744532	AXL	NM_021913	2	20	8	+	41744375	41744514
281794666	chr19	41744394	41744552	41744417	41744532	AXL	NM_001699	1	19	8	+	41744375	41744514
283360114	chr19	41748748	41748904	41748770	41748885	AXL	NM_021913	2	20	11	+	41748788	41748920
283360114	chr19	41748748	41748904	41748770	41748885	AXL	NM_001699	1	19	10	+	41748788	41748920
282960851	chr19	41754381	41754554	41754402	41754528	AXL	NM_021913	2	20	13	+	41754419	41754514
282960851	chr19	41754381	41754554	41754402	41754528	AXL	NM_001699	1	19	12	+	41754419	41754514
282880470	chr19	41759419	41759592	41759439	41759568	AXL	NM_021913	2	20	17	+	41759504	41759613
282880470	chr19	41759419	41759592	41759439	41759568	AXL	NM_001699	1	19	16	+	41759504	41759613
281411909	chr19	41763326	41763499	41763347	41763478	AXL	NM_021913	2	20	19	+	41763398	41763534
281411909	chr19	41763326	41763499	41763347	41763478	AXL	NM_001699	1	19	18	+	41763398	41763534
284503176	chr19	41765672	41765846	41765693	41765824	AXL	NM_021913	2	20	20	+	41765458	41767671
284503176	chr19	41765672	41765846	41765693	41765824	AXL	NM_001699	1	19	19	+	41765458	41767671
225845932	chr19	42383238	42383399	42383259	42383381	CD79A	NM_001783	1	5	2	+	42383060	42383359
225634648	chr19	42384951	42385116	42384975	42385095	CD79A	NM_001783	1	5	5	+	42384934	42385439
225634648	chr19	42384951	42385116	42384975	42385095	CD79A	NM_021601	2	5	5	+	42384934	42385439
225921729	chr19	42791112	42791265	42791130	42791248	CIC	NM_015125	1	20	3	+	42791158	42791392
225732730	chr19	42791552	42791703	42791572	42791682	CIC	NM_015125	1	20	4	+	42791472	42791601
226403604	chr19	42791990	42792116	42792012	42792099	CIC	NM_015125	1	20	6	+	42791962	42792127
226134213	chr19	42793206	42793341	42793228	42793319	CIC	NM_015125	1	20	7	+	42793040	42793242
225550183	chr19	42793960	42794134	42793980	42794116	CIC	NM_015125	1	20	9	+	42794000	42794103
225869103	chr19	42794659	42794809	42794678	42794787	CIC	NM_015125	1	20	10	+	42794385	42795618
225873579	chr19	42795084	42795221	42795102	42795204	CIC	NM_015125	1	20	10	+	42794385	42795618
225871061	chr19	42795503	42795658	42795522	42795639	CIC	NM_015125	1	20	10	+	42794385	42795618
226475571	chr19	42796414	42796578	42796436	42796558	CIC	NM_015125	1	20	13	+	42796452	42796618

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253711113	chr19	42796889	42797044	42796910	42797023	CIC	NM_015125	1	20	14	+	42796718	42797011
226103783	chr19	42797386	42797532	42797403	42797508	CIC	NM_015125	1	20	15	+	42797108	42797433
225439251	chr19	42797975	42798144	42797997	42798124	CIC	NM_015125	1	20	17	+	42798087	42798241
226506912	chr19	42798640	42798794	42798662	42798772	CIC	NM_015125	1	20	19	+	42798756	42798887
223635300	chr19	45252203	45252361	45252221	45252340	BCL3	NM_005178	1	9	1	+	45251978	45252303
223259539	chr19	45260174	45260340	45260195	45260321	BCL3	NM_005178	1	9	4	+	45260274	45260478
222398760	chr19	45260549	45260702	45260567	45260684	BCL3	NM_005178	1	9	5	+	45260584	45260672
222728834	chr19	45261511	45261643	45261530	45261625	BCL3	NM_005178	1	9	7	+	45261503	45261670
224631730	chr19	45262757	45262911	45262781	45262889	BCL3	NM_005178	1	9	9	+	45262685	45263301
290440703	chr19	45766539	45766676	45766562	45766654	MARK4	NM_031417	2	18	4	+	45766577	45766625
290440703	chr19	45766539	45766676	45766562	45766654	MARK4	NM_001199867	1	17	4	+	45766577	45766625
289336659	chr19	45768094	45768241	45768117	45768222	MARK4	NM_031417	2	18	6	+	45768098	45768168
289336659	chr19	45768094	45768241	45768117	45768222	MARK4	NM_001199867	1	17	6	+	45768098	45768168
290505083	chr19	45774777	45774933	45774798	45774914	MARK4	NM_031417	2	18	8	+	45774730	45774966
290505083	chr19	45774777	45774933	45774798	45774914	MARK4	NM_001199867	1	17	8	+	45774730	45774966
292541895	chr19	45781724	45781898	45781746	45781879	MARK4	NM_031417	2	18	10	+	45781774	45781873
292541895	chr19	45781724	45781898	45781746	45781879	MARK4	NM_001199867	1	17	10	+	45781774	45781873
289391194	chr19	45790666	45790834	45790685	45790817	MARK4	NM_031417	2	18	13	+	45790705	45790922
289391194	chr19	45790666	45790834	45790685	45790817	MARK4	NM_001199867	1	17	13	+	45790705	45790922
292306550	chr19	45800904	45801057	45800924	45801039	MARK4	NM_031417	2	18	15	+	45800934	45801212
292306550	chr19	45800904	45801057	45800924	45801039	MARK4	NM_001199867	1	17	15	+	45800934	45801212
293530175	chr19	45801400	45801546	45801421	45801525	MARK4	NM_031417	2	18	16	+	45801401	45801480
292531531	chr19	45805713	45805864	45805731	45805845	MARK4	NM_031417	2	18	18	+	45805632	45808541
292531531	chr19	45805713	45805864	45805731	45805845	MARK4	NM_001199867	1	17	17	+	45805632	45808541
227986788	chr19	45855420	45855554	45855438	45855533	ERCC2	NM_000400	1	23	22	-	45855467	45855610
227959097	chr19	45855950	45856124	45855973	45856104	ERCC2	NM_000400	1	23	20	-	45856004	45856074
230192636	chr19	45857881	45858055	45857903	45858036	ERCC2	NM_000400	1	23	17	-	45857988	45858109
228706599	chr19	45860688	45860822	45860707	45860801	ERCC2	NM_000400	1	23	14	-	45860732	45860801
230685005	chr19	45866945	45867114	45866964	45867093	ERCC2	NM_000400	1	23	11	-	45867001	45867169
230685005	chr19	45866945	45867114	45866964	45867093	ERCC2	NM_001130867	2	12	10	-	45867001	45867169
232399346	chr19	45867489	45867652	45867506	45867634	ERCC2	NM_000400	1	23	9	-	45867493	45867589
232399346	chr19	45867489	45867652	45867506	45867634	ERCC2	NM_001130867	2	12	8	-	45867493	45867589
228008295	chr19	45868200	45868345	45868222	45868324	ERCC2	NM_000400	1	23	6	-	45868300	45868416
228008295	chr19	45868200	45868345	45868222	45868324	ERCC2	NM_001130867	2	12	5	-	45868300	45868416
230519467	chr19	45872130	45872277	45872151	45872255	ERCC2	NM_000400	1	23	4	-	45872188	45872250
230519467	chr19	45872130	45872277	45872151	45872255	ERCC2	NM_001130867	2	12	3	-	45872188	45872250
230663064	chr19	45873726	45873863	45873747	45873844	ERCC2	NM_001130867	2	12	1	-	45873391	45873845
230663064	chr19	45873726	45873863	45873747	45873844	ERCC2	NM_000400	1	23	1	-	45873794	45873845
294290318	chr19	45917210	45917344	45917235	45917322	ERCC1	NM_202001	3	8	7	-	45917221	45917292
294290318	chr19	45917210	45917344	45917235	45917322	ERCC1	NM_001983	2	10	8	-	45917221	45917292
293778112	chr19	45922351	45922503	45922374	45922478	ERCC1	NM_202001	3	8	4	-	45922356	45922455

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293778112	chr19	45922351	45922503	45922374	45922478	ERCC1	NM_001983	2	10	5	-	45922356	45922455
293778112	chr19	45922351	45922503	45922374	45922478	ERCC1	NM_001166049	1	9	5	-	45922356	45922455
294493434	chr19	45924436	45924593	45924453	45924576	ERCC1	NM_202001	3	8	2	-	45924436	45924651
294493434	chr19	45924436	45924593	45924453	45924576	ERCC1	NM_001983	2	10	3	-	45924436	45924651
294493434	chr19	45924436	45924593	45924453	45924576	ERCC1	NM_001166049	1	9	3	-	45924436	45924651
237144676	chr19	52705170	52705341	52705193	52705320	PPP2R1A	NR_033500	2	14	2	+	52705197	52705287
237144676	chr19	52705170	52705341	52705193	52705320	PPP2R1A	NM_014225	1	15	2	+	52705197	52705287
236813774	chr19	52714687	52714832	52714707	52714810	PPP2R1A	NR_033500	2	14	3	+	52714513	52714745
236813774	chr19	52714687	52714832	52714707	52714810	PPP2R1A	NM_014225	1	15	4	+	52714513	52714745
236462084	chr19	52716307	52716468	52716327	52716447	PPP2R1A	NR_033500	2	14	5	+	52716208	52716363
236462084	chr19	52716307	52716468	52716327	52716447	PPP2R1A	NM_014225	1	15	6	+	52716208	52716363
241162426	chr19	52719693	52719867	52719720	52719846	PPP2R1A	NR_033500	2	14	8	+	52719782	52719916
241162426	chr19	52719693	52719867	52719720	52719846	PPP2R1A	NM_014225	1	15	9	+	52719782	52719916
237356033	chr19	52723084	52723230	52723106	52723209	PPP2R1A	NR_033500	2	14	9	+	52722944	52723117
237356033	chr19	52723084	52723230	52723106	52723209	PPP2R1A	NM_014225	1	15	10	+	52722944	52723117
235743010	chr19	52725308	52725478	52725330	52725456	PPP2R1A	NR_033500	2	14	12	+	52725352	52725494
235743010	chr19	52725308	52725478	52725330	52725456	PPP2R1A	NM_014225	1	15	13	+	52725352	52725494
293991877	chr19	57742343	57742513	57742366	57742494	AURKC	NM_001015878	1	7	1	+	57742428	57742674
293991877	chr19	57742343	57742513	57742366	57742494	AURKC	NM_003160	3	7	1	+	57742377	57742487
293991877	chr19	57742343	57742513	57742366	57742494	AURKC	NM_001015879	2	7	1	+	57742377	57742482
294461496	chr19	57743479	57743640	57743503	57743619	AURKC	NM_001015879	2	7	3	+	57743401	57743592
294461496	chr19	57743479	57743640	57743503	57743619	AURKC	NM_001015878	1	7	3	+	57743401	57743592
294461496	chr19	57743479	57743640	57743503	57743619	AURKC	NM_003160	3	7	3	+	57743401	57743592
293738975	chr19	57744852	57745014	57744874	57744991	AURKC	NM_001015879	2	7	5	+	57744828	57744976
293738975	chr19	57744852	57745014	57744874	57744991	AURKC	NM_001015878	1	7	5	+	57744828	57744976
293738975	chr19	57744852	57745014	57744874	57744991	AURKC	NM_003160	3	7	5	+	57744828	57744976
294573609	chr19	57746655	57746827	57746678	57746806	AURKC	NM_001015879	2	7	7	+	57746615	57746916
294573609	chr19	57746655	57746827	57746678	57746806	AURKC	NM_001015878	1	7	7	+	57746615	57746916
294573609	chr19	57746655	57746827	57746678	57746806	AURKC	NM_003160	3	7	7	+	57746615	57746916
272647003	chr20	30253852	30253994	30253872	30253969	BCL2L1	NM_138578	2	3	3	-	30252261	30253889
272647003	chr20	30253852	30253994	30253872	30253969	BCL2L1	NM_001191	1	3	3	-	30252261	30253889
271667326	chr20	30309748	30309902	30309768	30309880	BCL2L1	NM_001191	1	3	2	-	30309647	30310151
271667326	chr20	30309748	30309902	30309768	30309880	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
222321230	chr20	30956782	30956955	30956810	30956928	ASXL1	NM_015338	2	12	3	+	30956815	30956926
222321230	chr20	30956782	30956955	30956810	30956928	ASXL1	NM_001164603	1	4	3	+	30956815	30956926
224383150	chr20	31017101	31017262	31017124	31017236	ASXL1	NM_015338	2	12	6	+	31017141	31017234
222845942	chr20	31018996	31019168	31019020	31019140	ASXL1	NM_015338	2	12	8	+	31019124	31019287
222192581	chr20	31019414	31019561	31019438	31019534	ASXL1	NM_015338	2	12	9	+	31019386	31019482
225150291	chr20	31021255	31021381	31021279	31021361	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223756615	chr20	31021625	31021773	31021650	31021752	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223998169	chr20	31022480	31022640	31022499	31022621	ASXL1	NM_015338	2	12	12	+	31022235	31027122

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225291080	chr20	31022904	31023072	31022928	31023050	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225291009	chr20	31023370	31023542	31023394	31023519	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225280024	chr20	31023844	31024006	31023864	31023983	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225287268	chr20	31024272	31024435	31024297	31024412	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225273458	chr20	31024741	31024904	31024764	31024881	ASXL1	NM_015338	2	12	12	+	31022235	31027122
262487797	chr20	36012437	36012597	36012454	36012580	SRC	NM_198291	2	14	4	+	36012553	36012806
262487797	chr20	36012437	36012597	36012454	36012580	SRC	NM_005417	1	14	4	+	36012553	36012806
262401646	chr20	36022537	36022711	36022557	36022692	SRC	NM_198291	2	14	7	+	36022577	36022680
262401646	chr20	36022537	36022711	36022557	36022692	SRC	NM_005417	1	14	7	+	36022577	36022680
241084674	chr20	36026186	36026360	36026204	36026339	SRC	NM_198291	2	14	9	+	36026102	36026257
241084674	chr20	36026186	36026360	36026204	36026339	SRC	NM_005417	1	14	9	+	36026102	36026257
264586289	chr20	36030703	36030876	36030724	36030855	SRC	NM_198291	2	14	12	+	36030838	36030991
264586289	chr20	36030703	36030876	36030724	36030855	SRC	NM_005417	1	14	12	+	36030838	36030991
242072236	chr20	36031514	36031686	36031531	36031669	SRC	NM_198291	2	14	14	+	36031574	36033821
242072236	chr20	36031514	36031686	36031531	36031669	SRC	NM_005417	1	14	14	+	36031574	36033821
234397052	chr20	39316600	39316724	39316622	39316702	MAFB	NM_005461	1	1	1	-	39314517	39317876
232718674	chr20	39316978	39317136	39316995	39317118	MAFB	NM_005461	1	1	1	-	39314517	39317876
232731627	chr20	39317413	39317587	39317436	39317568	MAFB	NM_005461	1	1	1	-	39314517	39317876
264696291	chr20	39657696	39657851	39657713	39657834	TOP1	NM_003286	1	21	1	+	39657462	39657740
262063828	chr20	39704786	39704959	39704814	39704933	TOP1	NM_003286	1	21	4	+	39704811	39704934
261882862	chr20	39713075	39713236	39713100	39713209	TOP1	NM_003286	1	21	8	+	39713102	39713208
239230016	chr20	39725882	39726011	39725906	39725983	TOP1	NM_003286	1	21	10	+	39725860	39725981
290708959	chr20	39728749	39728906	39728774	39728884	TOP1	NM_003286	1	21	12	+	39728696	39728883
239575754	chr20	39741470	39741616	39741491	39741590	TOP1	NM_003286	1	21	14	+	39741422	39741565
242542626	chr20	39744883	39745057	39744909	39745033	TOP1	NM_003286	1	21	17	+	39744918	39745032
265964450	chr20	39750557	39750695	39750583	39750672	TOP1	NM_003286	1	21	20	+	39750646	39750795
271093356	chr20	39788149	39788320	39788176	39788300	PLCG1	NM_002660	1	32	2	+	39788246	39788398
271093356	chr20	39788149	39788320	39788176	39788300	PLCG1	NM_182811	2	32	2	+	39788246	39788398
271157808	chr20	39791040	39791214	39791063	39791194	PLCG1	NM_002660	1	32	5	+	39791092	39791176
271157808	chr20	39791040	39791214	39791063	39791194	PLCG1	NM_182811	2	32	5	+	39791092	39791176
271982450	chr20	39791791	39791935	39791814	39791915	PLCG1	NM_002660	1	32	8	+	39791843	39791915
271982450	chr20	39791791	39791935	39791814	39791915	PLCG1	NM_182811	2	32	8	+	39791843	39791915
270121229	chr20	39792426	39792598	39792450	39792576	PLCG1	NM_002660	1	32	10	+	39792355	39792473
270121229	chr20	39792426	39792598	39792450	39792576	PLCG1	NM_182811	2	32	10	+	39792355	39792473
270121229	chr20	39792426	39792598	39792450	39792576	PLCG1	NM_002660	1	32	11	+	39792561	39792646
270121229	chr20	39792426	39792598	39792450	39792576	PLCG1	NM_182811	2	32	11	+	39792561	39792646
271048834	chr20	39793631	39793791	39793654	39793771	PLCG1	NM_002660	1	32	13	+	39793573	39793741
271048834	chr20	39793631	39793791	39793654	39793771	PLCG1	NM_182811	2	32	13	+	39793573	39793741
272115530	chr20	39794237	39794392	39794259	39794368	PLCG1	NM_002660	1	32	16	+	39794279	39794466
272115530	chr20	39794237	39794392	39794259	39794368	PLCG1	NM_182811	2	32	16	+	39794279	39794466
270275456	chr20	39794961	39795118	39794981	39795097	PLCG1	NM_002660	1	32	17	+	39794834	39795034

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270275456	chr20	39794961	39795118	39794981	39795097	PLCG1	NM_182811	2	32	17	+	39794834	39795034
271997410	chr20	39796457	39796602	39796481	39796582	PLCG1	NM_002660	1	32	20	+	39796492	39796569
271997410	chr20	39796457	39796602	39796481	39796582	PLCG1	NM_182811	2	32	20	+	39796492	39796569
272617013	chr20	39798015	39798189	39798038	39798166	PLCG1	NM_002660	1	32	23	+	39798097	39798166
272617013	chr20	39798015	39798189	39798038	39798166	PLCG1	NM_182811	2	32	23	+	39798097	39798166
271445050	chr20	39800843	39800999	39800868	39800973	PLCG1	NM_002660	1	32	25	+	39800833	39800929
271445050	chr20	39800843	39800999	39800868	39800973	PLCG1	NM_182811	2	32	25	+	39800833	39800929
269982710	chr20	39801331	39801485	39801353	39801464	PLCG1	NM_002660	1	32	27	+	39801369	39801517
269982710	chr20	39801331	39801485	39801353	39801464	PLCG1	NM_182811	2	32	27	+	39801369	39801517
272582086	chr20	39802371	39802503	39802395	39802484	PLCG1	NM_002660	1	32	29	+	39802292	39802453
272582086	chr20	39802371	39802503	39802395	39802484	PLCG1	NM_182811	2	32	29	+	39802292	39802453
270161838	chr20	39802825	39802976	39802845	39802955	PLCG1	NM_182811	2	32	31	+	39802767	39802951
270161838	chr20	39802825	39802976	39802845	39802955	PLCG1	NM_002660	1	32	31	+	39802764	39802951
297115407	chr20	40710510	40710682	40710531	40710658	PTPRT	NM_007050	1	31	30	-	40710522	40710657
297115407	chr20	40710510	40710682	40710531	40710658	PTPRT	NM_133170	2	32	31	-	40710522	40710657
297880136	chr20	40726990	40727114	40727011	40727090	PTPRT	NM_007050	1	31	27	-	40727061	40727192
297880136	chr20	40726990	40727114	40727011	40727090	PTPRT	NM_133170	2	32	28	-	40727061	40727192
297918708	chr20	40733187	40733349	40733208	40733329	PTPRT	NM_007050	1	31	25	-	40733209	40733358
297918708	chr20	40733187	40733349	40733208	40733329	PTPRT	NM_133170	2	32	26	-	40733209	40733358
296754499	chr20	40738951	40739104	40738975	40739085	PTPRT	NM_007050	1	31	23	-	40738973	40739127
296754499	chr20	40738951	40739104	40738975	40739085	PTPRT	NM_133170	2	32	24	-	40738973	40739127
296386012	chr20	40746991	40747163	40747011	40747141	PTPRT	NM_007050	1	31	21	-	40747043	40747140
296386012	chr20	40746991	40747163	40747011	40747141	PTPRT	NM_133170	2	32	22	-	40747043	40747140
297245557	chr20	40789971	40790144	40789991	40790122	PTPRT	NM_007050	1	31	17	-	40789992	40790182
297245557	chr20	40789971	40790144	40789991	40790122	PTPRT	NM_133170	2	32	18	-	40789992	40790182
296524226	chr20	40864766	40864928	40864794	40864901	PTPRT	NM_007050	1	31	15	-	40864869	40864898
296524226	chr20	40864766	40864928	40864794	40864901	PTPRT	NM_133170	2	32	16	-	40864869	40864898
295948974	chr20	40911022	40911193	40911049	40911166	PTPRT	NM_007050	1	31	13	-	40911129	40911165
295948974	chr20	40911022	40911193	40911049	40911166	PTPRT	NM_133170	2	32	13	-	40911129	40911165
296221928	chr20	40979225	40979395	40979250	40979373	PTPRT	NM_007050	1	31	11	-	40979268	40979370
296221928	chr20	40979225	40979395	40979250	40979373	PTPRT	NM_133170	2	32	11	-	40979268	40979370
295507117	chr20	41076839	41077010	41076859	41076983	PTPRT	NM_007050	1	31	9	-	41076860	41076969
295507117	chr20	41076839	41077010	41076859	41076983	PTPRT	NM_133170	2	32	9	-	41076860	41076969
297684986	chr20	41306455	41306629	41306477	41306605	PTPRT	NM_007050	1	31	7	-	41306506	41306799
297684986	chr20	41306455	41306629	41306477	41306605	PTPRT	NM_133170	2	32	7	-	41306506	41306799
297857896	chr20	41385143	41385315	41385164	41385290	PTPRT	NM_007050	1	31	6	-	41385102	41385276
297857896	chr20	41385143	41385315	41385164	41385290	PTPRT	NM_133170	2	32	6	-	41385102	41385276
296495732	chr20	41419816	41419958	41419843	41419935	PTPRT	NM_007050	1	31	3	-	41419835	41420106
296495732	chr20	41419816	41419958	41419843	41419935	PTPRT	NM_133170	2	32	3	-	41419835	41420106
295999350	chr20	41514464	41514610	41514485	41514582	PTPRT	NM_007050	1	31	2	-	41514447	41514572
295999350	chr20	41514464	41514610	41514485	41514582	PTPRT	NM_133170	2	32	2	-	41514447	41514572

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_003600	1	9	8	-	54945541	54945715
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_198435	4	9	8	-	54945541	54945715
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_198436	5	10	9	-	54945541	54945715
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_198434	3	10	9	-	54945541	54945715
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_198433	2	11	10	-	54945541	54945715
270018960	chr20	54945473	54945630	54945495	54945604	AURKA	NM_198437	6	9	8	-	54945541	54945715
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_003600	1	9	6	-	54956489	54956627
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_198435	4	9	6	-	54956489	54956627
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_198436	5	10	7	-	54956489	54956627
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_198434	3	10	7	-	54956489	54956627
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_198433	2	11	8	-	54956489	54956627
269739012	chr20	54956418	54956592	54956443	54956564	AURKA	NM_198437	6	9	6	-	54956489	54956627
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_003600	1	9	5	-	54958041	54958232
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_198435	4	9	5	-	54958041	54958232
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_198436	5	10	6	-	54958041	54958232
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_198434	3	10	6	-	54958041	54958232
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_198433	2	11	7	-	54958041	54958232
270106496	chr20	54958195	54958351	54958218	54958323	AURKA	NM_198437	6	9	5	-	54958041	54958232
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_003600	1	9	3	-	54961313	54961589
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_198435	4	9	3	-	54961313	54961589
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_198436	5	10	4	-	54961313	54961589
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_198434	3	10	4	-	54961313	54961589
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_198433	2	11	5	-	54961313	54961589
270826879	chr20	54961440	54961603	54961463	54961579	AURKA	NM_198437	6	9	3	-	54961313	54961589
228094922	chr20	57415259	57415433	57415278	57415416	GNAS	NM_016592	5	13	1	+	57414795	57415941
228100342	chr20	57415674	57415840	57415691	57415823	GNAS	NM_016592	5	13	1	+	57414795	57415941
229418580	chr20	57428480	57428641	57428499	57428622	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229418580	chr20	57428480	57428641	57428499	57428622	GNAS	NM_080425	6	13	1	+	57428036	57430388
229424289	chr20	57428949	57429078	57428968	57429061	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229424289	chr20	57428949	57429078	57428968	57429061	GNAS	NM_080425	6	13	1	+	57428036	57430388
229439652	chr20	57429402	57429563	57429420	57429545	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229439652	chr20	57429402	57429563	57429420	57429545	GNAS	NM_080425	6	13	1	+	57428036	57430388
227515284	chr20	57430127	57430275	57430146	57430255	GNAS	NM_001077490	4	13	1	+	57428036	57430388
227515284	chr20	57430127	57430275	57430146	57430255	GNAS	NM_080425	6	13	1	+	57428036	57430388
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_016592	5	13	4	+	57478583	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_001077488	2	13	4	+	57478583	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_080426	7	12	3	+	57478583	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NR_003259	8	13	4	+	57478586	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_001077490	4	13	4	+	57478586	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_080425	6	13	4	+	57478586	57478640
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_001077489	3	12	3	+	57478586	57478640

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227236969	chr20	57478464	57478638	57478485	57478613	GNAS	NM_000516	1	13	4	+	57478586	57478640
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_016592	5	13	6	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_001077488	2	13	6	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NR_003259	8	13	6	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_001077490	4	13	6	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_080426	7	12	5	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_080425	6	13	6	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_001077489	3	12	5	+	57480438	57480535
227150064	chr20	57480383	57480556	57480408	57480535	GNAS	NM_000516	1	13	6	+	57480438	57480535
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_016592	5	13	10	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_001077488	2	13	10	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NR_003259	8	13	10	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_001077490	4	13	10	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_080426	7	12	9	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_080425	6	13	10	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_001077489	3	12	9	+	57484739	57484859
227244596	chr20	57484704	57484877	57484722	57484859	GNAS	NM_000516	1	13	10	+	57484739	57484859
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_016592	5	13	13	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_001077488	2	13	13	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_001077490	4	13	13	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_080426	7	12	12	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_080425	6	13	13	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_001077489	3	12	12	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NM_000516	1	13	13	+	57485738	57486250
230189710	chr20	57485806	57485973	57485825	57485948	GNAS	NR_003259	8	13	13	+	57485738	57486247
242435711	chr21	36164513	36164680	36164530	36164663	RUNX1	NM_001754	3	9	9	-	36160098	36164907
242435711	chr21	36164513	36164680	36164530	36164663	RUNX1	NM_001001890	1	6	6	-	36160098	36164907
264702858	chr21	36171558	36171726	36171579	36171701	RUNX1	NM_001754	3	9	8	-	36171598	36171759
264702858	chr21	36171558	36171726	36171579	36171701	RUNX1	NM_001001890	1	6	5	-	36171598	36171759
240196319	chr21	36206693	36206863	36206716	36206843	RUNX1	NM_001754	3	9	7	-	36206707	36206898
240196319	chr21	36206693	36206863	36206716	36206843	RUNX1	NM_001122607	2	5	4	-	36206707	36206898
240196319	chr21	36206693	36206863	36206716	36206843	RUNX1	NM_001001890	1	6	4	-	36206707	36206898
241363958	chr21	36252866	36253036	36252887	36253010	RUNX1	NM_001754	3	9	5	-	36252854	36253010
241363958	chr21	36252866	36253036	36252887	36253010	RUNX1	NM_001122607	2	5	2	-	36252854	36253010
241363958	chr21	36252866	36253036	36252887	36253010	RUNX1	NM_001001890	1	6	2	-	36252854	36253010
238333067	chr21	36265088	36265258	36265116	36265229	RUNX1	NM_001754	3	9	3	-	36265222	36265260
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_001136154	1	12	12	-	39751950	39755845
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_001136155	2	9	9	-	39751950	39755845
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_004449	6	11	11	-	39751950	39755845
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_182918	7	10	10	-	39751950	39755845
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_001243429	4	9	9	-	39751950	39755845

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230558801	chr21	39755394	39755542	39755419	39755519	ERG	NM_001243428	3	12	12	-	39751950	39755845
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_001136154	1	12	11	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_001136155	2	9	8	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_004449	6	11	10	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_182918	7	10	9	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_001243432	5	12	11	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_001243429	4	9	8	-	39762917	39762964
230132659	chr21	39762814	39762965	39762841	39762937	ERG	NM_001243428	3	12	11	-	39762917	39762964
230679219	chr21	39772430	39772599	39772451	39772571	ERG	NM_001136154	1	12	8	-	39772496	39772567
230679219	chr21	39772430	39772599	39772451	39772571	ERG	NM_001136155	2	9	5	-	39772496	39772567
230679219	chr21	39772430	39772599	39772451	39772571	ERG	NM_182918	7	10	6	-	39772496	39772567
230679219	chr21	39772430	39772599	39772451	39772571	ERG	NM_001243432	5	12	8	-	39772496	39772567
230679219	chr21	39772430	39772599	39772451	39772571	ERG	NM_001243428	3	12	8	-	39772496	39772567
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_001136154	1	12	6	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_001136155	2	9	3	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_004449	6	11	6	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_182918	7	10	4	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_001243432	5	12	6	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_001243429	4	9	4	-	39775428	39775631
228250309	chr21	39775481	39775653	39775501	39775632	ERG	NM_001243428	3	12	6	-	39775428	39775631
227941446	chr21	39817414	39817584	39817435	39817555	ERG	NM_001136154	1	12	4	-	39817327	39817544
227941446	chr21	39817414	39817584	39817435	39817555	ERG	NM_004449	6	11	4	-	39817327	39817544
227941446	chr21	39817414	39817584	39817435	39817555	ERG	NM_182918	7	10	2	-	39817327	39817544
227941446	chr21	39817414	39817584	39817435	39817555	ERG	NM_001243432	5	12	4	-	39817327	39817544
227941446	chr21	39817414	39817584	39817435	39817555	ERG	NM_001243428	3	12	4	-	39817327	39817544
279758838	chr21	46306582	46306730	46306601	46306709	ITGB2	NM_000211	1	16	15	-	46306651	46306817
279758838	chr21	46306582	46306730	46306601	46306709	ITGB2	NM_001127491	2	16	15	-	46306651	46306817
280295251	chr21	46308702	46308842	46308720	46308825	ITGB2	NM_000211	1	16	14	-	46308608	46308810
280295251	chr21	46308702	46308842	46308720	46308825	ITGB2	NM_001127491	2	16	14	-	46308608	46308810
279306495	chr21	46309805	46309977	46309827	46309957	ITGB2	NM_000211	1	16	12	-	46309893	46310137
279306495	chr21	46309805	46309977	46309827	46309957	ITGB2	NM_001127491	2	16	12	-	46309893	46310137
278404854	chr21	46311728	46311899	46311747	46311881	ITGB2	NM_000211	1	16	11	-	46311724	46311911
278404854	chr21	46311728	46311899	46311747	46311881	ITGB2	NM_001127491	2	16	11	-	46311724	46311911
279840143	chr21	46314852	46315005	46314871	46314984	ITGB2	NM_000211	1	16	9	-	46314886	46314975
279840143	chr21	46314852	46315005	46314871	46314984	ITGB2	NM_001127491	2	16	9	-	46314886	46314975
278026999	chr21	46320324	46320474	46320346	46320454	ITGB2	NM_000211	1	16	7	-	46320235	46320390
278026999	chr21	46320324	46320474	46320346	46320454	ITGB2	NM_001127491	2	16	7	-	46320235	46320390
280594190	chr21	46323191	46323362	46323211	46323339	ITGB2	NM_000211	1	16	5	-	46323280	46323450
280594190	chr21	46323191	46323362	46323211	46323339	ITGB2	NM_001127491	2	16	5	-	46323280	46323450
280502282	chr21	46326925	46327086	46326942	46327067	ITGB2	NM_000211	1	16	4	-	46326830	46327010
280502282	chr21	46326925	46327086	46326942	46327067	ITGB2	NM_001127491	2	16	4	-	46326830	46327010

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269826635	chr22	21272317	21272456	21272336	21272431	CRKL	NM_005207	1	3	1	+	21271714	21272533
271545807	chr22	21288257	21288409	21288276	21288388	CRKL	NM_005207	1	3	2	+	21288067	21288532
272274323	chr22	21304080	21304241	21304103	21304221	CRKL	NM_005207	1	3	3	+	21303999	21308037
294583170	chr22	22142451	22142619	22142476	22142591	MAPK1	NM_138957	2	8	6	-	22142546	22142677
294583170	chr22	22142451	22142619	22142476	22142591	MAPK1	NM_002745	1	9	6	-	22142546	22142677
294166190	chr22	22153226	22153399	22153250	22153382	MAPK1	NM_138957	2	8	4	-	22153301	22153417
294166190	chr22	22153226	22153399	22153250	22153382	MAPK1	NM_002745	1	9	4	-	22153301	22153417
294327369	chr22	22160261	22160390	22160284	22160363	MAPK1	NM_138957	2	8	3	-	22160139	22160328
294327369	chr22	22160261	22160390	22160284	22160363	MAPK1	NM_002745	1	9	3	-	22160139	22160328
293850803	chr22	22221634	22221780	22221653	22221763	MAPK1	NM_138957	2	8	1	-	22221612	22221970
293850803	chr22	22221634	22221780	22221653	22221763	MAPK1	NM_002745	1	9	1	-	22221612	22221970
223048617	chr22	23523503	23523632	23523521	23523614	BCR	NM_004327	1	23	1	+	23522552	23524426
223048617	chr22	23523503	23523632	23523521	23523614	BCR	NM_021574	2	22	1	+	23522552	23524426
223057680	chr22	23523769	23523941	23523790	23523923	BCR	NM_004327	1	23	1	+	23522552	23524426
223057680	chr22	23523769	23523941	23523790	23523923	BCR	NM_021574	2	22	1	+	23522552	23524426
224672554	chr22	23524255	23524429	23524273	23524410	BCR	NM_004327	1	23	1	+	23522552	23524426
224672554	chr22	23524255	23524429	23524273	23524410	BCR	NM_021574	2	22	1	+	23522552	23524426
222563980	chr22	23603102	23603263	23603125	23603241	BCR	NM_004327	1	23	3	+	23603137	23603241
222563980	chr22	23603102	23603263	23603125	23603241	BCR	NM_021574	2	22	3	+	23603137	23603241
224423966	chr22	23613629	23613803	23613653	23613782	BCR	NM_004327	1	23	6	+	23613719	23613779
224423966	chr22	23613629	23613803	23613653	23613782	BCR	NM_021574	2	22	6	+	23613719	23613779
223721909	chr22	23626139	23626304	23626156	23626286	BCR	NM_004327	1	23	9	+	23626164	23626285
223721909	chr22	23626139	23626304	23626156	23626286	BCR	NM_021574	2	22	9	+	23626164	23626285
222293302	chr22	23629381	23629548	23629402	23629525	BCR	NM_004327	1	23	11	+	23629346	23629465
222293302	chr22	23629381	23629548	23629402	23629525	BCR	NM_021574	2	22	11	+	23629346	23629465
222549675	chr22	23634678	23634851	23634701	23634830	BCR	NM_004327	1	23	15	+	23634728	23634825
222549675	chr22	23634678	23634851	23634701	23634830	BCR	NM_021574	2	22	15	+	23634728	23634825
223262376	chr22	23655020	23655188	23655040	23655166	BCR	NM_004327	1	23	20	+	23655074	23655208
223262376	chr22	23655020	23655188	23655040	23655166	BCR	NM_021574	2	22	19	+	23655074	23655208
224335792	chr22	23657583	23657725	23657606	23657702	BCR	NM_004327	1	23	23	+	23657620	23660224
224335792	chr22	23657583	23657725	23657606	23657702	BCR	NM_021574	2	22	22	+	23657620	23660224
238324054	chr22	24133930	24134101	24133957	24134082	SMARCB1	NM_001007468	1	9	2	+	24133943	24134054
238324054	chr22	24133930	24134101	24133957	24134082	SMARCB1	NM_003073	2	9	2	+	24133943	24134081
241223223	chr22	24145453	24145614	24145475	24145589	SMARCB1	NM_001007468	1	9	5	+	24145482	24145609
241223223	chr22	24145453	24145614	24145475	24145589	SMARCB1	NM_003073	2	9	5	+	24145482	24145609
242136767	chr22	24167388	24167555	24167409	24167533	SMARCB1	NM_001007468	1	9	7	+	24167412	24167602
242136767	chr22	24167388	24167555	24167409	24167533	SMARCB1	NM_003073	2	9	7	+	24167412	24167602
262827457	chr22	24176240	24176413	24176260	24176391	SMARCB1	NM_001007468	1	9	9	+	24176328	24176705
262827457	chr22	24176240	24176413	24176260	24176391	SMARCB1	NM_003073	2	9	9	+	24176328	24176705
235337345	chr22	28192719	28192892	28192742	28192871	MN1	NM_002430	1	2	1	-	28192751	28197486
235354152	chr22	28193173	28193340	28193190	28193321	MN1	NM_002430	1	2	1	-	28192751	28197486

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240191717	chr22	28193636	28193776	28193654	28193757	MN1	NM_002430	1	2	1	-	28192751	28197486
240216995	chr22	28194081	28194255	28194099	28194238	MN1	NM_002430	1	2	1	-	28192751	28197486
240207117	chr22	28194582	28194740	28194599	28194723	MN1	NM_002430	1	2	1	-	28192751	28197486
240220303	chr22	28194860	28195026	28194878	28195008	MN1	NM_002430	1	2	1	-	28192751	28197486
235391229	chr22	28195272	28195442	28195290	28195424	MN1	NM_002430	1	2	1	-	28192751	28197486
235399150	chr22	28195657	28195790	28195675	28195773	MN1	NM_002430	1	2	1	-	28192751	28197486
240245235	chr22	28196052	28196225	28196069	28196205	MN1	NM_002430	1	2	1	-	28192751	28197486
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_145862	3	14	13	-	29085123	29085203
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_007194	2	15	14	-	29085123	29085203
225636022	chr22	29085138	29085309	29085161	29085285	CHEK2	NM_001005735	1	16	15	-	29085123	29085203
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_145862	3	14	10	-	29091698	29091861
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_007194	2	15	11	-	29091698	29091861
226429377	chr22	29091662	29091809	29091682	29091787	CHEK2	NM_001005735	1	16	12	-	29091698	29091861
225435205	chr22	29099402	29099573	29099424	29099551	CHEK2	NM_145862	3	14	8	-	29099493	29099554
225435205	chr22	29099402	29099573	29099424	29099551	CHEK2	NM_007194	2	15	8	-	29099493	29099554
225435205	chr22	29099402	29099573	29099424	29099551	CHEK2	NM_001005735	1	16	9	-	29099493	29099554
226235931	chr22	29115309	29115447	29115335	29115418	CHEK2	NM_145862	3	14	5	-	29115383	29115473
226235931	chr22	29115309	29115447	29115335	29115418	CHEK2	NM_007194	2	15	5	-	29115383	29115473
226235931	chr22	29115309	29115447	29115335	29115418	CHEK2	NM_001005735	1	16	6	-	29115383	29115473
253756214	chr22	29121056	29121203	29121081	29121176	CHEK2	NM_145862	3	14	4	-	29120965	29121112
253756214	chr22	29121056	29121203	29121081	29121176	CHEK2	NM_007194	2	15	4	-	29120965	29121112
253756214	chr22	29121056	29121203	29121081	29121176	CHEK2	NM_001005735	1	16	5	-	29120965	29121112
226163432	chr22	29130470	29130604	29130495	29130584	CHEK2	NM_145862	3	14	2	-	29130391	29130715
226163432	chr22	29130470	29130604	29130495	29130584	CHEK2	NM_007194	2	15	2	-	29130391	29130715
226163432	chr22	29130470	29130604	29130495	29130584	CHEK2	NM_001005735	1	16	2	-	29130391	29130715
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_016418	2	17	2	+	30032740	30032865
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_000268	1	16	2	+	30032740	30032865
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_181833	9	5	2	+	30032740	30032865
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_181832	8	17	2	+	30032740	30032865
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_181825	3	16	2	+	30032740	30032865
240818195	chr22	30032611	30032763	30032634	30032741	NF2	NM_181829	5	16	2	+	30032740	30032865
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_016418	2	17	4	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_000268	1	16	4	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181833	9	5	4	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181832	8	17	4	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181828	4	16	3	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181825	3	16	4	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181831	7	15	2	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181830	6	15	2	+	30038191	30038274
237143564	chr22	30038153	30038320	30038178	30038293	NF2	NM_181829	5	16	3	+	30038191	30038274
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_016418	2	17	7	+	30054178	30054253

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_000268	1	16	7	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181832	8	17	7	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181828	4	16	6	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181825	3	16	7	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181831	7	15	5	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181830	6	15	5	+	30054178	30054253
235152124	chr22	30054122	30054276	30054144	30054253	NF2	NM_181829	5	16	6	+	30054178	30054253
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_016418	2	17	9	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_000268	1	16	9	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181832	8	17	9	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181828	4	16	8	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181825	3	16	9	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181831	7	15	7	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181830	6	15	7	+	30060979	30061053
257994467	chr22	30061012	30061172	30061040	30061144	NF2	NM_181829	5	16	8	+	30060979	30061053
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_016418	2	17	12	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_000268	1	16	12	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181832	8	17	12	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181828	4	16	11	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181825	3	16	12	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181831	7	15	10	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181830	6	15	10	+	30069258	30069475
238715650	chr22	30069227	30069396	30069249	30069379	NF2	NM_181829	5	16	11	+	30069258	30069475
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_016418	2	17	14	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_000268	1	16	14	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181832	8	17	14	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181828	4	16	13	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181825	3	16	14	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181831	7	15	12	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181830	6	15	12	+	30074185	30074312
239323364	chr22	30074102	30074250	30074122	30074228	NF2	NM_181829	5	16	13	+	30074185	30074312
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181825	3	16	16	+	30079009	30079904
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181832	8	17	16	+	30079009	30079068
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_016418	2	17	16	+	30079009	30079053
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181828	4	16	15	+	30079009	30079053
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181831	7	15	14	+	30079009	30079053
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181830	6	15	14	+	30079009	30079053
235167881	chr22	30078899	30079072	30078922	30079047	NF2	NM_181829	5	16	15	+	30079009	30079053
321817574	chr22	33253199	33253372	33253226	33253347	TIMP3	NM_000362	1	5	3	+	33253236	33253347
236695415	chr22	36678606	36678760	36678628	36678739	MYH9	NM_002473	1	41	41	-	36677323	36678831
241817164	chr22	36680421	36680582	36680440	36680561	MYH9	NM_002473	1	41	39	-	36680449	36680557

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236882906	chr22	36681609	36681747	36681628	36681727	MYH9	NM_002473	1	41	37	-	36681704	36681827
235894567	chr22	36682763	36682920	36682785	36682902	MYH9	NM_002473	1	41	35	-	36682764	36682892
237936866	chr22	36684777	36684937	36684799	36684916	MYH9	NM_002473	1	41	33	-	36684773	36684985
235702106	chr22	36685250	36685380	36685271	36685359	MYH9	NM_002473	1	41	32	-	36685131	36685343
242398855	chr22	36689333	36689470	36689350	36689448	MYH9	NM_002473	1	41	30	-	36689375	36689527
240845538	chr22	36690177	36690346	36690195	36690323	MYH9	NM_002473	1	41	28	-	36690138	36690344
241501340	chr22	36691518	36691670	36691536	36691651	MYH9	NM_002473	1	41	26	-	36691551	36691763
236341395	chr22	36694853	36695002	36694872	36694978	MYH9	NM_002473	1	41	24	-	36694965	36695088
237088586	chr22	36696814	36696978	36696833	36696960	MYH9	NM_002473	1	41	22	-	36696897	36697103
235084449	chr22	36697568	36697741	36697588	36697716	MYH9	NM_002473	1	41	21	-	36697580	36697711
238847556	chr22	36701059	36701183	36701078	36701158	MYH9	NM_002473	1	41	18	-	36701079	36701148
241138180	chr22	36702455	36702579	36702475	36702561	MYH9	NM_002473	1	41	16	-	36702460	36702653
238425414	chr22	36707966	36708137	36707987	36708112	MYH9	NM_002473	1	41	14	-	36708094	36708267
236786720	chr22	36710222	36710388	36710241	36710363	MYH9	NM_002473	1	41	13	-	36710190	36710363
235404687	chr22	36714312	36714485	36714335	36714464	MYH9	NM_002473	1	41	11	-	36714252	36714370
237490930	chr22	36716822	36716973	36716841	36716947	MYH9	NM_002473	1	41	8	-	36716843	36716941
237673045	chr22	36722557	36722729	36722577	36722707	MYH9	NM_002473	1	41	5	-	36722613	36722706
236923511	chr22	36744822	36744988	36744843	36744967	MYH9	NM_002473	1	41	2	-	36744949	36745300
237644166	chr22	39621710	39621882	39621727	39621856	PDGFB	NM_033016	2	7	6	-	39621700	39621852
237644166	chr22	39621710	39621882	39621727	39621856	PDGFB	NM_002608	1	7	6	-	39621700	39621852
235463674	chr22	39627663	39627833	39627681	39627812	PDGFB	NM_033016	2	7	4	-	39627627	39627832
235463674	chr22	39627663	39627833	39627681	39627812	PDGFB	NM_002608	1	7	4	-	39627627	39627832
235247847	chr22	39631814	39631987	39631836	39631964	PDGFB	NM_033016	2	7	2	-	39631783	39631879
235247847	chr22	39631814	39631987	39631836	39631964	PDGFB	NM_002608	1	7	2	-	39631783	39631879
231292723	chr22	41513146	41513303	41513174	41513277	EP300	NM_001429	1	31	2	+	41513191	41513825
231390045	chr22	41513582	41513754	41513605	41513732	EP300	NM_001429	1	31	2	+	41513191	41513825
230180169	chr22	41522009	41522164	41522030	41522138	EP300	NM_001429	1	31	3	+	41521868	41522044
229854786	chr22	41525877	41526019	41525903	41525992	EP300	NM_001429	1	31	5	+	41525894	41526007
229592211	chr22	41527534	41527687	41527559	41527659	EP300	NM_001429	1	31	6	+	41527392	41527637
229835374	chr22	41536101	41536225	41536129	41536201	EP300	NM_001429	1	31	9	+	41536144	41536261
230530162	chr22	41542666	41542820	41542689	41542795	EP300	NM_001429	1	31	11	+	41542743	41542820
229404678	chr22	41545001	41545133	41545028	41545108	EP300	NM_001429	1	31	13	+	41545042	41545179
229964583	chr22	41545971	41546100	41545992	41546080	EP300	NM_001429	1	31	14	+	41545765	41546202
229222079	chr22	41547916	41548071	41547937	41548046	EP300	NM_001429	1	31	15	+	41547837	41548016
228171474	chr22	41551009	41551133	41551031	41551106	EP300	NM_001429	1	31	17	+	41550999	41551117
228321124	chr22	41554350	41554523	41554376	41554504	EP300	NM_001429	1	31	19	+	41554416	41554504
230676205	chr22	41562555	41562722	41562583	41562695	EP300	NM_001429	1	31	23	+	41562603	41562670
232760371	chr22	41564732	41564896	41564755	41564872	EP300	NM_001429	1	31	25	+	41564725	41564871
232327091	chr22	41566435	41566595	41566456	41566575	EP300	NM_001429	1	31	27	+	41566410	41566575
229256427	chr22	41569636	41569809	41569664	41569789	EP300	NM_001429	1	31	29	+	41569627	41569788
231246379	chr22	41572663	41572836	41572690	41572809	EP300	NM_001429	1	31	31	+	41572777	41576081

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231317737	chr22	41573121	41573294	41573142	41573274	EP300	NM_001429	1	31	31	+	41572777	41576081
227995723	chr22	41573612	41573772	41573634	41573753	EP300	NM_001429	1	31	31	+	41572777	41576081
228066078	chr22	41574085	41574251	41574105	41574228	EP300	NM_001429	1	31	31	+	41572777	41576081
228152766	chr22	41574477	41574643	41574498	41574623	EP300	NM_001429	1	31	31	+	41572777	41576081
286102619	chr22	42522498	42522637	42522526	42522615	CYP2D6	NM_000106	1	9	9	-	42522501	42522754
286102619	chr22	42522498	42522637	42522526	42522615	CYP2D6	NM_001025161	2	8	8	-	42522501	42522754
285962936	chr22	42523855	42524023	42523878	42524003	CYP2D6	NM_000106	1	9	6	-	42523844	42523985
285962936	chr22	42523855	42524023	42523878	42524003	CYP2D6	NM_001025161	2	8	5	-	42523844	42523985
288329905	chr22	42525028	42525184	42525045	42525167	CYP2D6	NM_000106	1	9	3	-	42525035	42525187
286244707	chr22	42526504	42526666	42526524	42526649	CYP2D6	NM_000106	1	9	1	-	42526614	42526883
286244707	chr22	42526504	42526666	42526524	42526649	CYP2D6	NM_001025161	2	8	1	-	42526614	42526883
269541644	chrX	40988164	40988318	40988188	40988297	USP9X	NM_001039590	1	45	3	+	40988253	40988398
269541644	chrX	40988164	40988318	40988188	40988297	USP9X	NM_001039591	2	45	3	+	40988253	40988398
271060991	chrX	40993865	40994036	40993888	40994009	USP9X	NM_001039590	1	45	5	+	40993978	40994090
271060991	chrX	40993865	40994036	40993888	40994009	USP9X	NM_001039591	2	45	5	+	40993978	40994090
270120897	chrX	40996196	40996348	40996222	40996322	USP9X	NM_001039590	1	45	6	+	40996057	40996275
270120897	chrX	40996196	40996348	40996222	40996322	USP9X	NM_001039591	2	45	6	+	40996057	40996275
270256891	chrX	41000215	41000362	41000236	41000334	USP9X	NM_001039590	1	45	8	+	41000219	41000470
270256891	chrX	41000215	41000362	41000236	41000334	USP9X	NM_001039591	2	45	8	+	41000219	41000470
271529357	chrX	41000567	41000696	41000594	41000674	USP9X	NM_001039590	1	45	9	+	41000546	41000684
271529357	chrX	41000567	41000696	41000594	41000674	USP9X	NM_001039591	2	45	9	+	41000546	41000684
271934011	chrX	41003734	41003859	41003761	41003832	USP9X	NM_001039590	1	45	11	+	41003775	41003879
271934011	chrX	41003734	41003859	41003761	41003832	USP9X	NM_001039591	2	45	11	+	41003775	41003879
271323366	chrX	41007712	41007853	41007735	41007828	USP9X	NM_001039590	1	45	12	+	41007622	41007828
271323366	chrX	41007712	41007853	41007735	41007828	USP9X	NM_001039591	2	45	12	+	41007622	41007828
269688617	chrX	41012209	41012380	41012230	41012356	USP9X	NM_001039590	1	45	14	+	41012201	41012334
269688617	chrX	41012209	41012380	41012230	41012356	USP9X	NM_001039591	2	45	14	+	41012201	41012334
272432548	chrX	41025182	41025329	41025210	41025304	USP9X	NM_001039590	1	45	16	+	41025125	41025467
272432548	chrX	41025182	41025329	41025210	41025304	USP9X	NM_001039591	2	45	16	+	41025125	41025467
271844092	chrX	41027158	41027303	41027183	41027275	USP9X	NM_001039590	1	45	18	+	41027260	41027471
271844092	chrX	41027158	41027303	41027183	41027275	USP9X	NM_001039591	2	45	18	+	41027260	41027471
269737704	chrX	41029308	41029463	41029333	41029436	USP9X	NM_001039590	1	45	19	+	41029248	41029488
269737704	chrX	41029308	41029463	41029333	41029436	USP9X	NM_001039591	2	45	19	+	41029248	41029488
271072888	chrX	41031124	41031292	41031147	41031264	USP9X	NM_001039590	1	45	21	+	41031091	41031211
271072888	chrX	41031124	41031292	41031147	41031264	USP9X	NM_001039591	2	45	21	+	41031091	41031211
269613190	chrX	41043621	41043794	41043644	41043766	USP9X	NM_001039590	1	45	23	+	41043650	41043928
269613190	chrX	41043621	41043794	41043644	41043766	USP9X	NM_001039591	2	45	23	+	41043650	41043928
270584616	chrX	41045773	41045940	41045797	41045911	USP9X	NM_001039590	1	45	24	+	41045770	41045895
270584616	chrX	41045773	41045940	41045797	41045911	USP9X	NM_001039591	2	45	24	+	41045770	41045895
269815641	chrX	41048650	41048794	41048678	41048767	USP9X	NM_001039590	1	45	26	+	41048562	41048728
269815641	chrX	41048650	41048794	41048678	41048767	USP9X	NM_001039591	2	45	26	+	41048562	41048728

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272574905	chrX	41056545	41056714	41056573	41056688	USP9X	NM_001039590	1	45	29	+	41056617	41056763
272574905	chrX	41056545	41056714	41056573	41056688	USP9X	NM_001039591	2	45	29	+	41056617	41056763
269948892	chrX	41057883	41058009	41057911	41057982	USP9X	NM_001039590	1	45	30	+	41057781	41058003
269948892	chrX	41057883	41058009	41057911	41057982	USP9X	NM_001039591	2	45	30	+	41057781	41058003
271388743	chrX	41064473	41064617	41064501	41064589	USP9X	NM_001039590	1	45	32	+	41064556	41064746
271388743	chrX	41064473	41064617	41064501	41064589	USP9X	NM_001039591	2	45	32	+	41064556	41064746
271943508	chrX	41069769	41069904	41069790	41069878	USP9X	NM_001039590	1	45	33	+	41069762	41069935
271943508	chrX	41069769	41069904	41069790	41069878	USP9X	NM_001039591	2	45	33	+	41069762	41069935
270915624	chrX	41075099	41075232	41075130	41075204	USP9X	NM_001039590	1	45	35	+	41075152	41075905
270915624	chrX	41075099	41075232	41075130	41075204	USP9X	NM_001039591	2	45	35	+	41075152	41075905
270951751	chrX	41075480	41075652	41075503	41075632	USP9X	NM_001039590	1	45	35	+	41075152	41075905
270951751	chrX	41075480	41075652	41075503	41075632	USP9X	NM_001039591	2	45	35	+	41075152	41075905
271655774	chrX	41076353	41076510	41076378	41076486	USP9X	NM_001039590	1	45	36	+	41076473	41076596
271655774	chrX	41076353	41076510	41076378	41076486	USP9X	NM_001039591	2	45	36	+	41076473	41076596
270139196	chrX	41077718	41077882	41077741	41077854	USP9X	NM_001039590	1	45	37	+	41077625	41077850
270139196	chrX	41077718	41077882	41077741	41077854	USP9X	NM_001039591	2	45	37	+	41077625	41077850
269693888	chrX	41083911	41084061	41083939	41084033	USP9X	NM_001039590	1	45	40	+	41083995	41084215
269693888	chrX	41083911	41084061	41083939	41084033	USP9X	NM_001039591	2	45	40	+	41083995	41084215
270520216	chrX	41084281	41084418	41084309	41084391	USP9X	NM_001039590	1	45	41	+	41084302	41084390
270520216	chrX	41084281	41084418	41084309	41084391	USP9X	NM_001039591	2	45	41	+	41084302	41084390
271004239	chrX	41088817	41088963	41088844	41088939	USP9X	NM_001039591	2	45	43	+	41088820	41089032
271004239	chrX	41088817	41088963	41088844	41088939	USP9X	NM_001039590	1	45	43	+	41088820	41089080
271091463	chrX	41089743	41089880	41089769	41089853	USP9X	NM_001039590	1	45	44	+	41089754	41089849
271091463	chrX	41089743	41089880	41089769	41089853	USP9X	NM_001039591	2	45	44	+	41089754	41089849
232340060	chrX	44732847	44733015	44732874	44732998	KDM6A	NM_021140	1	29	1	+	44732423	44732958
233223429	chrX	44833818	44833990	44833840	44833963	KDM6A	NM_021140	1	29	4	+	44833911	44833960
234426180	chrX	44879919	44880093	44879947	44880060	KDM6A	NM_021140	1	29	6	+	44879855	44879975
233441895	chrX	44912988	44913127	44913017	44913103	KDM6A	NM_021140	1	29	10	+	44913074	44913200
233654655	chrX	44918237	44918361	44918260	44918336	KDM6A	NM_021140	1	29	11	+	44918251	44918349
234523872	chrX	44918619	44918777	44918647	44918756	KDM6A	NM_021140	1	29	12	+	44918492	44918711
232185712	chrX	44921776	44921949	44921801	44921921	KDM6A	NM_021140	1	29	15	+	44921892	44921993
231297238	chrX	44922717	44922890	44922737	44922865	KDM6A	NM_021140	1	29	16	+	44922667	44923062
232815250	chrX	44928929	44929082	44928951	44929058	KDM6A	NM_021140	1	29	17	+	44928824	44929602
234427537	chrX	44929370	44929543	44929393	44929518	KDM6A	NM_021140	1	29	17	+	44928824	44929602
231542054	chrX	44936025	44936169	44936046	44936142	KDM6A	NM_021140	1	29	18	+	44935942	44936071
230946397	chrX	44938379	44938515	44938406	44938489	KDM6A	NM_021140	1	29	20	+	44938391	44938596
230879724	chrX	44941925	44942087	44941954	44942062	KDM6A	NM_021140	1	29	22	+	44941960	44942034
232223103	chrX	44945174	44945348	44945199	44945324	KDM6A	NM_021140	1	29	24	+	44945110	44945224
232080424	chrX	44949889	44950022	44949911	44949996	KDM6A	NM_021140	1	29	26	+	44949968	44950109
232864769	chrX	44969220	44969392	44969249	44969364	KDM6A	NM_021140	1	29	28	+	44969324	44969494
262141959	chrX	48116642	48116809	48116665	48116787	SSX1	NM_005635	1	8	2	+	48116657	48116745

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264695625	chrX	48123214	48123384	48123235	48123357	SSX1	NM_005635	1	8	6	+	48123217	48123352
239105187	chrX	48542632	48542803	48542652	48542780	WAS	NM_000377	1	12	2	+	48542672	48542812
261955270	chrX	48544099	48544257	48544118	48544235	WAS	NM_000377	1	12	4	+	48544123	48544225
263120098	chrX	48545265	48545415	48545286	48545393	WAS	NM_000377	1	12	7	+	48545170	48545344
262401572	chrX	48547023	48547168	48547046	48547147	WAS	NM_000377	1	12	10	+	48547049	48547455
242464216	chrX	48547670	48547841	48547688	48547824	WAS	NM_000377	1	12	11	+	48547709	48547823
227543844	chrX	48650127	48650295	48650149	48650274	GATA1	NM_002049	1	6	3	+	48650251	48650628
228785921	chrX	48650670	48650844	48650690	48650818	GATA1	NM_002049	1	6	4	+	48650730	48650875
227646672	chrX	48652210	48652372	48652230	48652353	GATA1	NM_002049	1	6	6	+	48652200	48652717
265466525	chrX	48887706	48887860	48887724	48887842	TFE3	NM_006521	1	10	10	-	48886242	48888112
239311557	chrX	48888886	48889033	48888908	48889011	TFE3	NM_006521	1	10	9	-	48888912	48889059
242014400	chrX	48891627	48891794	48891648	48891774	TFE3	NM_006521	1	10	6	-	48891649	48891766
242128816	chrX	48895728	48895902	48895747	48895881	TFE3	NM_006521	1	10	4	-	48895722	48895967
241269419	chrX	48896757	48896897	48896774	48896874	TFE3	NM_006521	1	10	3	-	48896632	48896935
262446282	chrX	48900521	48900693	48900540	48900675	TFE3	NM_006521	1	10	1	-	48900637	48900990
232714540	chrX	53221960	53222086	53221982	53222065	KDM5C	NM_004187	2	26	26	-	53220503	53222514
232714540	chrX	53221960	53222086	53221982	53222065	KDM5C	NM_001146702	1	24	24	-	53220503	53222019
232724478	chrX	53222371	53222541	53222388	53222516	KDM5C	NM_004187	2	26	26	-	53220503	53222514
233912684	chrX	53223272	53223420	53223294	53223400	KDM5C	NM_004187	2	26	23	-	53223321	53223920
233912684	chrX	53223272	53223420	53223294	53223400	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
233924128	chrX	53223668	53223824	53223687	53223806	KDM5C	NM_004187	2	26	23	-	53223321	53223920
233924128	chrX	53223668	53223824	53223687	53223806	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
233292212	chrX	53224375	53224518	53224398	53224496	KDM5C	NM_004187	2	26	21	-	53224413	53224592
233292212	chrX	53224375	53224518	53224398	53224496	KDM5C	NM_001146702	1	24	19	-	53224413	53224592
232595919	chrX	53225797	53225965	53225819	53225943	KDM5C	NM_004187	2	26	19	-	53225868	53226226
232595919	chrX	53225797	53225965	53225819	53225943	KDM5C	NM_001146702	1	24	17	-	53225868	53226226
232618121	chrX	53226927	53227096	53226947	53227072	KDM5C	NM_004187	2	26	18	-	53226953	53227058
232618121	chrX	53226927	53227096	53226947	53227072	KDM5C	NM_001146702	1	24	16	-	53226953	53227058
233080283	chrX	53228008	53228153	53228028	53228133	KDM5C	NM_004187	2	26	16	-	53227946	53228070
233080283	chrX	53228008	53228153	53228028	53228133	KDM5C	NM_001146702	1	24	14	-	53227946	53228070
232493218	chrX	53230807	53230958	53230830	53230938	KDM5C	NM_004187	2	26	14	-	53230732	53230926
232493218	chrX	53230807	53230958	53230830	53230938	KDM5C	NM_001146702	1	24	12	-	53230732	53230926
233558101	chrX	53239819	53239991	53239840	53239967	KDM5C	NM_004187	2	26	11	-	53239858	53240039
233558101	chrX	53239819	53239991	53239840	53239967	KDM5C	NM_001146702	1	24	9	-	53239858	53240039
233020548	chrX	53240943	53241113	53240963	53241089	KDM5C	NM_004187	2	26	9	-	53240969	53241088
233020548	chrX	53240943	53241113	53240963	53241089	KDM5C	NM_001146702	1	24	7	-	53240969	53241088
232517022	chrX	53245038	53245206	53245059	53245180	KDM5C	NM_004187	2	26	7	-	53244977	53245158
232517022	chrX	53245038	53245206	53245059	53245180	KDM5C	NM_001146702	1	24	5	-	53244977	53245158
234214972	chrX	53246907	53247080	53246934	53247056	KDM5C	NM_004187	2	26	4	-	53246978	53247148
234214972	chrX	53246907	53247080	53246934	53247056	KDM5C	NM_001146702	1	24	2	-	53246978	53247148
234166650	chrX	53253861	53254005	53253883	53253985	KDM5C	NM_004187	2	26	1	-	53253922	53254604

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234166650	chrX	53253861	53254005	53253883	53253985	KDM5C	NM_001146702	1	24	1	-	53253922	53254604
231965079	chrX	63409966	63410109	63409988	63410088	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232009723	chrX	63410370	63410510	63410394	63410489	FAM123B	NM_152424	1	2	2	-	63404997	63413264
228941477	chrX	63410760	63410933	63410784	63410909	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232003118	chrX	63411237	63411375	63411258	63411352	FAM123B	NM_152424	1	2	2	-	63404997	63413264
229449892	chrX	63411683	63411846	63411703	63411822	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232020668	chrX	63412035	63412205	63412056	63412180	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232003803	chrX	63412500	63412649	63412522	63412629	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232012340	chrX	63412941	63413115	63412962	63413093	FAM123B	NM_152424	1	2	2	-	63404997	63413264
264347207	chrX	66765257	66765389	66765277	66765370	AR	NM_000044	1	8	1	+	66763874	66766604
264366735	chrX	66765680	66765821	66765702	66765803	AR	NM_000044	1	8	1	+	66763874	66766604
264358460	chrX	66766141	66766315	66766159	66766294	AR	NM_000044	1	8	1	+	66763874	66766604
259664452	chrX	66788764	66788921	66788784	66788895	AR	NM_001011645	2	8	1	+	66788683	66788864
265884179	chrX	66905917	66906072	66905938	66906046	AR	NM_001011645	2	8	3	+	66905852	66905968
265884179	chrX	66905917	66906072	66905938	66906046	AR	NM_000044	1	8	3	+	66905852	66905968
254456538	chrX	66937269	66937442	66937289	66937420	AR	NM_001011645	2	8	5	+	66937320	66937464
254456538	chrX	66937269	66937442	66937289	66937420	AR	NM_000044	1	8	5	+	66937320	66937464
266929317	chrX	66942643	66942808	66942665	66942786	AR	NM_001011645	2	8	7	+	66942669	66942826
266929317	chrX	66942643	66942808	66942665	66942786	AR	NM_000044	1	8	7	+	66942669	66942826
303242735	chrX	70586079	70586214	70586102	70586194	TAF1	NM_138923	2	38	1	+	70586114	70586344
303242735	chrX	70586079	70586214	70586102	70586194	TAF1	NM_004606	1	38	1	+	70586114	70586344
301340101	chrX	70587875	70588047	70587896	70588020	TAF1	NM_138923	2	38	3	+	70587904	70588020
301340101	chrX	70587875	70588047	70587896	70588020	TAF1	NM_004606	1	38	3	+	70587904	70588020
300407095	chrX	70596778	70596944	70596801	70596921	TAF1	NM_004606	1	38	5	+	70596800	70597041
300407095	chrX	70596778	70596944	70596801	70596921	TAF1	NM_138923	2	38	5	+	70596863	70597041
303971042	chrX	70598044	70598217	70598068	70598193	TAF1	NM_138923	2	38	7	+	70598085	70598303
303971042	chrX	70598044	70598217	70598068	70598193	TAF1	NM_004606	1	38	7	+	70598085	70598303
304873343	chrX	70601559	70601702	70601586	70601677	TAF1	NM_138923	2	38	9	+	70601593	70601769
304873343	chrX	70601559	70601702	70601586	70601677	TAF1	NM_004606	1	38	9	+	70601593	70601769
304840623	chrX	70602531	70602684	70602553	70602656	TAF1	NM_138923	2	38	11	+	70602611	70602718
304840623	chrX	70602531	70602684	70602553	70602656	TAF1	NM_004606	1	38	11	+	70602611	70602718
305878183	chrX	70603722	70603876	70603749	70603854	TAF1	NM_138923	2	38	13	+	70603812	70603985
305878183	chrX	70603722	70603876	70603749	70603854	TAF1	NM_004606	1	38	13	+	70603812	70603985
300780414	chrX	70604844	70604968	70604870	70604946	TAF1	NM_138923	2	38	14	+	70604795	70604899
300780414	chrX	70604844	70604968	70604870	70604946	TAF1	NM_004606	1	38	14	+	70604795	70604899
305647661	chrX	70607975	70608129	70608001	70608105	TAF1	NM_138923	2	38	16	+	70608087	70608228
305647661	chrX	70607975	70608129	70608001	70608105	TAF1	NM_004606	1	38	16	+	70608087	70608228
299799222	chrX	70612386	70612560	70612409	70612534	TAF1	NM_138923	2	38	19	+	70612419	70612568
299799222	chrX	70612386	70612560	70612409	70612534	TAF1	NM_004606	1	38	19	+	70612419	70612568
302850992	chrX	70613046	70613219	70613070	70613197	TAF1	NM_138923	2	38	21	+	70613151	70613326
302850992	chrX	70613046	70613219	70613070	70613197	TAF1	NM_004606	1	38	21	+	70613151	70613326

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300514290	chrX	70613961	70614117	70613986	70614095	TAF1	NM_138923	2	38	22	+	70613917	70614095
300514290	chrX	70613961	70614117	70613986	70614095	TAF1	NM_004606	1	38	22	+	70613917	70614095
301161627	chrX	70618447	70618620	70618468	70618596	TAF1	NM_138923	2	38	24	+	70618422	70618587
301161627	chrX	70618447	70618620	70618468	70618596	TAF1	NM_004606	1	38	24	+	70618422	70618587
304413905	chrX	70627391	70627565	70627419	70627537	TAF1	NM_138923	2	38	27	+	70627424	70627522
304413905	chrX	70627391	70627565	70627419	70627537	TAF1	NM_004606	1	38	27	+	70627424	70627522
300530438	chrX	70642885	70643036	70642908	70643014	TAF1	NM_138923	2	38	30	+	70642967	70643089
300530438	chrX	70642885	70643036	70642908	70643014	TAF1	NM_004606	1	38	30	+	70642967	70643089
299950708	chrX	70643967	70644131	70643989	70644104	TAF1	NM_138923	2	38	32	+	70644004	70644088
299950708	chrX	70643967	70644131	70643989	70644104	TAF1	NM_004606	1	38	32	+	70644004	70644088
301393202	chrX	70678091	70678265	70678118	70678239	TAF1	NM_138923	2	38	35	+	70678091	70678216
301393202	chrX	70678091	70678265	70678118	70678239	TAF1	NM_004606	1	38	35	+	70678091	70678216
302004365	chrX	70680544	70680677	70680565	70680653	TAF1	NM_138923	2	38	37	+	70680476	70680653
302004365	chrX	70680544	70680677	70680565	70680653	TAF1	NM_004606	1	38	37	+	70680476	70680653
273008565	chrX	76763742	76763911	76763771	76763890	ATRX	NM_000489	1	35	35	-	76760356	76764107
273008565	chrX	76763742	76763911	76763771	76763890	ATRX	NM_138270	2	34	34	-	76760356	76764107
273007400	chrX	76776149	76776311	76776175	76776284	ATRX	NM_000489	1	35	34	-	76776266	76776394
273007400	chrX	76776149	76776311	76776175	76776284	ATRX	NM_138270	2	34	33	-	76776266	76776394
274246902	chrX	76777644	76777775	76777672	76777754	ATRX	NM_000489	1	35	32	-	76777741	76777866
274246902	chrX	76777644	76777775	76777672	76777754	ATRX	NM_138270	2	34	31	-	76777741	76777866
274245997	chrX	76778758	76778908	76778784	76778879	ATRX	NM_000489	1	35	31	-	76778730	76778879
274245997	chrX	76778758	76778908	76778784	76778879	ATRX	NM_138270	2	34	30	-	76778730	76778879
273198237	chrX	76814038	76814188	76814066	76814166	ATRX	NM_000489	1	35	29	-	76814140	76814317
273198237	chrX	76814038	76814188	76814066	76814166	ATRX	NM_138270	2	34	28	-	76814140	76814317
272764204	chrX	76829727	76829887	76829755	76829859	ATRX	NM_000489	1	35	28	-	76829715	76829823
272764204	chrX	76829727	76829887	76829755	76829859	ATRX	NM_138270	2	34	27	-	76829715	76829823
273707434	chrX	76849158	76849284	76849184	76849257	ATRX	NM_000489	1	35	26	-	76849166	76849319
273707434	chrX	76849158	76849284	76849184	76849257	ATRX	NM_138270	2	34	25	-	76849166	76849319
272788559	chrX	76854975	76855145	76854999	76855117	ATRX	NM_000489	1	35	25	-	76854880	76855049
272788559	chrX	76854975	76855145	76854999	76855117	ATRX	NM_138270	2	34	24	-	76854880	76855049
273483827	chrX	76855920	76856045	76855944	76856022	ATRX	NM_000489	1	35	23	-	76855903	76856033
273483827	chrX	76855920	76856045	76855944	76856022	ATRX	NM_138270	2	34	22	-	76855903	76856033
273185038	chrX	76874263	76874415	76874291	76874389	ATRX	NM_000489	1	35	21	-	76874274	76874449
273185038	chrX	76874263	76874415	76874291	76874389	ATRX	NM_138270	2	34	20	-	76874274	76874449
272765791	chrX	76888655	76888814	76888682	76888789	ATRX	NM_000489	1	35	19	-	76888695	76888872
272765791	chrX	76888655	76888814	76888682	76888789	ATRX	NM_138270	2	34	18	-	76888695	76888872
272999734	chrX	76889068	76889223	76889095	76889195	ATRX	NM_000489	1	35	18	-	76889054	76889200
272999734	chrX	76889068	76889223	76889095	76889195	ATRX	NM_138270	2	34	17	-	76889054	76889200
273216623	chrX	76891337	76891488	76891358	76891459	ATRX	NM_000489	1	35	16	-	76891406	76891547
273216623	chrX	76891337	76891488	76891358	76891459	ATRX	NM_138270	2	34	15	-	76891406	76891547
273449324	chrX	76909495	76909669	76909524	76909642	ATRX	NM_000489	1	35	14	-	76909588	76909690

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273449324	chrX	76909495	76909669	76909524	76909642	ATRX	NM_138270	2	34	13	-	76909588	76909690
273174131	chrX	76918821	76918969	76918845	76918949	ATRX	NM_000489	1	35	12	-	76918871	76919047
273174131	chrX	76918821	76918969	76918845	76918949	ATRX	NM_138270	2	34	11	-	76918871	76919047
273268324	chrX	76931611	76931785	76931632	76931760	ATRX	NM_000489	1	35	10	-	76931721	76931793
273268324	chrX	76931611	76931785	76931632	76931760	ATRX	NM_138270	2	34	9	-	76931721	76931793
274007285	chrX	76937088	76937223	76937117	76937199	ATRX	NM_000489	1	35	9	-	76937012	76940085
274007285	chrX	76937088	76937223	76937117	76937199	ATRX	NM_138270	2	34	8	-	76937012	76940085
273990205	chrX	76937412	76937544	76937440	76937518	ATRX	NM_000489	1	35	9	-	76937012	76940085
273990205	chrX	76937412	76937544	76937440	76937518	ATRX	NM_138270	2	34	8	-	76937012	76940085
274006160	chrX	76937780	76937911	76937805	76937884	ATRX	NM_000489	1	35	9	-	76937012	76940085
274006160	chrX	76937780	76937911	76937805	76937884	ATRX	NM_138270	2	34	8	-	76937012	76940085
274013208	chrX	76938347	76938519	76938369	76938491	ATRX	NM_000489	1	35	9	-	76937012	76940085
274013208	chrX	76938347	76938519	76938369	76938491	ATRX	NM_138270	2	34	8	-	76937012	76940085
274009500	chrX	76938741	76938897	76938760	76938876	ATRX	NM_000489	1	35	9	-	76937012	76940085
274009500	chrX	76938741	76938897	76938760	76938876	ATRX	NM_138270	2	34	8	-	76937012	76940085
272793580	chrX	76939172	76939326	76939195	76939301	ATRX	NM_000489	1	35	9	-	76937012	76940085
272793580	chrX	76939172	76939326	76939195	76939301	ATRX	NM_138270	2	34	8	-	76937012	76940085
274019585	chrX	76939518	76939659	76939546	76939635	ATRX	NM_000489	1	35	9	-	76937012	76940085
274019585	chrX	76939518	76939659	76939546	76939635	ATRX	NM_138270	2	34	8	-	76937012	76940085
274024513	chrX	76939856	76940003	76939884	76939979	ATRX	NM_000489	1	35	9	-	76937012	76940085
274024513	chrX	76939856	76940003	76939884	76939979	ATRX	NM_138270	2	34	8	-	76937012	76940085
272810529	chrX	76949349	76949505	76949375	76949477	ATRX	NM_000489	1	35	6	-	76949313	76949426
273521490	chrX	76953975	76954108	76954002	76954079	ATRX	NM_000489	1	35	3	-	76954062	76954117
273521490	chrX	76953975	76954108	76954002	76954079	ATRX	NM_138270	2	34	3	-	76954062	76954117
272855174	chrX	77041408	77041578	77041425	77041553	ATRX	NM_000489	1	35	1	-	77041468	77041719
272855174	chrX	77041408	77041578	77041425	77041553	ATRX	NM_138270	2	34	1	-	77041468	77041719
269788816	chrX	79278631	79278772	79278656	79278751	TBX22	NM_016954	3	8	2	+	79278559	79278739
269788816	chrX	79278631	79278772	79278656	79278751	TBX22	NM_001109878	1	9	3	+	79278559	79278739
269788816	chrX	79278631	79278772	79278656	79278751	TBX22	NM_001109879	2	9	3	+	79278559	79278735
272544189	chrX	79282165	79282312	79282192	79282288	TBX22	NM_016954	3	8	5	+	79282203	79282367
272544189	chrX	79282165	79282312	79282192	79282288	TBX22	NM_001109879	2	9	6	+	79282203	79282367
272544189	chrX	79282165	79282312	79282192	79282288	TBX22	NM_001109878	1	9	6	+	79282203	79282367
271305198	chrX	79283545	79283675	79283569	79283647	TBX22	NM_016954	3	8	7	+	79283490	79283575
271305198	chrX	79283545	79283675	79283569	79283647	TBX22	NM_001109879	2	9	8	+	79283490	79283575
271305198	chrX	79283545	79283675	79283569	79283647	TBX22	NM_001109878	1	9	8	+	79283490	79283575
271689600	chrX	79286299	79286466	79286323	79286441	TBX22	NM_016954	3	8	8	+	79285997	79287268
271689600	chrX	79286299	79286466	79286323	79286441	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271689600	chrX	79286299	79286466	79286323	79286441	TBX22	NM_001109878	1	9	9	+	79285997	79287268
253941736	chrX	100608099	100608273	100608121	100608252	BTK	NM_000061	1	19	18	-	100608182	100608339
263782414	chrX	100609534	100609707	100609561	100609684	BTK	NM_000061	1	19	16	-	100609618	100609682
259163945	chrX	100611800	100611974	100611823	100611946	BTK	NM_000061	1	19	14	-	100611772	100611943

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258011862	chrX	100613537	100613710	100613561	100613684	BTK	NM_000061	1	19	11	-	100613605	100613684
265956189	chrX	100615542	100615671	100615563	100615643	BTK	NM_000061	1	19	8	-	100615556	100615743
254507753	chrX	100617562	100617704	100617585	100617678	BTK	NM_000061	1	19	6	-	100617549	100617677
253787706	chrX	100629999	100630173	100630027	100630148	BTK	NM_000061	1	19	2	-	100630132	100630302
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_001128172	4	15	2	+	110385324	110385424
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_001128168	3	16	2	+	110385324	110385424
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_001128173	5	15	2	+	110385324	110385424
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_001128166	1	16	4	+	110385324	110385424
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_001128167	2	15	3	+	110385324	110385424
270379172	chrX	110385248	110385404	110385277	110385379	PAK3	NM_002578	6	18	6	+	110385324	110385424
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_001128172	4	15	4	+	110390965	110391118
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_001128168	3	16	5	+	110390965	110391118
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_001128173	5	15	4	+	110390965	110391118
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_001128166	1	16	5	+	110390965	110391118
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_001128167	2	15	4	+	110390965	110391118
269573648	chrX	110390845	110391019	110390872	110390992	PAK3	NM_002578	6	18	7	+	110390965	110391118
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_001128172	4	15	6	+	110406143	110406274
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_001128168	3	16	7	+	110406143	110406274
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_001128173	5	15	6	+	110406143	110406274
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_001128166	1	16	7	+	110406143	110406274
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_001128167	2	15	6	+	110406143	110406274
269562850	chrX	110406134	110406258	110406161	110406237	PAK3	NM_002578	6	18	9	+	110406143	110406274
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_001128172	4	15	8	+	110416246	110416309
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_001128168	3	16	9	+	110416246	110416309
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_001128173	5	15	8	+	110416246	110416309
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_001128166	1	16	9	+	110416246	110416309
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_001128167	2	15	8	+	110416246	110416309
272684571	chrX	110416222	110416394	110416245	110416367	PAK3	NM_002578	6	18	11	+	110416246	110416309
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_001128172	4	15	10	+	110435734	110435846
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_001128168	3	16	11	+	110435734	110435846
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_001128173	5	15	10	+	110435734	110435846
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_001128166	1	16	11	+	110435734	110435846
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_001128167	2	15	10	+	110435734	110435846
269831716	chrX	110435798	110435944	110435823	110435916	PAK3	NM_002578	6	18	13	+	110435734	110435846
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_001128172	4	15	12	+	110439070	110439169
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_001128168	3	16	13	+	110439070	110439169
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_001128173	5	15	12	+	110439070	110439169
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_001128166	1	16	13	+	110439070	110439169
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_001128167	2	15	12	+	110439070	110439169
270033747	chrX	110439061	110439211	110439086	110439182	PAK3	NM_002578	6	18	15	+	110439070	110439169
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_001128172	4	15	14	+	110459649	110459786

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_001128168	3	16	15	+	110459649	110459786
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_001128173	5	15	14	+	110459649	110459786
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_001128166	1	16	15	+	110459649	110459786
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_001128167	2	15	14	+	110459649	110459786
270834982	chrX	110459672	110459838	110459694	110459811	PAK3	NM_002578	6	18	17	+	110459649	110459786
299281965	chrX	123480495	123480655	123480515	123480635	SH2D1A	NM_001114937	1	4	1	+	123480132	123480629
299281965	chrX	123480495	123480655	123480515	123480635	SH2D1A	NM_002351	2	4	1	+	123480132	123480629
298904286	chrX	123505184	123505337	123505217	123505309	SH2D1A	NM_001114937	1	4	4	+	123505201	123507010
298904286	chrX	123505184	123505337	123505217	123505309	SH2D1A	NM_002351	2	4	4	+	123505201	123507010
295163631	chrX	152482367	152482508	152482389	152482485	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
295167779	chrX	152482777	152482913	152482796	152482893	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
298955234	chrX	153760241	153760412	153760263	153760390	G6PD	NM_001042351	2	13	13	-	153759606	153760305
298955234	chrX	153760241	153760412	153760263	153760390	G6PD	NM_000402	1	13	13	-	153759606	153760305
299019388	chrX	153760750	153760900	153760769	153760883	G6PD	NM_001042351	2	13	10	-	153760782	153761017
299019388	chrX	153760750	153760900	153760769	153760883	G6PD	NM_000402	1	13	10	-	153760782	153761017
299118497	chrX	153761724	153761867	153761744	153761846	G6PD	NM_001042351	2	13	8	-	153761791	153761884
299118497	chrX	153761724	153761867	153761744	153761846	G6PD	NM_000402	1	13	8	-	153761791	153761884
299085019	chrX	153762496	153762651	153762516	153762630	G6PD	NM_001042351	2	13	6	-	153762553	153762711
299085019	chrX	153762496	153762651	153762516	153762630	G6PD	NM_000402	1	13	6	-	153762553	153762711
298974348	chrX	153763517	153763643	153763537	153763622	G6PD	NM_001042351	2	13	5	-	153763383	153763600
298974348	chrX	153763517	153763643	153763537	153763622	G6PD	NM_000402	1	13	5	-	153763383	153763600
298906497	chrX	153774168	153774293	153774190	153774265	G6PD	NM_001042351	2	13	2	-	153774251	153774378
298906497	chrX	153774168	153774293	153774190	153774265	G6PD	NM_000402	1	13	2	-	153774251	153774378
241330530	chr1	2489752	2489926	2489773	2489907	TNFRSF14	NM_003820	1	8	3	+	2489782	2489907
239707106	chr1	2493043	2493213	2493063	2493190	TNFRSF14	NM_003820	1	8	6	+	2493112	2493254
266254908	chr1	2494608	2494781	2494629	2494760	TNFRSF14	NM_003820	1	8	8	+	2494587	2495267
294023907	chr1	6528009	6528183	6528026	6528165	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294023907	chr1	6528009	6528183	6528026	6528165	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646
294023907	chr1	6528009	6528183	6528026	6528165	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294023907	chr1	6528009	6528183	6528026	6528165	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294023907	chr1	6528009	6528183	6528026	6528165	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
294048929	chr1	6528500	6528674	6528517	6528656	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294048929	chr1	6528500	6528674	6528517	6528656	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646
294048929	chr1	6528500	6528674	6528517	6528656	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294048929	chr1	6528500	6528674	6528517	6528656	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294048929	chr1	6528500	6528674	6528517	6528656	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042664	2	21	17	-	6529604	6529736
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042665	3	21	17	-	6529604	6529736
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_020631	4	21	17	-	6529604	6529736
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042663	1	22	18	-	6529604	6529736
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_198681	5	22	18	-	6529604	6529736

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042664	2	21	18	-	6529395	6529510
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042665	3	21	18	-	6529395	6529510
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_020631	4	21	18	-	6529395	6529510
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_001042663	1	22	19	-	6529395	6529510
295371486	chr1	6529471	6529644	6529496	6529623	PLEKHG5	NM_198681	5	22	19	-	6529395	6529510
293788128	chr1	6530286	6530456	6530308	6530437	PLEKHG5	NM_001042664	2	21	16	-	6530296	6530415
293788128	chr1	6530286	6530456	6530308	6530437	PLEKHG5	NM_001042665	3	21	16	-	6530296	6530415
293788128	chr1	6530286	6530456	6530308	6530437	PLEKHG5	NM_020631	4	21	16	-	6530296	6530415
293788128	chr1	6530286	6530456	6530308	6530437	PLEKHG5	NM_001042663	1	22	17	-	6530296	6530415
293788128	chr1	6530286	6530456	6530308	6530437	PLEKHG5	NM_198681	5	22	17	-	6530296	6530415
294266574	chr1	6530778	6530928	6530798	6530910	PLEKHG5	NM_001042664	2	21	14	-	6530795	6530944
294266574	chr1	6530778	6530928	6530798	6530910	PLEKHG5	NM_001042665	3	21	14	-	6530795	6530944
294266574	chr1	6530778	6530928	6530798	6530910	PLEKHG5	NM_020631	4	21	14	-	6530795	6530944
294266574	chr1	6530778	6530928	6530798	6530910	PLEKHG5	NM_001042663	1	22	15	-	6530795	6530944
294266574	chr1	6530778	6530928	6530798	6530910	PLEKHG5	NM_198681	5	22	15	-	6530795	6530944
293956644	chr1	6531478	6531639	6531495	6531621	PLEKHG5	NM_001042664	2	21	12	-	6531548	6531697
293956644	chr1	6531478	6531639	6531495	6531621	PLEKHG5	NM_001042665	3	21	12	-	6531548	6531697
293956644	chr1	6531478	6531639	6531495	6531621	PLEKHG5	NM_020631	4	21	12	-	6531548	6531697
293956644	chr1	6531478	6531639	6531495	6531621	PLEKHG5	NM_001042663	1	22	13	-	6531548	6531697
293956644	chr1	6531478	6531639	6531495	6531621	PLEKHG5	NM_198681	5	22	13	-	6531548	6531697
295272457	chr1	6532501	6532625	6532522	6532603	PLEKHG5	NM_001042664	2	21	10	-	6532587	6532682
295272457	chr1	6532501	6532625	6532522	6532603	PLEKHG5	NM_001042665	3	21	10	-	6532587	6532682
295272457	chr1	6532501	6532625	6532522	6532603	PLEKHG5	NM_020631	4	21	10	-	6532587	6532682
295272457	chr1	6532501	6532625	6532522	6532603	PLEKHG5	NM_001042663	1	22	11	-	6532587	6532682
295272457	chr1	6532501	6532625	6532522	6532603	PLEKHG5	NM_198681	5	22	11	-	6532587	6532682
294478446	chr1	6533226	6533395	6533250	6533377	PLEKHG5	NM_001042664	2	21	8	-	6533311	6533514
294478446	chr1	6533226	6533395	6533250	6533377	PLEKHG5	NM_001042665	3	21	8	-	6533311	6533514
294478446	chr1	6533226	6533395	6533250	6533377	PLEKHG5	NM_020631	4	21	8	-	6533311	6533514
294478446	chr1	6533226	6533395	6533250	6533377	PLEKHG5	NM_001042663	1	22	9	-	6533311	6533514
294478446	chr1	6533226	6533395	6533250	6533377	PLEKHG5	NM_198681	5	22	9	-	6533311	6533514
294008013	chr1	6534147	6534272	6534167	6534252	PLEKHG5	NM_001042664	2	21	7	-	6534073	6534224
294008013	chr1	6534147	6534272	6534167	6534252	PLEKHG5	NM_001042665	3	21	7	-	6534073	6534224
294008013	chr1	6534147	6534272	6534167	6534252	PLEKHG5	NM_020631	4	21	7	-	6534073	6534224
294008013	chr1	6534147	6534272	6534167	6534252	PLEKHG5	NM_001042663	1	22	8	-	6534073	6534224
294008013	chr1	6534147	6534272	6534167	6534252	PLEKHG5	NM_198681	5	22	8	-	6534073	6534224
294368728	chr1	6535468	6535621	6535485	6535603	PLEKHG5	NM_001042664	2	21	4	-	6535522	6535582
294368728	chr1	6535468	6535621	6535485	6535603	PLEKHG5	NM_001042665	3	21	4	-	6535522	6535582
294368728	chr1	6535468	6535621	6535485	6535603	PLEKHG5	NM_020631	4	21	4	-	6535522	6535582
294368728	chr1	6535468	6535621	6535485	6535603	PLEKHG5	NM_001042663	1	22	5	-	6535522	6535582
294368728	chr1	6535468	6535621	6535485	6535603	PLEKHG5	NM_198681	5	22	5	-	6535522	6535582
294593642	chr1	6556534	6556668	6556552	6556651	PLEKHG5	NM_001042663	1	22	2	-	6556553	6556629

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294593642	chr1	6556534	6556668	6556552	6556651	PLEKHG5	NM_198681	5	22	2	-	6556553	6556629
295326112	chr1	9770536	9770684	9770558	9770664	PIK3CD	NM_005026	1	24	3	+	9770482	9770654
294130274	chr1	9775784	9775955	9775810	9775933	PIK3CD	NM_005026	1	24	5	+	9775907	9776136
294130274	chr1	9775784	9775955	9775810	9775933	PIK3CD	NM_005026	1	24	4	+	9775599	9775827
294158643	chr1	9776468	9776625	9776487	9776605	PIK3CD	NM_005026	1	24	6	+	9776498	9776677
294862001	chr1	9777540	9777711	9777561	9777690	PIK3CD	NM_005026	1	24	8	+	9777595	9777684
294653147	chr1	9779955	9780128	9779974	9780108	PIK3CD	NM_005026	1	24	10	+	9779979	9780075
295267449	chr1	9780762	9780906	9780780	9780887	PIK3CD	NM_005026	1	24	13	+	9780800	9780967
294423471	chr1	9781538	9781686	9781559	9781666	PIK3CD	NM_005026	1	24	15	+	9781502	9781645
293823222	chr1	9782072	9782246	9782094	9782227	PIK3CD	NM_005026	1	24	17	+	9782033	9782211
294684623	chr1	9783151	9783290	9783171	9783268	PIK3CD	NM_005026	1	24	20	+	9783183	9783350
294693664	chr1	9784277	9784423	9784301	9784400	PIK3CD	NM_005026	1	24	22	+	9784334	9784479
295349603	chr1	9787023	9787182	9787044	9787161	PIK3CD	NM_005026	1	24	24	+	9786967	9789172
237591111	chr1	11169668	11169835	11169688	11169807	MTOR	NM_004958	1	58	55	-	11169706	11169786
235880812	chr1	11174845	11175003	11174865	11174975	MTOR	NM_004958	1	58	52	-	11174870	11174944
235621812	chr1	11181238	11181409	11181257	11181386	MTOR	NM_004958	1	58	49	-	11181303	11181425
237477988	chr1	11184513	11184684	11184541	11184659	MTOR	NM_004958	1	58	47	-	11184555	11184690
237214547	chr1	11186950	11187124	11186974	11187099	MTOR	NM_004958	1	58	45	-	11187067	11187201
237535029	chr1	11187981	11188129	11188006	11188105	MTOR	NM_004958	1	58	43	-	11188061	11188183
235519965	chr1	11188786	11188936	11188810	11188912	MTOR	NM_004958	1	58	41	-	11188912	11189008
236791511	chr1	11190620	11190766	11190637	11190741	MTOR	NM_004958	1	58	39	-	11190586	11190834
237165980	chr1	11193170	11193298	11193192	11193275	MTOR	NM_004958	1	58	38	-	11193137	11193254
235677538	chr1	11199366	11199532	11199389	11199505	MTOR	NM_004958	1	58	36	-	11199361	11199492
236326670	chr1	11204986	11205127	11205010	11205103	MTOR	NM_004958	1	58	33	-	11205025	11205102
238140375	chr1	11217128	11217295	11217150	11217271	MTOR	NM_004958	1	58	30	-	11217209	11217348
242148700	chr1	11259347	11259485	11259369	11259463	MTOR	NM_004958	1	58	28	-	11259315	11259460
236900732	chr1	11264673	11264810	11264695	11264784	MTOR	NM_004958	1	58	26	-	11264618	11264760
242158130	chr1	11272345	11272501	11272367	11272480	MTOR	NM_004958	1	58	23	-	11272369	11272531
237865860	chr1	11273549	11273673	11273572	11273650	MTOR	NM_004958	1	58	21	-	11273456	11273623
237287930	chr1	11288913	11289045	11288936	11289023	MTOR	NM_004958	1	58	19	-	11288725	11288975
242223119	chr1	11291366	11291515	11291387	11291492	MTOR	NM_004958	1	58	17	-	11291357	11291491
235773041	chr1	11294178	11294349	11294199	11294322	MTOR	NM_004958	1	58	14	-	11294200	11294322
238727223	chr1	11298521	11298686	11298543	11298663	MTOR	NM_004958	1	58	12	-	11298459	11298674
242436622	chr1	11300495	11300668	11300517	11300645	MTOR	NM_004958	1	58	11	-	11300360	11300604
238458768	chr1	11303221	11303386	11303245	11303358	MTOR	NM_004958	1	58	9	-	11303171	11303357
235283041	chr1	11308074	11308207	11308098	11308179	MTOR	NM_004958	1	58	7	-	11307876	11308151
237306608	chr1	11316158	11316282	11316179	11316257	MTOR	NM_004958	1	58	5	-	11316049	11316249
237736906	chr1	11318536	11318709	11318558	11318681	MTOR	NM_004958	1	58	3	-	11318542	11318650
239744790	chr1	17345387	17345536	17345414	17345512	SDHB	NM_003000	1	8	8	-	17345225	17345453
242019466	chr1	17354176	17354329	17354196	17354301	SDHB	NM_003000	1	8	5	-	17354244	17354360
240929067	chr1	17359516	17359688	17359538	17359661	SDHB	NM_003000	1	8	3	-	17359555	17359640

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240236189	chr1	18958051	18958201	18958072	18958182	PAX7	NM_002584	2	8	1	+	18957500	18958182
240236189	chr1	18958051	18958201	18958072	18958182	PAX7	NM_001135254	1	9	1	+	18957500	18958182
240236189	chr1	18958051	18958201	18958072	18958182	PAX7	NM_013945	3	8	1	+	18957500	18958182
235489147	chr1	18961579	18961753	18961599	18961735	PAX7	NM_002584	2	8	3	+	18961605	18961734
235489147	chr1	18961579	18961753	18961599	18961735	PAX7	NM_001135254	1	9	3	+	18961605	18961734
235489147	chr1	18961579	18961753	18961599	18961735	PAX7	NM_013945	3	8	3	+	18961605	18961734
239380625	chr1	19018190	19018337	19018212	19018318	PAX7	NM_002584	2	8	5	+	19018248	19018447
239380625	chr1	19018190	19018337	19018212	19018318	PAX7	NM_001135254	1	9	5	+	19018248	19018447
239380625	chr1	19018190	19018337	19018212	19018318	PAX7	NM_013945	3	8	5	+	19018248	19018447
235273298	chr1	19027205	19027351	19027224	19027333	PAX7	NM_002584	2	8	6	+	19027147	19027312
235273298	chr1	19027205	19027351	19027224	19027333	PAX7	NM_001135254	1	9	6	+	19027147	19027312
235273298	chr1	19027205	19027351	19027224	19027333	PAX7	NM_013945	3	8	6	+	19027147	19027312
237306504	chr1	19062213	19062337	19062231	19062320	PAX7	NM_001135254	1	9	8	+	19062126	19062372
237306504	chr1	19062213	19062337	19062231	19062320	PAX7	NM_002584	2	8	8	+	19062126	19062632
237306504	chr1	19062213	19062337	19062231	19062320	PAX7	NM_013945	3	8	8	+	19062126	19062632
225015307	chr1	27022953	27023121	27022970	27023103	ARID1A	NM_139135	2	20	1	+	27022522	27024031
225015307	chr1	27022953	27023121	27022970	27023103	ARID1A	NM_006015	1	20	1	+	27022522	27024031
225017167	chr1	27023393	27023542	27023414	27023517	ARID1A	NM_139135	2	20	1	+	27022522	27024031
225017167	chr1	27023393	27023542	27023414	27023517	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223547457	chr1	27023812	27023973	27023829	27023954	ARID1A	NM_139135	2	20	1	+	27022522	27024031
223547457	chr1	27023812	27023973	27023829	27023954	ARID1A	NM_006015	1	20	1	+	27022522	27024031
222689454	chr1	27057553	27057724	27057578	27057703	ARID1A	NM_139135	2	20	3	+	27057643	27058095
222689454	chr1	27057553	27057724	27057578	27057703	ARID1A	NM_006015	1	20	3	+	27057643	27058095
222375807	chr1	27059136	27059310	27059162	27059284	ARID1A	NM_139135	2	20	4	+	27059167	27059283
222375807	chr1	27059136	27059310	27059162	27059284	ARID1A	NM_006015	1	20	4	+	27059167	27059283
222554662	chr1	27087823	27087953	27087847	27087928	ARID1A	NM_139135	2	20	6	+	27087875	27087964
222554662	chr1	27087823	27087953	27087847	27087928	ARID1A	NM_006015	1	20	6	+	27087875	27087964
224704840	chr1	27089420	27089577	27089445	27089556	ARID1A	NM_139135	2	20	8	+	27089464	27089776
224704840	chr1	27089420	27089577	27089445	27089556	ARID1A	NM_006015	1	20	8	+	27089464	27089776
225180821	chr1	27092747	27092899	27092767	27092871	ARID1A	NM_139135	2	20	9	+	27092712	27092857
225180821	chr1	27092747	27092899	27092767	27092871	ARID1A	NM_006015	1	20	9	+	27092712	27092857
223482884	chr1	27094272	27094446	27094299	27094424	ARID1A	NM_139135	2	20	11	+	27094281	27094490
223482884	chr1	27094272	27094446	27094299	27094424	ARID1A	NM_006015	1	20	11	+	27094281	27094490
223115559	chr1	27098883	27099057	27098909	27099036	ARID1A	NM_139135	2	20	13	+	27098991	27099123
223115559	chr1	27098883	27099057	27098909	27099036	ARID1A	NM_006015	1	20	13	+	27098991	27099123
222657782	chr1	27099786	27099940	27099810	27099920	ARID1A	NM_139135	2	20	15	+	27099837	27099987
222657782	chr1	27099786	27099940	27099810	27099920	ARID1A	NM_006015	1	20	15	+	27099837	27099987
223571185	chr1	27100257	27100417	27100277	27100397	ARID1A	NM_139135	2	20	17	+	27100293	27100389
223571185	chr1	27100257	27100417	27100277	27100397	ARID1A	NM_006015	1	20	17	+	27100293	27100389
225170797	chr1	27101084	27101251	27101104	27101223	ARID1A	NM_006015	1	20	18	+	27100820	27101711
222561786	chr1	27101513	27101638	27101534	27101617	ARID1A	NM_006015	1	20	18	+	27100820	27101711

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222561786	chr1	27101513	27101638	27101534	27101617	ARID1A	NM_139135	2	20	18	+	27101471	27101711
223498571	chr1	27105402	27105565	27105424	27105540	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223498571	chr1	27105402	27105565	27105424	27105540	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223551163	chr1	27105822	27105983	27105850	27105962	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223551163	chr1	27105822	27105983	27105850	27105962	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223561744	chr1	27106260	27106385	27106283	27106363	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223561744	chr1	27106260	27106385	27106283	27106363	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224985943	chr1	27106611	27106784	27106632	27106761	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224985943	chr1	27106611	27106784	27106632	27106761	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224984253	chr1	27107049	27107212	27107069	27107185	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224984253	chr1	27107049	27107212	27107069	27107185	ARID1A	NM_006015	1	20	20	+	27105514	27108601
233218055	chr1	32740282	32740451	32740304	32740431	LCK	NM_005356	2	13	3	+	32740338	32740419
233218055	chr1	32740282	32740451	32740304	32740431	LCK	NM_001042771	1	13	3	+	32740338	32740419
231441371	chr1	32741226	32741371	32741244	32741354	LCK	NM_005356	2	13	6	+	32741170	32741273
231441371	chr1	32741226	32741371	32741244	32741354	LCK	NM_001042771	1	13	6	+	32741170	32741273
233224191	chr1	32742009	32742168	32742028	32742148	LCK	NM_005356	2	13	8	+	32741938	32742090
233224191	chr1	32742009	32742168	32742028	32742148	LCK	NM_001042771	1	13	8	+	32741938	32742090
233177631	chr1	32745385	32745542	32745407	32745522	LCK	NM_005356	2	13	11	+	32745442	32745595
233177631	chr1	32745385	32745542	32745407	32745522	LCK	NM_001042771	1	13	11	+	32745442	32745595
233334549	chr1	32751093	32751262	32751114	32751242	LCK	NM_005356	2	13	13	+	32751115	32751766
233334549	chr1	32751093	32751262	32751114	32751242	LCK	NM_001042771	1	13	13	+	32751115	32751766
241496606	chr1	40363136	40363308	40363157	40363285	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
241496606	chr1	40363136	40363308	40363157	40363285	MYCL1	NM_001033081	1	2	2	-	40361096	40363642
241866608	chr1	40366377	40366523	40366401	40366503	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235128370	chr1	40366852	40367014	40366870	40366993	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235128370	chr1	40366852	40367014	40366870	40366993	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235128370	chr1	40366852	40367014	40366870	40366993	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
236936286	chr1	43803468	43803635	43803489	43803614	MPL	NM_005373	1	12	1	+	43803475	43803598
238523219	chr1	43804882	43805017	43804903	43804995	MPL	NM_005373	1	12	4	+	43804942	43805240
236666148	chr1	43805683	43805839	43805703	43805815	MPL	NM_005373	1	12	5	+	43805635	43805797
241634684	chr1	43812188	43812329	43812209	43812301	MPL	NM_005373	1	12	7	+	43812116	43812300
239483569	chr1	43814563	43814709	43814583	43814692	MPL	NM_005373	1	12	9	+	43814514	43814673
241690821	chr1	43818266	43818437	43818286	43818415	MPL	NM_005373	1	12	12	+	43818189	43820135
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_012222	6	16	15	-	45796188	45796229
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_001048171	1	16	15	-	45796188	45796229
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_001128425	5	16	15	-	45796188	45796229
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_001048174	4	16	15	-	45796188	45796229
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_001048173	3	16	15	-	45796188	45796229
238651312	chr1	45796080	45796254	45796102	45796230	MUTYH	NM_001048172	2	16	15	-	45796188	45796229
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_012222	6	16	13	-	45797092	45797228
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_001048171	1	16	13	-	45797092	45797228

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_001128425	5	16	13	-	45797092	45797228
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_001048174	4	16	13	-	45797092	45797228
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_001048173	3	16	13	-	45797092	45797228
258600971	chr1	45797132	45797306	45797152	45797280	MUTYH	NM_001048172	2	16	13	-	45797092	45797228
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_012222	6	16	10	-	45797838	45797982
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_001048171	1	16	10	-	45797838	45797982
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_001128425	5	16	10	-	45797838	45797982
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_001048174	4	16	10	-	45797838	45797982
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_001048173	3	16	10	-	45797838	45797982
237745484	chr1	45797765	45797911	45797785	45797891	MUTYH	NM_001048172	2	16	10	-	45797838	45797982
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_012222	6	16	7	-	45798435	45798506
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_001048171	1	16	7	-	45798435	45798506
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_001128425	5	16	7	-	45798435	45798506
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_001048174	4	16	7	-	45798435	45798506
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_001048173	3	16	7	-	45798435	45798506
237824275	chr1	45798357	45798529	45798378	45798507	MUTYH	NM_001048172	2	16	7	-	45798435	45798506
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_012222	6	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048171	1	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001128425	5	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048174	4	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048173	3	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048172	2	16	4	-	45798957	45798996
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048172	2	16	3	-	45799085	45799236
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048171	1	16	3	-	45799085	45799233
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048174	4	16	3	-	45799085	45799233
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001048173	3	16	3	-	45799085	45799233
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_012222	6	16	3	-	45799085	45799266
237676414	chr1	45798969	45799134	45798990	45799113	MUTYH	NM_001128425	5	16	3	-	45799085	45799275
238464266	chr1	45805784	45805957	45805803	45805938	MUTYH	NM_012222	6	16	1	-	45805891	45806142
238464266	chr1	45805784	45805957	45805803	45805938	MUTYH	NM_001048171	1	16	1	-	45805891	45806142
238464266	chr1	45805784	45805957	45805803	45805938	MUTYH	NM_001128425	5	16	1	-	45805891	45806142
265147229	chr1	47685647	47685792	47685668	47685773	TAL1	NM_003189	1	4	4	-	47681963	47685846
240387103	chr1	47691027	47691157	47691045	47691139	TAL1	NM_003189	1	4	2	-	47691115	47691561
240390110	chr1	47691455	47691590	47691474	47691569	TAL1	NM_003189	1	4	2	-	47691115	47691561
321854627	chr1	47834167	47834311	47834187	47834288	CMPK1	NM_016308	2	6	2	+	47834141	47834287
321842830	chr1	47840780	47840947	47840801	47840919	CMPK1	NM_016308	2	6	5	+	47840869	47840965
321842830	chr1	47840780	47840947	47840801	47840919	CMPK1	NM_001136140	1	5	4	+	47840869	47840965
225615366	chr1	51436087	51436217	51436111	51436189	CDKN2C	NM_001262	1	3	2	+	51436030	51436169
225615366	chr1	51436087	51436217	51436111	51436189	CDKN2C	NM_078626	2	2	1	+	51435642	51436169
225617579	chr1	51439855	51440005	51439876	51439977	CDKN2C	NM_001262	1	3	3	+	51439565	51440306
225617579	chr1	51439855	51440005	51439876	51439977	CDKN2C	NM_078626	2	2	2	+	51439565	51440309

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232185765	chr1	59247956	59248114	59247975	59248097	JUN	NM_002228	1	1	1	-	59246463	59249785
232056349	chr1	65301015	65301189	65301042	65301164	JAK1	NM_002227	1	25	24	-	65301079	65301189
233093129	chr1	65303530	65303694	65303557	65303668	JAK1	NM_002227	1	25	22	-	65303615	65303787
233526725	chr1	65305210	65305384	65305231	65305357	JAK1	NM_002227	1	25	20	-	65305286	65305478
233082523	chr1	65307172	65307314	65307194	65307292	JAK1	NM_002227	1	25	18	-	65307134	65307284
232244465	chr1	65310441	65310612	65310462	65310590	JAK1	NM_002227	1	25	16	-	65310437	65310572
231761545	chr1	65313189	65313315	65313213	65313291	JAK1	NM_002227	1	25	13	-	65313215	65313358
233052589	chr1	65321119	65321290	65321140	65321271	JAK1	NM_002227	1	25	11	-	65321192	65321381
232279369	chr1	65325856	65326030	65325879	65326010	JAK1	NM_002227	1	25	9	-	65325788	65325945
232921230	chr1	65332574	65332738	65332596	65332714	JAK1	NM_002227	1	25	7	-	65332549	65332891
231457422	chr1	65335009	65335179	65335031	65335158	JAK1	NM_002227	1	25	6	-	65334994	65335157
232325641	chr1	65344765	65344938	65344786	65344910	JAK1	NM_002227	1	25	4	-	65344708	65344831
233197502	chr1	65351833	65351971	65351861	65351947	JAK1	NM_002227	1	25	2	-	65351942	65352024
223213616	chr1	85733478	85733640	85733504	85733619	BCL10	NM_003921	1	3	3	-	85731460	85733665
222967155	chr1	85736414	85736567	85736442	85736541	BCL10	NM_003921	1	3	2	-	85736301	85736589
299174492	chr1	97544440	97544610	97544464	97544586	DPYD	NM_000110	1	23	23	-	97543300	97544702
298936414	chr1	97564004	97564155	97564035	97564127	DPYD	NM_000110	1	23	21	-	97564045	97564188
298920356	chr1	97700298	97700461	97700320	97700438	DPYD	NM_000110	1	23	19	-	97700408	97700550
328847682	chr1	97771802	97771975	97771823	97771947	DPYD	NM_000110	1	23	17	-	97771733	97771853
299131980	chr1	97847942	97848074	97847965	97848043	DPYD	NM_000110	1	23	15	-	97847949	97848017
298970381	chr1	97981291	97981420	97981314	97981397	DPYD	NM_000110	1	23	13	-	97981282	97981497
299243469	chr1	98015195	98015352	98015217	98015324	DPYD	NM_000110	1	23	12	-	98015116	98015300
299038461	chr1	98058736	98058883	98058764	98058862	DPYD	NM_000110	1	23	10	-	98058774	98058943
299201595	chr1	98144568	98144739	98144594	98144712	DPYD	NM_000110	1	23	8	-	98144651	98144738
299244123	chr1	98164952	98165126	98164973	98165102	DPYD	NM_000110	1	23	6	-	98164907	98165103
298945880	chr1	98187181	98187307	98187209	98187276	DPYD	NM_001160301	2	6	5	-	98187066	98187227
298945880	chr1	98187181	98187307	98187209	98187276	DPYD	NM_000110	1	23	5	-	98187066	98187227
299168048	chr1	98293702	98293829	98293725	98293796	DPYD	NM_001160301	2	6	3	-	98293670	98293752
299168048	chr1	98293702	98293829	98293725	98293796	DPYD	NM_000110	1	23	3	-	98293670	98293752
262162995	chr1	114940287	114940456	114940311	114940428	TRIM33	NM_015906	1	20	20	-	114935399	114940482
262162995	chr1	114940287	114940456	114940311	114940428	TRIM33	NM_033020	2	19	19	-	114935399	114940482
238792478	chr1	114942114	114942267	114942133	114942238	TRIM33	NM_015906	1	20	18	-	114942079	114942231
238792478	chr1	114942114	114942267	114942133	114942238	TRIM33	NM_033020	2	19	18	-	114942079	114942231
264687061	chr1	114947916	114948074	114947944	114948046	TRIM33	NM_015906	1	20	15	-	114948032	114948381
264687061	chr1	114947916	114948074	114947944	114948046	TRIM33	NM_033020	2	19	15	-	114948032	114948381
241083391	chr1	114949497	114949652	114949524	114949625	TRIM33	NM_015906	1	20	14	-	114949563	114949722
241083391	chr1	114949497	114949652	114949524	114949625	TRIM33	NM_033020	2	19	14	-	114949563	114949722
263219607	chr1	114952905	114953061	114952934	114953033	TRIM33	NM_015906	1	20	12	-	114952806	114952938
263219607	chr1	114952905	114953061	114952934	114953033	TRIM33	NM_033020	2	19	12	-	114952806	114952938
266382136	chr1	114967196	114967322	114967224	114967297	TRIM33	NM_015906	1	20	10	-	114967213	114967377
266382136	chr1	114967196	114967322	114967224	114967297	TRIM33	NM_033020	2	19	10	-	114967213	114967377

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239393913	chr1	114968180	114968321	114968209	114968295	TRIM33	NM_015906	1	20	9	-	114968071	114968345
239393913	chr1	114968180	114968321	114968209	114968295	TRIM33	NM_033020	2	19	9	-	114968071	114968345
264656455	chr1	114969873	114970021	114969896	114969993	TRIM33	NM_015906	1	20	8	-	114969799	114969916
264656455	chr1	114969873	114970021	114969896	114969993	TRIM33	NM_033020	2	19	8	-	114969799	114969916
266290079	chr1	114976169	114976333	114976196	114976306	TRIM33	NM_015906	1	20	5	-	114976239	114976355
266290079	chr1	114976169	114976333	114976196	114976306	TRIM33	NM_033020	2	19	5	-	114976239	114976355
240577020	chr1	115005828	115005990	115005847	115005963	TRIM33	NM_015906	1	20	4	-	115005726	115005858
240577020	chr1	115005828	115005990	115005847	115005963	TRIM33	NM_033020	2	19	4	-	115005726	115005858
238816521	chr1	115006776	115006942	115006801	115006918	TRIM33	NM_015906	1	20	2	-	115006892	115007010
238816521	chr1	115006776	115006942	115006801	115006918	TRIM33	NM_033020	2	19	2	-	115006892	115007010
266355283	chr1	115053300	115053449	115053319	115053430	TRIM33	NM_015906	1	20	1	-	115053172	115053781
266355283	chr1	115053300	115053449	115053319	115053430	TRIM33	NM_033020	2	19	1	-	115053172	115053781
237210508	chr1	115252129	115252281	115252157	115252257	NRAS	NM_002524	1	7	4	-	115252190	115252349
237217291	chr1	115258600	115258729	115258628	115258704	NRAS	NM_002524	1	7	2	-	115258671	115258798
242070942	chr1	120458096	120458256	120458117	120458234	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242170242	chr1	120458520	120458688	120458539	120458666	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242214148	chr1	120458955	120459129	120458978	120459109	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237478313	chr1	120460307	120460463	120460328	120460435	NOTCH2	NM_024408	2	34	33	-	120460288	120460385
238357654	chr1	120461989	120462163	120462009	120462137	NOTCH2	NM_024408	2	34	31	-	120461935	120462236
237102665	chr1	120464229	120464403	120464256	120464376	NOTCH2	NM_024408	2	34	29	-	120464336	120464432
239263457	chr1	120465201	120465372	120465223	120465350	NOTCH2	NM_024408	2	34	27	-	120465259	120465401
235139142	chr1	120466443	120466604	120466463	120466579	NOTCH2	NM_024408	2	34	26	-	120466260	120466607
257686635	chr1	120468107	120468255	120468127	120468231	NOTCH2	NM_024408	2	34	25	-	120467928	120468433
236928340	chr1	120469139	120469287	120469163	120469264	NOTCH2	NM_024408	2	34	24	-	120469122	120469234
236906083	chr1	120477895	120478069	120477922	120478042	NOTCH2	NM_001200001	1	22	22	-	120477736	120478227
237768779	chr1	120479970	120480128	120479991	120480100	NOTCH2	NM_001200001	1	22	21	-	120479905	120480089
237768779	chr1	120479970	120480128	120479991	120480100	NOTCH2	NM_024408	2	34	21	-	120479905	120480089
235341253	chr1	120483242	120483405	120483263	120483379	NOTCH2	NM_001200001	1	22	19	-	120483178	120483379
235341253	chr1	120483242	120483405	120483263	120483379	NOTCH2	NM_024408	2	34	19	-	120483178	120483379
240726215	chr1	120490916	120491085	120490939	120491064	NOTCH2	NM_001200001	1	22	17	-	120491037	120491189
240726215	chr1	120490916	120491085	120490939	120491064	NOTCH2	NM_024408	2	34	17	-	120491037	120491189
236389810	chr1	120493276	120493403	120493297	120493378	NOTCH2	NM_001200001	1	22	15	-	120493347	120493460
236389810	chr1	120493276	120493403	120493297	120493378	NOTCH2	NM_024408	2	34	15	-	120493347	120493460
235595589	chr1	120497609	120497768	120497632	120497748	NOTCH2	NM_001200001	1	22	13	-	120497663	120497855
235595589	chr1	120497609	120497768	120497632	120497748	NOTCH2	NM_024408	2	34	13	-	120497663	120497855
237627770	chr1	120506242	120506371	120506261	120506349	NOTCH2	NM_001200001	1	22	11	-	120506197	120506430
237627770	chr1	120506242	120506371	120506261	120506349	NOTCH2	NM_024408	2	34	11	-	120506197	120506430
235339417	chr1	120509009	120509158	120509030	120509132	NOTCH2	NM_001200001	1	22	9	-	120508999	120509112
235339417	chr1	120509009	120509158	120509030	120509132	NOTCH2	NM_024408	2	34	9	-	120508999	120509112
236363607	chr1	120510733	120510896	120510753	120510869	NOTCH2	NM_001200001	1	22	7	-	120510700	120510855
236363607	chr1	120510733	120510896	120510753	120510869	NOTCH2	NM_024408	2	34	7	-	120510700	120510855

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236081261	chr1	120529631	120529761	120529653	120529734	NOTCH2	NM_001200001	1	22	5	-	120529583	120529705
236081261	chr1	120529631	120529761	120529653	120529734	NOTCH2	NM_024408	2	34	5	-	120529583	120529705
238084206	chr1	120539812	120539951	120539838	120539933	NOTCH2	NM_001200001	1	22	4	-	120539620	120539955
238084206	chr1	120539812	120539951	120539838	120539933	NOTCH2	NM_024408	2	34	4	-	120539620	120539955
238194370	chr1	144852424	144852594	144852443	144852573	PDE4DIP	NM_014644	8	44	44	-	144851427	144852499
238194370	chr1	144852424	144852594	144852443	144852573	PDE4DIP	NM_001198834	7	44	44	-	144851424	144852443
238194370	chr1	144852424	144852594	144852443	144852573	PDE4DIP	NM_001198832	6	46	46	-	144851424	144852499
235284518	chr1	144855716	144855883	144855736	144855861	PDE4DIP	NM_001198832	6	46	43	-	144855740	144855883
235284518	chr1	144855716	144855883	144855736	144855861	PDE4DIP	NM_001198834	7	44	41	-	144855740	144855883
235284518	chr1	144855716	144855883	144855736	144855861	PDE4DIP	NM_014644	8	44	41	-	144855740	144855883
241111211	chr1	144857550	144857691	144857578	144857670	PDE4DIP	NM_001198832	6	46	41	-	144857612	144857728
241111211	chr1	144857550	144857691	144857578	144857670	PDE4DIP	NM_001198834	7	44	39	-	144857612	144857728
241111211	chr1	144857550	144857691	144857578	144857670	PDE4DIP	NM_014644	8	44	39	-	144857612	144857728
237387880	chr1	144859878	144860025	144859901	144859999	PDE4DIP	NM_001198832	6	46	40	-	144859759	144859998
237387880	chr1	144859878	144860025	144859901	144859999	PDE4DIP	NM_001198834	7	44	38	-	144859759	144859998
237387880	chr1	144859878	144860025	144859901	144859999	PDE4DIP	NM_014644	8	44	38	-	144859759	144859998
236829186	chr1	144864179	144864351	144864200	144864326	PDE4DIP	NM_001198832	6	46	38	-	144864135	144864324
236829186	chr1	144864179	144864351	144864200	144864326	PDE4DIP	NM_001198834	7	44	36	-	144864135	144864324
236829186	chr1	144864179	144864351	144864200	144864326	PDE4DIP	NM_014644	8	44	36	-	144864135	144864324
235321911	chr1	144866593	144866754	144866614	144866732	PDE4DIP	NM_001198832	6	46	36	-	144866592	144866723
235321911	chr1	144866593	144866754	144866614	144866732	PDE4DIP	NM_001198834	7	44	34	-	144866592	144866723
235321911	chr1	144866593	144866754	144866614	144866732	PDE4DIP	NM_014644	8	44	34	-	144866592	144866723
236836354	chr1	144871658	144871792	144871675	144871774	PDE4DIP	NM_001198834	7	44	32	-	144871696	144871881
236836354	chr1	144871658	144871792	144871675	144871774	PDE4DIP	NM_014644	8	44	32	-	144871696	144871881
235804680	chr1	144873937	144874104	144873958	144874082	PDE4DIP	NM_001198832	6	46	34	-	144873877	144874029
235804680	chr1	144873937	144874104	144873958	144874082	PDE4DIP	NM_001198834	7	44	31	-	144873877	144874029
235804680	chr1	144873937	144874104	144873958	144874082	PDE4DIP	NM_014644	8	44	31	-	144873877	144874029
236254926	chr1	144875935	144876074	144875954	144876048	PDE4DIP	NM_001198832	6	46	32	-	144875977	144876028
236254926	chr1	144875935	144876074	144875954	144876048	PDE4DIP	NM_001198834	7	44	29	-	144875977	144876028
236254926	chr1	144875935	144876074	144875954	144876048	PDE4DIP	NM_014644	8	44	29	-	144875977	144876028
235371715	chr1	144879064	144879234	144879087	144879212	PDE4DIP	NM_001198832	6	46	30	-	144879035	144879563
235371715	chr1	144879064	144879234	144879087	144879212	PDE4DIP	NM_001198834	7	44	27	-	144879035	144879563
235371715	chr1	144879064	144879234	144879087	144879212	PDE4DIP	NM_014644	8	44	27	-	144879035	144879563
234941827	chr1	144880722	144880887	144880741	144880864	PDE4DIP	NM_001198832	6	46	29	-	144880742	144880861
234941827	chr1	144880722	144880887	144880741	144880864	PDE4DIP	NM_001198834	7	44	26	-	144880742	144880861
234941827	chr1	144880722	144880887	144880741	144880864	PDE4DIP	NM_014644	8	44	26	-	144880742	144880861
237716399	chr1	144882517	144882683	144882539	144882655	PDE4DIP	NM_001198834	7	44	24	-	144882446	144882881
237716399	chr1	144882517	144882683	144882539	144882655	PDE4DIP	NM_014644	8	44	24	-	144882446	144882881
235044843	chr1	144886005	144886151	144886033	144886127	PDE4DIP	NM_001198832	6	46	26	-	144886097	144886329
235044843	chr1	144886005	144886151	144886033	144886127	PDE4DIP	NM_001198834	7	44	23	-	144886097	144886329
235044843	chr1	144886005	144886151	144886033	144886127	PDE4DIP	NM_014644	8	44	23	-	144886097	144886329

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237818987	chr1	144892472	144892622	144892491	144892594	PDE4DIP	NM_001198832	6	46	25	-	144892501	144892589
237818987	chr1	144892472	144892622	144892491	144892594	PDE4DIP	NM_001198834	7	44	22	-	144892501	144892589
237818987	chr1	144892472	144892622	144892491	144892594	PDE4DIP	NM_014644	8	44	22	-	144892501	144892589
237818987	chr1	144892472	144892622	144892491	144892594	PDE4DIP	NM_001002812	3	23	22	-	144892501	144892589
237818987	chr1	144892472	144892622	144892491	144892594	PDE4DIP	NM_001002811	2	19	18	-	144892501	144892589
236593112	chr1	144906047	144906173	144906072	144906148	PDE4DIP	NM_001198832	6	46	22	-	144906059	144906196
236593112	chr1	144906047	144906173	144906072	144906148	PDE4DIP	NM_001198834	7	44	19	-	144906059	144906196
236593112	chr1	144906047	144906173	144906072	144906148	PDE4DIP	NM_014644	8	44	19	-	144906059	144906196
236593112	chr1	144906047	144906173	144906072	144906148	PDE4DIP	NM_001002812	3	23	19	-	144906059	144906196
236593112	chr1	144906047	144906173	144906072	144906148	PDE4DIP	NM_001002811	2	19	15	-	144906059	144906196
237023973	chr1	144911790	144911929	144911818	144911905	PDE4DIP	NM_001198832	6	46	19	-	144911882	144911963
237023973	chr1	144911790	144911929	144911818	144911905	PDE4DIP	NM_001198834	7	44	16	-	144911882	144911963
237023973	chr1	144911790	144911929	144911818	144911905	PDE4DIP	NM_014644	8	44	16	-	144911882	144911963
237023973	chr1	144911790	144911929	144911818	144911905	PDE4DIP	NM_001002812	3	23	16	-	144911882	144911963
237023973	chr1	144911790	144911929	144911818	144911905	PDE4DIP	NM_001002811	2	19	12	-	144911882	144911963
241080421	chr1	144912163	144912312	144912190	144912288	PDE4DIP	NM_001198832	6	46	18	-	144912130	144912294
241080421	chr1	144912163	144912312	144912190	144912288	PDE4DIP	NM_001198834	7	44	15	-	144912130	144912294
241080421	chr1	144912163	144912312	144912190	144912288	PDE4DIP	NM_014644	8	44	15	-	144912130	144912294
241080421	chr1	144912163	144912312	144912190	144912288	PDE4DIP	NM_001002812	3	23	15	-	144912130	144912294
241080421	chr1	144912163	144912312	144912190	144912288	PDE4DIP	NM_001002811	2	19	11	-	144912130	144912294
236455604	chr1	144916609	144916779	144916635	144916750	PDE4DIP	NM_001198832	6	46	16	-	144916570	144916749
236455604	chr1	144916609	144916779	144916635	144916750	PDE4DIP	NM_001198834	7	44	13	-	144916570	144916749
236455604	chr1	144916609	144916779	144916635	144916750	PDE4DIP	NM_014644	8	44	13	-	144916570	144916749
236455604	chr1	144916609	144916779	144916635	144916750	PDE4DIP	NM_001002812	3	23	13	-	144916570	144916749
236455604	chr1	144916609	144916779	144916635	144916750	PDE4DIP	NM_001002811	2	19	9	-	144916570	144916749
235537334	chr1	144918799	144918972	144918825	144918947	PDE4DIP	NM_001198832	6	46	13	-	144918833	144918991
235537334	chr1	144918799	144918972	144918825	144918947	PDE4DIP	NM_001198834	7	44	10	-	144918833	144918991
235537334	chr1	144918799	144918972	144918825	144918947	PDE4DIP	NM_014644	8	44	10	-	144918833	144918991
235537334	chr1	144918799	144918972	144918825	144918947	PDE4DIP	NM_001002812	3	23	10	-	144918833	144918991
235537334	chr1	144918799	144918972	144918825	144918947	PDE4DIP	NM_001002811	2	19	6	-	144918833	144918991
236272952	chr1	144921945	144922081	144921966	144922052	PDE4DIP	NM_001198832	6	46	12	-	144921835	144922047
236272952	chr1	144921945	144922081	144921966	144922052	PDE4DIP	NM_001198834	7	44	9	-	144921835	144922047
236272952	chr1	144921945	144922081	144921966	144922052	PDE4DIP	NM_014644	8	44	9	-	144921835	144922047
236272952	chr1	144921945	144922081	144921966	144922052	PDE4DIP	NM_001002812	3	23	9	-	144921835	144922047
236272952	chr1	144921945	144922081	144921966	144922052	PDE4DIP	NM_001002811	2	19	5	-	144921835	144922047
236253255	chr1	144923569	144923740	144923594	144923719	PDE4DIP	NM_001198832	6	46	9	-	144923690	144923821
236253255	chr1	144923569	144923740	144923594	144923719	PDE4DIP	NM_001198834	7	44	6	-	144923690	144923821
236253255	chr1	144923569	144923740	144923594	144923719	PDE4DIP	NM_014644	8	44	6	-	144923690	144923821
236253255	chr1	144923569	144923740	144923594	144923719	PDE4DIP	NM_001002812	3	23	6	-	144923690	144923821
236253255	chr1	144923569	144923740	144923594	144923719	PDE4DIP	NM_001002811	2	19	2	-	144923690	144923821
240397744	chr1	144930760	144930931	144930782	144930908	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236920642	chr1	144931252	144931421	144931273	144931394	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
235773943	chr1	144946595	144946769	144946617	144946743	PDE4DIP	NM_001198832	6	46	8	-	144946625	144946742
235773943	chr1	144946595	144946769	144946617	144946743	PDE4DIP	NM_001198834	7	44	5	-	144946625	144946742
235773943	chr1	144946595	144946769	144946617	144946743	PDE4DIP	NM_014644	8	44	5	-	144946625	144946742
235773943	chr1	144946595	144946769	144946617	144946743	PDE4DIP	NM_001002812	3	23	5	-	144946625	144946742
235194079	chr1	144994862	144995028	144994881	144995006	PDE4DIP	NM_001198834	7	44	1	-	144994591	144995033
235194079	chr1	144994862	144995028	144994881	144995006	PDE4DIP	NM_001002810	1	4	1	-	144994591	144995033
235194079	chr1	144994862	144995028	144994881	144995006	PDE4DIP	NM_014644	8	44	1	-	144994591	144995022
235194079	chr1	144994862	144995028	144994881	144995006	PDE4DIP	NM_001002812	3	23	1	-	144994591	144995022
235194079	chr1	144994862	144995028	144994881	144995006	PDE4DIP	NM_001195261	5	5	1	-	144994956	144995082
241291593	chr1	145021091	145021246	145021111	145021225	PDE4DIP	NM_001198832	6	46	2	-	145021112	145021167
241291593	chr1	145021091	145021246	145021111	145021225	PDE4DIP	NM_022359	9	7	2	-	145021112	145021167
240105442	chr1	145075758	145075906	145075775	145075885	PDE4DIP	NM_022359	9	7	1	-	145075630	145076186
233299248	chr1	145527887	145528060	145527910	145528038	ITGA10	NM_003637	1	30	3	+	145527928	145528037
231840684	chr1	145530259	145530419	145530281	145530394	ITGA10	NM_003637	1	30	6	+	145530267	145530394
233209387	chr1	145532159	145532294	145532179	145532270	ITGA10	NM_003637	1	30	8	+	145532115	145532265
233636429	chr1	145532999	145533160	145533027	145533140	ITGA10	NM_003637	1	30	11	+	145533055	145533199
231522019	chr1	145533746	145533919	145533772	145533896	ITGA10	NM_003637	1	30	13	+	145533798	145533941
231679108	chr1	145534862	145535036	145534888	145535019	ITGA10	NM_003637	1	30	15	+	145534889	145535019
232952206	chr1	145535996	145536162	145536017	145536140	ITGA10	NM_003637	1	30	17	+	145535998	145536140
232083975	chr1	145537461	145537635	145537486	145537614	ITGA10	NM_003637	1	30	20	+	145537423	145537564
233175955	chr1	145538674	145538847	145538697	145538824	ITGA10	NM_003637	1	30	24	+	145538724	145538808
232991263	chr1	145541330	145541465	145541352	145541445	ITGA10	NM_003637	1	30	28	+	145541441	145541536
223322098	chr1	147083599	147083749	147083619	147083728	BCL9	NM_004326	1	10	4	+	147083377	147083688
222520505	chr1	147084933	147085070	147084955	147085049	BCL9	NM_004326	1	10	5	+	147084682	147084998
223843295	chr1	147087615	147087754	147087637	147087726	BCL9	NM_004326	1	10	7	+	147087603	147087702
224764638	chr1	147090881	147091032	147090903	147091011	BCL9	NM_004326	1	10	8	+	147090622	147092863
223241048	chr1	147091300	147091466	147091324	147091445	BCL9	NM_004326	1	10	8	+	147090622	147092863
224767278	chr1	147091738	147091867	147091761	147091845	BCL9	NM_004326	1	10	8	+	147090622	147092863
224777109	chr1	147092201	147092359	147092221	147092339	BCL9	NM_004326	1	10	8	+	147090622	147092863
223254000	chr1	147092660	147092819	147092682	147092796	BCL9	NM_004326	1	10	8	+	147090622	147092863
223372348	chr1	147094224	147094358	147094244	147094332	BCL9	NM_004326	1	10	9	+	147094072	147094332
224499364	chr1	147095897	147096062	147095918	147096042	BCL9	NM_004326	1	10	10	+	147095643	147098015
224504696	chr1	147096332	147096466	147096354	147096445	BCL9	NM_004326	1	10	10	+	147095643	147098015
270683217	chr1	150549807	150549958	150549830	150549934	MCL1	NM_021960	2	3	3	-	150547027	150549967
270683217	chr1	150549807	150549958	150549830	150549934	MCL1	NM_001197320	1	4	4	-	150547027	150549967
270683217	chr1	150549807	150549958	150549830	150549934	MCL1	NM_182763	3	2	2	-	150547027	150549967
269811759	chr1	150550817	150550991	150550842	150550968	MCL1	NM_021960	2	3	2	-	150550720	150550967
269811759	chr1	150550817	150550991	150550842	150550968	MCL1	NM_001197320	1	4	3	-	150550720	150550967
271815492	chr1	150551532	150551687	150551555	150551667	MCL1	NM_021960	2	3	1	-	150551319	150552214
271815492	chr1	150551532	150551687	150551555	150551667	MCL1	NM_182763	3	2	1	-	150551319	150552214

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269963370	chr1	150551976	150552119	150551999	150552096	MCL1	NM_021960	2	3	1	-	150551319	150552214
269963370	chr1	150551976	150552119	150551999	150552096	MCL1	NM_182763	3	2	1	-	150551319	150552214
269963370	chr1	150551976	150552119	150551999	150552096	MCL1	NM_001197320	1	4	1	-	150551899	150552214
222513132	chr1	150786511	150786685	150786534	150786663	ARNT	NM_001197325	1	21	19	-	150786553	150786712
222513132	chr1	150786511	150786685	150786534	150786663	ARNT	NM_001668	2	22	20	-	150786553	150786715
222513132	chr1	150786511	150786685	150786534	150786663	ARNT	NM_178427	3	21	19	-	150786553	150786715
222771981	chr1	150789229	150789388	150789251	150789366	ARNT	NM_001668	2	22	18	-	150789264	150789366
222771981	chr1	150789229	150789388	150789251	150789366	ARNT	NM_178427	3	21	17	-	150789264	150789366
222771981	chr1	150789229	150789388	150789251	150789366	ARNT	NM_001197325	1	21	17	-	150789264	150789366
222179109	chr1	150789768	150789938	150789792	150789916	ARNT	NM_001668	2	22	16	-	150789837	150789909
222179109	chr1	150789768	150789938	150789792	150789916	ARNT	NM_178427	3	21	15	-	150789837	150789909
222179109	chr1	150789768	150789938	150789792	150789916	ARNT	NM_001197325	1	21	15	-	150789837	150789909
223029959	chr1	150798928	150799073	150798949	150799046	ARNT	NM_001668	2	22	13	-	150799019	150799093
223029959	chr1	150798928	150799073	150798949	150799046	ARNT	NM_178427	3	21	12	-	150799019	150799093
223029959	chr1	150798928	150799073	150798949	150799046	ARNT	NM_001197325	1	21	12	-	150799019	150799093
222201713	chr1	150804228	150804383	150804251	150804357	ARNT	NM_001668	2	22	10	-	150804294	150804379
222201713	chr1	150804228	150804383	150804251	150804357	ARNT	NM_178427	3	21	9	-	150804294	150804379
222201713	chr1	150804228	150804383	150804251	150804357	ARNT	NM_001197325	1	21	9	-	150804294	150804379
223096061	chr1	150808656	150808830	150808684	150808808	ARNT	NM_001668	2	22	7	-	150808756	150808969
223096061	chr1	150808656	150808830	150808684	150808808	ARNT	NM_178427	3	21	6	-	150808756	150808969
223096061	chr1	150808656	150808830	150808684	150808808	ARNT	NM_001197325	1	21	6	-	150808756	150808969
222895587	chr1	150811990	150812153	150812013	150812130	ARNT	NM_001668	2	22	6	-	150811917	150812130
222895587	chr1	150811990	150812153	150812013	150812130	ARNT	NM_178427	3	21	5	-	150811917	150812130
222895587	chr1	150811990	150812153	150812013	150812130	ARNT	NM_001197325	1	21	5	-	150811917	150812130
225109766	chr1	150825236	150825369	150825264	150825345	ARNT	NM_001668	2	22	3	-	150825238	150825282
225109766	chr1	150825236	150825369	150825264	150825345	ARNT	NM_178427	3	21	3	-	150825238	150825282
225109766	chr1	150825236	150825369	150825264	150825345	ARNT	NM_001197325	1	21	3	-	150825238	150825282
294912226	chr1	154947164	154947319	154947184	154947299	CKS1B	NM_001826	1	3	1	+	154947118	154947280
294912226	chr1	154947164	154947319	154947184	154947299	CKS1B	NR_024163	2	3	1	+	154947118	154947388
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001044391	4	5	5	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001044390	3	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204290	12	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204289	11	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204288	10	8	8	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_002456	20	8	8	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204286	8	9	9	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204294	16	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204293	15	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001044392	5	5	5	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001018017	2	8	8	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001044393	6	7	7	-	155158300	155158685

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204292	14	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204297	19	5	5	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204296	18	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204295	17	6	6	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204287	9	8	8	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204285	7	9	9	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001204291	13	7	7	-	155158300	155158685
238596346	chr1	155158545	155158716	155158567	155158693	MUC1	NM_001018016	1	8	8	-	155158300	155158685
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204288	10	8	6	-	155159931	155160020
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001044393	6	7	5	-	155159931	155160020
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204295	17	6	4	-	155159931	155160020
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001044390	3	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204290	12	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204289	11	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_002456	20	8	6	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204286	8	9	7	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204294	16	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001018017	2	8	6	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204292	14	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204296	18	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204287	9	8	6	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204285	7	9	7	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001204291	13	7	5	-	155159931	155160052
236328456	chr1	155159915	155160077	155159934	155160053	MUC1	NM_001018016	1	8	6	-	155159931	155160052
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204286	8	9	4	-	155160639	155161063
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204285	7	9	4	-	155160639	155161063
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_002456	20	8	3	-	155160639	155160761
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204293	15	7	3	-	155160639	155160761
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204297	19	5	3	-	155160639	155160761
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204287	9	8	3	-	155160639	155160761
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001044390	3	7	3	-	155160639	155160688
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204294	16	7	3	-	155160639	155160688
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001044393	6	7	3	-	155160639	155160688
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204292	14	7	3	-	155160639	155160688
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204296	18	7	3	-	155160639	155160688
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001044391	4	5	3	-	155160639	155160707
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204288	10	8	3	-	155160639	155160707
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001044392	5	5	3	-	155160639	155160707
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001018017	2	8	3	-	155160639	155160707
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001204295	17	6	3	-	155160639	155160707
235089199	chr1	155160617	155160774	155160638	155160752	MUC1	NM_001018016	1	8	3	-	155160639	155160707

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204286	8	9	2	-	155161699	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204285	7	9	2	-	155161699	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204289	11	7	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204288	10	8	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001044392	5	5	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204292	14	7	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204297	19	5	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204296	18	7	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204295	17	6	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204287	9	8	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204291	13	7	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001018016	1	8	2	-	155161974	155162101
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204290	12	7	2	-	155161974	155162038
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001044391	4	5	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001044390	3	7	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_002456	20	8	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204294	16	7	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001204293	15	7	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001018017	2	8	2	-	155161974	155162074
237024698	chr1	155161901	155162071	155161921	155162050	MUC1	NM_001044393	6	7	2	-	155161974	155162074
237931184	chr1	156811866	156812027	156811883	156812003	NTRK1	NM_001007792	1	17	2	+	156811873	156811985
238875930	chr1	156834084	156834240	156834103	156834221	NTRK1	NM_002529	3	17	2	+	156834146	156834220
238875930	chr1	156834084	156834240	156834103	156834221	NTRK1	NM_001012331	2	16	2	+	156834146	156834220
238875930	chr1	156834084	156834240	156834103	156834221	NTRK1	NM_001007792	1	17	3	+	156834146	156834220
241040592	chr1	156837907	156838072	156837928	156838052	NTRK1	NM_002529	3	17	5	+	156837896	156838041
241040592	chr1	156837907	156838072	156837928	156838052	NTRK1	NM_001012331	2	16	5	+	156837896	156838041
241040592	chr1	156837907	156838072	156837928	156838052	NTRK1	NM_001007792	1	17	6	+	156837896	156838041
235530862	chr1	156841455	156841602	156841477	156841578	NTRK1	NM_002529	3	17	7	+	156841415	156841547
235530862	chr1	156841455	156841602	156841477	156841578	NTRK1	NM_001012331	2	16	7	+	156841415	156841547
235530862	chr1	156841455	156841602	156841477	156841578	NTRK1	NM_001007792	1	17	8	+	156841415	156841547
237894933	chr1	156844057	156844213	156844076	156844193	NTRK1	NM_002529	3	17	9	+	156844175	156844192
235266569	chr1	156845291	156845464	156845311	156845441	NTRK1	NM_002529	3	17	12	+	156845312	156845458
235266569	chr1	156845291	156845464	156845311	156845441	NTRK1	NM_001012331	2	16	11	+	156845312	156845458
235266569	chr1	156845291	156845464	156845311	156845441	NTRK1	NM_001007792	1	17	12	+	156845312	156845458
237544747	chr1	156846174	156846347	156846191	156846330	NTRK1	NM_002529	3	17	14	+	156846192	156846364
237544747	chr1	156846174	156846347	156846191	156846330	NTRK1	NM_001012331	2	16	13	+	156846192	156846364
237544747	chr1	156846174	156846347	156846191	156846330	NTRK1	NM_001007792	1	17	14	+	156846192	156846364
238798543	chr1	156849109	156849279	156849131	156849257	NTRK1	NM_002529	3	17	15	+	156848914	156849154
238798543	chr1	156849109	156849279	156849131	156849257	NTRK1	NM_001012331	2	16	14	+	156848914	156849154
238798543	chr1	156849109	156849279	156849131	156849257	NTRK1	NM_001007792	1	17	15	+	156848914	156849154
241566602	chr1	156851302	156851475	156851323	156851453	NTRK1	NM_002529	3	17	17	+	156851249	156851642

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241566602	chr1	156851302	156851475	156851323	156851453	NTRK1	NM_001012331	2	16	16	+	156851249	156851642
241566602	chr1	156851302	156851475	156851323	156851453	NTRK1	NM_001007792	1	17	17	+	156851249	156851642
237929810	chr1	161298172	161298328	161298200	161298304	SDHC	NM_003001	4	6	3	+	161298186	161298287
237929810	chr1	161298172	161298328	161298200	161298304	SDHC	NM_001035511	1	5	3	+	161298186	161298287
240491736	chr1	161326498	161326661	161326520	161326633	SDHC	NM_003001	4	6	5	+	161326467	161326630
240491736	chr1	161326498	161326661	161326520	161326633	SDHC	NM_001035512	2	5	4	+	161326467	161326630
240491736	chr1	161326498	161326661	161326520	161326633	SDHC	NM_001035513	3	4	3	+	161326467	161326630
230614938	chr1	162722845	162723018	162722870	162722993	DDR2	NM_006182	2	18	4	+	162722885	162722987
230614938	chr1	162722845	162723018	162722870	162722993	DDR2	NM_001014796	1	19	5	+	162722885	162722987
227901591	chr1	162724829	162724995	162724851	162724967	DDR2	NM_006182	2	18	6	+	162724946	162725093
227901591	chr1	162724829	162724995	162724851	162724967	DDR2	NM_001014796	1	19	7	+	162724946	162725093
228252798	chr1	162729663	162729809	162729682	162729785	DDR2	NM_006182	2	18	8	+	162729586	162729769
228252798	chr1	162729663	162729809	162729682	162729785	DDR2	NM_001014796	1	19	9	+	162729586	162729769
232242025	chr1	162735762	162735905	162735784	162735880	DDR2	NM_006182	2	18	10	+	162735791	162735853
232242025	chr1	162735762	162735905	162735784	162735880	DDR2	NM_001014796	1	19	11	+	162735791	162735853
230169366	chr1	162740180	162740349	162740202	162740327	DDR2	NM_006182	2	18	12	+	162740092	162740302
230169366	chr1	162740180	162740349	162740202	162740327	DDR2	NM_001014796	1	19	13	+	162740092	162740302
229424328	chr1	162743183	162743326	162743205	162743301	DDR2	NM_006182	2	18	14	+	162743259	162743386
229424328	chr1	162743183	162743326	162743205	162743301	DDR2	NM_001014796	1	19	15	+	162743259	162743386
232575092	chr1	162745895	162746068	162745923	162746041	DDR2	NM_006182	2	18	16	+	162745926	162746160
232575092	chr1	162745895	162746068	162745923	162746041	DDR2	NM_001014796	1	19	17	+	162745926	162746160
229572416	chr1	162749839	162749998	162749867	162749977	DDR2	NM_006182	2	18	18	+	162749902	162750247
229572416	chr1	162749839	162749998	162749867	162749977	DDR2	NM_001014796	1	19	19	+	162749902	162750247
236986754	chr1	164529175	164529321	164529199	164529300	PBX1	NM_002585	3	9	1	+	164528597	164529250
236986754	chr1	164529175	164529321	164529199	164529300	PBX1	NM_001204963	2	9	1	+	164528597	164529250
236986754	chr1	164529175	164529321	164529199	164529300	PBX1	NM_001204961	1	8	1	+	164528597	164529250
238537422	chr1	164761886	164762033	164761909	164762011	PBX1	NM_002585	3	9	3	+	164761731	164761975
238537422	chr1	164761886	164762033	164761909	164762011	PBX1	NM_001204963	2	9	3	+	164761731	164761975
238537422	chr1	164761886	164762033	164761909	164762011	PBX1	NM_001204961	1	8	3	+	164761731	164761975
240558315	chr1	164776847	164777002	164776867	164776976	PBX1	NM_002585	3	9	5	+	164776779	164776914
240558315	chr1	164776847	164777002	164776867	164776976	PBX1	NM_001204963	2	9	5	+	164776779	164776914
240558315	chr1	164776847	164777002	164776867	164776976	PBX1	NM_001204961	1	8	5	+	164776779	164776914
237971446	chr1	164790692	164790827	164790712	164790804	PBX1	NM_002585	3	9	8	+	164790774	164790863
237971446	chr1	164790692	164790827	164790712	164790804	PBX1	NM_001204963	2	9	8	+	164790774	164790863
237971446	chr1	164790692	164790827	164790712	164790804	PBX1	NM_001204961	1	8	7	+	164790774	164790863
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_001168239	6	12	12	-	179068462	179078033
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_001168238	5	12	12	-	179068462	179078033
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_001136000	1	13	13	-	179068462	179078033
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_001168237	4	13	13	-	179068462	179078033
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_005158	7	12	12	-	179068462	179078576
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_007314	8	12	12	-	179068462	179078576

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224233178	chr1	179076809	179076982	179076831	179076961	ABL2	NM_001168236	3	11	11	-	179068462	179078576
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_001168239	6	12	12	-	179068462	179078033
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_001168238	5	12	12	-	179068462	179078033
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_001136000	1	13	13	-	179068462	179078033
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_001168237	4	13	13	-	179068462	179078033
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_005158	7	12	12	-	179068462	179078576
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_007314	8	12	12	-	179068462	179078576
224239366	chr1	179077241	179077413	179077263	179077391	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_005158	7	12	12	-	179068462	179078576
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_007314	8	12	12	-	179068462	179078576
223448345	chr1	179077690	179077831	179077710	179077808	ABL2	NM_001168236	3	11	11	-	179068462	179078576
224246137	chr1	179078108	179078272	179078130	179078252	ABL2	NM_005158	7	12	12	-	179068462	179078576
224246137	chr1	179078108	179078272	179078130	179078252	ABL2	NM_007314	8	12	12	-	179068462	179078576
224246137	chr1	179078108	179078272	179078130	179078252	ABL2	NM_001168236	3	11	11	-	179068462	179078576
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_005158	7	12	11	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_001168239	6	12	10	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_001168238	5	12	10	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_001136000	1	13	11	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_007314	8	12	11	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_001168237	4	13	11	-	179079417	179079590
222175751	chr1	179079325	179079499	179079349	179079474	ABL2	NM_001168236	3	11	10	-	179079417	179079590
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_005158	7	12	9	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001168239	6	12	8	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001168238	5	12	8	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001136001	2	10	8	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001136000	1	13	9	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_007314	8	12	9	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001168237	4	13	9	-	179084013	179084165
223696816	chr1	179084054	179084209	179084080	179084183	ABL2	NM_001168236	3	11	8	-	179084013	179084165
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_005158	7	12	7	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001168239	6	12	6	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001168238	5	12	6	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001136001	2	10	6	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001136000	1	13	7	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_007314	8	12	7	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001168237	4	13	7	-	179087722	179087899
222363434	chr1	179087800	179087962	179087821	179087936	ABL2	NM_001168236	3	11	6	-	179087722	179087899

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_005158	7	12	5	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001168239	6	12	4	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001168238	5	12	4	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001136001	2	10	4	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001136000	1	13	5	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_007314	8	12	5	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001168237	4	13	5	-	179090730	179091002
224171465	chr1	179090894	179091025	179090915	179090999	ABL2	NM_001168236	3	11	4	-	179090730	179091002
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_005158	7	12	3	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001168239	6	12	2	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001168238	5	12	2	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001136001	2	10	2	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001136000	1	13	3	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_007314	8	12	3	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001168237	4	13	3	-	179100446	179100616
222867868	chr1	179100376	179100526	179100397	179100502	ABL2	NM_001168236	3	11	2	-	179100446	179100616
321969906	chr1	182544416	182544586	182544438	182544564	RNASEL	NM_021133	1	7	7	-	182542769	182544713
321785802	chr1	182545398	182545567	182545424	182545541	RNASEL	NM_021133	1	7	6	-	182545391	182545524
321790851	chr1	182551259	182551426	182551283	182551402	RNASEL	NM_021133	1	7	4	-	182551188	182551393
322078141	chr1	182554606	182554777	182554627	182554754	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322086596	chr1	182555015	182555165	182555038	182555138	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322074609	chr1	182555480	182555630	182555508	182555607	RNASEL	NM_021133	1	7	2	-	182554462	182556105
312515056	chr1	185056628	185056798	185056656	185056772	RNF2	NM_007212	1	7	2	+	185056684	185056772
312218001	chr1	185062246	185062408	185062267	185062384	RNF2	NM_007212	1	7	4	+	185062193	185062408
312486346	chr1	185067276	185067441	185067302	185067413	RNF2	NM_007212	1	7	5	+	185067204	185067476
312225467	chr1	185069041	185069165	185069063	185069143	RNF2	NM_007212	1	7	6	+	185068923	185069094
264029401	chr1	186283681	186283853	186283709	186283826	TPR	NM_003292	1	51	50	-	186283761	186283856
242016876	chr1	186287480	186287627	186287505	186287600	TPR	NM_003292	1	51	48	-	186287579	186287735
264435251	chr1	186287868	186288035	186287888	186288009	TPR	NM_003292	1	51	47	-	186287865	186287960
264697653	chr1	186291538	186291707	186291566	186291687	TPR	NM_003292	1	51	44	-	186291650	186291718
242745839	chr1	186292849	186292990	186292870	186292966	TPR	NM_003292	1	51	43	-	186292818	186293002
241947393	chr1	186296642	186296795	186296670	186296773	TPR	NM_003292	1	51	40	-	186296592	186296792
242716979	chr1	186301334	186301462	186301359	186301440	TPR	NM_003292	1	51	38	-	186301327	186301475
264830392	chr1	186302444	186302610	186302470	186302582	TPR	NM_003292	1	51	37	-	186302254	186302526
242326507	chr1	186303627	186303797	186303649	186303769	TPR	NM_003292	1	51	36	-	186303457	186303665
265787695	chr1	186304578	186304751	186304599	186304725	TPR	NM_003292	1	51	34	-	186304470	186304675
239351398	chr1	186306042	186306200	186306067	186306172	TPR	NM_003292	1	51	32	-	186306145	186306288
239501016	chr1	186307197	186307369	186307225	186307341	TPR	NM_003292	1	51	31	-	186307165	186307375
241440252	chr1	186310121	186310295	186310145	186310267	TPR	NM_003292	1	51	29	-	186310160	186310291
265006874	chr1	186312407	186312541	186312435	186312514	TPR	NM_003292	1	51	27	-	186312458	186312605
264146363	chr1	186313099	186313247	186313122	186313222	TPR	NM_003292	1	51	26	-	186313038	186313222

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242257182	chr1	186315171	186315296	186315198	186315273	TPR	NM_003292	1	51	23	-	186315267	186315419
263022772	chr1	186316546	186316689	186316571	186316656	TPR	NM_003292	1	51	22	-	186316424	186316590
242450407	chr1	186320427	186320597	186320454	186320573	TPR	NM_003292	1	51	20	-	186320462	186320602
242571315	chr1	186322782	186322913	186322809	186322888	TPR	NM_003292	1	51	18	-	186322820	186322982
262303185	chr1	186324725	186324855	186324753	186324830	TPR	NM_003292	1	51	16	-	186324767	186324900
239063150	chr1	186326501	186326668	186326527	186326639	TPR	NM_003292	1	51	14	-	186326529	186326755
262623865	chr1	186327719	186327870	186327746	186327842	TPR	NM_003292	1	51	13	-	186327675	186327782
264426887	chr1	186329469	186329593	186329494	186329560	TPR	NM_003292	1	51	11	-	186329405	186329496
264985314	chr1	186330744	186330886	186330769	186330858	TPR	NM_003292	1	51	9	-	186330754	186330841
239443414	chr1	186332055	186332222	186332080	186332200	TPR	NM_003292	1	51	6	-	186331969	186332133
263331493	chr1	186336997	186337171	186337026	186337146	TPR	NM_003292	1	51	4	-	186337018	186337114
241380195	chr1	186342554	186342727	186342578	186342699	TPR	NM_003292	1	51	2	-	186342491	186342595
296644538	chr1	186643482	186643615	186643507	186643587	PTGS2	NM_000963	1	10	10	-	186640944	186643894
297088026	chr1	186644386	186644510	186644414	186644489	PTGS2	NM_000963	1	10	9	-	186644381	186644528
296102124	chr1	186645131	186645274	186645156	186645247	PTGS2	NM_000963	1	10	8	-	186645030	186645316
297549214	chr1	186645685	186645839	186645703	186645815	PTGS2	NM_000963	1	10	7	-	186645599	186645845
298339473	chr1	186646895	186647039	186646923	186647013	PTGS2	NM_000963	1	10	5	-	186646781	186646962
296838561	chr1	186648234	186648359	186648261	186648336	PTGS2	NM_000963	1	10	3	-	186648190	186648333
226605487	chr1	193091205	193091370	193091223	193091349	CDC73	NM_024529	1	17	1	+	193091088	193091461
225461361	chr1	193104555	193104709	193104582	193104682	CDC73	NM_024529	1	17	5	+	193104667	193104719
225461361	chr1	193104555	193104709	193104582	193104682	CDC73	NM_024529	1	17	4	+	193104521	193104583
225909414	chr1	193110916	193111087	193110946	193111059	CDC73	NM_024529	1	17	7	+	193110980	193111196
225666630	chr1	193119446	193119570	193119465	193119547	CDC73	NM_024529	1	17	9	+	193119434	193119512
225622350	chr1	193202060	193202208	193202087	193202180	CDC73	NM_024529	1	17	14	+	193202123	193202284
253630819	chr1	193205420	193205585	193205441	193205560	CDC73	NM_024529	1	17	15	+	193205386	193205486
226808649	chr1	193219803	193219964	193219829	193219936	CDC73	NM_024529	1	17	17	+	193219806	193223942
294763766	chr1	204394792	204394932	204394816	204394904	PIK3C2B	NM_002646	1	34	33	-	204394741	204394869
294538662	chr1	204398944	204399109	204398967	204399087	PIK3C2B	NM_002646	1	34	30	-	204399049	204399166
294361022	chr1	204401253	204401419	204401276	204401399	PIK3C2B	NM_002646	1	34	28	-	204401328	204401529
294822700	chr1	204402955	204403116	204402976	204403089	PIK3C2B	NM_002646	1	34	26	-	204402921	204403077
294093970	chr1	204408057	204408229	204408081	204408209	PIK3C2B	NM_002646	1	34	24	-	204408063	204408199
293909043	chr1	204412526	204412696	204412544	204412676	PIK3C2B	NM_002646	1	34	20	-	204412545	204412725
293991912	chr1	204415005	204415166	204415026	204415145	PIK3C2B	NM_002646	1	34	17	-	204415084	204415272
293739482	chr1	204416563	204416734	204416587	204416711	PIK3C2B	NM_002646	1	34	16	-	204416564	204416706
294003858	chr1	204423676	204423850	204423698	204423828	PIK3C2B	NM_002646	1	34	13	-	204423797	204423919
295198314	chr1	204425098	204425226	204425120	204425204	PIK3C2B	NM_002646	1	34	12	-	204424984	204425179
294394686	chr1	204428984	204429109	204429004	204429086	PIK3C2B	NM_002646	1	34	9	-	204429006	204429069
293866752	chr1	204433116	204433283	204433137	204433262	PIK3C2B	NM_002646	1	34	6	-	204433140	204433260
294438704	chr1	204434320	204434474	204434347	204434449	PIK3C2B	NM_002646	1	34	4	-	204434347	204434447
294291738	chr1	204438213	204438358	204438240	204438334	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
295195362	chr1	204438644	204438768	204438672	204438747	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232190910	chr1	204495414	204495575	204495442	204495547	MDM4	NM_002393	3	11	3	+	204495488	204495562
232190910	chr1	204495414	204495575	204495442	204495547	MDM4	NR_024171	4	10	3	+	204495488	204495562
232190910	chr1	204495414	204495575	204495442	204495547	MDM4	NM_001204171	1	10	3	+	204495488	204495562
233452486	chr1	204506484	204506657	204506507	204506634	MDM4	NM_002393	3	11	6	+	204506558	204506625
233452486	chr1	204506484	204506657	204506507	204506634	MDM4	NM_001204171	1	10	6	+	204506558	204506625
233107004	chr1	204511996	204512147	204512023	204512121	MDM4	NM_002393	3	11	8	+	204511912	204512072
233107004	chr1	204511996	204512147	204512023	204512121	MDM4	NR_024171	4	10	7	+	204511912	204512072
233107004	chr1	204511996	204512147	204512023	204512121	MDM4	NM_001204171	1	10	8	+	204511912	204512072
233309998	chr1	204515918	204516092	204515942	204516068	MDM4	NM_002393	3	11	10	+	204515925	204516005
233309998	chr1	204515918	204516092	204515942	204516068	MDM4	NR_024171	4	10	9	+	204515925	204516005
233309998	chr1	204515918	204516092	204515942	204516068	MDM4	NM_001204171	1	10	9	+	204515925	204516005
232000164	chr1	204518489	204518663	204518513	204518636	MDM4	NM_001204172	2	3	3	+	204518394	204527248
232000164	chr1	204518489	204518663	204518513	204518636	MDM4	NM_002393	3	11	11	+	204518241	204527248
232000164	chr1	204518489	204518663	204518513	204518636	MDM4	NR_024171	4	10	10	+	204518241	204527248
232000164	chr1	204518489	204518663	204518513	204518636	MDM4	NM_001204171	1	10	10	+	204518241	204527248
272124432	chr1	206647616	206647788	206647636	206647765	IKBKE	NM_014002	3	22	4	+	206647674	206647814
272124432	chr1	206647616	206647788	206647636	206647765	IKBKE	NM_001193322	2	21	4	+	206647674	206647814
272124432	chr1	206647616	206647788	206647636	206647765	IKBKE	NM_001193321	1	21	3	+	206647674	206647814
270046742	chr1	206649454	206649601	206649475	206649581	IKBKE	NM_014002	3	22	6	+	206649524	206649705
270046742	chr1	206649454	206649601	206649475	206649581	IKBKE	NM_001193322	2	21	6	+	206649524	206649705
270046742	chr1	206649454	206649601	206649475	206649581	IKBKE	NM_001193321	1	21	5	+	206649524	206649705
270475497	chr1	206650079	206650219	206650100	206650202	IKBKE	NM_014002	3	22	7	+	206650021	206650181
270475497	chr1	206650079	206650219	206650100	206650202	IKBKE	NM_001193322	2	21	7	+	206650021	206650181
270475497	chr1	206650079	206650219	206650100	206650202	IKBKE	NM_001193321	1	21	6	+	206650021	206650181
271437906	chr1	206652230	206652374	206652249	206652354	IKBKE	NM_014002	3	22	10	+	206652286	206652476
271437906	chr1	206652230	206652374	206652249	206652354	IKBKE	NM_001193322	2	21	10	+	206652286	206652476
271437906	chr1	206652230	206652374	206652249	206652354	IKBKE	NM_001193321	1	21	9	+	206652286	206652476
269969000	chr1	206653769	206653943	206653789	206653919	IKBKE	NM_014002	3	22	13	+	206653790	206653876
269969000	chr1	206653769	206653943	206653789	206653919	IKBKE	NM_001193322	2	21	13	+	206653790	206653876
269969000	chr1	206653769	206653943	206653789	206653919	IKBKE	NM_001193321	1	21	12	+	206653790	206653876
272417093	chr1	206661188	206661322	206661212	206661293	IKBKE	NM_014002	3	22	16	+	206661251	206661327
272417093	chr1	206661188	206661322	206661212	206661293	IKBKE	NM_001193322	2	21	16	+	206661251	206661327
272417093	chr1	206661188	206661322	206661212	206661293	IKBKE	NM_001193321	1	21	15	+	206661251	206661327
271919810	chr1	206664976	206665150	206665003	206665129	IKBKE	NM_014002	3	22	18	+	206664981	206665082
271919810	chr1	206664976	206665150	206665003	206665129	IKBKE	NM_001193322	2	21	18	+	206664981	206665082
271919810	chr1	206664976	206665150	206665003	206665129	IKBKE	NM_001193321	1	21	17	+	206664981	206665082
271630168	chr1	206669336	206669510	206669359	206669489	IKBKE	NM_014002	3	22	22	+	206669445	206670223
271630168	chr1	206669336	206669510	206669359	206669489	IKBKE	NM_001193322	2	21	21	+	206669445	206670223
271630168	chr1	206669336	206669510	206669359	206669489	IKBKE	NM_001193321	1	21	21	+	206669445	206670223
290934405	chr1	220752768	220752934	220752793	220752908	MARK1	NM_018650	1	18	2	+	220752696	220752899
290306010	chr1	220777387	220777530	220777413	220777502	MARK1	NM_018650	1	18	6	+	220777409	220777479

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289865538	chr1	220791768	220791894	220791788	220791866	MARK1	NM_018650	1	18	8	+	220791652	220791888
289617289	chr1	220804337	220804510	220804366	220804482	MARK1	NM_018650	1	18	10	+	220804377	220804476
289633834	chr1	220808646	220808797	220808668	220808770	MARK1	NM_018650	1	18	12	+	220808718	220808871
292892127	chr1	220823866	220824021	220823893	220823993	MARK1	NM_018650	1	18	14	+	220823962	220824062
290899997	chr1	220826337	220826508	220826359	220826486	MARK1	NM_018650	1	18	16	+	220826443	220826694
328501827	chr1	220831114	220831250	220831140	220831219	MARK1	NM_018650	1	18	17	+	220831132	220831176
290042554	chr1	220835383	220835542	220835404	220835514	MARK1	NM_018650	1	18	18	+	220835154	220837799
292787724	chr1	226551618	226551792	226551639	226551771	PARP1	NM_001618	1	23	20	-	226551644	226551771
290560703	chr1	226553638	226553797	226553666	226553773	PARP1	NM_001618	1	23	18	-	226553655	226553753
291340274	chr1	226558069	226558239	226558089	226558218	PARP1	NM_001618	1	23	15	-	226558135	226558218
289545078	chr1	226564905	226565038	226564927	226565014	PARP1	NM_001618	1	23	13	-	226564809	226565004
290409297	chr1	226567549	226567707	226567569	226567686	PARP1	NM_001618	1	23	10	-	226567623	226567865
292091297	chr1	226568732	226568865	226568753	226568844	PARP1	NM_001618	1	23	9	-	226568769	226568909
291787835	chr1	226570804	226570928	226570822	226570908	PARP1	NM_001618	1	23	8	-	226570737	226570884
292658032	chr1	226576309	226576482	226576332	226576456	PARP1	NM_001618	1	23	5	-	226576357	226576456
291088900	chr1	226579786	226579949	226579809	226579927	PARP1	NM_001618	1	23	3	-	226579900	226580015
291569246	chr1	226595444	226595603	226595464	226595583	PARP1	NM_001618	1	23	1	-	226595511	226595801
291609872	chr1	236966749	236966878	236966772	236966853	MTR	NM_000254	1	33	2	+	236966728	236966942
290394493	chr1	236973752	236973896	236973780	236973872	MTR	NM_000254	1	33	5	+	236973803	236973895
293182415	chr1	236979746	236979900	236979769	236979876	MTR	NM_000254	1	33	8	+	236979749	236979843
290718519	chr1	236988622	236988796	236988649	236988768	MTR	NM_000254	1	33	10	+	236988638	236988699
291859500	chr1	236995256	236995428	236995281	236995406	MTR	NM_000254	1	33	13	+	236995266	236995378
293219929	chr1	237001757	237001929	237001778	237001904	MTR	NM_000254	1	33	15	+	237001714	237001899
290504337	chr1	237015693	237015867	237015721	237015841	MTR	NM_000254	1	33	17	+	237015821	237015937
289294658	chr1	237023079	237023246	237023107	237023226	MTR	NM_000254	1	33	19	+	237023133	237023222
291323964	chr1	237026710	237026881	237026731	237026854	MTR	NM_000254	1	33	22	+	237026754	237026854
291996038	chr1	237043994	237044165	237044020	237044138	MTR	NM_000254	1	33	25	+	237044055	237044136
289908301	chr1	237052444	237052571	237052464	237052547	MTR	NM_000254	1	33	28	+	237052481	237052636
291910267	chr1	237054530	237054655	237054552	237054634	MTR	NM_000254	1	33	29	+	237054433	237054629
291504549	chr1	237058562	237058723	237058586	237058703	MTR	NM_000254	1	33	31	+	237058658	237058850
293469713	chr1	237060762	237060894	237060789	237060866	MTR	NM_000254	1	33	33	+	237060858	237067281
227252159	chr1	241663643	241663786	241663668	241663758	FH	NM_000143	1	10	9	-	241663737	241663890
228177075	chr1	241665737	241665902	241665762	241665874	FH	NM_000143	1	10	8	-	241665743	241665870
229373236	chr1	241669212	241669378	241669239	241669351	FH	NM_000143	1	10	6	-	241669303	241669468
227977990	chr1	241671889	241672026	241671913	241671999	FH	NM_000143	1	10	5	-	241671903	241672085
227865704	chr1	241675365	241675513	241675394	241675487	FH	NM_000143	1	10	4	-	241675267	241675443
227140502	chr1	241680490	241680662	241680517	241680633	FH	NM_000143	1	10	2	-	241680482	241680616
271453120	chr1	243663056	243663181	243663077	243663163	AKT3	NM_181690	3	14	13	-	243663039	243663088
271453120	chr1	243663056	243663181	243663077	243663163	AKT3	NM_001206729	1	14	14	-	243663021	243663088
271453120	chr1	243663056	243663181	243663077	243663163	AKT3	NM_005465	2	13	13	-	243663021	243668636
270348211	chr1	243715989	243716151	243716017	243716125	AKT3	NM_005465	2	13	10	-	243716031	243716245

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270348211	chr1	243715989	243716151	243716017	243716125	AKT3	NM_181690	3	14	10	-	243716031	243716245
270348211	chr1	243715989	243716151	243716017	243716125	AKT3	NM_001206729	1	14	11	-	243716031	243716245
271727076	chr1	243726999	243727155	243727024	243727130	AKT3	NM_005465	2	13	9	-	243727022	243727150
271727076	chr1	243726999	243727155	243727024	243727130	AKT3	NM_181690	3	14	9	-	243727022	243727150
271727076	chr1	243726999	243727155	243727024	243727130	AKT3	NM_001206729	1	14	10	-	243727022	243727150
269977028	chr1	243776861	243777030	243776890	243777006	AKT3	NM_005465	2	13	7	-	243776973	243777041
269977028	chr1	243776861	243777030	243776890	243777006	AKT3	NM_181690	3	14	7	-	243776973	243777041
269977028	chr1	243776861	243777030	243776890	243777006	AKT3	NM_001206729	1	14	8	-	243776973	243777041
270160793	chr1	243800968	243801138	243800995	243801110	AKT3	NM_005465	2	13	5	-	243800913	243801044
270160793	chr1	243800968	243801138	243800995	243801110	AKT3	NM_181690	3	14	5	-	243800913	243801044
270160793	chr1	243800968	243801138	243800995	243801110	AKT3	NM_001206729	1	14	6	-	243800913	243801044
272518057	chr1	243828136	243828291	243828164	243828267	AKT3	NM_005465	2	13	3	-	243828074	243828185
272518057	chr1	243828136	243828291	243828164	243828267	AKT3	NM_181690	3	14	3	-	243828074	243828185
272518057	chr1	243828136	243828291	243828164	243828267	AKT3	NM_001206729	1	14	4	-	243828074	243828185
297479520	chr2	5832920	5833058	5832940	5833036	SOX11	NM_003108	1	1	1	+	5832799	5841517
297471359	chr2	5833316	5833459	5833333	5833442	SOX11	NM_003108	1	1	1	+	5832799	5841517
297477134	chr2	5833645	5833819	5833664	5833798	SOX11	NM_003108	1	1	1	+	5832799	5841517
297497526	chr2	5834026	5834170	5834046	5834149	SOX11	NM_003108	1	1	1	+	5832799	5841517
241288575	chr2	16082411	16082538	16082430	16082519	MYCN	NM_005378	1	3	2	+	16082070	16082976
239178416	chr2	16085567	16085738	16085595	16085718	MYCN	NM_005378	1	3	3	+	16085615	16087129
239216566	chr2	16085968	16086117	16085989	16086096	MYCN	NM_005378	1	3	3	+	16085615	16087129
235882050	chr2	24888605	24888731	24888629	24888704	NCOA1	NM_147233	3	21	4	+	24888618	24888784
235882050	chr2	24888605	24888731	24888629	24888704	NCOA1	NM_147223	2	22	4	+	24888618	24888784
235882050	chr2	24888605	24888731	24888629	24888704	NCOA1	NM_003743	1	21	4	+	24888618	24888784
241649273	chr2	24905804	24905943	24905827	24905917	NCOA1	NM_147233	3	21	6	+	24905820	24905997
241649273	chr2	24905804	24905943	24905827	24905917	NCOA1	NM_147223	2	22	6	+	24905820	24905997
241649273	chr2	24905804	24905943	24905827	24905917	NCOA1	NM_003743	1	21	6	+	24905820	24905997
235534256	chr2	24914463	24914590	24914487	24914562	NCOA1	NM_147233	3	21	7	+	24914350	24914529
235534256	chr2	24914463	24914590	24914487	24914562	NCOA1	NM_147223	2	22	7	+	24914350	24914529
235534256	chr2	24914463	24914590	24914487	24914562	NCOA1	NM_003743	1	21	7	+	24914350	24914529
236548198	chr2	24920581	24920708	24920609	24920675	NCOA1	NM_147233	3	21	9	+	24920527	24920667
236548198	chr2	24920581	24920708	24920609	24920675	NCOA1	NM_147223	2	22	9	+	24920527	24920667
236548198	chr2	24920581	24920708	24920609	24920675	NCOA1	NM_003743	1	21	9	+	24920527	24920667
237981580	chr2	24929309	24929478	24929337	24929450	NCOA1	NM_147233	3	21	11	+	24929437	24930757
237981580	chr2	24929309	24929478	24929337	24929450	NCOA1	NM_147223	2	22	11	+	24929437	24930757
237981580	chr2	24929309	24929478	24929337	24929450	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238117887	chr2	24929789	24929954	24929811	24929926	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238117887	chr2	24929789	24929954	24929811	24929926	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238117887	chr2	24929789	24929954	24929811	24929926	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238138488	chr2	24930236	24930403	24930260	24930378	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238138488	chr2	24930236	24930403	24930260	24930378	NCOA1	NM_147223	2	22	11	+	24929437	24930757

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238138488	chr2	24930236	24930403	24930260	24930378	NCOA1	NM_003743	1	21	11	+	24929437	24930757
257731522	chr2	24930657	24930781	24930685	24930759	NCOA1	NM_147233	3	21	11	+	24929437	24930757
257731522	chr2	24930657	24930781	24930685	24930759	NCOA1	NM_147223	2	22	11	+	24929437	24930757
257731522	chr2	24930657	24930781	24930685	24930759	NCOA1	NM_003743	1	21	11	+	24929437	24930757
240413772	chr2	24949505	24949667	24949526	24949640	NCOA1	NM_147233	3	21	13	+	24949458	24949575
240413772	chr2	24949505	24949667	24949526	24949640	NCOA1	NM_147223	2	22	13	+	24949458	24949575
240413772	chr2	24949505	24949667	24949526	24949640	NCOA1	NM_003743	1	21	13	+	24949458	24949575
237661102	chr2	24952420	24952592	24952443	24952571	NCOA1	NM_147233	3	21	15	+	24952370	24952684
237661102	chr2	24952420	24952592	24952443	24952571	NCOA1	NM_147223	2	22	15	+	24952370	24952684
237661102	chr2	24952420	24952592	24952443	24952571	NCOA1	NM_003743	1	21	15	+	24952370	24952684
237534122	chr2	24964562	24964719	24964583	24964699	NCOA1	NM_147233	3	21	17	+	24964653	24965055
237534122	chr2	24964562	24964719	24964583	24964699	NCOA1	NM_147223	2	22	17	+	24964653	24965055
237534122	chr2	24964562	24964719	24964583	24964699	NCOA1	NM_003743	1	21	17	+	24964653	24965055
237581611	chr2	24964981	24965113	24965005	24965086	NCOA1	NM_147233	3	21	17	+	24964653	24965055
237581611	chr2	24964981	24965113	24965005	24965086	NCOA1	NM_147223	2	22	17	+	24964653	24965055
237581611	chr2	24964981	24965113	24965005	24965086	NCOA1	NM_003743	1	21	17	+	24964653	24965055
236264855	chr2	24980920	24981078	24980943	24981052	NCOA1	NM_147233	3	21	19	+	24980842	24981025
236264855	chr2	24980920	24981078	24980943	24981052	NCOA1	NM_147223	2	22	19	+	24980842	24981025
236264855	chr2	24980920	24981078	24980943	24981052	NCOA1	NM_003743	1	21	19	+	24980842	24981025
240769484	chr2	24991000	24991174	24991027	24991153	NCOA1	NM_147223	2	22	22	+	24991090	24993570
240769484	chr2	24991000	24991174	24991027	24991153	NCOA1	NM_003743	1	21	21	+	24991090	24993570
240769484	chr2	24991000	24991174	24991027	24991153	NCOA1	NM_147233	3	21	21	+	24991093	24993570
232898223	chr2	25457244	25457372	25457266	25457351	DNMT3A	NM_022552	1	23	23	-	25455830	25457289
232898223	chr2	25457244	25457372	25457266	25457351	DNMT3A	NM_153759	2	19	19	-	25455830	25457289
232898223	chr2	25457244	25457372	25457266	25457351	DNMT3A	NM_175629	3	23	23	-	25455830	25457289
230325182	chr2	25461867	25462022	25461888	25462001	DNMT3A	NM_022552	1	23	20	-	25461999	25462084
230325182	chr2	25461867	25462022	25461888	25462001	DNMT3A	NM_153759	2	19	16	-	25461999	25462084
230325182	chr2	25461867	25462022	25461888	25462001	DNMT3A	NM_175629	3	23	20	-	25461999	25462084
229776726	chr2	25463453	25463626	25463472	25463603	DNMT3A	NM_022552	1	23	18	-	25463509	25463599
229776726	chr2	25463453	25463626	25463472	25463603	DNMT3A	NM_153759	2	19	14	-	25463509	25463599
229776726	chr2	25463453	25463626	25463472	25463603	DNMT3A	NM_175629	3	23	18	-	25463509	25463599
230813536	chr2	25466925	25467062	25466943	25467036	DNMT3A	NM_022552	1	23	15	-	25467024	25467207
230813536	chr2	25466925	25467062	25466943	25467036	DNMT3A	NM_153759	2	19	11	-	25467024	25467207
230813536	chr2	25466925	25467062	25466943	25467036	DNMT3A	NM_175629	3	23	15	-	25467024	25467207
230723358	chr2	25467477	25467633	25467495	25467611	DNMT3A	NM_022552	1	23	14	-	25467409	25467521
230723358	chr2	25467477	25467633	25467495	25467611	DNMT3A	NM_153759	2	19	10	-	25467409	25467521
230723358	chr2	25467477	25467633	25467495	25467611	DNMT3A	NM_175629	3	23	14	-	25467409	25467521
232220542	chr2	25469016	25469187	25469036	25469164	DNMT3A	NM_022552	1	23	11	-	25469029	25469178
232220542	chr2	25469016	25469187	25469036	25469164	DNMT3A	NM_153759	2	19	7	-	25469029	25469178
232220542	chr2	25469016	25469187	25469036	25469164	DNMT3A	NM_175629	3	23	11	-	25469029	25469178
228040530	chr2	25469900	25470068	25469918	25470047	DNMT3A	NM_022552	1	23	9	-	25469920	25470027

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228040530	chr2	25469900	25470068	25469918	25470047	DNMT3A	NM_153759	2	19	5	-	25469920	25470027
228040530	chr2	25469900	25470068	25469918	25470047	DNMT3A	NM_175629	3	23	9	-	25469920	25470027
227747129	chr2	25470940	25471110	25470960	25471089	DNMT3A	NM_022552	1	23	7	-	25470906	25471121
227747129	chr2	25470940	25471110	25470960	25471089	DNMT3A	NM_153759	2	19	3	-	25470906	25471121
227747129	chr2	25470940	25471110	25470960	25471089	DNMT3A	NM_175629	3	23	7	-	25470906	25471121
230792239	chr2	25497708	25497870	25497733	25497848	DNMT3A	NM_022552	1	23	6	-	25497810	25497956
230792239	chr2	25497708	25497870	25497733	25497848	DNMT3A	NM_175629	3	23	6	-	25497810	25497956
228726104	chr2	25505356	25505511	25505378	25505491	DNMT3A	NM_175630	4	4	4	-	25504321	25505580
228726104	chr2	25505356	25505511	25505378	25505491	DNMT3A	NM_022552	1	23	4	-	25505310	25505580
228726104	chr2	25505356	25505511	25505378	25505491	DNMT3A	NM_175629	3	23	4	-	25505310	25505580
222613250	chr2	29416053	29416227	29416076	29416204	ALK	NM_004304	1	29	29	-	29415640	29416788
222658180	chr2	29416524	29416693	29416542	29416672	ALK	NM_004304	1	29	29	-	29415640	29416788
222176787	chr2	29420365	29420505	29420393	29420481	ALK	NM_004304	1	29	27	-	29420408	29420542
224503004	chr2	29436821	29436994	29436844	29436974	ALK	NM_004304	1	29	24	-	29436850	29436947
223795289	chr2	29445359	29445508	29445380	29445483	ALK	NM_004304	1	29	21	-	29445383	29445473
223272390	chr2	29448221	29448394	29448246	29448372	ALK	NM_004304	1	29	19	-	29448327	29448431
222597478	chr2	29450390	29450561	29450411	29450539	ALK	NM_004304	1	29	17	-	29450440	29450538
223532289	chr2	29455175	29455338	29455195	29455317	ALK	NM_004304	1	29	15	-	29455170	29455314
223161250	chr2	29462573	29462718	29462594	29462696	ALK	NM_004304	1	29	13	-	29462546	29462696
222378160	chr2	29498009	29498144	29498031	29498120	ALK	NM_004304	1	29	11	-	29497965	29498093
225086310	chr2	29519842	29519967	29519863	29519942	ALK	NM_004304	1	29	9	-	29519754	29519923
222219643	chr2	29551097	29551266	29551122	29551245	ALK	NM_004304	1	29	6	-	29551216	29551347
222650366	chr2	29754704	29754866	29754730	29754845	ALK	NM_004304	1	29	4	-	29754781	29754982
222436139	chr2	29917720	29917879	29917740	29917857	ALK	NM_004304	1	29	3	-	29917716	29917880
224300627	chr2	30142742	30142907	30142763	30142890	ALK	NM_004304	1	29	1	-	30142859	30144477
224313145	chr2	30143141	30143315	30143159	30143296	ALK	NM_004304	1	29	1	-	30142859	30144477
230687200	chr2	42396651	42396825	42396671	42396802	EML4	NM_019063	2	23	1	+	42396490	42396776
230687200	chr2	42396651	42396825	42396671	42396802	EML4	NM_001145076	1	22	1	+	42396490	42396776
229089321	chr2	42483550	42483691	42483572	42483666	EML4	NM_019063	2	23	3	+	42483641	42483770
229089321	chr2	42483550	42483691	42483572	42483666	EML4	NM_001145076	1	22	3	+	42483641	42483770
230512699	chr2	42490328	42490452	42490352	42490424	EML4	NM_019063	2	23	5	+	42490318	42490446
230512699	chr2	42490328	42490452	42490352	42490424	EML4	NM_001145076	1	22	4	+	42490318	42490446
233026044	chr2	42507972	42508143	42507999	42508117	EML4	NM_019063	2	23	7	+	42507990	42508113
233026044	chr2	42507972	42508143	42507999	42508117	EML4	NM_001145076	1	22	6	+	42507990	42508113
230325967	chr2	42511716	42511880	42511744	42511854	EML4	NM_019063	2	23	9	+	42511774	42511843
230325967	chr2	42511716	42511880	42511744	42511854	EML4	NM_001145076	1	22	8	+	42511774	42511843
228148641	chr2	42515408	42515572	42515432	42515546	EML4	NM_019063	2	23	11	+	42515367	42515462
228148641	chr2	42515408	42515572	42515432	42515546	EML4	NM_001145076	1	22	10	+	42515367	42515462
230323883	chr2	42522464	42522612	42522489	42522587	EML4	NM_019063	2	23	13	+	42522521	42522656
230323883	chr2	42522464	42522612	42522489	42522587	EML4	NM_001145076	1	22	12	+	42522521	42522656
227781072	chr2	42530161	42530286	42530185	42530262	EML4	NM_019063	2	23	15	+	42530244	42530369

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227781072	chr2	42530161	42530286	42530185	42530262	EML4	NM_001145076	1	22	14	+	42530244	42530369
228805660	chr2	42531561	42531729	42531582	42531701	EML4	NM_019063	2	23	17	+	42531624	42531691
228805660	chr2	42531561	42531729	42531582	42531701	EML4	NM_001145076	1	22	16	+	42531624	42531691
229787891	chr2	42552629	42552802	42552648	42552781	EML4	NM_019063	2	23	20	+	42552607	42552694
229787891	chr2	42552629	42552802	42552648	42552781	EML4	NM_001145076	1	22	19	+	42552607	42552694
229613949	chr2	42556065	42556202	42556086	42556173	EML4	NM_019063	2	23	22	+	42556026	42556156
229613949	chr2	42556065	42556202	42556086	42556173	EML4	NM_001145076	1	22	21	+	42556026	42556156
228818307	chr2	42557145	42557285	42557170	42557262	EML4	NM_019063	2	23	23	+	42556874	42559688
228818307	chr2	42557145	42557285	42557170	42557262	EML4	NM_001145076	1	22	22	+	42556874	42559688
236948093	chr2	47630491	47630617	47630510	47630598	MSH2	NM_000251	1	16	1	+	47630263	47630541
237768698	chr2	47637434	47637560	47637457	47637538	MSH2	NM_000251	1	16	3	+	47637233	47637511
235692657	chr2	47639670	47639829	47639693	47639797	MSH2	NM_000251	1	16	4	+	47639553	47639699
239694744	chr2	47641514	47641654	47641540	47641623	MSH2	NM_000251	1	16	5	+	47641408	47641557
239509741	chr2	47656907	47657045	47656931	47657017	MSH2	NM_000251	1	16	7	+	47656881	47657080
242651455	chr2	47690149	47690319	47690172	47690297	MSH2	NM_000251	1	16	9	+	47690170	47690293
236815587	chr2	47702160	47702285	47702184	47702262	MSH2	NM_000251	1	16	12	+	47702164	47702409
241390437	chr2	47703588	47703735	47703610	47703711	MSH2	NM_000251	1	16	13	+	47703506	47703710
240420862	chr2	47705568	47705714	47705596	47705686	MSH2	NM_000251	1	16	14	+	47705411	47705658
237702477	chr2	47709935	47710107	47709956	47710079	MSH2	NM_000251	1	16	16	+	47709918	47710360
236865027	chr2	48018000	48018173	48018027	48018152	MSH6	NM_000179	1	10	2	+	48018066	48018262
257735044	chr2	48025734	48025887	48025752	48025860	MSH6	NM_000179	1	10	4	+	48025750	48028294
257731000	chr2	48026163	48026335	48026183	48026309	MSH6	NM_000179	1	10	4	+	48025750	48028294
257927083	chr2	48026638	48026799	48026661	48026779	MSH6	NM_000179	1	10	4	+	48025750	48028294
238055250	chr2	48027020	48027194	48027047	48027169	MSH6	NM_000179	1	10	4	+	48025750	48028294
257775564	chr2	48027461	48027589	48027487	48027564	MSH6	NM_000179	1	10	4	+	48025750	48028294
257795953	chr2	48027820	48027976	48027848	48027948	MSH6	NM_000179	1	10	4	+	48025750	48028294
238205876	chr2	48030519	48030670	48030541	48030644	MSH6	NM_000179	1	10	5	+	48030559	48030824
235261220	chr2	48032037	48032203	48032062	48032174	MSH6	NM_000179	1	10	6	+	48032049	48032166
241841870	chr2	48033334	48033484	48033361	48033456	MSH6	NM_000179	1	10	8	+	48033343	48033497
235891398	chr2	48033702	48033868	48033727	48033843	MSH6	NM_000179	1	10	9	+	48033591	48033790
224663398	chr2	60687499	60687661	60687518	60687637	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224599382	chr2	60687859	60688033	60687879	60688011	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224599382	chr2	60687859	60688033	60687879	60688011	BCL11A	NM_018014	1	5	4	-	60687817	60689559
224592690	chr2	60688360	60688511	60688379	60688494	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224592690	chr2	60688360	60688511	60688379	60688494	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223023504	chr2	60688732	60688905	60688751	60688886	BCL11A	NM_022893	2	4	4	-	60684329	60689559
223023504	chr2	60688732	60688905	60688751	60688886	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223048618	chr2	60689197	60689371	60689214	60689346	BCL11A	NM_022893	2	4	4	-	60684329	60689559
223048618	chr2	60689197	60689371	60689214	60689346	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223719430	chr2	60773016	60773151	60773040	60773126	BCL11A	NM_018014	1	5	2	-	60773106	60773435
223719430	chr2	60773016	60773151	60773040	60773126	BCL11A	NM_022893	2	4	2	-	60773106	60773435

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223719430	chr2	60773016	60773151	60773040	60773126	BCL11A	NM_138559	3	5	2	-	60773106	60773435
223866047	chr2	60780298	60780471	60780317	60780454	BCL11A	NM_018014	1	5	1	-	60780351	60780633
223866047	chr2	60780298	60780471	60780317	60780454	BCL11A	NM_022893	2	4	1	-	60780351	60780633
223866047	chr2	60780298	60780471	60780317	60780454	BCL11A	NM_138559	3	5	1	-	60780351	60780633
240500706	chr2	61121585	61121751	61121613	61121725	REL	NM_002908	1	11	3	+	61121532	61121680
240130721	chr2	61145242	61145405	61145267	61145378	REL	NM_002908	1	11	6	+	61145326	61145430
263772176	chr2	61147629	61147760	61147653	61147738	REL	NM_002908	1	11	10	+	61147709	61147777
241931182	chr2	61148985	61149140	61149006	61149113	REL	NM_002908	1	11	11	+	61148898	61150178
264236203	chr2	61149447	61149619	61149470	61149591	REL	NM_002908	1	11	11	+	61148898	61150178
273201603	chr2	61708264	61708437	61708291	61708412	XPO1	NM_003400	1	25	24	-	61708320	61708416
273991601	chr2	61711033	61711184	61711061	61711158	XPO1	NM_003400	1	25	21	-	61711072	61711240
273161949	chr2	61713030	61713189	61713058	61713161	XPO1	NM_003400	1	25	20	-	61712903	61713097
273461244	chr2	61715722	61715875	61715750	61715852	XPO1	NM_003400	1	25	18	-	61715723	61715906
273139484	chr2	61719075	61719245	61719097	61719217	XPO1	NM_003400	1	25	16	-	61719170	61719333
273399183	chr2	61719580	61719735	61719608	61719707	XPO1	NM_003400	1	25	15	-	61719460	61719616
273399183	chr2	61719580	61719735	61719608	61719707	XPO1	NM_003400	1	25	14	-	61719702	61719883
273610266	chr2	61720967	61721099	61720991	61721075	XPO1	NM_003400	1	25	12	-	61721029	61721226
273188069	chr2	61722588	61722717	61722617	61722689	XPO1	NM_003400	1	25	11	-	61722590	61722748
274158694	chr2	61725753	61725906	61725781	61725882	XPO1	NM_003400	1	25	9	-	61725808	61725927
273466031	chr2	61726860	61727031	61726888	61727005	XPO1	NM_003400	1	25	7	-	61726848	61727029
273533565	chr2	61749731	61749894	61749757	61749868	XPO1	NM_003400	1	25	4	-	61749746	61749818
273424020	chr2	61760849	61760981	61760873	61760953	XPO1	NM_003400	1	25	2	-	61760907	61761038
299006727	chr2	85361418	85361567	85361435	85361550	TCF7L1	NM_031283	1	12	3	+	85361446	85361573
298992986	chr2	85529606	85529760	85529633	85529740	TCF7L1	NM_031283	1	12	5	+	85529607	85529739
299260804	chr2	85532378	85532550	85532397	85532531	TCF7L1	NM_031283	1	12	8	+	85532383	85532526
298916335	chr2	85534719	85534891	85534742	85534869	TCF7L1	NM_031283	1	12	11	+	85534765	85534840
299263215	chr2	85536358	85536482	85536376	85536464	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
225309080	chr2	100167923	100168097	100167944	100168073	AFF3	NM_002285	2	24	24	-	100163716	100168057
225309080	chr2	100167923	100168097	100167944	100168073	AFF3	NM_001025108	1	24	24	-	100163716	100168057
225066898	chr2	100171098	100171229	100171119	100171207	AFF3	NM_002285	2	24	22	-	100171145	100171194
225066898	chr2	100171098	100171229	100171119	100171207	AFF3	NM_001025108	1	24	22	-	100171145	100171194
224098398	chr2	100182019	100182184	100182046	100182156	AFF3	NM_002285	2	24	19	-	100181949	100182085
224098398	chr2	100182019	100182184	100182046	100182156	AFF3	NM_001025108	1	24	19	-	100181949	100182085
223275237	chr2	100199225	100199388	100199252	100199364	AFF3	NM_002285	2	24	16	-	100199260	100199461
223275237	chr2	100199225	100199388	100199252	100199364	AFF3	NM_001025108	1	24	16	-	100199260	100199461
225156035	chr2	100209567	100209713	100209589	100209694	AFF3	NM_002285	2	24	14	-	100209657	100210751
225156035	chr2	100209567	100209713	100209589	100209694	AFF3	NM_001025108	1	24	14	-	100209657	100210751
225190901	chr2	100210003	100210160	100210024	100210138	AFF3	NM_002285	2	24	14	-	100209657	100210751
225190901	chr2	100210003	100210160	100210024	100210138	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223846085	chr2	100210476	100210600	100210496	100210581	AFF3	NM_002285	2	24	14	-	100209657	100210751
223846085	chr2	100210476	100210600	100210496	100210581	AFF3	NM_001025108	1	24	14	-	100209657	100210751

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223745817	chr2	100217966	100218139	100217985	100218116	AFF3	NM_002285	2	24	13	-	100217897	100218083
223745817	chr2	100217966	100218139	100217985	100218116	AFF3	NM_001025108	1	24	13	-	100217897	100218083
224432485	chr2	100360525	100360697	100360546	100360668	AFF3	NM_002285	2	24	9	-	100360566	100360602
224432485	chr2	100360525	100360697	100360546	100360668	AFF3	NM_001025108	1	24	9	-	100360566	100360602
223069905	chr2	100623192	100623341	100623211	100623320	AFF3	NM_002285	2	24	6	-	100623094	100623479
223069905	chr2	100623192	100623341	100623211	100623320	AFF3	NM_001025108	1	24	6	-	100623094	100623479
225090146	chr2	100623693	100623830	100623714	100623808	AFF3	NM_002285	2	24	5	-	100623610	100623922
225090146	chr2	100623693	100623830	100623714	100623808	AFF3	NM_001025108	1	24	5	-	100623610	100623922
222582307	chr2	100627896	100628070	100627919	100628047	AFF3	NM_001025108	1	24	3	-	100627959	100628033
237530969	chr2	113984692	113984860	113984712	113984834	PAX8	NM_003466	1	12	10	-	113984732	113984833
237530969	chr2	113984692	113984860	113984712	113984834	PAX8	NM_013952	2	12	10	-	113984732	113984833
237530969	chr2	113984692	113984860	113984712	113984834	PAX8	NM_013953	3	10	8	-	113984732	113984833
234920506	chr2	113994194	113994348	113994215	113994329	PAX8	NM_003466	1	12	8	-	113994178	113994298
234920506	chr2	113994194	113994348	113994215	113994329	PAX8	NM_013952	2	12	8	-	113994178	113994298
239064384	chr2	113999507	113999681	113999529	113999661	PAX8	NM_003466	1	12	6	-	113999585	113999707
239064384	chr2	113999507	113999681	113999529	113999661	PAX8	NM_013992	4	9	6	-	113999585	113999707
239064384	chr2	113999507	113999681	113999529	113999661	PAX8	NM_013952	2	12	6	-	113999585	113999707
239064384	chr2	113999507	113999681	113999529	113999661	PAX8	NM_013953	3	10	6	-	113999585	113999707
235040578	chr2	114002093	114002240	114002114	114002211	PAX8	NM_003466	1	12	4	-	114002004	114002201
235040578	chr2	114002093	114002240	114002114	114002211	PAX8	NM_013992	4	9	4	-	114002004	114002201
235040578	chr2	114002093	114002240	114002114	114002211	PAX8	NM_013952	2	12	4	-	114002004	114002201
235040578	chr2	114002093	114002240	114002114	114002211	PAX8	NM_013953	3	10	4	-	114002004	114002201
229804987	chr2	128015076	128015212	128015098	128015191	ERCC3	NM_000122	1	15	15	-	128014866	128015303
230745406	chr2	128018750	128018874	128018772	128018851	ERCC3	NM_000122	1	15	13	-	128018804	128018922
228428556	chr2	128030419	128030566	128030440	128030538	ERCC3	NM_000122	1	15	11	-	128030441	128030537
231147136	chr2	128038065	128038231	128038085	128038207	ERCC3	NM_000122	1	15	9	-	128038023	128038207
232985420	chr2	128046197	128046371	128046219	128046347	ERCC3	NM_000122	1	15	7	-	128046236	128046440
229353274	chr2	128047181	128047351	128047205	128047331	ERCC3	NM_000122	1	15	5	-	128047265	128047400
231635036	chr2	128050281	128050451	128050304	128050423	ERCC3	NM_000122	1	15	3	-	128050186	128050422
271146404	chr2	140990650	140990815	140990675	140990788	LRP1B	NM_018557	1	91	91	-	140988996	140990895
270788021	chr2	140996943	140997107	140996970	140997086	LRP1B	NM_018557	1	91	88	-	140997011	140997101
271732426	chr2	141027844	141027977	141027865	141027950	LRP1B	NM_018557	1	91	86	-	141027811	141027915
269844984	chr2	141055305	141055454	141055332	141055433	LRP1B	NM_018557	1	91	84	-	141055377	141055538
271816064	chr2	141072627	141072787	141072655	141072756	LRP1B	NM_018557	1	91	83	-	141072504	141072668
271098474	chr2	141093167	141093304	141093195	141093282	LRP1B	NM_018557	1	91	78	-	141093184	141093407
269897900	chr2	141110421	141110570	141110445	141110542	LRP1B	NM_018557	1	91	76	-	141110522	141110641
271919485	chr2	141115451	141115611	141115478	141115588	LRP1B	NM_018557	1	91	74	-	141115548	141115685
270924938	chr2	141122118	141122285	141122145	141122264	LRP1B	NM_018557	1	91	72	-	141122230	141122352
271540405	chr2	141128607	141128780	141128639	141128753	LRP1B	NM_018557	1	91	70	-	141128748	141128854
270170343	chr2	141143387	141143561	141143413	141143533	LRP1B	NM_018557	1	91	67	-	141143462	141143578
271534733	chr2	141201855	141201982	141201882	141201955	LRP1B	NM_018557	1	91	65	-	141201899	141202018

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269713082	chr2	141208027	141208168	141208054	141208144	LRP1B	NM_018557	1	91	63	-	141208137	141208230
270026216	chr2	141214977	141215109	141215010	141215082	LRP1B	NM_018557	1	91	61	-	141215032	141215220
271064645	chr2	141232793	141232953	141232821	141232925	LRP1B	NM_018557	1	91	60	-	141232707	141232906
269533796	chr2	141245069	141245240	141245097	141245223	LRP1B	NM_018557	1	91	58	-	141245186	141245308
271973343	chr2	141253081	141253231	141253109	141253207	LRP1B	NM_018557	1	91	56	-	141253134	141253317
272604259	chr2	141259246	141259385	141259273	141259360	LRP1B	NM_018557	1	91	55	-	141259256	141259443
269960447	chr2	141260627	141260753	141260650	141260727	LRP1B	NM_018557	1	91	54	-	141260532	141260672
271099632	chr2	141267507	141267669	141267528	141267642	LRP1B	NM_018557	1	91	52	-	141267497	141267625
271224600	chr2	141274522	141274688	141274550	141274655	LRP1B	NM_018557	1	91	50	-	141274458	141274580
269490339	chr2	141283717	141283853	141283745	141283829	LRP1B	NM_018557	1	91	48	-	141283806	141283919
271797946	chr2	141294052	141294202	141294077	141294174	LRP1B	NM_018557	1	91	46	-	141294150	141294278
270024953	chr2	141299249	141299388	141299282	141299365	LRP1B	NM_018557	1	91	44	-	141299348	141299540
270985392	chr2	141356198	141356363	141356221	141356335	LRP1B	NM_018557	1	91	43	-	141356200	141356404
272069646	chr2	141359184	141359334	141359205	141359306	LRP1B	NM_018557	1	91	42	-	141359019	141359208
270659008	chr2	141458065	141458192	141458086	141458172	LRP1B	NM_018557	1	91	41	-	141457819	141458190
271060540	chr2	141459716	141459863	141459739	141459834	LRP1B	NM_018557	1	91	39	-	141459710	141459861
270361971	chr2	141473438	141473588	141473469	141473566	LRP1B	NM_018557	1	91	37	-	141473542	141473671
271163448	chr2	141526662	141526836	141526690	141526808	LRP1B	NM_018557	1	91	35	-	141526782	141526913
271073774	chr2	141533635	141533808	141533660	141533785	LRP1B	NM_018557	1	91	33	-	141533667	141533807
270952182	chr2	141597625	141597796	141597647	141597768	LRP1B	NM_018557	1	91	31	-	141597560	141597654
270454091	chr2	141607694	141607868	141607722	141607840	LRP1B	NM_018557	1	91	29	-	141607671	141607898
272189078	chr2	141625120	141625253	141625147	141625230	LRP1B	NM_018557	1	91	27	-	141625159	141625403
269596128	chr2	141625688	141625833	141625714	141625808	LRP1B	NM_018557	1	91	26	-	141625668	141625832
269889206	chr2	141643795	141643967	141643821	141643939	LRP1B	NM_018557	1	91	24	-	141643707	141643904
271173684	chr2	141665308	141665482	141665336	141665458	LRP1B	NM_018557	1	91	22	-	141665446	141665646
272189445	chr2	141680579	141680747	141680602	141680719	LRP1B	NM_018557	1	91	21	-	141680534	141680716
271928459	chr2	141709400	141709571	141709426	141709543	LRP1B	NM_018557	1	91	19	-	141709429	141709509
272704125	chr2	141747192	141747361	141747220	141747334	LRP1B	NM_018557	1	91	17	-	141747101	141747226
271629469	chr2	141762906	141763056	141762930	141763030	LRP1B	NM_018557	1	91	15	-	141762904	141763026
270919926	chr2	141773199	141773352	141773223	141773326	LRP1B	NM_018557	1	91	13	-	141773265	141773484
271432179	chr2	141777522	141777669	141777550	141777645	LRP1B	NM_018557	1	91	12	-	141777491	141777671
270190645	chr2	141812648	141812773	141812672	141812749	LRP1B	NM_018557	1	91	10	-	141812685	141812828
270044078	chr2	141819508	141819675	141819532	141819648	LRP1B	NM_018557	1	91	8	-	141819620	141819842
270968799	chr2	141946027	141946191	141946049	141946163	LRP1B	NM_018557	1	91	7	-	141945990	141946152
269725537	chr2	141986915	141987089	141986942	141987061	LRP1B	NM_018557	1	91	6	-	141986752	141987009
269519924	chr2	142012086	142012219	142012112	142012192	LRP1B	NM_018557	1	91	4	-	142012091	142012210
272582008	chr2	142567913	142568046	142567935	142568019	LRP1B	NM_018557	1	91	2	-	142567848	142567970
284766478	chr2	148602741	148602867	148602762	148602847	ACVR2A	NM_001616	1	11	1	+	148602570	148602776
282316828	chr2	148657053	148657181	148657079	148657153	ACVR2A	NM_001616	1	11	3	+	148657027	148657136
282112938	chr2	148672708	148672878	148672732	148672853	ACVR2A	NM_001616	1	11	5	+	148672760	148672903
281923114	chr2	148675912	148676068	148675935	148676043	ACVR2A	NM_001616	1	11	7	+	148676016	148676161

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
283877707	chr2	148677821	148677995	148677846	148677970	ACVR2A	NM_001616	1	11	8	+	148677799	148677913
284547951	chr2	148683483	148683657	148683511	148683635	ACVR2A	NM_001616	1	11	10	+	148683600	148683730
281384591	chr2	148684703	148684877	148684725	148684852	ACVR2A	NM_001616	1	11	11	+	148684649	148688393
235214512	chr2	178095679	178095848	178095707	178095820	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235214512	chr2	178095679	178095848	178095707	178095820	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235214512	chr2	178095679	178095848	178095707	178095820	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
239818754	chr2	178096142	178096315	178096168	178096291	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
239818754	chr2	178096142	178096315	178096168	178096291	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
239818754	chr2	178096142	178096315	178096168	178096291	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235099809	chr2	178096577	178096725	178096605	178096699	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235099809	chr2	178096577	178096725	178096605	178096699	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235099809	chr2	178096577	178096725	178096605	178096699	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235119720	chr2	178097206	178097355	178097230	178097329	NFE2L2	NM_001145412	1	5	4	-	178097120	178097311
235119720	chr2	178097206	178097355	178097230	178097329	NFE2L2	NM_006164	3	5	4	-	178097120	178097311
235119720	chr2	178097206	178097355	178097230	178097329	NFE2L2	NM_001145413	2	5	4	-	178097120	178097290
238577035	chr2	178098778	178098917	178098800	178098889	NFE2L2	NM_001145412	1	5	2	-	178098733	178098999
238577035	chr2	178098778	178098917	178098800	178098889	NFE2L2	NM_001145413	2	5	2	-	178098733	178098999
238577035	chr2	178098778	178098917	178098800	178098889	NFE2L2	NM_006164	3	5	2	-	178098733	178098999
237988103	chr2	190656462	190656594	190656486	190656566	PMS1	NM_001128144	3	12	2	+	190656516	190656667
237988103	chr2	190656462	190656594	190656486	190656566	PMS1	NM_000534	1	13	2	+	190656516	190656667
237988103	chr2	190656462	190656594	190656486	190656566	PMS1	NM_001128143	2	12	2	+	190656516	190656667
235899743	chr2	190660558	190660684	190660584	190660655	PMS1	NM_001128144	3	12	3	+	190660495	190660677
235899743	chr2	190660558	190660684	190660584	190660655	PMS1	NM_000534	1	13	3	+	190660495	190660677
235899743	chr2	190660558	190660684	190660584	190660655	PMS1	NM_001128143	2	12	3	+	190660495	190660677
237942399	chr2	190682687	190682858	190682712	190682833	PMS1	NM_001128144	3	12	5	+	190682743	190682906
237942399	chr2	190682687	190682858	190682712	190682833	PMS1	NM_000534	1	13	5	+	190682743	190682906
237942399	chr2	190682687	190682858	190682712	190682833	PMS1	NM_001128143	2	12	5	+	190682743	190682906
238518468	chr2	190717315	190717449	190717340	190717421	PMS1	NM_001128144	3	12	7	+	190717381	190717503
238518468	chr2	190717315	190717449	190717340	190717421	PMS1	NM_000534	1	13	7	+	190717381	190717503
238518468	chr2	190717315	190717449	190717340	190717421	PMS1	NM_001128143	2	12	6	+	190717381	190717503
241082013	chr2	190719000	190719171	190719028	190719143	PMS1	NM_001128144	3	12	9	+	190718965	190719854
241082013	chr2	190719000	190719171	190719028	190719143	PMS1	NM_000534	1	13	9	+	190718965	190719854
241082013	chr2	190719000	190719171	190719028	190719143	PMS1	NM_001128143	2	12	8	+	190718965	190719854
237598127	chr2	190719452	190719626	190719478	190719596	PMS1	NM_001128144	3	12	9	+	190718965	190719854
237598127	chr2	190719452	190719626	190719478	190719596	PMS1	NM_000534	1	13	9	+	190718965	190719854
237598127	chr2	190719452	190719626	190719478	190719596	PMS1	NM_001128143	2	12	8	+	190718965	190719854
238268147	chr2	190728540	190728674	190728568	190728648	PMS1	NM_000534	1	13	10	+	190728469	190728954
238268147	chr2	190728540	190728674	190728568	190728648	PMS1	NM_001128143	2	12	9	+	190728469	190728954
235202074	chr2	190732446	190732618	190732472	190732593	PMS1	NM_001128144	3	12	10	+	190732525	190732655
235202074	chr2	190732446	190732618	190732472	190732593	PMS1	NM_000534	1	13	11	+	190732525	190732655
235202074	chr2	190732446	190732618	190732472	190732593	PMS1	NM_001128143	2	12	10	+	190732525	190732655

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236314777	chr2	190742070	190742223	190742095	190742195	PMS1	NM_001128144	3	12	12	+	190741998	190742355
236314777	chr2	190742070	190742223	190742095	190742195	PMS1	NM_000534	1	13	13	+	190741998	190742355
236314777	chr2	190742070	190742223	190742095	190742195	PMS1	NM_001128143	2	12	12	+	190741998	190742355
273165502	chr2	198257886	198258013	198257908	198257984	SF3B1	NM_012433	2	25	24	-	198257696	198257912
273357212	chr2	198262594	198262749	198262618	198262727	SF3B1	NM_012433	2	25	22	-	198262709	198262840
274038201	chr2	198263191	198263365	198263219	198263337	SF3B1	NM_012433	2	25	21	-	198263185	198263305
273228059	chr2	198265050	198265220	198265078	198265192	SF3B1	NM_012433	2	25	19	-	198264976	198265158
273458756	chr2	198266004	198266171	198266034	198266151	SF3B1	NM_012433	2	25	17	-	198266124	198266249
273713635	chr2	198266488	198266614	198266512	198266593	SF3B1	NM_012433	2	25	16	-	198266466	198266612
272949310	chr2	198267355	198267497	198267382	198267471	SF3B1	NM_012433	2	25	14	-	198267280	198267550
272983143	chr2	198268192	198268346	198268215	198268319	SF3B1	NM_012433	2	25	12	-	198268309	198268488
273564146	chr2	198269973	198270101	198270005	198270073	SF3B1	NM_012433	2	25	10	-	198269999	198270196
274403011	chr2	198272720	198272857	198272747	198272829	SF3B1	NM_012433	2	25	9	-	198272722	198272843
273061413	chr2	198273192	198273316	198273218	198273289	SF3B1	NM_012433	2	25	8	-	198273093	198273305
273975316	chr2	198281454	198281614	198281479	198281587	SF3B1	NM_012433	2	25	6	-	198281465	198281635
272956066	chr2	198285052	198285180	198285076	198285160	SF3B1	NM_012433	2	25	4	-	198285152	198285266
272956066	chr2	198285052	198285180	198285076	198285160	SF3B1	NM_001005526	1	5	4	-	198285152	198285266
273789607	chr2	198285744	198285871	198285769	198285849	SF3B1	NM_012433	2	25	3	-	198285753	198285857
273789607	chr2	198285744	198285871	198285769	198285849	SF3B1	NM_001005526	1	5	3	-	198285753	198285857
273521664	chr2	198299588	198299746	198299608	198299724	SF3B1	NM_012433	2	25	1	-	198299696	198299771
273521664	chr2	198299588	198299746	198299608	198299724	SF3B1	NM_001005526	1	5	1	-	198299696	198299771
226988760	chr2	208424975	208425104	208424996	208425078	CREB1	NM_134442	2	9	3	+	208424950	208425096
226988760	chr2	208424975	208425104	208424996	208425078	CREB1	NM_004379	1	8	3	+	208424950	208425096
225326238	chr2	208434791	208434959	208434813	208434936	CREB1	NM_134442	2	9	6	+	208434903	208435045
225326238	chr2	208434791	208434959	208434813	208434936	CREB1	NM_004379	1	8	5	+	208434903	208435045
225411455	chr2	208440057	208440208	208440082	208440183	CREB1	NM_134442	2	9	7	+	208439996	208440178
225411455	chr2	208440057	208440208	208440082	208440183	CREB1	NM_004379	1	8	6	+	208439996	208440178
225813804	chr2	208461696	208461826	208461719	208461801	CREB1	NM_134442	2	9	9	+	208461638	208470284
225813804	chr2	208461696	208461826	208461719	208461801	CREB1	NM_004379	1	8	8	+	208461638	208470284
228765454	chr2	209103833	209104000	209103855	209103972	IDH1	NM_005896	1	10	9	-	209103795	209103957
227425846	chr2	209106767	209106941	209106789	209106913	IDH1	NM_005896	1	10	7	-	209106718	209106869
227333601	chr2	209110020	209110168	209110048	209110143	IDH1	NM_005896	1	10	5	-	209110043	209110148
227229303	chr2	209113189	209113349	209113211	209113328	IDH1	NM_005896	1	10	4	-	209113093	209113384
230956728	chr2	212248207	212248371	212248231	212248347	ERBB4	NM_001042599	1	27	27	-	212240442	212248785
230956728	chr2	212248207	212248371	212248231	212248347	ERBB4	NM_005235	2	28	28	-	212240442	212248785
227784624	chr2	212248658	212248782	212248680	212248760	ERBB4	NM_001042599	1	27	27	-	212240442	212248785
227784624	chr2	212248658	212248782	212248680	212248760	ERBB4	NM_005235	2	28	28	-	212240442	212248785
231895395	chr2	212252560	212252713	212252581	212252692	ERBB4	NM_005235	2	28	26	-	212252670	212252717
232483524	chr2	212286672	212286846	212286696	212286819	ERBB4	NM_001042599	1	27	24	-	212286732	212286829
232483524	chr2	212286672	212286846	212286696	212286819	ERBB4	NM_005235	2	28	24	-	212286732	212286829
228333610	chr2	212293129	212293296	212293153	212293273	ERBB4	NM_001042599	1	27	22	-	212293133	212293208

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228333610	chr2	212293129	212293296	212293153	212293273	ERBB4	NM_005235	2	28	22	-	212293133	212293208
230761339	chr2	212426621	212426782	212426646	212426763	ERBB4	NM_001042599	1	27	20	-	212426628	212426813
230761339	chr2	212426621	212426782	212426646	212426763	ERBB4	NM_005235	2	28	20	-	212426628	212426813
229788737	chr2	212488654	212488821	212488674	212488797	ERBB4	NM_001042599	1	27	18	-	212488647	212488769
229788737	chr2	212488654	212488821	212488674	212488797	ERBB4	NM_005235	2	28	18	-	212488647	212488769
231404672	chr2	212529979	212530148	212530007	212530123	ERBB4	NM_001042599	1	27	15	-	212530048	212530202
231404672	chr2	212529979	212530148	212530007	212530123	ERBB4	NM_005235	2	28	15	-	212530048	212530202
230412616	chr2	212543861	212544035	212543882	212544008	ERBB4	NM_001042599	1	27	13	-	212543777	212543909
230412616	chr2	212543861	212544035	212543882	212544008	ERBB4	NM_005235	2	28	13	-	212543777	212543909
230576288	chr2	212568757	212568894	212568783	212568870	ERBB4	NM_001042599	1	27	11	-	212568829	212568919
230576288	chr2	212568757	212568894	212568783	212568870	ERBB4	NM_005235	2	28	11	-	212568829	212568919
228394464	chr2	212576672	212576827	212576696	212576799	ERBB4	NM_001042599	1	27	9	-	212576775	212576901
228394464	chr2	212576672	212576827	212576696	212576799	ERBB4	NM_005235	2	28	9	-	212576775	212576901
227685062	chr2	212587106	212587242	212587134	212587219	ERBB4	NM_001042599	1	27	7	-	212587118	212587259
227685062	chr2	212587106	212587242	212587134	212587219	ERBB4	NM_005235	2	28	7	-	212587118	212587259
230441605	chr2	212615286	212615457	212615309	212615432	ERBB4	NM_001042599	1	27	5	-	212615364	212615429
230441605	chr2	212615286	212615457	212615309	212615432	ERBB4	NM_005235	2	28	5	-	212615364	212615429
229760520	chr2	212812149	212812294	212812178	212812272	ERBB4	NM_001042599	1	27	3	-	212812155	212812341
229760520	chr2	212812149	212812294	212812178	212812272	ERBB4	NM_005235	2	28	3	-	212812155	212812341
232528324	chr2	213403082	213403228	213403100	213403209	ERBB4	NM_001042599	1	27	1	-	213403173	213403352
232528324	chr2	213403082	213403228	213403100	213403209	ERBB4	NM_005235	2	28	1	-	213403173	213403352
280412479	chr2	216226655	216226827	216226678	216226803	FN1	NM_212476	4	44	43	-	216226692	216226802
280412479	chr2	216226655	216226827	216226678	216226803	FN1	NM_212478	5	46	45	-	216226692	216226802
280412479	chr2	216226655	216226827	216226678	216226803	FN1	NM_212482	6	46	45	-	216226692	216226802
280412479	chr2	216226655	216226827	216226678	216226803	FN1	NM_212474	3	44	43	-	216226692	216226802
280412479	chr2	216226655	216226827	216226678	216226803	FN1	NM_002026	1	46	45	-	216226692	216226802
280699501	chr2	216232530	216232699	216232553	216232677	FN1	NM_212476	4	44	40	-	216232586	216232750
280699501	chr2	216232530	216232699	216232553	216232677	FN1	NM_212478	5	46	42	-	216232586	216232750
280699501	chr2	216232530	216232699	216232553	216232677	FN1	NM_212482	6	46	42	-	216232586	216232750
280699501	chr2	216232530	216232699	216232553	216232677	FN1	NM_212474	3	44	40	-	216232586	216232750
280699501	chr2	216232530	216232699	216232553	216232677	FN1	NM_002026	1	46	42	-	216232586	216232750
279018110	chr2	216236599	216236748	216236621	216236726	FN1	NM_212476	4	44	38	-	216236632	216237098
279018110	chr2	216236599	216236748	216236621	216236726	FN1	NM_212482	6	46	40	-	216236632	216237098
279018110	chr2	216236599	216236748	216236621	216236726	FN1	NM_212478	5	46	40	-	216236632	216236738
279018110	chr2	216236599	216236748	216236621	216236726	FN1	NM_212474	3	44	38	-	216236632	216236738
279018110	chr2	216236599	216236748	216236621	216236726	FN1	NM_002026	1	46	40	-	216236632	216236738
279617495	chr2	216238008	216238173	216238034	216238145	FN1	NM_212476	4	44	37	-	216238045	216238134
279617495	chr2	216238008	216238173	216238034	216238145	FN1	NM_212478	5	46	38	-	216238045	216238134
279617495	chr2	216238008	216238173	216238034	216238145	FN1	NM_212482	6	46	39	-	216238045	216238134
279617495	chr2	216238008	216238173	216238034	216238145	FN1	NM_212474	3	44	37	-	216238045	216238134
279617495	chr2	216238008	216238173	216238034	216238145	FN1	NM_002026	1	46	38	-	216238045	216238134

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278066288	chr2	216240383	216240520	216240405	216240495	FN1	NM_212476	4	44	35	-	216240352	216240441
278066288	chr2	216240383	216240520	216240405	216240495	FN1	NM_212478	5	46	36	-	216240352	216240441
278066288	chr2	216240383	216240520	216240405	216240495	FN1	NM_212482	6	46	37	-	216240352	216240441
278066288	chr2	216240383	216240520	216240405	216240495	FN1	NM_212474	3	44	35	-	216240352	216240441
278066288	chr2	216240383	216240520	216240405	216240495	FN1	NM_002026	1	46	36	-	216240352	216240441
279997833	chr2	216242911	216243054	216242931	216243030	FN1	NM_212476	4	44	33	-	216242898	216242985
279997833	chr2	216242911	216243054	216242931	216243030	FN1	NM_212478	5	46	34	-	216242898	216242985
279997833	chr2	216242911	216243054	216242931	216243030	FN1	NM_212482	6	46	35	-	216242898	216242985
279997833	chr2	216242911	216243054	216242931	216243030	FN1	NM_212474	3	44	33	-	216242898	216242985
279997833	chr2	216242911	216243054	216242931	216243030	FN1	NM_002026	1	46	34	-	216242898	216242985
278595982	chr2	216245630	216245780	216245652	216245755	FN1	NM_212478	5	46	32	-	216245534	216245803
278595982	chr2	216245630	216245780	216245652	216245755	FN1	NM_212482	6	46	33	-	216245534	216245803
278595982	chr2	216245630	216245780	216245652	216245755	FN1	NM_002026	1	46	32	-	216245534	216245803
278061167	chr2	216248027	216248176	216248050	216248154	FN1	NM_212476	4	44	30	-	216248051	216248206
278061167	chr2	216248027	216248176	216248050	216248154	FN1	NM_212478	5	46	30	-	216248051	216248206
278061167	chr2	216248027	216248176	216248050	216248154	FN1	NM_212482	6	46	31	-	216248051	216248206
278061167	chr2	216248027	216248176	216248050	216248154	FN1	NM_212474	3	44	30	-	216248051	216248206
278061167	chr2	216248027	216248176	216248050	216248154	FN1	NM_002026	1	46	30	-	216248051	216248206
279947219	chr2	216249518	216249687	216249546	216249667	FN1	NM_212476	4	44	28	-	216249583	216249699
279947219	chr2	216249518	216249687	216249546	216249667	FN1	NM_212478	5	46	28	-	216249583	216249699
279947219	chr2	216249518	216249687	216249546	216249667	FN1	NM_212482	6	46	29	-	216249583	216249699
279947219	chr2	216249518	216249687	216249546	216249667	FN1	NM_212474	3	44	28	-	216249583	216249699
279947219	chr2	216249518	216249687	216249546	216249667	FN1	NM_002026	1	46	28	-	216249583	216249699
279095618	chr2	216252905	216253077	216252929	216253049	FN1	NM_212476	4	44	26	-	216252935	216253024
279095618	chr2	216252905	216253077	216252929	216253049	FN1	NM_212478	5	46	26	-	216252935	216253024
279095618	chr2	216252905	216253077	216252929	216253049	FN1	NM_212482	6	46	27	-	216252935	216253024
279095618	chr2	216252905	216253077	216252929	216253049	FN1	NM_212474	3	44	26	-	216252935	216253024
279095618	chr2	216252905	216253077	216252929	216253049	FN1	NM_002026	1	46	26	-	216252935	216253024
278752590	chr2	216257642	216257809	216257667	216257781	FN1	NM_212482	6	46	25	-	216257654	216257926
278934621	chr2	216259327	216259479	216259347	216259453	FN1	NM_212476	4	44	24	-	216259251	216259442
278934621	chr2	216259327	216259479	216259347	216259453	FN1	NM_212478	5	46	24	-	216259251	216259442
278934621	chr2	216259327	216259479	216259347	216259453	FN1	NM_212482	6	46	24	-	216259251	216259442
278934621	chr2	216259327	216259479	216259347	216259453	FN1	NM_212474	3	44	24	-	216259251	216259442
278934621	chr2	216259327	216259479	216259347	216259453	FN1	NM_002026	1	46	24	-	216259251	216259442
281118981	chr2	216263937	216264068	216263959	216264045	FN1	NM_212476	4	44	21	-	216263980	216264074
281118981	chr2	216263937	216264068	216263959	216264045	FN1	NM_212478	5	46	21	-	216263980	216264074
281118981	chr2	216263937	216264068	216263959	216264045	FN1	NM_212482	6	46	21	-	216263980	216264074
281118981	chr2	216263937	216264068	216263959	216264045	FN1	NM_212474	3	44	21	-	216263980	216264074
281118981	chr2	216263937	216264068	216263959	216264045	FN1	NM_002026	1	46	21	-	216263980	216264074
278526579	chr2	216269315	216269483	216269340	216269455	FN1	NM_212476	4	44	20	-	216269112	216269378
278526579	chr2	216269315	216269483	216269340	216269455	FN1	NM_212478	5	46	20	-	216269112	216269378

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278526579	chr2	216269315	216269483	216269340	216269455	FN1	NM_212482	6	46	20	-	216269112	216269378
278526579	chr2	216269315	216269483	216269340	216269455	FN1	NM_212474	3	44	20	-	216269112	216269378
278526579	chr2	216269315	216269483	216269340	216269455	FN1	NM_002026	1	46	20	-	216269112	216269378
279157869	chr2	216271781	216271911	216271804	216271882	FN1	NM_212476	4	44	18	-	216271850	216272044
279157869	chr2	216271781	216271911	216271804	216271882	FN1	NM_212478	5	46	18	-	216271850	216272044
279157869	chr2	216271781	216271911	216271804	216271882	FN1	NM_212482	6	46	18	-	216271850	216272044
279157869	chr2	216271781	216271911	216271804	216271882	FN1	NM_212474	3	44	18	-	216271850	216272044
279157869	chr2	216271781	216271911	216271804	216271882	FN1	NM_002026	1	46	18	-	216271850	216272044
278014888	chr2	216272850	216273023	216272871	216272995	FN1	NM_212476	4	44	17	-	216272831	216272920
278014888	chr2	216272850	216273023	216272871	216272995	FN1	NM_212478	5	46	17	-	216272831	216272920
278014888	chr2	216272850	216273023	216272871	216272995	FN1	NM_212482	6	46	17	-	216272831	216272920
278014888	chr2	216272850	216273023	216272871	216272995	FN1	NM_212474	3	44	17	-	216272831	216272920
278014888	chr2	216272850	216273023	216272871	216272995	FN1	NM_002026	1	46	17	-	216272831	216272920
279917202	chr2	216274374	216274502	216274398	216274480	FN1	NM_212476	4	44	15	-	216274286	216274462
279917202	chr2	216274374	216274502	216274398	216274480	FN1	NM_212478	5	46	15	-	216274286	216274462
279917202	chr2	216274374	216274502	216274398	216274480	FN1	NM_212482	6	46	15	-	216274286	216274462
279917202	chr2	216274374	216274502	216274398	216274480	FN1	NM_212474	3	44	15	-	216274286	216274462
279917202	chr2	216274374	216274502	216274398	216274480	FN1	NM_002026	1	46	15	-	216274286	216274462
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_212476	4	44	13	-	216279560	216279681
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_212478	5	46	13	-	216279560	216279681
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_212482	6	46	13	-	216279560	216279681
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_212474	3	44	13	-	216279560	216279681
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_002026	1	46	13	-	216279560	216279681
278045847	chr2	216279471	216279596	216279494	216279568	FN1	NM_054034	2	13	13	-	216279384	216279681
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_054034	2	13	12	-	216283965	216284108
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_212476	4	44	12	-	216283965	216284108
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_212478	5	46	12	-	216283965	216284108
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_212482	6	46	12	-	216283965	216284108
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_212474	3	44	12	-	216283965	216284108
280812582	chr2	216284011	216284141	216284032	216284115	FN1	NM_002026	1	46	12	-	216283965	216284108
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_054034	2	13	10	-	216286814	216286966
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_212476	4	44	10	-	216286814	216286966
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_212478	5	46	10	-	216286814	216286966
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_212482	6	46	10	-	216286814	216286966
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_212474	3	44	10	-	216286814	216286966
279265333	chr2	216286872	216287011	216286893	216286983	FN1	NM_002026	1	46	10	-	216286814	216286966
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_054034	2	13	8	-	216288869	216289048
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_212476	4	44	8	-	216288869	216289048
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_212478	5	46	8	-	216288869	216289048
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_212482	6	46	8	-	216288869	216289048
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_212474	3	44	8	-	216288869	216289048

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280439481	chr2	216288928	216289088	216288949	216289061	FN1	NM_002026	1	46	8	-	216288869	216289048
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_054034	2	13	6	-	216292903	216293061
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_212476	4	44	6	-	216292903	216293061
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_212478	5	46	6	-	216292903	216293061
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_212482	6	46	6	-	216292903	216293061
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_212474	3	44	6	-	216292903	216293061
279912750	chr2	216292976	216293100	216292996	216293075	FN1	NM_002026	1	46	6	-	216292903	216293061
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_054034	2	13	4	-	216296556	216296687
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_212476	4	44	4	-	216296556	216296687
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_212478	5	46	4	-	216296556	216296687
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_212482	6	46	4	-	216296556	216296687
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_212474	3	44	4	-	216296556	216296687
279976555	chr2	216296562	216296721	216296584	216296692	FN1	NM_002026	1	46	4	-	216296556	216296687
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_054034	2	13	2	-	216299419	216299547
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_212476	4	44	2	-	216299419	216299547
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_212478	5	46	2	-	216299419	216299547
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_212482	6	46	2	-	216299419	216299547
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_212474	3	44	2	-	216299419	216299547
328497062	chr2	216299497	216299641	216299524	216299608	FN1	NM_002026	1	46	2	-	216299419	216299547
237782758	chr2	219538297	219538437	219538324	219538413	STK36	NM_015690	2	27	3	+	219538348	219538488
237782758	chr2	219538297	219538437	219538324	219538413	STK36	NM_001243313	1	27	3	+	219538348	219538488
240858263	chr2	219540110	219540235	219540130	219540211	STK36	NM_015690	2	27	5	+	219540066	219540196
240858263	chr2	219540110	219540235	219540130	219540211	STK36	NM_001243313	1	27	5	+	219540066	219540196
261080083	chr2	219543848	219544005	219543874	219543984	STK36	NM_015690	2	27	7	+	219543891	219543984
261080083	chr2	219543848	219544005	219543874	219543984	STK36	NM_001243313	1	27	7	+	219543891	219543984
241158331	chr2	219544702	219544869	219544723	219544843	STK36	NM_015690	2	27	9	+	219544616	219544803
241158331	chr2	219544702	219544869	219544723	219544843	STK36	NM_001243313	1	27	9	+	219544616	219544803
240322795	chr2	219553376	219553533	219553404	219553511	STK36	NM_015690	2	27	12	+	219553420	219553599
240322795	chr2	219553376	219553533	219553404	219553511	STK36	NM_001243313	1	27	12	+	219553420	219553599
238667783	chr2	219555199	219555328	219555221	219555304	STK36	NM_015690	2	27	14	+	219555173	219555278
238667783	chr2	219555199	219555328	219555221	219555304	STK36	NM_001243313	1	27	14	+	219555173	219555278
242312366	chr2	219557330	219557457	219557351	219557434	STK36	NM_015690	2	27	16	+	219557306	219557433
242312366	chr2	219557330	219557457	219557351	219557434	STK36	NM_001243313	1	27	16	+	219557306	219557433
242189409	chr2	219558929	219559099	219558951	219559076	STK36	NM_015690	2	27	20	+	219558987	219559050
242189409	chr2	219558929	219559099	219558951	219559076	STK36	NM_001243313	1	27	20	+	219558987	219559050
238248381	chr2	219561736	219561889	219561760	219561868	STK36	NM_015690	2	27	23	+	219561762	219561936
238248381	chr2	219561736	219561889	219561760	219561868	STK36	NM_001243313	1	27	23	+	219561762	219561936
240802338	chr2	219562515	219562689	219562542	219562667	STK36	NM_015690	2	27	25	+	219562577	219562724
240802338	chr2	219562515	219562689	219562542	219562667	STK36	NM_001243313	1	27	25	+	219562577	219562724
240854577	chr2	219563526	219563688	219563546	219563668	STK36	NM_015690	2	27	26	+	219563325	219564071
240854577	chr2	219563526	219563688	219563546	219563668	STK36	NM_001243313	1	27	26	+	219563325	219564071

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263778772	chr2	219563948	219564111	219563970	219564090	STK36	NM_015690	2	27	26	+	219563325	219564071
263778772	chr2	219563948	219564111	219563970	219564090	STK36	NM_001243313	1	27	26	+	219563325	219564071
237313575	chr2	223066058	223066183	223066083	223066162	PAX3	NM_001127366	2	9	9	-	223064606	223066161
237313575	chr2	223066058	223066183	223066083	223066162	PAX3	NM_181461	8	8	8	-	223064606	223066161
237313575	chr2	223066058	223066183	223066083	223066162	PAX3	NM_181458	5	9	9	-	223064606	223066161
237313575	chr2	223066058	223066183	223066083	223066162	PAX3	NM_181459	6	10	9	-	223066131	223066161
237313575	chr2	223066058	223066183	223066083	223066162	PAX3	NM_181460	7	9	8	-	223066131	223066161
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_001127366	2	9	7	-	223084859	223085073
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_181461	8	8	7	-	223084859	223085073
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_181459	6	10	7	-	223084859	223085073
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_181460	7	9	7	-	223084859	223085073
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_181458	5	9	7	-	223084859	223085073
236039709	chr2	223084835	223085007	223084858	223084987	PAX3	NM_181457	4	8	7	-	223084859	223085073
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_001127366	2	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181461	8	8	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181459	6	10	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181460	7	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181458	5	9	6	-	223085941	223086106
234927801	chr2	223086062	223086204	223086081	223086175	PAX3	NM_181457	4	8	6	-	223085941	223086106
237582644	chr2	223158726	223158900	223158749	223158881	PAX3	NM_000438	1	4	4	-	223158349	223159020
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_000438	1	4	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_181461	8	8	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_181459	6	10	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_013942	3	5	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_181460	7	9	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_181458	5	9	2	-	223161697	223161932
235285458	chr2	223161593	223161766	223161614	223161744	PAX3	NM_181457	4	8	2	-	223161697	223161932
304767668	chr2	234668908	234669066	234668928	234669047	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
304766493	chr2	234669351	234669512	234669373	234669491	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
300035759	chr2	234675555	234675723	234675576	234675695	UGT1A1	NM_000463	1	5	2	+	234675680	234675811
304614255	chr2	234676830	234676993	234676852	234676972	UGT1A1	NM_000463	1	5	4	+	234676866	234677085
305745974	chr2	234681100	234681257	234681121	234681228	UGT1A1	NM_000463	1	5	5	+	234680908	234681945
295313710	chr3	3192690	3192819	3192712	3192791	CRBN	NM_016302	2	11	11	-	3191317	3192729
295313710	chr3	3192690	3192819	3192712	3192791	CRBN	NM_001173482	1	11	11	-	3191317	3192729
293865602	chr3	3195144	3195296	3195171	3195268	CRBN	NM_016302	2	11	9	-	3195108	3195172
293865602	chr3	3195144	3195296	3195171	3195268	CRBN	NM_001173482	1	11	9	-	3195108	3195172
293809138	chr3	3197804	3197974	3197831	3197946	CRBN	NM_016302	2	11	6	-	3197903	3197965
293809138	chr3	3197804	3197974	3197831	3197946	CRBN	NM_001173482	1	11	6	-	3197903	3197965
295206131	chr3	3209406	3209533	3209433	3209500	CRBN	NM_016302	2	11	5	-	3209318	3209477
295206131	chr3	3209406	3209533	3209433	3209500	CRBN	NM_001173482	1	11	5	-	3209318	3209477

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294811908	chr3	3215674	3215825	3215696	3215800	CRBN	NM_016302	2	11	3	-	3215743	3215945
294811908	chr3	3215674	3215825	3215696	3215800	CRBN	NM_001173482	1	11	3	-	3215743	3215945
293979537	chr3	3216894	3217053	3216922	3217025	CRBN	NM_001173482	1	11	2	-	3216847	3216950
293979537	chr3	3216894	3217053	3216922	3217025	CRBN	NM_016302	2	11	2	-	3216847	3216953
230649010	chr3	10074563	10074724	10074591	10074697	FANCD2	NM_033084	2	43	3	+	10074516	10074656
230649010	chr3	10074563	10074724	10074591	10074697	FANCD2	NM_001018115	1	44	3	+	10074516	10074656
228609358	chr3	10076804	10076959	10076831	10076932	FANCD2	NM_033084	2	43	6	+	10076857	10076917
228609358	chr3	10076804	10076959	10076831	10076932	FANCD2	NM_001018115	1	44	6	+	10076857	10076917
229459160	chr3	10081324	10081455	10081346	10081432	FANCD2	NM_033084	2	43	9	+	10081405	10081529
229459160	chr3	10081324	10081455	10081346	10081432	FANCD2	NM_001018115	1	44	9	+	10081405	10081529
230474380	chr3	10084238	10084376	10084260	10084347	FANCD2	NM_033084	2	43	11	+	10084243	10084347
230474380	chr3	10084238	10084376	10084260	10084347	FANCD2	NM_001018115	1	44	11	+	10084243	10084347
228280083	chr3	10088183	10088355	10088207	10088327	FANCD2	NM_033084	2	43	15	+	10088264	10088407
228280083	chr3	10088183	10088355	10088207	10088327	FANCD2	NM_001018115	1	44	15	+	10088264	10088407
229778349	chr3	10090932	10091106	10090954	10091083	FANCD2	NM_033084	2	43	17	+	10091058	10091189
229778349	chr3	10090932	10091106	10090954	10091083	FANCD2	NM_001018115	1	44	17	+	10091058	10091189
232429859	chr3	10105556	10105684	10105581	10105656	FANCD2	NM_033084	2	43	21	+	10105476	10105595
232429859	chr3	10105556	10105684	10105581	10105656	FANCD2	NM_001018115	1	44	21	+	10105476	10105595
228538049	chr3	10107103	10107274	10107129	10107250	FANCD2	NM_033084	2	43	24	+	10107078	10107178
228538049	chr3	10107103	10107274	10107129	10107250	FANCD2	NM_001018115	1	44	24	+	10107078	10107178
230820839	chr3	10108901	10109061	10108921	10109037	FANCD2	NM_033084	2	43	26	+	10108893	10109001
230820839	chr3	10108901	10109061	10108921	10109037	FANCD2	NM_001018115	1	44	26	+	10108893	10109001
228528732	chr3	10116190	10116325	10116213	10116298	FANCD2	NM_033084	2	43	29	+	10116214	10116357
228528732	chr3	10116190	10116325	10116213	10116298	FANCD2	NM_001018115	1	44	29	+	10116214	10116357
230817110	chr3	10122790	10122939	10122814	10122915	FANCD2	NM_033084	2	43	31	+	10122784	10122912
230817110	chr3	10122790	10122939	10122814	10122915	FANCD2	NM_001018115	1	44	31	+	10122784	10122912
231173790	chr3	10128786	10128928	10128814	10128901	FANCD2	NM_033084	2	43	34	+	10128818	10128948
231173790	chr3	10128786	10128928	10128814	10128901	FANCD2	NM_001018115	1	44	34	+	10128818	10128948
232779422	chr3	10130508	10130665	10130530	10130640	FANCD2	NM_033084	2	43	36	+	10130512	10130634
232779422	chr3	10130508	10130665	10130530	10130640	FANCD2	NM_001018115	1	44	36	+	10130512	10130634
229617041	chr3	10135918	10136078	10135939	10136050	FANCD2	NM_033084	2	43	40	+	10135973	10136047
229617041	chr3	10135918	10136078	10135939	10136050	FANCD2	NM_001018115	1	44	40	+	10135973	10136047
227771785	chr3	10138022	10138180	10138043	10138157	FANCD2	NM_033084	2	43	42	+	10138010	10138156
227771785	chr3	10138022	10138180	10138043	10138157	FANCD2	NM_001018115	1	44	42	+	10138010	10138156
231769447	chr3	10142823	10142997	10142848	10142977	FANCD2	NM_001018115	1	44	44	+	10142872	10143614
264393987	chr3	10183787	10183928	10183808	10183909	VHL	NM_000551	1	3	1	+	10183319	10183871
264393987	chr3	10183787	10183928	10183808	10183909	VHL	NM_198156	2	2	1	+	10183319	10183871
263315434	chr3	10191520	10191690	10191543	10191662	VHL	NM_000551	1	3	3	+	10191471	10195354
263315434	chr3	10191520	10191690	10191543	10191662	VHL	NM_198156	2	2	2	+	10191471	10195354
240291536	chr3	12421315	12421480	12421341	12421452	PPARG	NM_138711	3	8	3	+	12421203	12421430
240291536	chr3	12421315	12421480	12421341	12421452	PPARG	NM_015869	2	7	2	+	12421203	12421430

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240291536	chr3	12421315	12421480	12421341	12421452	PPARG	NM_138712	4	8	3	+	12421203	12421430
240291536	chr3	12421315	12421480	12421341	12421452	PPARG	NM_005037	1	7	2	+	12421203	12421430
236904400	chr3	12434160	12434312	12434187	12434291	PPARG	NM_138711	3	8	5	+	12434113	12434251
236904400	chr3	12434160	12434312	12434187	12434291	PPARG	NM_015869	2	7	4	+	12434113	12434251
236904400	chr3	12434160	12434312	12434187	12434291	PPARG	NM_138712	4	8	5	+	12434113	12434251
236904400	chr3	12434160	12434312	12434187	12434291	PPARG	NM_005037	1	7	4	+	12434113	12434251
234958934	chr3	12458297	12458466	12458317	12458445	PPARG	NM_138711	3	8	7	+	12458203	12458653
234958934	chr3	12458297	12458466	12458317	12458445	PPARG	NM_015869	2	7	6	+	12458203	12458653
234958934	chr3	12458297	12458466	12458317	12458445	PPARG	NM_138712	4	8	7	+	12458203	12458653
234958934	chr3	12458297	12458466	12458317	12458445	PPARG	NM_005037	1	7	6	+	12458203	12458653
236611759	chr3	12475406	12475557	12475428	12475534	PPARG	NM_138711	3	8	8	+	12475397	12475855
236611759	chr3	12475406	12475557	12475428	12475534	PPARG	NM_015869	2	7	7	+	12475397	12475855
236611759	chr3	12475406	12475557	12475428	12475534	PPARG	NM_138712	4	8	8	+	12475397	12475855
236611759	chr3	12475406	12475557	12475428	12475534	PPARG	NM_005037	1	7	7	+	12475397	12475855
236218670	chr3	12626239	12626406	12626259	12626385	RAF1	NM_002880	1	17	16	-	12626346	12626480
237667756	chr3	12627090	12627228	12627116	12627206	RAF1	NM_002880	1	17	14	-	12627180	12627298
235053623	chr3	12632364	12632531	12632386	12632510	RAF1	NM_002880	1	17	12	-	12632297	12632473
237422949	chr3	12641622	12641793	12641644	12641766	RAF1	NM_002880	1	17	9	-	12641651	12641778
234934204	chr3	12645665	12645818	12645686	12645789	RAF1	NM_002880	1	17	7	-	12645635	12645788
235630572	chr3	12650278	12650452	12650303	12650424	RAF1	NM_002880	1	17	5	-	12650265	12650422
236777546	chr3	12659930	12660062	12659957	12660037	RAF1	NM_002880	1	17	2	-	12660014	12660246
241216202	chr3	14187508	14187680	14187528	14187662	XPC	NR_027299	3	15	15	-	14186648	14187659
241216202	chr3	14187508	14187680	14187528	14187662	XPC	NM_001145769	1	16	16	-	14186648	14187659
241216202	chr3	14187508	14187680	14187528	14187662	XPC	NM_004628	2	16	16	-	14186648	14187659
240326122	chr3	14190109	14190261	14190130	14190240	XPC	NR_027299	3	15	12	-	14190062	14190231
240326122	chr3	14190109	14190261	14190130	14190240	XPC	NM_001145769	1	16	13	-	14190062	14190231
240326122	chr3	14190109	14190261	14190130	14190240	XPC	NM_004628	2	16	13	-	14190062	14190231
241450232	chr3	14193819	14193944	14193841	14193922	XPC	NR_027299	3	15	10	-	14193835	14193916
241450232	chr3	14193819	14193944	14193841	14193922	XPC	NM_001145769	1	16	11	-	14193835	14193916
241450232	chr3	14193819	14193944	14193841	14193922	XPC	NM_004628	2	16	11	-	14193835	14193916
266257695	chr3	14199615	14199781	14199635	14199758	XPC	NR_027299	3	15	8	-	14199511	14200392
266257695	chr3	14199615	14199781	14199635	14199758	XPC	NM_001145769	1	16	9	-	14199511	14200392
266257695	chr3	14199615	14199781	14199635	14199758	XPC	NM_004628	2	16	9	-	14199511	14200392
262310836	chr3	14200034	14200193	14200058	14200173	XPC	NR_027299	3	15	8	-	14199511	14200392
262310836	chr3	14200034	14200193	14200058	14200173	XPC	NM_001145769	1	16	9	-	14199511	14200392
262310836	chr3	14200034	14200193	14200058	14200173	XPC	NM_004628	2	16	9	-	14199511	14200392
264720484	chr3	14201123	14201297	14201147	14201277	XPC	NR_027299	3	15	7	-	14201241	14201330
264720484	chr3	14201123	14201297	14201147	14201277	XPC	NM_001145769	1	16	8	-	14201241	14201330
264720484	chr3	14201123	14201297	14201147	14201277	XPC	NM_004628	2	16	8	-	14201241	14201330
239958349	chr3	14206982	14207152	14207002	14207130	XPC	NR_027299	3	15	5	-	14206928	14207085
239958349	chr3	14206982	14207152	14207002	14207130	XPC	NM_001145769	1	16	6	-	14206928	14207085

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239958349	chr3	14206982	14207152	14207002	14207130	XPC	NM_004628	2	16	6	-	14206928	14207085
240935006	chr3	14211814	14211973	14211842	14211945	XPC	NM_001145769	1	16	3	-	14211945	14212050
240935006	chr3	14211814	14211973	14211842	14211945	XPC	NR_027299	3	15	3	-	14211938	14212050
240935006	chr3	14211814	14211973	14211842	14211945	XPC	NM_004628	2	16	3	-	14211938	14212050
239502432	chr3	14219878	14220026	14219895	14220006	XPC	NR_027299	3	15	1	-	14219966	14220172
239502432	chr3	14219878	14220026	14219895	14220006	XPC	NM_001145769	1	16	1	-	14219966	14220172
239502432	chr3	14219878	14220026	14219895	14220006	XPC	NM_004628	2	16	1	-	14219966	14220172
328198328	chr3	30664741	30664913	30664760	30664885	TGFBR2	NM_001024847	1	8	2	+	30664691	30664765
271953393	chr3	30691728	30691854	30691748	30691830	TGFBR2	NM_001024847	1	8	4	+	30691762	30691952
271953393	chr3	30691728	30691854	30691748	30691830	TGFBR2	NM_003242	2	7	3	+	30691762	30691952
272357451	chr3	30713318	30713492	30713339	30713467	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272357451	chr3	30713318	30713492	30713339	30713467	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
272311041	chr3	30713807	30713955	30713827	30713929	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272311041	chr3	30713807	30713955	30713827	30713929	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
270841379	chr3	30729922	30730047	30729943	30730020	TGFBR2	NM_001024847	1	8	7	+	30729876	30730003
270841379	chr3	30729922	30730047	30729943	30730020	TGFBR2	NM_003242	2	7	6	+	30729876	30730003
233153276	chr3	37037999	37038157	37038027	37038128	MLH1	NM_001167618	3	19	2	+	37038115	37038200
233153276	chr3	37037999	37038157	37038027	37038128	MLH1	NM_001167619	4	18	2	+	37038110	37038200
233153276	chr3	37037999	37038157	37038027	37038128	MLH1	NM_001167617	2	19	2	+	37038110	37038200
233153276	chr3	37037999	37038157	37038027	37038128	MLH1	NM_000249	1	19	2	+	37038110	37038200
233503974	chr3	37045789	37045951	37045812	37045924	MLH1	NM_001167619	4	18	4	+	37045892	37045965
233503974	chr3	37045789	37045951	37045812	37045924	MLH1	NM_001167618	3	19	4	+	37045892	37045965
233503974	chr3	37045789	37045951	37045812	37045924	MLH1	NM_001167617	2	19	4	+	37045892	37045965
233503974	chr3	37045789	37045951	37045812	37045924	MLH1	NM_000249	1	19	4	+	37045892	37045965
233353634	chr3	37050296	37050420	37050317	37050397	MLH1	NM_001167618	3	19	6	+	37050305	37050396
233353634	chr3	37050296	37050420	37050317	37050397	MLH1	NM_001167617	2	19	6	+	37050305	37050396
233353634	chr3	37050296	37050420	37050317	37050397	MLH1	NM_000249	1	19	6	+	37050305	37050396
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167619	4	18	8	+	37055923	37056035
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167618	3	19	9	+	37055923	37056035
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_001167617	2	19	9	+	37055923	37056035
232266922	chr3	37055816	37055977	37055844	37055949	MLH1	NM_000249	1	19	9	+	37055923	37056035
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167619	4	18	10	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167618	3	19	11	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_001167617	2	19	11	+	37061801	37061954
233202774	chr3	37061826	37061990	37061849	37061969	MLH1	NM_000249	1	19	11	+	37061801	37061954
233225221	chr3	37067314	37067444	37067335	37067423	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233225221	chr3	37067314	37067444	37067335	37067423	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233225221	chr3	37067314	37067444	37067335	37067423	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233225221	chr3	37067314	37067444	37067335	37067423	MLH1	NM_000249	1	19	12	+	37067128	37067498
232033913	chr3	37081561	37081711	37081585	37081689	MLH1	NM_001167619	4	18	13	+	37081677	37081785
232033913	chr3	37081561	37081711	37081585	37081689	MLH1	NM_001167618	3	19	14	+	37081677	37081785

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232033913	chr3	37081561	37081711	37081585	37081689	MLH1	NM_001167617	2	19	14	+	37081677	37081785
232033913	chr3	37081561	37081711	37081585	37081689	MLH1	NM_000249	1	19	14	+	37081677	37081785
232921900	chr3	37088944	37089118	37088968	37089091	MLH1	NM_001167619	4	18	15	+	37089010	37089174
232921900	chr3	37088944	37089118	37088968	37089091	MLH1	NM_001167618	3	19	16	+	37089010	37089174
232921900	chr3	37088944	37089118	37088968	37089091	MLH1	NM_001167617	2	19	16	+	37089010	37089174
232921900	chr3	37088944	37089118	37088968	37089091	MLH1	NM_000249	1	19	16	+	37089010	37089174
234743582	chr3	37090391	37090530	37090413	37090509	MLH1	NM_001167619	4	18	17	+	37090395	37090508
234743582	chr3	37090391	37090530	37090413	37090509	MLH1	NM_001167618	3	19	18	+	37090395	37090508
234743582	chr3	37090391	37090530	37090413	37090509	MLH1	NM_001167617	2	19	18	+	37090395	37090508
234743582	chr3	37090391	37090530	37090413	37090509	MLH1	NM_000249	1	19	18	+	37090395	37090508
234105891	chr3	37512414	37512558	37512435	37512537	ITGA9	NM_002207	1	28	2	+	37512498	37512625
231247801	chr3	37522869	37523022	37522891	37522998	ITGA9	NM_002207	1	28	4	+	37522975	37523098
233681968	chr3	37544686	37544829	37544709	37544804	ITGA9	NM_002207	1	28	6	+	37544669	37544798
234425985	chr3	37555217	37555391	37555241	37555364	ITGA9	NM_002207	1	28	9	+	37555254	37555391
231637702	chr3	37560714	37560875	37560739	37560847	ITGA9	NM_002207	1	28	11	+	37560751	37560845
232802474	chr3	37574846	37575016	37574867	37574996	ITGA9	NM_002207	1	28	14	+	37574805	37574959
232442521	chr3	37670781	37670906	37670802	37670879	ITGA9	NM_002207	1	28	16	+	37670678	37670827
231442945	chr3	37774176	37774310	37774198	37774290	ITGA9	NM_002207	1	28	19	+	37774203	37774289
232908591	chr3	37791884	37792026	37791907	37792001	ITGA9	NM_002207	1	28	23	+	37791953	37792060
232956961	chr3	37821270	37821426	37821293	37821399	ITGA9	NM_002207	1	28	25	+	37821393	37821512
234733194	chr3	37845288	37845455	37845309	37845434	ITGA9	NM_002207	1	28	27	+	37845314	37845433
274100283	chr3	38180258	38180397	38180278	38180377	MYD88	NM_002468	5	5	1	+	38179969	38180519
274100283	chr3	38180258	38180397	38180278	38180377	MYD88	NM_001172569	4	4	1	+	38179969	38180519
274100283	chr3	38180258	38180397	38180278	38180377	MYD88	NM_001172568	3	4	1	+	38179969	38180519
274100283	chr3	38180258	38180397	38180278	38180377	MYD88	NM_001172567	2	5	1	+	38179969	38180519
274100283	chr3	38180258	38180397	38180278	38180377	MYD88	NM_001172566	1	3	1	+	38179969	38180519
273169715	chr3	38181350	38181514	38181374	38181491	MYD88	NM_002468	5	5	2	+	38181355	38181489
273169715	chr3	38181350	38181514	38181374	38181491	MYD88	NM_001172569	4	4	2	+	38181355	38181489
273169715	chr3	38181350	38181514	38181374	38181491	MYD88	NM_001172567	2	5	2	+	38181355	38181489
273955008	chr3	38182194	38182360	38182219	38182339	MYD88	NM_002468	5	5	4	+	38182248	38182339
273955008	chr3	38182194	38182360	38182219	38182339	MYD88	NM_001172569	4	4	3	+	38182248	38182339
273955008	chr3	38182194	38182360	38182219	38182339	MYD88	NM_001172568	3	4	3	+	38182248	38182339
273955008	chr3	38182194	38182360	38182219	38182339	MYD88	NM_001172567	2	5	4	+	38182248	38182339
273955008	chr3	38182194	38182360	38182219	38182339	MYD88	NM_001172566	1	3	2	+	38182248	38182339
326726865	chr3	41265929	41266093	41265956	41266072	CTNNB1	NM_001904	3	15	3	+	41266017	41266244
326726865	chr3	41265929	41266093	41265956	41266072	CTNNB1	NM_001098209	1	16	3	+	41266017	41266244
326726865	chr3	41265929	41266093	41265956	41266072	CTNNB1	NM_001098210	2	16	3	+	41266017	41266244
226801798	chr3	41266478	41266620	41266499	41266594	CTNNB1	NM_001904	3	15	4	+	41266445	41266698
226801798	chr3	41266478	41266620	41266499	41266594	CTNNB1	NM_001098209	1	16	4	+	41266445	41266698
226801798	chr3	41266478	41266620	41266499	41266594	CTNNB1	NM_001098210	2	16	4	+	41266445	41266698
225704086	chr3	41267003	41267171	41267023	41267148	CTNNB1	NM_001904	3	15	5	+	41266825	41267063

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225704086	chr3	41267003	41267171	41267023	41267148	CTNNB1	NM_001098209	1	16	5	+	41266825	41267063
225704086	chr3	41267003	41267171	41267023	41267148	CTNNB1	NM_001098210	2	16	5	+	41266825	41267063
226481749	chr3	41268635	41268807	41268659	41268785	CTNNB1	NM_001904	3	15	7	+	41268699	41268843
226481749	chr3	41268635	41268807	41268659	41268785	CTNNB1	NM_001098209	1	16	7	+	41268699	41268843
226481749	chr3	41268635	41268807	41268659	41268785	CTNNB1	NM_001098210	2	16	7	+	41268699	41268843
226034552	chr3	41275047	41275220	41275071	41275198	CTNNB1	NM_001904	3	15	9	+	41275020	41275358
226034552	chr3	41275047	41275220	41275071	41275198	CTNNB1	NM_001098209	1	16	9	+	41275020	41275358
226034552	chr3	41275047	41275220	41275071	41275198	CTNNB1	NM_001098210	2	16	9	+	41275020	41275358
226563461	chr3	41275696	41275833	41275718	41275805	CTNNB1	NM_001904	3	15	10	+	41275630	41275788
226563461	chr3	41275696	41275833	41275718	41275805	CTNNB1	NM_001098209	1	16	10	+	41275630	41275788
226563461	chr3	41275696	41275833	41275718	41275805	CTNNB1	NM_001098210	2	16	10	+	41275630	41275788
253668904	chr3	41277970	41278122	41277993	41278099	CTNNB1	NM_001904	3	15	13	+	41278079	41278200
253668904	chr3	41277970	41278122	41277993	41278099	CTNNB1	NM_001098209	1	16	13	+	41278079	41278200
253668904	chr3	41277970	41278122	41277993	41278099	CTNNB1	NM_001098210	2	16	13	+	41278079	41278200
226047692	chr3	41280713	41280840	41280733	41280812	CTNNB1	NM_001098209	1	16	15	+	41280625	41280845
226047692	chr3	41280713	41280840	41280733	41280812	CTNNB1	NM_001098210	2	16	15	+	41280625	41280845
226047692	chr3	41280713	41280840	41280733	41280812	CTNNB1	NM_001904	3	15	15	+	41280625	41281939
279543782	chr3	46479520	46479649	46479541	46479627	LTF	NM_002343	2	17	16	-	46479431	46479620
279543782	chr3	46479520	46479649	46479541	46479627	LTF	NM_001199149	1	17	16	-	46479431	46479620
280590363	chr3	46484840	46484990	46484862	46484969	LTF	NM_002343	2	17	13	-	46484932	46485073
280590363	chr3	46484840	46484990	46484862	46484969	LTF	NM_001199149	1	17	13	-	46484932	46485073
279836018	chr3	46487853	46488013	46487877	46487985	LTF	NM_002343	2	17	11	-	46487931	46487984
279836018	chr3	46487853	46488013	46487877	46487985	LTF	NM_001199149	1	17	11	-	46487931	46487984
279150282	chr3	46491217	46491376	46491238	46491353	LTF	NM_002343	2	17	8	-	46491344	46491518
279150282	chr3	46491217	46491376	46491238	46491353	LTF	NM_001199149	1	17	8	-	46491344	46491518
281140222	chr3	46492080	46492234	46492103	46492211	LTF	NM_002343	2	17	7	-	46491985	46492163
281140222	chr3	46492080	46492234	46492103	46492211	LTF	NM_001199149	1	17	7	-	46491985	46492163
278491863	chr3	46497263	46497414	46497285	46497394	LTF	NM_002343	2	17	4	-	46497286	46497468
278491863	chr3	46497263	46497414	46497285	46497394	LTF	NM_001199149	1	17	4	-	46497286	46497468
280554192	chr3	46501082	46501245	46501108	46501221	LTF	NM_002343	2	17	2	-	46501146	46501309
280554192	chr3	46501082	46501245	46501108	46501221	LTF	NM_001199149	1	17	2	-	46501146	46501309
241374655	chr3	47059099	47059256	47059119	47059233	SETD2	NM_014159	1	21	20	-	47059128	47059229
241310393	chr3	47084081	47084229	47084103	47084201	SETD2	NM_014159	1	21	17	-	47084051	47084190
261192714	chr3	47098396	47098552	47098417	47098532	SETD2	NM_014159	1	21	15	-	47098311	47098980
261184968	chr3	47098865	47099037	47098885	47099009	SETD2	NM_014159	1	21	15	-	47098311	47098980
263434637	chr3	47108522	47108657	47108549	47108632	SETD2	NM_014159	1	21	13	-	47108560	47108608
264322175	chr3	47125509	47125651	47125536	47125623	SETD2	NM_014159	1	21	12	-	47125210	47125872
264240877	chr3	47129542	47129669	47129568	47129641	SETD2	NM_014159	1	21	10	-	47129603	47129737
264430446	chr3	47142893	47143033	47142916	47143010	SETD2	NM_014159	1	21	8	-	47142948	47143045
242027077	chr3	47147414	47147543	47147442	47147516	SETD2	NM_014159	1	21	6	-	47147487	47147610
239825252	chr3	47158076	47158231	47158098	47158204	SETD2	NM_014159	1	21	4	-	47158113	47158244

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262501849	chr3	47161886	47162027	47161912	47162005	SETD2	NM_014159	1	21	3	-	47161672	47166038
239132213	chr3	47162312	47162486	47162338	47162461	SETD2	NM_014159	1	21	3	-	47161672	47166038
239065059	chr3	47162749	47162896	47162778	47162872	SETD2	NM_014159	1	21	3	-	47161672	47166038
239142882	chr3	47163160	47163311	47163187	47163288	SETD2	NM_014159	1	21	3	-	47161672	47166038
239193281	chr3	47163550	47163709	47163574	47163682	SETD2	NM_014159	1	21	3	-	47161672	47166038
262516884	chr3	47163928	47164093	47163956	47164073	SETD2	NM_014159	1	21	3	-	47161672	47166038
262464947	chr3	47164333	47164507	47164361	47164481	SETD2	NM_014159	1	21	3	-	47161672	47166038
238792819	chr3	47164749	47164873	47164774	47164845	SETD2	NM_014159	1	21	3	-	47161672	47166038
238833111	chr3	47165133	47165267	47165160	47165239	SETD2	NM_014159	1	21	3	-	47161672	47166038
239087853	chr3	47165398	47165522	47165426	47165500	SETD2	NM_014159	1	21	3	-	47161672	47166038
262560298	chr3	47165824	47165998	47165850	47165975	SETD2	NM_014159	1	21	3	-	47161672	47166038
223438220	chr3	52436189	52436340	52436210	52436322	BAP1	NM_004656	1	17	17	-	52435025	52436437
223702035	chr3	52437105	52437252	52437127	52437232	BAP1	NM_004656	1	17	14	-	52437154	52437314
222332343	chr3	52437647	52437821	52437667	52437798	BAP1	NM_004656	1	17	13	-	52437432	52437910
223804202	chr3	52439081	52439253	52439109	52439230	BAP1	NM_004656	1	17	11	-	52439126	52439310
223265514	chr3	52440168	52440338	52440195	52440317	BAP1	NM_004656	1	17	9	-	52440269	52440392
222216268	chr3	52441234	52441362	52441255	52441341	BAP1	NM_004656	1	17	7	-	52441190	52441332
223155579	chr3	52442380	52442546	52442403	52442518	BAP1	NM_004656	1	17	4	-	52442490	52442622
222164848	chr3	52443731	52443905	52443752	52443884	BAP1	NM_004656	1	17	2	-	52443730	52443759
222164848	chr3	52443731	52443905	52443752	52443884	BAP1	NM_004656	1	17	1	-	52443858	52444009
237395866	chr3	52582185	52582325	52582208	52582297	PBRM1	NM_018165	1	28	28	-	52579368	52582251
237395866	chr3	52582185	52582325	52582208	52582297	PBRM1	NM_018313	2	30	30	-	52579368	52582251
237395866	chr3	52582185	52582325	52582208	52582297	PBRM1	NM_181042	3	28	28	-	52579368	52582251
235077810	chr3	52588672	52588846	52588696	52588825	PBRM1	NM_018165	1	28	25	-	52588740	52588895
235077810	chr3	52588672	52588846	52588696	52588825	PBRM1	NM_018313	2	30	27	-	52588740	52588895
235674202	chr3	52597222	52597395	52597249	52597367	PBRM1	NM_018165	1	28	23	-	52597299	52597509
235674202	chr3	52597222	52597395	52597249	52597367	PBRM1	NM_181042	3	28	24	-	52597299	52597509
236639693	chr3	52598135	52598260	52598157	52598236	PBRM1	NM_018165	1	28	22	-	52598066	52598249
236639693	chr3	52598135	52598260	52598157	52598236	PBRM1	NM_018313	2	30	24	-	52598066	52598249
236639693	chr3	52598135	52598260	52598157	52598236	PBRM1	NM_181042	3	28	23	-	52598066	52598249
235569124	chr3	52612985	52613149	52613007	52613124	PBRM1	NM_018165	1	28	20	-	52613070	52613215
235569124	chr3	52612985	52613149	52613007	52613124	PBRM1	NM_018313	2	30	22	-	52613070	52613215
235569124	chr3	52612985	52613149	52613007	52613124	PBRM1	NM_181042	3	28	21	-	52613070	52613215
237564353	chr3	52620477	52620611	52620505	52620588	PBRM1	NM_018165	1	28	19	-	52620441	52620704
237564353	chr3	52620477	52620611	52620505	52620588	PBRM1	NM_018313	2	30	21	-	52620441	52620704
237564353	chr3	52620477	52620611	52620505	52620588	PBRM1	NM_181042	3	28	20	-	52620441	52620704
237753037	chr3	52621387	52621521	52621416	52621494	PBRM1	NM_018165	1	28	18	-	52621369	52621526
237753037	chr3	52621387	52621521	52621416	52621494	PBRM1	NM_181042	3	28	19	-	52621369	52621526
237753037	chr3	52621387	52621521	52621416	52621494	PBRM1	NM_018313	2	30	20	-	52621369	52621451
235516511	chr3	52637621	52637787	52637647	52637759	PBRM1	NM_018165	1	28	16	-	52637537	52637748
235516511	chr3	52637621	52637787	52637647	52637759	PBRM1	NM_018313	2	30	18	-	52637537	52637748

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235516511	chr3	52637621	52637787	52637647	52637759	PBRM1	NM_181042	3	28	17	-	52637537	52637748
239446871	chr3	52643493	52643652	52643516	52643627	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239446871	chr3	52643493	52643652	52643516	52643627	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239446871	chr3	52643493	52643652	52643516	52643627	PBRM1	NM_181042	3	28	16	-	52643329	52643971
239427313	chr3	52643918	52644069	52643947	52644043	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239427313	chr3	52643918	52644069	52643947	52644043	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239427313	chr3	52643918	52644069	52643947	52644043	PBRM1	NM_181042	3	28	16	-	52643329	52643971
235045412	chr3	52651455	52651579	52651483	52651557	PBRM1	NM_018165	1	28	13	-	52651278	52651554
235045412	chr3	52651455	52651579	52651483	52651557	PBRM1	NM_018313	2	30	15	-	52651278	52651554
235045412	chr3	52651455	52651579	52651483	52651557	PBRM1	NM_181042	3	28	14	-	52651278	52651554
237512401	chr3	52668563	52668702	52668589	52668674	PBRM1	NM_018165	1	28	10	-	52668618	52668831
237512401	chr3	52668563	52668702	52668589	52668674	PBRM1	NM_018313	2	30	12	-	52668618	52668831
237512401	chr3	52668563	52668702	52668589	52668674	PBRM1	NM_181042	3	28	11	-	52668618	52668831
236159641	chr3	52677178	52677312	52677201	52677290	PBRM1	NM_018313	2	30	10	-	52677264	52677359
236159641	chr3	52677178	52677312	52677201	52677290	PBRM1	NM_181042	3	28	9	-	52677264	52677359
235863494	chr3	52685691	52685865	52685718	52685837	PBRM1	NM_018165	1	28	6	-	52685758	52685826
235863494	chr3	52685691	52685865	52685718	52685837	PBRM1	NM_018313	2	30	7	-	52685758	52685826
235863494	chr3	52685691	52685865	52685718	52685837	PBRM1	NM_181042	3	28	6	-	52685758	52685826
238149566	chr3	52696200	52696372	52696226	52696345	PBRM1	NM_018165	1	28	4	-	52696149	52696292
238149566	chr3	52696200	52696372	52696226	52696345	PBRM1	NM_018313	2	30	5	-	52696149	52696292
238149566	chr3	52696200	52696372	52696226	52696345	PBRM1	NM_181042	3	28	4	-	52696149	52696292
236069946	chr3	52713557	52713724	52713579	52713699	PBRM1	NM_018165	1	28	1	-	52713590	52713739
236069946	chr3	52713557	52713724	52713579	52713699	PBRM1	NM_018313	2	30	2	-	52713590	52713739
236069946	chr3	52713557	52713724	52713579	52713699	PBRM1	NM_181042	3	28	1	-	52713590	52713739
312296361	chr3	65342456	65342630	65342473	65342604	MAGI1	NM_015520	3	25	25	-	65339906	65342807
312296361	chr3	65342456	65342630	65342473	65342604	MAGI1	NM_001033057	1	23	23	-	65339906	65342807
312550768	chr3	65346754	65346924	65346775	65346901	MAGI1	NM_015520	3	25	23	-	65346874	65347012
312550768	chr3	65346754	65346924	65346775	65346901	MAGI1	NM_001033057	1	23	22	-	65346874	65347012
312550768	chr3	65346754	65346924	65346775	65346901	MAGI1	NM_004742	2	23	23	-	65344944	65347012
312165990	chr3	65350275	65350449	65350302	65350421	MAGI1	NM_004742	2	23	21	-	65350340	65350400
312165990	chr3	65350275	65350449	65350302	65350421	MAGI1	NM_015520	3	25	21	-	65350340	65350400
312165990	chr3	65350275	65350449	65350302	65350421	MAGI1	NM_001033057	1	23	20	-	65350340	65350400
312196064	chr3	65361506	65361678	65361531	65361652	MAGI1	NM_015520	3	25	19	-	65361420	65361620
312196064	chr3	65361506	65361678	65361531	65361652	MAGI1	NM_001033057	1	23	18	-	65361420	65361620
312196064	chr3	65361506	65361678	65361531	65361652	MAGI1	NM_004742	2	23	19	-	65361420	65361623
312405832	chr3	65365107	65365258	65365127	65365237	MAGI1	NM_004742	2	23	18	-	65364936	65365229
312405832	chr3	65365107	65365258	65365127	65365237	MAGI1	NM_015520	3	25	18	-	65364936	65365229
312405832	chr3	65365107	65365258	65365127	65365237	MAGI1	NM_001033057	1	23	17	-	65364936	65365229
312477718	chr3	65369214	65369380	65369236	65369357	MAGI1	NM_004742	2	23	16	-	65369207	65369298
312477718	chr3	65369214	65369380	65369236	65369357	MAGI1	NM_015520	3	25	16	-	65369207	65369298
312477718	chr3	65369214	65369380	65369236	65369357	MAGI1	NM_001033057	1	23	15	-	65369207	65369298

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312201018	chr3	65387007	65387173	65387035	65387151	MAGI1	NM_004742	2	23	13	-	65387114	65387145
312201018	chr3	65387007	65387173	65387035	65387151	MAGI1	NM_015520	3	25	13	-	65387114	65387145
312201018	chr3	65387007	65387173	65387035	65387151	MAGI1	NM_001033057	1	23	13	-	65387114	65387145
312397125	chr3	65415454	65415591	65415476	65415568	MAGI1	NM_004742	2	23	12	-	65415195	65415815
312397125	chr3	65415454	65415591	65415476	65415568	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312397125	chr3	65415454	65415591	65415476	65415568	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312375193	chr3	65416426	65416595	65416451	65416573	MAGI1	NM_004742	2	23	11	-	65416374	65416556
312375193	chr3	65416426	65416595	65416451	65416573	MAGI1	NM_015520	3	25	11	-	65416374	65416556
312375193	chr3	65416426	65416595	65416451	65416573	MAGI1	NM_001033057	1	23	11	-	65416374	65416556
312195965	chr3	65425620	65425744	65425641	65425722	MAGI1	NM_004742	2	23	9	-	65425554	65425687
312195965	chr3	65425620	65425744	65425641	65425722	MAGI1	NM_015520	3	25	9	-	65425554	65425687
312195965	chr3	65425620	65425744	65425641	65425722	MAGI1	NM_001033057	1	23	9	-	65425554	65425687
312366887	chr3	65438942	65439096	65438963	65439074	MAGI1	NM_004742	2	23	6	-	65438933	65439015
312366887	chr3	65438942	65439096	65438963	65439074	MAGI1	NM_015520	3	25	6	-	65438933	65439015
312366887	chr3	65438942	65439096	65438963	65439074	MAGI1	NM_001033057	1	23	6	-	65438933	65439015
312216531	chr3	65464333	65464501	65464362	65464477	MAGI1	NM_004742	2	23	4	-	65464267	65464473
312216531	chr3	65464333	65464501	65464362	65464477	MAGI1	NM_015520	3	25	4	-	65464267	65464473
312216531	chr3	65464333	65464501	65464362	65464477	MAGI1	NM_001033057	1	23	4	-	65464267	65464473
312222574	chr3	65607652	65607806	65607672	65607777	MAGI1	NM_004742	2	23	2	-	65607647	65607763
312222574	chr3	65607652	65607806	65607672	65607777	MAGI1	NM_015520	3	25	2	-	65607647	65607763
312222574	chr3	65607652	65607806	65607672	65607777	MAGI1	NM_001033057	1	23	2	-	65607647	65607763
233325728	chr3	69788699	69788871	69788719	69788852	MITF	NM_198159	6	10	1	+	69788586	69788852
231556993	chr3	69928316	69928476	69928338	69928453	MITF	NM_001184967	2	10	2	+	69928285	69928534
231556993	chr3	69928316	69928476	69928338	69928453	MITF	NM_006722	4	10	2	+	69928285	69928534
231556993	chr3	69928316	69928476	69928338	69928453	MITF	NM_198177	7	10	2	+	69928285	69928534
231556993	chr3	69928316	69928476	69928338	69928453	MITF	NM_198159	6	10	2	+	69928285	69928534
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_198178	8	9	2	+	69986973	69987032
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_001184968	3	3	2	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_001184967	2	10	3	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_006722	4	10	3	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_000248	1	9	2	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_198177	7	10	3	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_198159	6	10	3	+	69986973	69987200
232614404	chr3	69986942	69987104	69986967	69987083	MITF	NM_198158	5	9	2	+	69986973	69987200
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_001184967	2	10	4	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_006722	4	10	4	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_000248	1	9	3	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_198177	7	10	4	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_198159	6	10	4	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_198178	8	9	3	+	69988249	69988332
233774929	chr3	69988213	69988355	69988241	69988333	MITF	NM_198158	5	9	3	+	69988249	69988332

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231455123	chr3	70000866	70000996	70000893	70000974	MITF	NM_000248	1	9	6	+	70000963	70001037
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_001184967	2	10	9	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_006722	4	10	9	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_000248	1	9	8	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_198177	7	10	9	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_198159	6	10	9	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_198178	8	9	8	+	70008424	70008571
233279805	chr3	70008469	70008623	70008495	70008597	MITF	NM_198158	5	9	8	+	70008424	70008571
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244816	8	20	20	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244815	7	16	16	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244814	6	17	17	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244813	5	15	15	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_032682	9	21	21	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244812	4	16	16	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244808	2	21	21	-	71003865	71008542
228669968	chr3	71008277	71008448	71008301	71008421	FOXP1	NM_001244810	3	21	21	-	71003865	71008542
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244816	8	20	18	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244815	7	16	14	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244814	6	17	15	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244813	5	15	13	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_032682	9	21	19	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244812	4	16	14	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244808	2	21	19	-	71019887	71019956
227344561	chr3	71019845	71020001	71019866	71019973	FOXP1	NM_001244810	3	21	19	-	71019887	71019956
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244816	8	20	17	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244815	7	16	13	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244814	6	17	14	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244813	5	15	12	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_032682	9	21	18	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244812	4	16	13	-	71021706	71021827
227301777	chr3	71021755	71021900	71021778	71021872	FOXP1	NM_001244808	2	21	18	-	71021706	71021827
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244808	2	21	16	-	71026794	71026870
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244816	8	20	15	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244815	7	16	11	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244814	6	17	12	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244813	5	15	10	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_032682	9	21	16	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244812	4	16	11	-	71026794	71026873
228450133	chr3	71026816	71026962	71026841	71026937	FOXP1	NM_001244810	3	21	16	-	71026794	71026873
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244816	8	20	13	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244815	7	16	9	-	71037145	71037228

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244814	6	17	10	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244813	5	15	8	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_032682	9	21	14	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244812	4	16	9	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244808	2	21	14	-	71037145	71037228
227821568	chr3	71037025	71037196	71037048	71037176	FOXP1	NM_001244810	3	21	14	-	71037145	71037228
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244816	8	20	11	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244815	7	16	7	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244814	6	17	8	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244813	5	15	6	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_032682	9	21	12	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244812	4	16	7	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244808	2	21	12	-	71064700	71064804
229235447	chr3	71064618	71064786	71064645	71064764	FOXP1	NM_001244810	3	21	12	-	71064700	71064804
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244816	8	20	9	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244815	7	16	5	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244814	6	17	6	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244813	5	15	4	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_032682	9	21	10	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244812	4	16	5	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244808	2	21	10	-	71096093	71096246
229339090	chr3	71096048	71096220	71096072	71096197	FOXP1	NM_001244810	3	21	10	-	71096093	71096246
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244816	8	20	7	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244815	7	16	3	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244814	6	17	4	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244813	5	15	2	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_032682	9	21	8	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244808	2	21	8	-	71102787	71102924
227460346	chr3	71102880	71103017	71102904	71102996	FOXP1	NM_001244810	3	21	8	-	71102787	71102924
227458238	chr3	71179687	71179857	71179709	71179836	FOXP1	NM_001244815	7	16	1	-	71179649	71180092
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001244816	8	20	5	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001244814	6	17	2	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_032682	9	21	6	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001244812	4	16	3	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001244808	2	21	6	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001012505	1	7	6	-	71247353	71247543
228707482	chr3	71247443	71247615	71247464	71247590	FOXP1	NM_001244810	3	21	6	-	71247353	71247543
270935418	chr3	89176390	89176529	89176411	89176502	EPHA3	NM_005233	1	17	2	+	89176359	89176423
270935418	chr3	89176390	89176529	89176411	89176502	EPHA3	NM_182644	2	7	2	+	89176359	89176423
271570488	chr3	89259329	89259503	89259351	89259482	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271570488	chr3	89259329	89259503	89259351	89259482	EPHA3	NM_182644	2	7	3	+	89259010	89259670

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272653826	chr3	89390052	89390183	89390077	89390155	EPHA3	NM_005233	1	17	4	+	89390066	89390221
272653826	chr3	89390052	89390183	89390077	89390155	EPHA3	NM_182644	2	7	4	+	89390066	89390221
270733049	chr3	89391038	89391190	89391065	89391168	EPHA3	NM_005233	1	17	5	+	89390905	89391240
270733049	chr3	89391038	89391190	89391065	89391168	EPHA3	NM_182644	2	7	5	+	89390905	89391240
271498646	chr3	89448382	89448543	89448406	89448522	EPHA3	NM_182644	2	7	7	+	89448468	89449495
271498646	chr3	89448382	89448543	89448406	89448522	EPHA3	NM_005233	1	17	7	+	89448468	89448630
271140070	chr3	89456444	89456583	89456465	89456561	EPHA3	NM_005233	1	17	8	+	89456419	89456521
269675474	chr3	89468321	89468455	89468347	89468430	EPHA3	NM_005233	1	17	11	+	89468355	89468540
272701752	chr3	89480168	89480341	89480195	89480319	EPHA3	NM_005233	1	17	13	+	89480300	89480509
271430294	chr3	89498287	89498434	89498314	89498412	EPHA3	NM_005233	1	17	14	+	89498375	89498524
272277838	chr3	89499402	89499553	89499422	89499524	EPHA3	NM_005233	1	17	15	+	89499327	89499520
272453373	chr3	89528581	89528734	89528608	89528708	EPHA3	NM_005233	1	17	17	+	89528547	89531284
227635602	chr3	128200593	128200767	128200611	128200744	GATA2	NM_001145662	2	6	5	-	128200662	128200745
227635602	chr3	128200593	128200767	128200611	128200744	GATA2	NM_032638	3	6	5	-	128200662	128200787
227635602	chr3	128200593	128200767	128200611	128200744	GATA2	NM_001145661	1	7	6	-	128200662	128200787
229069206	chr3	128204532	128204702	128204551	128204681	GATA2	NM_032638	3	6	3	-	128204570	128205211
229069206	chr3	128204532	128204702	128204551	128204681	GATA2	NM_001145661	1	7	4	-	128204570	128205211
229069206	chr3	128204532	128204702	128204551	128204681	GATA2	NM_001145662	2	6	3	-	128204570	128205211
227230833	chr3	128205007	128205160	128205024	128205143	GATA2	NM_032638	3	6	3	-	128204570	128205211
227230833	chr3	128205007	128205160	128205024	128205143	GATA2	NM_001145661	1	7	4	-	128204570	128205211
227230833	chr3	128205007	128205160	128205024	128205143	GATA2	NM_001145662	2	6	3	-	128204570	128205211
271689328	chr3	134514470	134514638	134514487	134514620	EPHB1	NM_004441	1	16	1	+	134514099	134514531
270984674	chr3	134670334	134670483	134670356	134670462	EPHB1	NM_004441	1	16	3	+	134670213	134670894
272498146	chr3	134670791	134670917	134670813	134670895	EPHB1	NM_004441	1	16	3	+	134670213	134670894
270591010	chr3	134851644	134851818	134851666	134851797	EPHB1	NM_004441	1	16	5	+	134851556	134851891
270666198	chr3	134880829	134880995	134880852	134880975	EPHB1	NM_004441	1	16	7	+	134880860	134881022
270048524	chr3	134898606	134898757	134898627	134898735	EPHB1	NM_004441	1	16	10	+	134898702	134898824
272384413	chr3	134911549	134911704	134911568	134911681	EPHB1	NM_004441	1	16	11	+	134911418	134911665
270342683	chr3	134960055	134960196	134960075	134960174	EPHB1	NM_004441	1	16	13	+	134959990	134960139
270129156	chr3	134968243	134968405	134968263	134968383	EPHB1	NM_004441	1	16	15	+	134968178	134968333
294181567	chr3	138374905	138375075	138374930	138375052	PIK3CB	NM_001256045	1	13	12	-	138374984	138375116
294181567	chr3	138374905	138375075	138374930	138375052	PIK3CB	NM_006219	2	22	21	-	138374984	138375116
294709692	chr3	138382649	138382812	138382675	138382787	PIK3CB	NM_001256045	1	13	10	-	138382748	138382871
294709692	chr3	138382649	138382812	138382675	138382787	PIK3CB	NM_006219	2	22	19	-	138382748	138382871
294660223	chr3	138400757	138400881	138400786	138400855	PIK3CB	NM_001256045	1	13	8	-	138400809	138400887
294660223	chr3	138400757	138400881	138400786	138400855	PIK3CB	NM_006219	2	22	17	-	138400809	138400887
293810657	chr3	138403438	138403611	138403458	138403583	PIK3CB	NM_001256045	1	13	6	-	138403467	138403645
293810657	chr3	138403438	138403611	138403458	138403583	PIK3CB	NM_006219	2	22	15	-	138403467	138403645
294625539	chr3	138409806	138409952	138409829	138409924	PIK3CB	NM_001256045	1	13	4	-	138409842	138409985
294625539	chr3	138409806	138409952	138409829	138409924	PIK3CB	NM_006219	2	22	13	-	138409842	138409985
293917641	chr3	138417697	138417827	138417721	138417806	PIK3CB	NM_001256045	1	13	2	-	138417749	138417937

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293917641	chr3	138417697	138417827	138417721	138417806	PIK3CB	NM_006219	2	22	11	-	138417749	138417937
293874503	chr3	138423284	138423445	138423310	138423420	PIK3CB	NM_006219	2	22	10	-	138423285	138423335
293805218	chr3	138431084	138431215	138431112	138431189	PIK3CB	NM_006219	2	22	8	-	138431050	138431146
293780301	chr3	138452159	138452284	138452181	138452258	PIK3CB	NM_006219	2	22	6	-	138452203	138452280
294581633	chr3	138456544	138456676	138456571	138456649	PIK3CB	NM_006219	2	22	4	-	138456549	138456728
294175255	chr3	138461473	138461631	138461495	138461603	PIK3CB	NM_006219	2	22	3	-	138461400	138461623
293759193	chr3	138477955	138478113	138477980	138478091	PIK3CB	NM_006219	2	22	1	-	138478015	138478201
229746471	chr3	138664949	138665123	138664967	138665104	FOXL2	NM_023067	1	1	1	-	138663066	138665982
229756001	chr3	138665374	138665522	138665391	138665505	FOXL2	NM_023067	1	1	1	-	138663066	138665982
284006355	chr3	142171923	142172060	142171948	142172034	ATR	NM_001184	1	47	46	-	142171970	142172075
284765480	chr3	142176542	142176686	142176568	142176658	ATR	NM_001184	1	47	45	-	142176446	142176597
284428752	chr3	142177949	142178122	142177974	142178094	ATR	NM_001184	1	47	43	-	142178069	142178225
282578325	chr3	142180797	142180925	142180823	142180898	ATR	NM_001184	1	47	42	-	142180782	142180932
282268085	chr3	142183961	142184087	142183989	142184059	ATR	NM_001184	1	47	41	-	142183939	142184082
281330379	chr3	142185235	142185360	142185261	142185332	ATR	NM_001184	1	47	40	-	142185166	142185375
283071903	chr3	142188077	142188238	142188097	142188210	ATR	NM_001184	1	47	38	-	142188179	142188411
283165738	chr3	142188840	142189006	142188866	142188979	ATR	NM_001184	1	47	37	-	142188928	142189025
282754712	chr3	142211932	142212078	142211959	142212051	ATR	NM_001184	1	47	35	-	142211974	142212153
281378196	chr3	142215840	142215988	142215867	142215966	ATR	NM_001184	1	47	33	-	142215855	142216034
284237796	chr3	142218425	142218549	142218449	142218521	ATR	NM_001184	1	47	31	-	142218469	142218560
283604607	chr3	142224011	142224150	142224032	142224122	ATR	NM_001184	1	47	29	-	142223981	142224145
282725734	chr3	142231027	142231166	142231055	142231143	ATR	NM_001184	1	47	27	-	142231102	142231312
283590722	chr3	142232365	142232520	142232390	142232493	ATR	NM_001184	1	47	26	-	142232343	142232480
284675777	chr3	142241553	142241677	142241580	142241650	ATR	NM_001184	1	47	23	-	142241570	142241683
281817538	chr3	142242962	142243114	142242985	142243088	ATR	NM_001184	1	47	22	-	142242835	142243041
283727830	chr3	142257231	142257389	142257257	142257362	ATR	NM_001184	1	47	19	-	142257324	142257467
283958763	chr3	142261422	142261552	142261451	142261528	ATR	NM_001184	1	47	17	-	142261507	142261599
282012566	chr3	142268221	142268380	142268249	142268354	ATR	NM_001184	1	47	15	-	142268321	142268515
283007813	chr3	142269004	142269151	142269029	142269124	ATR	NM_001184	1	47	14	-	142268974	142269144
282319604	chr3	142272413	142272559	142272441	142272531	ATR	NM_001184	1	47	12	-	142272482	142272582
284564354	chr3	142274612	142274772	142274641	142274747	ATR	NM_001184	1	47	10	-	142274719	142274981
285702179	chr3	142275136	142275301	142275162	142275275	ATR	NM_001184	1	47	9	-	142275225	142275417
282752384	chr3	142278005	142278167	142278027	142278145	ATR	NM_001184	1	47	7	-	142278093	142278283
281465474	chr3	142279159	142279297	142279187	142279267	ATR	NM_001184	1	47	6	-	142279105	142279296
281384992	chr3	142281069	142281221	142281095	142281196	ATR	NM_001184	1	47	4	-	142281074	142281951
281404698	chr3	142281439	142281564	142281459	142281537	ATR	NM_001184	1	47	4	-	142281074	142281951
283784323	chr3	142281740	142281887	142281764	142281859	ATR	NM_001184	1	47	4	-	142281074	142281951
281776362	chr3	142285017	142285179	142285041	142285152	ATR	NM_001184	1	47	3	-	142284963	142285103
237445932	chr3	178916703	178916851	178916728	178916824	PIK3CA	NM_006218	1	21	2	+	178916538	178916965
236853594	chr3	178917490	178917624	178917513	178917596	PIK3CA	NM_006218	1	21	3	+	178917478	178917687
241327232	chr3	178919164	178919299	178919191	178919273	PIK3CA	NM_006218	1	21	4	+	178919078	178919328

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240944402	chr3	178922222	178922385	178922248	178922362	PIK3CA	NM_006218	1	21	6	+	178922291	178922376
236064411	chr3	178928164	178928296	178928190	178928268	PIK3CA	NM_006218	1	21	9	+	178928219	178928353
235951539	chr3	178936067	178936208	178936093	178936181	PIK3CA	NM_006218	1	21	10	+	178935998	178936122
236365247	chr3	178938776	178938938	178938803	178938911	PIK3CA	NM_006218	1	21	14	+	178938774	178938945
236986278	chr3	178942485	178942631	178942511	178942603	PIK3CA	NM_006218	1	21	16	+	178942488	178942609
235022560	chr3	178947112	178947236	178947139	178947209	PIK3CA	NM_006218	1	21	18	+	178947060	178947230
237320198	chr3	178947887	178948055	178947910	178948028	PIK3CA	NM_006218	1	21	20	+	178948013	178948164
235581427	chr3	178951919	178952063	178951941	178952038	PIK3CA	NM_006218	1	21	21	+	178951882	178952497
263670306	chr3	181430268	181430410	181430285	181430391	SOX2	NM_003106	1	1	1	+	181429712	181432223
263674303	chr3	181430694	181430832	181430711	181430810	SOX2	NM_003106	1	1	1	+	181429712	181432223
263699335	chr3	181431066	181431220	181431085	181431198	SOX2	NM_003106	1	1	1	+	181429712	181432223
223484216	chr3	187442607	187442772	187442629	187442752	BCL6	NM_001706	3	10	9	-	187442729	187442866
223484216	chr3	187442607	187442772	187442629	187442752	BCL6	NM_001134738	2	8	7	-	187442729	187442866
223484216	chr3	187442607	187442772	187442629	187442752	BCL6	NM_001130845	1	10	9	-	187442729	187442866
222786472	chr3	187444462	187444615	187444482	187444595	BCL6	NM_001706	3	10	7	-	187444519	187444686
222786472	chr3	187444462	187444615	187444482	187444595	BCL6	NM_001130845	1	10	7	-	187444519	187444686
225150085	chr3	187446812	187446986	187446832	187446966	BCL6	NM_001706	3	10	5	-	187446838	187447809
225150085	chr3	187446812	187446986	187446832	187446966	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225150085	chr3	187446812	187446986	187446832	187446966	BCL6	NM_001130845	1	10	5	-	187446838	187447809
225146179	chr3	187447268	187447426	187447290	187447397	BCL6	NM_001706	3	10	5	-	187446838	187447809
225146179	chr3	187447268	187447426	187447290	187447397	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225146179	chr3	187447268	187447426	187447290	187447397	BCL6	NM_001130845	1	10	5	-	187446838	187447809
225185808	chr3	187447698	187447842	187447718	187447820	BCL6	NM_001706	3	10	5	-	187446838	187447809
225185808	chr3	187447698	187447842	187447718	187447820	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225185808	chr3	187447698	187447842	187447718	187447820	BCL6	NM_001130845	1	10	5	-	187446838	187447809
223170095	chr3	187451229	187451402	187451251	187451377	BCL6	NM_001706	3	10	3	-	187451321	187451491
223170095	chr3	187451229	187451402	187451251	187451377	BCL6	NM_001134738	2	8	2	-	187451321	187451491
223170095	chr3	187451229	187451402	187451251	187451377	BCL6	NM_001130845	1	10	3	-	187451321	187451491
232739288	chr3	188202321	188202455	188202346	188202429	LPP	NM_001167672	2	10	3	+	188202380	188202492
232739288	chr3	188202321	188202455	188202346	188202429	LPP	NM_001167671	1	11	4	+	188202380	188202492
232739288	chr3	188202321	188202455	188202346	188202429	LPP	NM_005578	3	11	4	+	188202380	188202492
233629447	chr3	188327027	188327201	188327047	188327177	LPP	NM_001167671	1	11	6	+	188326949	188327632
233629447	chr3	188327027	188327201	188327047	188327177	LPP	NM_005578	3	11	6	+	188326949	188327632
233629447	chr3	188327027	188327201	188327047	188327177	LPP	NM_001167672	2	10	5	+	188326949	188327191
233634153	chr3	188327506	188327671	188327526	188327647	LPP	NM_001167671	1	11	6	+	188326949	188327632
233634153	chr3	188327506	188327671	188327526	188327647	LPP	NM_005578	3	11	6	+	188326949	188327632
234160390	chr3	188477954	188478096	188477975	188478070	LPP	NM_001167672	2	10	7	+	188477901	188478070
234160390	chr3	188477954	188478096	188477975	188478070	LPP	NM_001167671	1	11	8	+	188477901	188478070
234160390	chr3	188477954	188478096	188477975	188478070	LPP	NM_005578	3	11	8	+	188477901	188478070
233478904	chr3	188592045	188592219	188592068	188592198	LPP	NM_001167672	2	10	10	+	188592139	188608460
233478904	chr3	188592045	188592219	188592068	188592198	LPP	NM_001167671	1	11	11	+	188592139	188608460

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233478904	chr3	188592045	188592219	188592068	188592198	LPP	NM_005578	3	11	11	+	188592139	188608460
302476427	chr3	195593807	195593951	195593827	195593931	TNK2	NM_001010938	1	15	14	-	195593760	195593887
302476427	chr3	195593807	195593951	195593827	195593931	TNK2	NM_005781	2	15	14	-	195593760	195593887
304436290	chr3	195594494	195594664	195594511	195594644	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304436290	chr3	195594494	195594664	195594511	195594644	TNK2	NM_005781	2	15	12	-	195594232	195595580
300730821	chr3	195594749	195594906	195594767	195594887	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300730821	chr3	195594749	195594906	195594767	195594887	TNK2	NM_005781	2	15	12	-	195594232	195595580
300737129	chr3	195595100	195595229	195595120	195595212	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300737129	chr3	195595100	195595229	195595120	195595212	TNK2	NM_005781	2	15	12	-	195594232	195595580
305859235	chr3	195596284	195596435	195596303	195596416	TNK2	NM_001010938	1	15	12	-	195596368	195596412
303995073	chr3	195605069	195605239	195605087	195605218	TNK2	NM_001010938	1	15	9	-	195605124	195605218
303995073	chr3	195605069	195605239	195605087	195605218	TNK2	NM_005781	2	15	9	-	195605124	195605218
305815511	chr3	195605961	195606087	195605984	195606065	TNK2	NM_001010938	1	15	7	-	195605920	195606046
305815511	chr3	195605961	195606087	195605984	195606065	TNK2	NM_005781	2	15	7	-	195605920	195606046
302431663	chr3	195609936	195610091	195609958	195610073	TNK2	NM_001010938	1	15	5	-	195610028	195610180
302431663	chr3	195609936	195610091	195609958	195610073	TNK2	NM_005781	2	15	5	-	195610028	195610180
304388306	chr3	195613738	195613872	195613756	195613852	TNK2	NM_001010938	1	15	3	-	195613848	195613918
304388306	chr3	195613738	195613872	195613756	195613852	TNK2	NM_005781	2	15	3	-	195613848	195613918
302253771	chr3	195622077	195622213	195622097	195622194	TNK2	NM_001010938	1	15	1	-	195622117	195622432
227847409	chr4	1801159	1801293	1801177	1801272	FGFR3	NM_000142	1	18	3	+	1800981	1801250
227847409	chr4	1801159	1801293	1801177	1801272	FGFR3	NM_022965	3	16	3	+	1800981	1801250
227847409	chr4	1801159	1801293	1801177	1801272	FGFR3	NM_001163213	2	18	3	+	1800981	1801250
227973420	chr4	1803308	1803446	1803325	1803428	FGFR3	NM_000142	1	18	6	+	1803347	1803470
227973420	chr4	1803308	1803446	1803325	1803428	FGFR3	NM_022965	3	16	6	+	1803347	1803470
227973420	chr4	1803308	1803446	1803325	1803428	FGFR3	NM_001163213	2	18	6	+	1803347	1803470
227443116	chr4	1803694	1803858	1803714	1803837	FGFR3	NM_000142	1	18	7	+	1803562	1803752
227443116	chr4	1803694	1803858	1803714	1803837	FGFR3	NM_022965	3	16	7	+	1803562	1803752
227443116	chr4	1803694	1803858	1803714	1803837	FGFR3	NM_001163213	2	18	7	+	1803562	1803752
227392369	chr4	1805504	1805667	1805524	1805646	FGFR3	NM_000142	1	18	8	+	1805419	1805563
227915472	chr4	1806550	1806714	1806569	1806697	FGFR3	NM_000142	1	18	10	+	1806551	1806696
227915472	chr4	1806550	1806714	1806569	1806697	FGFR3	NM_022965	3	16	8	+	1806551	1806696
227915472	chr4	1806550	1806714	1806569	1806697	FGFR3	NM_001163213	2	18	10	+	1806551	1806696
228340627	chr4	1807282	1807413	1807302	1807396	FGFR3	NM_000142	1	18	12	+	1807286	1807396
228340627	chr4	1807282	1807413	1807302	1807396	FGFR3	NM_022965	3	16	10	+	1807286	1807396
228340627	chr4	1807282	1807413	1807302	1807396	FGFR3	NM_001163213	2	18	12	+	1807286	1807396
227994902	chr4	1807733	1807905	1807753	1807882	FGFR3	NM_000142	1	18	14	+	1807778	1807900
227994902	chr4	1807733	1807905	1807753	1807882	FGFR3	NM_022965	3	16	12	+	1807778	1807900
227994902	chr4	1807733	1807905	1807753	1807882	FGFR3	NM_001163213	2	18	14	+	1807778	1807900
227609865	chr4	1808345	1808518	1808366	1808499	FGFR3	NM_000142	1	18	16	+	1808273	1808410
227609865	chr4	1808345	1808518	1808366	1808499	FGFR3	NM_022965	3	16	14	+	1808273	1808410
227609865	chr4	1808345	1808518	1808366	1808499	FGFR3	NM_001163213	2	18	16	+	1808273	1808410

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_000142	1	18	18	+	1808843	1810599
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_022965	3	16	16	+	1808843	1810599
228971278	chr4	1808862	1809027	1808882	1809006	FGFR3	NM_001163213	2	18	18	+	1808843	1810599
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_007331	2	11	4	+	1902353	1902978
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_133330	3	24	4	+	1902353	1902978
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_133335	6	22	2	+	1902353	1902978
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_133334	5	9	1	+	1902353	1902978
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_133331	4	23	3	+	1902353	1902978
294637354	chr4	1902713	1902886	1902738	1902863	WHSC1	NM_001042424	1	22	2	+	1902353	1902978
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_007331	2	11	6	+	1918598	1918764
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_133330	3	24	6	+	1918598	1918764
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_133335	6	22	4	+	1918598	1918764
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_133334	5	9	3	+	1918598	1918764
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_133331	4	23	5	+	1918598	1918764
293960108	chr4	1918530	1918690	1918558	1918666	WHSC1	NM_001042424	1	22	4	+	1918598	1918764
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_007331	2	11	7	+	1919868	1920350
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_133330	3	24	7	+	1919868	1920350
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_133335	6	22	5	+	1919868	1920350
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_133334	5	9	4	+	1919868	1920350
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_133331	4	23	6	+	1919868	1920350
294413684	chr4	1920031	1920169	1920052	1920147	WHSC1	NM_001042424	1	22	5	+	1919868	1920350
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_007331	2	11	8	+	1932353	1932497
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_133330	3	24	8	+	1932353	1932497
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_133335	6	22	6	+	1932353	1932497
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_133334	5	9	5	+	1932353	1932497
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_133331	4	23	7	+	1932353	1932497
294573897	chr4	1932365	1932532	1932386	1932508	WHSC1	NM_001042424	1	22	6	+	1932353	1932497
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_133330	3	24	11	+	1941381	1941505
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_133335	6	22	9	+	1941381	1941505
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_133334	5	9	8	+	1941381	1941505
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_133331	4	23	10	+	1941381	1941505
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_001042424	1	22	9	+	1941381	1941505
294481931	chr4	1941257	1941429	1941285	1941406	WHSC1	NM_007331	2	11	11	+	1941381	1944302
294462278	chr4	1952776	1952950	1952798	1952930	WHSC1	NM_133330	3	24	12	+	1952799	1952930
294462278	chr4	1952776	1952950	1952798	1952930	WHSC1	NM_133335	6	22	10	+	1952799	1952930
294462278	chr4	1952776	1952950	1952798	1952930	WHSC1	NM_133331	4	23	11	+	1952799	1952930
294462278	chr4	1952776	1952950	1952798	1952930	WHSC1	NM_001042424	1	22	10	+	1952799	1952930
293900474	chr4	1955121	1955292	1955149	1955272	WHSC1	NM_133330	3	24	14	+	1955051	1955251
293900474	chr4	1955121	1955292	1955149	1955272	WHSC1	NM_133335	6	22	12	+	1955051	1955251
293900474	chr4	1955121	1955292	1955149	1955272	WHSC1	NM_133331	4	23	13	+	1955051	1955251
293900474	chr4	1955121	1955292	1955149	1955272	WHSC1	NM_001042424	1	22	12	+	1955051	1955251

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294562663	chr4	1957472	1957642	1957494	1957616	WHSC1	NM_133330	3	24	16	+	1957420	1957576
294562663	chr4	1957472	1957642	1957494	1957616	WHSC1	NM_133335	6	22	14	+	1957420	1957576
294562663	chr4	1957472	1957642	1957494	1957616	WHSC1	NM_133331	4	23	15	+	1957420	1957576
294562663	chr4	1957472	1957642	1957494	1957616	WHSC1	NM_001042424	1	22	14	+	1957420	1957576
294723476	chr4	1959685	1959847	1959711	1959827	WHSC1	NM_133330	3	24	18	+	1959660	1959763
294723476	chr4	1959685	1959847	1959711	1959827	WHSC1	NM_133335	6	22	16	+	1959660	1959763
294723476	chr4	1959685	1959847	1959711	1959827	WHSC1	NM_133331	4	23	17	+	1959660	1959763
294723476	chr4	1959685	1959847	1959711	1959827	WHSC1	NM_001042424	1	22	16	+	1959660	1959763
294442325	chr4	1962728	1962900	1962750	1962878	WHSC1	NM_133330	3	24	20	+	1962762	1962878
294442325	chr4	1962728	1962900	1962750	1962878	WHSC1	NM_133335	6	22	18	+	1962762	1962878
294442325	chr4	1962728	1962900	1962750	1962878	WHSC1	NM_133331	4	23	19	+	1962762	1962878
294442325	chr4	1962728	1962900	1962750	1962878	WHSC1	NM_001042424	1	22	18	+	1962762	1962878
294861159	chr4	1977018	1977180	1977039	1977158	WHSC1	NM_133330	3	24	22	+	1977021	1977127
294861159	chr4	1977018	1977180	1977039	1977158	WHSC1	NM_133335	6	22	20	+	1977021	1977127
294861159	chr4	1977018	1977180	1977039	1977158	WHSC1	NM_133331	4	23	21	+	1977021	1977127
294861159	chr4	1977018	1977180	1977039	1977158	WHSC1	NM_001042424	1	22	20	+	1977021	1977127
294938610	chr4	1980262	1980432	1980287	1980409	WHSC1	NM_133335	6	22	22	+	1980365	1983934
294938610	chr4	1980262	1980432	1980287	1980409	WHSC1	NM_001042424	1	22	22	+	1980365	1983934
294938610	chr4	1980262	1980432	1980287	1980409	WHSC1	NM_133330	3	24	24	+	1980365	1983930
294938610	chr4	1980262	1980432	1980287	1980409	WHSC1	NM_133331	4	23	23	+	1980365	1983930
238620393	chr4	40245090	40245259	40245109	40245238	RHOH	NM_004310	1	3	3	+	40244798	40246281
262109848	chr4	40245504	40245669	40245522	40245649	RHOH	NM_004310	1	3	3	+	40244798	40246281
238989438	chr4	41748185	41748344	41748202	41748325	PHOX2B	NM_003924	1	3	3	-	41746099	41748339
238068373	chr4	41749527	41749652	41749548	41749632	PHOX2B	NM_003924	1	3	2	-	41749366	41749553
239924520	chr4	55127215	55127389	55127239	55127368	PDGFRA	NM_006206	1	23	3	+	55127262	55127579
235188251	chr4	55129866	55130025	55129892	55130006	PDGFRA	NM_006206	1	23	4	+	55129834	55130094
238700031	chr4	55133431	55133605	55133455	55133581	PDGFRA	NM_006206	1	23	6	+	55133456	55133627
236402038	chr4	55136745	55136869	55136773	55136841	PDGFRA	NM_006206	1	23	8	+	55136800	55136915
235225467	chr4	55139643	55139795	55139665	55139774	PDGFRA	NM_006206	1	23	10	+	55139704	55139897
235351598	chr4	55140989	55141163	55141015	55141140	PDGFRA	NM_006206	1	23	12	+	55141008	55141140
236495223	chr4	55144495	55144640	55144518	55144617	PDGFRA	NM_006206	1	23	15	+	55144529	55144682
237913176	chr4	55151470	55151616	55151491	55151589	PDGFRA	NM_006206	1	23	17	+	55151538	55151653
236661574	chr4	55153568	55153739	55153591	55153717	PDGFRA	NM_006206	1	23	19	+	55153597	55153708
235008307	chr4	55156490	55156649	55156515	55156631	PDGFRA	NM_006206	1	23	22	+	55156480	55156721
233652131	chr4	55524150	55524299	55524169	55524280	KIT	NM_000222	1	21	1	+	55524095	55524248
233652131	chr4	55524150	55524299	55524169	55524280	KIT	NM_001093772	2	21	1	+	55524095	55524248
233639192	chr4	55564404	55564564	55564425	55564541	KIT	NM_000222	1	21	3	+	55564450	55564731
233639192	chr4	55564404	55564564	55564425	55564541	KIT	NM_001093772	2	21	3	+	55564450	55564731
232356272	chr4	55565797	55565959	55565818	55565933	KIT	NM_000222	1	21	4	+	55565796	55565932
232356272	chr4	55565797	55565959	55565818	55565933	KIT	NM_001093772	2	21	4	+	55565796	55565932
233959039	chr4	55573337	55573476	55573365	55573453	KIT	NM_000222	1	21	6	+	55573264	55573453

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233959039	chr4	55573337	55573476	55573365	55573453	KIT	NM_001093772	2	21	6	+	55573264	55573453
233402386	chr4	55589729	55589902	55589753	55589874	KIT	NM_000222	1	21	8	+	55589750	55589864
233402386	chr4	55589729	55589902	55589753	55589874	KIT	NM_001093772	2	21	8	+	55589750	55589864
326944562	chr4	55593451	55593621	55593477	55593597	KIT	NM_000222	1	21	10	+	55593384	55593490
326944562	chr4	55593451	55593621	55593477	55593597	KIT	NM_001093772	2	21	10	+	55593384	55593490
326944562	chr4	55593451	55593621	55593477	55593597	KIT	NM_000222	1	21	11	+	55593582	55593708
326944562	chr4	55593451	55593621	55593477	55593597	KIT	NM_001093772	2	21	11	+	55593582	55593708
234736983	chr4	55595501	55595633	55595518	55595605	KIT	NM_000222	1	21	14	+	55595501	55595651
234736983	chr4	55595501	55595633	55595518	55595605	KIT	NM_001093772	2	21	14	+	55595501	55595651
233452214	chr4	55598084	55598258	55598108	55598231	KIT	NM_000222	1	21	16	+	55598037	55598164
233452214	chr4	55598084	55598258	55598108	55598231	KIT	NM_001093772	2	21	16	+	55598037	55598164
232113009	chr4	55602638	55602805	55602665	55602780	KIT	NM_000222	1	21	18	+	55602664	55602775
232113009	chr4	55602638	55602805	55602665	55602780	KIT	NM_001093772	2	21	18	+	55602664	55602775
230915896	chr4	55603327	55603499	55603351	55603478	KIT	NM_000222	1	21	20	+	55603341	55603446
230915896	chr4	55603327	55603499	55603351	55603478	KIT	NM_001093772	2	21	20	+	55603341	55603446
234730332	chr4	55946191	55946361	55946217	55946335	KDR	NM_002253	1	30	30	-	55944426	55946330
233303345	chr4	55948714	55948862	55948742	55948836	KDR	NM_002253	1	30	28	-	55948703	55948802
233713304	chr4	55955471	55955615	55955494	55955586	KDR	NM_002253	1	30	25	-	55955541	55955640
233564417	chr4	55956166	55956311	55956190	55956284	KDR	NM_002253	1	30	23	-	55956123	55956245
232047089	chr4	55961696	55961867	55961723	55961843	KDR	NM_002253	1	30	20	-	55961744	55961832
231737830	chr4	55963833	55963959	55963858	55963935	KDR	NM_002253	1	30	18	-	55963829	55963933
233328658	chr4	55964919	55965065	55964940	55965040	KDR	NM_002253	1	30	16	-	55964864	55964970
233158008	chr4	55968599	55968741	55968621	55968714	KDR	NM_002253	1	30	14	-	55968529	55968675
232865451	chr4	55971035	55971183	55971056	55971155	KDR	NM_002253	1	30	13	-	55970810	55971151
231555966	chr4	55973841	55974014	55973867	55973994	KDR	NM_002253	1	30	10	-	55973904	55974060
232832391	chr4	55976766	55976937	55976790	55976909	KDR	NM_002253	1	30	8	-	55976821	55976935
234384237	chr4	55980205	55980368	55980226	55980340	KDR	NM_002253	1	30	6	-	55980293	55980432
233171607	chr4	55981155	55981279	55981179	55981251	KDR	NM_002253	1	30	5	-	55981041	55981209
233588863	chr4	55984835	55985007	55984860	55984979	KDR	NM_002253	1	30	3	-	55984771	55984967
294419032	chr4	62452872	62453027	62452900	62453002	LPHN3	NM_015236	1	23	2	+	62452945	62453158
294789044	chr4	62542597	62542721	62542620	62542698	LPHN3	NM_015236	1	23	3	+	62542544	62542653
294449085	chr4	62598580	62598751	62598607	62598729	LPHN3	NM_015236	1	23	5	+	62598472	62599272
295340564	chr4	62599028	62599177	62599055	62599152	LPHN3	NM_015236	1	23	5	+	62598472	62599272
294756414	chr4	62758565	62758718	62758587	62758690	LPHN3	NM_015236	1	23	7	+	62758374	62758676
294965234	chr4	62775290	62775456	62775312	62775436	LPHN3	NM_015236	1	23	9	+	62775278	62775463
294388921	chr4	62800643	62800768	62800664	62800741	LPHN3	NM_015236	1	23	11	+	62800558	62800741
294284051	chr4	62812732	62812871	62812760	62812843	LPHN3	NM_015236	1	23	13	+	62812632	62812840
294430352	chr4	62845356	62845519	62845384	62845493	LPHN3	NM_015236	1	23	15	+	62845281	62845490
294042767	chr4	62861958	62862124	62861979	62862096	LPHN3	NM_015236	1	23	17	+	62862009	62862075
294345021	chr4	62897078	62897206	62897106	62897179	LPHN3	NM_015236	1	23	20	+	62897160	62897328
294085884	chr4	62903472	62903643	62903493	62903615	LPHN3	NM_015236	1	23	21	+	62903449	62903574

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294687841	chr4	62935874	62936045	62935896	62936021	LPHN3	NM_015236	1	23	23	+	62935827	62938168
294695050	chr4	62936323	62936482	62936345	62936461	LPHN3	NM_015236	1	23	23	+	62935827	62938168
224099404	chr4	87928467	87928615	87928485	87928592	AFF1	NM_005935	2	20	1	+	87928153	87928576
223613512	chr4	87967900	87968067	87967925	87968046	AFF1	NM_005935	2	20	3	+	87967847	87968746
223613512	chr4	87967900	87968067	87967925	87968046	AFF1	NM_001166693	1	21	4	+	87967847	87968746
225033011	chr4	87968328	87968483	87968349	87968458	AFF1	NM_005935	2	20	3	+	87967847	87968746
225033011	chr4	87968328	87968483	87968349	87968458	AFF1	NM_001166693	1	21	4	+	87967847	87968746
223358944	chr4	88005208	88005382	88005231	88005357	AFF1	NM_005935	2	20	4	+	88005272	88005316
223358944	chr4	88005208	88005382	88005231	88005357	AFF1	NM_001166693	1	21	5	+	88005272	88005316
222727607	chr4	88016086	88016250	88016113	88016226	AFF1	NM_005935	2	20	7	+	88016067	88016121
222727607	chr4	88016086	88016250	88016113	88016226	AFF1	NM_001166693	1	21	8	+	88016067	88016121
224085470	chr4	88029248	88029406	88029273	88029382	AFF1	NM_005935	2	20	10	+	88029311	88029467
224085470	chr4	88029248	88029406	88029273	88029382	AFF1	NM_001166693	1	21	11	+	88029311	88029467
225152679	chr4	88035650	88035810	88035669	88035789	AFF1	NM_005935	2	20	11	+	88035519	88036451
225152679	chr4	88035650	88035810	88035669	88035789	AFF1	NM_001166693	1	21	12	+	88035519	88036451
223720140	chr4	88036105	88036252	88036127	88036231	AFF1	NM_005935	2	20	11	+	88035519	88036451
223720140	chr4	88036105	88036252	88036127	88036231	AFF1	NM_001166693	1	21	12	+	88035519	88036451
222302327	chr4	88046075	88046248	88046099	88046220	AFF1	NM_005935	2	20	12	+	88046189	88046295
222302327	chr4	88046075	88046248	88046099	88046220	AFF1	NM_001166693	1	21	13	+	88046189	88046295
222575058	chr4	88047389	88047530	88047411	88047505	AFF1	NM_005935	2	20	13	+	88047251	88047488
222575058	chr4	88047389	88047530	88047411	88047505	AFF1	NM_001166693	1	21	14	+	88047251	88047488
225188467	chr4	88052112	88052279	88052134	88052257	AFF1	NM_005935	2	20	16	+	88052235	88052371
225188467	chr4	88052112	88052279	88052134	88052257	AFF1	NM_001166693	1	21	17	+	88052235	88052371
223053703	chr4	88053388	88053560	88053410	88053539	AFF1	NM_005935	2	20	18	+	88053423	88053560
223053703	chr4	88053388	88053560	88053410	88053539	AFF1	NM_001166693	1	21	19	+	88053423	88053560
222857638	chr4	88055763	88055891	88055787	88055866	AFF1	NM_005935	2	20	19	+	88055626	88055846
222857638	chr4	88055763	88055891	88055787	88055866	AFF1	NM_001166693	1	21	20	+	88055623	88055846
291145028	chr4	103446655	103446797	103446682	103446770	NFKB1	NM_001165412	1	24	2	+	103446669	103446714
291145028	chr4	103446655	103446797	103446682	103446770	NFKB1	NM_003998	2	24	2	+	103446669	103446714
293283547	chr4	103488090	103488220	103488111	103488197	NFKB1	NM_001165412	1	24	6	+	103488144	103488292
293283547	chr4	103488090	103488220	103488111	103488197	NFKB1	NM_003998	2	24	6	+	103488144	103488292
292495736	chr4	103500003	103500141	103500023	103500118	NFKB1	NM_001165412	1	24	8	+	103500038	103500196
292495736	chr4	103500003	103500141	103500023	103500118	NFKB1	NM_003998	2	24	8	+	103500038	103500196
293543761	chr4	103505749	103505920	103505778	103505900	NFKB1	NM_001165412	1	24	11	+	103505839	103505977
293543761	chr4	103505749	103505920	103505778	103505900	NFKB1	NM_003998	2	24	11	+	103505839	103505977
293373573	chr4	103514669	103514842	103514689	103514809	NFKB1	NM_001165412	1	24	12	+	103514582	103514725
293373573	chr4	103514669	103514842	103514689	103514809	NFKB1	NM_003998	2	24	12	+	103514582	103514725
291812909	chr4	103517425	103517561	103517446	103517535	NFKB1	NM_001165412	1	24	14	+	103517295	103517489
291812909	chr4	103517425	103517561	103517446	103517535	NFKB1	NM_003998	2	24	14	+	103517295	103517489
289884780	chr4	103522034	103522197	103522061	103522169	NFKB1	NM_001165412	1	24	16	+	103522052	103522166
289884780	chr4	103522034	103522197	103522061	103522169	NFKB1	NM_003998	2	24	16	+	103522052	103522166

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
290363468	chr4	103528387	103528561	103528408	103528537	NFKB1	NM_001165412	1	24	18	+	103528307	103528476
290363468	chr4	103528387	103528561	103528408	103528537	NFKB1	NM_003998	2	24	18	+	103528307	103528476
292818304	chr4	103533157	103533331	103533183	103533303	NFKB1	NM_001165412	1	24	21	+	103533201	103533267
292818304	chr4	103533157	103533331	103533183	103533303	NFKB1	NM_003998	2	24	21	+	103533201	103533267
291595161	chr4	103534617	103534779	103534639	103534752	NFKB1	NM_001165412	1	24	23	+	103534582	103534738
291595161	chr4	103534617	103534779	103534639	103534752	NFKB1	NM_003998	2	24	23	+	103534582	103534738
242140500	chr4	106155137	106155306	106155164	106155279	TET2	NM_001127208	1	11	3	+	106155054	106158508
242140500	chr4	106155137	106155306	106155164	106155279	TET2	NM_017628	2	3	3	+	106155054	106163928
265686344	chr4	106155617	106155773	106155639	106155751	TET2	NM_001127208	1	11	3	+	106155054	106158508
265686344	chr4	106155617	106155773	106155639	106155751	TET2	NM_017628	2	3	3	+	106155054	106163928
265699905	chr4	106156002	106156168	106156028	106156143	TET2	NM_001127208	1	11	3	+	106155054	106158508
265699905	chr4	106156002	106156168	106156028	106156143	TET2	NM_017628	2	3	3	+	106155054	106163928
242090206	chr4	106156469	106156613	106156490	106156586	TET2	NM_001127208	1	11	3	+	106155054	106158508
242090206	chr4	106156469	106156613	106156490	106156586	TET2	NM_017628	2	3	3	+	106155054	106163928
242326573	chr4	106156942	106157071	106156962	106157048	TET2	NM_001127208	1	11	3	+	106155054	106158508
242326573	chr4	106156942	106157071	106156962	106157048	TET2	NM_017628	2	3	3	+	106155054	106163928
261976420	chr4	106157372	106157519	106157394	106157494	TET2	NM_001127208	1	11	3	+	106155054	106158508
261976420	chr4	106157372	106157519	106157394	106157494	TET2	NM_017628	2	3	3	+	106155054	106163928
242165703	chr4	106157716	106157890	106157741	106157865	TET2	NM_001127208	1	11	3	+	106155054	106158508
242165703	chr4	106157716	106157890	106157741	106157865	TET2	NM_017628	2	3	3	+	106155054	106163928
242169295	chr4	106158130	106158279	106158154	106158251	TET2	NM_001127208	1	11	3	+	106155054	106158508
242169295	chr4	106158130	106158279	106158154	106158251	TET2	NM_017628	2	3	3	+	106155054	106163928
261889368	chr4	106158535	106158676	106158562	106158650	TET2	NM_017628	2	3	3	+	106155054	106163928
264911362	chr4	106162384	106162550	106162412	106162525	TET2	NM_001127208	1	11	4	+	106162496	106162586
264911362	chr4	106162384	106162550	106162412	106162525	TET2	NM_017628	2	3	3	+	106155054	106163928
264058006	chr4	106163948	106164112	106163977	106164087	TET2	NM_001127208	1	11	5	+	106163991	106164084
262367284	chr4	106180826	106180954	106180851	106180925	TET2	NM_001127208	1	11	7	+	106180776	106180926
262550671	chr4	106190765	106190925	106190791	106190905	TET2	NM_001127208	1	11	9	+	106190767	106190904
240672581	chr4	106193978	106194118	106194004	106194090	TET2	NM_001127208	1	11	10	+	106193721	106194075
241716240	chr4	106196436	106196571	106196457	106196543	TET2	NM_001127208	1	11	11	+	106196205	106200960
265250376	chr4	106196862	106197036	106196883	106197011	TET2	NM_001127208	1	11	11	+	106196205	106200960
265226917	chr4	106197352	106197477	106197375	106197453	TET2	NM_001127208	1	11	11	+	106196205	106200960
231679449	chr4	123372967	123373102	123372991	123373075	IL2	NM_000586	1	4	4	-	123372626	123373017
234304351	chr4	123377310	123377482	123377338	123377454	IL2	NM_000586	1	4	2	-	123377299	123377358
234304351	chr4	123377310	123377482	123377338	123377454	IL2	NM_000586	1	4	1	-	123377449	123377650
231811541	chr4	153243919	153244066	153243942	153244045	FBXW7	NM_033632	3	12	12	-	153242410	153244301
231811541	chr4	153243919	153244066	153243942	153244045	FBXW7	NM_001013415	1	11	11	-	153242410	153244301
231811541	chr4	153243919	153244066	153243942	153244045	FBXW7	NM_018315	2	11	11	-	153242410	153244301
232190402	chr4	153245240	153245406	153245267	153245379	FBXW7	NM_033632	3	12	11	-	153245336	153245546
232190402	chr4	153245240	153245406	153245267	153245379	FBXW7	NM_001013415	1	11	10	-	153245336	153245546
232190402	chr4	153245240	153245406	153245267	153245379	FBXW7	NM_018315	2	11	10	-	153245336	153245546

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229630761	chr4	153247216	153247390	153247239	153247369	FBXW7	NM_033632	3	12	10	-	153247158	153247383
229630761	chr4	153247216	153247390	153247239	153247369	FBXW7	NM_001013415	1	11	9	-	153247158	153247383
229630761	chr4	153247216	153247390	153247239	153247369	FBXW7	NM_018315	2	11	9	-	153247158	153247383
230233743	chr4	153250757	153250912	153250784	153250884	FBXW7	NM_033632	3	12	8	-	153250824	153250937
230233743	chr4	153250757	153250912	153250784	153250884	FBXW7	NM_001013415	1	11	7	-	153250824	153250937
230233743	chr4	153250757	153250912	153250784	153250884	FBXW7	NM_018315	2	11	7	-	153250824	153250937
230789109	chr4	153253676	153253801	153253705	153253776	FBXW7	NM_033632	3	12	6	-	153253748	153253871
230789109	chr4	153253676	153253801	153253705	153253776	FBXW7	NM_001013415	1	11	5	-	153253748	153253871
230789109	chr4	153253676	153253801	153253705	153253776	FBXW7	NM_018315	2	11	5	-	153253748	153253871
230151224	chr4	153258993	153259153	153259021	153259124	FBXW7	NM_033632	3	12	5	-	153258954	153259088
230151224	chr4	153258993	153259153	153259021	153259124	FBXW7	NM_001013415	1	11	4	-	153258954	153259088
230151224	chr4	153258993	153259153	153259021	153259124	FBXW7	NM_018315	2	11	4	-	153258954	153259088
231761358	chr4	153271078	153271249	153271105	153271227	FBXW7	NM_033632	3	12	3	-	153271194	153271276
231761358	chr4	153271078	153271249	153271105	153271227	FBXW7	NM_001013415	1	11	2	-	153271194	153271276
231761358	chr4	153271078	153271249	153271105	153271227	FBXW7	NM_018315	2	11	2	-	153271194	153271276
229451556	chr4	153273818	153273948	153273842	153273920	FBXW7	NM_018315	2	11	1	-	153273622	153274110
228107362	chr4	153332479	153332650	153332499	153332626	FBXW7	NM_033632	3	12	2	-	153332455	153333024
294345660	chr5	224429	224601	224453	224574	SDHA	NM_004168	1	15	3	+	224475	224636
294209953	chr5	225625	225770	225646	225751	SDHA	NM_004168	1	15	4	+	225534	225677
294614326	chr5	228295	228454	228323	228434	SDHA	NM_004168	1	15	6	+	228300	228448
293709989	chr5	233478	233641	233504	233621	SDHA	NM_004168	1	15	8	+	233592	233760
294316532	chr5	235331	235463	235351	235445	SDHA	NM_004168	1	15	9	+	235259	235454
294437722	chr5	251051	251206	251075	251183	SDHA	NM_004168	1	15	12	+	251107	251218
290542980	chr5	7870779	7870942	7870805	7870914	MTRR	NM_002454	1	15	2	+	7870883	7871036
290542980	chr5	7870779	7870942	7870805	7870914	MTRR	NM_024010	2	15	2	+	7870883	7871036
289666258	chr5	7875237	7875408	7875265	7875382	MTRR	NM_002454	1	15	4	+	7875371	7875488
289666258	chr5	7875237	7875408	7875265	7875382	MTRR	NM_024010	2	15	4	+	7875371	7875488
293615996	chr5	7878223	7878393	7878247	7878367	MTRR	NM_002454	1	15	5	+	7878057	7878435
293615996	chr5	7878223	7878393	7878247	7878367	MTRR	NM_024010	2	15	5	+	7878057	7878435
290001558	chr5	7885748	7885917	7885776	7885892	MTRR	NM_002454	1	15	7	+	7885814	7885967
290001558	chr5	7885748	7885917	7885776	7885892	MTRR	NM_024010	2	15	7	+	7885814	7885967
289747898	chr5	7889261	7889413	7889284	7889391	MTRR	NM_002454	1	15	9	+	7889208	7889388
289747898	chr5	7889261	7889413	7889284	7889391	MTRR	NM_024010	2	15	9	+	7889208	7889388
290252723	chr5	7895797	7895929	7895826	7895906	MTRR	NM_002454	1	15	12	+	7895847	7895965
290252723	chr5	7895797	7895929	7895826	7895906	MTRR	NM_024010	2	15	12	+	7895847	7895965
292372050	chr5	7897135	7897294	7897161	7897269	MTRR	NM_002454	1	15	14	+	7897178	7897360
292372050	chr5	7897135	7897294	7897161	7897269	MTRR	NM_024010	2	15	14	+	7897178	7897360
274207048	chr5	35856938	35857112	35856965	35857086	IL7R	NM_002185	1	8	1	+	35856991	35857161
272987754	chr5	35867349	35867518	35867372	35867490	IL7R	NM_002185	1	8	3	+	35867408	35867565
273070820	chr5	35871232	35871384	35871259	35871356	IL7R	NM_002185	1	8	4	+	35871158	35871315
273496925	chr5	35875572	35875728	35875598	35875703	IL7R	NM_002185	1	8	7	+	35875614	35875689

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274656543	chr5	35876394	35876565	35876415	35876537	IL7R	NM_002185	1	8	8	+	35876085	35876923
299014461	chr5	37815879	37816041	37815907	37816015	GDNF	NM_199231	4	3	3	-	37812779	37816237
299014461	chr5	37815879	37816041	37815907	37816015	GDNF	NM_001190468	2	3	3	-	37812779	37816237
299014461	chr5	37815879	37816041	37815907	37816015	GDNF	NM_001190469	3	3	3	-	37812779	37816237
299014461	chr5	37815879	37816041	37815907	37816015	GDNF	NM_000514	1	3	3	-	37812779	37816237
299022024	chr5	37834730	37834896	37834751	37834874	GDNF	NM_199231	4	3	2	-	37834826	37834924
299022024	chr5	37834730	37834896	37834751	37834874	GDNF	NM_001190469	3	3	2	-	37834826	37834924
299022024	chr5	37834730	37834896	37834751	37834874	GDNF	NM_001190468	2	3	2	-	37834748	37834924
299022024	chr5	37834730	37834896	37834751	37834874	GDNF	NM_000514	1	3	2	-	37834748	37834924
233035864	chr5	38481776	38481950	38481802	38481922	LIFR	NM_001127671	1	20	20	-	38475065	38482320
233035864	chr5	38481776	38481950	38481802	38481922	LIFR	NM_002310	2	20	20	-	38475065	38482320
234474926	chr5	38482246	38482374	38482270	38482347	LIFR	NM_001127671	1	20	20	-	38475065	38482320
234474926	chr5	38482246	38482374	38482270	38482347	LIFR	NM_002310	2	20	20	-	38475065	38482320
231782048	chr5	38485866	38486030	38485889	38486001	LIFR	NM_001127671	1	20	17	-	38485921	38486082
231782048	chr5	38485866	38486030	38485889	38486001	LIFR	NM_002310	2	20	17	-	38485921	38486082
234711171	chr5	38490231	38490402	38490261	38490374	LIFR	NM_001127671	1	20	15	-	38490292	38490393
234711171	chr5	38490231	38490402	38490261	38490374	LIFR	NM_002310	2	20	15	-	38490292	38490393
233084770	chr5	38496361	38496519	38496382	38496494	LIFR	NM_001127671	1	20	13	-	38496484	38496697
233084770	chr5	38496361	38496519	38496382	38496494	LIFR	NM_002310	2	20	13	-	38496484	38496697
233146204	chr5	38499639	38499795	38499662	38499767	LIFR	NM_001127671	1	20	12	-	38499615	38499685
233146204	chr5	38499639	38499795	38499662	38499767	LIFR	NM_002310	2	20	12	-	38499615	38499685
232206013	chr5	38504169	38504333	38504197	38504311	LIFR	NM_001127671	1	20	10	-	38504078	38504223
232206013	chr5	38504169	38504333	38504197	38504311	LIFR	NM_002310	2	20	10	-	38504078	38504223
232642702	chr5	38506573	38506744	38506599	38506717	LIFR	NM_001127671	1	20	8	-	38506605	38506734
232642702	chr5	38506573	38506744	38506599	38506717	LIFR	NM_002310	2	20	8	-	38506605	38506734
230843385	chr5	38510700	38510828	38510725	38510800	LIFR	NM_001127671	1	20	7	-	38510566	38510820
230843385	chr5	38510700	38510828	38510725	38510800	LIFR	NM_002310	2	20	7	-	38510566	38510820
233530458	chr5	38523531	38523655	38523558	38523627	LIFR	NM_001127671	1	20	5	-	38523521	38523684
233530458	chr5	38523531	38523655	38523558	38523627	LIFR	NM_002310	2	20	5	-	38523521	38523684
232601250	chr5	38530532	38530706	38530559	38530679	LIFR	NM_001127671	1	20	2	-	38530608	38530768
232601250	chr5	38530532	38530706	38530559	38530679	LIFR	NM_002310	2	20	2	-	38530608	38530768
231675990	chr5	55237034	55237204	55237057	55237176	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231675990	chr5	55237034	55237204	55237057	55237176	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231675990	chr5	55237034	55237204	55237057	55237176	IL6ST	NM_002184	2	17	17	-	55230925	55237647
234055713	chr5	55237451	55237613	55237474	55237586	IL6ST	NM_175767	3	16	16	-	55230925	55237647
234055713	chr5	55237451	55237613	55237474	55237586	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
234055713	chr5	55237451	55237613	55237474	55237586	IL6ST	NM_002184	2	17	17	-	55230925	55237647
233350209	chr5	55247178	55247347	55247210	55247325	IL6ST	NM_175767	3	16	13	-	55247292	55247432
233350209	chr5	55247178	55247347	55247210	55247325	IL6ST	NM_001190981	1	16	13	-	55247292	55247432
233350209	chr5	55247178	55247347	55247210	55247325	IL6ST	NM_002184	2	17	14	-	55247292	55247432
232863869	chr5	55248076	55248205	55248103	55248177	IL6ST	NM_175767	3	16	11	-	55248078	55248179

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232863869	chr5	55248076	55248205	55248103	55248177	IL6ST	NM_001190981	1	16	11	-	55248078	55248179
232863869	chr5	55248076	55248205	55248103	55248177	IL6ST	NM_002184	2	17	12	-	55248078	55248179
232565747	chr5	55251789	55251945	55251812	55251919	IL6ST	NM_175767	3	16	9	-	55251853	55252063
232565747	chr5	55251789	55251945	55251812	55251919	IL6ST	NM_001190981	1	16	10	-	55251853	55252063
232565747	chr5	55251789	55251945	55251812	55251919	IL6ST	NM_002184	2	17	10	-	55251853	55252063
233716567	chr5	55256248	55256422	55256271	55256397	IL6ST	NM_175767	3	16	8	-	55256230	55256389
233716567	chr5	55256248	55256422	55256271	55256397	IL6ST	NM_001190981	1	16	8	-	55256230	55256389
233716567	chr5	55256248	55256422	55256271	55256397	IL6ST	NM_002184	2	17	8	-	55256230	55256389
233043561	chr5	55260067	55260234	55260095	55260206	IL6ST	NM_175767	3	16	6	-	55259974	55260140
233043561	chr5	55260067	55260234	55260095	55260206	IL6ST	NM_001190981	1	16	6	-	55259974	55260140
233043561	chr5	55260067	55260234	55260095	55260206	IL6ST	NM_002184	2	17	6	-	55259974	55260140
232207325	chr5	55272034	55272206	55272060	55272179	IL6ST	NM_175767	3	16	3	-	55272043	55272121
232207325	chr5	55272034	55272206	55272060	55272179	IL6ST	NM_001190981	1	16	3	-	55272043	55272121
232207325	chr5	55272034	55272206	55272060	55272179	IL6ST	NM_002184	2	17	3	-	55272043	55272121
236495108	chr5	67569157	67569331	67569184	67569310	PIK3R1	NM_181523	3	16	3	+	67569218	67569310
234918963	chr5	67576306	67576480	67576333	67576452	PIK3R1	NM_181523	3	16	6	+	67576356	67576557
239923757	chr5	67584483	67584628	67584504	67584605	PIK3R1	NM_181524	4	10	1	+	67584252	67584579
241219798	chr5	67588118	67588254	67588144	67588226	PIK3R1	NM_181523	3	16	8	+	67588087	67588189
241219798	chr5	67588118	67588254	67588144	67588226	PIK3R1	NM_181524	4	10	2	+	67588087	67588189
241219798	chr5	67588118	67588254	67588144	67588226	PIK3R1	NM_181504	2	10	2	+	67588087	67588189
235874208	chr5	67590290	67590438	67590311	67590410	PIK3R1	NM_181523	3	16	12	+	67590364	67590506
235874208	chr5	67590290	67590438	67590311	67590410	PIK3R1	NM_001242466	1	9	5	+	67590364	67590506
235874208	chr5	67590290	67590438	67590311	67590410	PIK3R1	NM_181524	4	10	6	+	67590364	67590506
235874208	chr5	67590290	67590438	67590311	67590410	PIK3R1	NM_181504	2	10	6	+	67590364	67590506
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181523	3	16	13	+	67590976	67591152
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_001242466	1	9	6	+	67590976	67591152
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181524	4	10	7	+	67590976	67591152
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181504	2	10	7	+	67590976	67591152
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181523	3	16	14	+	67591248	67591316
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_001242466	1	9	7	+	67591248	67591316
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181524	4	10	8	+	67591248	67591316
237500383	chr5	67591098	67591271	67591124	67591248	PIK3R1	NM_181504	2	10	8	+	67591248	67591316
240266433	chr5	67593166	67593336	67593193	67593310	PIK3R1	NM_181523	3	16	16	+	67593240	67597649
240266433	chr5	67593166	67593336	67593193	67593310	PIK3R1	NM_001242466	1	9	9	+	67593240	67597649
240266433	chr5	67593166	67593336	67593193	67593310	PIK3R1	NM_181524	4	10	10	+	67593240	67597649
240266433	chr5	67593166	67593336	67593193	67593310	PIK3R1	NM_181504	2	10	10	+	67593240	67597649
223858394	chr5	112090500	112090670	112090527	112090643	APC	NM_000038	1	16	2	+	112090570	112090722
223858394	chr5	112090500	112090670	112090527	112090643	APC	NM_001127510	2	17	3	+	112090570	112090722
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_000038	1	16	4	+	112102886	112103087
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_001127510	2	17	5	+	112102886	112103087
329273555	chr5	112102831	112102958	112102863	112102935	APC	NM_001127511	3	14	3	+	112102886	112103087

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_000038	1	16	5	+	112111326	112111434
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_001127510	2	17	6	+	112111326	112111434
223558752	chr5	112111329	112111454	112111355	112111425	APC	NM_001127511	3	14	4	+	112111326	112111434
223258804	chr5	112136915	112137080	112136937	112137057	APC	NM_000038	1	16	8	+	112136976	112137080
223258804	chr5	112136915	112137080	112136937	112137057	APC	NM_001127510	2	17	9	+	112136976	112137080
223258804	chr5	112136915	112137080	112136937	112137057	APC	NM_001127511	3	14	6	+	112136976	112137080
222846722	chr5	112154591	112154731	112154619	112154707	APC	NM_000038	1	16	10	+	112154663	112155041
222846722	chr5	112154591	112154731	112154619	112154707	APC	NM_001127510	2	17	11	+	112154663	112155041
222846722	chr5	112154591	112154731	112154619	112154707	APC	NM_001127511	3	14	8	+	112154663	112155041
222513007	chr5	112157649	112157815	112157677	112157787	APC	NM_000038	1	16	11	+	112157593	112157688
222513007	chr5	112157649	112157815	112157677	112157787	APC	NM_001127510	2	17	12	+	112157593	112157688
222513007	chr5	112157649	112157815	112157677	112157787	APC	NM_001127511	3	14	9	+	112157593	112157688
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_000038	1	16	13	+	112163626	112163703
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_001127510	2	17	14	+	112163626	112163703
222301696	chr5	112163576	112163707	112163604	112163681	APC	NM_001127511	3	14	11	+	112163626	112163703
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_000038	1	16	15	+	112170648	112170862
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_001127510	2	17	16	+	112170648	112170862
222403679	chr5	112170634	112170773	112170662	112170751	APC	NM_001127511	3	14	13	+	112170648	112170862
224539101	chr5	112173404	112173576	112173427	112173548	APC	NM_000038	1	16	16	+	112173250	112181936
224539101	chr5	112173404	112173576	112173427	112173548	APC	NM_001127510	2	17	17	+	112173250	112181936
224539101	chr5	112173404	112173576	112173427	112173548	APC	NM_001127511	3	14	14	+	112173250	112181936
224545285	chr5	112173858	112174012	112173880	112173989	APC	NM_000038	1	16	16	+	112173250	112181936
224545285	chr5	112173858	112174012	112173880	112173989	APC	NM_001127510	2	17	17	+	112173250	112181936
224545285	chr5	112173858	112174012	112173880	112173989	APC	NM_001127511	3	14	14	+	112173250	112181936
222798076	chr5	112174269	112174443	112174295	112174418	APC	NM_000038	1	16	16	+	112173250	112181936
222798076	chr5	112174269	112174443	112174295	112174418	APC	NM_001127510	2	17	17	+	112173250	112181936
222798076	chr5	112174269	112174443	112174295	112174418	APC	NM_001127511	3	14	14	+	112173250	112181936
222756079	chr5	112174708	112174869	112174736	112174841	APC	NM_000038	1	16	16	+	112173250	112181936
222756079	chr5	112174708	112174869	112174736	112174841	APC	NM_001127510	2	17	17	+	112173250	112181936
222756079	chr5	112174708	112174869	112174736	112174841	APC	NM_001127511	3	14	14	+	112173250	112181936
326755794	chr5	112175083	112175239	112175115	112175211	APC	NM_000038	1	16	16	+	112173250	112181936
326755794	chr5	112175083	112175239	112175115	112175211	APC	NM_001127510	2	17	17	+	112173250	112181936
326755794	chr5	112175083	112175239	112175115	112175211	APC	NM_001127511	3	14	14	+	112173250	112181936
326844609	chr5	112175538	112175704	112175564	112175684	APC	NM_000038	1	16	16	+	112173250	112181936
326844609	chr5	112175538	112175704	112175564	112175684	APC	NM_001127510	2	17	17	+	112173250	112181936
326844609	chr5	112175538	112175704	112175564	112175684	APC	NM_001127511	3	14	14	+	112173250	112181936
224578555	chr5	112176016	112176161	112176044	112176134	APC	NM_000038	1	16	16	+	112173250	112181936
224578555	chr5	112176016	112176161	112176044	112176134	APC	NM_001127510	2	17	17	+	112173250	112181936
224578555	chr5	112176016	112176161	112176044	112176134	APC	NM_001127511	3	14	14	+	112173250	112181936
224579341	chr5	112176473	112176633	112176498	112176605	APC	NM_000038	1	16	16	+	112173250	112181936
224579341	chr5	112176473	112176633	112176498	112176605	APC	NM_001127510	2	17	17	+	112173250	112181936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224579341	chr5	112176473	112176633	112176498	112176605	APC	NM_001127511	3	14	14	+	112173250	112181936
222822985	chr5	112176965	112177093	112176988	112177065	APC	NM_000038	1	16	16	+	112173250	112181936
222822985	chr5	112176965	112177093	112176988	112177065	APC	NM_001127510	2	17	17	+	112173250	112181936
222822985	chr5	112176965	112177093	112176988	112177065	APC	NM_001127511	3	14	14	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_000038	1	16	16	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_001127510	2	17	17	+	112173250	112181936
224547648	chr5	112177354	112177500	112177382	112177475	APC	NM_001127511	3	14	14	+	112173250	112181936
224532793	chr5	112177769	112177938	112177795	112177918	APC	NM_000038	1	16	16	+	112173250	112181936
224532793	chr5	112177769	112177938	112177795	112177918	APC	NM_001127510	2	17	17	+	112173250	112181936
224532793	chr5	112177769	112177938	112177795	112177918	APC	NM_001127511	3	14	14	+	112173250	112181936
224553937	chr5	112178282	112178447	112178310	112178420	APC	NM_000038	1	16	16	+	112173250	112181936
224553937	chr5	112178282	112178447	112178310	112178420	APC	NM_001127510	2	17	17	+	112173250	112181936
224553937	chr5	112178282	112178447	112178310	112178420	APC	NM_001127511	3	14	14	+	112173250	112181936
222755331	chr5	112178694	112178864	112178718	112178842	APC	NM_000038	1	16	16	+	112173250	112181936
222755331	chr5	112178694	112178864	112178718	112178842	APC	NM_001127510	2	17	17	+	112173250	112181936
222755331	chr5	112178694	112178864	112178718	112178842	APC	NM_001127511	3	14	14	+	112173250	112181936
222833299	chr5	112179156	112179297	112179184	112179273	APC	NM_000038	1	16	16	+	112173250	112181936
222833299	chr5	112179156	112179297	112179184	112179273	APC	NM_001127510	2	17	17	+	112173250	112181936
222833299	chr5	112179156	112179297	112179184	112179273	APC	NM_001127511	3	14	14	+	112173250	112181936
224608621	chr5	112179574	112179738	112179597	112179712	APC	NM_000038	1	16	16	+	112173250	112181936
224608621	chr5	112179574	112179738	112179597	112179712	APC	NM_001127510	2	17	17	+	112173250	112181936
224608621	chr5	112179574	112179738	112179597	112179712	APC	NM_001127511	3	14	14	+	112173250	112181936
236369236	chr5	131893053	131893178	131893078	131893157	RAD50	NM_005732	1	25	1	+	131892616	131893145
236512430	chr5	131914888	131915042	131914909	131915017	RAD50	NM_005732	1	25	4	+	131915009	131915194
237200288	chr5	131915589	131915716	131915617	131915691	RAD50	NM_005732	1	25	5	+	131915554	131915758
234920707	chr5	131923658	131923788	131923683	131923766	RAD50	NM_005732	1	25	7	+	131923616	131923781
235876260	chr5	131925324	131925480	131925351	131925452	RAD50	NM_005732	1	25	9	+	131925323	131925529
239786724	chr5	131927002	131927159	131927025	131927132	RAD50	NM_005732	1	25	10	+	131926916	131927098
237562108	chr5	131930462	131930635	131930489	131930607	RAD50	NM_005732	1	25	12	+	131930561	131930736
235132261	chr5	131931258	131931385	131931279	131931360	RAD50	NM_005732	1	25	13	+	131931265	131931502
235558608	chr5	131939072	131939232	131939101	131939207	RAD50	NM_005732	1	25	14	+	131938992	131939181
236253784	chr5	131944314	131944484	131944335	131944456	RAD50	NM_005732	1	25	17	+	131944307	131944417
237782721	chr5	131951636	131951807	131951669	131951784	RAD50	NM_005732	1	25	20	+	131951695	131951822
235670531	chr5	131953890	131954024	131953918	131953995	RAD50	NM_005732	1	25	21	+	131953762	131953986
235935034	chr5	131973817	131973941	131973842	131973919	RAD50	NM_005732	1	25	23	+	131973773	131973915
234928292	chr5	131977894	131978032	131977916	131978006	RAD50	NM_005732	1	25	25	+	131977870	131980313
273192649	chr5	138118749	138118917	138118775	138118890	CTNNA1	NM_001903	1	18	3	+	138118866	138119061
274304312	chr5	138145786	138145960	138145804	138145936	CTNNA1	NM_001903	1	18	4	+	138145727	138145893
273792248	chr5	138160274	138160411	138160300	138160391	CTNNA1	NM_001903	1	18	6	+	138160219	138160488
272907578	chr5	138221827	138222000	138221855	138221975	CTNNA1	NM_001903	1	18	8	+	138221901	138221981
273760220	chr5	138223246	138223371	138223273	138223344	CTNNA1	NM_001903	1	18	9	+	138223179	138223331

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273407536	chr5	138253443	138253578	138253464	138253550	CTNNA1	NM_001903	1	18	11	+	138253431	138253587
273663821	chr5	138260905	138261047	138260927	138261026	CTNNA1	NM_001903	1	18	13	+	138260945	138261096
273515705	chr5	138266242	138266393	138266265	138266373	CTNNA1	NM_001903	1	18	15	+	138266162	138266343
273961901	chr5	138269460	138269588	138269481	138269565	CTNNA1	NM_001903	1	18	18	+	138269491	138270723
226688060	chr5	149433571	149433713	149433594	149433692	CSF1R	NM_005211	1	22	22	-	149432854	149433787
225525028	chr5	149435510	149435674	149435531	149435652	CSF1R	NM_005211	1	22	19	-	149435589	149435700
225819257	chr5	149436806	149436973	149436824	149436956	CSF1R	NM_005211	1	22	17	-	149436850	149436947
227017797	chr5	149440307	149440462	149440327	149440440	CSF1R	NM_005211	1	22	14	-	149440425	149440535
225691124	chr5	149441247	149441392	149441270	149441367	CSF1R	NM_005211	1	22	12	-	149441286	149441412
225521189	chr5	149449425	149449555	149449445	149449536	CSF1R	NM_005211	1	22	10	-	149449436	149449626
253704306	chr5	149450009	149450165	149450029	149450143	CSF1R	NM_005211	1	22	8	-	149450019	149450134
225830363	chr5	149456904	149457034	149456924	149457006	CSF1R	NM_005211	1	22	6	-	149456839	149456998
225568061	chr5	149459676	149459837	149459700	149459817	CSF1R	NM_005211	1	22	4	-	149459615	149459899
225397029	chr5	149460487	149460633	149460506	149460611	CSF1R	NM_005211	1	22	3	-	149460330	149460587
239118617	chr5	149495427	149495569	149495445	149495550	PDGFRB	NM_002609	1	23	23	-	149493402	149495509
237298095	chr5	149498288	149498441	149498309	149498420	PDGFRB	NM_002609	1	23	21	-	149498310	149498415
236298246	chr5	149500341	149500492	149500363	149500472	PDGFRB	NM_002609	1	23	18	-	149500451	149500573
236558450	chr5	149501386	149501517	149501408	149501491	PDGFRB	NM_002609	1	23	16	-	149501443	149501603
236518302	chr5	149503713	149503882	149503733	149503858	PDGFRB	NM_002609	1	23	14	-	149503813	149503923
235155127	chr5	149505095	149505219	149505118	149505199	PDGFRB	NM_002609	1	23	12	-	149505008	149505140
240564374	chr5	149509442	149509601	149509462	149509577	PDGFRB	NM_002609	1	23	10	-	149509320	149509531
237614401	chr5	149511542	149511674	149511566	149511654	PDGFRB	NM_002609	1	23	8	-	149511542	149511657
237894640	chr5	149513214	149513388	149513234	149513368	PDGFRB	NM_002609	1	23	6	-	149513149	149513323
236108869	chr5	149514393	149514529	149514418	149514504	PDGFRB	NM_002609	1	23	4	-	149514313	149514579
237399394	chr5	149515309	149515483	149515327	149515462	PDGFRB	NM_002609	1	23	3	-	149515118	149515441
238082176	chr5	170817067	170817214	170817094	170817186	NPM1	NM_002520	2	11	2	+	170817055	170817134
238082176	chr5	170817067	170817214	170817094	170817186	NPM1	NM_001037738	1	10	2	+	170817055	170817134
238082176	chr5	170817067	170817214	170817094	170817186	NPM1	NM_199185	3	10	2	+	170817055	170817134
236526400	chr5	170818724	170818857	170818749	170818830	NPM1	NM_002520	2	11	4	+	170818710	170818803
236526400	chr5	170818724	170818857	170818749	170818830	NPM1	NM_001037738	1	10	4	+	170818710	170818803
236526400	chr5	170818724	170818857	170818749	170818830	NPM1	NM_199185	3	10	4	+	170818710	170818803
236854141	chr5	170832298	170832467	170832325	170832444	NPM1	NM_002520	2	11	9	+	170832306	170832407
236854141	chr5	170832298	170832467	170832325	170832444	NPM1	NM_001037738	1	10	9	+	170832306	170832407
236854141	chr5	170832298	170832467	170832325	170832444	NPM1	NM_199185	3	10	8	+	170832306	170832407
269879314	chr5	176516558	176516716	176516578	176516695	FGFR4	NM_022963	2	16	1	+	176516551	176516694
269879314	chr5	176516558	176516716	176516578	176516695	FGFR4	NM_002011	1	18	2	+	176516551	176516694
269879314	chr5	176516558	176516716	176516578	176516695	FGFR4	NM_213647	3	18	2	+	176516551	176516694
270172444	chr5	176517700	176517849	176517720	176517826	FGFR4	NM_022963	2	16	3	+	176517746	176517826
270172444	chr5	176517700	176517849	176517720	176517826	FGFR4	NM_002011	1	18	4	+	176517746	176517826
270172444	chr5	176517700	176517849	176517720	176517826	FGFR4	NM_213647	3	18	4	+	176517746	176517826
272012489	chr5	176518698	176518860	176518718	176518839	FGFR4	NM_022963	2	16	5	+	176518686	176518809

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272012489	chr5	176518698	176518860	176518718	176518839	FGFR4	NM_002011	1	18	6	+	176518686	176518809
272012489	chr5	176518698	176518860	176518718	176518839	FGFR4	NM_213647	3	18	6	+	176518686	176518809
271001230	chr5	176519639	176519812	176519659	176519794	FGFR4	NM_022963	2	16	7	+	176519647	176519785
271001230	chr5	176519639	176519812	176519659	176519794	FGFR4	NM_002011	1	18	8	+	176519647	176519785
271001230	chr5	176519639	176519812	176519659	176519794	FGFR4	NM_213647	3	18	8	+	176519647	176519785
271301469	chr5	176520402	176520540	176520422	176520519	FGFR4	NM_002011	1	18	10	+	176520407	176520552
271301469	chr5	176520402	176520540	176520422	176520519	FGFR4	NM_213647	3	18	10	+	176520407	176520552
271301469	chr5	176520402	176520540	176520422	176520519	FGFR4	NM_022963	2	16	8	+	176520333	176520552
270155134	chr5	176522473	176522647	176522493	176522629	FGFR4	NM_022963	2	16	11	+	176522534	176522724
270155134	chr5	176522473	176522647	176522493	176522629	FGFR4	NM_002011	1	18	13	+	176522534	176522724
270155134	chr5	176522473	176522647	176522493	176522629	FGFR4	NM_213647	3	18	13	+	176522534	176522724
271196139	chr5	176523056	176523207	176523075	176523186	FGFR4	NM_022963	2	16	12	+	176523058	176523180
271196139	chr5	176523056	176523207	176523075	176523186	FGFR4	NM_002011	1	18	14	+	176523058	176523180
271196139	chr5	176523056	176523207	176523075	176523186	FGFR4	NM_213647	3	18	14	+	176523058	176523180
270068802	chr5	176524185	176524349	176524206	176524329	FGFR4	NM_022963	2	16	15	+	176524293	176524398
270068802	chr5	176524185	176524349	176524206	176524329	FGFR4	NM_002011	1	18	17	+	176524293	176524398
270068802	chr5	176524185	176524349	176524206	176524329	FGFR4	NM_213647	3	18	17	+	176524293	176524398
237799191	chr5	176562057	176562229	176562085	176562204	NSD1	NM_022455	1	23	2	+	176562088	176563031
237799191	chr5	176562057	176562229	176562085	176562204	NSD1	NM_172349	2	24	2	+	176562088	176562201
235752028	chr5	176562507	176562669	176562532	176562642	NSD1	NM_022455	1	23	2	+	176562088	176563031
235832644	chr5	176562948	176563102	176562976	176563074	NSD1	NM_172349	2	24	3	+	176562942	176563031
235832644	chr5	176562948	176563102	176562976	176563074	NSD1	NM_022455	1	23	2	+	176562088	176563031
236775332	chr5	176631190	176631346	176631211	176631318	NSD1	NM_022455	1	23	4	+	176631121	176631293
236775332	chr5	176631190	176631346	176631211	176631318	NSD1	NM_172349	2	24	5	+	176631121	176631293
242619885	chr5	176636905	176637072	176636933	176637044	NSD1	NM_022455	1	23	5	+	176636637	176639196
242619885	chr5	176636905	176637072	176636933	176637044	NSD1	NM_172349	2	24	6	+	176636637	176639196
237633763	chr5	176637330	176637503	176637351	176637476	NSD1	NM_022455	1	23	5	+	176636637	176639196
237633763	chr5	176637330	176637503	176637351	176637476	NSD1	NM_172349	2	24	6	+	176636637	176639196
257590446	chr5	176637753	176637912	176637779	176637887	NSD1	NM_022455	1	23	5	+	176636637	176639196
257590446	chr5	176637753	176637912	176637779	176637887	NSD1	NM_172349	2	24	6	+	176636637	176639196
242560505	chr5	176638180	176638321	176638203	176638298	NSD1	NM_022455	1	23	5	+	176636637	176639196
242560505	chr5	176638180	176638321	176638203	176638298	NSD1	NM_172349	2	24	6	+	176636637	176639196
242558690	chr5	176638577	176638739	176638600	176638714	NSD1	NM_022455	1	23	5	+	176636637	176639196
242558690	chr5	176638577	176638739	176638600	176638714	NSD1	NM_172349	2	24	6	+	176636637	176639196
257654704	chr5	176638998	176639133	176639020	176639109	NSD1	NM_022455	1	23	5	+	176636637	176639196
257654704	chr5	176638998	176639133	176639020	176639109	NSD1	NM_172349	2	24	6	+	176636637	176639196
236181961	chr5	176665194	176665320	176665218	176665298	NSD1	NM_022455	1	23	7	+	176665238	176665508
236181961	chr5	176665194	176665320	176665218	176665298	NSD1	NM_172349	2	24	8	+	176665238	176665508
235405862	chr5	176666821	176666993	176666844	176666968	NSD1	NM_022455	1	23	8	+	176666757	176666866
235405862	chr5	176666821	176666993	176666844	176666968	NSD1	NM_172349	2	24	9	+	176666757	176666866
238143557	chr5	176675083	176675257	176675110	176675237	NSD1	NM_022455	1	23	11	+	176675182	176675325

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238143557	chr5	176675083	176675257	176675110	176675237	NSD1	NM_172349	2	24	12	+	176675182	176675325
240337490	chr5	176683935	176684073	176683960	176684052	NSD1	NM_022455	1	23	13	+	176683952	176684152
240337490	chr5	176683935	176684073	176683960	176684052	NSD1	NM_172349	2	24	14	+	176683952	176684152
238549388	chr5	176687133	176687264	176687159	176687233	NSD1	NM_022455	1	23	14	+	176686990	176687169
238549388	chr5	176687133	176687264	176687159	176687233	NSD1	NM_172349	2	24	15	+	176686990	176687169
236728736	chr5	176696627	176696775	176696647	176696753	NSD1	NM_022455	1	23	16	+	176696603	176696808
236728736	chr5	176696627	176696775	176696647	176696753	NSD1	NM_172349	2	24	17	+	176696603	176696808
235842889	chr5	176707643	176707774	176707666	176707753	NSD1	NM_022455	1	23	18	+	176707566	176707835
235842889	chr5	176707643	176707774	176707666	176707753	NSD1	NM_172349	2	24	19	+	176707566	176707835
235225796	chr5	176710659	176710833	176710682	176710809	NSD1	NM_022455	1	23	20	+	176710788	176710929
235225796	chr5	176710659	176710833	176710682	176710809	NSD1	NM_172349	2	24	21	+	176710788	176710929
240594775	chr5	176718904	176719075	176718931	176719049	NSD1	NM_022455	1	23	22	+	176718955	176719159
240594775	chr5	176718904	176719075	176718931	176719049	NSD1	NM_172349	2	24	23	+	176718955	176719159
239827046	chr5	176720973	176721137	176720994	176721111	NSD1	NM_022455	1	23	23	+	176720833	176727214
239827046	chr5	176720973	176721137	176720994	176721111	NSD1	NM_172349	2	24	24	+	176720833	176727214
235277065	chr5	176721360	176721511	176721381	176721488	NSD1	NM_022455	1	23	23	+	176720833	176727214
235277065	chr5	176721360	176721511	176721381	176721488	NSD1	NM_172349	2	24	24	+	176720833	176727214
235340993	chr5	176721794	176721925	176721815	176721902	NSD1	NM_022455	1	23	23	+	176720833	176727214
235340993	chr5	176721794	176721925	176721815	176721902	NSD1	NM_172349	2	24	24	+	176720833	176727214
235232963	chr5	176722246	176722407	176722267	176722382	NSD1	NM_022455	1	23	23	+	176720833	176727214
235232963	chr5	176722246	176722407	176722267	176722382	NSD1	NM_172349	2	24	24	+	176720833	176727214
272479307	chr5	180030265	180030417	180030284	180030394	FLT4	NM_182925	2	30	30	-	180028506	180030390
271123845	chr5	180038389	180038525	180038408	180038506	FLT4	NM_182925	2	30	27	-	180038331	180038479
271123845	chr5	180038389	180038525	180038408	180038506	FLT4	NM_002020	1	30	27	-	180038331	180038479
270286743	chr5	180043334	180043464	180043355	180043442	FLT4	NM_182925	2	30	23	-	180043367	180043489
270286743	chr5	180043334	180043464	180043355	180043442	FLT4	NM_002020	1	30	23	-	180043367	180043489
269651552	chr5	180045801	180045947	180045819	180045930	FLT4	NM_182925	2	30	21	-	180045770	180045920
269651552	chr5	180045801	180045947	180045819	180045930	FLT4	NM_002020	1	30	21	-	180045770	180045920
269588655	chr5	180046652	180046818	180046672	180046800	FLT4	NM_182925	2	30	18	-	180046665	180046769
269588655	chr5	180046652	180046818	180046672	180046800	FLT4	NM_002020	1	30	18	-	180046665	180046769
271443705	chr5	180047616	180047773	180047641	180047754	FLT4	NM_182925	2	30	16	-	180047609	180047715
271443705	chr5	180047616	180047773	180047641	180047754	FLT4	NM_002020	1	30	16	-	180047609	180047715
270122464	chr5	180048096	180048231	180048118	180048211	FLT4	NM_182925	2	30	14	-	180048106	180048252
270122464	chr5	180048096	180048231	180048118	180048211	FLT4	NM_002020	1	30	14	-	180048106	180048252
271355932	chr5	180048711	180048875	180048730	180048854	FLT4	NM_182925	2	30	13	-	180048542	180048904
271355932	chr5	180048711	180048875	180048730	180048854	FLT4	NM_002020	1	30	13	-	180048542	180048904
271131662	chr5	180050863	180050998	180050884	180050979	FLT4	NM_182925	2	30	11	-	180050935	180051061
271131662	chr5	180050863	180050998	180050884	180050979	FLT4	NM_002020	1	30	11	-	180050935	180051061
272531392	chr5	180053091	180053263	180053110	180053241	FLT4	NM_182925	2	30	9	-	180053111	180053265
272531392	chr5	180053091	180053263	180053110	180053241	FLT4	NM_002020	1	30	9	-	180053111	180053265
269687060	chr5	180056228	180056376	180056247	180056355	FLT4	NM_182925	2	30	7	-	180056259	180056427

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269687060	chr5	180056228	180056376	180056247	180056355	FLT4	NM_002020	1	30	7	-	180056259	180056427
271910403	chr5	180056837	180057007	180056857	180056989	FLT4	NM_182925	2	30	5	-	180056943	180057105
271910403	chr5	180056837	180057007	180056857	180056989	FLT4	NM_002020	1	30	5	-	180056943	180057105
270892862	chr5	180057653	180057827	180057670	180057808	FLT4	NM_182925	2	30	3	-	180057555	180057799
270892862	chr5	180057653	180057827	180057670	180057808	FLT4	NM_002020	1	30	3	-	180057555	180057799
233364698	chr6	393228	393354	393248	393337	IRF4	NM_001195286	1	9	2	+	393098	393368
233364698	chr6	393228	393354	393248	393337	IRF4	NR_046000	4	10	2	+	393098	393368
233364698	chr6	393228	393354	393248	393337	IRF4	NM_002460	2	9	2	+	393098	393368
232244328	chr6	395870	396043	395889	396020	IRF4	NM_001195286	1	9	4	+	395847	395935
232244328	chr6	395870	396043	395889	396020	IRF4	NR_046000	4	10	4	+	395847	395935
232244328	chr6	395870	396043	395889	396020	IRF4	NM_002460	2	9	4	+	395847	395935
232244328	chr6	395870	396043	395889	396020	IRF4	NR_036585	3	8	3	+	395847	395935
233720488	chr6	398904	399043	398925	399019	IRF4	NM_001195286	1	9	6	+	398828	398935
233720488	chr6	398904	399043	398925	399019	IRF4	NR_046000	4	10	6	+	398828	398935
233720488	chr6	398904	399043	398925	399019	IRF4	NM_002460	2	9	6	+	398828	398935
233720488	chr6	398904	399043	398925	399019	IRF4	NR_036585	3	8	5	+	398828	398935
234185337	chr6	401643	401804	401664	401777	IRF4	NM_001195286	1	9	7	+	401424	401777
234185337	chr6	401643	401804	401664	401777	IRF4	NR_046000	4	10	7	+	401424	401777
234185337	chr6	401643	401804	401664	401777	IRF4	NM_002460	2	9	7	+	401424	401777
234185337	chr6	401643	401804	401664	401777	IRF4	NR_036585	3	8	6	+	401424	401777
228009583	chr6	18236589	18236733	18236617	18236714	DEK	NM_003472	2	11	9	-	18236683	18236831
228009583	chr6	18236589	18236733	18236617	18236714	DEK	NM_001134709	1	10	8	-	18236683	18236831
227712800	chr6	18249820	18249984	18249848	18249956	DEK	NM_003472	2	11	7	-	18249882	18250070
227712800	chr6	18249820	18249984	18249848	18249956	DEK	NM_001134709	1	10	6	-	18249882	18250070
230693331	chr6	18255972	18256113	18256001	18256087	DEK	NM_003472	2	11	6	-	18255962	18256082
230693331	chr6	18255972	18256113	18256001	18256087	DEK	NM_001134709	1	10	5	-	18255962	18256082
230030492	chr6	18258599	18258764	18258622	18258736	DEK	NM_003472	2	11	3	-	18258535	18258636
235195444	chr6	31132970	31133133	31132993	31133112	POU5F1	NM_002701	2	5	4	-	31132905	31133063
235195444	chr6	31132970	31133133	31132993	31133112	POU5F1	NM_203289	3	4	3	-	31132905	31133063
235195444	chr6	31132970	31133133	31132993	31133112	POU5F1	NM_001173531	1	5	4	-	31132905	31133063
235017110	chr6	31133727	31133883	31133746	31133855	POU5F1	NM_002701	2	5	2	-	31133704	31133824
235017110	chr6	31133727	31133883	31133746	31133855	POU5F1	NM_001173531	1	5	2	-	31133704	31133824
235017110	chr6	31133727	31133883	31133746	31133855	POU5F1	NM_203289	3	4	1	-	31133704	31134615
290125061	chr6	32163187	32163359	32163213	32163341	NOTCH4	NM_004557	1	30	30	-	32162620	32163927
292643503	chr6	32163673	32163813	32163691	32163794	NOTCH4	NM_004557	1	30	30	-	32162620	32163927
291205814	chr6	32164780	32164904	32164800	32164885	NOTCH4	NM_004557	1	30	28	-	32164702	32164849
289630689	chr6	32166131	32166269	32166159	32166249	NOTCH4	NM_004557	1	30	26	-	32166198	32166336
291225154	chr6	32166766	32166916	32166784	32166898	NOTCH4	NM_004557	1	30	24	-	32166703	32166922
293598118	chr6	32168941	32169113	32168962	32169092	NOTCH4	NM_004557	1	30	22	-	32168894	32169277
292908914	chr6	32169906	32170079	32169924	32170061	NOTCH4	NM_004557	1	30	21	-	32169853	32170376
289280089	chr6	32171521	32171690	32171544	32171663	NOTCH4	NM_004557	1	30	20	-	32171547	32171659

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289581629	chr6	32178481	32178632	32178500	32178613	NOTCH4	NM_004557	1	30	18	-	32178529	32178713
291693774	chr6	32180373	32180524	32180393	32180500	NOTCH4	NM_004557	1	30	17	-	32180251	32180404
290148217	chr6	32181470	32181637	32181493	32181617	NOTCH4	NM_004557	1	30	14	-	32181465	32181617
289763646	chr6	32183079	32183205	32183100	32183180	NOTCH4	NM_004557	1	30	12	-	32183003	32183162
291243141	chr6	32185747	32185920	32185767	32185902	NOTCH4	NM_004557	1	30	9	-	32185772	32185885
292328108	chr6	32187946	32188120	32187966	32188099	NOTCH4	NM_004557	1	30	7	-	32187906	32188061
290802552	chr6	32188507	32188676	32188532	32188656	NOTCH4	NM_004557	1	30	5	-	32188533	32188655
290073841	chr6	32189050	32189180	32189072	32189159	NOTCH4	NM_004557	1	30	4	-	32188755	32189102
290225645	chr6	32190761	32190903	32190780	32190885	NOTCH4	NM_004557	1	30	2	-	32190782	32190863
273614818	chr6	33286885	33287034	33286906	33287012	DAXX	NM_001254717	3	7	6	-	33286774	33286996
273614818	chr6	33286885	33287034	33286906	33287012	DAXX	NM_001350	4	8	7	-	33286774	33286996
273614818	chr6	33286885	33287034	33286906	33287012	DAXX	NM_001141969	1	8	7	-	33286774	33286996
273614818	chr6	33286885	33287034	33286906	33287012	DAXX	NM_001141970	2	8	7	-	33286774	33286996
273100131	chr6	33287446	33287617	33287472	33287596	DAXX	NM_001254717	3	7	5	-	33287157	33287631
273100131	chr6	33287446	33287617	33287472	33287596	DAXX	NM_001350	4	8	6	-	33287157	33287631
273100131	chr6	33287446	33287617	33287472	33287596	DAXX	NM_001141969	1	8	6	-	33287157	33287631
273100131	chr6	33287446	33287617	33287472	33287596	DAXX	NM_001141970	2	8	6	-	33287157	33287631
273103793	chr6	33287915	33288039	33287938	33288014	DAXX	NM_001254717	3	7	4	-	33287788	33288001
273103793	chr6	33287915	33288039	33287938	33288014	DAXX	NM_001350	4	8	5	-	33287788	33288001
273103793	chr6	33287915	33288039	33287938	33288014	DAXX	NM_001141969	1	8	5	-	33287788	33288001
273103793	chr6	33287915	33288039	33287938	33288014	DAXX	NM_001141970	2	8	5	-	33287788	33288001
274326728	chr6	33288572	33288743	33288592	33288723	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274326728	chr6	33288572	33288743	33288592	33288723	DAXX	NM_001350	4	8	3	-	33288513	33289344
274326728	chr6	33288572	33288743	33288592	33288723	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274326728	chr6	33288572	33288743	33288592	33288723	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274314469	chr6	33289017	33289191	33289040	33289164	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274314469	chr6	33289017	33289191	33289040	33289164	DAXX	NM_001350	4	8	3	-	33288513	33289344
274314469	chr6	33289017	33289191	33289040	33289164	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274314469	chr6	33289017	33289191	33289040	33289164	DAXX	NM_001141970	2	8	3	-	33288513	33289344
272971131	chr6	33289466	33289596	33289489	33289576	DAXX	NM_001141970	2	8	2	-	33289496	33289685
272971131	chr6	33289466	33289596	33289489	33289576	DAXX	NM_001350	4	8	2	-	33289496	33289751
272971131	chr6	33289466	33289596	33289489	33289576	DAXX	NM_001141969	1	8	2	-	33289496	33289754
237812660	chr6	37138049	37138193	37138068	37138174	PIM1	NM_002648	2	6	1	+	37137922	37138433
237812660	chr6	37138049	37138193	37138068	37138174	PIM1	NM_001243186	1	6	1	+	37137922	37138433
236977505	chr6	37138701	37138850	37138718	37138832	PIM1	NM_002648	2	6	3	+	37138757	37138807
236977505	chr6	37138701	37138850	37138718	37138832	PIM1	NM_001243186	1	6	3	+	37138757	37138807
238261997	chr6	37139150	37139278	37139168	37139260	PIM1	NM_002648	2	6	4	+	37138901	37139267
238261997	chr6	37139150	37139278	37139168	37139260	PIM1	NM_001243186	1	6	4	+	37138901	37139267
237437042	chr6	37141741	37141912	37141764	37141892	PIM1	NM_002648	2	6	6	+	37141710	37143204
237437042	chr6	37141741	37141912	37141764	37141892	PIM1	NM_001243186	1	6	6	+	37141710	37143204
271318530	chr6	41545790	41545936	41545811	41545913	FOXP4	NM_138457	3	17	3	+	41545724	41545819

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271318530	chr6	41545790	41545936	41545811	41545913	FOXP4	NM_001012427	2	17	3	+	41545724	41545819
271318530	chr6	41545790	41545936	41545811	41545913	FOXP4	NM_001012426	1	17	3	+	41545724	41545819
270348472	chr6	41554683	41554831	41554702	41554812	FOXP4	NM_138457	3	17	6	+	41554747	41554894
270348472	chr6	41554683	41554831	41554702	41554812	FOXP4	NM_001012427	2	17	6	+	41554747	41554894
270348472	chr6	41554683	41554831	41554702	41554812	FOXP4	NM_001012426	1	17	6	+	41554747	41554894
269970090	chr6	41555147	41555303	41555165	41555286	FOXP4	NM_138457	3	17	7	+	41555040	41555250
269970090	chr6	41555147	41555303	41555165	41555286	FOXP4	NM_001012427	2	17	7	+	41555037	41555250
269970090	chr6	41555147	41555303	41555165	41555286	FOXP4	NM_001012426	1	17	7	+	41555037	41555250
272109858	chr6	41557480	41557650	41557499	41557632	FOXP4	NM_138457	3	17	10	+	41557509	41557592
272109858	chr6	41557480	41557650	41557499	41557632	FOXP4	NM_001012427	2	17	10	+	41557509	41557592
272109858	chr6	41557480	41557650	41557499	41557632	FOXP4	NM_001012426	1	17	10	+	41557509	41557592
271300540	chr6	41557945	41558119	41557967	41558099	FOXP4	NM_138457	3	17	12	+	41558009	41558085
271300540	chr6	41557945	41558119	41557967	41558099	FOXP4	NM_001012427	2	17	12	+	41558009	41558085
271300540	chr6	41557945	41558119	41557967	41558099	FOXP4	NM_001012426	1	17	12	+	41558009	41558085
271420102	chr6	41564838	41564970	41564866	41564946	FOXP4	NM_138457	3	17	15	+	41564914	41564980
271420102	chr6	41564838	41564970	41564866	41564946	FOXP4	NM_001012427	2	17	15	+	41564914	41564980
271420102	chr6	41564838	41564970	41564866	41564946	FOXP4	NM_001012426	1	17	15	+	41564914	41564980
271754661	chr6	41566431	41566572	41566449	41566552	FOXP4	NM_138457	3	17	17	+	41566527	41570122
271754661	chr6	41566431	41566572	41566449	41566552	FOXP4	NM_001012427	2	17	17	+	41566527	41570122
271754661	chr6	41566431	41566572	41566449	41566552	FOXP4	NM_001012426	1	17	17	+	41566527	41570122
228024922	chr6	44217096	44217225	44217119	44217204	HSP90AB1	NM_007355	1	12	3	+	44217114	44217320
227810152	chr6	44217692	44217828	44217716	44217799	HSP90AB1	NM_007355	1	12	5	+	44217758	44217891
227476693	chr6	44218846	44219004	44218874	44218981	HSP90AB1	NM_007355	1	12	7	+	44218785	44218950
228043678	chr6	44219535	44219659	44219557	44219636	HSP90AB1	NM_007355	1	12	9	+	44219474	44219621
228602982	chr6	44219961	44220126	44219989	44220103	HSP90AB1	NM_007355	1	12	10	+	44219736	44220004
227215247	chr6	44221044	44221216	44221067	44221191	HSP90AB1	NM_007355	1	12	11	+	44220782	44221115
272233055	chr6	51484042	51484196	51484064	51484173	PKHD1	NM_138694	1	67	67	-	51480145	51484318
271279045	chr6	51491799	51491973	51491822	51491951	PKHD1	NM_138694	1	67	66	-	51491795	51491914
270998513	chr6	51503560	51503719	51503587	51503695	PKHD1	NM_138694	1	67	64	-	51503647	51503754
269733843	chr6	51513914	51514080	51513937	51514052	PKHD1	NM_138694	1	67	62	-	51513883	51514018
271126645	chr6	51524009	51524157	51524032	51524133	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271103391	chr6	51524448	51524618	51524473	51524590	PKHD1	NM_138694	1	67	61	-	51523750	51524767
269827132	chr6	51609081	51609246	51609108	51609222	PKHD1	NM_138694	1	67	60	-	51609183	51609340
269827132	chr6	51609081	51609246	51609108	51609222	PKHD1	NM_170724	2	61	60	-	51609183	51609340
272261323	chr6	51612544	51612684	51612572	51612662	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272261323	chr6	51612544	51612684	51612572	51612662	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270519182	chr6	51612989	51613152	51613014	51613131	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270519182	chr6	51612989	51613152	51613014	51613131	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272648525	chr6	51617924	51618098	51617946	51618070	PKHD1	NM_138694	1	67	57	-	51617999	51618151
272648525	chr6	51617924	51618098	51617946	51618070	PKHD1	NM_170724	2	61	57	-	51617999	51618151
270770335	chr6	51637469	51637643	51637497	51637615	PKHD1	NM_138694	1	67	55	-	51637500	51637587

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270770335	chr6	51637469	51637643	51637497	51637615	PKHD1	NM_170724	2	61	55	-	51637500	51637587
272541778	chr6	51656068	51656241	51656089	51656214	PKHD1	NM_138694	1	67	53	-	51656034	51656171
272541778	chr6	51656068	51656241	51656089	51656214	PKHD1	NM_170724	2	61	53	-	51656034	51656171
271346489	chr6	51712529	51712703	51712557	51712681	PKHD1	NM_138694	1	67	50	-	51712573	51712768
271346489	chr6	51712529	51712703	51712557	51712681	PKHD1	NM_170724	2	61	50	-	51712573	51712768
272215074	chr6	51732586	51732760	51732610	51732737	PKHD1	NM_138694	1	67	48	-	51732661	51732907
272215074	chr6	51732586	51732760	51732610	51732737	PKHD1	NM_170724	2	61	48	-	51732661	51732907
269753164	chr6	51735333	51735489	51735356	51735460	PKHD1	NM_138694	1	67	47	-	51735302	51735437
269753164	chr6	51735333	51735489	51735356	51735460	PKHD1	NM_170724	2	61	47	-	51735302	51735437
271044659	chr6	51750716	51750890	51750739	51750862	PKHD1	NM_138694	1	67	45	-	51750665	51750770
271044659	chr6	51750716	51750890	51750739	51750862	PKHD1	NM_170724	2	61	45	-	51750665	51750770
272635116	chr6	51768408	51768555	51768431	51768532	PKHD1	NM_138694	1	67	43	-	51768395	51768525
272635116	chr6	51768408	51768555	51768431	51768532	PKHD1	NM_170724	2	61	43	-	51768395	51768525
269708291	chr6	51771093	51771223	51771116	51771197	PKHD1	NM_138694	1	67	41	-	51771013	51771138
269708291	chr6	51771093	51771223	51771116	51771197	PKHD1	NM_170724	2	61	41	-	51771013	51771138
269947043	chr6	51776630	51776802	51776653	51776774	PKHD1	NM_138694	1	67	39	-	51776597	51776754
269947043	chr6	51776630	51776802	51776653	51776774	PKHD1	NM_170724	2	61	39	-	51776597	51776754
269986456	chr6	51798993	51799157	51799014	51799135	PKHD1	NM_138694	1	67	37	-	51798908	51799120
269986456	chr6	51798993	51799157	51799014	51799135	PKHD1	NM_170724	2	61	37	-	51798908	51799120
271400962	chr6	51875119	51875282	51875138	51875258	PKHD1	NM_138694	1	67	35	-	51875107	51875257
271400962	chr6	51875119	51875282	51875138	51875258	PKHD1	NM_170724	2	61	35	-	51875107	51875257
270333464	chr6	51887482	51887646	51887510	51887622	PKHD1	NM_138694	1	67	33	-	51887599	51887742
270333464	chr6	51887482	51887646	51887510	51887622	PKHD1	NM_170724	2	61	33	-	51887599	51887742
271897489	chr6	51889433	51889575	51889455	51889550	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271897489	chr6	51889433	51889575	51889455	51889550	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271880464	chr6	51889889	51890047	51889916	51890019	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271880464	chr6	51889889	51890047	51889916	51890019	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271926688	chr6	51890269	51890406	51890290	51890383	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271926688	chr6	51890269	51890406	51890290	51890383	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271948789	chr6	51890733	51890906	51890753	51890884	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271948789	chr6	51890733	51890906	51890753	51890884	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271373916	chr6	51892838	51893005	51892865	51892979	PKHD1	NM_138694	1	67	30	-	51892954	51893149
271373916	chr6	51892838	51893005	51892865	51892979	PKHD1	NM_170724	2	61	30	-	51892954	51893149
272126825	chr6	51897838	51897962	51897866	51897939	PKHD1	NM_138694	1	67	29	-	51897828	51897963
272126825	chr6	51897838	51897962	51897866	51897939	PKHD1	NM_170724	2	61	29	-	51897828	51897963
271955264	chr6	51907614	51907788	51907638	51907765	PKHD1	NM_138694	1	67	27	-	51907657	51907932
271955264	chr6	51907614	51907788	51907638	51907765	PKHD1	NM_170724	2	61	27	-	51907657	51907932
270826529	chr6	51908441	51908614	51908462	51908586	PKHD1	NM_138694	1	67	26	-	51908423	51908528
270826529	chr6	51908441	51908614	51908462	51908586	PKHD1	NM_170724	2	61	26	-	51908423	51908528
270930444	chr6	51910890	51911054	51910912	51911026	PKHD1	NM_138694	1	67	24	-	51910802	51910986
270930444	chr6	51910890	51911054	51910912	51911026	PKHD1	NM_170724	2	61	24	-	51910802	51910986

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269595909	chr6	51917803	51917955	51917828	51917933	PKHD1	NM_138694	1	67	21	-	51917874	51918049
269595909	chr6	51917803	51917955	51917828	51917933	PKHD1	NM_170724	2	61	21	-	51917874	51918049
272726522	chr6	51920276	51920449	51920299	51920427	PKHD1	NM_138694	1	67	19	-	51920385	51920527
272726522	chr6	51920276	51920449	51920299	51920427	PKHD1	NM_170724	2	61	19	-	51920385	51920527
271189876	chr6	51921651	51921814	51921672	51921786	PKHD1	NM_138694	1	67	17	-	51921688	51921777
271189876	chr6	51921651	51921814	51921672	51921786	PKHD1	NM_170724	2	61	17	-	51921688	51921777
270972182	chr6	51924601	51924758	51924624	51924734	PKHD1	NM_138694	1	67	15	-	51924726	51924840
270972182	chr6	51924601	51924758	51924624	51924734	PKHD1	NM_170724	2	61	15	-	51924726	51924840
271088511	chr6	51929689	51929863	51929710	51929836	PKHD1	NM_138694	1	67	13	-	51929753	51929848
271088511	chr6	51929689	51929863	51929710	51929836	PKHD1	NM_170724	2	61	13	-	51929753	51929848
271383969	chr6	51934246	51934403	51934271	51934382	PKHD1	NM_138694	1	67	11	-	51934255	51934325
271383969	chr6	51934246	51934403	51934271	51934382	PKHD1	NM_170724	2	61	11	-	51934255	51934325
270750272	chr6	51938163	51938330	51938190	51938302	PKHD1	NM_138694	1	67	7	-	51938261	51938339
270750272	chr6	51938163	51938330	51938190	51938302	PKHD1	NM_170724	2	61	7	-	51938261	51938339
272535480	chr6	51947073	51947244	51947097	51947219	PKHD1	NM_138694	1	67	4	-	51947190	51947340
272535480	chr6	51947073	51947244	51947097	51947219	PKHD1	NM_170724	2	61	4	-	51947190	51947340
280723064	chr6	52869885	52870059	52869908	52870038	ICK	NM_016513	2	15	15	-	52866098	52870101
280723064	chr6	52869885	52870059	52869908	52870038	ICK	NM_014920	1	14	14	-	52866098	52870101
280912370	chr6	52874292	52874466	52874320	52874437	ICK	NM_016513	2	15	13	-	52874237	52874365
280912370	chr6	52874292	52874466	52874320	52874437	ICK	NM_014920	1	14	12	-	52874237	52874365
280395776	chr6	52876911	52877074	52876934	52877047	ICK	NM_016513	2	15	11	-	52876835	52877025
280395776	chr6	52876911	52877074	52876934	52877047	ICK	NM_014920	1	14	10	-	52876835	52877025
278308084	chr6	52880865	52880997	52880892	52880969	ICK	NM_016513	2	15	9	-	52880881	52881048
278308084	chr6	52880865	52880997	52880892	52880969	ICK	NM_014920	1	14	8	-	52880881	52881048
279987408	chr6	52883919	52884083	52883950	52884062	ICK	NM_016513	2	15	7	-	52884025	52884157
279987408	chr6	52883919	52884083	52883950	52884062	ICK	NM_014920	1	14	6	-	52884025	52884157
280209396	chr6	52897325	52897485	52897353	52897457	ICK	NM_016513	2	15	5	-	52897331	52897452
280209396	chr6	52897325	52897485	52897353	52897457	ICK	NM_014920	1	14	4	-	52897331	52897452
286499106	chr6	56323801	56323972	56323827	56323947	DST	NM_015548	2	84	84	-	56322785	56324065
288390205	chr6	56327753	56327898	56327779	56327875	DST	NM_015548	2	84	82	-	56327844	56327954
284746756	chr6	56330799	56330948	56330822	56330926	DST	NM_015548	2	84	80	-	56330876	56330993
285191869	chr6	56334705	56334876	56334729	56334848	DST	NM_015548	2	84	78	-	56334681	56334755
288174682	chr6	56335919	56336075	56335944	56336051	DST	NM_015548	2	84	76	-	56335904	56336066
286731775	chr6	56338572	56338722	56338595	56338695	DST	NM_015548	2	84	74	-	56338671	56338800
287911951	chr6	56340959	56341128	56340983	56341108	DST	NM_015548	2	84	73	-	56340947	56341135
286809608	chr6	56346726	56346900	56346754	56346879	DST	NM_015548	2	84	71	-	56346848	56346976
286887004	chr6	56350040	56350164	56350069	56350143	DST	NM_015548	2	84	69	-	56350110	56350269
288272097	chr6	56351976	56352132	56351997	56352105	DST	NM_015548	2	84	68	-	56351902	56352071
286255776	chr6	56356924	56357098	56356952	56357075	DST	NM_015548	2	84	66	-	56357025	56357231
287394214	chr6	56357766	56357928	56357788	56357900	DST	NM_015548	2	84	65	-	56357732	56357887
288177953	chr6	56362104	56362235	56362123	56362214	DST	NM_015548	2	84	63	-	56362177	56362305

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
285716837	chr6	56362791	56362950	56362815	56362922	DST	NM_015548	2	84	62	-	56362654	56362851
285230068	chr6	56366189	56366347	56366219	56366324	DST	NM_015548	2	84	60	-	56366318	56366491
287326855	chr6	56368750	56368917	56368775	56368896	DST	NM_015548	2	84	59	-	56368795	56368896
286092481	chr6	56371507	56371631	56371528	56371603	DST	NM_015548	2	84	57	-	56371465	56371587
286570546	chr6	56374365	56374523	56374387	56374496	DST	NM_015548	2	84	55	-	56374440	56374671
284744507	chr6	56375916	56376078	56375944	56376052	DST	NM_015548	2	84	54	-	56375995	56376198
285182434	chr6	56380253	56380377	56380274	56380349	DST	NM_015548	2	84	53	-	56380248	56380466
286944371	chr6	56382227	56382352	56382254	56382331	DST	NM_015548	2	84	51	-	56382299	56382418
286979686	chr6	56391274	56391417	56391294	56391389	DST	NM_015548	2	84	50	-	56391159	56391365
288227046	chr6	56393599	56393753	56393626	56393726	DST	NM_015548	2	84	48	-	56393639	56393723
287522598	chr6	56394446	56394578	56394474	56394553	DST	NM_015548	2	84	47	-	56394246	56394572
288826965	chr6	56397082	56397226	56397105	56397201	DST	NM_015548	2	84	45	-	56397142	56397308
286192273	chr6	56399989	56400152	56400009	56400124	DST	NM_015548	2	84	44	-	56399920	56400090
285767745	chr6	56416900	56417041	56416929	56417019	DST	NM_015548	2	84	42	-	56416982	56418453
285904863	chr6	56417341	56417495	56417362	56417469	DST	NM_015548	2	84	42	-	56416982	56418453
288179385	chr6	56417783	56417956	56417811	56417931	DST	NM_015548	2	84	42	-	56416982	56418453
288142149	chr6	56418219	56418375	56418246	56418350	DST	NM_015548	2	84	42	-	56416982	56418453
287234862	chr6	56420177	56420335	56420203	56420310	DST	NM_015548	2	84	41	-	56420143	56420638
286175635	chr6	56422056	56422201	56422083	56422173	DST	NM_015548	2	84	40	-	56422117	56422316
286644168	chr6	56425175	56425349	56425203	56425321	DST	NM_015548	2	84	39	-	56425092	56425221
287626344	chr6	56426844	56426975	56426877	56426950	DST	NM_015548	2	84	37	-	56426936	56426998
287150916	chr6	56434638	56434790	56434668	56434766	DST	NM_015548	2	84	35	-	56434654	56434810
286294374	chr6	56436959	56437123	56436983	56437097	DST	NM_015548	2	84	34	-	56436898	56437064
285860264	chr6	56437809	56437969	56437837	56437947	DST	NM_015548	2	84	33	-	56437545	56437862
286304307	chr6	56457035	56457188	56457057	56457160	DST	NM_015548	2	84	30	-	56456980	56457156
288855621	chr6	56458740	56458912	56458763	56458888	DST	NM_015548	2	84	29	-	56458461	56458991
287013749	chr6	56462710	56462834	56462732	56462809	DST	NM_015548	2	84	28	-	56462538	56462804
288489431	chr6	56464738	56464906	56464762	56464877	DST	NM_015548	2	84	26	-	56464867	56465019
286254843	chr6	56475233	56475407	56475260	56475382	DST	NM_015548	2	84	25	-	56475225	56475360
287067777	chr6	56479153	56479306	56479176	56479283	DST	NM_015548	2	84	23	-	56479154	56479282
287173840	chr6	56480597	56480764	56480624	56480744	DST	NM_001723	1	24	24	-	56479375	56482216
289083142	chr6	56481032	56481202	56481060	56481175	DST	NM_001723	1	24	24	-	56479375	56482216
289066247	chr6	56481486	56481651	56481508	56481627	DST	NM_001723	1	24	24	-	56479375	56482216
287482402	chr6	56481943	56482111	56481965	56482088	DST	NM_001723	1	24	24	-	56479375	56482216
288267742	chr6	56482833	56483004	56482861	56482983	DST	NM_001723	1	24	23	-	56482784	56485513
288256383	chr6	56483298	56483465	56483320	56483437	DST	NM_001723	1	24	23	-	56482784	56485513
286169645	chr6	56483710	56483876	56483735	56483852	DST	NM_001723	1	24	23	-	56482784	56485513
286215694	chr6	56484117	56484272	56484143	56484244	DST	NM_001723	1	24	23	-	56482784	56485513
288289691	chr6	56484528	56484698	56484550	56484674	DST	NM_001723	1	24	23	-	56482784	56485513
286160963	chr6	56484941	56485115	56484968	56485091	DST	NM_001723	1	24	23	-	56482784	56485513
286122015	chr6	56485392	56485551	56485421	56485528	DST	NM_001723	1	24	23	-	56482784	56485513

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
287224892	chr6	56489991	56490117	56490013	56490088	DST	NM_015548	2	84	21	-	56489955	56490062
287224892	chr6	56489991	56490117	56490013	56490088	DST	NM_001723	1	24	21	-	56489955	56490062
289134880	chr6	56492824	56492997	56492853	56492976	DST	NM_015548	2	84	19	-	56492797	56492959
289134880	chr6	56492824	56492997	56492853	56492976	DST	NM_001723	1	24	19	-	56492797	56492959
288567490	chr6	56496016	56496169	56496046	56496141	DST	NM_015548	2	84	16	-	56496009	56496187
288567490	chr6	56496016	56496169	56496046	56496141	DST	NM_001723	1	24	16	-	56496009	56496187
287394696	chr6	56496744	56496893	56496768	56496865	DST	NM_015548	2	84	15	-	56496681	56496838
287394696	chr6	56496744	56496893	56496768	56496865	DST	NM_001723	1	24	15	-	56496681	56496838
287533358	chr6	56498969	56499115	56498997	56499089	DST	NM_015548	2	84	13	-	56498930	56499056
287533358	chr6	56498969	56499115	56498997	56499089	DST	NM_001723	1	24	13	-	56498930	56499056
288038277	chr6	56500275	56500434	56500303	56500410	DST	NM_015548	2	84	10	-	56500387	56500512
288038277	chr6	56500275	56500434	56500303	56500410	DST	NM_001723	1	24	10	-	56500387	56500512
284843518	chr6	56503963	56504104	56503990	56504078	DST	NM_015548	2	84	8	-	56504057	56504161
284843518	chr6	56503963	56504104	56503990	56504078	DST	NM_001723	1	24	8	-	56504057	56504161
287933693	chr6	56504351	56504514	56504379	56504486	DST	NM_015548	2	84	7	-	56504248	56504409
287933693	chr6	56504351	56504514	56504379	56504486	DST	NM_001723	1	24	7	-	56504248	56504409
287183806	chr6	56504805	56504977	56504830	56504949	DST	NM_015548	2	84	4	-	56504941	56505403
287183806	chr6	56504805	56504977	56504830	56504949	DST	NM_001723	1	24	4	-	56504941	56505403
287183806	chr6	56504805	56504977	56504830	56504949	DST	NM_015548	2	84	5	-	56504727	56504855
287183806	chr6	56504805	56504977	56504830	56504949	DST	NM_001723	1	24	5	-	56504727	56504855
287016724	chr6	56505112	56505284	56505137	56505259	DST	NM_015548	2	84	4	-	56504941	56505403
287016724	chr6	56505112	56505284	56505137	56505259	DST	NM_001723	1	24	4	-	56504941	56505403
288650843	chr6	56507099	56507258	56507126	56507232	DST	NM_015548	2	84	2	-	56507208	56507301
288650843	chr6	56507099	56507258	56507126	56507232	DST	NM_001723	1	24	2	-	56507208	56507301
284117222	chr6	69348468	69348628	69348494	69348599	BAI3	NM_001704	1	32	3	+	69348553	69349324
284142331	chr6	69348819	69348983	69348847	69348955	BAI3	NM_001704	1	32	3	+	69348553	69349324
284140973	chr6	69349199	69349347	69349227	69349325	BAI3	NM_001704	1	32	3	+	69348553	69349324
283314925	chr6	69646433	69646602	69646453	69646580	BAI3	NM_001704	1	32	5	+	69646411	69646572
281319925	chr6	69665950	69666112	69665971	69666089	BAI3	NM_001704	1	32	7	+	69665916	69666080
283588639	chr6	69685099	69685257	69685124	69685233	BAI3	NM_001704	1	32	10	+	69685126	69685232
281766210	chr6	69728292	69728465	69728317	69728437	BAI3	NM_001704	1	32	13	+	69728283	69728391
283864949	chr6	69759177	69759343	69759200	69759316	BAI3	NM_001704	1	32	15	+	69759163	69759238
283662385	chr6	69785886	69786014	69785915	69785991	BAI3	NM_001704	1	32	17	+	69785887	69785930
283714100	chr6	69944929	69945067	69944950	69945039	BAI3	NM_001704	1	32	19	+	69944924	69945027
282242303	chr6	70034680	70034831	70034707	70034807	BAI3	NM_001704	1	32	21	+	70034764	70034914
282681634	chr6	70040414	70040540	70040441	70040510	BAI3	NM_001704	1	32	23	+	70040398	70040464
281788759	chr6	70049179	70049353	70049205	70049325	BAI3	NM_001704	1	32	26	+	70049225	70049396
283144502	chr6	70065590	70065742	70065617	70065714	BAI3	NM_001704	1	32	28	+	70065713	70065752
284270557	chr6	70070990	70071132	70071013	70071104	BAI3	NM_001704	1	32	29	+	70070761	70071404
282164552	chr6	70071357	70071509	70071385	70071487	BAI3	NM_001704	1	32	29	+	70070761	70071404
283485642	chr6	70098566	70098733	70098592	70098712	BAI3	NM_001704	1	32	32	+	70098595	70099403

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294843971	chr6	91228072	91228246	91228104	91228219	MAP3K7	NM_145331	2	17	16	-	91228166	91228281
294843971	chr6	91228072	91228246	91228104	91228219	MAP3K7	NM_003188	1	16	15	-	91228166	91228281
294295348	chr6	91233285	91233420	91233313	91233398	MAP3K7	NM_145333	4	15	13	-	91233397	91233502
294295348	chr6	91233285	91233420	91233313	91233398	MAP3K7	NM_145332	3	16	14	-	91233397	91233502
294295348	chr6	91233285	91233420	91233313	91233398	MAP3K7	NM_145331	2	17	14	-	91233397	91233502
294295348	chr6	91233285	91233420	91233313	91233398	MAP3K7	NM_003188	1	16	13	-	91233397	91233502
294816247	chr6	91256915	91257069	91256938	91257049	MAP3K7	NM_145333	4	15	11	-	91256977	91257106
294816247	chr6	91256915	91257069	91256938	91257049	MAP3K7	NM_145332	3	16	11	-	91256977	91257106
294816247	chr6	91256915	91257069	91256938	91257049	MAP3K7	NM_145331	2	17	11	-	91256977	91257106
294816247	chr6	91256915	91257069	91256938	91257049	MAP3K7	NM_003188	1	16	11	-	91256977	91257106
294257169	chr6	91261740	91261864	91261764	91261843	MAP3K7	NM_145333	4	15	8	-	91261768	91261898
294257169	chr6	91261740	91261864	91261764	91261843	MAP3K7	NM_145332	3	16	8	-	91261768	91261898
294257169	chr6	91261740	91261864	91261764	91261843	MAP3K7	NM_145331	2	17	8	-	91261768	91261898
294257169	chr6	91261740	91261864	91261764	91261843	MAP3K7	NM_003188	1	16	8	-	91261768	91261898
294787101	chr6	91266159	91266286	91266185	91266262	MAP3K7	NM_145333	4	15	6	-	91266219	91266343
294787101	chr6	91266159	91266286	91266185	91266262	MAP3K7	NM_145332	3	16	6	-	91266219	91266343
294787101	chr6	91266159	91266286	91266185	91266262	MAP3K7	NM_145331	2	17	6	-	91266219	91266343
294787101	chr6	91266159	91266286	91266185	91266262	MAP3K7	NM_003188	1	16	6	-	91266219	91266343
294529830	chr6	91271230	91271381	91271251	91271356	MAP3K7	NM_145333	4	15	4	-	91271341	91271386
294529830	chr6	91271230	91271381	91271251	91271356	MAP3K7	NM_145332	3	16	4	-	91271341	91271386
294529830	chr6	91271230	91271381	91271251	91271356	MAP3K7	NM_145331	2	17	4	-	91271341	91271386
294529830	chr6	91271230	91271381	91271251	91271356	MAP3K7	NM_003188	1	16	4	-	91271341	91271386
293837270	chr6	91281469	91281598	91281495	91281571	MAP3K7	NM_145333	4	15	2	-	91281416	91281526
293837270	chr6	91281469	91281598	91281495	91281571	MAP3K7	NM_145332	3	16	2	-	91281416	91281526
293837270	chr6	91281469	91281598	91281495	91281571	MAP3K7	NM_145331	2	17	2	-	91281416	91281526
293837270	chr6	91281469	91281598	91281495	91281571	MAP3K7	NM_003188	1	16	2	-	91281416	91281526
272286291	chr6	93953155	93953323	93953179	93953294	EPHA7	NM_004440	1	17	17	-	93949740	93953258
271557778	chr6	93956609	93956782	93956635	93956756	EPHA7	NM_004440	1	17	15	-	93956510	93956703
269616513	chr6	93965438	93965601	93965464	93965577	EPHA7	NM_004440	1	17	13	-	93965546	93965755
270811721	chr6	93967163	93967289	93967191	93967268	EPHA7	NM_004440	1	17	12	-	93967180	93967241
270490301	chr6	93969057	93969230	93969080	93969202	EPHA7	NM_004440	1	17	10	-	93969072	93969197
270674236	chr6	93979165	93979313	93979191	93979287	EPHA7	NM_004440	1	17	7	-	93979195	93979378
270889606	chr6	94066376	94066544	94066401	94066518	EPHA7	NM_004440	1	17	5	-	94066435	94066770
271434621	chr6	94067910	94068039	94067936	94068015	EPHA7	NM_004440	1	17	4	-	94067974	94068129
270615043	chr6	94120351	94120479	94120372	94120453	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270573646	chr6	94120690	94120843	94120712	94120822	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270651937	chr6	94128897	94129049	94128918	94129022	EPHA7	NM_004440	1	17	1	-	94128963	94129300
273442304	chr6	106536180	106536352	106536203	106536324	PRDM1	NM_001198	1	7	2	+	106536076	106536324
272964489	chr6	106546820	106546994	106546840	106546969	PRDM1	NM_182907	2	5	1	+	106546737	106546969
272753550	chr6	106552611	106552781	106552634	106552756	PRDM1	NM_182907	2	5	3	+	106552700	106553808
272753550	chr6	106552611	106552781	106552634	106552756	PRDM1	NM_001198	1	7	5	+	106552700	106553808

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272820430	chr6	106553105	106553267	106553124	106553247	PRDM1	NM_182907	2	5	3	+	106552700	106553808
272820430	chr6	106553105	106553267	106553124	106553247	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273927941	chr6	106553511	106553681	106553533	106553661	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273927941	chr6	106553511	106553681	106553533	106553661	PRDM1	NM_001198	1	7	5	+	106552700	106553808
272770967	chr6	106554264	106554406	106554285	106554379	PRDM1	NM_182907	2	5	4	+	106554246	106554374
272770967	chr6	106554264	106554406	106554285	106554379	PRDM1	NM_001198	1	7	6	+	106554246	106554374
273026586	chr6	106555040	106555206	106555064	106555183	PRDM1	NM_182907	2	5	5	+	106554786	106557814
273026586	chr6	106555040	106555206	106555064	106555183	PRDM1	NM_001198	1	7	7	+	106554786	106557814
228909210	chr6	108882980	108883117	108883002	108883099	FOXO3	NM_201559	2	4	2	+	108882289	108883032
228909210	chr6	108882980	108883117	108883002	108883099	FOXO3	NM_001455	1	3	1	+	108882069	108883032
227532890	chr6	108985171	108985345	108985194	108985328	FOXO3	NM_001455	1	3	2	+	108984658	108986092
227532890	chr6	108985171	108985345	108985194	108985328	FOXO3	NM_201559	2	4	3	+	108984658	108986092
242587898	chr6	117609629	117609777	117609654	117609751	ROS1	NM_002944	1	43	43	-	117609530	117609965
241734255	chr6	117622140	117622301	117622168	117622277	ROS1	NM_002944	1	43	42	-	117622137	117622300
262582706	chr6	117631207	117631368	117631232	117631341	ROS1	NM_002944	1	43	40	-	117631244	117631444
263877317	chr6	117638204	117638354	117638227	117638332	ROS1	NM_002944	1	43	38	-	117638306	117638435
239821359	chr6	117641125	117641263	117641147	117641235	ROS1	NM_002944	1	43	36	-	117641031	117641193
237794627	chr6	117645490	117645656	117645514	117645633	ROS1	NM_002944	1	43	34	-	117645495	117645578
240780532	chr6	117650468	117650618	117650494	117650597	ROS1	NM_002944	1	43	32	-	117650492	117650609
240773779	chr6	117658452	117658588	117658471	117658558	ROS1	NM_002944	1	43	31	-	117658335	117658503
240344039	chr6	117662582	117662718	117662606	117662692	ROS1	NM_002944	1	43	29	-	117662563	117662795
242661804	chr6	117665286	117665426	117665307	117665399	ROS1	NM_002944	1	43	27	-	117665223	117665425
238464566	chr6	117677664	117677834	117677687	117677812	ROS1	NM_002944	1	43	25	-	117677792	117678078
239464738	chr6	117679016	117679173	117679044	117679145	ROS1	NM_002944	1	43	24	-	117678967	117679172
242355829	chr6	117681090	117681254	117681118	117681227	ROS1	NM_002944	1	43	23	-	117680972	117681174
262251545	chr6	117683903	117684053	117683931	117684028	ROS1	NM_002944	1	43	21	-	117683766	117684028
240984644	chr6	117686733	117686882	117686760	117686854	ROS1	NM_002944	1	43	19	-	117686744	117686904
262601651	chr6	117687362	117687496	117687386	117687471	ROS1	NM_002944	1	43	18	-	117687239	117687453
238470625	chr6	117704501	117704626	117704527	117704602	ROS1	NM_002944	1	43	16	-	117704480	117704671
262168487	chr6	117708017	117708168	117708043	117708141	ROS1	NM_002944	1	43	14	-	117708052	117708162
242253254	chr6	117710380	117710553	117710403	117710530	ROS1	NM_002944	1	43	12	-	117710513	117711009
260464926	chr6	117710862	117711035	117710887	117711010	ROS1	NM_002944	1	43	12	-	117710513	117711009
260545990	chr6	117715316	117715490	117715340	117715462	ROS1	NM_002944	1	43	10	-	117715325	117715509
237927515	chr6	117718156	117718308	117718183	117718280	ROS1	NM_002944	1	43	7	-	117718078	117718279
239110577	chr6	117725501	117725649	117725526	117725629	ROS1	NM_002944	1	43	5	-	117725443	117725591
241821278	chr6	117746572	117746745	117746593	117746717	ROS1	NM_002944	1	43	1	-	117746697	117747018
293713309	chr6	134491919	134492091	134491942	134492063	SGK1	NM_001143676	1	14	13	-	134491964	134492053
293713309	chr6	134491919	134492091	134491942	134492063	SGK1	NM_001143677	2	12	11	-	134491964	134492053
293713309	chr6	134491919	134492091	134491942	134492063	SGK1	NM_005627	4	12	11	-	134491964	134492053
293713309	chr6	134491919	134492091	134491942	134492063	SGK1	NM_001143678	3	12	11	-	134491964	134492053
294369853	chr6	134493264	134493438	134493290	134493410	SGK1	NM_001143676	1	14	10	-	134493331	134493454

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294369853	chr6	134493264	134493438	134493290	134493410	SGK1	NM_001143677	2	12	8	-	134493331	134493454
294369853	chr6	134493264	134493438	134493290	134493410	SGK1	NM_005627	4	12	8	-	134493331	134493454
294369853	chr6	134493264	134493438	134493290	134493410	SGK1	NM_001143678	3	12	8	-	134493331	134493454
293976103	chr6	134494162	134494326	134494190	134494300	SGK1	NM_001143676	1	14	8	-	134494161	134494292
293976103	chr6	134494162	134494326	134494190	134494300	SGK1	NM_001143677	2	12	6	-	134494161	134494292
293976103	chr6	134494162	134494326	134494190	134494300	SGK1	NM_005627	4	12	6	-	134494161	134494292
293976103	chr6	134494162	134494326	134494190	134494300	SGK1	NM_001143678	3	12	6	-	134494161	134494292
293710649	chr6	134495092	134495263	134495115	134495239	SGK1	NM_001143676	1	14	5	-	134495143	134495218
293710649	chr6	134495092	134495263	134495115	134495239	SGK1	NM_001143677	2	12	3	-	134495143	134495218
293710649	chr6	134495092	134495263	134495115	134495239	SGK1	NM_005627	4	12	3	-	134495143	134495218
293710649	chr6	134495092	134495263	134495115	134495239	SGK1	NM_001143678	3	12	3	-	134495143	134495218
294759137	chr6	134498755	134498926	134498780	134498904	SGK1	NM_001143677	2	12	1	-	134498801	134499010
294771437	chr6	134582987	134583161	134583014	134583140	SGK1	NM_001143676	1	14	2	-	134583071	134583286
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001130173	2	16	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001130172	1	15	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001161657	4	14	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001161656	3	16	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_005375	8	15	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001161658	5	16	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001161660	7	14	2	+	135507041	135507158
236113776	chr6	135507000	135507130	135507022	135507109	MYB	NM_001161659	6	14	2	+	135507041	135507158
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001130173	2	16	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001130172	1	15	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001161657	4	14	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001161656	3	16	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_005375	8	15	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001161658	5	16	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001161660	7	14	4	+	135510929	135511021
239633077	chr6	135510829	135510993	135510857	135510970	MYB	NM_001161659	6	14	4	+	135510929	135511021
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001130173	2	16	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001130172	1	15	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001161657	4	14	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001161656	3	16	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_005375	8	15	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001161658	5	16	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001161660	7	14	5	+	135511265	135511485
239043292	chr6	135511356	135511530	135511379	135511507	MYB	NM_001161659	6	14	5	+	135511265	135511485
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001130173	2	16	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001130172	1	15	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001161657	4	14	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001161656	3	16	7	+	135514976	135515056

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_005375	8	15	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001161658	5	16	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001161660	7	14	7	+	135514976	135515056
239364548	chr6	135514920	135515092	135514942	135515068	MYB	NM_001161659	6	14	7	+	135514976	135515056
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001130173	2	16	9	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001130172	1	15	9	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001161656	3	16	9	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_005375	8	15	9	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001161660	7	14	8	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001161659	6	14	9	+	135516886	135517140
237146843	chr6	135516952	135517124	135516973	135517096	MYB	NM_001161658	5	16	9	+	135516886	135517092
239301823	chr6	135518319	135518493	135518343	135518468	MYB	NM_001130173	2	16	10	+	135518099	135518461
239301823	chr6	135518319	135518493	135518343	135518468	MYB	NM_001161656	3	16	10	+	135518099	135518461
239301823	chr6	135518319	135518493	135518343	135518468	MYB	NM_001161658	5	16	10	+	135518099	135518461
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001130173	2	16	12	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001130172	1	15	11	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001161657	4	14	10	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001161656	3	16	12	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_005375	8	15	11	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001161658	5	16	12	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001161660	7	14	10	+	135521223	135521337
236637797	chr6	135521242	135521402	135521270	135521373	MYB	NM_001161659	6	14	11	+	135521223	135521337
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001130173	2	16	15	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001130172	1	15	14	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001161657	4	14	13	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001161656	3	16	15	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_005375	8	15	14	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001161658	5	16	15	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001161660	7	14	13	+	135524355	135524462
236527079	chr6	135524283	135524447	135524310	135524420	MYB	NM_001161659	6	14	13	+	135524355	135524462
238849816	chr6	138192278	138192448	138192301	138192424	TNFAIP3	NM_006290	1	9	2	+	138192350	138192659
264670224	chr6	138196062	138196216	138196081	138196188	TNFAIP3	NM_006290	1	9	3	+	138195982	138196172
264859916	chr6	138197216	138197359	138197238	138197332	TNFAIP3	NM_006290	1	9	5	+	138197133	138197303
263758827	chr6	138199551	138199711	138199575	138199690	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
263789696	chr6	138199925	138200080	138199945	138200058	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
263800053	chr6	138200353	138200524	138200372	138200504	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
240201794	chr6	138202274	138202433	138202294	138202411	TNFAIP3	NM_006290	1	9	9	+	138202172	138204449
272094659	chr6	152129128	152129267	152129146	152129250	ESR1	NM_000125	1	8	1	+	152128814	152129499
272094659	chr6	152129128	152129267	152129146	152129250	ESR1	NM_001122740	2	9	2	+	152128978	152129499
272094659	chr6	152129128	152129267	152129146	152129250	ESR1	NM_001122742	4	10	3	+	152128978	152129499
272094659	chr6	152129128	152129267	152129146	152129250	ESR1	NM_001122741	3	9	2	+	152128978	152129499

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272570275	chr6	152163638	152163804	152163665	152163781	ESR1	NM_000125	1	8	2	+	152163732	152163922
272570275	chr6	152163638	152163804	152163665	152163781	ESR1	NM_001122740	2	9	3	+	152163732	152163922
272570275	chr6	152163638	152163804	152163665	152163781	ESR1	NM_001122742	4	10	4	+	152163732	152163922
272570275	chr6	152163638	152163804	152163665	152163781	ESR1	NM_001122741	3	9	3	+	152163732	152163922
270181083	chr6	152201792	152201928	152201817	152201907	ESR1	NM_000125	1	8	3	+	152201790	152201906
270181083	chr6	152201792	152201928	152201817	152201907	ESR1	NM_001122740	2	9	4	+	152201790	152201906
270181083	chr6	152201792	152201928	152201817	152201907	ESR1	NM_001122742	4	10	5	+	152201790	152201906
270181083	chr6	152201792	152201928	152201817	152201907	ESR1	NM_001122741	3	9	4	+	152201790	152201906
269931208	chr6	152265513	152265663	152265535	152265643	ESR1	NM_000125	1	8	4	+	152265308	152265643
269931208	chr6	152265513	152265663	152265535	152265643	ESR1	NM_001122740	2	9	5	+	152265308	152265643
269931208	chr6	152265513	152265663	152265535	152265643	ESR1	NM_001122742	4	10	6	+	152265308	152265643
269931208	chr6	152265513	152265663	152265535	152265643	ESR1	NM_001122741	3	9	5	+	152265308	152265643
272240847	chr6	152382134	152382296	152382157	152382269	ESR1	NM_000125	1	8	6	+	152382126	152382259
272240847	chr6	152382134	152382296	152382157	152382269	ESR1	NM_001122740	2	9	7	+	152382126	152382259
272240847	chr6	152382134	152382296	152382157	152382269	ESR1	NM_001122742	4	10	8	+	152382126	152382259
272240847	chr6	152382134	152382296	152382157	152382269	ESR1	NM_001122741	3	9	7	+	152382126	152382259
272090476	chr6	152419920	152420077	152419942	152420056	ESR1	NM_000125	1	8	8	+	152419867	152424408
272090476	chr6	152419920	152420077	152419942	152420056	ESR1	NM_001122740	2	9	9	+	152419867	152424408
272090476	chr6	152419920	152420077	152419942	152420056	ESR1	NM_001122742	4	10	10	+	152419867	152424408
272090476	chr6	152419920	152420077	152419942	152420056	ESR1	NM_001122741	3	9	9	+	152419867	152424408
305022289	chr6	152443774	152443902	152443795	152443881	SYNE1	NM_033071	1	146	146	-	152442819	152443811
305022289	chr6	152443774	152443902	152443795	152443881	SYNE1	NM_182961	2	146	146	-	152442819	152443811
302865849	chr6	152454411	152454562	152454434	152454540	SYNE1	NM_033071	1	146	143	-	152454411	152454623
302865849	chr6	152454411	152454562	152454434	152454540	SYNE1	NM_182961	2	146	143	-	152454411	152454623
302294946	chr6	152457728	152457892	152457748	152457872	SYNE1	NM_033071	1	146	141	-	152457753	152457953
302294946	chr6	152457728	152457892	152457748	152457872	SYNE1	NM_182961	2	146	141	-	152457753	152457953
299304626	chr6	152461089	152461249	152461112	152461226	SYNE1	NM_033071	1	146	140	-	152461085	152461296
299304626	chr6	152461089	152461249	152461112	152461226	SYNE1	NM_182961	2	146	140	-	152461085	152461296
300141127	chr6	152464793	152464934	152464817	152464907	SYNE1	NM_033071	1	146	138	-	152464758	152464900
300141127	chr6	152464793	152464934	152464817	152464907	SYNE1	NM_182961	2	146	138	-	152464758	152464900
302564151	chr6	152469383	152469542	152469404	152469522	SYNE1	NM_033071	1	146	136	-	152469180	152469513
302564151	chr6	152469383	152469542	152469404	152469522	SYNE1	NM_182961	2	146	137	-	152469180	152469513
300986139	chr6	152472731	152472903	152472758	152472880	SYNE1	NM_033071	1	146	134	-	152472688	152472825
300986139	chr6	152472731	152472903	152472758	152472880	SYNE1	NM_182961	2	146	135	-	152472688	152472825
302524649	chr6	152476082	152476229	152476105	152476201	SYNE1	NM_033071	1	146	132	-	152476027	152476177
302524649	chr6	152476082	152476229	152476105	152476201	SYNE1	NM_182961	2	146	133	-	152476027	152476177
302553248	chr6	152485326	152485500	152485351	152485480	SYNE1	NM_033071	1	146	130	-	152485298	152485460
302553248	chr6	152485326	152485500	152485351	152485480	SYNE1	NM_182961	2	146	131	-	152485298	152485460
299720388	chr6	152501310	152501481	152501337	152501453	SYNE1	NM_033071	1	146	128	-	152501271	152501429
299720388	chr6	152501310	152501481	152501337	152501453	SYNE1	NM_182961	2	146	129	-	152501271	152501429
302377295	chr6	152523003	152523139	152523026	152523111	SYNE1	NM_033071	1	146	126	-	152522959	152523084

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
302377295	chr6	152523003	152523139	152523026	152523111	SYNE1	NM_182961	2	146	127	-	152522959	152523084
301435956	chr6	152529056	152529224	152529076	152529202	SYNE1	NM_033071	1	146	124	-	152529107	152529341
301435956	chr6	152529056	152529224	152529076	152529202	SYNE1	NM_182961	2	146	125	-	152529107	152529341
301778378	chr6	152532624	152532796	152532648	152532768	SYNE1	NM_033071	1	146	123	-	152532629	152532723
301778378	chr6	152532624	152532796	152532648	152532768	SYNE1	NM_182961	2	146	124	-	152532629	152532723
303077854	chr6	152536129	152536274	152536156	152536250	SYNE1	NM_033071	1	146	121	-	152536041	152536195
303077854	chr6	152536129	152536274	152536156	152536250	SYNE1	NM_182961	2	146	122	-	152536041	152536195
303178379	chr6	152540175	152540347	152540196	152540321	SYNE1	NM_033071	1	146	119	-	152540138	152540320
303178379	chr6	152540175	152540347	152540196	152540321	SYNE1	NM_182961	2	146	120	-	152540138	152540320
299937233	chr6	152542606	152542735	152542634	152542707	SYNE1	NM_033071	1	146	117	-	152542561	152542694
299937233	chr6	152542606	152542735	152542634	152542707	SYNE1	NM_182961	2	146	118	-	152542561	152542694
305363493	chr6	152546830	152546954	152546853	152546928	SYNE1	NM_033071	1	146	115	-	152546856	152547011
305363493	chr6	152546830	152546954	152546853	152546928	SYNE1	NM_182961	2	146	116	-	152546856	152547011
303975722	chr6	152551803	152551937	152551828	152551906	SYNE1	NM_033071	1	146	114	-	152551682	152551837
303975722	chr6	152551803	152551937	152551828	152551906	SYNE1	NM_182961	2	146	115	-	152551682	152551837
300832859	chr6	152554874	152555042	152554899	152555016	SYNE1	NM_033071	1	146	111	-	152554916	152555098
300832859	chr6	152554874	152555042	152554899	152555016	SYNE1	NM_182961	2	146	112	-	152554916	152555098
299705079	chr6	152557172	152557314	152557194	152557285	SYNE1	NM_033071	1	146	109	-	152557242	152557438
299705079	chr6	152557172	152557314	152557194	152557285	SYNE1	NM_182961	2	146	110	-	152557242	152557438
302107421	chr6	152558054	152558209	152558074	152558186	SYNE1	NM_033071	1	146	108	-	152557952	152558083
302107421	chr6	152558054	152558209	152558074	152558186	SYNE1	NM_182961	2	146	109	-	152557952	152558083
302592688	chr6	152563443	152563600	152563467	152563575	SYNE1	NM_033071	1	146	106	-	152563375	152563575
302592688	chr6	152563443	152563600	152563467	152563575	SYNE1	NM_182961	2	146	107	-	152563375	152563575
300419782	chr6	152570301	152570425	152570321	152570403	SYNE1	NM_033071	1	146	104	-	152570296	152570397
300419782	chr6	152570301	152570425	152570321	152570403	SYNE1	NM_182961	2	146	105	-	152570296	152570397
305338851	chr6	152576663	152576831	152576690	152576810	SYNE1	NM_033071	1	146	102	-	152576726	152576881
305338851	chr6	152576663	152576831	152576690	152576810	SYNE1	NM_182961	2	146	103	-	152576726	152576881
305196559	chr6	152583090	152583219	152583115	152583191	SYNE1	NM_033071	1	146	100	-	152583167	152583323
305196559	chr6	152583090	152583219	152583115	152583191	SYNE1	NM_182961	2	146	101	-	152583167	152583323
299382653	chr6	152590262	152590436	152590288	152590414	SYNE1	NM_033071	1	146	98	-	152590290	152590421
299382653	chr6	152590262	152590436	152590288	152590414	SYNE1	NM_182961	2	146	99	-	152590290	152590421
305432639	chr6	152599340	152599483	152599361	152599461	SYNE1	NM_033071	1	146	97	-	152599224	152599415
305432639	chr6	152599340	152599483	152599361	152599461	SYNE1	NM_182961	2	146	98	-	152599224	152599415
301726971	chr6	152605176	152605346	152605195	152605318	SYNE1	NM_033071	1	146	95	-	152605113	152605307
301726971	chr6	152605176	152605346	152605195	152605318	SYNE1	NM_182961	2	146	96	-	152605113	152605307
299979246	chr6	152615153	152615287	152615173	152615263	SYNE1	NM_033071	1	146	93	-	152615095	152615262
299979246	chr6	152615153	152615287	152615173	152615263	SYNE1	NM_182961	2	146	94	-	152615095	152615262
300108595	chr6	152622985	152623159	152623005	152623133	SYNE1	NM_033071	1	146	91	-	152623004	152623198
300108595	chr6	152622985	152623159	152623005	152623133	SYNE1	NM_182961	2	146	92	-	152623004	152623198
302624184	chr6	152630914	152631081	152630937	152631062	SYNE1	NM_182961	2	146	90	-	152630970	152631152
302624184	chr6	152630914	152631081	152630937	152631062	SYNE1	NM_033071	1	146	89	-	152630966	152631152

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305959282	chr6	152631705	152631878	152631733	152631853	SYNE1	NM_033071	1	146	87	-	152631823	152632008
305959282	chr6	152631705	152631878	152631733	152631853	SYNE1	NM_182961	2	146	88	-	152631823	152632008
304575889	chr6	152638009	152638176	152638030	152638148	SYNE1	NM_033071	1	146	86	-	152637984	152638121
304575889	chr6	152638009	152638176	152638030	152638148	SYNE1	NM_182961	2	146	87	-	152637984	152638121
300379443	chr6	152640031	152640183	152640058	152640155	SYNE1	NM_033071	1	146	84	-	152639998	152640150
300379443	chr6	152640031	152640183	152640058	152640155	SYNE1	NM_182961	2	146	85	-	152639998	152640150
300573111	chr6	152642912	152643065	152642936	152643037	SYNE1	NM_033071	1	146	82	-	152642856	152643021
300573111	chr6	152642912	152643065	152642936	152643037	SYNE1	NM_182961	2	146	83	-	152642856	152643021
304735387	chr6	152646197	152646368	152646218	152646346	SYNE1	NM_033071	1	146	80	-	152646219	152646437
304735387	chr6	152646197	152646368	152646218	152646346	SYNE1	NM_182961	2	146	81	-	152646219	152646437
303820640	chr6	152647322	152647487	152647350	152647466	SYNE1	NM_033071	1	146	78	-	152647431	152647768
303820640	chr6	152647322	152647487	152647350	152647466	SYNE1	NM_182961	2	146	79	-	152647431	152647768
305390854	chr6	152650808	152650954	152650836	152650933	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305390854	chr6	152650808	152650954	152650836	152650933	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305480200	chr6	152651244	152651392	152651265	152651369	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305480200	chr6	152651244	152651392	152651265	152651369	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305450852	chr6	152651712	152651838	152651733	152651809	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305450852	chr6	152651712	152651838	152651733	152651809	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305424981	chr6	152652089	152652242	152652114	152652220	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305424981	chr6	152652089	152652242	152652114	152652220	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305447579	chr6	152652533	152652704	152652556	152652684	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305447579	chr6	152652533	152652704	152652556	152652684	SYNE1	NM_182961	2	146	78	-	152650865	152653025
299861569	chr6	152655111	152655283	152655134	152655263	SYNE1	NM_033071	1	146	76	-	152655143	152655408
299861569	chr6	152655111	152655283	152655134	152655263	SYNE1	NM_182961	2	146	77	-	152655143	152655408
304416803	chr6	152657958	152658108	152657983	152658084	SYNE1	NM_033071	1	146	75	-	152657976	152658152
304416803	chr6	152657958	152658108	152657983	152658084	SYNE1	NM_182961	2	146	76	-	152657976	152658152
305185762	chr6	152665199	152665370	152665227	152665345	SYNE1	NM_033071	1	146	73	-	152665216	152665362
305185762	chr6	152665199	152665370	152665227	152665345	SYNE1	NM_182961	2	146	74	-	152665216	152665362
305169528	chr6	152671257	152671431	152671278	152671407	SYNE1	NM_182961	2	146	72	-	152671303	152671470
301047275	chr6	152673127	152673283	152673152	152673255	SYNE1	NM_033071	1	146	70	-	152673162	152673488
301047275	chr6	152673127	152673283	152673152	152673255	SYNE1	NM_182961	2	146	70	-	152673162	152673488
305788085	chr6	152674449	152674608	152674476	152674580	SYNE1	NM_033071	1	146	69	-	152674398	152674568
305788085	chr6	152674449	152674608	152674476	152674580	SYNE1	NM_182961	2	146	69	-	152674398	152674568
302441696	chr6	152675872	152676044	152675898	152676022	SYNE1	NM_033071	1	146	67	-	152675860	152676111
302441696	chr6	152675872	152676044	152675898	152676022	SYNE1	NM_182961	2	146	67	-	152675794	152676111
302190707	chr6	152679579	152679745	152679601	152679717	SYNE1	NM_033071	1	146	66	-	152679508	152679672
302190707	chr6	152679579	152679745	152679601	152679717	SYNE1	NM_182961	2	146	66	-	152679508	152679672
302836932	chr6	152683344	152683510	152683365	152683482	SYNE1	NM_033071	1	146	64	-	152683305	152683458
302836932	chr6	152683344	152683510	152683365	152683482	SYNE1	NM_182961	2	146	64	-	152683305	152683458
303427728	chr6	152688392	152688547	152688412	152688521	SYNE1	NM_033071	1	146	62	-	152688353	152688517
303427728	chr6	152688392	152688547	152688412	152688521	SYNE1	NM_182961	2	146	62	-	152688353	152688517

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300222427	chr6	152690625	152690775	152690646	152690749	SYNE1	NM_033071	1	146	60	-	152690606	152690749
300222427	chr6	152690625	152690775	152690646	152690749	SYNE1	NM_182961	2	146	60	-	152690606	152690749
300292186	chr6	152697557	152697721	152697583	152697693	SYNE1	NM_033071	1	146	58	-	152697516	152697693
300292186	chr6	152697557	152697721	152697583	152697693	SYNE1	NM_182961	2	146	58	-	152697516	152697693
304651168	chr6	152702104	152702243	152702131	152702221	SYNE1	NM_033071	1	146	56	-	152702141	152702497
304651168	chr6	152702104	152702243	152702131	152702221	SYNE1	NM_182961	2	146	56	-	152702141	152702497
302790818	chr6	152706750	152706877	152706778	152706856	SYNE1	NM_033071	1	146	55	-	152706809	152706973
302790818	chr6	152706750	152706877	152706778	152706856	SYNE1	NM_182961	2	146	55	-	152706809	152706973
304614594	chr6	152708325	152708495	152708346	152708468	SYNE1	NM_033071	1	146	54	-	152708207	152708516
304614594	chr6	152708325	152708495	152708346	152708468	SYNE1	NM_182961	2	146	54	-	152708207	152708516
300477595	chr6	152712364	152712519	152712390	152712498	SYNE1	NM_033071	1	146	52	-	152712412	152712703
300477595	chr6	152712364	152712519	152712390	152712498	SYNE1	NM_182961	2	146	52	-	152712412	152712703
304091090	chr6	152716608	152716761	152716633	152716733	SYNE1	NM_033071	1	146	51	-	152716651	152716806
304091090	chr6	152716608	152716761	152716633	152716733	SYNE1	NM_182961	2	146	51	-	152716651	152716806
305278422	chr6	152718037	152718177	152718065	152718149	SYNE1	NM_033071	1	146	50	-	152717910	152718115
305278422	chr6	152718037	152718177	152718065	152718149	SYNE1	NM_182961	2	146	50	-	152717910	152718115
303402572	chr6	152720823	152720949	152720850	152720921	SYNE1	NM_033071	1	146	48	-	152720751	152720958
303402572	chr6	152720823	152720949	152720850	152720921	SYNE1	NM_182961	2	146	48	-	152720751	152720958
300698363	chr6	152725348	152725504	152725367	152725476	SYNE1	NM_033071	1	146	46	-	152725348	152725449
300698363	chr6	152725348	152725504	152725367	152725476	SYNE1	NM_182961	2	146	46	-	152725348	152725449
304606183	chr6	152730187	152730353	152730214	152730324	SYNE1	NM_033071	1	146	44	-	152730203	152730361
304606183	chr6	152730187	152730353	152730214	152730324	SYNE1	NM_182961	2	146	44	-	152730203	152730361
305944841	chr6	152730785	152730917	152730813	152730896	SYNE1	NM_033071	1	146	43	-	152730694	152730844
305944841	chr6	152730785	152730917	152730813	152730896	SYNE1	NM_182961	2	146	43	-	152730694	152730844
305253150	chr6	152737494	152737652	152737514	152737629	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305253150	chr6	152737494	152737652	152737514	152737629	SYNE1	NM_182961	2	146	41	-	152737522	152738150
305309899	chr6	152737908	152738065	152737927	152738046	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305309899	chr6	152737908	152738065	152737927	152738046	SYNE1	NM_182961	2	146	41	-	152737522	152738150
301379015	chr6	152746388	152746562	152746415	152746537	SYNE1	NM_033071	1	146	39	-	152746516	152746682
301379015	chr6	152746388	152746562	152746415	152746537	SYNE1	NM_182961	2	146	39	-	152746516	152746682
303400275	chr6	152749246	152749420	152749270	152749398	SYNE1	NM_033071	1	146	37	-	152749340	152749527
303400275	chr6	152749246	152749420	152749270	152749398	SYNE1	NM_182961	2	146	37	-	152749340	152749527
304729426	chr6	152751645	152751773	152751670	152751747	SYNE1	NM_033071	1	146	35	-	152751617	152751844
304729426	chr6	152751645	152751773	152751670	152751747	SYNE1	NM_182961	2	146	35	-	152751617	152751844
304006583	chr6	152754998	152755157	152755022	152755129	SYNE1	NM_033071	1	146	34	-	152754930	152755080
304006583	chr6	152754998	152755157	152755022	152755129	SYNE1	NM_182961	2	146	34	-	152754930	152755080
303772478	chr6	152762322	152762494	152762349	152762469	SYNE1	NM_033071	1	146	32	-	152762265	152762405
303772478	chr6	152762322	152762494	152762349	152762469	SYNE1	NM_182961	2	146	32	-	152762265	152762405
302715945	chr6	152765559	152765715	152765584	152765687	SYNE1	NM_033071	1	146	30	-	152765546	152765713
302715945	chr6	152765559	152765715	152765584	152765687	SYNE1	NM_182961	2	146	30	-	152765546	152765713
305653145	chr6	152770721	152770878	152770749	152770845	SYNE1	NM_033071	1	146	28	-	152770668	152770776

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305653145	chr6	152770721	152770878	152770749	152770845	SYNE1	NM_182961	2	146	28	-	152770668	152770776
302308380	chr6	152772134	152772304	152772157	152772275	SYNE1	NM_033071	1	146	26	-	152772182	152772340
302308380	chr6	152772134	152772304	152772157	152772275	SYNE1	NM_182961	2	146	26	-	152772182	152772340
304573280	chr6	152776497	152776649	152776520	152776628	SYNE1	NM_033071	1	146	24	-	152776561	152776725
304573280	chr6	152776497	152776649	152776520	152776628	SYNE1	NM_182961	2	146	24	-	152776561	152776725
302795749	chr6	152779822	152779947	152779844	152779926	SYNE1	NM_033071	1	146	22	-	152779892	152780065
302795749	chr6	152779822	152779947	152779844	152779926	SYNE1	NM_182961	2	146	22	-	152779892	152780065
300475835	chr6	152782801	152782933	152782825	152782904	SYNE1	NM_033071	1	146	21	-	152782732	152782875
300475835	chr6	152782801	152782933	152782825	152782904	SYNE1	NM_182961	2	146	21	-	152782732	152782875
304018953	chr6	152784480	152784643	152784508	152784616	SYNE1	NM_033071	1	146	19	-	152784488	152784652
304018953	chr6	152784480	152784643	152784508	152784616	SYNE1	NM_182961	2	146	19	-	152784488	152784652
299688548	chr6	152786545	152786696	152786566	152786670	SYNE1	NM_033071	1	146	18	-	152786393	152786595
299688548	chr6	152786545	152786696	152786566	152786670	SYNE1	NM_182961	2	146	18	-	152786393	152786595
301575485	chr6	152793325	152793492	152793347	152793469	SYNE1	NM_033071	1	146	15	-	152793436	152793548
301575485	chr6	152793325	152793492	152793347	152793469	SYNE1	NM_182961	2	146	15	-	152793436	152793548
301003795	chr6	152805856	152806029	152805878	152806003	SYNE1	NM_033071	1	146	13	-	152805970	152806107
301003795	chr6	152805856	152806029	152805878	152806003	SYNE1	NM_182961	2	146	13	-	152805970	152806107
302331361	chr6	152823712	152823838	152823734	152823810	SYNE1	NM_033071	1	146	10	-	152823768	152823877
302331361	chr6	152823712	152823838	152823734	152823810	SYNE1	NM_182961	2	146	10	-	152823768	152823877
305442465	chr6	152826436	152826584	152826456	152826555	SYNE1	NM_033071	1	146	9	-	152826336	152826532
305442465	chr6	152826436	152826584	152826456	152826555	SYNE1	NM_182961	2	146	9	-	152826336	152826532
305528362	chr6	152832198	152832368	152832221	152832341	SYNE1	NM_033071	1	146	7	-	152832146	152832238
305528362	chr6	152832198	152832368	152832221	152832341	SYNE1	NM_182961	2	146	7	-	152832146	152832238
302837380	chr6	152841636	152841807	152841658	152841783	SYNE1	NM_033071	1	146	5	-	152841594	152841677
302837380	chr6	152841636	152841807	152841658	152841783	SYNE1	NM_182961	2	146	6	-	152841594	152841677
303421953	chr6	152949339	152949501	152949368	152949481	SYNE1	NM_033071	1	146	2	-	152949400	152949689
303421953	chr6	152949339	152949501	152949368	152949481	SYNE1	NM_182961	2	146	3	-	152949400	152949689
272690724	chr6	160431605	160431768	160431628	160431743	IGF2R	NM_000876	1	48	4	+	160431719	160431817
271086330	chr6	160448147	160448292	160448169	160448272	IGF2R	NM_000876	1	48	6	+	160448217	160448346
269774675	chr6	160453645	160453796	160453668	160453774	IGF2R	NM_000876	1	48	8	+	160453583	160453745
271331496	chr6	160461506	160461679	160461529	160461657	IGF2R	NM_000876	1	48	11	+	160461592	160461756
271167515	chr6	160465475	160465643	160465498	160465615	IGF2R	NM_000876	1	48	13	+	160465546	160465689
271507997	chr6	160467436	160467592	160467460	160467564	IGF2R	NM_000876	1	48	15	+	160467530	160467677
272227493	chr6	160468270	160468394	160468290	160468372	IGF2R	NM_000876	1	48	16	+	160468191	160468368
270127397	chr6	160469429	160469602	160469452	160469576	IGF2R	NM_000876	1	48	18	+	160469407	160469575
270169604	chr6	160477523	160477692	160477544	160477667	IGF2R	NM_000876	1	48	20	+	160477456	160477557
270189817	chr6	160481523	160481668	160481543	160481642	IGF2R	NM_000876	1	48	23	+	160481579	160481749
270303848	chr6	160482756	160482907	160482780	160482883	IGF2R	NM_000876	1	48	25	+	160482785	160482960
270832113	chr6	160484530	160484685	160484555	160484660	IGF2R	NM_000876	1	48	27	+	160484447	160484662
271079720	chr6	160485791	160485954	160485822	160485927	IGF2R	NM_000876	1	48	29	+	160485836	160485933
271173372	chr6	160490964	160491117	160490984	160491096	IGF2R	NM_000876	1	48	31	+	160490900	160491090

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269638396	chr6	160493838	160493996	160493858	160493972	IGF2R	NM_000876	1	48	33	+	160493797	160493916
271041190	chr6	160494760	160494904	160494788	160494884	IGF2R	NM_000876	1	48	35	+	160494789	160495007
271276077	chr6	160499162	160499315	160499182	160499292	IGF2R	NM_000876	1	48	37	+	160499233	160499394
270105628	chr6	160500752	160500896	160500773	160500868	IGF2R	NM_000876	1	48	38	+	160500612	160500819
272024217	chr6	160505097	160505271	160505120	160505249	IGF2R	NM_000876	1	48	40	+	160504982	160505216
271137283	chr6	160509087	160509236	160509109	160509213	IGF2R	NM_000876	1	48	42	+	160509065	160509179
269870694	chr6	160510983	160511157	160511007	160511136	IGF2R	NM_000876	1	48	44	+	160510948	160511135
272057281	chr6	160523555	160523720	160523575	160523703	IGF2R	NM_000876	1	48	46	+	160523551	160523703
272101653	chr6	160525932	160526089	160525952	160526069	IGF2R	NM_000876	1	48	48	+	160525706	160527583
238205322	chr6	166827200	166827370	166827224	166827349	RPS6KA2	NM_001006932	1	22	21	-	166827282	166827419
238205322	chr6	166827200	166827370	166827224	166827349	RPS6KA2	NM_021135	2	21	20	-	166827282	166827419
242121248	chr6	166833333	166833467	166833355	166833447	RPS6KA2	NM_001006932	1	22	19	-	166833370	166833446
242121248	chr6	166833333	166833467	166833355	166833447	RPS6KA2	NM_021135	2	21	18	-	166833370	166833446
241960906	chr6	166843822	166843992	166843845	166843973	RPS6KA2	NM_001006932	1	22	17	-	166843941	166844099
241960906	chr6	166843822	166843992	166843845	166843973	RPS6KA2	NM_021135	2	21	16	-	166843941	166844099
262585883	chr6	166862141	166862303	166862161	166862280	RPS6KA2	NM_001006932	1	22	15	-	166862212	166862337
262585883	chr6	166862141	166862303	166862161	166862280	RPS6KA2	NM_021135	2	21	14	-	166862212	166862337
264055689	chr6	166872907	166873068	166872928	166873042	RPS6KA2	NM_001006932	1	22	13	-	166872937	166873039
264055689	chr6	166872907	166873068	166872928	166873042	RPS6KA2	NM_021135	2	21	12	-	166872937	166873039
262215139	chr6	166904092	166904260	166904113	166904237	RPS6KA2	NM_001006932	1	22	10	-	166904159	166904229
262215139	chr6	166904092	166904260	166904113	166904237	RPS6KA2	NM_021135	2	21	9	-	166904159	166904229
240381311	chr6	166917920	166918054	166917944	166918031	RPS6KA2	NM_001006932	1	22	7	-	166917994	166918100
240381311	chr6	166917920	166918054	166917944	166918031	RPS6KA2	NM_021135	2	21	6	-	166917994	166918100
242751048	chr6	166944653	166944827	166944681	166944801	RPS6KA2	NM_001006932	1	22	4	-	166944720	166944801
242751048	chr6	166944653	166944827	166944681	166944801	RPS6KA2	NM_021135	2	21	3	-	166944720	166944801
260331512	chr6	167271629	167271788	167271649	167271760	RPS6KA2	NM_001006932	1	22	2	-	167271688	167271747
223178786	chr7	2949554	2949713	2949576	2949688	CARD11	NM_032415	1	25	24	-	2949684	2949799
223186865	chr7	2952858	2953013	2952878	2952995	CARD11	NM_032415	1	25	22	-	2952921	2953100
222691654	chr7	2956912	2957051	2956933	2957025	CARD11	NM_032415	1	25	20	-	2956924	2957019
224147413	chr7	2959178	2959332	2959198	2959311	CARD11	NM_032415	1	25	18	-	2959006	2959246
223246682	chr7	2962883	2963034	2962901	2963013	CARD11	NM_032415	1	25	16	-	2962766	2962967
222673281	chr7	2968197	2968359	2968215	2968336	CARD11	NM_032415	1	25	13	-	2968232	2968332
222340350	chr7	2974031	2974174	2974049	2974155	CARD11	NM_032415	1	25	10	-	2974087	2974263
225198494	chr7	2976796	2976957	2976822	2976937	CARD11	NM_032415	1	25	9	-	2976671	2976868
223888229	chr7	2979302	2979443	2979321	2979421	CARD11	NM_032415	1	25	6	-	2979383	2979562
222289513	chr7	2983904	2984045	2983924	2984023	CARD11	NM_032415	1	25	5	-	2983846	2984171
222351381	chr7	2985481	2985615	2985504	2985591	CARD11	NM_032415	1	25	4	-	2985453	2985590
240499849	chr7	6026398	6026547	6026423	6026520	PMS2	NM_000535	1	15	11	-	6026390	6027251
240499849	chr7	6026398	6026547	6026423	6026520	PMS2	NR_003085	2	15	11	-	6026390	6027251
240559019	chr7	6026684	6026858	6026708	6026839	PMS2	NM_000535	1	15	11	-	6026390	6027251
240559019	chr7	6026684	6026858	6026708	6026839	PMS2	NR_003085	2	15	11	-	6026390	6027251

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240529325	chr7	6027014	6027188	6027036	6027164	PMS2	NM_000535	1	15	11	-	6026390	6027251
240529325	chr7	6027014	6027188	6027036	6027164	PMS2	NR_003085	2	15	11	-	6026390	6027251
235070609	chr7	6035068	6035229	6035087	6035205	PMS2	NM_000535	1	15	8	-	6035165	6035264
235070609	chr7	6035068	6035229	6035087	6035205	PMS2	NR_003085	2	15	8	-	6035165	6035264
234994316	chr7	6038681	6038854	6038708	6038833	PMS2	NM_000535	1	15	6	-	6038739	6038906
234994316	chr7	6038681	6038854	6038708	6038833	PMS2	NR_003085	2	15	6	-	6038739	6038906
235544452	chr7	6042180	6042324	6042208	6042305	PMS2	NM_000535	1	15	5	-	6042084	6042267
235544452	chr7	6042180	6042324	6042208	6042305	PMS2	NR_003085	2	15	5	-	6042084	6042267
238434888	chr7	6048562	6048702	6048582	6048682	PMS2	NM_000535	1	15	1	-	6048628	6048737
238434888	chr7	6048562	6048702	6048582	6048682	PMS2	NR_003085	2	15	1	-	6048628	6048737
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163151	5	9	8	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163150	4	10	9	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163149	3	12	11	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163148	2	13	12	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163147	1	12	11	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_004956	7	14	13	-	13940363	13940464
229169527	chr7	13940393	13940565	13940413	13940537	ETV1	NM_001163152	6	9	8	-	13940363	13940464
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_001163151	5	9	5	-	13950864	13950932
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_001163150	4	10	6	-	13950864	13950932
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_001163149	3	12	8	-	13950864	13950932
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_001163148	2	13	9	-	13950864	13950932
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_004956	7	14	10	-	13950864	13950932
229754964	chr7	13950804	13950971	13950830	13950943	ETV1	NM_001163152	6	9	5	-	13950864	13950932
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_001163151	5	9	3	-	13975333	13975521
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_001163150	4	10	4	-	13975333	13975521
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_001163149	3	12	6	-	13975333	13975521
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_001163148	2	13	7	-	13975333	13975521
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_001163147	1	12	7	-	13975333	13975521
228494382	chr7	13975305	13975441	13975330	13975416	ETV1	NM_004956	7	14	8	-	13975333	13975521
233019725	chr7	14016936	14017098	14016961	14017074	ETV1	NM_001163150	4	10	2	-	14017052	14017105
233019725	chr7	14016936	14017098	14016961	14017074	ETV1	NM_001163147	1	12	5	-	14017052	14017105
233019725	chr7	14016936	14017098	14016961	14017074	ETV1	NM_004956	7	14	6	-	14017052	14017105
233019725	chr7	14016936	14017098	14016961	14017074	ETV1	NM_001163152	6	9	2	-	14017052	14017105
229556175	chr7	14026134	14026298	14026156	14026270	ETV1	NM_001163149	3	12	4	-	14026263	14026310
229556175	chr7	14026134	14026298	14026156	14026270	ETV1	NM_001163148	2	13	5	-	14026263	14026310
229556175	chr7	14026134	14026298	14026156	14026270	ETV1	NM_001163147	1	12	4	-	14026263	14026310
229556175	chr7	14026134	14026298	14026156	14026270	ETV1	NM_004956	7	14	5	-	14026263	14026310
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_006060	13	8	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220771	7	5	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220770	6	6	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220769	5	6	3	+	50367234	50367353

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220768	4	6	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220767	3	7	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220766	2	7	3	+	50367234	50367353
228316772	chr7	50367201	50367372	50367220	50367353	IKZF1	NM_001220765	1	7	3	+	50367234	50367353
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_006060	13	8	5	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220770	6	6	4	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220769	5	6	4	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220768	4	6	5	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220767	3	7	4	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220766	2	7	4	+	50450238	50450405
227828085	chr7	50450170	50450343	50450191	50450322	IKZF1	NM_001220765	1	7	5	+	50450238	50450405
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220770	6	6	5	+	50459427	50459531
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220774	10	5	4	+	50459427	50459531
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220767	3	7	6	+	50459427	50459531
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220776	12	4	3	+	50459427	50459531
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_006060	13	8	7	+	50459427	50459561
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220773	9	5	4	+	50459427	50459561
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220769	5	6	5	+	50459427	50459561
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220766	2	7	6	+	50459427	50459561
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220765	1	7	6	+	50459427	50459561
227312943	chr7	50459322	50459495	50459343	50459469	IKZF1	NM_001220775	11	4	3	+	50459427	50459561
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_006060	13	8	8	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
228277925	chr7	50467781	50467954	50467799	50467935	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_006060	13	8	8	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220769	5	6	6	+	50467616	50472798

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
230045709	chr7	50468223	50468385	50468245	50468364	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
229608278	chr7	55210953	55211116	55210978	55211088	EGFR	NM_005228	1	28	3	+	55210998	55211181
229608278	chr7	55210953	55211116	55210978	55211088	EGFR	NM_201284	4	16	3	+	55210998	55211181
229608278	chr7	55210953	55211116	55210978	55211088	EGFR	NM_201283	3	10	3	+	55210998	55211181
229608278	chr7	55210953	55211116	55210978	55211088	EGFR	NM_201282	2	16	3	+	55210998	55211181
230461276	chr7	55218907	55219079	55218927	55219055	EGFR	NM_005228	1	28	5	+	55218987	55219055
230461276	chr7	55218907	55219079	55218927	55219055	EGFR	NM_201284	4	16	5	+	55218987	55219055
230461276	chr7	55218907	55219079	55218927	55219055	EGFR	NM_201283	3	10	5	+	55218987	55219055
230461276	chr7	55218907	55219079	55218927	55219055	EGFR	NM_201282	2	16	5	+	55218987	55219055
228035285	chr7	55221751	55221891	55221772	55221869	EGFR	NM_005228	1	28	7	+	55221704	55221845
228035285	chr7	55221751	55221891	55221772	55221869	EGFR	NM_201284	4	16	7	+	55221704	55221845
228035285	chr7	55221751	55221891	55221772	55221869	EGFR	NM_201283	3	10	7	+	55221704	55221845
228035285	chr7	55221751	55221891	55221772	55221869	EGFR	NM_201282	2	16	7	+	55221704	55221845
230683371	chr7	55224225	55224375	55224253	55224353	EGFR	NM_005228	1	28	9	+	55224226	55224352
230683371	chr7	55224225	55224375	55224253	55224353	EGFR	NM_201284	4	16	9	+	55224226	55224352
230683371	chr7	55224225	55224375	55224253	55224353	EGFR	NM_201283	3	10	9	+	55224226	55224352
230683371	chr7	55224225	55224375	55224253	55224353	EGFR	NM_201282	2	16	9	+	55224226	55224352
230173849	chr7	55227705	55227879	55227729	55227856	EGFR	NM_005228	1	28	12	+	55227832	55228031
230173849	chr7	55227705	55227879	55227729	55227856	EGFR	NM_201284	4	16	12	+	55227832	55228031
230173849	chr7	55227705	55227879	55227729	55227856	EGFR	NM_201282	2	16	12	+	55227832	55228031
228744254	chr7	55229262	55229406	55229283	55229378	EGFR	NM_005228	1	28	13	+	55229192	55229324
228744254	chr7	55229262	55229406	55229283	55229378	EGFR	NM_201284	4	16	13	+	55229192	55229324
228744254	chr7	55229262	55229406	55229283	55229378	EGFR	NM_201282	2	16	13	+	55229192	55229324
330137554	chr7	55236078	55236251	55236105	55236223	EGFR	NM_201282	2	16	16	+	55236216	55236328
228857751	chr7	55238848	55238991	55238874	55238966	EGFR	NM_005228	1	28	16	+	55238868	55238906
230742871	chr7	55241655	55241827	55241680	55241801	EGFR	NM_005228	1	28	18	+	55241614	55241736
232237229	chr7	55259345	55259512	55259368	55259486	EGFR	NM_005228	1	28	21	+	55259412	55259567
228956984	chr7	55266419	55266578	55266443	55266558	EGFR	NM_005228	1	28	23	+	55266410	55266556
228732632	chr7	55269353	55269511	55269375	55269483	EGFR	NM_005228	1	28	26	+	55269428	55269475
231222418	chr7	55273081	55273231	55273103	55273210	EGFR	NM_005228	1	28	28	+	55272949	55275031
241508632	chr7	66456183	66456317	66456209	66456290	SBDS	NM_016038	1	5	4	-	66456124	66456288
261508003	chr7	66458350	66458517	66458378	66458486	SBDS	NM_016038	1	5	3	-	66458204	66458404
224038045	chr7	91570328	91570481	91570345	91570464	AKAP9	NM_005751	1	50	1	+	91570189	91570461
224038045	chr7	91570328	91570481	91570345	91570464	AKAP9	NM_147185	2	50	1	+	91570189	91570461
224098602	chr7	91603181	91603339	91603209	91603312	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224098602	chr7	91603181	91603339	91603209	91603312	AKAP9	NM_147185	2	50	2	+	91603025	91603282

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224460718	chr7	91621468	91621622	91621493	91621594	AKAP9	NM_005751	1	50	4	+	91621472	91621525
224460718	chr7	91621468	91621622	91621493	91621594	AKAP9	NM_147185	2	50	4	+	91621472	91621525
223420515	chr7	91623937	91624062	91623965	91624031	AKAP9	NM_005751	1	50	6	+	91623935	91624090
223420515	chr7	91623937	91624062	91623965	91624031	AKAP9	NM_147185	2	50	6	+	91623935	91624090
222713530	chr7	91630426	91630561	91630447	91630540	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222713530	chr7	91630426	91630561	91630447	91630540	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224468823	chr7	91630748	91630875	91630776	91630850	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224468823	chr7	91630748	91630875	91630776	91630850	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224487846	chr7	91631089	91631251	91631114	91631221	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224487846	chr7	91631089	91631251	91631114	91631221	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224472290	chr7	91631542	91631676	91631567	91631648	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224472290	chr7	91631542	91631676	91631567	91631648	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222654021	chr7	91632094	91632249	91632119	91632221	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222654021	chr7	91632094	91632249	91632119	91632221	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222664184	chr7	91632465	91632622	91632493	91632595	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222664184	chr7	91632465	91632622	91632493	91632595	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222270072	chr7	91641897	91642065	91641925	91642043	AKAP9	NM_005751	1	50	9	+	91641743	91641956
222270072	chr7	91641897	91642065	91641925	91642043	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222536443	chr7	91646382	91646537	91646408	91646509	AKAP9	NM_005751	1	50	12	+	91646331	91646416
222536443	chr7	91646382	91646537	91646408	91646509	AKAP9	NM_147185	2	50	12	+	91646331	91646416
223255532	chr7	91652288	91652447	91652311	91652422	AKAP9	NM_005751	1	50	14	+	91652128	91652323
223255532	chr7	91652288	91652447	91652311	91652422	AKAP9	NM_147185	2	50	14	+	91652128	91652323
222546482	chr7	91667739	91667900	91667767	91667872	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222546482	chr7	91667739	91667900	91667767	91667872	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222164938	chr7	91669870	91670021	91669900	91669997	AKAP9	NM_005751	1	50	18	+	91669988	91670212
222164938	chr7	91669870	91670021	91669900	91669997	AKAP9	NM_147185	2	50	18	+	91669988	91670212
222167339	chr7	91671382	91671556	91671405	91671528	AKAP9	NM_005751	1	50	19	+	91671360	91671500
222167339	chr7	91671382	91671556	91671405	91671528	AKAP9	NM_147185	2	50	19	+	91671360	91671500
223889694	chr7	91674411	91674564	91674436	91674536	AKAP9	NM_005751	1	50	21	+	91674322	91674527
223889694	chr7	91674411	91674564	91674436	91674536	AKAP9	NM_147185	2	50	21	+	91674322	91674527
222691663	chr7	91682228	91682377	91682255	91682349	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222691663	chr7	91682228	91682377	91682255	91682349	AKAP9	NM_147185	2	50	22	+	91682040	91682272
224122610	chr7	91691663	91691837	91691687	91691810	AKAP9	NM_005751	1	50	24	+	91691588	91691800
224122610	chr7	91691663	91691837	91691687	91691810	AKAP9	NM_147185	2	50	24	+	91691588	91691800
223778582	chr7	91695614	91695781	91695640	91695753	AKAP9	NM_005751	1	50	26	+	91695741	91695860
223778582	chr7	91695614	91695781	91695640	91695753	AKAP9	NM_147185	2	50	26	+	91695741	91695860
223209775	chr7	91700099	91700273	91700122	91700247	AKAP9	NM_005751	1	50	28	+	91700219	91700323
223209775	chr7	91700099	91700273	91700122	91700247	AKAP9	NM_147185	2	50	28	+	91700219	91700323
224431601	chr7	91707052	91707180	91707076	91707153	AKAP9	NM_005751	1	50	30	+	91707010	91707189
224431601	chr7	91707052	91707180	91707076	91707153	AKAP9	NM_147185	2	50	30	+	91707010	91707189
223500523	chr7	91708625	91708770	91708646	91708745	AKAP9	NM_005751	1	50	31	+	91708393	91709466

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223500523	chr7	91708625	91708770	91708646	91708745	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223513338	chr7	91708976	91709133	91709004	91709107	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223513338	chr7	91708976	91709133	91709004	91709107	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223529483	chr7	91709287	91709460	91709315	91709436	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223529483	chr7	91709287	91709460	91709315	91709436	AKAP9	NM_147185	2	50	31	+	91708393	91709466
224046182	chr7	91712517	91712664	91712542	91712637	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224046182	chr7	91712517	91712664	91712542	91712637	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224076414	chr7	91712908	91713072	91712935	91713047	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224076414	chr7	91712908	91713072	91712935	91713047	AKAP9	NM_147185	2	50	33	+	91712484	91712969
222167391	chr7	91714149	91714306	91714175	91714279	AKAP9	NM_005751	1	50	35	+	91714133	91714254
222167391	chr7	91714149	91714306	91714175	91714279	AKAP9	NM_147185	2	50	35	+	91714133	91714254
222611830	chr7	91715571	91715731	91715590	91715703	AKAP9	NM_005751	1	50	37	+	91715542	91715730
222611830	chr7	91715571	91715731	91715590	91715703	AKAP9	NM_147185	2	50	37	+	91715542	91715730
224418822	chr7	91722432	91722565	91722454	91722542	AKAP9	NM_005751	1	50	39	+	91722411	91722630
224418822	chr7	91722432	91722565	91722454	91722542	AKAP9	NM_147185	2	50	39	+	91722411	91722630
224218883	chr7	91725985	91726134	91726012	91726109	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224218883	chr7	91725985	91726134	91726012	91726109	AKAP9	NM_147185	2	50	41	+	91726003	91726671
222164840	chr7	91726403	91726577	91726428	91726549	AKAP9	NM_005751	1	50	41	+	91726003	91726671
222164840	chr7	91726403	91726577	91726428	91726549	AKAP9	NM_147185	2	50	41	+	91726003	91726671
225156157	chr7	91726909	91727070	91726937	91727044	AKAP9	NM_005751	1	50	42	+	91726900	91727108
225156157	chr7	91726909	91727070	91726937	91727044	AKAP9	NM_147185	2	50	42	+	91726900	91727108
223664384	chr7	91729086	91729243	91729114	91729215	AKAP9	NM_005751	1	50	44	+	91729001	91729183
223664384	chr7	91729086	91729243	91729114	91729215	AKAP9	NM_147185	2	50	44	+	91729001	91729183
223664421	chr7	91731940	91732112	91731966	91732092	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223664421	chr7	91731940	91732112	91731966	91732092	AKAP9	NM_147185	2	50	46	+	91731908	91732140
223235434	chr7	91736596	91736765	91736622	91736738	AKAP9	NM_005751	1	50	48	+	91736607	91736736
223235434	chr7	91736596	91736765	91736622	91736738	AKAP9	NM_147185	2	50	48	+	91736607	91736736
225815096	chr7	92244419	92244582	92244440	92244557	CDK6	NM_001145306	1	8	8	-	92234235	92244600
225815096	chr7	92244419	92244582	92244440	92244557	CDK6	NM_001259	2	8	8	-	92234235	92244600
253699002	chr7	92252272	92252409	92252298	92252384	CDK6	NM_001145306	1	8	6	-	92252350	92252400
253699002	chr7	92252272	92252409	92252298	92252384	CDK6	NM_001259	2	8	6	-	92252350	92252400
226229404	chr7	92354996	92355169	92355018	92355144	CDK6	NM_001145306	1	8	4	-	92354940	92355107
226229404	chr7	92354996	92355169	92355018	92355144	CDK6	NM_001259	2	8	4	-	92354940	92355107
227040507	chr7	92462428	92462599	92462446	92462581	CDK6	NM_001145306	1	8	2	-	92462405	92463004
227040507	chr7	92462428	92462599	92462446	92462581	CDK6	NM_001259	2	8	2	-	92462405	92463004
294113623	chr7	92730841	92731015	92730865	92730987	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294113623	chr7	92730841	92731015	92730865	92730987	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294029711	chr7	92731233	92731382	92731261	92731353	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294029711	chr7	92731233	92731382	92731261	92731353	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294044289	chr7	92731675	92731819	92731701	92731794	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294044289	chr7	92731675	92731819	92731701	92731794	SAMD9	NM_017654	2	3	3	-	92728826	92735418

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294103183	chr7	92732104	92732262	92732128	92732234	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294103183	chr7	92732104	92732262	92732128	92732234	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295066797	chr7	92732483	92732623	92732507	92732596	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295066797	chr7	92732483	92732623	92732507	92732596	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295041637	chr7	92732812	92732986	92732836	92732958	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295041637	chr7	92732812	92732986	92732836	92732958	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295075583	chr7	92733189	92733362	92733218	92733340	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295075583	chr7	92733189	92733362	92733218	92733340	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294145530	chr7	92733562	92733722	92733586	92733694	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294145530	chr7	92733562	92733722	92733586	92733694	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294089965	chr7	92733978	92734150	92734007	92734122	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294089965	chr7	92733978	92734150	92734007	92734122	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295050590	chr7	92734348	92734482	92734374	92734458	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295050590	chr7	92734348	92734482	92734374	92734458	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295087643	chr7	92734653	92734825	92734678	92734798	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295087643	chr7	92734653	92734825	92734678	92734798	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294152247	chr7	92735077	92735232	92735104	92735204	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294152247	chr7	92735077	92735232	92735104	92735204	SAMD9	NM_017654	2	3	3	-	92728826	92735418
302877341	chr7	98479573	98479734	98479595	98479707	TRRAP	NM_003496	2	71	3	+	98479598	98479647
302877341	chr7	98479573	98479734	98479595	98479707	TRRAP	NM_001244580	1	72	3	+	98479598	98479647
299708217	chr7	98490051	98490199	98490076	98490170	TRRAP	NM_003496	2	71	5	+	98490047	98490151
299708217	chr7	98490051	98490199	98490076	98490170	TRRAP	NM_001244580	1	72	5	+	98490047	98490151
304012324	chr7	98497316	98497440	98497339	98497416	TRRAP	NM_003496	2	71	10	+	98497302	98497390
304012324	chr7	98497316	98497440	98497339	98497416	TRRAP	NM_001244580	1	72	10	+	98497302	98497390
305640540	chr7	98501028	98501161	98501051	98501141	TRRAP	NM_003496	2	71	12	+	98501002	98501140
305640540	chr7	98501028	98501161	98501051	98501141	TRRAP	NM_001244580	1	72	12	+	98501002	98501140
301095747	chr7	98507616	98507786	98507642	98507768	TRRAP	NM_003496	2	71	15	+	98507679	98508042
301095747	chr7	98507616	98507786	98507642	98507768	TRRAP	NM_001244580	1	72	15	+	98507679	98508042
301114842	chr7	98507982	98508142	98508003	98508116	TRRAP	NM_003496	2	71	15	+	98507679	98508042
301114842	chr7	98507982	98508142	98508003	98508116	TRRAP	NM_001244580	1	72	15	+	98507679	98508042
299902356	chr7	98508701	98508868	98508725	98508844	TRRAP	NM_003496	2	71	17	+	98508700	98508894
299902356	chr7	98508701	98508868	98508725	98508844	TRRAP	NM_001244580	1	72	17	+	98508700	98508894
302641739	chr7	98513256	98513430	98513279	98513407	TRRAP	NM_003496	2	71	19	+	98513346	98513511
302641739	chr7	98513256	98513430	98513279	98513407	TRRAP	NM_001244580	1	72	19	+	98513346	98513511
305231466	chr7	98515170	98515333	98515191	98515312	TRRAP	NM_003496	2	71	20	+	98515046	98515302
305231466	chr7	98515170	98515333	98515191	98515312	TRRAP	NM_001244580	1	72	20	+	98515046	98515302
304997576	chr7	98522799	98522947	98522822	98522925	TRRAP	NM_003496	2	71	22	+	98522735	98522886
304997576	chr7	98522799	98522947	98522822	98522925	TRRAP	NM_001244580	1	72	22	+	98522735	98522886
300528953	chr7	98527557	98527731	98527579	98527703	TRRAP	NM_003496	2	71	24	+	98527612	98527829
300528953	chr7	98527557	98527731	98527579	98527703	TRRAP	NM_001244580	1	72	24	+	98527612	98527829
300060992	chr7	98528987	98529129	98529009	98529108	TRRAP	NM_003496	2	71	26	+	98529028	98529288

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300060992	chr7	98528987	98529129	98529009	98529108	TRRAP	NM_001244580	1	72	26	+	98529028	98529288
302096772	chr7	98530966	98531107	98530986	98531087	TRRAP	NM_003496	2	71	27	+	98530864	98531025
302096772	chr7	98530966	98531107	98530986	98531087	TRRAP	NM_001244580	1	72	27	+	98530864	98531025
304785317	chr7	98534853	98535022	98534876	98534995	TRRAP	NM_003496	2	71	29	+	98534779	98534900
304785317	chr7	98534853	98535022	98534876	98534995	TRRAP	NM_001244580	1	72	29	+	98534779	98534900
300896048	chr7	98543258	98543395	98543285	98543375	TRRAP	NM_001244580	1	72	32	+	98543370	98543423
300393881	chr7	98546162	98546329	98546184	98546308	TRRAP	NM_003496	2	71	33	+	98546189	98546308
300393881	chr7	98546162	98546329	98546184	98546308	TRRAP	NM_001244580	1	72	34	+	98546189	98546308
299973096	chr7	98547246	98547388	98547271	98547365	TRRAP	NM_003496	2	71	35	+	98547283	98547464
299973096	chr7	98547246	98547388	98547271	98547365	TRRAP	NM_001244580	1	72	36	+	98547283	98547464
299354001	chr7	98548381	98548542	98548403	98548517	TRRAP	NM_003496	2	71	37	+	98548499	98548627
299354001	chr7	98548381	98548542	98548403	98548517	TRRAP	NM_001244580	1	72	38	+	98548499	98548627
301008324	chr7	98550986	98551117	98551006	98551096	TRRAP	NM_003496	2	71	38	+	98550790	98551056
301008324	chr7	98550986	98551117	98551006	98551096	TRRAP	NM_001244580	1	72	39	+	98550790	98551056
301158138	chr7	98553732	98553897	98553750	98553874	TRRAP	NM_003496	2	71	40	+	98553769	98553927
301158138	chr7	98553732	98553897	98553750	98553874	TRRAP	NM_001244580	1	72	41	+	98553769	98553927
305675697	chr7	98555566	98555734	98555587	98555715	TRRAP	NM_003496	2	71	42	+	98555604	98555714
305675697	chr7	98555566	98555734	98555587	98555715	TRRAP	NM_001244580	1	72	43	+	98555604	98555714
302901641	chr7	98558970	98559144	98558994	98559121	TRRAP	NM_003496	2	71	44	+	98558884	98559097
302901641	chr7	98558970	98559144	98558994	98559121	TRRAP	NM_001244580	1	72	45	+	98558884	98559097
299841625	chr7	98562282	98562444	98562304	98562420	TRRAP	NM_003496	2	71	46	+	98562252	98562398
299841625	chr7	98562282	98562444	98562304	98562420	TRRAP	NM_001244580	1	72	47	+	98562252	98562398
300111057	chr7	98564664	98564838	98564684	98564812	TRRAP	NM_003496	2	71	48	+	98564664	98564785
300111057	chr7	98564664	98564838	98564684	98564812	TRRAP	NM_001244580	1	72	49	+	98564664	98564785
300291835	chr7	98567794	98567921	98567813	98567902	TRRAP	NM_003496	2	71	50	+	98567735	98567914
300291835	chr7	98567794	98567921	98567813	98567902	TRRAP	NM_001244580	1	72	51	+	98567735	98567914
302284694	chr7	98573840	98573978	98573861	98573950	TRRAP	NM_003496	2	71	52	+	98573772	98573891
302284694	chr7	98573840	98573978	98573861	98573950	TRRAP	NM_001244580	1	72	53	+	98573772	98573891
305816919	chr7	98574466	98574618	98574493	98574591	TRRAP	NM_003496	2	71	54	+	98574562	98574699
305816919	chr7	98574466	98574618	98574493	98574591	TRRAP	NM_001244580	1	72	55	+	98574562	98574699
305476986	chr7	98576450	98576624	98576470	98576597	TRRAP	NM_003496	2	71	56	+	98576392	98576527
305476986	chr7	98576450	98576624	98576470	98576597	TRRAP	NM_001244580	1	72	57	+	98576392	98576527
300262504	chr7	98580794	98580965	98580817	98580944	TRRAP	NM_003496	2	71	58	+	98580887	98581082
300262504	chr7	98580794	98580965	98580817	98580944	TRRAP	NM_001244580	1	72	59	+	98580887	98581115
300958678	chr7	98581748	98581918	98581772	98581894	TRRAP	NM_003496	2	71	59	+	98581716	98581981
300958678	chr7	98581748	98581918	98581772	98581894	TRRAP	NM_001244580	1	72	60	+	98581716	98581981
304232467	chr7	98586354	98586501	98586380	98586481	TRRAP	NM_003496	2	71	61	+	98586388	98586589
304232467	chr7	98586354	98586501	98586380	98586481	TRRAP	NM_001244580	1	72	62	+	98586388	98586589
303749660	chr7	98589702	98589843	98589726	98589822	TRRAP	NM_003496	2	71	63	+	98589760	98589850
303749660	chr7	98589702	98589843	98589726	98589822	TRRAP	NM_001244580	1	72	64	+	98589760	98589850
299782144	chr7	98592169	98592339	98592190	98592317	TRRAP	NM_003496	2	71	65	+	98592210	98592471

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299782144	chr7	98592169	98592339	98592190	98592317	TRRAP	NM_001244580	1	72	66	+	98592210	98592471
300491615	chr7	98601824	98601968	98601845	98601947	TRRAP	NM_003496	2	71	66	+	98601813	98602038
300491615	chr7	98601824	98601968	98601845	98601947	TRRAP	NM_001244580	1	72	67	+	98601813	98602038
303192736	chr7	98602913	98603078	98602935	98603057	TRRAP	NM_003496	2	71	67	+	98602754	98602971
303192736	chr7	98602913	98603078	98602935	98603057	TRRAP	NM_001244580	1	72	68	+	98602754	98602971
304210428	chr7	98608759	98608902	98608779	98608879	TRRAP	NM_003496	2	71	69	+	98608675	98608878
304210428	chr7	98608759	98608902	98608779	98608879	TRRAP	NM_001244580	1	72	70	+	98608675	98608878
306010580	chr7	98609759	98609911	98609780	98609890	TRRAP	NM_003496	2	71	71	+	98609694	98610866
306010580	chr7	98609759	98609911	98609780	98609890	TRRAP	NM_001244580	1	72	72	+	98609694	98610866
272022662	chr7	100402768	100402940	100402787	100402921	EPHB4	NM_004444	1	17	16	-	100402788	100402943
270055294	chr7	100403949	100404118	100403970	100404097	EPHB4	NM_004444	1	17	14	-	100404042	100404191
271666697	chr7	100410281	100410433	100410303	100410414	EPHB4	NM_004444	1	17	12	-	100410369	100410616
270779598	chr7	100410714	100410884	100410735	100410861	EPHB4	NM_004444	1	17	11	-	100410717	100410830
270911584	chr7	100414923	100415087	100414942	100415067	EPHB4	NM_004444	1	17	8	-	100414814	100414979
271321976	chr7	100417264	100417435	100417290	100417417	EPHB4	NM_004444	1	17	6	-	100417179	100417511
270686382	chr7	100419874	100420040	100419892	100420022	EPHB4	NM_004444	1	17	4	-	100419893	100420289
269698358	chr7	100421220	100421356	100421240	100421335	EPHB4	NM_004444	1	17	3	-	100421266	100421553
270827588	chr7	100424529	100424683	100424548	100424663	EPHB4	NM_004444	1	17	1	-	100424601	100425143
294978723	chr7	106508324	106508497	106508349	106508474	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294991368	chr7	106508761	106508933	106508785	106508913	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294019663	chr7	106509232	106509389	106509253	106509367	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294032471	chr7	106509662	106509804	106509682	106509776	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294526156	chr7	106513071	106513216	106513099	106513194	PIK3CG	NM_002649	1	11	4	+	106513158	106513383
293936253	chr7	106519938	106520088	106519963	106520060	PIK3CG	NM_002649	1	11	6	+	106519964	106520110
293747925	chr7	106523385	106523532	106523408	106523508	PIK3CG	NM_002649	1	11	8	+	106523478	106523608
294107756	chr7	106526486	106526654	106526514	106526626	PIK3CG	NM_002649	1	11	10	+	106526580	106526737
294631932	chr7	106545631	106545780	106545653	106545754	PIK3CG	NM_002649	1	11	11	+	106545554	106547592
234556338	chr7	116339328	116339496	116339357	116339468	MET	NM_001127500	2	21	2	+	116339125	116340338
234556338	chr7	116339328	116339496	116339357	116339468	MET	NM_000245	1	21	2	+	116339125	116340338
234557893	chr7	116339756	116339904	116339780	116339879	MET	NM_001127500	2	21	2	+	116339125	116340338
234557893	chr7	116339756	116339904	116339780	116339879	MET	NM_000245	1	21	2	+	116339125	116340338
233160766	chr7	116340130	116340300	116340152	116340274	MET	NM_001127500	2	21	2	+	116339125	116340338
233160766	chr7	116340130	116340300	116340152	116340274	MET	NM_000245	1	21	2	+	116339125	116340338
233368471	chr7	116379898	116380058	116379919	116380033	MET	NM_001127500	2	21	4	+	116380004	116380138
233368471	chr7	116379898	116380058	116379919	116380033	MET	NM_000245	1	21	4	+	116380004	116380138
230824453	chr7	116395388	116395534	116395416	116395507	MET	NM_001127500	2	21	6	+	116395409	116395569
230824453	chr7	116395388	116395534	116395416	116395507	MET	NM_000245	1	21	6	+	116395409	116395569
231229586	chr7	116397668	116397807	116397695	116397779	MET	NM_001127500	2	21	8	+	116397692	116397828
231229586	chr7	116397668	116397807	116397695	116397779	MET	NM_000245	1	21	8	+	116397692	116397828
233120383	chr7	116399291	116399448	116399317	116399422	MET	NM_001127500	2	21	10	+	116399391	116399544
234441712	chr7	116403198	116403366	116403226	116403338	MET	NM_001127500	2	21	11	+	116403104	116403322

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234441712	chr7	116403198	116403366	116403226	116403338	MET	NM_000245	1	21	11	+	116403104	116403322
233289389	chr7	116411565	116411698	116411591	116411674	MET	NM_001127500	2	21	13	+	116411552	116411708
233289389	chr7	116411565	116411698	116411591	116411674	MET	NM_000245	1	21	13	+	116411552	116411708
230868083	chr7	116414864	116415003	116414886	116414981	MET	NM_001127500	2	21	15	+	116414935	116415165
230868083	chr7	116414864	116415003	116414886	116414981	MET	NM_000245	1	21	15	+	116414935	116415165
234182548	chr7	116418798	116418940	116418825	116418919	MET	NM_001127500	2	21	17	+	116418830	116419011
234182548	chr7	116418798	116418940	116418825	116418919	MET	NM_000245	1	21	17	+	116418830	116419011
231135341	chr7	116423432	116423556	116423457	116423527	MET	NM_001127500	2	21	19	+	116423358	116423523
231135341	chr7	116423432	116423556	116423457	116423527	MET	NM_000245	1	21	19	+	116423358	116423523
234553950	chr7	116435977	116436103	116435998	116436079	MET	NM_001127500	2	21	21	+	116435941	116438440
234553950	chr7	116435977	116436103	116435998	116436079	MET	NM_000245	1	21	21	+	116435941	116438440
294689974	chr7	124465261	124465432	124465289	124465399	POT1	NR_003103	4	18	17	-	124465306	124465411
294689974	chr7	124465261	124465432	124465289	124465399	POT1	NR_003104	5	20	19	-	124465306	124465411
294689974	chr7	124465261	124465432	124465289	124465399	POT1	NR_003102	3	20	19	-	124465306	124465411
294689974	chr7	124465261	124465432	124465289	124465399	POT1	NM_001042594	1	18	17	-	124465306	124465411
294689974	chr7	124465261	124465432	124465289	124465399	POT1	NM_015450	2	19	18	-	124465306	124465411
294340986	chr7	124475401	124475548	124475427	124475518	POT1	NR_003103	4	18	15	-	124475333	124475468
294340986	chr7	124475401	124475548	124475427	124475518	POT1	NR_003104	5	20	16	-	124475333	124475468
294340986	chr7	124475401	124475548	124475427	124475518	POT1	NR_003102	3	20	16	-	124475333	124475468
294340986	chr7	124475401	124475548	124475427	124475518	POT1	NM_001042594	1	18	14	-	124475333	124475468
294340986	chr7	124475401	124475548	124475427	124475518	POT1	NM_015450	2	19	15	-	124475333	124475468
294177180	chr7	124482848	124482987	124482878	124482961	POT1	NR_003103	4	18	13	-	124482861	124483017
294177180	chr7	124482848	124482987	124482878	124482961	POT1	NR_003104	5	20	13	-	124482861	124483017
294177180	chr7	124482848	124482987	124482878	124482961	POT1	NR_003102	3	20	14	-	124482861	124483017
294177180	chr7	124482848	124482987	124482878	124482961	POT1	NM_001042594	1	18	12	-	124482861	124483017
294177180	chr7	124482848	124482987	124482878	124482961	POT1	NM_015450	2	19	13	-	124482861	124483017
294422256	chr7	124492938	124493100	124492960	124493078	POT1	NR_003103	4	18	10	-	124493026	124493192
294422256	chr7	124492938	124493100	124492960	124493078	POT1	NR_003104	5	20	10	-	124493026	124493192
294422256	chr7	124492938	124493100	124492960	124493078	POT1	NR_003102	3	20	10	-	124493026	124493192
294422256	chr7	124492938	124493100	124492960	124493078	POT1	NM_001042594	1	18	9	-	124493026	124493192
294422256	chr7	124492938	124493100	124492960	124493078	POT1	NM_015450	2	19	10	-	124493026	124493192
294636781	chr7	124499132	124499285	124499155	124499258	POT1	NR_003103	4	18	9	-	124499011	124499166
294636781	chr7	124499132	124499285	124499155	124499258	POT1	NR_003104	5	20	9	-	124499011	124499166
294636781	chr7	124499132	124499285	124499155	124499258	POT1	NR_003102	3	20	9	-	124499011	124499166
294636781	chr7	124499132	124499285	124499155	124499258	POT1	NM_001042594	1	18	8	-	124499011	124499166
294636781	chr7	124499132	124499285	124499155	124499258	POT1	NM_015450	2	19	9	-	124499011	124499166
293999246	chr7	124510886	124511044	124510914	124511018	POT1	NR_003103	4	18	7	-	124510965	124511095
293999246	chr7	124510886	124511044	124510914	124511018	POT1	NR_003104	5	20	7	-	124510965	124511095
293999246	chr7	124510886	124511044	124510914	124511018	POT1	NR_003102	3	20	7	-	124510965	124511095
293999246	chr7	124510886	124511044	124510914	124511018	POT1	NM_015450	2	19	7	-	124510965	124511095
294118155	chr7	124532297	124532446	124532324	124532418	POT1	NR_003103	4	18	6	-	124532320	124532434

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294118155	chr7	124532297	124532446	124532324	124532418	POT1	NR_003104	5	20	6	-	124532320	124532434
294118155	chr7	124532297	124532446	124532324	124532418	POT1	NR_003102	3	20	6	-	124532320	124532434
294118155	chr7	124532297	124532446	124532324	124532418	POT1	NM_001042594	1	18	6	-	124532320	124532434
294118155	chr7	124532297	124532446	124532324	124532418	POT1	NM_015450	2	19	6	-	124532320	124532434
295051388	chr7	126086019	126086193	126086047	126086166	GRM8	NM_001127323	2	11	10	-	126086125	126086426
293753214	chr7	126172885	126173059	126172913	126173033	GRM8	NR_028041	3	11	9	-	126173006	126173941
293753214	chr7	126172885	126173059	126172913	126173033	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293753214	chr7	126172885	126173059	126172913	126173033	GRM8	NM_000845	1	10	8	-	126173006	126173941
293799071	chr7	126173340	126173508	126173361	126173482	GRM8	NR_028041	3	11	9	-	126173006	126173941
293799071	chr7	126173340	126173508	126173361	126173482	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293799071	chr7	126173340	126173508	126173361	126173482	GRM8	NM_000845	1	10	8	-	126173006	126173941
293832025	chr7	126173769	126173933	126173792	126173911	GRM8	NR_028041	3	11	9	-	126173006	126173941
293832025	chr7	126173769	126173933	126173792	126173911	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293832025	chr7	126173769	126173933	126173792	126173911	GRM8	NM_000845	1	10	8	-	126173006	126173941
293838914	chr7	126409830	126409992	126409853	126409971	GRM8	NR_028041	3	11	6	-	126409919	126410119
293838914	chr7	126409830	126409992	126409853	126409971	GRM8	NM_001127323	2	11	7	-	126409919	126410119
293838914	chr7	126409830	126409992	126409853	126409971	GRM8	NM_000845	1	10	6	-	126409919	126410119
294593201	chr7	126543968	126544141	126543992	126544117	GRM8	NR_028041	3	11	4	-	126544026	126544180
294593201	chr7	126543968	126544141	126543992	126544117	GRM8	NM_001127323	2	11	5	-	126544026	126544180
294593201	chr7	126543968	126544141	126543992	126544117	GRM8	NM_000845	1	10	4	-	126544026	126544180
293902855	chr7	126746588	126746735	126746611	126746709	GRM8	NR_028041	3	11	2	-	126746550	126746766
293902855	chr7	126746588	126746735	126746611	126746709	GRM8	NM_001127323	2	11	3	-	126746550	126746766
293902855	chr7	126746588	126746735	126746611	126746709	GRM8	NM_000845	1	10	2	-	126746550	126746766
295248843	chr7	126882900	126883032	126882925	126883010	GRM8	NR_028041	3	11	1	-	126882749	126883569
295248843	chr7	126882900	126883032	126882925	126883010	GRM8	NM_001127323	2	11	2	-	126882749	126883569
295248843	chr7	126882900	126883032	126882925	126883010	GRM8	NM_000845	1	10	1	-	126882749	126883569
260964772	chr7	128829301	128829427	128829318	128829410	SMO	NM_005631	1	12	1	+	128828713	128829323
262583639	chr7	128845040	128845208	128845064	128845187	SMO	NM_005631	1	12	3	+	128845044	128845253
238157881	chr7	128845934	128846108	128845956	128846087	SMO	NM_005631	1	12	5	+	128845991	128846210
240722804	chr7	128848577	128848751	128848597	128848733	SMO	NM_005631	1	12	7	+	128848600	128848692
242195741	chr7	128850769	128850926	128850791	128850906	SMO	NM_005631	1	12	10	+	128850806	128850954
241159884	chr7	128851770	128851915	128851791	128851894	SMO	NM_005631	1	12	12	+	128851865	128853385
241187296	chr7	128852230	128852394	128852251	128852373	SMO	NM_005631	1	12	12	+	128851865	128853385
274232217	chr7	138189027	138189187	138189050	138189165	TRIM24	NM_015905	2	19	2	+	138189035	138189153
274232217	chr7	138189027	138189187	138189050	138189165	TRIM24	NM_003852	1	19	2	+	138189035	138189153
273476603	chr7	138203991	138204131	138204013	138204108	TRIM24	NM_015905	2	19	4	+	138203934	138204066
273476603	chr7	138203991	138204131	138204013	138204108	TRIM24	NM_003852	1	19	4	+	138203934	138204066
273229750	chr7	138235734	138235892	138235761	138235866	TRIM24	NM_015905	2	19	8	+	138235808	138235925
273229750	chr7	138235734	138235892	138235761	138235866	TRIM24	NM_003852	1	19	8	+	138235808	138235925
274471475	chr7	138239577	138239735	138239597	138239712	TRIM24	NM_003852	1	19	9	+	138239443	138239609
274471475	chr7	138239577	138239735	138239597	138239712	TRIM24	NM_015905	2	19	9	+	138239443	138239711

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273619831	chr7	138255533	138255676	138255559	138255651	TRIM24	NM_015905	2	19	11	+	138255575	138255748
273619831	chr7	138255533	138255676	138255559	138255651	TRIM24	NM_003852	1	19	11	+	138255575	138255748
273123962	chr7	138261092	138261263	138261115	138261235	TRIM24	NM_015905	2	19	13	+	138261118	138261190
273123962	chr7	138261092	138261263	138261115	138261235	TRIM24	NM_003852	1	19	13	+	138261118	138261190
273593196	chr7	138263943	138264112	138263970	138264087	TRIM24	NM_015905	2	19	15	+	138263949	138264277
273593196	chr7	138263943	138264112	138263970	138264087	TRIM24	NM_003852	1	19	15	+	138263949	138264277
274480689	chr7	138265328	138265496	138265353	138265468	TRIM24	NM_015905	2	19	16	+	138265307	138265439
274480689	chr7	138265328	138265496	138265353	138265468	TRIM24	NM_003852	1	19	16	+	138265307	138265439
273230023	chr7	138268624	138268792	138268650	138268769	TRIM24	NM_015905	2	19	18	+	138268595	138268744
273230023	chr7	138268624	138268792	138268650	138268769	TRIM24	NM_003852	1	19	18	+	138268595	138268744
222629880	chr7	140434365	140434517	140434390	140434494	BRAF	NM_004333	1	18	18	-	140433813	140434570
223175118	chr7	140449052	140449217	140449079	140449190	BRAF	NM_004333	1	18	16	-	140449087	140449218
223719489	chr7	140453920	140454078	140453948	140454053	BRAF	NM_004333	1	18	14	-	140453987	140454033
225222024	chr7	140477762	140477904	140477789	140477876	BRAF	NM_004333	1	18	12	-	140477791	140477875
222684242	chr7	140482865	140483020	140482886	140482992	BRAF	NM_004333	1	18	10	-	140482821	140482957
223700378	chr7	140500104	140500235	140500128	140500214	BRAF	NM_004333	1	18	7	-	140500162	140500281
222258987	chr7	140507637	140507806	140507665	140507784	BRAF	NM_004333	1	18	5	-	140507760	140507862
222895407	chr7	140534279	140534444	140534302	140534421	BRAF	NM_004333	1	18	3	-	140534409	140534672
223103332	chr7	140549794	140549966	140549820	140549943	BRAF	NM_004333	1	18	2	-	140549911	140550012
270958700	chr7	142560963	142561129	142560982	142561108	EPHB6	NM_004445	1	20	5	+	142560885	142561085
271207883	chr7	142561819	142561969	142561843	142561950	EPHB6	NM_004445	1	20	7	+	142561724	142562504
272595776	chr7	142562259	142562433	142562277	142562416	EPHB6	NM_004445	1	20	7	+	142561724	142562504
271794522	chr7	142563681	142563848	142563700	142563829	EPHB6	NM_004445	1	20	9	+	142563715	142564071
271518803	chr7	142564192	142564331	142564213	142564309	EPHB6	NM_004445	1	20	10	+	142564236	142564360
269651002	chr7	142565292	142565416	142565310	142565398	EPHB6	NM_004445	1	20	12	+	142565363	142565477
271144346	chr7	142566067	142566194	142566087	142566173	EPHB6	NM_004445	1	20	14	+	142565996	142566115
272729953	chr7	142566780	142566926	142566798	142566908	EPHB6	NM_004445	1	20	16	+	142566727	142566900
272249633	chr7	142567966	142568131	142567994	142568110	EPHB6	NM_004445	1	20	18	+	142567967	142568160
271543759	chr7	142568509	142568680	142568530	142568658	EPHB6	NM_004445	1	20	20	+	142568549	142568847
229288067	chr7	148507403	148507558	148507424	148507530	EZH2	NM_001203248	2	20	17	-	148507425	148507506
229288067	chr7	148507403	148507558	148507424	148507530	EZH2	NM_152998	5	19	16	-	148507425	148507506
229288067	chr7	148507403	148507558	148507424	148507530	EZH2	NM_001203247	1	20	17	-	148507425	148507506
229288067	chr7	148507403	148507558	148507424	148507530	EZH2	NM_001203249	3	19	16	-	148507425	148507506
229288067	chr7	148507403	148507558	148507424	148507530	EZH2	NM_004456	4	20	17	-	148507425	148507506
228088143	chr7	148511112	148511254	148511132	148511230	EZH2	NM_001203248	2	20	15	-	148511051	148511229
228088143	chr7	148511112	148511254	148511132	148511230	EZH2	NM_152998	5	19	14	-	148511051	148511229
228088143	chr7	148511112	148511254	148511132	148511230	EZH2	NM_001203247	1	20	15	-	148511051	148511229
228088143	chr7	148511112	148511254	148511132	148511230	EZH2	NM_001203249	3	19	14	-	148511051	148511229
228088143	chr7	148511112	148511254	148511132	148511230	EZH2	NM_004456	4	20	15	-	148511051	148511229
227956383	chr7	148513721	148513895	148513745	148513874	EZH2	NM_001203248	2	20	12	-	148513776	148513870
227956383	chr7	148513721	148513895	148513745	148513874	EZH2	NM_152998	5	19	11	-	148513776	148513870

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227956383	chr7	148513721	148513895	148513745	148513874	EZH2	NM_001203247	1	20	12	-	148513776	148513870
227956383	chr7	148513721	148513895	148513745	148513874	EZH2	NM_001203249	3	19	12	-	148513776	148513870
227956383	chr7	148513721	148513895	148513745	148513874	EZH2	NM_004456	4	20	12	-	148513776	148513870
228985079	chr7	148514971	148515125	148514997	148515102	EZH2	NM_001203248	2	20	10	-	148514969	148515209
228985079	chr7	148514971	148515125	148514997	148515102	EZH2	NM_152998	5	19	9	-	148514969	148515209
228985079	chr7	148514971	148515125	148514997	148515102	EZH2	NM_001203247	1	20	10	-	148514969	148515209
228985079	chr7	148514971	148515125	148514997	148515102	EZH2	NM_001203249	3	19	10	-	148514969	148515209
228985079	chr7	148514971	148515125	148514997	148515102	EZH2	NM_004456	4	20	10	-	148514969	148515209
230192237	chr7	148523483	148523623	148523505	148523597	EZH2	NM_001203248	2	20	8	-	148523561	148523724
230192237	chr7	148523483	148523623	148523505	148523597	EZH2	NM_152998	5	19	7	-	148523561	148523724
230192237	chr7	148523483	148523623	148523505	148523597	EZH2	NM_001203247	1	20	8	-	148523561	148523724
230192237	chr7	148523483	148523623	148523505	148523597	EZH2	NM_001203249	3	19	8	-	148523561	148523724
230192237	chr7	148523483	148523623	148523505	148523597	EZH2	NM_004456	4	20	8	-	148523546	148523724
230533775	chr7	148525784	148525935	148525810	148525907	EZH2	NM_001203248	2	20	6	-	148525832	148525972
230533775	chr7	148525784	148525935	148525810	148525907	EZH2	NM_152998	5	19	5	-	148525832	148525972
230533775	chr7	148525784	148525935	148525810	148525907	EZH2	NM_001203247	1	20	6	-	148525832	148525972
230533775	chr7	148525784	148525935	148525810	148525907	EZH2	NM_001203249	3	19	6	-	148525832	148525972
230533775	chr7	148525784	148525935	148525810	148525907	EZH2	NM_004456	4	20	6	-	148525832	148525972
231128405	chr7	148529628	148529784	148529659	148529760	EZH2	NM_001203248	2	20	4	-	148529726	148529842
231128405	chr7	148529628	148529784	148529659	148529760	EZH2	NM_001203247	1	20	4	-	148529726	148529842
231128405	chr7	148529628	148529784	148529659	148529760	EZH2	NM_001203249	3	19	4	-	148529726	148529842
231128405	chr7	148529628	148529784	148529659	148529760	EZH2	NM_004456	4	20	4	-	148529726	148529842
230774505	chr7	148544273	148544405	148544297	148544378	EZH2	NM_001203248	2	20	2	-	148544274	148544397
230774505	chr7	148544273	148544405	148544297	148544378	EZH2	NM_152998	5	19	2	-	148544274	148544397
230774505	chr7	148544273	148544405	148544297	148544378	EZH2	NM_001203247	1	20	2	-	148544274	148544397
230774505	chr7	148544273	148544405	148544297	148544378	EZH2	NM_001203249	3	19	2	-	148544274	148544397
230774505	chr7	148544273	148544405	148544297	148544378	EZH2	NM_004456	4	20	2	-	148544274	148544397
273613242	chr7	151836249	151836383	151836269	151836358	MLL3	NM_170606	1	59	57	-	151836271	151836344
274336215	chr7	151841855	151842027	151841877	151841998	MLL3	NM_170606	1	59	55	-	151841798	151841966
273150942	chr7	151843751	151843906	151843774	151843878	MLL3	NM_170606	1	59	53	-	151843684	151843820
273116363	chr7	151845415	151845584	151845435	151845556	MLL3	NM_170606	1	59	52	-	151845118	151846237
274182987	chr7	151845887	151846047	151845911	151846025	MLL3	NM_170606	1	59	52	-	151845118	151846237
273690484	chr7	151848003	151848134	151848032	151848110	MLL3	NM_170606	1	59	51	-	151847985	151848092
274031429	chr7	151849786	151849960	151849807	151849938	MLL3	NM_170606	1	59	49	-	151849790	151850039
273420976	chr7	151851178	151851323	151851203	151851294	MLL3	NM_170606	1	59	48	-	151851095	151851231
274362413	chr7	151853002	151853152	151853028	151853125	MLL3	NM_170606	1	59	46	-	151852995	151853142
273383375	chr7	151855924	151856098	151855947	151856072	MLL3	NM_170606	1	59	44	-	151855948	151856157
274530885	chr7	151859319	151859463	151859346	151859438	MLL3	NM_170606	1	59	43	-	151859202	151860911
274538891	chr7	151859739	151859904	151859762	151859876	MLL3	NM_170606	1	59	43	-	151859202	151860911
274550060	chr7	151860138	151860307	151860161	151860282	MLL3	NM_170606	1	59	43	-	151859202	151860911
274611718	chr7	151860565	151860701	151860593	151860680	MLL3	NM_170606	1	59	43	-	151859202	151860911

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273796572	chr7	151864150	151864324	151864177	151864304	MLL3	NM_170606	1	59	42	-	151864231	151864463
273655585	chr7	151868286	151868455	151868308	151868428	MLL3	NM_170606	1	59	40	-	151868349	151868427
274275690	chr7	151873337	151873497	151873360	151873475	MLL3	NM_170606	1	59	38	-	151873276	151875095
273336836	chr7	151873731	151873901	151873756	151873875	MLL3	NM_170606	1	59	38	-	151873276	151875095
273365629	chr7	151874058	151874215	151874084	151874188	MLL3	NM_170606	1	59	38	-	151873276	151875095
273299217	chr7	151874423	151874564	151874449	151874540	MLL3	NM_170606	1	59	38	-	151873276	151875095
274268865	chr7	151874835	151875005	151874855	151874977	MLL3	NM_170606	1	59	38	-	151873276	151875095
272988802	chr7	151876960	151877126	151876980	151877108	MLL3	NM_170606	1	59	37	-	151876919	151877211
273844314	chr7	151877976	151878140	151877997	151878115	MLL3	NM_170606	1	59	36	-	151877796	151879679
273849478	chr7	151878411	151878535	151878431	151878508	MLL3	NM_170606	1	59	36	-	151877796	151879679
273845717	chr7	151878832	151878972	151878854	151878949	MLL3	NM_170606	1	59	36	-	151877796	151879679
273830178	chr7	151879273	151879439	151879294	151879414	MLL3	NM_170606	1	59	36	-	151877796	151879679
273828717	chr7	151879987	151880141	151880014	151880113	MLL3	NM_170606	1	59	35	-	151880059	151880241
273698951	chr7	151884341	151884488	151884369	151884460	MLL3	NM_170606	1	59	33	-	151884347	151884561
273234654	chr7	151884780	151884916	151884807	151884892	MLL3	NM_170606	1	59	32	-	151884800	151884932
273007098	chr7	151891481	151891609	151891509	151891584	MLL3	NM_170606	1	59	29	-	151891525	151891653
272911081	chr7	151896262	151896403	151896288	151896381	MLL3	NM_170606	1	59	27	-	151896364	151896544
273301515	chr7	151900006	151900143	151900036	151900115	MLL3	NM_170606	1	59	26	-	151900019	151900149
273688298	chr7	151904428	151904602	151904454	151904575	MLL3	NM_170606	1	59	24	-	151904385	151904513
272778397	chr7	151921454	151921618	151921480	151921596	MLL3	NM_170606	1	59	19	-	151921520	151921701
273457724	chr7	151944896	151945062	151944917	151945038	MLL3	NM_170606	1	59	14	-	151944987	151945705
273488966	chr7	151945373	151945545	151945399	151945523	MLL3	NM_170606	1	59	14	-	151944987	151945705
274566705	chr7	151947833	151948007	151947857	151947985	MLL3	NM_170606	1	59	12	-	151947938	151948051
272921329	chr7	151949550	151949723	151949577	151949696	MLL3	NM_170606	1	59	10	-	151949631	151949800
273954148	chr7	151960163	151960309	151960186	151960288	MLL3	NM_170606	1	59	9	-	151960101	151960215
273500770	chr7	152007045	152007195	152007068	152007168	MLL3	NM_170606	1	59	6	-	152007051	152007160
273332112	chr7	152012300	152012466	152012328	152012438	MLL3	NM_170606	1	59	4	-	152012223	152012423
273242886	chr7	152132735	152132897	152132753	152132873	MLL3	NM_170606	1	59	1	-	152132711	152133090
294951237	chr7	152346041	152346200	152346068	152346171	XRCC2	NM_005431	1	3	3	-	152343587	152346448
294730514	chr7	152357699	152357869	152357727	152357851	XRCC2	NM_005431	1	3	2	-	152357786	152357867
240009248	chr8	30916718	30916882	30916746	30916854	WRN	NM_000553	1	35	3	+	30916669	30916781
239082857	chr8	30922437	30922568	30922463	30922541	WRN	NM_000553	1	35	5	+	30922431	30922579
262086869	chr8	30924656	30924807	30924679	30924779	WRN	NM_000553	1	35	6	+	30924549	30924698
239979260	chr8	30933745	30933919	30933769	30933891	WRN	NM_000553	1	35	8	+	30933689	30933803
240024290	chr8	30938630	30938775	30938659	30938751	WRN	NM_000553	1	35	9	+	30938383	30938812
262065201	chr8	30946291	30946464	30946314	30946440	WRN	NM_000553	1	35	13	+	30946406	30946481
264510772	chr8	30949350	30949524	30949370	30949496	WRN	NM_000553	1	35	16	+	30949346	30949414
264511104	chr8	30969073	30969228	30969097	30969203	WRN	NM_000553	1	35	19	+	30969131	30969315
262978854	chr8	30973917	30974078	30973945	30974055	WRN	NM_000553	1	35	20	+	30973870	30974044
238916496	chr8	30982020	30982144	30982045	30982116	WRN	NM_000553	1	35	22	+	30982038	30982139
264609210	chr8	30989836	30989975	30989861	30989950	WRN	NM_000553	1	35	24	+	30989881	30990022

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240577165	chr8	30999026	30999181	30999047	30999154	WRN	NM_000553	1	35	25	+	30998946	30999116
242598639	chr8	31000148	31000322	31000170	31000295	WRN	NM_000553	1	35	27	+	31000142	31000217
264777981	chr8	31004789	31004923	31004819	31004900	WRN	NM_000553	1	35	30	+	31004880	31004992
240510024	chr8	31012133	31012298	31012161	31012271	WRN	NM_000553	1	35	32	+	31012140	31012271
239404253	chr8	31024565	31024689	31024593	31024665	WRN	NM_000553	1	35	34	+	31024538	31024746
228266244	chr8	37654774	37654919	37654791	37654900	GPR124	NM_032777	1	19	1	+	37654401	37655052
227180775	chr8	37672377	37672545	37672398	37672525	GPR124	NM_032777	1	19	2	+	37672414	37672485
228993618	chr8	37686964	37687107	37686986	37687086	GPR124	NM_032777	1	19	5	+	37687006	37687077
227392596	chr8	37688321	37688490	37688340	37688472	GPR124	NM_032777	1	19	7	+	37688228	37688441
227671500	chr8	37690547	37690709	37690567	37690690	GPR124	NM_032777	1	19	9	+	37690528	37690726
229077372	chr8	37691369	37691535	37691389	37691516	GPR124	NM_032777	1	19	11	+	37691485	37691646
227894304	chr8	37692879	37693035	37692900	37693014	GPR124	NM_032777	1	19	12	+	37692692	37692916
229079003	chr8	37695198	37695323	37695217	37695305	GPR124	NM_032777	1	19	14	+	37695249	37695457
228103822	chr8	37696551	37696681	37696569	37696661	GPR124	NM_032777	1	19	15	+	37696474	37696601
227341007	chr8	37698251	37698420	37698271	37698396	GPR124	NM_032777	1	19	18	+	37698278	37698367
227508650	chr8	37698919	37699093	37698937	37699075	GPR124	NM_032777	1	19	19	+	37698604	37701504
227560037	chr8	37699540	37699705	37699557	37699688	GPR124	NM_032777	1	19	19	+	37698604	37701504
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_001174066	4	17	17	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_001174065	3	18	18	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_001174063	1	18	18	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_023110	9	18	18	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_023106	8	17	17	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_023105	7	17	17	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_015850	6	18	18	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_001174067	5	19	19	-	38268656	38271322
230392972	chr8	38271105	38271266	38271124	38271249	FGFR1	NM_001174064	2	19	19	-	38268656	38271322
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_001174066	4	17	15	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_001174065	3	18	16	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_001174063	1	18	16	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_023110	9	18	16	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_023106	8	17	15	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_023105	7	17	15	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_015850	6	18	16	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_001174067	5	19	17	-	38271670	38271807
229661236	chr8	38271681	38271853	38271702	38271833	FGFR1	NM_001174064	2	19	17	-	38271670	38271807
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_001174066	4	17	13	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_001174065	3	18	14	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_001174063	1	18	14	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_023110	9	18	14	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_023106	8	17	13	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_023105	7	17	13	-	38272297	38272419

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_015850	6	18	14	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_001174067	5	19	15	-	38272297	38272419
227958806	chr8	38272341	38272510	38272363	38272489	FGFR1	NM_001174064	2	19	15	-	38272297	38272419
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_001174066	4	17	11	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_001174065	3	18	12	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_001174063	1	18	12	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_023110	9	18	12	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_023106	8	17	11	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_023105	7	17	11	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_015850	6	18	12	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_001174067	5	19	13	-	38274824	38274934
228571915	chr8	38274839	38274966	38274861	38274938	FGFR1	NM_001174064	2	19	13	-	38274824	38274934
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_001174066	4	17	9	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_001174065	3	18	10	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_001174063	1	18	10	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_023110	9	18	10	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_023106	8	17	9	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_023105	7	17	9	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_015850	6	18	10	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_001174067	5	19	11	-	38275746	38275891
228890947	chr8	38275833	38276005	38275852	38275981	FGFR1	NM_001174064	2	19	11	-	38275746	38275891
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_001174066	4	17	7	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_001174065	3	18	8	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_001174063	1	18	8	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_023110	9	18	8	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_023106	8	17	7	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_023105	7	17	7	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_015850	6	18	8	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_001174067	5	19	9	-	38279315	38279459
232425795	chr8	38279320	38279486	38279341	38279460	FGFR1	NM_001174064	2	19	9	-	38279315	38279459
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_001174066	4	17	5	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_001174065	3	18	6	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_001174063	1	18	6	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_023110	9	18	6	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_023106	8	17	5	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_023105	7	17	5	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_015850	6	18	6	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_001174067	5	19	7	-	38283640	38283763
229771207	chr8	38283632	38283796	38283653	38283772	FGFR1	NM_001174064	2	19	7	-	38283640	38283763
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_001174063	1	18	3	-	38287200	38287466

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_023110	9	18	3	-	38287200	38287466
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_015850	6	18	3	-	38287200	38287466
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
227973101	chr8	38287114	38287268	38287137	38287246	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
232244408	chr8	38297788	38297913	38297815	38297891	FGFR1	NM_001174064	2	19	3	-	38297824	38297891
232838090	chr8	38318535	38318698	38318553	38318673	FGFR1	NM_001174067	5	19	2	-	38318614	38318773
312166891	chr8	41789904	41790061	41789928	41790041	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312166891	chr8	41789904	41790061	41789928	41790041	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312166891	chr8	41789904	41790061	41789928	41790041	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312238708	chr8	41790356	41790514	41790377	41790492	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312238708	chr8	41790356	41790514	41790377	41790492	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312238708	chr8	41790356	41790514	41790377	41790492	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312336682	chr8	41791017	41791148	41791037	41791127	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312336682	chr8	41791017	41791148	41791037	41791127	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312336682	chr8	41791017	41791148	41791037	41791127	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312406126	chr8	41791420	41791590	41791444	41791570	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312406126	chr8	41791420	41791590	41791444	41791570	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312406126	chr8	41791420	41791590	41791444	41791570	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312654869	chr8	41791801	41791975	41791821	41791954	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312654869	chr8	41791801	41791975	41791821	41791954	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312654869	chr8	41791801	41791975	41791821	41791954	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312377486	chr8	41792206	41792352	41792230	41792326	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312377486	chr8	41792206	41792352	41792230	41792326	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312377486	chr8	41792206	41792352	41792230	41792326	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312361590	chr8	41794905	41795041	41794930	41795013	KAT6A	NM_001099412	1	18	17	-	41794774	41795086
312361590	chr8	41794905	41795041	41794930	41795013	KAT6A	NM_006766	3	17	16	-	41794774	41795086
312361590	chr8	41794905	41795041	41794930	41795013	KAT6A	NM_001099413	2	18	17	-	41794774	41795086
312408288	chr8	41798467	41798607	41798487	41798585	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312408288	chr8	41798467	41798607	41798487	41798585	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312408288	chr8	41798467	41798607	41798487	41798585	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312390829	chr8	41798883	41799051	41798911	41799020	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312390829	chr8	41798883	41799051	41798911	41799020	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312390829	chr8	41798883	41799051	41798911	41799020	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312371398	chr8	41801325	41801462	41801347	41801436	KAT6A	NM_001099412	1	18	14	-	41801266	41801497
312371398	chr8	41801325	41801462	41801347	41801436	KAT6A	NM_006766	3	17	13	-	41801266	41801497
312371398	chr8	41801325	41801462	41801347	41801436	KAT6A	NM_001099413	2	18	14	-	41801266	41801497
312308632	chr8	41805297	41805471	41805326	41805446	KAT6A	NM_001099412	1	18	12	-	41805269	41805430
312308632	chr8	41805297	41805471	41805326	41805446	KAT6A	NM_006766	3	17	11	-	41805269	41805430
312308632	chr8	41805297	41805471	41805326	41805446	KAT6A	NM_001099413	2	18	12	-	41805269	41805430
312349897	chr8	41812838	41812990	41812864	41812960	KAT6A	NM_001099412	1	18	10	-	41812814	41812929
312349897	chr8	41812838	41812990	41812864	41812960	KAT6A	NM_006766	3	17	9	-	41812814	41812929

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312349897	chr8	41812838	41812990	41812864	41812960	KAT6A	NM_001099413	2	18	10	-	41812814	41812929
312428143	chr8	41834548	41834697	41834571	41834670	KAT6A	NM_001099412	1	18	8	-	41834526	41834845
312428143	chr8	41834548	41834697	41834571	41834670	KAT6A	NM_006766	3	17	7	-	41834526	41834845
312428143	chr8	41834548	41834697	41834571	41834670	KAT6A	NM_001099413	2	18	8	-	41834526	41834845
312263150	chr8	41836220	41836353	41836247	41836324	KAT6A	NM_001099412	1	18	7	-	41836160	41836295
312263150	chr8	41836220	41836353	41836247	41836324	KAT6A	NM_006766	3	17	6	-	41836160	41836295
312263150	chr8	41836220	41836353	41836247	41836324	KAT6A	NM_001099413	2	18	7	-	41836160	41836295
312381179	chr8	41844923	41845097	41844948	41845075	KAT6A	NM_001099412	1	18	4	-	41844973	41845081
312381179	chr8	41844923	41845097	41844948	41845075	KAT6A	NM_006766	3	17	3	-	41844973	41845081
312381179	chr8	41844923	41845097	41844948	41845075	KAT6A	NM_001099413	2	18	4	-	41844973	41845081
312539061	chr8	41906224	41906376	41906248	41906349	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312539061	chr8	41906224	41906376	41906248	41906349	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312539061	chr8	41906224	41906376	41906248	41906349	KAT6A	NM_001099413	2	18	3	-	41905896	41906820
280897554	chr8	42129532	42129704	42129554	42129682	IKBKB	NM_001242778	2	21	2	+	42129601	42129723
280897554	chr8	42129532	42129704	42129554	42129682	IKBKB	NR_033819	5	21	2	+	42129601	42129723
280897554	chr8	42129532	42129704	42129554	42129682	IKBKB	NR_033818	4	22	2	+	42129601	42129723
280897554	chr8	42129532	42129704	42129554	42129682	IKBKB	NM_001556	3	22	2	+	42129601	42129723
280897554	chr8	42129532	42129704	42129554	42129682	IKBKB	NR_040009	6	22	2	+	42129601	42129723
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NM_001242778	2	21	3	+	42147674	42147791
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NR_033819	5	21	4	+	42147674	42147791
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NR_033818	4	22	4	+	42147674	42147791
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NM_001556	3	22	4	+	42147674	42147791
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NM_001190720	1	21	3	+	42147674	42147791
278648093	chr8	42147725	42147891	42147744	42147866	IKBKB	NR_040009	6	22	4	+	42147674	42147791
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NM_001242778	2	21	6	+	42163861	42163950
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NR_033819	5	21	7	+	42163861	42163950
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NR_033818	4	22	7	+	42163861	42163950
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NM_001556	3	22	7	+	42163861	42163950
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NM_001190720	1	21	6	+	42163861	42163950
279941344	chr8	42163798	42163971	42163823	42163951	IKBKB	NR_040009	6	22	7	+	42163861	42163950
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NM_001242778	2	21	9	+	42173728	42173857
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NR_033819	5	21	10	+	42173728	42173857
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NR_033818	4	22	10	+	42173728	42173857
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NM_001556	3	22	10	+	42173728	42173857
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NM_001190720	1	21	9	+	42173728	42173857
279726858	chr8	42173705	42173879	42173727	42173858	IKBKB	NR_040009	6	22	10	+	42173728	42173857
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NR_040009	6	22	12	+	42175228	42175289
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NM_001242778	2	21	11	+	42175175	42175289
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NR_033819	5	21	12	+	42175175	42175289
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NR_033818	4	22	12	+	42175175	42175289
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NM_001556	3	22	12	+	42175175	42175289

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279036646	chr8	42175191	42175348	42175219	42175320	IKBKB	NM_001190720	1	21	11	+	42175175	42175289
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NM_001242778	2	21	13	+	42176788	42176939
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NR_033819	5	21	14	+	42176788	42176939
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NR_033818	4	22	14	+	42176788	42176939
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NM_001556	3	22	14	+	42176788	42176939
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NM_001190720	1	21	13	+	42176788	42176939
281261580	chr8	42176805	42176962	42176826	42176940	IKBKB	NR_040009	6	22	14	+	42176788	42176939
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NM_001242778	2	21	17	+	42179572	42179671
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NR_033819	5	21	17	+	42179572	42179671
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NR_033818	4	22	18	+	42179572	42179671
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NM_001556	3	22	18	+	42179572	42179671
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NM_001190720	1	21	17	+	42179572	42179671
279175606	chr8	42179545	42179716	42179568	42179695	IKBKB	NR_040009	6	22	18	+	42179572	42179671
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NM_001242778	2	21	19	+	42183488	42183615
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NR_033819	5	21	19	+	42183488	42183615
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NR_033818	4	22	20	+	42183488	42183615
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NM_001556	3	22	20	+	42183488	42183615
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NM_001190720	1	21	19	+	42183488	42183615
280374446	chr8	42183506	42183657	42183526	42183636	IKBKB	NR_040009	6	22	20	+	42183488	42183615
227481668	chr8	42761261	42761394	42761289	42761373	HOOK3	NM_032410	1	22	2	+	42761316	42761401
227247139	chr8	42785216	42785358	42785241	42785330	HOOK3	NM_032410	1	22	4	+	42785265	42785315
227248023	chr8	42805459	42805624	42805484	42805597	HOOK3	NM_032410	1	22	6	+	42805531	42805598
227631818	chr8	42814361	42814485	42814389	42814463	HOOK3	NM_032410	1	22	8	+	42814374	42814457
229956014	chr8	42821658	42821807	42821686	42821783	HOOK3	NM_032410	1	22	10	+	42821616	42821756
227961502	chr8	42828305	42828479	42828330	42828452	HOOK3	NM_032410	1	22	12	+	42828432	42828542
227217160	chr8	42841701	42841860	42841728	42841836	HOOK3	NM_032410	1	22	15	+	42841798	42841938
227671727	chr8	42865431	42865582	42865451	42865554	HOOK3	NM_032410	1	22	19	+	42865448	42865548
230352458	chr8	42873405	42873548	42873435	42873525	HOOK3	NM_032410	1	22	22	+	42873501	42885682
269827770	chr8	48689293	48689467	48689319	48689438	PRKDC	NM_001081640	1	85	84	-	48689405	48689544
269827770	chr8	48689293	48689467	48689319	48689438	PRKDC	NM_006904	2	86	85	-	48689405	48689544
269469367	chr8	48690945	48691118	48690972	48691096	PRKDC	NM_001081640	1	85	82	-	48691020	48691221
269469367	chr8	48690945	48691118	48690972	48691096	PRKDC	NM_006904	2	86	83	-	48691020	48691221
270171105	chr8	48691466	48691637	48691491	48691608	PRKDC	NM_001081640	1	85	80	-	48691565	48691654
270171105	chr8	48691466	48691637	48691491	48691608	PRKDC	NM_006904	2	86	81	-	48691565	48691654
270325844	chr8	48694920	48695081	48694938	48695063	PRKDC	NM_001081640	1	85	79	-	48694939	48695159
270325844	chr8	48694920	48695081	48694938	48695063	PRKDC	NM_006904	2	86	79	-	48694939	48695159
270794573	chr8	48697672	48697839	48697692	48697811	PRKDC	NM_001081640	1	85	77	-	48697674	48697878
270794573	chr8	48697672	48697839	48697692	48697811	PRKDC	NM_006904	2	86	77	-	48697674	48697878
270920204	chr8	48701667	48701792	48701696	48701767	PRKDC	NM_001081640	1	85	75	-	48701712	48701799
270920204	chr8	48701667	48701792	48701696	48701767	PRKDC	NM_006904	2	86	75	-	48701712	48701799
270010294	chr8	48706926	48707091	48706949	48707064	PRKDC	NM_001081640	1	85	74	-	48706851	48707062

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270010294	chr8	48706926	48707091	48706949	48707064	PRKDC	NM_006904	2	86	74	-	48706851	48707062
271959196	chr8	48711822	48711993	48711845	48711970	PRKDC	NM_001081640	1	85	72	-	48711771	48711951
271959196	chr8	48711822	48711993	48711845	48711970	PRKDC	NM_006904	2	86	72	-	48711771	48711951
269838052	chr8	48715845	48716013	48715869	48715987	PRKDC	NM_001081640	1	85	70	-	48715867	48716041
269838052	chr8	48715845	48716013	48715869	48715987	PRKDC	NM_006904	2	86	70	-	48715867	48716041
269562787	chr8	48729986	48730158	48730007	48730130	PRKDC	NM_001081640	1	85	68	-	48730011	48730122
269562787	chr8	48729986	48730158	48730007	48730130	PRKDC	NM_006904	2	86	68	-	48730011	48730122
272003272	chr8	48733401	48733550	48733421	48733523	PRKDC	NM_001081640	1	85	66	-	48733280	48733504
272003272	chr8	48733401	48733550	48733421	48733523	PRKDC	NM_006904	2	86	66	-	48733280	48733504
271585946	chr8	48736360	48736514	48736387	48736486	PRKDC	NM_001081640	1	85	64	-	48736419	48736557
271585946	chr8	48736360	48736514	48736387	48736486	PRKDC	NM_006904	2	86	64	-	48736419	48736557
271990230	chr8	48740633	48740801	48740656	48740773	PRKDC	NM_001081640	1	85	62	-	48740729	48740908
271990230	chr8	48740633	48740801	48740656	48740773	PRKDC	NM_006904	2	86	62	-	48740729	48740908
269807753	chr8	48743191	48743364	48743211	48743342	PRKDC	NM_001081640	1	85	61	-	48743166	48743297
269807753	chr8	48743191	48743364	48743211	48743342	PRKDC	NM_006904	2	86	61	-	48743166	48743297
270616609	chr8	48746821	48746984	48746842	48746961	PRKDC	NM_001081640	1	85	59	-	48746757	48746957
270616609	chr8	48746821	48746984	48746842	48746961	PRKDC	NM_006904	2	86	59	-	48746757	48746957
270207430	chr8	48749685	48749859	48749707	48749833	PRKDC	NM_001081640	1	85	57	-	48749773	48749980
270207430	chr8	48749685	48749859	48749707	48749833	PRKDC	NM_006904	2	86	57	-	48749773	48749980
271420682	chr8	48752661	48752820	48752682	48752795	PRKDC	NM_001081640	1	85	55	-	48752577	48752750
271420682	chr8	48752661	48752820	48752682	48752795	PRKDC	NM_006904	2	86	55	-	48752577	48752750
272506810	chr8	48761953	48762117	48761975	48762090	PRKDC	NM_001081640	1	85	53	-	48761940	48762064
272506810	chr8	48761953	48762117	48761975	48762090	PRKDC	NM_006904	2	86	53	-	48761940	48762064
269652441	chr8	48766647	48766810	48766668	48766784	PRKDC	NM_001081640	1	85	51	-	48766644	48766775
269652441	chr8	48766647	48766810	48766668	48766784	PRKDC	NM_006904	2	86	51	-	48766644	48766775
272486207	chr8	48769583	48769754	48769604	48769729	PRKDC	NM_001081640	1	85	49	-	48769717	48769860
272486207	chr8	48769583	48769754	48769604	48769729	PRKDC	NM_006904	2	86	49	-	48769717	48769860
272652098	chr8	48771385	48771529	48771409	48771508	PRKDC	NM_001081640	1	85	47	-	48771410	48771547
272652098	chr8	48771385	48771529	48771409	48771508	PRKDC	NM_006904	2	86	47	-	48771410	48771547
270243638	chr8	48772273	48772446	48772297	48772419	PRKDC	NM_001081640	1	85	46	-	48772172	48772320
270243638	chr8	48772273	48772446	48772297	48772419	PRKDC	NM_006904	2	86	46	-	48772172	48772320
270406257	chr8	48774895	48775024	48774921	48775002	PRKDC	NM_001081640	1	85	43	-	48774934	48775102
270406257	chr8	48774895	48775024	48774921	48775002	PRKDC	NM_006904	2	86	43	-	48774934	48775102
271078910	chr8	48776094	48776260	48776120	48776229	PRKDC	NM_001081640	1	85	42	-	48775960	48776138
271078910	chr8	48776094	48776260	48776120	48776229	PRKDC	NM_006904	2	86	42	-	48775960	48776138
272416716	chr8	48790232	48790405	48790256	48790378	PRKDC	NM_001081640	1	85	40	-	48790285	48790412
272416716	chr8	48790232	48790405	48790256	48790378	PRKDC	NM_006904	2	86	40	-	48790285	48790412
271117563	chr8	48793975	48794114	48794003	48794086	PRKDC	NM_001081640	1	85	38	-	48793977	48794081
271117563	chr8	48793975	48794114	48794003	48794086	PRKDC	NM_006904	2	86	38	-	48793977	48794081
270543661	chr8	48798576	48798749	48798604	48798727	PRKDC	NM_001081640	1	85	36	-	48798505	48798708
270543661	chr8	48798576	48798749	48798604	48798727	PRKDC	NM_006904	2	86	36	-	48798505	48798708

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270951624	chr8	48801089	48801246	48801115	48801218	PRKDC	NM_001081640	1	85	34	-	48801079	48801211
270951624	chr8	48801089	48801246	48801115	48801218	PRKDC	NM_006904	2	86	34	-	48801079	48801211
269948255	chr8	48802844	48802994	48802866	48802969	PRKDC	NM_001081640	1	85	32	-	48802818	48803041
269948255	chr8	48802844	48802994	48802866	48802969	PRKDC	NM_006904	2	86	32	-	48802818	48803041
271169332	chr8	48805906	48806078	48805931	48806049	PRKDC	NM_001081640	1	85	31	-	48805700	48805947
271169332	chr8	48805906	48806078	48805931	48806049	PRKDC	NM_006904	2	86	31	-	48805700	48805947
271332733	chr8	48811070	48811238	48811094	48811205	PRKDC	NM_001081640	1	85	29	-	48811030	48811129
271332733	chr8	48811070	48811238	48811094	48811205	PRKDC	NM_006904	2	86	29	-	48811030	48811129
271568793	chr8	48815293	48815421	48815317	48815393	PRKDC	NM_001081640	1	85	27	-	48815129	48815355
271568793	chr8	48815293	48815421	48815317	48815393	PRKDC	NM_006904	2	86	27	-	48815129	48815355
271916095	chr8	48824999	48825145	48825019	48825124	PRKDC	NM_001081640	1	85	25	-	48824970	48825122
271916095	chr8	48824999	48825145	48825019	48825124	PRKDC	NM_006904	2	86	25	-	48824970	48825122
270249449	chr8	48827821	48827945	48827849	48827918	PRKDC	NM_001081640	1	85	23	-	48827888	48827978
270249449	chr8	48827821	48827945	48827849	48827918	PRKDC	NM_006904	2	86	23	-	48827888	48827978
271283241	chr8	48839632	48839789	48839660	48839766	PRKDC	NM_001081640	1	85	21	-	48839754	48839913
271283241	chr8	48839632	48839789	48839660	48839766	PRKDC	NM_006904	2	86	21	-	48839754	48839913
272034430	chr8	48840404	48840563	48840429	48840535	PRKDC	NM_001081640	1	85	20	-	48840331	48840450
272034430	chr8	48840404	48840563	48840429	48840535	PRKDC	NM_006904	2	86	20	-	48840331	48840450
270102898	chr8	48842515	48842657	48842541	48842629	PRKDC	NM_001081640	1	85	18	-	48842413	48842572
270102898	chr8	48842515	48842657	48842541	48842629	PRKDC	NM_006904	2	86	18	-	48842413	48842572
271550480	chr8	48845589	48845720	48845617	48845693	PRKDC	NM_001081640	1	85	16	-	48845580	48845732
271550480	chr8	48845589	48845720	48845617	48845693	PRKDC	NM_006904	2	86	16	-	48845580	48845732
271325100	chr8	48847495	48847624	48847518	48847595	PRKDC	NM_001081640	1	85	14	-	48847569	48847618
271325100	chr8	48847495	48847624	48847518	48847595	PRKDC	NM_006904	2	86	14	-	48847569	48847618
270609937	chr8	48848368	48848495	48848389	48848467	PRKDC	NM_001081640	1	85	13	-	48848292	48848460
270609937	chr8	48848368	48848495	48848389	48848467	PRKDC	NM_006904	2	86	13	-	48848292	48848460
270046793	chr8	48852056	48852199	48852083	48852170	PRKDC	NM_001081640	1	85	11	-	48852111	48852257
270046793	chr8	48852056	48852199	48852083	48852170	PRKDC	NM_006904	2	86	11	-	48852111	48852257
269603279	chr8	48855826	48855980	48855848	48855952	PRKDC	NM_001081640	1	85	10	-	48855769	48855926
269603279	chr8	48855826	48855980	48855848	48855952	PRKDC	NM_006904	2	86	10	-	48855769	48855926
270711249	chr8	48866114	48866249	48866138	48866228	PRKDC	NM_001081640	1	85	7	-	48866180	48866279
270711249	chr8	48866114	48866249	48866138	48866228	PRKDC	NM_006904	2	86	7	-	48866180	48866279
271044401	chr8	48866879	48867044	48866907	48867016	PRKDC	NM_001081640	1	85	5	-	48866898	48867006
271044401	chr8	48866879	48867044	48866907	48867016	PRKDC	NM_006904	2	86	5	-	48866898	48867006
269462910	chr8	48869732	48869872	48869760	48869843	PRKDC	NM_001081640	1	85	3	-	48869731	48869823
269462910	chr8	48869732	48869872	48869760	48869843	PRKDC	NM_006904	2	86	3	-	48869731	48869823
237042741	chr8	57078858	57078984	57078879	57078959	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237042741	chr8	57078858	57078984	57078879	57078959	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237042741	chr8	57078858	57078984	57078879	57078959	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
240894156	chr8	57079280	57079447	57079308	57079421	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240894156	chr8	57079280	57079447	57079308	57079421	PLAG1	NM_001114634	1	4	4	-	57073468	57080062

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240894156	chr8	57079280	57079447	57079308	57079421	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
237178442	chr8	57079776	57079932	57079797	57079905	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237178442	chr8	57079776	57079932	57079797	57079905	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237178442	chr8	57079776	57079932	57079797	57079905	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
238266569	chr8	57080605	57080756	57080626	57080732	PLAG1	NM_002655	3	5	4	-	57080587	57080945
238266569	chr8	57080605	57080756	57080626	57080732	PLAG1	NM_001114634	1	4	3	-	57080587	57080945
237143684	chr8	71033529	71033689	71033552	71033666	NCOA2	NM_006540	1	23	22	-	71033537	71033626
236273997	chr8	71036990	71037141	71037012	71037113	NCOA2	NM_006540	1	23	20	-	71036923	71037100
258689379	chr8	71040536	71040697	71040560	71040676	NCOA2	NM_006540	1	23	18	-	71040668	71040745
235671193	chr8	71041162	71041291	71041186	71041263	NCOA2	NM_006540	1	23	17	-	71040937	71041215
239985956	chr8	71050513	71050680	71050537	71050655	NCOA2	NM_006540	1	23	15	-	71050438	71050567
236831140	chr8	71056922	71057048	71056945	71057020	NCOA2	NM_006540	1	23	13	-	71056877	71057083
236294835	chr8	71060644	71060778	71060668	71060754	NCOA2	NM_006540	1	23	12	-	71060508	71060718
240225755	chr8	71068504	71068628	71068525	71068607	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240192613	chr8	71068851	71069022	71068875	71068998	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240210093	chr8	71069297	71069465	71069319	71069442	NCOA2	NM_006540	1	23	11	-	71068206	71069475
237963221	chr8	71074825	71074995	71074847	71074973	NCOA2	NM_006540	1	23	9	-	71074946	71075089
235736180	chr8	71078714	71078888	71078741	71078860	NCOA2	NM_006540	1	23	7	-	71078801	71078989
235564745	chr8	71082547	71082691	71082573	71082664	NCOA2	NM_006540	1	23	6	-	71082437	71082614
240423850	chr8	71126279	71126430	71126305	71126399	NCOA2	NM_006540	1	23	4	-	71126138	71126310
236268705	chr8	90949219	90949344	90949247	90949315	NBN	NM_002485	1	16	15	-	90949254	90949303
241230625	chr8	90958341	90958515	90958370	90958488	NBN	NM_002485	1	16	13	-	90958368	90958523
258706709	chr8	90965555	90965699	90965583	90965671	NBN	NM_002485	1	16	11	-	90965472	90965919
235638295	chr8	90967398	90967572	90967424	90967554	NBN	NM_002485	1	16	10	-	90967511	90967783
238079093	chr8	90970824	90970998	90970847	90970972	NBN	NM_002485	1	16	9	-	90970953	90971082
236514340	chr8	90982591	90982747	90982619	90982719	NBN	NM_002485	1	16	7	-	90982592	90982785
237177776	chr8	90990337	90990492	90990364	90990469	NBN	NM_002485	1	16	5	-	90990448	90990551
235144027	chr8	90993549	90993673	90993572	90993650	NBN	NM_002485	1	16	3	-	90993603	90993751
236160438	chr8	90995006	90995145	90995033	90995117	NBN	NM_002485	1	16	2	-	90994950	90995083
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_004349	12	11	11	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198625	1	15	15	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198626	2	13	13	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198627	3	14	14	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198679	11	12	12	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_175636	15	10	10	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198630	6	13	13	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_175635	14	11	11	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_175634	13	12	12	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198633	9	11	11	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198632	8	12	12	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198631	7	12	12	-	92967195	92972745

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198634	10	11	11	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198629	5	12	12	-	92967195	92972745
240190808	chr8	92972646	92972794	92972668	92972766	RUNX1T1	NM_001198628	4	12	12	-	92967195	92972745
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_004349	12	11	8	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198625	1	15	12	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198626	2	13	10	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198627	3	14	11	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198679	11	12	9	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_175636	15	10	7	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198630	6	13	10	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_175635	14	11	8	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_175634	13	12	9	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198633	9	11	8	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198632	8	12	9	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198631	7	12	9	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198634	10	11	8	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198629	5	12	9	-	92998352	92998553
241661028	chr8	92998332	92998504	92998361	92998483	RUNX1T1	NM_001198628	4	12	9	-	92998352	92998553
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_004349	12	11	6	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198625	1	15	10	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198626	2	13	8	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198627	3	14	9	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198679	11	12	7	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_175636	15	10	5	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198630	6	13	8	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_175635	14	11	6	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_175634	13	12	7	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198633	9	11	6	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198632	8	12	7	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198631	7	12	7	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198634	10	11	6	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198629	5	12	7	-	93003867	93004117
242674741	chr8	93003802	93003974	93003828	93003954	RUNX1T1	NM_001198628	4	12	7	-	93003867	93004117
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_004349	12	11	5	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198625	1	15	9	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198626	2	13	7	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198627	3	14	8	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198679	11	12	6	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_175636	15	10	4	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198630	6	13	7	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_175635	14	11	5	-	93017344	93017525

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_175634	13	12	6	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198633	9	11	5	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198632	8	12	6	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198631	7	12	6	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198634	10	11	5	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198629	5	12	6	-	93017344	93017525
241705064	chr8	93017376	93017548	93017397	93017525	RUNX1T1	NM_001198628	4	12	6	-	93017344	93017525
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_004349	12	11	3	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198625	1	15	7	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198626	2	13	5	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198627	3	14	6	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198679	11	12	4	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_175636	15	10	2	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198630	6	13	5	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_175635	14	11	3	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_175634	13	12	4	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198633	9	11	3	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198632	8	12	4	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198631	7	12	4	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198634	10	11	3	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198629	5	12	4	-	93026807	93027048
240949849	chr8	93026818	93026982	93026837	93026960	RUNX1T1	NM_001198628	4	12	4	-	93026807	93027048
238458948	chr8	93074655	93074803	93074676	93074781	RUNX1T1	NM_001198625	1	15	5	-	93074774	93074855
238458948	chr8	93074655	93074803	93074676	93074781	RUNX1T1	NM_004349	12	11	1	-	93074774	93075191
238458948	chr8	93074655	93074803	93074676	93074781	RUNX1T1	NM_001198632	8	12	2	-	93074774	93074937
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198625	1	15	1	-	93107575	93107882
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198626	2	13	1	-	93107575	93107882
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198627	3	14	1	-	93107575	93107882
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198679	11	12	1	-	93107575	93107882
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198631	7	12	1	-	93107575	93107882
238947202	chr8	93107552	93107677	93107572	93107649	RUNX1T1	NM_001198634	10	11	1	-	93107575	93107882
303472489	chr8	103266545	103266681	103266572	103266656	UBR5	NM_015902	1	59	59	-	103264502	103266742
302819106	chr8	103271221	103271348	103271249	103271320	UBR5	NM_015902	1	59	57	-	103271213	103271357
305621970	chr8	103274028	103274184	103274053	103274156	UBR5	NM_015902	1	59	55	-	103274143	103274298
304022779	chr8	103277393	103277534	103277418	103277507	UBR5	NM_015902	1	59	53	-	103277328	103277506
299494310	chr8	103281234	103281387	103281255	103281358	UBR5	NM_015902	1	59	51	-	103281206	103281336
300345607	chr8	103284665	103284799	103284693	103284771	UBR5	NM_015902	1	59	48	-	103284757	103285000
299283946	chr8	103287811	103287971	103287837	103287945	UBR5	NM_015902	1	59	47	-	103287749	103287847
299283946	chr8	103287811	103287971	103287837	103287945	UBR5	NM_015902	1	59	46	-	103287936	103288056
302478055	chr8	103289370	103289541	103289398	103289517	UBR5	NM_015902	1	59	45	-	103289200	103289420
303848648	chr8	103291263	103291395	103291284	103291372	UBR5	NM_015902	1	59	43	-	103291264	103291436

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299304443	chr8	103293508	103293679	103293535	103293652	UBR5	NM_015902	1	59	41	-	103293517	103293747
300460465	chr8	103297616	103297786	103297642	103297762	UBR5	NM_015902	1	59	39	-	103297741	103298009
301353734	chr8	103298684	103298855	103298705	103298829	UBR5	NM_015902	1	59	38	-	103298588	103298845
303130176	chr8	103300432	103300571	103300455	103300542	UBR5	NM_015902	1	59	36	-	103300383	103300494
302137715	chr8	103305859	103305994	103305880	103305971	UBR5	NM_015902	1	59	34	-	103305833	103306072
300346018	chr8	103306172	103306300	103306200	103306272	UBR5	NM_015902	1	59	33	-	103306183	103306343
301940968	chr8	103307322	103307496	103307345	103307473	UBR5	NM_015902	1	59	31	-	103307432	103307558
305537880	chr8	103307753	103307921	103307775	103307896	UBR5	NM_015902	1	59	29	-	103307864	103308010
302049127	chr8	103309596	103309770	103309624	103309741	UBR5	NM_015902	1	59	27	-	103309686	103309834
302762039	chr8	103311020	103311161	103311052	103311133	UBR5	NM_015902	1	59	25	-	103311076	103311199
302041350	chr8	103312170	103312334	103312195	103312311	UBR5	NM_015902	1	59	23	-	103312228	103312379
303258340	chr8	103316344	103316482	103316365	103316449	UBR5	NM_015902	1	59	22	-	103316271	103316397
301804586	chr8	103323480	103323635	103323508	103323607	UBR5	NM_015902	1	59	20	-	103323527	103323724
299454121	chr8	103323966	103324096	103323988	103324068	UBR5	NM_015902	1	59	19	-	103323963	103324117
300636997	chr8	103324518	103324655	103324543	103324631	UBR5	NM_015902	1	59	17	-	103324570	103324713
300603061	chr8	103326027	103326173	103326050	103326143	UBR5	NM_015902	1	59	16	-	103326032	103326144
302563128	chr8	103338646	103338811	103338669	103338785	UBR5	NM_015902	1	59	13	-	103338774	103338891
303220266	chr8	103341189	103341363	103341217	103341337	UBR5	NM_015902	1	59	11	-	103341318	103341428
300325928	chr8	103357656	103357802	103357683	103357774	UBR5	NM_015902	1	59	8	-	103357624	103357773
300206062	chr8	103359208	103359333	103359229	103359309	UBR5	NM_015902	1	59	6	-	103359131	103359320
302196986	chr8	103372839	103372978	103372862	103372950	UBR5	NM_015902	1	59	4	-	103372817	103372893
286559822	chr8	113236944	113237097	113236966	113237070	CSMD3	NM_052900	1	69	69	-	113235159	113237159
286559822	chr8	113236944	113237097	113236966	113237070	CSMD3	NM_198123	2	71	71	-	113235159	113237159
286559822	chr8	113236944	113237097	113236966	113237070	CSMD3	NM_198124	3	72	72	-	113235159	113237159
286218972	chr8	113243788	113243920	113243816	113243895	CSMD3	NM_052900	1	69	67	-	113243774	113243861
286218972	chr8	113243788	113243920	113243816	113243895	CSMD3	NM_198123	2	71	69	-	113243774	113243861
286218972	chr8	113243788	113243920	113243816	113243895	CSMD3	NM_198124	3	72	70	-	113243774	113243861
287664314	chr8	113249457	113249582	113249478	113249557	CSMD3	NM_052900	1	69	65	-	113249419	113249577
287664314	chr8	113249457	113249582	113249478	113249557	CSMD3	NM_198123	2	71	67	-	113249419	113249577
287664314	chr8	113249457	113249582	113249478	113249557	CSMD3	NM_198124	3	72	68	-	113249419	113249577
288958612	chr8	113259196	113259368	113259227	113259340	CSMD3	NM_052900	1	69	62	-	113259249	113259360
288958612	chr8	113259196	113259368	113259227	113259340	CSMD3	NM_198123	2	71	64	-	113259249	113259360
288958612	chr8	113259196	113259368	113259227	113259340	CSMD3	NM_198124	3	72	65	-	113259249	113259360
288634708	chr8	113267445	113267609	113267472	113267581	CSMD3	NM_052900	1	69	60	-	113267483	113267656
288634708	chr8	113267445	113267609	113267472	113267581	CSMD3	NM_198123	2	71	62	-	113267483	113267656
288634708	chr8	113267445	113267609	113267472	113267581	CSMD3	NM_198124	3	72	63	-	113267483	113267656
285286225	chr8	113275956	113276091	113275983	113276066	CSMD3	NM_052900	1	69	59	-	113275868	113276041
285286225	chr8	113275956	113276091	113275983	113276066	CSMD3	NM_198123	2	71	61	-	113275868	113276041
285286225	chr8	113275956	113276091	113275983	113276066	CSMD3	NM_198124	3	72	62	-	113275868	113276041
289036770	chr8	113293404	113293532	113293432	113293504	CSMD3	NM_052900	1	69	57	-	113293403	113293579
289036770	chr8	113293404	113293532	113293432	113293504	CSMD3	NM_198123	2	71	59	-	113293403	113293579

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
289036770	chr8	113293404	113293532	113293432	113293504	CSMD3	NM_198124	3	72	60	-	113293403	113293579
286719198	chr8	113299361	113299508	113299389	113299480	CSMD3	NM_052900	1	69	56	-	113299293	113299475
286719198	chr8	113299361	113299508	113299389	113299480	CSMD3	NM_198123	2	71	58	-	113299293	113299475
286719198	chr8	113299361	113299508	113299389	113299480	CSMD3	NM_198124	3	72	59	-	113299293	113299475
286337436	chr8	113303743	113303867	113303769	113303840	CSMD3	NM_052900	1	69	54	-	113303739	113303924
286337436	chr8	113303743	113303867	113303769	113303840	CSMD3	NM_198123	2	71	56	-	113303739	113303924
286337436	chr8	113303743	113303867	113303769	113303840	CSMD3	NM_198124	3	72	57	-	113303739	113303924
287757594	chr8	113304818	113304981	113304840	113304958	CSMD3	NM_052900	1	69	53	-	113304766	113304939
287757594	chr8	113304818	113304981	113304840	113304958	CSMD3	NM_198123	2	71	55	-	113304766	113304939
287757594	chr8	113304818	113304981	113304840	113304958	CSMD3	NM_198124	3	72	56	-	113304766	113304939
288076698	chr8	113313956	113314086	113313979	113314065	CSMD3	NM_052900	1	69	51	-	113314022	113314195
288076698	chr8	113313956	113314086	113313979	113314065	CSMD3	NM_198123	2	71	53	-	113314022	113314195
288076698	chr8	113313956	113314086	113313979	113314065	CSMD3	NM_198124	3	72	54	-	113314022	113314195
286329954	chr8	113316961	113317110	113316988	113317087	CSMD3	NM_198123	2	71	52	-	113316950	113317144
286329954	chr8	113316961	113317110	113316988	113317087	CSMD3	NM_198124	3	72	53	-	113316950	113317144
287832487	chr8	113323098	113323272	113323126	113323250	CSMD3	NM_052900	1	69	49	-	113323207	113323395
287832487	chr8	113323098	113323272	113323126	113323250	CSMD3	NM_198123	2	71	50	-	113323207	113323395
287832487	chr8	113323098	113323272	113323126	113323250	CSMD3	NM_198124	3	72	51	-	113323207	113323395
287631286	chr8	113326230	113326395	113326255	113326367	CSMD3	NM_052900	1	69	48	-	113326135	113326281
287631286	chr8	113326230	113326395	113326255	113326367	CSMD3	NM_198123	2	71	49	-	113326135	113326281
287631286	chr8	113326230	113326395	113326255	113326367	CSMD3	NM_198124	3	72	50	-	113326135	113326281
287436207	chr8	113331054	113331216	113331080	113331190	CSMD3	NM_052900	1	69	46	-	113331066	113331179
287436207	chr8	113331054	113331216	113331080	113331190	CSMD3	NM_198123	2	71	47	-	113331066	113331179
287436207	chr8	113331054	113331216	113331080	113331190	CSMD3	NM_198124	3	72	48	-	113331066	113331179
284874763	chr8	113348858	113349022	113348889	113348994	CSMD3	NM_052900	1	69	43	-	113348881	113349058
284874763	chr8	113348858	113349022	113348889	113348994	CSMD3	NM_198123	2	71	44	-	113348881	113349058
284874763	chr8	113348858	113349022	113348889	113348994	CSMD3	NM_198124	3	72	45	-	113348881	113349058
288739686	chr8	113349879	113350041	113349907	113350016	CSMD3	NM_052900	1	69	42	-	113349772	113349960
288739686	chr8	113349879	113350041	113349907	113350016	CSMD3	NM_198123	2	71	43	-	113349772	113349960
288739686	chr8	113349879	113350041	113349907	113350016	CSMD3	NM_198124	3	72	44	-	113349772	113349960
285905566	chr8	113358336	113358462	113358363	113358436	CSMD3	NM_052900	1	69	40	-	113358326	113358442
285905566	chr8	113358336	113358462	113358363	113358436	CSMD3	NM_198123	2	71	41	-	113358326	113358442
285905566	chr8	113358336	113358462	113358363	113358436	CSMD3	NM_198124	3	72	42	-	113358326	113358442
284765703	chr8	113364605	113364769	113364630	113364743	CSMD3	NM_052900	1	69	38	-	113364645	113364763
284765703	chr8	113364605	113364769	113364630	113364743	CSMD3	NM_198123	2	71	39	-	113364645	113364763
284765703	chr8	113364605	113364769	113364630	113364743	CSMD3	NM_198124	3	72	40	-	113364645	113364763
287937230	chr8	113395705	113395879	113395736	113395851	CSMD3	NM_052900	1	69	36	-	113395796	113395892
287937230	chr8	113395705	113395879	113395736	113395851	CSMD3	NM_198123	2	71	37	-	113395796	113395892
287937230	chr8	113395705	113395879	113395736	113395851	CSMD3	NM_198124	3	72	38	-	113395796	113395892
288469338	chr8	113418723	113418879	113418756	113418859	CSMD3	NM_052900	1	69	34	-	113418753	113418956
288469338	chr8	113418723	113418879	113418756	113418859	CSMD3	NM_198123	2	71	35	-	113418753	113418956

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288469338	chr8	113418723	113418879	113418756	113418859	CSMD3	NM_198124	3	72	36	-	113418753	113418956
287117354	chr8	113420618	113420750	113420642	113420718	CSMD3	NM_052900	1	69	33	-	113420547	113420642
287117354	chr8	113420618	113420750	113420642	113420718	CSMD3	NM_198123	2	71	34	-	113420547	113420642
287117354	chr8	113420618	113420750	113420642	113420718	CSMD3	NM_198124	3	72	35	-	113420547	113420642
286748836	chr8	113504591	113504764	113504614	113504741	CSMD3	NM_052900	1	69	30	-	113504718	113504912
286748836	chr8	113504591	113504764	113504614	113504741	CSMD3	NM_198123	2	71	31	-	113504718	113504912
286748836	chr8	113504591	113504764	113504614	113504741	CSMD3	NM_198124	3	72	32	-	113504718	113504912
284766325	chr8	113516054	113516179	113516076	113516151	CSMD3	NM_052900	1	69	29	-	113516019	113516206
284766325	chr8	113516054	113516179	113516076	113516151	CSMD3	NM_198123	2	71	30	-	113516019	113516206
284766325	chr8	113516054	113516179	113516076	113516151	CSMD3	NM_198124	3	72	31	-	113516019	113516206
288898222	chr8	113519002	113519168	113519028	113519142	CSMD3	NM_052900	1	69	28	-	113518920	113519058
288898222	chr8	113519002	113519168	113519028	113519142	CSMD3	NM_198123	2	71	29	-	113518920	113519058
288898222	chr8	113519002	113519168	113519028	113519142	CSMD3	NM_198124	3	72	30	-	113518920	113519058
288871443	chr8	113562942	113563073	113562965	113563047	CSMD3	NM_052900	1	69	26	-	113562900	113563102
288871443	chr8	113562942	113563073	113562965	113563047	CSMD3	NM_198123	2	71	27	-	113562900	113563102
288871443	chr8	113562942	113563073	113562965	113563047	CSMD3	NM_198124	3	72	28	-	113562900	113563102
286255182	chr8	113568882	113569017	113568914	113568993	CSMD3	NM_052900	1	69	24	-	113568992	113569183
286255182	chr8	113568882	113569017	113568914	113568993	CSMD3	NM_198123	2	71	25	-	113568992	113569183
286255182	chr8	113568882	113569017	113568914	113568993	CSMD3	NM_198124	3	72	26	-	113568992	113569183
287542937	chr8	113585669	113585824	113585698	113585796	CSMD3	NM_052900	1	69	23	-	113585730	113585886
287542937	chr8	113585669	113585824	113585698	113585796	CSMD3	NM_198123	2	71	24	-	113585730	113585886
287542937	chr8	113585669	113585824	113585698	113585796	CSMD3	NM_198124	3	72	25	-	113585730	113585886
286423964	chr8	113599328	113599453	113599355	113599425	CSMD3	NM_052900	1	69	22	-	113599295	113599464
286423964	chr8	113599328	113599453	113599355	113599425	CSMD3	NM_198123	2	71	23	-	113599295	113599464
286423964	chr8	113599328	113599453	113599355	113599425	CSMD3	NM_198124	3	72	24	-	113599295	113599464
288912015	chr8	113649173	113649297	113649198	113649268	CSMD3	NM_052900	1	69	21	-	113649046	113649234
288912015	chr8	113649173	113649297	113649198	113649268	CSMD3	NM_198123	2	71	22	-	113649046	113649234
288912015	chr8	113649173	113649297	113649198	113649268	CSMD3	NM_198124	3	72	23	-	113649046	113649234
285179532	chr8	113657226	113657364	113657252	113657341	CSMD3	NM_052900	1	69	19	-	113657338	113657454
285179532	chr8	113657226	113657364	113657252	113657341	CSMD3	NM_198123	2	71	20	-	113657338	113657454
285179532	chr8	113657226	113657364	113657252	113657341	CSMD3	NM_198124	3	72	21	-	113657338	113657454
284949116	chr8	113668332	113668478	113668358	113668453	CSMD3	NM_052900	1	69	17	-	113668383	113668570
284949116	chr8	113668332	113668478	113668358	113668453	CSMD3	NM_198123	2	71	18	-	113668383	113668570
284949116	chr8	113668332	113668478	113668358	113668453	CSMD3	NM_198124	3	72	19	-	113668383	113668570
286457207	chr8	113678522	113678658	113678546	113678632	CSMD3	NM_052900	1	69	16	-	113678506	113678644
286457207	chr8	113678522	113678658	113678546	113678632	CSMD3	NM_198123	2	71	17	-	113678506	113678644
286457207	chr8	113678522	113678658	113678546	113678632	CSMD3	NM_198124	3	72	18	-	113678506	113678644
286416802	chr8	113694726	113694851	113694751	113694828	CSMD3	NM_052900	1	69	15	-	113694671	113694865
286416802	chr8	113694726	113694851	113694751	113694828	CSMD3	NM_198123	2	71	16	-	113694671	113694865
286416802	chr8	113694726	113694851	113694751	113694828	CSMD3	NM_198124	3	72	17	-	113694671	113694865
285118642	chr8	113697761	113697915	113697784	113697891	CSMD3	NM_052900	1	69	14	-	113697635	113697961

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
285118642	chr8	113697761	113697915	113697784	113697891	CSMD3	NM_198123	2	71	15	-	113697635	113697961
285118642	chr8	113697761	113697915	113697784	113697891	CSMD3	NM_198124	3	72	16	-	113697635	113697961
287681705	chr8	113812276	113812440	113812301	113812417	CSMD3	NM_052900	1	69	12	-	113812391	113812503
287681705	chr8	113812276	113812440	113812301	113812417	CSMD3	NM_198123	2	71	13	-	113812391	113812503
287681705	chr8	113812276	113812440	113812301	113812417	CSMD3	NM_198124	3	72	14	-	113812391	113812503
289063264	chr8	113871373	113871503	113871401	113871477	CSMD3	NM_052900	1	69	10	-	113871374	113871495
289063264	chr8	113871373	113871503	113871401	113871477	CSMD3	NM_198123	2	71	11	-	113871374	113871495
289063264	chr8	113871373	113871503	113871401	113871477	CSMD3	NM_198124	3	72	12	-	113871374	113871495
288713001	chr8	113960065	113960236	113960090	113960206	CSMD3	NM_052900	1	69	8	-	113960019	113960106
288713001	chr8	113960065	113960236	113960090	113960206	CSMD3	NM_198123	2	71	9	-	113960019	113960106
288713001	chr8	113960065	113960236	113960090	113960206	CSMD3	NM_198124	3	72	10	-	113960019	113960106
287622293	chr8	113988226	113988400	113988249	113988378	CSMD3	NM_198123	2	71	7	-	113988066	113988377
287622293	chr8	113988226	113988400	113988249	113988378	CSMD3	NM_198124	3	72	8	-	113988066	113988377
285129480	chr8	114111063	114111189	114111084	114111165	CSMD3	NM_052900	1	69	5	-	114110985	114111192
285129480	chr8	114111063	114111189	114111084	114111165	CSMD3	NM_198123	2	71	5	-	114110985	114111192
285129480	chr8	114111063	114111189	114111084	114111165	CSMD3	NM_198124	3	72	6	-	114110985	114111192
286373934	chr8	114186101	114186270	114186122	114186243	CSMD3	NM_052900	1	69	4	-	114185951	114186145
286373934	chr8	114186101	114186270	114186122	114186243	CSMD3	NM_198123	2	71	4	-	114185951	114186145
286373934	chr8	114186101	114186270	114186122	114186243	CSMD3	NM_198124	3	72	5	-	114185951	114186145
288175942	chr8	114326922	114327047	114326944	114327019	CSMD3	NM_052900	1	69	2	-	114326800	114327022
288175942	chr8	114326922	114327047	114326944	114327019	CSMD3	NM_198123	2	71	2	-	114326800	114327022
288175942	chr8	114326922	114327047	114326944	114327019	CSMD3	NM_198124	3	72	3	-	114326800	114327022
288957366	chr8	114448835	114449000	114448856	114448979	CSMD3	NM_052900	1	69	1	-	114448906	114449242
288957366	chr8	114448835	114449000	114448856	114448979	CSMD3	NM_198123	2	71	1	-	114448906	114449242
227704017	chr8	118816921	118817057	118816943	118817032	EXT1	NM_000127	1	11	10	-	118816961	118817132
230119681	chr8	118825089	118825224	118825110	118825201	EXT1	NM_000127	1	11	8	-	118825111	118825200
228009831	chr8	118834730	118834870	118834757	118834842	EXT1	NM_000127	1	11	5	-	118834704	118834836
231347581	chr8	119122285	119122459	119122306	119122436	EXT1	NM_000127	1	11	1	-	119122324	119124058
231358520	chr8	119122752	119122912	119122778	119122886	EXT1	NM_000127	1	11	1	-	119122324	119124058
231420020	chr8	119123185	119123341	119123204	119123314	EXT1	NM_000127	1	11	1	-	119122324	119124058
240727865	chr8	128750639	128750769	128750657	128750750	MYC	NM_002467	1	3	2	+	128750494	128751265
240720488	chr8	128751029	128751197	128751049	128751178	MYC	NM_002467	1	3	2	+	128750494	128751265
242605495	chr8	128752763	128752916	128752783	128752894	MYC	NM_002467	1	3	3	+	128752642	128753680
237602572	chr8	128753169	128753300	128753193	128753276	MYC	NM_002467	1	3	3	+	128752642	128753680
238904882	chr8	145737265	145737393	145737284	145737374	RECQL4	NM_004260	1	22	20	-	145737294	145737450
238597033	chr8	145737709	145737882	145737729	145737861	RECQL4	NM_004260	1	22	18	-	145737775	145737944
264232370	chr8	145738205	145738370	145738224	145738352	RECQL4	NM_004260	1	22	16	-	145738230	145738521
240943413	chr8	145738663	145738824	145738682	145738807	RECQL4	NM_004260	1	22	14	-	145738769	145738864
240943413	chr8	145738663	145738824	145738682	145738807	RECQL4	NM_004260	1	22	15	-	145738601	145738767
238535271	chr8	145739281	145739406	145739298	145739388	RECQL4	NM_004260	1	22	12	-	145739312	145739491
238175328	chr8	145739636	145739769	145739658	145739748	RECQL4	NM_004260	1	22	11	-	145739573	145739746

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264214685	chr8	145740400	145740554	145740420	145740534	RECQL4	NM_004260	1	22	8	-	145740534	145740626
264214685	chr8	145740400	145740554	145740420	145740534	RECQL4	NM_004260	1	22	9	-	145740320	145740456
264249865	chr8	145740738	145740905	145740756	145740885	RECQL4	NM_004260	1	22	7	-	145740710	145740841
264065193	chr8	145741409	145741562	145741429	145741542	RECQL4	NM_004260	1	22	5	-	145741372	145742148
264055490	chr8	145741827	145741951	145741848	145741929	RECQL4	NM_004260	1	22	5	-	145741372	145742148
240784107	chr8	145742504	145742628	145742523	145742611	RECQL4	NM_004260	1	22	4	-	145742434	145742574
233790238	chr9	5022166	5022333	5022190	5022311	JAK2	NM_004972	1	25	3	+	5021963	5022213
234417516	chr9	5044468	5044631	5044490	5044603	JAK2	NM_004972	1	25	5	+	5044403	5044520
233547824	chr9	5054557	5054707	5054585	5054681	JAK2	NM_004972	1	25	7	+	5054563	5054884
234712047	chr9	5055617	5055771	5055643	5055745	JAK2	NM_004972	1	25	8	+	5055669	5055788
234421514	chr9	5066594	5066725	5066624	5066700	JAK2	NM_004972	1	25	10	+	5066678	5066789
232040857	chr9	5069861	5070035	5069889	5070007	JAK2	NM_004972	1	25	12	+	5069925	5070052
232783578	chr9	5073651	5073815	5073679	5073787	JAK2	NM_004972	1	25	14	+	5073698	5073785
231872431	chr9	5078252	5078421	5078274	5078393	JAK2	NM_004972	1	25	16	+	5078306	5078444
230825726	chr9	5080475	5080649	5080498	5080629	JAK2	NM_004972	1	25	18	+	5080533	5080683
234401133	chr9	5089673	5089822	5089696	5089795	JAK2	NM_004972	1	25	20	+	5089674	5089863
233274780	chr9	5090733	5090903	5090760	5090877	JAK2	NM_004972	1	25	22	+	5090739	5090911
233700554	chr9	5126253	5126383	5126279	5126358	JAK2	NM_004972	1	25	24	+	5126333	5126446
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_001040712	1	30	30	-	8314246	8317942
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_001171025	2	29	29	-	8314246	8317942
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_130393	6	29	29	-	8314246	8317942
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_130392	5	31	31	-	8314246	8317942
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_130391	4	31	31	-	8314246	8317942
269473453	chr9	8317800	8317970	8317823	8317947	PTPRD	NM_002839	3	46	46	-	8314246	8317942
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_001040712	1	30	28	-	8331582	8331736
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_001171025	2	29	27	-	8331582	8331736
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_130393	6	29	27	-	8331582	8331736
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_130392	5	31	29	-	8331582	8331736
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_130391	4	31	29	-	8331582	8331736
271446164	chr9	8331609	8331761	8331636	8331736	PTPRD	NM_002839	3	46	44	-	8331582	8331736
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_001040712	1	30	26	-	8340343	8340469
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_001171025	2	29	25	-	8340343	8340469
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_130393	6	29	25	-	8340343	8340469
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_130392	5	31	27	-	8340343	8340469
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_130391	4	31	27	-	8340343	8340469
269731758	chr9	8340358	8340531	8340379	8340504	PTPRD	NM_002839	3	46	42	-	8340343	8340469
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_001040712	1	30	24	-	8341693	8341978
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_001171025	2	29	23	-	8341693	8341978
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_130393	6	29	23	-	8341693	8341978
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_130392	5	31	25	-	8341693	8341978
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_130391	4	31	25	-	8341693	8341978

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271227613	chr9	8341611	8341780	8341637	8341756	PTPRD	NM_002839	3	46	40	-	8341693	8341978
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_001040712	1	30	23	-	8375936	8376090
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_001171025	2	29	22	-	8375936	8376090
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_130393	6	29	22	-	8375936	8376090
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_130392	5	31	24	-	8375936	8376090
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_130391	4	31	24	-	8375936	8376090
270156257	chr9	8375961	8376131	8375982	8376103	PTPRD	NM_002839	3	46	39	-	8375936	8376090
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_001040712	1	30	21	-	8389232	8389407
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_001171025	2	29	20	-	8389232	8389407
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_130393	6	29	20	-	8389232	8389407
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_130392	5	31	22	-	8389232	8389407
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_130391	4	31	22	-	8389232	8389407
269467762	chr9	8389263	8389437	8389282	8389410	PTPRD	NM_002839	3	46	37	-	8389232	8389407
271168745	chr9	8437108	8437259	8437133	8437235	PTPRD	NM_001171025	2	29	17	-	8437198	8437239
270028870	chr9	8454496	8454648	8454518	8454620	PTPRD	NM_130392	5	31	18	-	8454580	8454594
270028870	chr9	8454496	8454648	8454518	8454620	PTPRD	NM_001040712	1	30	17	-	8454580	8454591
270028870	chr9	8454496	8454648	8454518	8454620	PTPRD	NM_130391	4	31	18	-	8454580	8454591
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_001040712	1	30	15	-	8465466	8465675
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_001171025	2	29	14	-	8465466	8465675
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_130393	6	29	15	-	8465466	8465675
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_130392	5	31	16	-	8465466	8465675
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_130391	4	31	16	-	8465466	8465675
270215975	chr9	8465385	8465553	8465410	8465526	PTPRD	NM_002839	3	46	32	-	8465466	8465675
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_001040712	1	30	13	-	8484119	8484378
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_001171025	2	29	12	-	8484119	8484378
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_130393	6	29	13	-	8484119	8484378
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_130392	5	31	14	-	8484119	8484378
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_130391	4	31	14	-	8484119	8484378
270017832	chr9	8484083	8484232	8484105	8484210	PTPRD	NM_002839	3	46	30	-	8484119	8484378
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_130393	6	29	12	-	8485227	8485327
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_001040712	1	30	12	-	8485227	8485324
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_001171025	2	29	11	-	8485227	8485324
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_130392	5	31	13	-	8485227	8485324
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_130391	4	31	13	-	8485227	8485324
270711559	chr9	8485228	8485386	8485249	8485358	PTPRD	NM_002839	3	46	29	-	8485227	8485324
272607132	chr9	8486112	8486262	8486133	8486238	PTPRD	NM_002839	3	46	28	-	8485762	8486349
270199623	chr9	8497123	8497295	8497151	8497268	PTPRD	NM_002839	3	46	26	-	8497242	8497268
270836797	chr9	8500816	8500982	8500836	8500958	PTPRD	NM_002839	3	46	24	-	8500754	8501059
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_001040712	1	30	10	-	8507301	8507434
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_001171025	2	29	9	-	8507301	8507434
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_130393	6	29	10	-	8507301	8507434

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_130392	5	31	11	-	8507301	8507434
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_130391	4	31	11	-	8507301	8507434
270607507	chr9	8507198	8507342	8507222	8507315	PTPRD	NM_002839	3	46	22	-	8507301	8507434
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_130393	6	29	9	-	8517848	8518429
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_130392	5	31	10	-	8517848	8518429
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_130391	4	31	10	-	8517848	8518429
269891202	chr9	8518067	8518230	8518090	8518204	PTPRD	NM_002839	3	46	21	-	8517848	8518429
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_001040712	1	30	8	-	8521277	8521546
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_001171025	2	29	7	-	8521277	8521546
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_130393	6	29	8	-	8521277	8521546
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_130392	5	31	9	-	8521277	8521546
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_130391	4	31	9	-	8521277	8521546
271212018	chr9	8521201	8521328	8521223	8521305	PTPRD	NM_002839	3	46	20	-	8521277	8521546
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_001040712	1	30	6	-	8524925	8525035
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_001171025	2	29	6	-	8524925	8525035
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_130393	6	29	6	-	8524925	8525035
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_130392	5	31	7	-	8524925	8525035
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_130391	4	31	7	-	8524925	8525035
270592827	chr9	8524877	8525016	8524898	8524990	PTPRD	NM_002839	3	46	18	-	8524925	8525035
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_001040712	1	30	4	-	8528591	8528779
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_001171025	2	29	4	-	8528591	8528779
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_130393	6	29	4	-	8528591	8528779
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_130392	5	31	4	-	8528591	8528779
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_130391	4	31	4	-	8528591	8528779
270396736	chr9	8528632	8528763	8528661	8528742	PTPRD	NM_002839	3	46	15	-	8528591	8528779
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_001040712	1	30	2	-	8636699	8636844
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_001171025	2	29	2	-	8636699	8636844
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_130393	6	29	2	-	8636699	8636844
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_130392	5	31	2	-	8636699	8636844
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_130391	4	31	2	-	8636699	8636844
271793572	chr9	8636621	8636791	8636645	8636769	PTPRD	NM_002839	3	46	13	-	8636699	8636844
235015095	chr9	15466714	15466883	15466742	15466858	PSIP1	NM_001128217	1	16	15	-	15466746	15466857
235015095	chr9	15466714	15466883	15466742	15466858	PSIP1	NM_033222	3	16	15	-	15466746	15466857
240151927	chr9	15468989	15469163	15469011	15469137	PSIP1	NM_001128217	1	16	13	-	15468955	15469056
240151927	chr9	15468989	15469163	15469011	15469137	PSIP1	NM_033222	3	16	13	-	15468955	15469056
236262341	chr9	15472675	15472831	15472699	15472803	PSIP1	NM_001128217	1	16	10	-	15472630	15472748
236262341	chr9	15472675	15472831	15472699	15472803	PSIP1	NM_033222	3	16	10	-	15472630	15472748
236262341	chr9	15472675	15472831	15472699	15472803	PSIP1	NM_021144	2	10	9	-	15472630	15472748
236216934	chr9	15479519	15479647	15479544	15479623	PSIP1	NM_001128217	1	16	7	-	15479589	15479685

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236216934	chr9	15479519	15479647	15479544	15479623	PSIP1	NM_033222	3	16	7	-	15479589	15479685
236216934	chr9	15479519	15479647	15479544	15479623	PSIP1	NM_021144	2	10	6	-	15479589	15479685
236433598	chr9	15486735	15486865	15486768	15486840	PSIP1	NM_001128217	1	16	5	-	15486825	15486929
236433598	chr9	15486735	15486865	15486768	15486840	PSIP1	NM_033222	3	16	5	-	15486825	15486929
236433598	chr9	15486735	15486865	15486768	15486840	PSIP1	NM_021144	2	10	4	-	15486825	15486929
235107329	chr9	15506586	15506724	15506608	15506696	PSIP1	NM_001128217	1	16	3	-	15506559	15506635
235107329	chr9	15506586	15506724	15506608	15506696	PSIP1	NM_033222	3	16	3	-	15506559	15506635
235107329	chr9	15506586	15506724	15506608	15506696	PSIP1	NM_021144	2	10	2	-	15506559	15506635
225941304	chr9	21970834	21971005	21970858	21970987	CDKN2A	NM_058195	3	3	2	-	21970901	21971207
225941304	chr9	21970834	21971005	21970858	21970987	CDKN2A	NM_058197	4	3	2	-	21970901	21971207
225941304	chr9	21970834	21971005	21970858	21970987	CDKN2A	NM_001195132	2	4	2	-	21970901	21971207
225941304	chr9	21970834	21971005	21970858	21970987	CDKN2A	NM_000077	1	3	2	-	21970901	21971207
225529900	chr9	21974543	21974708	21974565	21974687	CDKN2A	NM_058197	4	3	1	-	21974403	21974826
225529900	chr9	21974543	21974708	21974565	21974687	CDKN2A	NM_001195132	2	4	1	-	21974677	21975132
225529900	chr9	21974543	21974708	21974565	21974687	CDKN2A	NM_000077	1	3	1	-	21974677	21975132
226279815	chr9	22005859	22006025	22005879	22006007	CDKN2B	NM_004936	1	2	2	-	22002902	22006246
226279815	chr9	22005859	22006025	22005879	22006007	CDKN2B	NM_078487	2	2	2	-	22002902	22006246
227019787	chr9	22008680	22008834	22008701	22008814	CDKN2B	NM_078487	2	2	1	-	22008674	22009312
227019787	chr9	22008680	22008834	22008701	22008814	CDKN2B	NM_004936	1	2	1	-	22008797	22009312
261345239	chr9	32630119	32630254	32630142	32630233	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261250832	chr9	32630485	32630633	32630510	32630608	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261455594	chr9	32630845	32630977	32630873	32630954	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237884501	chr9	32631204	32631375	32631229	32631355	TAF1L	NM_153809	1	1	1	-	32629452	32635667
238020841	chr9	32631624	32631765	32631645	32631740	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237810345	chr9	32631969	32632136	32631994	32632115	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237923738	chr9	32632366	32632490	32632390	32632464	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261379135	chr9	32632733	32632865	32632759	32632837	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261297042	chr9	32633081	32633222	32633109	32633195	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237802439	chr9	32633491	32633662	32633513	32633635	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237861438	chr9	32633968	32634113	32633996	32634087	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237949761	chr9	32634354	32634511	32634383	32634491	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261471352	chr9	32634778	32634946	32634802	32634926	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261493209	chr9	32635236	32635409	32635264	32635383	TAF1L	NM_153809	1	1	1	-	32629452	32635667
230745595	chr9	35074074	35074237	35074095	35074213	FANCG	NM_004629	1	14	14	-	35073835	35074213
229535277	chr9	35074952	35075120	35074976	35075099	FANCG	NM_004629	1	14	12	-	35074924	35075079
228798297	chr9	35075672	35075796	35075692	35075775	FANCG	NM_004629	1	14	10	-	35075462	35075751
231258570	chr9	35076694	35076867	35076715	35076844	FANCG	NM_004629	1	14	7	-	35076721	35076867
228442590	chr9	35077230	35077394	35077254	35077373	FANCG	NM_004629	1	14	5	-	35077261	35077396
230959346	chr9	35078291	35078427	35078309	35078406	FANCG	NM_004629	1	14	4	-	35078138	35078340
230445320	chr9	35079392	35079561	35079413	35079540	FANCG	NM_004629	1	14	1	-	35079438	35080013
237640009	chr9	36923268	36923440	36923289	36923419	PAX5	NM_016734	1	10	7	-	36923352	36923481

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236641827	chr9	37002529	37002703	37002548	37002686	PAX5	NM_016734	1	10	5	-	37002645	37002773
235290452	chr9	37014950	37015103	37014971	37015077	PAX5	NM_016734	1	10	3	-	37014994	37015191
235029520	chr9	37033940	37034065	37033960	37034041	PAX5	NM_016734	1	10	1	-	37033983	37034476
228768728	chr9	80343448	80343592	80343473	80343568	GNAQ	NM_002072	1	7	6	-	80343430	80343583
227452153	chr9	80412422	80412591	80412450	80412565	GNAQ	NM_002072	1	7	4	-	80412436	80412564
228935464	chr9	80537165	80537293	80537186	80537268	GNAQ	NM_002072	1	7	2	-	80537077	80537261
237996715	chr9	93606219	93606375	93606241	93606355	SYK	NM_001135052	1	13	2	+	93606140	93606597
237996715	chr9	93606219	93606375	93606241	93606355	SYK	NM_001174167	2	14	2	+	93606140	93606597
237996715	chr9	93606219	93606375	93606241	93606355	SYK	NM_001174168	3	13	2	+	93606140	93606597
237996715	chr9	93606219	93606375	93606241	93606355	SYK	NM_003177	4	14	2	+	93606140	93606597
238026020	chr9	93606548	93606673	93606575	93606651	SYK	NM_001135052	1	13	2	+	93606140	93606597
238026020	chr9	93606548	93606673	93606575	93606651	SYK	NM_001174167	2	14	2	+	93606140	93606597
238026020	chr9	93606548	93606673	93606575	93606651	SYK	NM_001174168	3	13	2	+	93606140	93606597
238026020	chr9	93606548	93606673	93606575	93606651	SYK	NM_003177	4	14	2	+	93606140	93606597
241577803	chr9	93624544	93624670	93624564	93624649	SYK	NM_001135052	1	13	4	+	93624488	93624626
241577803	chr9	93624544	93624670	93624564	93624649	SYK	NM_001174167	2	14	4	+	93624488	93624626
241577803	chr9	93624544	93624670	93624564	93624649	SYK	NM_001174168	3	13	4	+	93624488	93624626
241577803	chr9	93624544	93624670	93624564	93624649	SYK	NM_003177	4	14	4	+	93624488	93624626
242688090	chr9	93636440	93636599	93636468	93636574	SYK	NM_001135052	1	13	7	+	93636486	93636573
242688090	chr9	93636440	93636599	93636468	93636574	SYK	NM_001174167	2	14	8	+	93636486	93636573
242688090	chr9	93636440	93636599	93636468	93636574	SYK	NM_001174168	3	13	7	+	93636486	93636573
242688090	chr9	93636440	93636599	93636468	93636574	SYK	NM_003177	4	14	8	+	93636486	93636573
237819391	chr9	93639895	93640069	93639918	93640042	SYK	NM_001135052	1	13	9	+	93639853	93640062
237819391	chr9	93639895	93640069	93639918	93640042	SYK	NM_001174167	2	14	10	+	93639853	93640062
237819391	chr9	93639895	93640069	93639918	93640042	SYK	NM_001174168	3	13	9	+	93639853	93640062
237819391	chr9	93639895	93640069	93639918	93640042	SYK	NM_003177	4	14	10	+	93639853	93640062
239224463	chr9	93649978	93650104	93650002	93650077	SYK	NM_001135052	1	13	11	+	93650031	93650171
239224463	chr9	93649978	93650104	93650002	93650077	SYK	NM_001174167	2	14	12	+	93650031	93650171
239224463	chr9	93649978	93650104	93650002	93650077	SYK	NM_001174168	3	13	11	+	93650031	93650171
239224463	chr9	93649978	93650104	93650002	93650077	SYK	NM_003177	4	14	12	+	93650031	93650171
242255840	chr9	93657763	93657933	93657790	93657909	SYK	NM_001135052	1	13	13	+	93657810	93660842
242255840	chr9	93657763	93657933	93657790	93657909	SYK	NM_001174167	2	14	14	+	93657810	93660842
242255840	chr9	93657763	93657933	93657790	93657909	SYK	NM_001174168	3	13	13	+	93657810	93660842
242255840	chr9	93657763	93657933	93657790	93657909	SYK	NM_003177	4	14	14	+	93657810	93660842
230202649	chr9	97869414	97869587	97869434	97869565	FANCC	NM_001243743	2	15	14	-	97869348	97869551
230202649	chr9	97869414	97869587	97869434	97869565	FANCC	NM_000136	1	15	14	-	97869348	97869551
232665698	chr9	97873832	97873976	97873855	97873949	FANCC	NM_001243744	3	14	13	-	97873745	97873919
232665698	chr9	97873832	97873976	97873855	97873949	FANCC	NM_001243743	2	15	13	-	97873745	97873919
232665698	chr9	97873832	97873976	97873855	97873949	FANCC	NM_000136	1	15	13	-	97873745	97873919
230070772	chr9	97888720	97888891	97888743	97888863	FANCC	NM_001243744	3	14	9	-	97888811	97888863
230070772	chr9	97888720	97888891	97888743	97888863	FANCC	NM_001243743	2	15	9	-	97888811	97888863

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230070772	chr9	97888720	97888891	97888743	97888863	FANCC	NM_000136	1	15	9	-	97888811	97888863
232122553	chr9	97912118	97912291	97912140	97912270	FANCC	NM_001243744	3	14	7	-	97912205	97912369
232122553	chr9	97912118	97912291	97912140	97912270	FANCC	NM_001243743	2	15	7	-	97912205	97912369
232122553	chr9	97912118	97912291	97912140	97912270	FANCC	NM_000136	1	15	7	-	97912205	97912369
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_001243744	3	14	5	-	97934319	97934429
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_001243743	2	15	5	-	97934319	97934429
229976759	chr9	97934353	97934497	97934378	97934471	FANCC	NM_000136	1	15	5	-	97934319	97934429
232580732	chr9	98011469	98011599	98011490	98011574	FANCC	NM_001243744	3	14	2	-	98011409	98011651
232580732	chr9	98011469	98011599	98011490	98011574	FANCC	NM_001243743	2	15	2	-	98011409	98011651
232580732	chr9	98011469	98011599	98011490	98011574	FANCC	NM_000136	1	15	2	-	98011409	98011651
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237372755	chr9	98209466	98209621	98209483	98209602	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083605	5	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083602	2	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_000264	1	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083604	4	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083606	6	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083607	7	24	22	-	98211351	98211605
235192189	chr9	98211453	98211625	98211471	98211599	PTCH1	NM_001083603	3	24	22	-	98211351	98211605
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083605	5	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083602	2	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_000264	1	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083604	4	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083606	6	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083607	7	24	20	-	98215760	98215902
239402030	chr9	98215763	98215936	98215787	98215912	PTCH1	NM_001083603	3	24	20	-	98215760	98215902
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083605	5	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083602	2	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_000264	1	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083604	4	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083606	6	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083607	7	24	18	-	98220295	98220575
234954334	chr9	98220354	98220510	98220374	98220487	PTCH1	NM_001083603	3	24	18	-	98220295	98220575
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083605	5	24	16	-	98224138	98224280
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083602	2	24	16	-	98224138	98224280
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_000264	1	24	16	-	98224138	98224280

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083604	4	24	16	-	98224138	98224280
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083606	6	24	16	-	98224138	98224280
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083607	7	24	16	-	98224138	98224280
236780496	chr9	98224054	98224227	98224072	98224199	PTCH1	NM_001083603	3	24	16	-	98224138	98224280
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083605	5	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083602	2	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_000264	1	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083604	4	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083606	6	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083607	7	24	15	-	98229398	98229707
235708083	chr9	98229578	98229733	98229605	98229711	PTCH1	NM_001083603	3	24	15	-	98229398	98229707
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235341576	chr9	98231303	98231458	98231324	98231435	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083605	5	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083602	2	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_000264	1	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083604	4	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083606	6	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083607	7	24	12	-	98238316	98238441
237668837	chr9	98238347	98238521	98238366	98238499	PTCH1	NM_001083603	3	24	12	-	98238316	98238441
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083605	5	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083602	2	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_000264	1	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083604	4	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083606	6	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083607	7	24	9	-	98240337	98240468
236664818	chr9	98240282	98240453	98240308	98240432	PTCH1	NM_001083603	3	24	9	-	98240337	98240468
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083605	5	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083602	2	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_000264	1	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083604	4	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083606	6	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083607	7	24	7	-	98242251	98242372
237855594	chr9	98242183	98242337	98242205	98242309	PTCH1	NM_001083603	3	24	7	-	98242251	98242372
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083605	5	24	5	-	98244231	98244322
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083602	2	24	5	-	98244231	98244322

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_000264	1	24	5	-	98244231	98244322
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083604	4	24	5	-	98244231	98244322
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083606	6	24	5	-	98244231	98244322
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083607	7	24	5	-	98244231	98244322
235566054	chr9	98244179	98244350	98244204	98244323	PTCH1	NM_001083603	3	24	5	-	98244231	98244322
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083605	5	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083602	2	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_000264	1	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083604	4	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083606	6	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083607	7	24	2	-	98268689	98268881
237782565	chr9	98268680	98268846	98268699	98268819	PTCH1	NM_001083603	3	24	2	-	98268689	98268881
235586852	chr9	98270486	98270643	98270504	98270625	PTCH1	NM_000264	1	24	1	-	98270443	98270831
264389483	chr9	100437730	100437870	100437754	100437850	XPA	NR_027302	2	7	7	-	100437191	100437869
264389483	chr9	100437730	100437870	100437754	100437850	XPA	NM_000380	1	6	6	-	100437191	100437869
241658440	chr9	100449285	100449435	100449308	100449407	XPA	NR_027302	2	7	4	-	100449378	100449543
241658440	chr9	100449285	100449435	100449308	100449407	XPA	NM_000380	1	6	4	-	100449378	100449543
241029567	chr9	100451818	100451942	100451845	100451914	XPA	NR_027302	2	7	3	-	100451816	100451921
241029567	chr9	100451818	100451942	100451845	100451914	XPA	NM_000380	1	6	3	-	100451816	100451921
238373880	chr9	100459332	100459500	100459350	100459482	XPA	NR_027302	2	7	1	-	100459403	100459691
238373880	chr9	100459332	100459500	100459350	100459482	XPA	NM_000380	1	6	1	-	100459403	100459691
293909498	chr9	120470897	120471038	120470919	120471010	TLR4	NR_024168	4	4	3	+	120470841	120471007
293909498	chr9	120470897	120471038	120470919	120471010	TLR4	NM_003266	1	4	3	+	120470841	120471007
293909498	chr9	120470897	120471038	120470919	120471010	TLR4	NM_138554	2	3	2	+	120470841	120471007
295084127	chr9	120474836	120474993	120474860	120474965	TLR4	NM_003266	1	4	4	+	120474667	120479769
295084127	chr9	120474836	120474993	120474860	120474965	TLR4	NM_138554	2	3	3	+	120474667	120479769
295084127	chr9	120474836	120474993	120474860	120474965	TLR4	NM_138557	3	2	2	+	120474667	120479769
295084127	chr9	120474836	120474993	120474860	120474965	TLR4	NR_024169	5	2	2	+	120474667	120479766
295084127	chr9	120474836	120474993	120474860	120474965	TLR4	NR_024168	4	4	4	+	120474667	120479766
294052358	chr9	120475233	120475377	120475253	120475350	TLR4	NM_003266	1	4	4	+	120474667	120479769
294052358	chr9	120475233	120475377	120475253	120475350	TLR4	NM_138554	2	3	3	+	120474667	120479769
294052358	chr9	120475233	120475377	120475253	120475350	TLR4	NM_138557	3	2	2	+	120474667	120479769
294052358	chr9	120475233	120475377	120475253	120475350	TLR4	NR_024169	5	2	2	+	120474667	120479766
294052358	chr9	120475233	120475377	120475253	120475350	TLR4	NR_024168	4	4	4	+	120474667	120479766
295066826	chr9	120475649	120475810	120475675	120475784	TLR4	NM_003266	1	4	4	+	120474667	120479769
295066826	chr9	120475649	120475810	120475675	120475784	TLR4	NM_138554	2	3	3	+	120474667	120479769
295066826	chr9	120475649	120475810	120475675	120475784	TLR4	NM_138557	3	2	2	+	120474667	120479769
295066826	chr9	120475649	120475810	120475675	120475784	TLR4	NR_024169	5	2	2	+	120474667	120479766
295066826	chr9	120475649	120475810	120475675	120475784	TLR4	NR_024168	4	4	4	+	120474667	120479766
294118651	chr9	120476100	120476259	120476128	120476237	TLR4	NM_003266	1	4	4	+	120474667	120479769
294118651	chr9	120476100	120476259	120476128	120476237	TLR4	NM_138554	2	3	3	+	120474667	120479769

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294118651	chr9	120476100	120476259	120476128	120476237	TLR4	NM_138557	3	2	2	+	120474667	120479769
294118651	chr9	120476100	120476259	120476128	120476237	TLR4	NR_024169	5	2	2	+	120474667	120479766
294118651	chr9	120476100	120476259	120476128	120476237	TLR4	NR_024168	4	4	4	+	120474667	120479766
294191255	chr9	120476557	120476731	120476578	120476710	TLR4	NM_003266	1	4	4	+	120474667	120479769
294191255	chr9	120476557	120476731	120476578	120476710	TLR4	NM_138554	2	3	3	+	120474667	120479769
294191255	chr9	120476557	120476731	120476578	120476710	TLR4	NM_138557	3	2	2	+	120474667	120479769
294191255	chr9	120476557	120476731	120476578	120476710	TLR4	NR_024169	5	2	2	+	120474667	120479766
294191255	chr9	120476557	120476731	120476578	120476710	TLR4	NR_024168	4	4	4	+	120474667	120479766
224727001	chr9	133589754	133589880	133589776	133589852	ABL1	NM_007313	2	11	1	+	133589268	133589842
222574295	chr9	133730152	133730320	133730179	133730298	ABL1	NM_005157	1	11	3	+	133730188	133730483
222574295	chr9	133730152	133730320	133730179	133730298	ABL1	NM_007313	2	11	3	+	133730188	133730483
224076188	chr9	133738182	133738327	133738202	133738307	ABL1	NM_005157	1	11	4	+	133738150	133738422
224076188	chr9	133738182	133738327	133738202	133738307	ABL1	NM_007313	2	11	4	+	133738150	133738422
222742444	chr9	133747531	133747705	133747556	133747684	ABL1	NM_005157	1	11	5	+	133747516	133747600
222742444	chr9	133747531	133747705	133747556	133747684	ABL1	NM_007313	2	11	5	+	133747516	133747600
223580432	chr9	133750186	133750359	133750208	133750339	ABL1	NM_005157	1	11	7	+	133750255	133750439
223580432	chr9	133750186	133750359	133750208	133750339	ABL1	NM_007313	2	11	7	+	133750255	133750439
225062040	chr9	133755416	133755584	133755441	133755564	ABL1	NM_005157	1	11	9	+	133755455	133755544
225062040	chr9	133755416	133755584	133755441	133755564	ABL1	NM_007313	2	11	9	+	133755455	133755544
224383411	chr9	133759442	133759602	133759463	133759582	ABL1	NM_005157	1	11	11	+	133759356	133763062
224383411	chr9	133759442	133759602	133759463	133759582	ABL1	NM_007313	2	11	11	+	133759356	133763062
224372544	chr9	133759833	133759959	133759850	133759939	ABL1	NM_005157	1	11	11	+	133759356	133763062
224372544	chr9	133759833	133759959	133759850	133759939	ABL1	NM_007313	2	11	11	+	133759356	133763062
224381820	chr9	133760185	133760329	133760205	133760308	ABL1	NM_005157	1	11	11	+	133759356	133763062
224381820	chr9	133760185	133760329	133760205	133760308	ABL1	NM_007313	2	11	11	+	133759356	133763062
224378730	chr9	133760562	133760712	133760582	133760688	ABL1	NM_005157	1	11	11	+	133759356	133763062
224378730	chr9	133760562	133760712	133760582	133760688	ABL1	NM_007313	2	11	11	+	133759356	133763062
224395176	chr9	133761029	133761166	133761053	133761145	ABL1	NM_005157	1	11	11	+	133759356	133763062
224395176	chr9	133761029	133761166	133761053	133761145	ABL1	NM_007313	2	11	11	+	133759356	133763062
235080295	chr9	134002888	134003017	134002916	134002993	NUP214	NM_005085	1	36	2	+	134002911	134003106
241093452	chr9	134004561	134004722	134004589	134004697	NUP214	NM_005085	1	36	4	+	134004666	134004864
236293900	chr9	134007874	134008047	134007896	134008019	NUP214	NM_005085	1	36	6	+	134007983	134008046
236334375	chr9	134010216	134010343	134010241	134010320	NUP214	NM_005085	1	36	8	+	134010285	134010391
238523315	chr9	134014667	134014819	134014694	134014794	NUP214	NM_005085	1	36	10	+	134014668	134014794
237086914	chr9	134019701	134019862	134019723	134019841	NUP214	NM_005085	1	36	12	+	134019667	134020141
235114450	chr9	134021436	134021560	134021463	134021537	NUP214	NM_005085	1	36	13	+	134021516	134021691
235999576	chr9	134022860	134023002	134022885	134022974	NUP214	NM_005085	1	36	14	+	134022877	134022971
236042712	chr9	134027049	134027223	134027075	134027195	NUP214	NM_005085	1	36	17	+	134027123	134027281
235156091	chr9	134038416	134038587	134038437	134038562	NUP214	NM_005085	1	36	19	+	134038378	134038560
236788575	chr9	134049387	134049560	134049408	134049540	NUP214	NM_005085	1	36	22	+	134049442	134049705
237004269	chr9	134050897	134051067	134050918	134051045	NUP214	NM_005085	1	36	23	+	134050847	134051008

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239193372	chr9	134064457	134064619	134064478	134064596	NUP214	NM_005085	1	36	26	+	134064440	134064518
238002517	chr9	134072553	134072715	134072580	134072694	NUP214	NM_005085	1	36	29	+	134072603	134074402
238104976	chr9	134072924	134073085	134072949	134073065	NUP214	NM_005085	1	36	29	+	134072603	134074402
234942390	chr9	134073363	134073516	134073385	134073494	NUP214	NM_005085	1	36	29	+	134072603	134074402
238014183	chr9	134073830	134073966	134073851	134073947	NUP214	NM_005085	1	36	29	+	134072603	134074402
238024680	chr9	134074289	134074439	134074309	134074413	NUP214	NM_005085	1	36	29	+	134072603	134074402
236751123	chr9	134098132	134098288	134098154	134098268	NUP214	NM_005085	1	36	32	+	134098165	134098317
235654215	chr9	134105982	134106116	134106004	134106094	NUP214	NM_005085	1	36	34	+	134106017	134106156
241851713	chr9	135771592	135771766	135771619	135771742	TSC1	NM_000368	1	23	23	-	135766735	135772141
241851713	chr9	135771592	135771766	135771619	135771742	TSC1	NM_001162427	3	22	22	-	135766735	135772141
241851713	chr9	135771592	135771766	135771619	135771742	TSC1	NM_001162426	2	23	23	-	135766735	135772141
265456452	chr9	135772059	135772232	135772079	135772207	TSC1	NM_000368	1	23	23	-	135766735	135772141
265456452	chr9	135772059	135772232	135772079	135772207	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265456452	chr9	135772059	135772232	135772079	135772207	TSC1	NM_001162426	2	23	23	-	135766735	135772141
261816662	chr9	135772813	135772977	135772840	135772955	TSC1	NM_000368	1	23	21	-	135772810	135772997
261816662	chr9	135772813	135772977	135772840	135772955	TSC1	NM_001162427	3	22	20	-	135772810	135772997
261816662	chr9	135772813	135772977	135772840	135772955	TSC1	NM_001162426	2	23	21	-	135772810	135772997
240431165	chr9	135776945	135777113	135776966	135777090	TSC1	NM_000368	1	23	19	-	135776976	135777086
240431165	chr9	135776945	135777113	135776966	135777090	TSC1	NM_001162427	3	22	18	-	135776976	135777086
240431165	chr9	135776945	135777113	135776966	135777090	TSC1	NM_001162426	2	23	19	-	135776976	135777086
262446132	chr9	135779070	135779229	135779091	135779207	TSC1	NM_000368	1	23	17	-	135779038	135779204
262446132	chr9	135779070	135779229	135779091	135779207	TSC1	NM_001162427	3	22	16	-	135779038	135779204
262446132	chr9	135779070	135779229	135779091	135779207	TSC1	NM_001162426	2	23	17	-	135779038	135779204
240564668	chr9	135781188	135781361	135781211	135781338	TSC1	NM_000368	1	23	15	-	135780968	135781526
240564668	chr9	135781188	135781361	135781211	135781338	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240564668	chr9	135781188	135781361	135781211	135781338	TSC1	NM_001162426	2	23	15	-	135780968	135781526
265005986	chr9	135782633	135782806	135782661	135782778	TSC1	NM_000368	1	23	13	-	135782688	135782757
265005986	chr9	135782633	135782806	135782661	135782778	TSC1	NM_001162427	3	22	12	-	135782688	135782757
265005986	chr9	135782633	135782806	135782661	135782778	TSC1	NM_001162426	2	23	13	-	135782688	135782757
261953775	chr9	135786811	135786982	135786832	135786955	TSC1	NM_000368	1	23	10	-	135786840	135786955
261953775	chr9	135786811	135786982	135786832	135786955	TSC1	NM_001162427	3	22	9	-	135786840	135786955
261953775	chr9	135786811	135786982	135786832	135786955	TSC1	NM_001162426	2	23	10	-	135786840	135786955
241051217	chr9	135796737	135796872	135796763	135796844	TSC1	NM_000368	1	23	8	-	135796750	135796823
241051217	chr9	135796737	135796872	135796763	135796844	TSC1	NM_001162427	3	22	7	-	135796750	135796823
241051217	chr9	135796737	135796872	135796763	135796844	TSC1	NM_001162426	2	23	8	-	135796750	135796823
239660886	chr9	135798736	135798908	135798757	135798884	TSC1	NM_000368	1	23	6	-	135798735	135798879
239660886	chr9	135798736	135798908	135798757	135798884	TSC1	NM_001162427	3	22	5	-	135798735	135798879
239660886	chr9	135798736	135798908	135798757	135798884	TSC1	NM_001162426	2	23	6	-	135798735	135798879
239621783	chr9	135802577	135802722	135802600	135802694	TSC1	NM_000368	1	23	4	-	135802588	135802691
239621783	chr9	135802577	135802722	135802600	135802694	TSC1	NM_001162427	3	22	4	-	135802588	135802691
239621783	chr9	135802577	135802722	135802600	135802694	TSC1	NM_001162426	2	23	4	-	135802588	135802691

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273804615	chr9	135974043	135974183	135974064	135974163	RALGDS	NM_001042368	1	18	18	-	135973107	135974149
273804615	chr9	135974043	135974183	135974064	135974163	RALGDS	NM_006266	2	18	18	-	135973107	135974149
273039257	chr9	135977100	135977258	135977118	135977238	RALGDS	NM_001042368	1	18	16	-	135976907	135977149
273039257	chr9	135977100	135977258	135977118	135977238	RALGDS	NM_006266	2	18	16	-	135976907	135977149
272740330	chr9	135977807	135977978	135977827	135977958	RALGDS	NM_001042368	1	18	14	-	135977863	135977958
272740330	chr9	135977807	135977978	135977827	135977958	RALGDS	NM_006266	2	18	14	-	135977863	135977958
272768567	chr9	135979078	135979248	135979099	135979227	RALGDS	NM_001042368	1	18	11	-	135979134	135979220
272768567	chr9	135979078	135979248	135979099	135979227	RALGDS	NM_006266	2	18	11	-	135979134	135979220
274051863	chr9	135982091	135982242	135982113	135982219	RALGDS	NM_001042368	1	18	8	-	135982032	135982135
274051863	chr9	135982091	135982242	135982113	135982219	RALGDS	NM_006266	2	18	8	-	135982032	135982135
273165897	chr9	135983369	135983502	135983389	135983478	RALGDS	NM_001042368	1	18	6	-	135983375	135983793
273165897	chr9	135983369	135983502	135983389	135983478	RALGDS	NM_006266	2	18	6	-	135983375	135983793
273585600	chr9	135984947	135985104	135984968	135985085	RALGDS	NM_001042368	1	18	4	-	135985013	135985108
273585600	chr9	135984947	135985104	135984968	135985085	RALGDS	NM_006266	2	18	4	-	135985013	135985108
273709097	chr9	135987479	135987646	135987503	135987624	RALGDS	NM_001042368	1	18	2	-	135987429	135987539
273709097	chr9	135987479	135987646	135987503	135987624	RALGDS	NM_006266	2	18	2	-	135987429	135987539
224323988	chr9	136898680	136898853	136898703	136898834	BRD3	NM_007371	1	12	12	-	136895446	136898827
223031596	chr9	136901210	136901381	136901231	136901358	BRD3	NM_007371	1	12	10	-	136901154	136901446
224456610	chr9	136905199	136905361	136905219	136905341	BRD3	NM_007371	1	12	9	-	136905156	136905391
222193202	chr9	136910326	136910499	136910345	136910480	BRD3	NM_007371	1	12	7	-	136910415	136910543
222647379	chr9	136913332	136913499	136913352	136913482	BRD3	NM_007371	1	12	6	-	136913205	136913576
222520150	chr9	136916585	136916754	136916607	136916728	BRD3	NM_007371	1	12	4	-	136916684	136916831
223867689	chr9	136918347	136918498	136918366	136918477	BRD3	NM_007371	1	12	2	-	136918387	136918712
240916162	chr9	139390595	139390738	139390615	139390720	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236042835	chr9	139391094	139391241	139391116	139391224	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240923175	chr9	139391480	139391614	139391498	139391597	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236207033	chr9	139391837	139392011	139391857	139391990	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
238439241	chr9	139393564	139393735	139393584	139393717	NOTCH1	NM_017617	1	34	32	-	139393564	139393711
237161024	chr9	139396182	139396354	139396199	139396335	NOTCH1	NM_017617	1	34	30	-	139396200	139396365
238886124	chr9	139396647	139396819	139396666	139396802	NOTCH1	NM_017617	1	34	28	-	139396724	139396940
241010738	chr9	139399310	139399475	139399328	139399458	NOTCH1	NM_017617	1	34	26	-	139399125	139399556
235679711	chr9	139399819	139399976	139399838	139399959	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
240377565	chr9	139400260	139400409	139400277	139400392	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
239238083	chr9	139401250	139401410	139401271	139401390	NOTCH1	NM_017617	1	34	23	-	139401168	139401425
236231008	chr9	139402375	139402509	139402396	139402488	NOTCH1	NM_017617	1	34	21	-	139402407	139402591
236356680	chr9	139403287	139403458	139403305	139403440	NOTCH1	NM_017617	1	34	19	-	139403322	139403523
236511370	chr9	139404297	139404442	139404316	139404423	NOTCH1	NM_017617	1	34	18	-	139404185	139404413
239883973	chr9	139405499	139405645	139405523	139405621	NOTCH1	NM_017617	1	34	16	-	139405604	139405723
242098368	chr9	139407809	139407960	139407829	139407939	NOTCH1	NM_017617	1	34	14	-	139407844	139407989
236466569	chr9	139409122	139409284	139409148	139409262	NOTCH1	NM_017617	1	34	13	-	139408962	139409154
235383157	chr9	139410039	139410213	139410056	139410193	NOTCH1	NM_017617	1	34	11	-	139409935	139410168

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237691270	chr9	139412117	139412287	139412138	139412268	NOTCH1	NM_017617	1	34	8	-	139412204	139412389
242589945	chr9	139413025	139413172	139413042	139413154	NOTCH1	NM_017617	1	34	6	-	139413043	139413276
238630712	chr9	139417173	139417332	139417191	139417314	NOTCH1	NM_017617	1	34	4	-	139417302	139417640
238635564	chr9	139417495	139417665	139417515	139417645	NOTCH1	NM_017617	1	34	4	-	139417302	139417640
235502541	chr9	139438429	139438588	139438448	139438565	NOTCH1	NM_017617	1	34	2	-	139438476	139438554
234826403	chr10	3823721	3823880	3823742	3823856	KLF6	NM_001300	3	4	2	-	3823833	3824406
234826403	chr10	3823721	3823880	3823742	3823856	KLF6	NM_001160125	2	3	2	-	3823833	3824406
233087051	chr10	3824162	3824332	3824182	3824311	KLF6	NM_001160124	1	4	2	-	3823959	3824406
233087051	chr10	3824162	3824332	3824182	3824311	KLF6	NR_027653	4	4	2	-	3823987	3824406
233087051	chr10	3824162	3824332	3824182	3824311	KLF6	NM_001300	3	4	2	-	3823833	3824406
233087051	chr10	3824162	3824332	3824182	3824311	KLF6	NM_001160125	2	3	2	-	3823833	3824406
227404319	chr10	8097487	8097661	8097511	8097644	GATA3	NM_002051	2	6	2	+	8097250	8097859
227404319	chr10	8097487	8097661	8097511	8097644	GATA3	NM_001002295	1	6	2	+	8097250	8097859
229535241	chr10	8100359	8100533	8100380	8100516	GATA3	NM_002051	2	6	3	+	8100268	8100804
229535241	chr10	8100359	8100533	8100380	8100516	GATA3	NM_001002295	1	6	3	+	8100268	8100804
228329940	chr10	8105923	8106097	8105947	8106076	GATA3	NM_002051	2	6	4	+	8105959	8106101
228329940	chr10	8105923	8106097	8105947	8106076	GATA3	NM_001002295	1	6	4	+	8105956	8106101
228214393	chr10	8115634	8115804	8115655	8115781	GATA3	NM_002051	2	6	6	+	8115702	8117164
228214393	chr10	8115634	8115804	8115655	8115781	GATA3	NM_001002295	1	6	6	+	8115702	8117164
233104626	chr10	21823519	21823647	21823540	21823622	MLLT10	NM_004641	5	24	2	+	21823574	21823733
233104626	chr10	21823519	21823647	21823540	21823622	MLLT10	NM_001195627	2	5	2	+	21823574	21823733
233104626	chr10	21823519	21823647	21823540	21823622	MLLT10	NM_001195626	1	22	1	+	21823574	21823733
233104626	chr10	21823519	21823647	21823540	21823622	MLLT10	NM_001195628	3	4	2	+	21823574	21823733
233104626	chr10	21823519	21823647	21823540	21823622	MLLT10	NM_001195630	4	4	2	+	21823574	21823733
234729836	chr10	21845814	21845967	21845841	21845939	MLLT10	NM_001195627	2	5	5	+	21845572	21846114
234729836	chr10	21845814	21845967	21845841	21845939	MLLT10	NM_001195628	3	4	4	+	21845572	21846114
234729836	chr10	21845814	21845967	21845841	21845939	MLLT10	NM_001195630	4	4	4	+	21845572	21846114
231113718	chr10	21901160	21901313	21901193	21901288	MLLT10	NM_004641	5	24	6	+	21901277	21901380
231113718	chr10	21901160	21901313	21901193	21901288	MLLT10	NM_001195626	1	22	5	+	21901277	21901380
233620582	chr10	21906088	21906260	21906113	21906228	MLLT10	NM_004641	5	24	8	+	21906041	21906136
233620582	chr10	21906088	21906260	21906113	21906228	MLLT10	NM_001195626	1	22	7	+	21906041	21906136
232506811	chr10	21959389	21959555	21959417	21959531	MLLT10	NM_004641	5	24	10	+	21959378	21959633
232506811	chr10	21959389	21959555	21959417	21959531	MLLT10	NM_001195626	1	22	9	+	21959378	21959633
234532251	chr10	21962288	21962433	21962310	21962406	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234532251	chr10	21962288	21962433	21962310	21962406	MLLT10	NM_001195626	1	22	10	+	21962279	21962848
234532976	chr10	21962719	21962892	21962743	21962864	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234532976	chr10	21962719	21962892	21962743	21962864	MLLT10	NM_001195626	1	22	10	+	21962279	21962848
233655744	chr10	22002642	22002791	22002668	22002769	MLLT10	NM_004641	5	24	15	+	22002701	22002879
233655744	chr10	22002642	22002791	22002668	22002769	MLLT10	NM_001195626	1	22	13	+	22002701	22002879
231986513	chr10	22016744	22016894	22016770	22016866	MLLT10	NM_004641	5	24	17	+	22016785	22016857
231986513	chr10	22016744	22016894	22016770	22016866	MLLT10	NM_001195626	1	22	15	+	22016785	22016857

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232708871	chr10	22021862	22022025	22021890	22022002	MLLT10	NM_004641	5	24	19	+	22021828	22022016
232708871	chr10	22021862	22022025	22021890	22022002	MLLT10	NM_001195626	1	22	17	+	22021828	22022016
234676688	chr10	22022775	22022937	22022796	22022912	MLLT10	NM_004641	5	24	21	+	22022697	22023058
234676688	chr10	22022775	22022937	22022796	22022912	MLLT10	NM_001195626	1	22	19	+	22022697	22023058
231642163	chr10	22024086	22024250	22024109	22024225	MLLT10	NM_004641	5	24	22	+	22024068	22024164
231642163	chr10	22024086	22024250	22024109	22024225	MLLT10	NM_001195626	1	22	20	+	22024068	22024164
234406497	chr10	22030777	22030947	22030805	22030919	MLLT10	NM_004641	5	24	24	+	22030868	22032559
234406497	chr10	22030777	22030947	22030805	22030919	MLLT10	NM_001195626	1	22	22	+	22030868	22032559
242191185	chr10	43597763	43597919	43597784	43597896	RET	NM_020630	1	19	3	+	43597790	43598077
242191185	chr10	43597763	43597919	43597784	43597896	RET	NM_020975	2	20	3	+	43597790	43598077
242042773	chr10	43600475	43600643	43600494	43600623	RET	NM_020630	1	19	4	+	43600400	43600641
242042773	chr10	43600475	43600643	43600494	43600623	RET	NM_020975	2	20	4	+	43600400	43600641
238117251	chr10	43604454	43604598	43604475	43604576	RET	NM_020630	1	19	6	+	43604479	43604678
238117251	chr10	43604454	43604598	43604475	43604576	RET	NM_020975	2	20	6	+	43604479	43604678
238719671	chr10	43606779	43606909	43606804	43606888	RET	NM_020630	1	19	7	+	43606655	43606913
238719671	chr10	43606779	43606909	43606804	43606888	RET	NM_020975	2	20	7	+	43606655	43606913
240419617	chr10	43608926	43609097	43608947	43609076	RET	NM_020630	1	19	10	+	43609004	43609123
240419617	chr10	43608926	43609097	43608947	43609076	RET	NM_020975	2	20	10	+	43609004	43609123
264081824	chr10	43610131	43610304	43610148	43610287	RET	NM_020630	1	19	11	+	43609928	43610184
264081824	chr10	43610131	43610304	43610148	43610287	RET	NM_020975	2	20	11	+	43609928	43610184
238814598	chr10	43613750	43613901	43613772	43613879	RET	NM_020630	1	19	13	+	43613821	43613928
238814598	chr10	43613750	43613901	43613772	43613879	RET	NM_020975	2	20	13	+	43613821	43613928
241510364	chr10	43615060	43615220	43615077	43615202	RET	NM_020630	1	19	14	+	43614979	43615193
241510364	chr10	43615060	43615220	43615077	43615202	RET	NM_020975	2	20	14	+	43614979	43615193
242431976	chr10	43619092	43619244	43619115	43619224	RET	NM_020630	1	19	17	+	43619119	43619256
242431976	chr10	43619092	43619244	43619115	43619224	RET	NM_020975	2	20	17	+	43619119	43619256
238926165	chr10	43622064	43622235	43622086	43622212	RET	NM_020630	1	19	19	+	43622023	43622952
238926165	chr10	43622064	43622235	43622086	43622212	RET	NM_020975	2	20	19	+	43622023	43622170
294678301	chr10	49609714	49609886	49609742	49609858	MAPK8	NM_002750	1	11	1	+	49609687	49609825
294678301	chr10	49609714	49609886	49609742	49609858	MAPK8	NM_139049	4	11	1	+	49609687	49609825
294678301	chr10	49609714	49609886	49609742	49609858	MAPK8	NM_139046	2	11	1	+	49609687	49609825
294678301	chr10	49609714	49609886	49609742	49609858	MAPK8	NM_139047	3	11	1	+	49609687	49609825
294288824	chr10	49617879	49618048	49617912	49618023	MAPK8	NM_002750	1	11	3	+	49617922	49617980
294288824	chr10	49617879	49618048	49617912	49618023	MAPK8	NM_139049	4	11	3	+	49617922	49617980
294288824	chr10	49617879	49618048	49617912	49618023	MAPK8	NM_139046	2	11	3	+	49617922	49617980
294288824	chr10	49617879	49618048	49617912	49618023	MAPK8	NM_139047	3	11	3	+	49617922	49617980
294209889	chr10	49628228	49628373	49628256	49628352	MAPK8	NM_002750	1	11	5	+	49628198	49628363
294209889	chr10	49628228	49628373	49628256	49628352	MAPK8	NM_139049	4	11	5	+	49628198	49628363
294209889	chr10	49628228	49628373	49628256	49628352	MAPK8	NM_139046	2	11	5	+	49628198	49628363
294209889	chr10	49628228	49628373	49628256	49628352	MAPK8	NM_139047	3	11	5	+	49628198	49628363
295372078	chr10	49632536	49632698	49632563	49632670	MAPK8	NM_139046	2	11	6	+	49632557	49632628

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
295372078	chr10	49632536	49632698	49632563	49632670	MAPK8	NM_139047	3	11	6	+	49632557	49632628
294338759	chr10	49634400	49634540	49634426	49634515	MAPK8	NM_002750	1	11	8	+	49634423	49634547
294338759	chr10	49634400	49634540	49634426	49634515	MAPK8	NM_139049	4	11	8	+	49634423	49634547
294338759	chr10	49634400	49634540	49634426	49634515	MAPK8	NM_139046	2	11	8	+	49634423	49634547
294338759	chr10	49634400	49634540	49634426	49634515	MAPK8	NM_139047	3	11	8	+	49634423	49634547
293925353	chr10	49639249	49639409	49639274	49639382	MAPK8	NM_002750	1	11	10	+	49639236	49639313
293925353	chr10	49639249	49639409	49639274	49639382	MAPK8	NM_139049	4	11	10	+	49639236	49639313
293925353	chr10	49639249	49639409	49639274	49639382	MAPK8	NM_139046	2	11	10	+	49639236	49639313
293925353	chr10	49639249	49639409	49639274	49639382	MAPK8	NM_139047	3	11	10	+	49639236	49639313
236182614	chr10	51579056	51579210	51579081	51579187	NCOA4	NM_001145261	2	11	3	+	51579128	51579282
236182614	chr10	51579056	51579210	51579081	51579187	NCOA4	NM_005437	5	10	2	+	51579128	51579282
236182614	chr10	51579056	51579210	51579081	51579187	NCOA4	NM_001145262	3	10	2	+	51579128	51579282
236182614	chr10	51579056	51579210	51579081	51579187	NCOA4	NM_001145263	4	10	2	+	51579128	51579282
236182614	chr10	51579056	51579210	51579081	51579187	NCOA4	NM_001145260	1	12	3	+	51579128	51579282
236459549	chr10	51580807	51580931	51580835	51580906	NCOA4	NM_001145261	2	11	5	+	51580880	51580968
236459549	chr10	51580807	51580931	51580835	51580906	NCOA4	NM_005437	5	10	4	+	51580880	51580968
236459549	chr10	51580807	51580931	51580835	51580906	NCOA4	NM_001145262	3	10	4	+	51580880	51580968
236459549	chr10	51580807	51580931	51580835	51580906	NCOA4	NM_001145263	4	10	4	+	51580880	51580968
236459549	chr10	51580807	51580931	51580835	51580906	NCOA4	NM_001145260	1	12	5	+	51580880	51580968
257916240	chr10	51582171	51582331	51582199	51582303	NCOA4	NM_001145261	2	11	7	+	51582183	51582272
257916240	chr10	51582171	51582331	51582199	51582303	NCOA4	NM_005437	5	10	6	+	51582183	51582272
257916240	chr10	51582171	51582331	51582199	51582303	NCOA4	NM_001145262	3	10	6	+	51582183	51582272
257916240	chr10	51582171	51582331	51582199	51582303	NCOA4	NM_001145263	4	10	6	+	51582183	51582272
257916240	chr10	51582171	51582331	51582199	51582303	NCOA4	NM_001145260	1	12	7	+	51582183	51582272
241411031	chr10	51584674	51584798	51584698	51584773	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
241411031	chr10	51584674	51584798	51584698	51584773	NCOA4	NM_005437	5	10	8	+	51584616	51585599
241411031	chr10	51584674	51584798	51584698	51584773	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
241411031	chr10	51584674	51584798	51584698	51584773	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
241411031	chr10	51584674	51584798	51584698	51584773	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
236581146	chr10	51585075	51585249	51585098	51585229	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
236581146	chr10	51585075	51585249	51585098	51585229	NCOA4	NM_005437	5	10	8	+	51584616	51585599
236581146	chr10	51585075	51585249	51585098	51585229	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
236581146	chr10	51585075	51585249	51585098	51585229	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
236581146	chr10	51585075	51585249	51585098	51585229	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
236643853	chr10	51585461	51585627	51585489	51585600	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
236643853	chr10	51585461	51585627	51585489	51585600	NCOA4	NM_005437	5	10	8	+	51584616	51585599
236643853	chr10	51585461	51585627	51585489	51585600	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
236643853	chr10	51585461	51585627	51585489	51585600	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
236643853	chr10	51585461	51585627	51585489	51585600	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
258193740	chr10	51589115	51589255	51589142	51589233	NCOA4	NM_001145261	2	11	11	+	51589225	51590734
258193740	chr10	51589115	51589255	51589142	51589233	NCOA4	NM_005437	5	10	10	+	51589225	51590734

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258193740	chr10	51589115	51589255	51589142	51589233	NCOA4	NM_001145262	3	10	10	+	51589225	51590734
258193740	chr10	51589115	51589255	51589142	51589233	NCOA4	NM_001145263	4	10	10	+	51589225	51590734
258193740	chr10	51589115	51589255	51589142	51589233	NCOA4	NM_001145260	1	12	12	+	51589225	51590734
262811566	chr10	70332286	70332418	70332305	70332396	TET1	NM_030625	1	12	2	+	70331974	70334009
262809742	chr10	70332668	70332841	70332692	70332820	TET1	NM_030625	1	12	2	+	70331974	70334009
262907864	chr10	70333146	70333320	70333171	70333298	TET1	NM_030625	1	12	2	+	70331974	70334009
262848358	chr10	70333580	70333725	70333608	70333702	TET1	NM_030625	1	12	2	+	70331974	70334009
264370105	chr10	70360702	70360872	70360729	70360844	TET1	NM_030625	1	12	3	+	70360738	70360791
262690718	chr10	70404713	70404846	70404742	70404818	TET1	NM_030625	1	12	4	+	70404455	70406762
262730460	chr10	70405102	70405274	70405131	70405249	TET1	NM_030625	1	12	4	+	70404455	70406762
262707280	chr10	70405448	70405621	70405475	70405594	TET1	NM_030625	1	12	4	+	70404455	70406762
262770683	chr10	70405823	70405993	70405849	70405966	TET1	NM_030625	1	12	4	+	70404455	70406762
262869728	chr10	70406260	70406433	70406287	70406414	TET1	NM_030625	1	12	4	+	70404455	70406762
265061481	chr10	70411542	70411715	70411565	70411693	TET1	NM_030625	1	12	5	+	70411603	70411693
240769424	chr10	70426865	70427015	70426886	70426990	TET1	NM_030625	1	12	7	+	70426802	70427013
265895719	chr10	70441074	70441244	70441102	70441219	TET1	NM_030625	1	12	9	+	70441156	70441245
238865858	chr10	70446091	70446256	70446119	70446232	TET1	NM_030625	1	12	11	+	70446113	70446464
239089702	chr10	70450563	70450736	70450584	70450716	TET1	NM_030625	1	12	12	+	70450565	70454239
239174145	chr10	70451005	70451160	70451027	70451137	TET1	NM_030625	1	12	12	+	70450565	70454239
239238296	chr10	70451416	70451578	70451437	70451552	TET1	NM_030625	1	12	12	+	70450565	70454239
312568060	chr10	76602715	76602888	76602736	76602864	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312568060	chr10	76602715	76602888	76602736	76602864	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312568060	chr10	76602715	76602888	76602736	76602864	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312261652	chr10	76719720	76719844	76719738	76719819	KAT6B	NM_012330	3	18	4	+	76719728	76719836
312261652	chr10	76719720	76719844	76719738	76719819	KAT6B	NM_001256468	1	18	4	+	76719728	76719836
312261652	chr10	76719720	76719844	76719738	76719819	KAT6B	NM_001256469	2	18	4	+	76719728	76719836
312473688	chr10	76729713	76729861	76729741	76729838	KAT6B	NM_012330	3	18	6	+	76729778	76729859
312473688	chr10	76729713	76729861	76729741	76729838	KAT6B	NM_001256468	1	18	6	+	76729778	76729859
312473688	chr10	76729713	76729861	76729741	76729838	KAT6B	NM_001256469	2	18	6	+	76729778	76729859
312305787	chr10	76732356	76732483	76732381	76732455	KAT6B	NM_012330	3	18	7	+	76732265	76732397
312305787	chr10	76732356	76732483	76732381	76732455	KAT6B	NM_001256468	1	18	7	+	76732265	76732397
312305787	chr10	76732356	76732483	76732381	76732455	KAT6B	NM_001256469	2	18	7	+	76732265	76732397
312425979	chr10	76735347	76735488	76735375	76735461	KAT6B	NM_001256468	1	18	8	+	76735157	76735539
312425979	chr10	76735347	76735488	76735375	76735461	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312427143	chr10	76735719	76735867	76735744	76735845	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312468743	chr10	76737095	76737227	76737124	76737203	KAT6B	NM_012330	3	18	9	+	76737074	76737195
312468743	chr10	76737095	76737227	76737124	76737203	KAT6B	NM_001256468	1	18	9	+	76737074	76737195
312468743	chr10	76737095	76737227	76737124	76737203	KAT6B	NM_001256469	2	18	9	+	76737074	76737195
312398870	chr10	76741641	76741772	76741667	76741744	KAT6B	NM_012330	3	18	11	+	76741545	76741686
312398870	chr10	76741641	76741772	76741667	76741744	KAT6B	NM_001256468	1	18	11	+	76741545	76741686
312398870	chr10	76741641	76741772	76741667	76741744	KAT6B	NM_001256469	2	18	11	+	76741545	76741686

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312289608	chr10	76748740	76748914	76748766	76748886	KAT6B	NM_012330	3	18	13	+	76748777	76748870
312289608	chr10	76748740	76748914	76748766	76748886	KAT6B	NM_001256468	1	18	13	+	76748777	76748870
312289608	chr10	76748740	76748914	76748766	76748886	KAT6B	NM_001256469	2	18	13	+	76748777	76748870
312359002	chr10	76780804	76780963	76780827	76780940	KAT6B	NM_012330	3	18	15	+	76780884	76781043
312359002	chr10	76780804	76780963	76780827	76780940	KAT6B	NM_001256468	1	18	15	+	76780884	76781043
312359002	chr10	76780804	76780963	76780827	76780940	KAT6B	NM_001256469	2	18	15	+	76780884	76781043
312534963	chr10	76781797	76781968	76781818	76781946	KAT6B	NM_012330	3	18	16	+	76781639	76781989
312534963	chr10	76781797	76781968	76781818	76781946	KAT6B	NM_001256468	1	18	16	+	76781639	76781989
312534963	chr10	76781797	76781968	76781818	76781946	KAT6B	NM_001256469	2	18	16	+	76781639	76781989
312263003	chr10	76784902	76785063	76784926	76785037	KAT6B	NM_012330	3	18	17	+	76784716	76785007
312263003	chr10	76784902	76785063	76784926	76785037	KAT6B	NM_001256468	1	18	17	+	76784716	76785007
312263003	chr10	76784902	76785063	76784926	76785037	KAT6B	NM_001256469	2	18	17	+	76784716	76785007
312645099	chr10	76788570	76788743	76788591	76788716	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312645099	chr10	76788570	76788743	76788591	76788716	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312645099	chr10	76788570	76788743	76788591	76788716	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312607621	chr10	76788967	76789139	76788988	76789116	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312607621	chr10	76788967	76789139	76788988	76789116	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312607621	chr10	76788967	76789139	76788988	76789116	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312636599	chr10	76789439	76789603	76789461	76789582	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312636599	chr10	76789439	76789603	76789461	76789582	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312636599	chr10	76789439	76789603	76789461	76789582	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312602954	chr10	76789945	76790087	76789965	76790059	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312602954	chr10	76789945	76790087	76789965	76790059	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312602954	chr10	76789945	76790087	76789965	76790059	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312622664	chr10	76790389	76790563	76790409	76790541	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312622664	chr10	76790389	76790563	76790409	76790541	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312622664	chr10	76790389	76790563	76790409	76790541	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
223430086	chr10	88635723	88635854	88635751	88635827	BMPR1A	NM_004329	1	13	3	+	88635624	88635842
222166546	chr10	88651777	88651932	88651805	88651905	BMPR1A	NM_004329	1	13	5	+	88651884	88651986
222898859	chr10	88659663	88659837	88659685	88659812	BMPR1A	NM_004329	1	13	7	+	88659784	88659883
223148608	chr10	88676820	88676988	88676841	88676967	BMPR1A	NM_004329	1	13	9	+	88676891	88677083
223058787	chr10	88679068	88679241	88679087	88679213	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
222673095	chr10	88681346	88681474	88681367	88681450	BMPR1A	NM_004329	1	13	11	+	88681277	88681452
224587150	chr10	88683336	88683506	88683363	88683479	BMPR1A	NM_004329	1	13	13	+	88683351	88684945
241268004	chr10	89690796	89690945	89690826	89690917	PTEN	NM_000314	1	9	4	+	89690803	89690846
235014683	chr10	89692896	89693063	89692921	89693034	PTEN	NM_000314	1	9	5	+	89692770	89693008
236173397	chr10	89717598	89717769	89717623	89717744	PTEN	NM_000314	1	9	7	+	89717610	89717776
238889089	chr10	89724922	89725085	89724955	89725061	PTEN	NM_000314	1	9	9	+	89725044	89728532
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NM_152872	3	8	2	+	90762786	90762951
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NM_152871	2	8	2	+	90762786	90762951
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NR_028036	7	8	2	+	90762786	90762951

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NR_028035	6	7	2	+	90762786	90762951
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NR_028034	5	6	2	+	90762786	90762951
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NR_028033	4	7	2	+	90762786	90762951
228683242	chr10	90762812	90762986	90762836	90762958	FAS	NM_000043	1	9	2	+	90762786	90762951
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NM_152872	3	8	5	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NM_152871	2	8	5	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NR_028036	7	8	4	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NR_028035	6	7	3	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NR_028034	5	6	3	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NR_028033	4	7	4	+	90770296	90770357
230600404	chr10	90770258	90770429	90770283	90770401	FAS	NM_000043	1	9	5	+	90770296	90770357
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NM_152872	3	8	8	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NM_152871	2	8	8	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NR_028036	7	8	8	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NR_028035	6	7	7	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NR_028034	5	6	6	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NR_028033	4	7	7	+	90773876	90775542
231206913	chr10	90773759	90773929	90773788	90773905	FAS	NM_000043	1	9	9	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NM_152872	3	8	8	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NM_152871	2	8	8	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NR_028036	7	8	8	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NR_028035	6	7	7	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NR_028034	5	6	6	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NR_028033	4	7	7	+	90773876	90775542
231220326	chr10	90774142	90774291	90774170	90774267	FAS	NM_000043	1	9	9	+	90773876	90775542
284896146	chr10	96534777	96534946	96534806	96534922	CYP2C19	NM_000769	1	9	2	+	96534815	96534977
287058234	chr10	96535267	96535407	96535289	96535379	CYP2C19	NM_000769	1	9	3	+	96535147	96535296
328502380	chr10	96541563	96541702	96541596	96541674	CYP2C19	NM_000769	1	9	5	+	96541578	96541754
287776993	chr10	96602549	96602720	96602576	96602698	CYP2C19	NM_000769	1	9	7	+	96602594	96602781
286701320	chr10	96612454	96612628	96612481	96612604	CYP2C19	NM_000769	1	9	9	+	96612490	96612671
294026393	chr10	97956567	97956709	97956595	97956685	BLNK	NM_013314	2	17	16	-	97956664	97956819
294026393	chr10	97956567	97956709	97956595	97956685	BLNK	NM_001114094	1	16	15	-	97956664	97956819
293996898	chr10	97959834	97959968	97959857	97959940	BLNK	NM_013314	2	17	15	-	97959831	97959914
293996898	chr10	97959834	97959968	97959857	97959940	BLNK	NM_001114094	1	16	14	-	97959831	97959914
294781783	chr10	97964300	97964457	97964321	97964434	BLNK	NM_013314	2	17	12	-	97964288	97964372
294781783	chr10	97964300	97964457	97964321	97964434	BLNK	NM_001114094	1	16	11	-	97964288	97964372
294425130	chr10	97974957	97975130	97974983	97975105	BLNK	NM_013314	2	17	8	-	97975077	97975145
293834652	chr10	97983658	97983826	97983680	97983802	BLNK	NM_013314	2	17	6	-	97983582	97983745
293834652	chr10	97983658	97983826	97983680	97983802	BLNK	NM_001114094	1	16	6	-	97983582	97983745
294743909	chr10	98002398	98002568	98002422	98002540	BLNK	NM_013314	2	17	3	-	98002491	98002540
294743909	chr10	98002398	98002568	98002422	98002540	BLNK	NM_001114094	1	16	3	-	98002491	98002540

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264720059	chr10	102891294	102891446	102891311	102891428	TLX1	NM_005521	2	3	1	+	102891061	102891866
264720059	chr10	102891294	102891446	102891311	102891428	TLX1	NM_001195517	1	3	1	+	102891061	102891866
262935731	chr10	102893898	102894039	102893920	102894020	TLX1	NM_005521	2	3	2	+	102893932	102894133
262935731	chr10	102893898	102894039	102893920	102894020	TLX1	NM_001195517	1	3	2	+	102893932	102894133
266222200	chr10	102896419	102896590	102896437	102896571	TLX1	NM_001195517	1	3	3	+	102896425	102897546
266222200	chr10	102896419	102896590	102896437	102896571	TLX1	NM_005521	2	3	3	+	102896448	102897546
236503284	chr10	104155988	104156114	104156008	104156091	NFKB2	NM_002502	3	23	3	+	104156010	104156091
236503284	chr10	104155988	104156114	104156008	104156091	NFKB2	NM_001077494	2	23	3	+	104156010	104156091
236503284	chr10	104155988	104156114	104156008	104156091	NFKB2	NM_001077493	1	23	3	+	104156010	104156091
239093243	chr10	104156657	104156831	104156682	104156813	NFKB2	NM_002502	3	23	6	+	104156661	104156812
239093243	chr10	104156657	104156831	104156682	104156813	NFKB2	NM_001077494	2	23	6	+	104156661	104156812
239093243	chr10	104156657	104156831	104156682	104156813	NFKB2	NM_001077493	1	23	6	+	104156661	104156812
236870605	chr10	104157312	104157466	104157335	104157445	NFKB2	NM_002502	3	23	8	+	104157284	104157442
236870605	chr10	104157312	104157466	104157335	104157445	NFKB2	NM_001077494	2	23	8	+	104157284	104157442
236870605	chr10	104157312	104157466	104157335	104157445	NFKB2	NM_001077493	1	23	8	+	104157284	104157442
240612755	chr10	104158192	104158349	104158214	104158327	NFKB2	NM_002502	3	23	11	+	104158142	104158280
240612755	chr10	104158192	104158349	104158214	104158327	NFKB2	NM_001077494	2	23	11	+	104158142	104158280
240612755	chr10	104158192	104158349	104158214	104158327	NFKB2	NM_001077493	1	23	11	+	104158142	104158280
237227347	chr10	104159105	104159272	104159122	104159255	NFKB2	NM_002502	3	23	13	+	104159045	104159254
237227347	chr10	104159105	104159272	104159122	104159255	NFKB2	NM_001077494	2	23	13	+	104159045	104159254
237227347	chr10	104159105	104159272	104159122	104159255	NFKB2	NM_001077493	1	23	13	+	104159045	104159254
235080126	chr10	104159862	104160004	104159883	104159984	NFKB2	NM_002502	3	23	15	+	104159837	104159951
235080126	chr10	104159862	104160004	104159883	104159984	NFKB2	NM_001077494	2	23	15	+	104159837	104159951
235080126	chr10	104159862	104160004	104159883	104159984	NFKB2	NM_001077493	1	23	15	+	104159837	104159951
237352417	chr10	104160459	104160608	104160479	104160586	NFKB2	NM_002502	3	23	17	+	104160412	104160581
237352417	chr10	104160459	104160608	104160479	104160586	NFKB2	NM_001077494	2	23	17	+	104160412	104160581
237352417	chr10	104160459	104160608	104160479	104160586	NFKB2	NM_001077493	1	23	17	+	104160412	104160581
238264710	chr10	104161135	104161296	104161163	104161275	NFKB2	NM_002502	3	23	20	+	104161206	104161275
238264710	chr10	104161135	104161296	104161163	104161275	NFKB2	NM_001077494	2	23	20	+	104161206	104161275
238264710	chr10	104161135	104161296	104161163	104161275	NFKB2	NM_001077493	1	23	20	+	104161206	104161275
238894902	chr10	104161978	104162145	104162001	104162127	NFKB2	NM_001077494	2	23	23	+	104162009	104162281
238894902	chr10	104161978	104162145	104162001	104162127	NFKB2	NM_002502	3	23	23	+	104162012	104162281
238894902	chr10	104161978	104162145	104162001	104162127	NFKB2	NM_001077493	1	23	23	+	104162012	104162281
237896197	chr10	104268925	104269088	104268942	104269061	SUFU	NM_016169	2	12	2	+	104268926	104269060
237896197	chr10	104268925	104269088	104268942	104269061	SUFU	NM_001178133	1	11	2	+	104268926	104269060
240709447	chr10	104352373	104352525	104352395	104352505	SUFU	NM_016169	2	12	4	+	104352339	104352481
240709447	chr10	104352373	104352525	104352395	104352505	SUFU	NM_001178133	1	11	4	+	104352339	104352481
240156431	chr10	104356904	104357078	104356927	104357057	SUFU	NM_016169	2	12	7	+	104356897	104357050
240156431	chr10	104356904	104357078	104356927	104357057	SUFU	NM_001178133	1	11	7	+	104356897	104357050
241852237	chr10	104375102	104375228	104375127	104375210	SUFU	NM_016169	2	12	9	+	104375025	104375159
241852237	chr10	104375102	104375228	104375127	104375210	SUFU	NM_001178133	1	11	9	+	104375025	104375159

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238439385	chr10	104386863	104387031	104386884	104387005	SUFU	NM_016169	2	12	11	+	104386932	104387000
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001146283	2	13	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198526	7	13	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_030756	13	14	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001146286	5	12	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001146285	4	13	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198530	11	11	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198529	10	13	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198525	6	15	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198531	12	13	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001146274	1	14	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198528	9	15	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001198527	8	15	1	+	114710009	114710704
274205736	chr10	114710563	114710696	114710588	114710673	TCF7L2	NM_001146284	3	13	1	+	114710009	114710704
272761644	chr10	114724270	114724408	114724295	114724383	TCF7L2	NM_001198531	12	13	4	+	114724315	114724383
272761644	chr10	114724270	114724408	114724295	114724383	TCF7L2	NM_001146274	1	14	4	+	114724315	114724383
273020157	chr10	114849215	114849385	114849238	114849360	TCF7L2	NM_001146283	2	13	5	+	114849159	114849299
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001146283	2	13	7	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198526	7	13	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_030756	13	14	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001146286	5	12	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001146285	4	13	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198530	11	11	5	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198529	10	13	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198525	6	15	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198531	12	13	7	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001146274	1	14	7	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198528	9	15	6	+	114903682	114903784
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001198527	8	15	6	+	114903682	114903772
273593056	chr10	114903699	114903833	114903723	114903806	TCF7L2	NM_001146284	3	13	6	+	114903682	114903772
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001146283	2	13	10	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198526	7	13	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_030756	13	14	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001146286	5	12	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001146285	4	13	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198530	11	11	8	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198529	10	13	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198525	6	15	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198531	12	13	10	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001146274	1	14	10	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198528	9	15	9	+	114911484	114911643

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001198527	8	15	9	+	114911484	114911643
273592866	chr10	114911432	114911584	114911453	114911555	TCF7L2	NM_001146284	3	13	9	+	114911484	114911643
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_030756	13	14	12	+	114918426	114918476
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_001198529	10	13	12	+	114918426	114918476
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_001198525	6	15	12	+	114918426	114918476
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_001198528	9	15	12	+	114918426	114918476
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_001198527	8	15	12	+	114918426	114918476
273374406	chr10	114918324	114918498	114918347	114918470	TCF7L2	NM_001146284	3	13	12	+	114918426	114918476
273586380	chr10	114921213	114921384	114921238	114921356	TCF7L2	NM_001198528	9	15	14	+	114921338	114921362
273586380	chr10	114921213	114921384	114921238	114921356	TCF7L2	NM_001198527	8	15	14	+	114921338	114921362
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001146283	2	13	13	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198526	7	13	13	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_030756	13	14	14	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001146286	5	12	12	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001146285	4	13	13	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198530	11	11	11	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198529	10	13	13	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198525	6	15	15	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198531	12	13	13	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001146274	1	14	14	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198528	9	15	15	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001198527	8	15	15	+	114925314	114927436
274221897	chr10	114925701	114925856	114925718	114925829	TCF7L2	NM_001146284	3	13	13	+	114925314	114927436
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_001144918	7	16	16	-	123237844	123239535
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_000141	1	18	18	-	123237844	123239535
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_001144917	6	16	16	-	123237844	123239535
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_001144916	5	15	15	-	123237844	123239535
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_022970	9	18	18	-	123237844	123239535
228319748	chr10	123239414	123239577	123239434	123239550	FGFR2	NM_001144914	3	15	15	-	123237844	123239535
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144913	2	17	15	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144918	7	16	14	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_000141	1	18	16	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144917	6	16	14	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144916	5	15	13	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_022970	9	18	16	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144914	3	15	13	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144915	4	17	15	-	123244909	123245046
228913018	chr10	123244775	123244946	123244797	123244924	FGFR2	NM_001144919	8	17	15	-	123244909	123245046
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144913	2	17	13	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144918	7	16	12	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_000141	1	18	14	-	123247505	123247627

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144917	6	16	12	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144916	5	15	11	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_022970	9	18	14	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144914	3	15	11	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144915	4	17	13	-	123247505	123247627
232231008	chr10	123247435	123247608	123247458	123247580	FGFR2	NM_001144919	8	17	13	-	123247505	123247627
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144913	2	17	11	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144918	7	16	10	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_000141	1	18	12	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144917	6	16	10	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144916	5	15	9	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_022970	9	18	12	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144914	3	15	9	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144915	4	17	11	-	123258009	123258119
228307739	chr10	123257978	123258150	123257999	123258122	FGFR2	NM_001144919	8	17	11	-	123258009	123258119
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144913	2	17	9	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144918	7	16	8	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_000141	1	18	10	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144917	6	16	8	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144916	5	15	7	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_022970	9	18	10	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144914	3	15	7	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144915	4	17	9	-	123263304	123263455
228474926	chr10	123263374	123263507	123263394	123263483	FGFR2	NM_001144919	8	17	9	-	123263304	123263455
228077410	chr10	123276849	123277007	123276873	123276983	FGFR2	NM_001144918	7	16	6	-	123276833	123276977
228077410	chr10	123276849	123277007	123276873	123276983	FGFR2	NM_000141	1	18	8	-	123276833	123276977
228077410	chr10	123276849	123277007	123276873	123276983	FGFR2	NM_001144916	5	15	5	-	123276833	123276977
228077410	chr10	123276849	123277007	123276873	123276983	FGFR2	NM_001144915	4	17	7	-	123276833	123276977
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144913	2	17	6	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144918	7	16	5	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_000141	1	18	7	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144917	6	16	7	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144916	5	15	4	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_022970	9	18	7	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144915	4	17	6	-	123279493	123279683
228055766	chr10	123279581	123279705	123279605	123279683	FGFR2	NM_001144919	8	17	6	-	123279493	123279683
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144913	2	17	4	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144918	7	16	3	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_000141	1	18	5	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144917	6	16	5	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144916	5	15	2	-	123310804	123310973

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_022970	9	18	5	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144914	3	15	4	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144915	4	17	4	-	123310804	123310973
229691846	chr10	123310860	123311020	123310880	123310997	FGFR2	NM_001144919	8	17	4	-	123310804	123310973
231612233	chr10	123325097	123325256	123325119	123325233	FGFR2	NM_001144913	2	17	2	-	123324952	123325218
231612233	chr10	123325097	123325256	123325119	123325233	FGFR2	NM_000141	1	18	3	-	123324952	123325218
231612233	chr10	123325097	123325256	123325119	123325233	FGFR2	NM_001144917	6	16	3	-	123324952	123325218
231612233	chr10	123325097	123325256	123325119	123325233	FGFR2	NM_022970	9	18	3	-	123324952	123325218
231612233	chr10	123325097	123325256	123325119	123325233	FGFR2	NM_001144914	3	15	2	-	123324952	123325218
227387562	chr11	533362	533499	533382	533480	HRAS	NM_001130442	1	5	4	-	533453	533612
227387562	chr11	533362	533499	533382	533480	HRAS	NM_176795	3	6	4	-	533453	533612
227387562	chr11	533362	533499	533382	533480	HRAS	NM_005343	2	6	4	-	533453	533612
227470067	chr11	533881	534031	533902	534009	HRAS	NM_001130442	1	5	3	-	533766	533944
227470067	chr11	533881	534031	533902	534009	HRAS	NM_176795	3	6	3	-	533766	533944
227470067	chr11	533881	534031	533902	534009	HRAS	NM_005343	2	6	3	-	533766	533944
330092138	chr11	2154267	2154440	2154289	2154421	IGF2	NM_000612	1	4	4	-	2150347	2154453
330092138	chr11	2154267	2154440	2154289	2154421	IGF2	NM_001127598	3	5	5	-	2150347	2154453
330092138	chr11	2154267	2154440	2154289	2154421	IGF2	NM_001007139	2	5	5	-	2150347	2154453
330129946	chr11	2156535	2156694	2156555	2156674	IGF2	NM_000612	1	4	2	-	2156597	2156759
330129946	chr11	2156535	2156694	2156555	2156674	IGF2	NM_001127598	3	5	3	-	2156597	2156759
330129946	chr11	2156535	2156694	2156555	2156674	IGF2	NM_001007139	2	5	3	-	2156597	2156759
235760009	chr11	3697305	3697461	3697326	3697439	NUP98	NM_016320	2	33	33	-	3696240	3697606
235760009	chr11	3697305	3697461	3697326	3697439	NUP98	NM_139132	4	32	32	-	3696240	3697606
237192792	chr11	3700696	3700868	3700723	3700844	NUP98	NM_016320	2	33	31	-	3700784	3700938
237192792	chr11	3700696	3700868	3700723	3700844	NUP98	NM_139132	4	32	30	-	3700784	3700938
235849170	chr11	3704562	3704718	3704582	3704690	NUP98	NM_016320	2	33	30	-	3704430	3704671
235849170	chr11	3704562	3704718	3704582	3704690	NUP98	NM_139132	4	32	29	-	3704430	3704671
235047653	chr11	3712599	3712725	3712622	3712700	NUP98	NM_016320	2	33	28	-	3712577	3712719
235047653	chr11	3712599	3712725	3712622	3712700	NUP98	NM_139132	4	32	28	-	3712577	3712719
235021062	chr11	3716723	3716895	3716745	3716869	NUP98	NM_016320	2	33	26	-	3716679	3716836
235021062	chr11	3716723	3716895	3716745	3716869	NUP98	NM_139132	4	32	26	-	3716679	3716836
236608020	chr11	3721725	3721899	3721748	3721871	NUP98	NM_016320	2	33	24	-	3721840	3722069
236608020	chr11	3721725	3721899	3721748	3721871	NUP98	NM_139132	4	32	24	-	3721840	3722069
237333164	chr11	3723737	3723911	3723765	3723891	NUP98	NM_016320	2	33	23	-	3723693	3724122
237333164	chr11	3723737	3723911	3723765	3723891	NUP98	NM_139132	4	32	23	-	3723693	3724122
235462079	chr11	3726470	3726634	3726495	3726607	NUP98	NM_016320	2	33	22	-	3726430	3726586
235462079	chr11	3726470	3726634	3726495	3726607	NUP98	NM_139132	4	32	22	-	3726430	3726586
237076108	chr11	3733859	3734015	3733883	3733986	NUP98	NM_016320	2	33	20	-	3733794	3733958
237076108	chr11	3733859	3734015	3733883	3733986	NUP98	NM_139132	4	32	20	-	3733794	3733958
237076108	chr11	3733859	3734015	3733883	3733986	NUP98	NM_005387	1	20	20	-	3733059	3733958
237076108	chr11	3733859	3734015	3733883	3733986	NUP98	NM_139131	3	20	20	-	3733059	3733958

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236647397	chr11	3740546	3740719	3740574	3740696	NUP98	NM_005387	1	20	18	-	3740642	3740780
236647397	chr11	3740546	3740719	3740574	3740696	NUP98	NM_139131	3	20	18	-	3740642	3740780
236647397	chr11	3740546	3740719	3740574	3740696	NUP98	NM_016320	2	33	18	-	3740642	3740780
236647397	chr11	3740546	3740719	3740574	3740696	NUP98	NM_139132	4	32	18	-	3740642	3740780
235480103	chr11	3744538	3744695	3744563	3744668	NUP98	NM_005387	1	20	16	-	3744387	3744685
235480103	chr11	3744538	3744695	3744563	3744668	NUP98	NM_139131	3	20	16	-	3744387	3744685
235480103	chr11	3744538	3744695	3744563	3744668	NUP98	NM_016320	2	33	16	-	3744387	3744685
235480103	chr11	3744538	3744695	3744563	3744668	NUP98	NM_139132	4	32	16	-	3744387	3744685
237938099	chr11	3752713	3752878	3752733	3752853	NUP98	NM_005387	1	20	14	-	3752621	3752808
237938099	chr11	3752713	3752878	3752733	3752853	NUP98	NM_139131	3	20	14	-	3752621	3752808
237938099	chr11	3752713	3752878	3752733	3752853	NUP98	NM_016320	2	33	14	-	3752621	3752808
237938099	chr11	3752713	3752878	3752733	3752853	NUP98	NM_139132	4	32	14	-	3752621	3752808
236378571	chr11	3765824	3765949	3765849	3765926	NUP98	NM_005387	1	20	12	-	3765739	3765879
236378571	chr11	3765824	3765949	3765849	3765926	NUP98	NM_139131	3	20	12	-	3765739	3765879
236378571	chr11	3765824	3765949	3765849	3765926	NUP98	NM_016320	2	33	12	-	3765739	3765879
236378571	chr11	3765824	3765949	3765849	3765926	NUP98	NM_139132	4	32	12	-	3765739	3765879
237786090	chr11	3784103	3784239	3784131	3784217	NUP98	NM_005387	1	20	9	-	3784132	3784269
237786090	chr11	3784103	3784239	3784131	3784217	NUP98	NM_139131	3	20	9	-	3784132	3784269
237786090	chr11	3784103	3784239	3784131	3784217	NUP98	NM_016320	2	33	9	-	3784132	3784269
237786090	chr11	3784103	3784239	3784131	3784217	NUP98	NM_139132	4	32	9	-	3784132	3784269
236100522	chr11	3792970	3793098	3792994	3793076	NUP98	NM_005387	1	20	7	-	3792978	3793158
236100522	chr11	3792970	3793098	3792994	3793076	NUP98	NM_139131	3	20	7	-	3792978	3793158
236100522	chr11	3792970	3793098	3792994	3793076	NUP98	NM_016320	2	33	7	-	3792978	3793158
236100522	chr11	3792970	3793098	3792994	3793076	NUP98	NM_139132	4	32	7	-	3792978	3793158
237216370	chr11	3797052	3797220	3797077	3797193	NUP98	NM_005387	1	20	5	-	3797112	3797251
237216370	chr11	3797052	3797220	3797077	3797193	NUP98	NM_139131	3	20	5	-	3797112	3797251
237216370	chr11	3797052	3797220	3797077	3797193	NUP98	NM_016320	2	33	5	-	3797112	3797251
237216370	chr11	3797052	3797220	3797077	3797193	NUP98	NM_139132	4	32	5	-	3797112	3797251
236409008	chr11	3800277	3800448	3800299	3800420	NUP98	NM_005387	1	20	3	-	3800386	3800487
236409008	chr11	3800277	3800448	3800299	3800420	NUP98	NM_139131	3	20	3	-	3800386	3800487
236409008	chr11	3800277	3800448	3800299	3800420	NUP98	NM_016320	2	33	3	-	3800386	3800487
236409008	chr11	3800277	3800448	3800299	3800420	NUP98	NM_139132	4	32	3	-	3800386	3800487
293988127	chr11	4116142	4116305	4116163	4116284	RRM1	NM_001033	1	19	1	+	4115924	4116261
294652721	chr11	4127316	4127478	4127336	4127451	RRM1	NM_001033	1	19	3	+	4127276	4127453
293895601	chr11	4132732	4132895	4132759	4132868	RRM1	NM_001033	1	19	6	+	4132831	4132870
294737461	chr11	4139568	4139741	4139592	4139713	RRM1	NM_001033	1	19	8	+	4139550	4139691
293960858	chr11	4143254	4143405	4143280	4143383	RRM1	NM_001033	1	19	11	+	4143371	4143450
293729148	chr11	4144559	4144731	4144581	4144704	RRM1	NM_001033	1	19	12	+	4144413	4144614
293944473	chr11	4148284	4148419	4148304	4148390	RRM1	NM_001033	1	19	14	+	4148265	4148486
294919863	chr11	4153533	4153683	4153555	4153662	RRM1	NM_001033	1	19	16	+	4153516	4153651
295399556	chr11	4156294	4156467	4156320	4156445	RRM1	NM_001033	1	19	18	+	4156312	4156500

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293740973	chr11	4159561	4159685	4159583	4159656	RRM1	NM_001033	1	19	19	+	4159425	4160106
230642947	chr11	22646488	22646654	22646512	22646634	FANCF	NM_022725	1	1	1	-	22644079	22647387
230657001	chr11	22646961	22647125	22646984	22647104	FANCF	NM_022725	1	1	1	-	22644079	22647387
239513624	chr11	32410486	32410656	32410514	32410633	WT1	NM_000378	1	9	9	-	32409322	32410725
239513624	chr11	32410486	32410656	32410514	32410633	WT1	NM_001198552	3	9	9	-	32409322	32410725
239513624	chr11	32410486	32410656	32410514	32410633	WT1	NM_001198551	2	10	10	-	32409322	32410725
239513624	chr11	32410486	32410656	32410514	32410633	WT1	NM_024426	5	10	10	-	32409322	32410725
239513624	chr11	32410486	32410656	32410514	32410633	WT1	NM_024424	4	10	10	-	32409322	32410725
240494321	chr11	32414181	32414353	32414203	32414324	WT1	NM_000378	1	9	7	-	32414212	32414301
240494321	chr11	32414181	32414353	32414203	32414324	WT1	NM_001198552	3	9	7	-	32414212	32414301
240494321	chr11	32414181	32414353	32414203	32414324	WT1	NM_001198551	2	10	8	-	32414212	32414301
240494321	chr11	32414181	32414353	32414203	32414324	WT1	NM_024426	5	10	8	-	32414212	32414301
240494321	chr11	32414181	32414353	32414203	32414324	WT1	NM_024424	4	10	8	-	32414212	32414301
240970430	chr11	32421488	32421620	32421509	32421596	WT1	NM_000378	1	9	5	-	32421494	32421590
240970430	chr11	32421488	32421620	32421509	32421596	WT1	NM_001198552	3	9	5	-	32421494	32421590
240970430	chr11	32421488	32421620	32421509	32421596	WT1	NM_001198551	2	10	6	-	32421494	32421590
240970430	chr11	32421488	32421620	32421509	32421596	WT1	NM_024426	5	10	6	-	32421494	32421590
240970430	chr11	32421488	32421620	32421509	32421596	WT1	NM_024424	4	10	6	-	32421494	32421590
238648460	chr11	32449371	32449532	32449390	32449513	WT1	NM_000378	1	9	3	-	32449502	32449604
238648460	chr11	32449371	32449532	32449390	32449513	WT1	NM_001198552	3	9	3	-	32449502	32449604
238648460	chr11	32449371	32449532	32449390	32449513	WT1	NM_001198551	2	10	3	-	32449502	32449604
238648460	chr11	32449371	32449532	32449390	32449513	WT1	NM_024426	5	10	3	-	32449502	32449604
238648460	chr11	32449371	32449532	32449390	32449513	WT1	NM_024424	4	10	3	-	32449502	32449604
241420276	chr11	32452048	32452213	32452074	32452194	WT1	NM_001198552	3	9	1	-	32452076	32452363
241420276	chr11	32452048	32452213	32452074	32452194	WT1	NM_001198551	2	10	1	-	32452076	32452363
262327650	chr11	32456462	32456619	32456485	32456602	WT1	NM_000378	1	9	1	-	32456246	32457081
262327650	chr11	32456462	32456619	32456485	32456602	WT1	NM_024426	5	10	1	-	32456246	32457081
262327650	chr11	32456462	32456619	32456485	32456602	WT1	NM_024424	4	10	1	-	32456246	32457081
229914948	chr11	44117801	44117967	44117818	44117950	EXT2	NM_000401	1	14	1	+	44117747	44117871
230562535	chr11	44129533	44129707	44129556	44129681	EXT2	NM_000401	1	14	2	+	44129233	44129798
230562535	chr11	44129533	44129707	44129556	44129681	EXT2	NM_001178083	2	15	2	+	44129233	44129798
230562535	chr11	44129533	44129707	44129556	44129681	EXT2	NM_207122	3	14	2	+	44129233	44129798
229252734	chr11	44135653	44135795	44135678	44135775	EXT2	NM_000401	1	14	4	+	44135735	44135851
229252734	chr11	44135653	44135795	44135678	44135775	EXT2	NM_001178083	2	15	4	+	44135735	44135851
229252734	chr11	44135653	44135795	44135678	44135775	EXT2	NM_207122	3	14	4	+	44135735	44135851
229903863	chr11	44148327	44148498	44148355	44148469	EXT2	NM_000401	1	14	6	+	44148366	44148505
229903863	chr11	44148327	44148498	44148355	44148469	EXT2	NM_001178083	2	15	6	+	44148366	44148505
229903863	chr11	44148327	44148498	44148355	44148469	EXT2	NM_207122	3	14	6	+	44148366	44148505
229160551	chr11	44165818	44165953	44165840	44165927	EXT2	NM_001178083	2	15	8	+	44165797	44165889
230145713	chr11	44219431	44219592	44219451	44219568	EXT2	NM_000401	1	14	9	+	44219379	44219568
230145713	chr11	44219431	44219592	44219451	44219568	EXT2	NM_001178083	2	15	10	+	44219379	44219568

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230145713	chr11	44219431	44219592	44219451	44219568	EXT2	NM_207122	3	14	9	+	44219379	44219568
230423770	chr11	44253828	44254001	44253853	44253978	EXT2	NM_000401	1	14	11	+	44253903	44254046
230423770	chr11	44253828	44254001	44253853	44253978	EXT2	NM_001178083	2	15	12	+	44253903	44254046
230423770	chr11	44253828	44254001	44253853	44253978	EXT2	NM_207122	3	14	11	+	44253903	44254046
230829554	chr11	44265597	44265737	44265625	44265715	EXT2	NM_000401	1	14	14	+	44265699	44266980
230829554	chr11	44265597	44265737	44265625	44265715	EXT2	NM_001178083	2	15	15	+	44265699	44266980
230829554	chr11	44265597	44265737	44265625	44265715	EXT2	NM_207122	3	14	14	+	44265699	44266980
228063208	chr11	47237784	47237921	47237808	47237901	DDB2	NM_000107	1	10	2	+	47237887	47238023
230324108	chr11	47238474	47238646	47238495	47238622	DDB2	NM_000107	1	10	3	+	47238409	47238600
229966463	chr11	47256108	47256233	47256129	47256214	DDB2	NM_000107	1	10	5	+	47256124	47256223
228812840	chr11	47256733	47256902	47256753	47256882	DDB2	NM_000107	1	10	7	+	47256821	47256963
228356960	chr11	47259585	47259759	47259607	47259734	DDB2	NM_000107	1	10	9	+	47259689	47259734
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130800	3	10	10	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130803	6	10	10	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130802	5	10	10	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130801	4	10	10	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130804	7	11	11	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_000244	1	10	10	-	64570986	64572288
234682987	chr11	64571950	64572120	64571974	64572103	MEN1	NM_130799	2	10	10	-	64570986	64572288
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130800	3	10	9	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130803	6	10	9	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130802	5	10	9	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130801	4	10	9	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130804	7	11	10	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_000244	1	10	9	-	64572506	64572670
233524283	chr11	64572582	64572716	64572602	64572693	MEN1	NM_130799	2	10	9	-	64572506	64572670
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130800	3	10	7	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130803	6	10	7	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130802	5	10	7	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130801	4	10	7	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130804	7	11	8	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_000244	1	10	7	-	64573704	64573840
233058491	chr11	64573770	64573943	64573789	64573923	MEN1	NM_130799	2	10	7	-	64573704	64573840
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130800	3	10	3	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130803	6	10	3	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130802	5	10	3	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130801	4	10	3	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130804	7	11	4	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_000244	1	10	3	-	64575363	64575571
233660564	chr11	64575308	64575477	64575329	64575456	MEN1	NM_130799	2	10	3	-	64575363	64575571
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130800	3	10	2	-	64577122	64577604

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130803	6	10	2	-	64577122	64577604
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130802	5	10	2	-	64577122	64577604
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130801	4	10	2	-	64577122	64577604
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130804	7	11	3	-	64577122	64577604
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_000244	1	10	2	-	64577122	64577604
231204216	chr11	64577299	64577458	64577318	64577437	MEN1	NM_130799	2	10	2	-	64577137	64577604
253635139	chr11	69456078	69456238	69456097	69456219	CCND1	NM_053056	1	5	1	+	69455873	69456279
226296830	chr11	69457961	69458129	69457982	69458107	CCND1	NM_053056	1	5	2	+	69457799	69458014
226687535	chr11	69462845	69462979	69462869	69462959	CCND1	NM_053056	1	5	4	+	69462762	69462910
241838789	chr11	71714489	71714624	71714510	71714603	NUMA1	NM_006185	1	27	27	-	71713911	71714584
236049186	chr11	71715642	71715787	71715662	71715765	NUMA1	NM_006185	1	27	24	-	71715686	71715862
236635075	chr11	71717058	71717227	71717080	71717206	NUMA1	NM_006185	1	27	22	-	71717081	71717309
235537909	chr11	71718360	71718505	71718382	71718481	NUMA1	NM_006185	1	27	21	-	71718235	71718481
238718325	chr11	71720058	71720227	71720079	71720201	NUMA1	NM_006185	1	27	19	-	71720013	71720231
241248460	chr11	71721761	71721931	71721783	71721908	NUMA1	NM_006185	1	27	17	-	71721832	71721900
258184281	chr11	71724104	71724265	71724127	71724245	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238440324	chr11	71724517	71724687	71724535	71724670	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258132064	chr11	71724923	71725069	71724945	71725048	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238399756	chr11	71725371	71725496	71725392	71725477	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238433972	chr11	71725798	71725966	71725816	71725945	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258225961	chr11	71726195	71726348	71726217	71726325	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258213716	chr11	71726623	71726779	71726641	71726759	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238129858	chr11	71727114	71727281	71727135	71727259	NUMA1	NM_006185	1	27	15	-	71723941	71727306
237028820	chr11	71728819	71728993	71728839	71728969	NUMA1	NM_006185	1	27	13	-	71728733	71728873
239159418	chr11	71729501	71729645	71729523	71729623	NUMA1	NM_006185	1	27	11	-	71729442	71729559
242004903	chr11	71730557	71730726	71730580	71730697	NUMA1	NM_006185	1	27	9	-	71730540	71730663
237036021	chr11	71735275	71735445	71735298	71735417	NUMA1	NM_006185	1	27	5	-	71735320	71735399
235531762	chr11	94163001	94163136	94163023	94163113	MRE11A	NM_005591	2	20	19	-	94163077	94163152
235531762	chr11	94163001	94163136	94163023	94163113	MRE11A	NM_005590	1	19	18	-	94163077	94163152
236760864	chr11	94178847	94179012	94178873	94178985	MRE11A	NM_005591	2	20	16	-	94178976	94179059
257718834	chr11	94189410	94189540	94189439	94189514	MRE11A	NM_005591	2	20	14	-	94189442	94189504
257718834	chr11	94189410	94189540	94189439	94189514	MRE11A	NM_005590	1	19	14	-	94189442	94189504
235716971	chr11	94197215	94197345	94197248	94197318	MRE11A	NM_005591	2	20	11	-	94197279	94197405
235716971	chr11	94197215	94197345	94197248	94197318	MRE11A	NM_005590	1	19	11	-	94197279	94197405
237411139	chr11	94203516	94203686	94203544	94203659	MRE11A	NM_005591	2	20	9	-	94203637	94203808
237411139	chr11	94203516	94203686	94203544	94203659	MRE11A	NM_005590	1	19	9	-	94203637	94203808
239332380	chr11	94204731	94204856	94204757	94204832	MRE11A	NM_005591	2	20	8	-	94204740	94204925
239332380	chr11	94204731	94204856	94204757	94204832	MRE11A	NM_005590	1	19	8	-	94204740	94204925
237373600	chr11	94211969	94212114	94211995	94212086	MRE11A	NM_005591	2	20	6	-	94211901	94212042
237373600	chr11	94211969	94212114	94211995	94212086	MRE11A	NM_005590	1	19	6	-	94211901	94212042
235434292	chr11	94219141	94219270	94219169	94219246	MRE11A	NM_005591	2	20	4	-	94219090	94219250

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235434292	chr11	94219141	94219270	94219169	94219246	MRE11A	NM_005590	1	19	4	-	94219090	94219250
234477984	chr11	95712003	95712173	95712030	95712146	MAML2	NM_032427	1	5	5	-	95711440	95713127
234484139	chr11	95712467	95712617	95712490	95712596	MAML2	NM_032427	1	5	5	-	95711440	95713127
234484925	chr11	95712879	95713052	95712905	95713030	MAML2	NM_032427	1	5	5	-	95711440	95713127
232905933	chr11	95724744	95724916	95724769	95724892	MAML2	NM_032427	1	5	3	-	95724684	95724887
234514466	chr11	95825641	95825801	95825662	95825780	MAML2	NM_032427	1	5	2	-	95825056	95826681
234513998	chr11	95826082	95826254	95826105	95826232	MAML2	NM_032427	1	5	2	-	95825056	95826681
234511001	chr11	95826557	95826681	95826581	95826656	MAML2	NM_032427	1	5	2	-	95825056	95826681
233186400	chr11	96074834	96074983	96074856	96074964	MAML2	NM_032427	1	5	1	-	96074547	96076344
223940369	chr11	102195389	102195563	102195413	102195536	BIRC3	NM_182962	2	10	3	+	102195192	102196093
223940369	chr11	102195389	102195563	102195413	102195536	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222459888	chr11	102195854	102195998	102195875	102195972	BIRC3	NM_182962	2	10	3	+	102195192	102196093
222459888	chr11	102195854	102195998	102195875	102195972	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222486702	chr11	102196196	102196364	102196224	102196335	BIRC3	NM_182962	2	10	4	+	102196197	102196296
222486702	chr11	102196196	102196364	102196224	102196335	BIRC3	NM_001165	1	9	3	+	102196197	102196296
222996668	chr11	102201595	102201765	102201627	102201741	BIRC3	NM_182962	2	10	7	+	102201730	102201972
222996668	chr11	102201595	102201765	102201627	102201741	BIRC3	NM_001165	1	9	6	+	102201730	102201972
222719457	chr11	102206714	102206849	102206742	102206825	BIRC3	NM_182962	2	10	8	+	102206697	102206951
222719457	chr11	102206714	102206849	102206742	102206825	BIRC3	NM_001165	1	9	7	+	102206697	102206951
224046808	chr11	102207587	102207714	102207611	102207686	BIRC3	NM_182962	2	10	10	+	102207640	102210135
224046808	chr11	102207587	102207714	102207611	102207686	BIRC3	NM_001165	1	9	9	+	102207640	102210135
295145414	chr11	102220619	102220785	102220647	102220763	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294247179	chr11	102221033	102221202	102221056	102221177	BIRC2	NM_001166	1	9	2	+	102219329	102221480
295164599	chr11	102221415	102221587	102221438	102221563	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294612858	chr11	102239040	102239190	102239067	102239161	BIRC2	NM_001166	1	9	6	+	102239037	102239279
294116556	chr11	102248372	102248531	102248397	102248504	BIRC2	NM_001166	1	9	7	+	102248227	102248481
293821663	chr11	102248836	102248988	102248860	102248960	BIRC2	NM_001166	1	9	9	+	102248721	102249401
270818401	chr11	106579242	106579391	106579264	106579367	GUCY1A2	NM_000855	1	8	7	-	106579238	106579392
270818401	chr11	106579242	106579391	106579264	106579367	GUCY1A2	NM_001256424	2	9	8	-	106579238	106579392
272130408	chr11	106680826	106680993	106680851	106680967	GUCY1A2	NM_000855	1	8	5	-	106680719	106681204
272130408	chr11	106680826	106680993	106680851	106680967	GUCY1A2	NM_001256424	2	9	5	-	106680719	106681204
272631873	chr11	106810045	106810212	106810068	106810186	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
272631873	chr11	106810045	106810212	106810068	106810186	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
272698141	chr11	106810528	106810700	106810550	106810677	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
272698141	chr11	106810528	106810700	106810550	106810677	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
271406310	chr11	106849356	106849523	106849382	106849500	GUCY1A2	NM_000855	1	8	3	-	106849345	106849466
271406310	chr11	106849356	106849523	106849382	106849500	GUCY1A2	NM_001256424	2	9	3	-	106849345	106849466
270720926	chr11	106888659	106888786	106888676	106888764	GUCY1A2	NM_000855	1	8	1	-	106888479	106889171
270720926	chr11	106888659	106888786	106888676	106888764	GUCY1A2	NM_001256424	2	9	1	-	106888479	106889171
225127853	chr11	108099813	108099983	108099836	108099959	ATM	NM_000051	1	63	4	+	108099905	108100050
222453945	chr11	108106478	108106644	108106506	108106618	ATM	NM_000051	1	63	5	+	108106397	108106561

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222538939	chr11	108114824	108114980	108114845	108114952	ATM	NM_000051	1	63	6	+	108114680	108114845
224033491	chr11	108117681	108117811	108117708	108117783	ATM	NM_000051	1	63	8	+	108117691	108117854
225125930	chr11	108119752	108119926	108119781	108119900	ATM	NM_000051	1	63	9	+	108119660	108119829
223558525	chr11	108121687	108121826	108121715	108121799	ATM	NM_000051	1	63	10	+	108121428	108121799
222801826	chr11	108123493	108123639	108123521	108123616	ATM	NM_000051	1	63	12	+	108123544	108123639
223082092	chr11	108124661	108124832	108124681	108124804	ATM	NM_000051	1	63	13	+	108124541	108124766
224417294	chr11	108128126	108128300	108128155	108128273	ATM	NM_000051	1	63	15	+	108128208	108128333
223753735	chr11	108137977	108138142	108138003	108138117	ATM	NM_000051	1	63	17	+	108137898	108138069
223505437	chr11	108141849	108142016	108141878	108141992	ATM	NM_000051	1	63	20	+	108141978	108142133
329370991	chr11	108143284	108143446	108143310	108143418	ATM	NM_000051	1	63	21	+	108143259	108143334
222421876	chr11	108150136	108150301	108150162	108150276	ATM	NM_000051	1	63	23	+	108150218	108150335
222187255	chr11	108151837	108151982	108151862	108151955	ATM	NM_000051	1	63	24	+	108151722	108151895
223777262	chr11	108158248	108158409	108158277	108158385	ATM	NM_000051	1	63	27	+	108158327	108158442
222737398	chr11	108160340	108160471	108160367	108160443	ATM	NM_000051	1	63	29	+	108160329	108160528
222323044	chr11	108163341	108163480	108163368	108163452	ATM	NM_000051	1	63	30	+	108163346	108163520
223690725	chr11	108170319	108170480	108170347	108170456	ATM	NM_000051	1	63	34	+	108170441	108170612
223709468	chr11	108172428	108172580	108172454	108172555	ATM	NM_000051	1	63	35	+	108172375	108172516
223037706	chr11	108175355	108175508	108175385	108175481	ATM	NM_000051	1	63	37	+	108175402	108175579
222602826	chr11	108180786	108180960	108180815	108180936	ATM	NM_000051	1	63	39	+	108180887	108181042
224716824	chr11	108186448	108186587	108186479	108186560	ATM	NM_000051	1	63	41	+	108186550	108186638
222233370	chr11	108188088	108188214	108188109	108188191	ATM	NM_000051	1	63	43	+	108188100	108188248
223107583	chr11	108192045	108192194	108192065	108192167	ATM	NM_000051	1	63	45	+	108192028	108192147
223557787	chr11	108196763	108196914	108196791	108196890	ATM	NM_000051	1	63	47	+	108196785	108196952
222347382	chr11	108199723	108199847	108199751	108199822	ATM	NM_000051	1	63	49	+	108199748	108199965
222177921	chr11	108200960	108201123	108200985	108201099	ATM	NM_000051	1	63	50	+	108200941	108201148
222589963	chr11	108202617	108202753	108202641	108202725	ATM	NM_000051	1	63	52	+	108202606	108202764
222309251	chr11	108203491	108203615	108203518	108203591	ATM	NM_000051	1	63	53	+	108203489	108203627
222974856	chr11	108205705	108205878	108205733	108205853	ATM	NM_000051	1	63	55	+	108205696	108205836
224111881	chr11	108213999	108214165	108214026	108214142	ATM	NM_000051	1	63	57	+	108213949	108214098
223619994	chr11	108217997	108218159	108218024	108218132	ATM	NM_000051	1	63	59	+	108218006	108218092
223012860	chr11	108235706	108235877	108235734	108235850	ATM	NM_000051	1	63	62	+	108235809	108235945
238676901	chr11	111957569	111957721	111957589	111957701	SDHD	NM_003002	1	4	1	+	111957571	111957683
242193785	chr11	111959638	111959798	111959659	111959772	SDHD	NM_003002	1	4	3	+	111959591	111959735
234191801	chr11	118339408	118339582	118339431	118339560	MLL	NM_005933	2	36	2	+	118339490	118339559
234191801	chr11	118339408	118339582	118339431	118339560	MLL	NM_001197104	1	36	2	+	118339490	118339559
234020203	chr11	118342551	118342719	118342579	118342695	MLL	NM_005933	2	36	3	+	118342377	118345030
234020203	chr11	118342551	118342719	118342579	118342695	MLL	NM_001197104	1	36	3	+	118342377	118345030
231617896	chr11	118342969	118343113	118342992	118343087	MLL	NM_005933	2	36	3	+	118342377	118345030
231617896	chr11	118342969	118343113	118342992	118343087	MLL	NM_001197104	1	36	3	+	118342377	118345030
231662993	chr11	118343382	118343555	118343402	118343536	MLL	NM_005933	2	36	3	+	118342377	118345030
231662993	chr11	118343382	118343555	118343402	118343536	MLL	NM_001197104	1	36	3	+	118342377	118345030

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231748789	chr11	118343818	118343948	118343840	118343922	MLL	NM_005933	2	36	3	+	118342377	118345030
231748789	chr11	118343818	118343948	118343840	118343922	MLL	NM_001197104	1	36	3	+	118342377	118345030
234044328	chr11	118344200	118344370	118344226	118344344	MLL	NM_005933	2	36	3	+	118342377	118345030
234044328	chr11	118344200	118344370	118344226	118344344	MLL	NM_001197104	1	36	3	+	118342377	118345030
234036728	chr11	118344585	118344733	118344608	118344705	MLL	NM_005933	2	36	3	+	118342377	118345030
234036728	chr11	118344585	118344733	118344608	118344705	MLL	NM_001197104	1	36	3	+	118342377	118345030
232227053	chr11	118347486	118347638	118347513	118347617	MLL	NM_005933	2	36	4	+	118347520	118347697
232227053	chr11	118347486	118347638	118347513	118347617	MLL	NM_001197104	1	36	4	+	118347520	118347697
232741236	chr11	118350806	118350978	118350832	118350951	MLL	NM_005933	2	36	6	+	118350889	118350953
232741236	chr11	118350806	118350978	118350832	118350951	MLL	NM_001197104	1	36	6	+	118350889	118350953
233131985	chr11	118352599	118352765	118352625	118352738	MLL	NM_005933	2	36	7	+	118352430	118352807
233131985	chr11	118352599	118352765	118352625	118352738	MLL	NM_001197104	1	36	7	+	118352430	118352807
233954563	chr11	118354935	118355108	118354958	118355080	MLL	NM_005933	2	36	9	+	118354898	118355029
233954563	chr11	118354935	118355108	118354958	118355080	MLL	NM_001197104	1	36	9	+	118354898	118355029
233393848	chr11	118360394	118360554	118360421	118360531	MLL	NM_005933	2	36	12	+	118360507	118360602
233393848	chr11	118360394	118360554	118360421	118360531	MLL	NM_001197104	1	36	12	+	118360507	118360602
233048323	chr11	118361841	118361979	118361861	118361950	MLL	NM_001197104	1	36	14	+	118361911	118362033
233048323	chr11	118361841	118361979	118361861	118361950	MLL	NM_005933	2	36	14	+	118361911	118362024
234506989	chr11	118363712	118363880	118363739	118363856	MLL	NM_005933	2	36	16	+	118363772	118363945
234506989	chr11	118363712	118363880	118363739	118363856	MLL	NM_001197104	1	36	16	+	118363772	118363945
232465884	chr11	118365288	118365449	118365311	118365423	MLL	NM_005933	2	36	18	+	118365409	118365482
232465884	chr11	118365288	118365449	118365311	118365423	MLL	NM_001197104	1	36	18	+	118365409	118365482
233273746	chr11	118366497	118366631	118366518	118366608	MLL	NM_005933	2	36	19	+	118366415	118366608
233273746	chr11	118366497	118366631	118366518	118366608	MLL	NM_001197104	1	36	19	+	118366415	118366608
233399223	chr11	118369004	118369174	118369028	118369154	MLL	NM_005933	2	36	22	+	118369085	118369243
233399223	chr11	118369004	118369174	118369028	118369154	MLL	NM_001197104	1	36	22	+	118369085	118369243
232542114	chr11	118370503	118370658	118370531	118370630	MLL	NM_005933	2	36	24	+	118370550	118370628
232542114	chr11	118370503	118370658	118370531	118370630	MLL	NM_001197104	1	36	24	+	118370550	118370628
233068008	chr11	118372364	118372488	118372392	118372462	MLL	NM_005933	2	36	26	+	118372387	118372572
233068008	chr11	118372364	118372488	118372392	118372462	MLL	NM_001197104	1	36	26	+	118372387	118372572
231258378	chr11	118373280	118373431	118373306	118373404	MLL	NM_005933	2	36	27	+	118373113	118377361
231258378	chr11	118373280	118373431	118373306	118373404	MLL	NM_001197104	1	36	27	+	118373113	118377361
233875108	chr11	118373721	118373894	118373743	118373866	MLL	NM_005933	2	36	27	+	118373113	118377361
233875108	chr11	118373721	118373894	118373743	118373866	MLL	NM_001197104	1	36	27	+	118373113	118377361
231311108	chr11	118374163	118374326	118374184	118374304	MLL	NM_005933	2	36	27	+	118373113	118377361
231311108	chr11	118374163	118374326	118374184	118374304	MLL	NM_001197104	1	36	27	+	118373113	118377361
233864390	chr11	118374586	118374726	118374608	118374699	MLL	NM_005933	2	36	27	+	118373113	118377361
233864390	chr11	118374586	118374726	118374608	118374699	MLL	NM_001197104	1	36	27	+	118373113	118377361
233880502	chr11	118374948	118375101	118374975	118375073	MLL	NM_005933	2	36	27	+	118373113	118377361
233880502	chr11	118374948	118375101	118374975	118375073	MLL	NM_001197104	1	36	27	+	118373113	118377361
233888141	chr11	118375361	118375534	118375384	118375510	MLL	NM_005933	2	36	27	+	118373113	118377361

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TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233888141	chr11	118375361	118375534	118375384	118375510	MLL	NM_001197104	1	36	27	+	118373113	118377361
233898710	chr11	118375869	118376043	118375892	118376020	MLL	NM_005933	2	36	27	+	118373113	118377361
233898710	chr11	118375869	118376043	118375892	118376020	MLL	NM_001197104	1	36	27	+	118373113	118377361
233923261	chr11	118376346	118376511	118376370	118376483	MLL	NM_005933	2	36	27	+	118373113	118377361
233923261	chr11	118376346	118376511	118376370	118376483	MLL	NM_001197104	1	36	27	+	118373113	118377361
233908520	chr11	118376727	118376856	118376753	118376835	MLL	NM_005933	2	36	27	+	118373113	118377361
233908520	chr11	118376727	118376856	118376753	118376835	MLL	NM_001197104	1	36	27	+	118373113	118377361
233904598	chr11	118377113	118377287	118377135	118377264	MLL	NM_005933	2	36	27	+	118373113	118377361
233904598	chr11	118377113	118377287	118377135	118377264	MLL	NM_001197104	1	36	27	+	118373113	118377361
230977265	chr11	118380620	118380753	118380646	118380729	MLL	NM_005933	2	36	30	+	118380663	118380833
230977265	chr11	118380620	118380753	118380646	118380729	MLL	NM_001197104	1	36	30	+	118380663	118380833
233114794	chr11	118390402	118390536	118390422	118390512	MLL	NM_005933	2	36	32	+	118390333	118390507
233114794	chr11	118390402	118390536	118390422	118390512	MLL	NM_001197104	1	36	32	+	118390333	118390507
233090072	chr11	118391499	118391672	118391526	118391646	MLL	NM_005933	2	36	34	+	118391517	118391600
233090072	chr11	118391499	118391672	118391526	118391646	MLL	NM_001197104	1	36	34	+	118391517	118391600
232556238	chr11	118392709	118392836	118392733	118392816	MLL	NM_005933	2	36	36	+	118392612	118397539
232556238	chr11	118392709	118392836	118392733	118392816	MLL	NM_001197104	1	36	36	+	118392612	118397539
253778207	chr11	119077209	119077340	119077229	119077323	CBL	NM_005188	1	16	1	+	119076990	119077322
226308315	chr11	119142303	119142475	119142329	119142450	CBL	NM_005188	1	16	3	+	119142445	119142591
225873536	chr11	119144649	119144779	119144673	119144754	CBL	NM_005188	1	16	4	+	119144578	119144734
226129361	chr11	119146725	119146876	119146746	119146850	CBL	NM_005188	1	16	6	+	119146707	119146844
226429415	chr11	119148951	119149097	119148974	119149076	CBL	NM_005188	1	16	8	+	119148876	119149007
253652619	chr11	119155736	119155891	119155757	119155869	CBL	NM_005188	1	16	10	+	119155679	119155810
225907585	chr11	119156153	119156326	119156175	119156298	CBL	NM_005188	1	16	11	+	119155899	119156276
227086677	chr11	119167628	119167802	119167650	119167777	CBL	NM_005188	1	16	13	+	119167628	119167744
226205447	chr11	119169102	119169273	119169122	119169250	CBL	NM_005188	1	16	15	+	119169068	119169250
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NM_001244846	3	12	2	+	125496644	125496728
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NR_045205	6	13	2	+	125496644	125496728
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NM_001114121	1	14	2	+	125496644	125496728
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NM_001114122	2	13	2	+	125496644	125496728
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NM_001274	4	13	2	+	125496644	125496728
253763811	chr11	125496583	125496754	125496604	125496729	CHEK1	NR_045204	5	12	2	+	125496644	125496728
226465840	chr11	125497684	125497827	125497708	125497801	CHEK1	NM_001244846	3	12	3	+	125497502	125497725
226465840	chr11	125497684	125497827	125497708	125497801	CHEK1	NR_045205	6	13	3	+	125497502	125497725
226465840	chr11	125497684	125497827	125497708	125497801	CHEK1	NM_001114121	1	14	3	+	125497502	125497725
226465840	chr11	125497684	125497827	125497708	125497801	CHEK1	NM_001114122	2	13	3	+	125497502	125497725
226465840	chr11	125497684	125497827	125497708	125497801	CHEK1	NM_001274	4	13	3	+	125497502	125497725
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NM_001244846	3	12	5	+	125499286	125499355
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NR_045205	6	13	5	+	125499286	125499355
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NM_001114121	1	14	5	+	125499286	125499355
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NM_001114122	2	13	5	+	125499286	125499355

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NM_001274	4	13	5	+	125499286	125499355
226159954	chr11	125499295	125499461	125499321	125499434	CHEK1	NR_045204	5	12	4	+	125499286	125499355
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NM_001244846	3	12	7	+	125505324	125505428
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NR_045205	6	13	7	+	125505324	125505428
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NM_001114121	1	14	7	+	125505324	125505428
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NM_001114122	2	13	7	+	125505324	125505428
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NM_001274	4	13	7	+	125505324	125505428
226208233	chr11	125505185	125505349	125505211	125505330	CHEK1	NR_045204	5	12	6	+	125505324	125505428
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NM_001244846	3	12	9	+	125513687	125513795
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NR_045205	6	13	9	+	125513687	125513795
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NM_001114121	1	14	9	+	125513687	125513795
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NM_001114122	2	13	9	+	125513687	125513795
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NM_001274	4	13	9	+	125513687	125513795
225331053	chr11	125513641	125513805	125513669	125513777	CHEK1	NR_045204	5	12	8	+	125513687	125513795
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NM_001244846	3	12	11	+	125514407	125514538
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NR_045205	6	13	11	+	125514407	125514538
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NM_001114121	1	14	11	+	125514407	125514538
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NM_001114122	2	13	11	+	125514407	125514538
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NM_001274	4	13	11	+	125514407	125514538
253761334	chr11	125514302	125514462	125514323	125514435	CHEK1	NR_045204	5	12	10	+	125514407	125514538
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NM_001244846	3	12	12	+	125525120	125527042
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NR_045205	6	13	13	+	125525120	125527042
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NM_001114122	2	13	13	+	125525120	125527042
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NM_001274	4	13	13	+	125525120	125527042
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NR_045204	5	12	12	+	125525120	125527042
227076499	chr11	125524982	125525153	125525009	125525129	CHEK1	NM_001114121	1	14	13	+	125525120	125525242
294573284	chr11	128332367	128332520	128332394	128332492	ETS1	NM_005238	3	8	8	-	128328656	128332471
294573284	chr11	128332367	128332520	128332394	128332492	ETS1	NM_001143820	1	10	10	-	128328656	128332471
294573284	chr11	128332367	128332520	128332394	128332492	ETS1	NM_001162422	2	4	4	-	128328656	128332471
294046785	chr11	128350128	128350271	128350149	128350249	ETS1	NM_005238	3	8	6	-	128350086	128350346
294046785	chr11	128350128	128350271	128350149	128350249	ETS1	NM_001143820	1	10	8	-	128350086	128350346
294046785	chr11	128350128	128350271	128350149	128350249	ETS1	NM_001162422	2	4	2	-	128350086	128350346
293796462	chr11	128354874	128355000	128354894	128354975	ETS1	NM_005238	3	8	5	-	128354718	128354966
293796462	chr11	128354874	128355000	128354894	128354975	ETS1	NM_001143820	1	10	7	-	128354718	128354966
293967518	chr11	128360296	128360460	128360317	128360434	ETS1	NM_005238	3	8	2	-	128360352	128360471
293967518	chr11	128360296	128360460	128360317	128360434	ETS1	NM_001143820	1	10	4	-	128360352	128360471
294496317	chr11	128426126	128426299	128426154	128426276	ETS1	NM_001143820	1	10	3	-	128426186	128426330
227982321	chr11	128627934	128628065	128627956	128628044	FLI1	NM_002017	2	9	2	+	128628010	128628221
227982321	chr11	128627934	128628065	128627956	128628044	FLI1	NM_001167681	1	10	3	+	128628010	128628221
229389465	chr11	128638031	128638189	128638052	128638168	FLI1	NM_002017	2	9	3	+	128638013	128638167
229389465	chr11	128638031	128638189	128638052	128638168	FLI1	NM_001167681	1	10	4	+	128638013	128638167

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229806631	chr11	128651831	128651975	128651857	128651954	FLI1	NM_002017	2	9	5	+	128651853	128651918
229806631	chr11	128651831	128651975	128651857	128651954	FLI1	NM_001167681	1	10	6	+	128651853	128651918
229090101	chr11	128680316	128680457	128680338	128680435	FLI1	NM_002017	2	9	9	+	128680354	128683162
229090101	chr11	128680316	128680457	128680338	128680435	FLI1	NM_001167681	1	10	10	+	128680354	128683162
229143130	chr11	128680750	128680911	128680772	128680888	FLI1	NM_002017	2	9	9	+	128680354	128683162
229143130	chr11	128680750	128680911	128680772	128680888	FLI1	NM_001167681	1	10	10	+	128680354	128683162
226084686	chr12	4383331	4383491	4383353	4383469	CCND2	NM_001759	1	5	1	+	4382902	4383401
226669094	chr12	4387870	4388011	4387891	4387990	CCND2	NM_001759	1	5	3	+	4387926	4388085
226799646	chr12	4408954	4409121	4408979	4409101	CCND2	NM_001759	1	5	5	+	4409026	4414522
281125773	chr12	6761320	6761485	6761345	6761463	ING4	NM_001127584	3	8	6	-	6761437	6761584
281125773	chr12	6761320	6761485	6761345	6761463	ING4	NM_001127583	2	8	6	-	6761437	6761584
281125773	chr12	6761320	6761485	6761345	6761463	ING4	NM_016162	6	8	6	-	6761437	6761584
281125773	chr12	6761320	6761485	6761345	6761463	ING4	NM_001127582	1	8	6	-	6761437	6761584
281125773	chr12	6761320	6761485	6761345	6761463	ING4	NM_001127585	4	7	5	-	6761437	6761584
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_016162	6	8	4	-	6762102	6762216
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_001127582	1	8	4	-	6762102	6762216
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_001127586	5	7	4	-	6762102	6762216
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_001127585	4	7	3	-	6762102	6762216
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_001127584	3	8	4	-	6762111	6762216
278251277	chr12	6762095	6762248	6762118	6762223	ING4	NM_001127583	2	8	4	-	6762111	6762216
278296948	chr12	6765888	6766029	6765913	6766002	ING4	NM_001127584	3	8	2	-	6765893	6765964
278296948	chr12	6765888	6766029	6765913	6766002	ING4	NM_001127583	2	8	2	-	6765893	6765964
278296948	chr12	6765888	6766029	6765913	6766002	ING4	NM_016162	6	8	2	-	6765893	6765964
278296948	chr12	6765888	6766029	6765913	6766002	ING4	NM_001127582	1	8	2	-	6765893	6765964
278296948	chr12	6765888	6766029	6765913	6766002	ING4	NM_001127586	5	7	2	-	6765893	6765964
264684273	chr12	6777001	6777129	6777020	6777112	ZNF384	NM_133476	3	10	10	-	6775643	6777281
264684273	chr12	6777001	6777129	6777020	6777112	ZNF384	NM_001135734	2	11	11	-	6775643	6777281
264684273	chr12	6777001	6777129	6777020	6777112	ZNF384	NM_001039920	1	9	9	-	6775643	6777281
238421227	chr12	6779878	6780048	6779899	6780023	ZNF384	NM_133476	3	10	8	-	6779926	6780004
238421227	chr12	6779878	6780048	6779899	6780023	ZNF384	NM_001135734	2	11	9	-	6779926	6780004
238421227	chr12	6779878	6780048	6779899	6780023	ZNF384	NM_001039920	1	9	7	-	6779926	6780004
240062998	chr12	6782318	6782476	6782339	6782453	ZNF384	NM_133476	3	10	7	-	6782382	6782606
240062998	chr12	6782318	6782476	6782339	6782453	ZNF384	NM_001135734	2	11	7	-	6782382	6782606
240062998	chr12	6782318	6782476	6782339	6782453	ZNF384	NM_001039920	1	9	6	-	6782382	6782606
239062394	chr12	6787337	6787496	6787363	6787474	ZNF384	NM_133476	3	10	6	-	6787293	6787626
239062394	chr12	6787337	6787496	6787363	6787474	ZNF384	NM_001135734	2	11	6	-	6787293	6787626
239062394	chr12	6787337	6787496	6787363	6787474	ZNF384	NM_001039920	1	9	5	-	6787293	6787509
240589268	chr12	6788063	6788231	6788089	6788209	ZNF384	NM_133476	3	10	4	-	6788112	6788349
240589268	chr12	6788063	6788231	6788089	6788209	ZNF384	NM_001135734	2	11	4	-	6788112	6788349
240589268	chr12	6788063	6788231	6788089	6788209	ZNF384	NM_001039920	1	9	4	-	6788112	6788349
234764991	chr12	25362740	25362903	25362770	25362877	KRAS	NM_004985	1	5	5	-	25358180	25362845

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234764991	chr12	25362740	25362903	25362770	25362877	KRAS	NM_033360	2	6	6	-	25358180	25362845
233467720	chr12	25378620	25378773	25378648	25378745	KRAS	NM_004985	1	5	4	-	25378548	25378707
233467720	chr12	25378620	25378773	25378648	25378745	KRAS	NM_033360	2	6	4	-	25378548	25378707
231133990	chr12	25398284	25398415	25398305	25398388	KRAS	NM_004985	1	5	2	-	25398208	25398329
231133990	chr12	25398284	25398415	25398305	25398388	KRAS	NM_033360	2	6	2	-	25398208	25398329
282752754	chr12	43750331	43750472	43750352	43750445	ADAMTS20	NM_025003	1	39	38	-	43750287	43750391
283127011	chr12	43769220	43769362	43769245	43769334	ADAMTS20	NM_025003	1	39	36	-	43769182	43769315
282554656	chr12	43770071	43770234	43770099	43770206	ADAMTS20	NM_025003	1	39	34	-	43770039	43770133
281583697	chr12	43771112	43771285	43771139	43771262	ADAMTS20	NM_025003	1	39	32	-	43771168	43771365
282869649	chr12	43777464	43777614	43777489	43777586	ADAMTS20	NM_025003	1	39	31	-	43777361	43777531
283700663	chr12	43792860	43792999	43792887	43792974	ADAMTS20	NM_025003	1	39	29	-	43792869	43793036
282556394	chr12	43819388	43819530	43819414	43819498	ADAMTS20	NM_025003	1	39	28	-	43819317	43819493
281755492	chr12	43822023	43822193	43822051	43822171	ADAMTS20	NM_025003	1	39	26	-	43822044	43822334
282278952	chr12	43822428	43822584	43822452	43822563	ADAMTS20	NM_025003	1	39	25	-	43822438	43822602
281752762	chr12	43823468	43823626	43823496	43823602	ADAMTS20	NM_025003	1	39	24	-	43823420	43823527
282478237	chr12	43825149	43825293	43825173	43825266	ADAMTS20	NM_025003	1	39	22	-	43825135	43825299
284456269	chr12	43826127	43826274	43826152	43826252	ADAMTS20	NM_025003	1	39	21	-	43826107	43826271
282542800	chr12	43826572	43826728	43826596	43826699	ADAMTS20	NM_025003	1	39	20	-	43826404	43826614
282776170	chr12	43833377	43833547	43833399	43833519	ADAMTS20	NM_025003	1	39	18	-	43833425	43833554
282762575	chr12	43833747	43833871	43833775	43833844	ADAMTS20	NM_025003	1	39	17	-	43833700	43833872
283058118	chr12	43840397	43840525	43840424	43840505	ADAMTS20	NM_025003	1	39	15	-	43840398	43840515
282127298	chr12	43846197	43846347	43846220	43846323	ADAMTS20	NM_025003	1	39	13	-	43846317	43846498
283497024	chr12	43847742	43847896	43847763	43847868	ADAMTS20	NM_025003	1	39	12	-	43847710	43847855
283121544	chr12	43860360	43860527	43860389	43860500	ADAMTS20	NM_025003	1	39	9	-	43860455	43860598
328492587	chr12	43884203	43884348	43884236	43884320	ADAMTS20	NM_025003	1	39	7	-	43884198	43884238
283836053	chr12	43895984	43896139	43896009	43896110	ADAMTS20	NM_025003	1	39	4	-	43895955	43896208
283594981	chr12	43944616	43944765	43944637	43944741	ADAMTS20	NM_025003	1	39	2	-	43944712	43945073
282178889	chr12	43945595	43945743	43945612	43945726	ADAMTS20	NM_025003	1	39	1	-	43945634	43945724
274078500	chr12	46124954	46125100	46124982	46125072	ARID2	NM_152641	1	21	3	+	46125000	46125097
273375148	chr12	46211366	46211538	46211394	46211510	ARID2	NM_152641	1	21	5	+	46211453	46211671
272861795	chr12	46215201	46215331	46215230	46215305	ARID2	NM_152641	1	21	6	+	46215203	46215270
273647102	chr12	46230519	46230683	46230546	46230658	ARID2	NM_152641	1	21	8	+	46230524	46230774
273580586	chr12	46231302	46231429	46231330	46231402	ARID2	NM_152641	1	21	10	+	46231281	46231490
272971441	chr12	46233157	46233322	46233177	46233296	ARID2	NM_152641	1	21	11	+	46233112	46233279
274565212	chr12	46242655	46242808	46242682	46242780	ARID2	NM_152641	1	21	13	+	46242619	46242753
273523154	chr12	46243511	46243675	46243536	46243646	ARID2	NM_152641	1	21	14	+	46243363	46243559
274484547	chr12	46244119	46244250	46244145	46244226	ARID2	NM_152641	1	21	15	+	46243819	46246679
274491275	chr12	46244539	46244710	46244563	46244690	ARID2	NM_152641	1	21	15	+	46243819	46246679
274473710	chr12	46245003	46245135	46245026	46245113	ARID2	NM_152641	1	21	15	+	46243819	46246679
273556611	chr12	46245459	46245611	46245481	46245587	ARID2	NM_152641	1	21	15	+	46243819	46246679
273578432	chr12	46245922	46246072	46245950	46246044	ARID2	NM_152641	1	21	15	+	46243819	46246679

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274432685	chr12	46246267	46246428	46246293	46246403	ARID2	NM_152641	1	21	15	+	46243819	46246679
272831478	chr12	46254544	46254669	46254568	46254645	ARID2	NM_152641	1	21	16	+	46254584	46254732
273971325	chr12	46285563	46285707	46285584	46285680	ARID2	NM_152641	1	21	17	+	46285563	46285701
273679425	chr12	46287122	46287267	46287143	46287243	ARID2	NM_152641	1	21	19	+	46287203	46287326
273977618	chr12	46298747	46298917	46298773	46298891	ARID2	NM_152641	1	21	21	+	46298717	46301819
273864922	chr12	49416290	49416460	49416311	49416434	MLL2	NM_003482	1	54	51	-	49416373	49416658
273234980	chr12	49418350	49418523	49418372	49418498	MLL2	NM_003482	1	54	50	-	49418361	49418491
273627933	chr12	49420037	49420197	49420060	49420179	MLL2	NM_003482	1	54	48	-	49419965	49421105
274604614	chr12	49420498	49420651	49420519	49420628	MLL2	NM_003482	1	54	48	-	49419965	49421105
273670519	chr12	49420920	49421082	49420938	49421059	MLL2	NM_003482	1	54	48	-	49419965	49421105
274407115	chr12	49421843	49421968	49421865	49421942	MLL2	NM_003482	1	54	46	-	49421792	49421924
273162458	chr12	49422913	49423059	49422934	49423039	MLL2	NM_003482	1	54	44	-	49422844	49423019
273417522	chr12	49424334	49424508	49424359	49424486	MLL2	NM_003482	1	54	41	-	49424384	49424551
274231820	chr12	49424925	49425097	49424948	49425077	MLL2	NM_003482	1	54	39	-	49424958	49427747
274252586	chr12	49425315	49425481	49425335	49425463	MLL2	NM_003482	1	54	39	-	49424958	49427747
274235326	chr12	49425773	49425907	49425791	49425889	MLL2	NM_003482	1	54	39	-	49424958	49427747
273259318	chr12	49426157	49426298	49426178	49426276	MLL2	NM_003482	1	54	39	-	49424958	49427747
273248173	chr12	49426782	49426949	49426804	49426929	MLL2	NM_003482	1	54	39	-	49424958	49427747
273257548	chr12	49427124	49427250	49427142	49427229	MLL2	NM_003482	1	54	39	-	49424958	49427747
273199204	chr12	49427486	49427651	49427506	49427633	MLL2	NM_003482	1	54	39	-	49424958	49427747
273561533	chr12	49427996	49428162	49428017	49428140	MLL2	NM_003482	1	54	38	-	49427850	49428082
274267917	chr12	49430869	49431015	49430892	49430993	MLL2	NM_003482	1	54	34	-	49430908	49432772
273262849	chr12	49431353	49431523	49431376	49431502	MLL2	NM_003482	1	54	34	-	49430908	49432772
273279233	chr12	49431761	49431932	49431779	49431912	MLL2	NM_003482	1	54	34	-	49430908	49432772
273357097	chr12	49432260	49432434	49432279	49432411	MLL2	NM_003482	1	54	34	-	49430908	49432772
274301341	chr12	49432724	49432856	49432745	49432832	MLL2	NM_003482	1	54	34	-	49430908	49432772
273588213	chr12	49433213	49433378	49433234	49433358	MLL2	NM_003482	1	54	32	-	49433218	49433400
274203322	chr12	49433711	49433841	49433728	49433822	MLL2	NM_003482	1	54	31	-	49433507	49435318
273173188	chr12	49434086	49434252	49434106	49434231	MLL2	NM_003482	1	54	31	-	49433507	49435318
273149596	chr12	49434463	49434607	49434484	49434587	MLL2	NM_003482	1	54	31	-	49433507	49435318
273155130	chr12	49434833	49434979	49434851	49434962	MLL2	NM_003482	1	54	31	-	49433507	49435318
274188775	chr12	49435232	49435404	49435252	49435384	MLL2	NM_003482	1	54	31	-	49433507	49435318
273363644	chr12	49435968	49436102	49435988	49436082	MLL2	NM_003482	1	54	28	-	49435872	49436113
273088370	chr12	49436575	49436707	49436596	49436685	MLL2	NM_003482	1	54	26	-	49436524	49436661
273844133	chr12	49437358	49437528	49437382	49437506	MLL2	NM_003482	1	54	23	-	49437418	49437565
273551757	chr12	49437957	49438110	49437974	49438088	MLL2	NM_003482	1	54	21	-	49437983	49438087
274279238	chr12	49438566	49438724	49438587	49438703	MLL2	NM_003482	1	54	19	-	49438527	49438748
273184333	chr12	49439951	49440106	49439973	49440083	MLL2	NM_003482	1	54	16	-	49440043	49440207
272909360	chr12	49441709	49441883	49441730	49441859	MLL2	NM_003482	1	54	14	-	49441748	49441852
273738559	chr12	49443540	49443664	49443560	49443644	MLL2	NM_003482	1	54	11	-	49443465	49444573
273723726	chr12	49443958	49444101	49443976	49444082	MLL2	NM_003482	1	54	11	-	49443465	49444573

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273724891	chr12	49444393	49444561	49444414	49444539	MLL2	NM_003482	1	54	11	-	49443465	49444573
273084092	chr12	49444833	49444990	49444851	49444970	MLL2	NM_003482	1	54	10	-	49444669	49446207
273132694	chr12	49445171	49445336	49445190	49445318	MLL2	NM_003482	1	54	10	-	49444669	49446207
273092150	chr12	49445640	49445796	49445664	49445776	MLL2	NM_003482	1	54	10	-	49444669	49446207
273104619	chr12	49445920	49446051	49445946	49446033	MLL2	NM_003482	1	54	10	-	49444669	49446207
274423175	chr12	49446425	49446560	49446446	49446536	MLL2	NM_003482	1	54	9	-	49446347	49446492
273558187	chr12	49447210	49447384	49447234	49447361	MLL2	NM_003482	1	54	6	-	49447259	49447424
273794115	chr12	49448054	49448227	49448075	49448201	MLL2	NM_003482	1	54	4	-	49448090	49448199
272932976	chr12	49448596	49448750	49448618	49448729	MLL2	NM_003482	1	54	2	-	49448683	49448809
222382863	chr12	51173922	51174050	51173950	51174028	ATF1	NM_005171	1	7	2	+	51173923	51174021
224786698	chr12	51207842	51208016	51207865	51207989	ATF1	NM_005171	1	7	5	+	51207793	51207975
223613698	chr12	51213332	51213506	51213358	51213477	ATF1	NM_005171	1	7	7	+	51213418	51214943
321682712	chr12	54576039	54576208	54576056	54576184	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321682712	chr12	54576039	54576208	54576056	54576184	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321682712	chr12	54576039	54576208	54576056	54576184	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_014311	6	4	3	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NR_045039	7	5	3	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_001243791	5	4	2	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_001243790	4	5	3	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_001243789	3	6	4	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_001243788	2	3	2	-	54577440	54577743
321760113	chr12	54577506	54577655	54577528	54577635	SMUG1	NM_001243787	1	4	3	-	54577440	54577743
272524148	chr12	56477569	56477730	56477590	56477705	ERBB3	NM_001005915	1	3	2	+	56477535	56477686
272524148	chr12	56477569	56477730	56477590	56477705	ERBB3	NM_001982	2	28	2	+	56477535	56477686
271200159	chr12	56479008	56479170	56479030	56479149	ERBB3	NM_001005915	1	3	3	+	56478779	56479401
270091733	chr12	56481717	56481889	56481740	56481866	ERBB3	NM_001982	2	28	7	+	56481805	56481946
269653501	chr12	56486493	56486654	56486522	56486630	ERBB3	NM_001982	2	28	10	+	56486531	56486604
270846919	chr12	56487480	56487654	56487505	56487631	ERBB3	NM_001982	2	28	13	+	56487548	56487680
272033016	chr12	56488269	56488412	56488292	56488389	ERBB3	NM_001982	2	28	15	+	56488186	56488340
270781461	chr12	56490257	56490430	56490281	56490406	ERBB3	NM_001982	2	28	18	+	56490287	56490406
271083103	chr12	56491503	56491665	56491528	56491644	ERBB3	NM_001982	2	28	21	+	56491569	56491724
271339603	chr12	56492582	56492712	56492603	56492692	ERBB3	NM_001982	2	28	23	+	56492543	56492689
271588830	chr12	56493879	56494052	56493903	56494029	ERBB3	NM_001982	2	28	26	+	56493958	56494029
269732277	chr12	56495255	56495383	56495278	56495359	ERBB3	NM_001982	2	28	28	+	56495313	56497291
269783789	chr12	56495658	56495803	56495681	56495777	ERBB3	NM_001982	2	28	28	+	56495313	56497291
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_001195055	3	4	4	-	57910371	57910963
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_001195054	2	4	4	-	57910371	57910963
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_001195053	1	4	4	-	57910371	57910963
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_001195057	5	4	4	-	57910371	57910963
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_001195056	4	3	3	-	57910371	57910963
231122767	chr12	57910710	57910870	57910738	57910849	DDIT3	NM_004083	6	4	4	-	57910371	57910963

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_001195053	1	4	3	-	57911052	57911378
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_001195056	4	3	2	-	57911052	57911536
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_001195057	5	4	3	-	57911052	57911207
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_001195054	2	4	3	-	57911052	57911325
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_001195055	3	4	3	-	57911052	57911302
228195374	chr12	57911151	57911284	57911172	57911259	DDIT3	NM_004083	6	4	3	-	57911052	57911221
225991712	chr12	58143175	58143315	58143196	58143287	CDK4	NM_000075	1	8	6	-	58143237	58143287
253738432	chr12	58144894	58145064	58144916	58145041	CDK4	NM_000075	1	8	3	-	58144990	58145125
226610226	chr12	58145432	58145582	58145454	58145560	CDK4	NM_000075	1	8	2	-	58145283	58145519
230908059	chr12	69207261	69207425	69207285	69207396	MDM2	NM_002392	1	11	3	+	69207334	69207408
231179114	chr12	69218041	69218211	69218068	69218186	MDM2	NM_002392	1	11	6	+	69218143	69218210
234463139	chr12	69222561	69222723	69222589	69222699	MDM2	NM_002392	1	11	8	+	69222551	69222711
233429649	chr12	69230480	69230626	69230508	69230594	MDM2	NM_002392	1	11	10	+	69230452	69230529
234792805	chr12	69233337	69233487	69233366	69233464	MDM2	NM_002392	1	11	11	+	69233054	69239212
236452546	chr12	112884078	112884238	112884104	112884211	PTPN11	NM_002834	1	16	2	+	112884080	112884202
235149460	chr12	112891058	112891228	112891086	112891204	PTPN11	NM_002834	1	16	4	+	112890999	112891191
237504870	chr12	112910667	112910792	112910692	112910767	PTPN11	NM_002834	1	16	7	+	112910748	112910844
235535964	chr12	112915727	112915883	112915750	112915856	PTPN11	NM_002834	1	16	9	+	112915661	112915819
237942008	chr12	112924375	112924525	112924395	112924501	PTPN11	NM_002834	1	16	11	+	112924279	112924433
237762210	chr12	112939919	112940093	112939941	112940066	PTPN11	NM_002834	1	16	14	+	112939948	112940060
227192043	chr12	121416676	121416817	121416696	121416797	HNF1A	NM_000545	1	10	1	+	121416549	121416897
227538470	chr12	121426710	121426854	121426730	121426832	HNF1A	NM_000545	1	10	2	+	121426636	121426835
227422404	chr12	121431477	121431602	121431496	121431578	HNF1A	NM_000545	1	10	3	+	121431323	121431509
227371495	chr12	121433976	121434150	121433999	121434127	HNF1A	NM_000545	1	10	5	+	121434065	121434216
227482950	chr12	121435249	121435411	121435268	121435392	HNF1A	NM_000545	1	10	7	+	121435277	121435468
227542030	chr12	121437301	121437448	121437320	121437431	HNF1A	NM_000545	1	10	9	+	121437286	121437430
280166064	chr12	123213901	123214056	123213925	123214029	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280136303	chr12	123214293	123214461	123214320	123214437	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280130525	chr12	123214712	123214886	123214737	123214867	HCAR1	NM_032554	1	1	1	-	123212153	123215129
288124928	chr12	132445049	132445223	132445075	132445206	EP400	NM_015409	1	53	2	+	132445130	132446499
288123915	chr12	132446237	132446401	132446255	132446373	EP400	NM_015409	1	53	2	+	132445130	132446499
287961753	chr12	132466040	132466207	132466060	132466187	EP400	NM_015409	1	53	4	+	132466034	132466141
287516435	chr12	132466916	132467084	132466934	132467063	EP400	NM_015409	1	53	5	+	132466638	132467023
287585042	chr12	132471303	132471433	132471324	132471405	EP400	NM_015409	1	53	6	+	132471059	132471352
288808126	chr12	132474540	132474699	132474562	132474676	EP400	NM_015409	1	53	8	+	132474509	132474649
288588300	chr12	132479367	132479531	132479388	132479503	EP400	NM_015409	1	53	12	+	132479412	132479501
287801609	chr12	132490699	132490869	132490722	132490848	EP400	NM_015409	1	53	14	+	132490657	132490847
328497846	chr12	132496119	132496276	132496141	132496248	EP400	NM_015409	1	53	16	+	132496043	132496179
288328104	chr12	132498039	132498210	132498061	132498186	EP400	NM_015409	1	53	18	+	132498035	132498209
288493129	chr12	132501964	132502132	132501986	132502111	EP400	NM_015409	1	53	20	+	132502080	132502266
287277983	chr12	132502837	132503008	132502858	132502985	EP400	NM_015409	1	53	21	+	132502755	132502921

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288760522	chr12	132505691	132505839	132505708	132505822	EP400	NM_015409	1	53	23	+	132505624	132505866
284866094	chr12	132508352	132508521	132508374	132508499	EP400	NM_015409	1	53	24	+	132508322	132508486
288227869	chr12	132512493	132512620	132512514	132512592	EP400	NM_015409	1	53	27	+	132512562	132512833
287410691	chr12	132514212	132514385	132514234	132514366	EP400	NM_015409	1	53	28	+	132514246	132514448
288628510	chr12	132516444	132516611	132516472	132516589	EP400	NM_015409	1	53	30	+	132516498	132516694
286860432	chr12	132522502	132522672	132522524	132522644	EP400	NM_015409	1	53	32	+	132522498	132522641
288193957	chr12	132528103	132528270	132528134	132528242	EP400	NM_015409	1	53	34	+	132528190	132528273
288395643	chr12	132529296	132529432	132529318	132529411	EP400	NM_015409	1	53	37	+	132529345	132529498
289036643	chr12	132530046	132530220	132530067	132530198	EP400	NM_015409	1	53	38	+	132529864	132530105
287080425	chr12	132534864	132535034	132534887	132535006	EP400	NM_015409	1	53	40	+	132534868	132535004
328493086	chr12	132537779	132537920	132537796	132537903	EP400	NM_015409	1	53	43	+	132537888	132538142
288151934	chr12	132546627	132546788	132546650	132546768	EP400	NM_015409	1	53	46	+	132546655	132546868
286325784	chr12	132547155	132547283	132547174	132547264	EP400	NM_015409	1	53	47	+	132547011	132547246
286526587	chr12	132551279	132551451	132551304	132551432	EP400	NM_015409	1	53	49	+	132551319	132551514
285572889	chr12	132554004	132554131	132554025	132554106	EP400	NM_015409	1	53	51	+	132554040	132554186
286158915	chr12	132562029	132562196	132562050	132562175	EP400	NM_015409	1	53	53	+	132561946	132565011
271159078	chr13	26927970	26928097	26927995	26928069	CDK8	NM_001260	1	13	4	+	26927877	26928017
272640997	chr13	26967418	26967565	26967444	26967537	CDK8	NM_001260	1	13	7	+	26967504	26967647
271180151	chr13	26971297	26971471	26971326	26971446	CDK8	NM_001260	1	13	9	+	26971290	26971362
270901352	chr13	26975685	26975809	26975706	26975781	CDK8	NM_001260	1	13	12	+	26975603	26975761
228493439	chr13	28578250	28578387	28578270	28578359	FLT3	NM_004119	1	24	24	-	28577411	28578311
228118059	chr13	28589707	28589864	28589726	28589839	FLT3	NM_004119	1	24	21	-	28589727	28589838
227351007	chr13	28597478	28597644	28597503	28597619	FLT3	NM_004119	1	24	19	-	28597487	28597614
230144073	chr13	28602242	28602407	28602267	28602383	FLT3	NM_004119	1	24	16	-	28602315	28602425
227220326	chr13	28608293	28608467	28608315	28608441	FLT3	NM_004119	1	24	14	-	28608219	28608351
227220326	chr13	28608293	28608467	28608315	28608441	FLT3	NM_004119	1	24	13	-	28608438	28608544
228532997	chr13	28609695	28609854	28609718	28609827	FLT3	NM_004119	1	24	12	-	28609632	28609810
229765066	chr13	28611331	28611469	28611357	28611441	FLT3	NM_004119	1	24	10	-	28611322	28611425
227869979	chr13	28623651	28623810	28623678	28623787	FLT3	NM_004119	1	24	7	-	28623772	28623911
229265400	chr13	28626654	28626822	28626678	28626795	FLT3	NM_004119	1	24	5	-	28626682	28626811
228774349	chr13	28635987	28636157	28636015	28636136	FLT3	NM_004119	1	24	3	-	28636004	28636206
228850403	chr13	28877188	28877341	28877211	28877320	FLT1	NM_002019	4	30	30	-	28874483	28877505
228070591	chr13	28880766	28880936	28880786	28880910	FLT1	NM_002019	4	30	29	-	28880815	28880909
227794227	chr13	28886081	28886255	28886105	28886235	FLT1	NM_002019	4	30	26	-	28886130	28886235
228733500	chr13	28893560	28893714	28893584	28893691	FLT1	NM_002019	4	30	24	-	28893560	28893671
227236675	chr13	28896376	28896522	28896401	28896497	FLT1	NM_002019	4	30	22	-	28896399	28896496
228410885	chr13	28901628	28901770	28901655	28901749	FLT1	NM_002019	4	30	20	-	28901599	28901687
227563986	chr13	28919511	28919680	28919534	28919654	FLT1	NM_002019	4	30	16	-	28919582	28919688
229294358	chr13	28958945	28959119	28958965	28959095	FLT1	NM_002019	4	30	14	-	28959022	28959168
229294358	chr13	28958945	28959119	28958965	28959095	FLT1	NM_001160030	2	15	14	-	28959022	28959168
227293926	chr13	28963971	28964142	28963995	28964115	FLT1	NM_001159920	1	13	13	-	28959688	28964241

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227293926	chr13	28963971	28964142	28963995	28964115	FLT1	NM_002019	4	30	13	-	28963933	28964241
227293926	chr13	28963971	28964142	28963995	28964115	FLT1	NM_001160030	2	15	13	-	28963933	28964241
229356259	chr13	28973143	28973278	28973169	28973256	FLT1	NM_001160031	3	12	12	-	28973181	28973255
228587413	chr13	29001323	29001478	29001344	29001455	FLT1	NM_002019	4	30	10	-	29001296	29001455
228587413	chr13	29001323	29001478	29001344	29001455	FLT1	NM_001159920	1	13	10	-	29001296	29001455
228587413	chr13	29001323	29001478	29001344	29001455	FLT1	NM_001160031	3	12	10	-	29001296	29001455
228587413	chr13	29001323	29001478	29001344	29001455	FLT1	NM_001160030	2	15	10	-	29001296	29001455
229965034	chr13	29004200	29004371	29004222	29004346	FLT1	NM_002019	4	30	8	-	29004187	29004304
229965034	chr13	29004200	29004371	29004222	29004346	FLT1	NM_001159920	1	13	8	-	29004187	29004304
229965034	chr13	29004200	29004371	29004222	29004346	FLT1	NM_001160031	3	12	8	-	29004187	29004304
229965034	chr13	29004200	29004371	29004222	29004346	FLT1	NM_001160030	2	15	8	-	29004187	29004304
227351614	chr13	29007990	29008163	29008012	29008135	FLT1	NM_002019	4	30	6	-	29007956	29008092
227351614	chr13	29007990	29008163	29008012	29008135	FLT1	NM_001159920	1	13	6	-	29007956	29008092
227351614	chr13	29007990	29008163	29008012	29008135	FLT1	NM_001160031	3	12	6	-	29007956	29008092
227351614	chr13	29007990	29008163	29008012	29008135	FLT1	NM_001160030	2	15	6	-	29007956	29008092
227250651	chr13	29012400	29012544	29012420	29012519	FLT1	NM_002019	4	30	4	-	29012358	29012482
227250651	chr13	29012400	29012544	29012420	29012519	FLT1	NM_001159920	1	13	4	-	29012358	29012482
227250651	chr13	29012400	29012544	29012420	29012519	FLT1	NM_001160031	3	12	4	-	29012358	29012482
227250651	chr13	29012400	29012544	29012420	29012519	FLT1	NM_001160030	2	15	4	-	29012358	29012482
227389291	chr13	29041578	29041730	29041603	29041703	FLT1	NM_002019	4	30	2	-	29041658	29041754
227389291	chr13	29041578	29041730	29041603	29041703	FLT1	NM_001159920	1	13	2	-	29041658	29041754
227389291	chr13	29041578	29041730	29041603	29041703	FLT1	NM_001160031	3	12	2	-	29041658	29041754
227389291	chr13	29041578	29041730	29041603	29041703	FLT1	NM_001160030	2	15	2	-	29041658	29041754
230247996	chr13	41133634	41133767	41133655	41133742	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230307348	chr13	41134019	41134146	41134040	41134126	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230314694	chr13	41134447	41134572	41134471	41134548	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230282076	chr13	41134793	41134956	41134817	41134934	FOXO1	NM_002015	1	3	2	-	41133646	41134997
229111222	chr13	41240017	41240153	41240034	41240134	FOXO1	NM_002015	1	3	1	-	41239720	41240734
264234263	chr13	48881405	48881532	48881431	48881507	RB1	NM_000321	1	27	2	+	48881416	48881542
240121645	chr13	48919301	48919470	48919326	48919442	RB1	NM_000321	1	27	4	+	48919216	48919335
261119226	chr13	48936844	48937018	48936876	48936999	RB1	NM_000321	1	27	8	+	48936951	48937093
241484257	chr13	48951135	48951305	48951153	48951277	RB1	NM_000321	1	27	13	+	48951054	48951170
326867697	chr13	49027076	49027203	49027106	49027179	RB1	NM_000321	1	27	18	+	49027129	49027247
242205246	chr13	49033892	49034022	49033918	49033994	RB1	NM_000321	1	27	20	+	49033824	49033969
241677346	chr13	49039195	49039367	49039218	49039343	RB1	NM_000321	1	27	23	+	49039341	49039504
241677346	chr13	49039195	49039367	49039218	49039343	RB1	NM_000321	1	27	22	+	49039134	49039247
239932898	chr13	49050768	49050910	49050796	49050887	RB1	NM_000321	1	27	25	+	49050837	49050979
262117124	chr13	49054074	49054241	49054096	49054220	RB1	NM_000321	1	27	27	+	49054134	49056026
230571820	chr13	103506041	103506170	103506069	103506147	ERCC5	NM_000123	1	15	3	+	103506107	103506222
231395819	chr13	103510581	103510741	103510611	103510720	ERCC5	NM_000123	1	15	6	+	103510625	103510768
227930926	chr13	103513912	103514038	103513940	103514015	ERCC5	NM_000123	1	15	7	+	103513857	103514064

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227776768	chr13	103514552	103514711	103514573	103514685	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230975468	chr13	103515003	103515148	103515025	103515125	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230602394	chr13	103517946	103518117	103517971	103518096	ERCC5	NM_000123	1	15	9	+	103518017	103518261
232978203	chr13	103518615	103518774	103518638	103518749	ERCC5	NM_000123	1	15	10	+	103518612	103518731
231226755	chr13	103520353	103520523	103520386	103520495	ERCC5	NM_000123	1	15	12	+	103520463	103520607
227784698	chr13	103524588	103524731	103524616	103524709	ERCC5	NM_000123	1	15	13	+	103524548	103524748
231457477	chr13	103527572	103527746	103527598	103527720	ERCC5	NM_000123	1	15	15	+	103527657	103528351
231498739	chr13	103528053	103528225	103528075	103528198	ERCC5	NM_000123	1	15	15	+	103527657	103528351
272380559	chr13	110434381	110434528	110434402	110434510	IRS2	NM_003749	1	2	1	-	110434389	110438914
272379017	chr13	110434840	110434964	110434861	110434945	IRS2	NM_003749	1	2	1	-	110434389	110438914
272380095	chr13	110435425	110435574	110435443	110435557	IRS2	NM_003749	1	2	1	-	110434389	110438914
272382748	chr13	110435871	110436002	110435888	110435983	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383486	chr13	110436206	110436349	110436223	110436330	IRS2	NM_003749	1	2	1	-	110434389	110438914
272386578	chr13	110436593	110436750	110436611	110436733	IRS2	NM_003749	1	2	1	-	110434389	110438914
270670428	chr13	110437046	110437200	110437063	110437183	IRS2	NM_003749	1	2	1	-	110434389	110438914
272387519	chr13	110437620	110437753	110437638	110437733	IRS2	NM_003749	1	2	1	-	110434389	110438914
272386942	chr13	110438056	110438183	110438077	110438161	IRS2	NM_003749	1	2	1	-	110434389	110438914
280714748	chr13	113964042	113964204	113964065	113964178	LAMP1	NM_005561	1	9	3	+	113963958	113964177
280870270	chr13	113973943	113974074	113973966	113974052	LAMP1	NM_005561	1	9	5	+	113973784	113973971
278131676	chr13	113975835	113976009	113975859	113975982	LAMP1	NM_005561	1	9	8	+	113975872	113976042
269585490	chr14	23777119	23777248	23777141	23777228	BCL2L2	NM_004050	2	4	3	+	23776969	23777408
269585490	chr14	23777119	23777248	23777141	23777228	BCL2L2	NM_001199839	1	4	3	+	23776969	23777408
272052400	chr14	23778085	23778248	23778105	23778224	BCL2L2	NM_004050	2	4	4	+	23778025	23780968
272052400	chr14	23778085	23778248	23778105	23778224	BCL2L2	NM_001199839	1	4	4	+	23778025	23780968
258656292	chr14	36986938	36987106	36986955	36987089	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
258656292	chr14	36986938	36987106	36986955	36987089	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
237518084	chr14	36988211	36988368	36988228	36988351	NKX2-1	NM_003317	2	2	1	-	36988190	36988903
237518084	chr14	36988211	36988368	36988228	36988351	NKX2-1	NM_001079668	1	3	2	-	36988190	36988575
235772800	chr14	51190143	51190314	51190171	51190292	NIN	NM_020921	2	31	31	-	51186481	51190390
237144528	chr14	51192665	51192839	51192689	51192814	NIN	NM_020921	2	31	30	-	51192671	51192784
237144528	chr14	51192665	51192839	51192689	51192814	NIN	NM_016350	1	29	29	-	51192546	51192784
237144528	chr14	51192665	51192839	51192689	51192814	NIN	NM_182946	4	30	30	-	51192546	51192784
257415226	chr14	51196381	51196529	51196402	51196505	NIN	NM_016350	1	29	28	-	51196241	51196441
257415226	chr14	51196381	51196529	51196402	51196505	NIN	NM_182946	4	30	29	-	51196241	51196441
257415226	chr14	51196381	51196529	51196402	51196505	NIN	NM_182944	3	30	29	-	51196241	51196441
257415226	chr14	51196381	51196529	51196402	51196505	NIN	NM_020921	2	31	29	-	51196241	51196441
236555372	chr14	51204881	51205054	51204908	51205028	NIN	NM_016350	1	29	26	-	51204858	51205004
236555372	chr14	51204881	51205054	51204908	51205028	NIN	NM_182946	4	30	27	-	51204858	51205004
236555372	chr14	51204881	51205054	51204908	51205028	NIN	NM_182944	3	30	27	-	51204858	51205004
236555372	chr14	51204881	51205054	51204908	51205028	NIN	NM_020921	2	31	27	-	51204858	51205004
236808323	chr14	51208396	51208526	51208417	51208498	NIN	NM_016350	1	29	24	-	51208300	51208446

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236808323	chr14	51208396	51208526	51208417	51208498	NIN	NM_182946	4	30	25	-	51208300	51208446
236808323	chr14	51208396	51208526	51208417	51208498	NIN	NM_182944	3	30	25	-	51208300	51208446
236808323	chr14	51208396	51208526	51208417	51208498	NIN	NM_020921	2	31	25	-	51208300	51208446
237077862	chr14	51214581	51214754	51214602	51214728	NIN	NM_016350	1	29	21	-	51214710	51214823
237077862	chr14	51214581	51214754	51214602	51214728	NIN	NM_182946	4	30	22	-	51214710	51214823
237077862	chr14	51214581	51214754	51214602	51214728	NIN	NM_182944	3	30	22	-	51214710	51214823
237077862	chr14	51214581	51214754	51214602	51214728	NIN	NM_020921	2	31	22	-	51214710	51214823
240699467	chr14	51221179	51221344	51221206	51221316	NIN	NM_016350	1	29	19	-	51221281	51221350
240699467	chr14	51221179	51221344	51221206	51221316	NIN	NM_182946	4	30	20	-	51221281	51221350
240699467	chr14	51221179	51221344	51221206	51221316	NIN	NM_182944	3	30	20	-	51221281	51221350
240699467	chr14	51221179	51221344	51221206	51221316	NIN	NM_020921	2	31	20	-	51221281	51221350
236000518	chr14	51223933	51224082	51223956	51224054	NIN	NM_182946	4	30	18	-	51223210	51225348
236000518	chr14	51223933	51224082	51223956	51224054	NIN	NM_182944	3	30	18	-	51223210	51225348
236000518	chr14	51223933	51224082	51223956	51224054	NIN	NM_020921	2	31	18	-	51223210	51225348
240862655	chr14	51224348	51224483	51224373	51224456	NIN	NM_182946	4	30	18	-	51223210	51225348
240862655	chr14	51224348	51224483	51224373	51224456	NIN	NM_182944	3	30	18	-	51223210	51225348
240862655	chr14	51224348	51224483	51224373	51224456	NIN	NM_020921	2	31	18	-	51223210	51225348
236117111	chr14	51224793	51224942	51224816	51224917	NIN	NM_182946	4	30	18	-	51223210	51225348
236117111	chr14	51224793	51224942	51224816	51224917	NIN	NM_182944	3	30	18	-	51223210	51225348
236117111	chr14	51224793	51224942	51224816	51224917	NIN	NM_020921	2	31	18	-	51223210	51225348
240836757	chr14	51225255	51225385	51225280	51225357	NIN	NM_182946	4	30	18	-	51223210	51225348
240836757	chr14	51225255	51225385	51225280	51225357	NIN	NM_182944	3	30	18	-	51223210	51225348
240836757	chr14	51225255	51225385	51225280	51225357	NIN	NM_020921	2	31	18	-	51223210	51225348
235486033	chr14	51226848	51227019	51226873	51226995	NIN	NM_016350	1	29	17	-	51226575	51227077
235486033	chr14	51226848	51227019	51226873	51226995	NIN	NM_182946	4	30	17	-	51226575	51227077
235486033	chr14	51226848	51227019	51226873	51226995	NIN	NM_182944	3	30	17	-	51226575	51227077
235486033	chr14	51226848	51227019	51226873	51226995	NIN	NM_020921	2	31	17	-	51226575	51227077
237314829	chr14	51230580	51230705	51230605	51230680	NIN	NM_016350	1	29	15	-	51230544	51230682
237314829	chr14	51230580	51230705	51230605	51230680	NIN	NM_182946	4	30	15	-	51230544	51230682
237314829	chr14	51230580	51230705	51230605	51230680	NIN	NM_182944	3	30	15	-	51230544	51230682
237314829	chr14	51230580	51230705	51230605	51230680	NIN	NM_020921	2	31	15	-	51230544	51230682
236735027	chr14	51237029	51237195	51237051	51237173	NIN	NM_016350	1	29	12	-	51237106	51237280
236735027	chr14	51237029	51237195	51237051	51237173	NIN	NM_182946	4	30	12	-	51237106	51237280
236735027	chr14	51237029	51237195	51237051	51237173	NIN	NM_182944	3	30	12	-	51237106	51237280
236735027	chr14	51237029	51237195	51237051	51237173	NIN	NM_020921	2	31	12	-	51237106	51237280
236111424	chr14	51237972	51238136	51237993	51238111	NIN	NM_016350	1	29	10	-	51238050	51238186
236111424	chr14	51237972	51238136	51237993	51238111	NIN	NM_182946	4	30	10	-	51238050	51238186
236111424	chr14	51237972	51238136	51237993	51238111	NIN	NM_182944	3	30	10	-	51238050	51238186
236111424	chr14	51237972	51238136	51237993	51238111	NIN	NM_020921	2	31	10	-	51238050	51238186
239218253	chr14	51239544	51239718	51239569	51239691	NIN	NM_016350	1	29	8	-	51239667	51239813
239218253	chr14	51239544	51239718	51239569	51239691	NIN	NM_182946	4	30	8	-	51239667	51239813

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239218253	chr14	51239544	51239718	51239569	51239691	NIN	NM_182944	3	30	8	-	51239667	51239813
239218253	chr14	51239544	51239718	51239569	51239691	NIN	NM_020921	2	31	8	-	51239667	51239813
257703329	chr14	51243740	51243881	51243761	51243857	NIN	NM_016350	1	29	7	-	51243667	51243857
257703329	chr14	51243740	51243881	51243761	51243857	NIN	NM_182946	4	30	7	-	51243667	51243857
257703329	chr14	51243740	51243881	51243761	51243857	NIN	NM_182944	3	30	7	-	51243667	51243857
257703329	chr14	51243740	51243881	51243761	51243857	NIN	NM_020921	2	31	7	-	51243667	51243857
241773827	chr14	51273426	51273589	51273449	51273560	NIN	NM_016350	1	29	4	-	51273455	51273536
241773827	chr14	51273426	51273589	51273449	51273560	NIN	NM_182946	4	30	4	-	51273455	51273536
241773827	chr14	51273426	51273589	51273449	51273560	NIN	NM_182944	3	30	4	-	51273455	51273536
241773827	chr14	51273426	51273589	51273449	51273560	NIN	NM_020921	2	31	4	-	51273455	51273536
278551515	chr14	62164518	62164644	62164539	62164617	HIF1A	NM_001243084	1	15	1	+	62164340	62164672
279377701	chr14	62187216	62187380	62187239	62187353	HIF1A	NM_001530	2	15	2	+	62187100	62187290
279377701	chr14	62187216	62187380	62187239	62187353	HIF1A	NM_181054	3	14	2	+	62187100	62187290
279377701	chr14	62187216	62187380	62187239	62187353	HIF1A	NM_001243084	1	15	2	+	62187097	62187290
280413127	chr14	62188467	62188640	62188494	62188612	HIF1A	NM_001243084	1	15	4	+	62188457	62188541
280413127	chr14	62188467	62188640	62188494	62188612	HIF1A	NM_001530	2	15	4	+	62188457	62188541
280413127	chr14	62188467	62188640	62188494	62188612	HIF1A	NM_181054	3	14	4	+	62188457	62188541
279944514	chr14	62194065	62194228	62194090	62194203	HIF1A	NM_001243084	1	15	6	+	62194171	62194373
279944514	chr14	62194065	62194228	62194090	62194203	HIF1A	NM_001530	2	15	6	+	62194171	62194373
279944514	chr14	62194065	62194228	62194090	62194203	HIF1A	NM_181054	3	14	6	+	62194171	62194373
279575836	chr14	62199142	62199303	62199166	62199275	HIF1A	NM_001243084	1	15	7	+	62199136	62199242
279575836	chr14	62199142	62199303	62199166	62199275	HIF1A	NM_001530	2	15	7	+	62199136	62199242
279575836	chr14	62199142	62199303	62199166	62199275	HIF1A	NM_181054	3	14	7	+	62199136	62199242
279022950	chr14	62203490	62203657	62203517	62203632	HIF1A	NM_001243084	1	15	9	+	62203607	62203827
279022950	chr14	62203490	62203657	62203517	62203632	HIF1A	NM_001530	2	15	9	+	62203607	62203827
279022950	chr14	62203490	62203657	62203517	62203632	HIF1A	NM_181054	3	14	9	+	62203607	62203827
280351319	chr14	62204865	62205011	62204891	62204986	HIF1A	NM_001243084	1	15	10	+	62204805	62205091
280351319	chr14	62204865	62205011	62204891	62204986	HIF1A	NM_001530	2	15	10	+	62204805	62205091
280351319	chr14	62204865	62205011	62204891	62204986	HIF1A	NM_181054	3	14	10	+	62204805	62205091
280786127	chr14	62207291	62207452	62207319	62207428	HIF1A	NM_001243084	1	15	11	+	62207223	62207345
280786127	chr14	62207291	62207452	62207319	62207428	HIF1A	NM_001530	2	15	11	+	62207223	62207345
280786127	chr14	62207291	62207452	62207319	62207428	HIF1A	NM_181054	3	14	11	+	62207223	62207345
278430502	chr14	62207733	62207901	62207758	62207875	HIF1A	NM_001243084	1	15	12	+	62207473	62207906
278430502	chr14	62207733	62207901	62207758	62207875	HIF1A	NM_001530	2	15	12	+	62207473	62207906
278430502	chr14	62207733	62207901	62207758	62207875	HIF1A	NM_181054	3	14	12	+	62207473	62207906
278365715	chr14	62212332	62212462	62212360	62212436	HIF1A	NM_001243084	1	15	14	+	62212409	62212535
278365715	chr14	62212332	62212462	62212360	62212436	HIF1A	NM_001530	2	15	14	+	62212409	62212535
263042228	chr14	81421997	81422160	81422017	81422135	TSHR	NM_001142626	3	9	1	+	81421869	81422194
263042228	chr14	81421997	81422160	81422017	81422135	TSHR	NM_000369	1	10	1	+	81421869	81422194
263042228	chr14	81421997	81422160	81422017	81422135	TSHR	NM_001018036	2	9	1	+	81421869	81422194
262030444	chr14	81534492	81534657	81534513	81534629	TSHR	NM_001142626	3	9	3	+	81534598	81534672

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262030444	chr14	81534492	81534657	81534513	81534629	TSHR	NM_000369	1	10	3	+	81534598	81534672
262030444	chr14	81534492	81534657	81534513	81534629	TSHR	NM_001018036	2	9	3	+	81534598	81534672
239587376	chr14	81558819	81558982	81558841	81558955	TSHR	NM_001142626	3	9	6	+	81558875	81558952
239587376	chr14	81558819	81558982	81558841	81558955	TSHR	NM_000369	1	10	6	+	81558875	81558952
239587376	chr14	81558819	81558982	81558841	81558955	TSHR	NM_001018036	2	9	6	+	81558875	81558952
241141553	chr14	81574916	81575072	81574938	81575051	TSHR	NM_001142626	3	9	9	+	81574893	81575294
241141553	chr14	81574916	81575072	81574938	81575051	TSHR	NM_001018036	2	9	9	+	81574956	81575294
262672324	chr14	81609381	81609548	81609403	81609522	TSHR	NM_000369	1	10	10	+	81609284	81612646
266460279	chr14	81609807	81609979	81609830	81609958	TSHR	NM_000369	1	10	10	+	81609284	81612646
262692944	chr14	81610304	81610454	81610326	81610429	TSHR	NM_000369	1	10	10	+	81609284	81612646
264363696	chr14	92435924	92436091	92435945	92436070	TRIP11	NM_004239	1	21	21	-	92434243	92436237
240726027	chr14	92440970	92441094	92440998	92441068	TRIP11	NM_004239	1	21	19	-	92440971	92441087
241380240	chr14	92454667	92454825	92454695	92454800	TRIP11	NM_004239	1	21	16	-	92454628	92454727
239046000	chr14	92461786	92461932	92461808	92461910	TRIP11	NM_004239	1	21	14	-	92461696	92461859
264835303	chr14	92466312	92466451	92466339	92466423	TRIP11	NM_004239	1	21	12	-	92466312	92466452
266124842	chr14	92469893	92470067	92469919	92470039	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266126580	chr14	92470313	92470454	92470340	92470432	TRIP11	NM_004239	1	21	11	-	92469763	92472792
242755858	chr14	92470712	92470878	92470740	92470849	TRIP11	NM_004239	1	21	11	-	92469763	92472792
262000221	chr14	92471081	92471241	92471109	92471213	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266136322	chr14	92471437	92471561	92471462	92471533	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266158967	chr14	92471763	92471932	92471791	92471905	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266164756	chr14	92472112	92472254	92472134	92472227	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266165505	chr14	92472443	92472587	92472471	92472559	TRIP11	NM_004239	1	21	11	-	92469763	92472792
240284872	chr14	92473910	92474042	92473933	92474014	TRIP11	NM_004239	1	21	10	-	92473984	92474196
242084209	chr14	92477327	92477501	92477355	92477474	TRIP11	NM_004239	1	21	9	-	92477330	92477416
263730624	chr14	92482171	92482327	92482196	92482299	TRIP11	NM_004239	1	21	6	-	92482040	92482205
240242108	chr14	92488007	92488177	92488030	92488151	TRIP11	NM_004239	1	21	4	-	92487900	92488175
240233374	chr14	92499435	92499583	92499465	92499556	TRIP11	NM_004239	1	21	2	-	92499536	92499597
229996143	chr14	95556721	95556878	95556745	95556855	DICER1	NM_177438	3	27	27	-	95552565	95557000
229996143	chr14	95556721	95556878	95556745	95556855	DICER1	NM_001195573	1	25	25	-	95552565	95557000
229996143	chr14	95556721	95556878	95556745	95556855	DICER1	NM_030621	2	28	28	-	95552565	95557000
231482571	chr14	95557366	95557540	95557393	95557514	DICER1	NM_177438	3	27	26	-	95557371	95557446
231482571	chr14	95557366	95557540	95557393	95557514	DICER1	NM_001195573	1	25	24	-	95557371	95557446
231482571	chr14	95557366	95557540	95557393	95557514	DICER1	NM_030621	2	28	27	-	95557371	95557446
229746968	chr14	95560171	95560344	95560199	95560319	DICER1	NM_177438	3	27	24	-	95560225	95560493
229746968	chr14	95560171	95560344	95560199	95560319	DICER1	NM_001195573	1	25	23	-	95560225	95560493
229746968	chr14	95560171	95560344	95560199	95560319	DICER1	NM_030621	2	28	25	-	95560225	95560493
232982509	chr14	95562165	95562336	95562191	95562308	DICER1	NM_177438	3	27	23	-	95562162	95563050
232982509	chr14	95562165	95562336	95562191	95562308	DICER1	NM_001195573	1	25	22	-	95562162	95563050
232982509	chr14	95562165	95562336	95562191	95562308	DICER1	NM_030621	2	28	24	-	95562162	95563050
230658591	chr14	95562603	95562746	95562625	95562724	DICER1	NM_177438	3	27	23	-	95562162	95563050

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230658591	chr14	95562603	95562746	95562625	95562724	DICER1	NM_001195573	1	25	22	-	95562162	95563050
230658591	chr14	95562603	95562746	95562625	95562724	DICER1	NM_030621	2	28	24	-	95562162	95563050
232741936	chr14	95566039	95566183	95566062	95566156	DICER1	NM_177438	3	27	22	-	95566117	95566272
232741936	chr14	95566039	95566183	95566062	95566156	DICER1	NM_001195573	1	25	21	-	95566117	95566272
232741936	chr14	95566039	95566183	95566062	95566156	DICER1	NM_030621	2	28	23	-	95566117	95566272
228144654	chr14	95569741	95569915	95569767	95569893	DICER1	NM_177438	3	27	21	-	95569683	95570463
228144654	chr14	95569741	95569915	95569767	95569893	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228144654	chr14	95569741	95569915	95569767	95569893	DICER1	NM_030621	2	28	22	-	95569683	95570463
228124408	chr14	95570202	95570340	95570229	95570318	DICER1	NM_177438	3	27	21	-	95569683	95570463
228124408	chr14	95570202	95570340	95570229	95570318	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228124408	chr14	95570202	95570340	95570229	95570318	DICER1	NM_030621	2	28	22	-	95569683	95570463
230561874	chr14	95571463	95571609	95571484	95571582	DICER1	NM_177438	3	27	20	-	95571408	95571583
230561874	chr14	95571463	95571609	95571484	95571582	DICER1	NM_001195573	1	25	19	-	95571408	95571583
230561874	chr14	95571463	95571609	95571484	95571582	DICER1	NM_030621	2	28	21	-	95571408	95571583
227802474	chr14	95572421	95572562	95572449	95572536	DICER1	NM_177438	3	27	18	-	95572378	95572560
227802474	chr14	95572421	95572562	95572449	95572536	DICER1	NM_001195573	1	25	17	-	95572378	95572560
227802474	chr14	95572421	95572562	95572449	95572536	DICER1	NM_030621	2	28	19	-	95572378	95572560
228801263	chr14	95574083	95574257	95574111	95574234	DICER1	NM_177438	3	27	16	-	95574217	95574430
228801263	chr14	95574083	95574257	95574111	95574234	DICER1	NM_001195573	1	25	15	-	95574217	95574430
228801263	chr14	95574083	95574257	95574111	95574234	DICER1	NM_030621	2	28	17	-	95574217	95574430
228284244	chr14	95574606	95574742	95574633	95574718	DICER1	NM_177438	3	27	15	-	95574661	95574840
228284244	chr14	95574606	95574742	95574633	95574718	DICER1	NM_001195573	1	25	14	-	95574661	95574840
228284244	chr14	95574606	95574742	95574633	95574718	DICER1	NM_030621	2	28	16	-	95574661	95574840
228097614	chr14	95578392	95578547	95578418	95578522	DICER1	NM_177438	3	27	13	-	95578509	95578584
228097614	chr14	95578392	95578547	95578418	95578522	DICER1	NM_001195573	1	25	12	-	95578509	95578584
228097614	chr14	95578392	95578547	95578418	95578522	DICER1	NM_030621	2	28	14	-	95578509	95578584
230456073	chr14	95581956	95582094	95581977	95582071	DICER1	NM_177438	3	27	11	-	95582004	95582158
230456073	chr14	95581956	95582094	95581977	95582071	DICER1	NM_001195573	1	25	10	-	95582004	95582158
230456073	chr14	95581956	95582094	95581977	95582071	DICER1	NM_030621	2	28	12	-	95582004	95582158
230703626	chr14	95582947	95583071	95582974	95583044	DICER1	NM_177438	3	27	10	-	95582790	95583032
230703626	chr14	95582947	95583071	95582974	95583044	DICER1	NM_001195573	1	25	9	-	95582790	95583032
230703626	chr14	95582947	95583071	95582974	95583044	DICER1	NM_030621	2	28	11	-	95582790	95583032
232508541	chr14	95590613	95590775	95590640	95590748	DICER1	NM_177438	3	27	8	-	95590533	95591005
232508541	chr14	95590613	95590775	95590640	95590748	DICER1	NM_001195573	1	25	7	-	95590533	95591005
232508541	chr14	95590613	95590775	95590640	95590748	DICER1	NM_030621	2	28	9	-	95590533	95591005
231603895	chr14	95592986	95593122	95593012	95593094	DICER1	NM_177438	3	27	7	-	95592917	95593085
231603895	chr14	95592986	95593122	95593012	95593094	DICER1	NM_001195573	1	25	6	-	95592917	95593085
231603895	chr14	95592986	95593122	95593012	95593094	DICER1	NM_030621	2	28	8	-	95592917	95593085
232997278	chr14	95596414	95596573	95596435	95596545	DICER1	NM_177438	3	27	5	-	95596395	95596529
232997278	chr14	95596414	95596573	95596435	95596545	DICER1	NM_001195573	1	25	4	-	95596395	95596529
232997278	chr14	95596414	95596573	95596435	95596545	DICER1	NM_030621	2	28	6	-	95596395	95596529

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230027566	chr14	95598889	95599027	95598911	95599003	DICER1	NM_177438	3	27	3	-	95598852	95599014
230027566	chr14	95598889	95599027	95598911	95599003	DICER1	NM_001195573	1	25	2	-	95598852	95599014
230027566	chr14	95598889	95599027	95598911	95599003	DICER1	NM_030621	2	28	4	-	95598852	95599014
242342378	chr14	96178023	96178173	96178048	96178148	TCL1A	NM_001098725	1	4	3	-	96178091	96178139
242342378	chr14	96178023	96178173	96178048	96178148	TCL1A	NM_021966	2	4	3	-	96178086	96178139
238523658	chr14	96180274	96180448	96180297	96180427	TCL1A	NM_021966	2	4	1	-	96180284	96180533
238523658	chr14	96180274	96180448	96180297	96180427	TCL1A	NM_001098725	1	4	1	-	96180284	96180533
225215312	chr14	99640757	99640929	99640776	99640912	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225215312	chr14	99640757	99640929	99640776	99640912	BCL11B	NM_022898	1	3	3	-	99635625	99642532
223929301	chr14	99641487	99641638	99641505	99641621	BCL11B	NM_138576	2	4	4	-	99635625	99642532
223929301	chr14	99641487	99641638	99641505	99641621	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225214534	chr14	99641994	99642145	99642012	99642127	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225214534	chr14	99641994	99642145	99642012	99642127	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225214480	chr14	99642315	99642486	99642336	99642467	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225214480	chr14	99642315	99642486	99642336	99642467	BCL11B	NM_022898	1	3	3	-	99635625	99642532
222199718	chr14	99697804	99697931	99697824	99697907	BCL11B	NM_138576	2	4	3	-	99697682	99697894
222980066	chr14	99724104	99724233	99724124	99724212	BCL11B	NM_138576	2	4	2	-	99723808	99724176
222980066	chr14	99724104	99724233	99724124	99724212	BCL11B	NM_022898	1	3	2	-	99723808	99724176
227269096	chr14	102548362	102548536	102548390	102548515	HSP90AA1	NM_005348	2	11	10	-	102548448	102548781
227269096	chr14	102548362	102548536	102548390	102548515	HSP90AA1	NM_001017963	1	12	11	-	102548448	102548781
227285334	chr14	102548750	102548906	102548773	102548874	HSP90AA1	NM_005348	2	11	10	-	102548448	102548781
227285334	chr14	102548750	102548906	102548773	102548874	HSP90AA1	NM_001017963	1	12	11	-	102548448	102548781
227139038	chr14	102549822	102549995	102549846	102549968	HSP90AA1	NM_005348	2	11	8	-	102549883	102550030
227139038	chr14	102549822	102549995	102549846	102549968	HSP90AA1	NM_001017963	1	12	9	-	102549883	102550030
227292504	chr14	102550185	102550358	102550213	102550335	HSP90AA1	NM_005348	2	11	7	-	102550130	102550320
227292504	chr14	102550185	102550358	102550213	102550335	HSP90AA1	NM_001017963	1	12	8	-	102550130	102550320
227310356	chr14	102551114	102551251	102551136	102551225	HSP90AA1	NM_005348	2	11	5	-	102551018	102551335
227310356	chr14	102551114	102551251	102551136	102551225	HSP90AA1	NM_001017963	1	12	6	-	102551018	102551335
228655984	chr14	102551674	102551823	102551703	102551795	HSP90AA1	NM_005348	2	11	4	-	102551635	102551768
228655984	chr14	102551674	102551823	102551703	102551795	HSP90AA1	NM_001017963	1	12	5	-	102551635	102551768
227778156	chr14	102552422	102552553	102552446	102552525	HSP90AA1	NM_005348	2	11	3	-	102552095	102552461
227778156	chr14	102552422	102552553	102552446	102552525	HSP90AA1	NM_001017963	1	12	4	-	102552095	102552461
227409291	chr14	102568217	102568385	102568243	102568362	HSP90AA1	NM_001017963	1	12	2	-	102568212	102568422
223745545	chr14	105236632	105236778	105236654	105236757	AKT1	NM_005163	3	14	14	-	105235687	105236757
223745545	chr14	105236632	105236778	105236654	105236757	AKT1	NM_001014432	2	15	15	-	105235687	105236757
223745545	chr14	105236632	105236778	105236654	105236757	AKT1	NM_001014431	1	14	14	-	105235687	105236757
223729103	chr14	105238716	105238876	105238734	105238855	AKT1	NM_005163	3	14	12	-	105238702	105238789
223729103	chr14	105238716	105238876	105238734	105238855	AKT1	NM_001014432	2	15	13	-	105238702	105238789
223729103	chr14	105238716	105238876	105238734	105238855	AKT1	NM_001014431	1	14	12	-	105238702	105238789
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_005163	3	14	10	-	105239588	105239716
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_001014432	2	15	11	-	105239588	105239716

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_001014431	1	14	10	-	105239588	105239716
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_005163	3	14	9	-	105239792	105239917
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_001014432	2	15	10	-	105239792	105239917
223656075	chr14	105239660	105239826	105239682	105239806	AKT1	NM_001014431	1	14	9	-	105239792	105239917
222523072	chr14	105241331	105241460	105241351	105241438	AKT1	NM_005163	3	14	6	-	105241413	105241544
222523072	chr14	105241331	105241460	105241351	105241438	AKT1	NM_001014432	2	15	7	-	105241413	105241544
222523072	chr14	105241331	105241460	105241351	105241438	AKT1	NM_001014431	1	14	6	-	105241413	105241544
224109544	chr14	105242063	105242188	105242085	105242167	AKT1	NM_005163	3	14	5	-	105241989	105242136
224109544	chr14	105242063	105242188	105242085	105242167	AKT1	NM_001014432	2	15	6	-	105241989	105242136
224109544	chr14	105242063	105242188	105242085	105242167	AKT1	NM_001014431	1	14	5	-	105241989	105242136
223631289	chr14	105246394	105246527	105246413	105246502	AKT1	NM_005163	3	14	3	-	105246425	105246553
223631289	chr14	105246394	105246527	105246413	105246502	AKT1	NM_001014432	2	15	4	-	105246425	105246553
223631289	chr14	105246394	105246527	105246413	105246502	AKT1	NM_001014431	1	14	3	-	105246425	105246553
304176184	chr15	39874401	39874553	39874422	39874531	THBS1	NM_003246	1	22	3	+	39874394	39874953
304170277	chr15	39874822	39874994	39874846	39874974	THBS1	NM_003246	1	22	3	+	39874394	39874953
300862091	chr15	39876272	39876441	39876294	39876419	THBS1	NM_003246	1	22	5	+	39876189	39876388
303351631	chr15	39879609	39879773	39879630	39879750	THBS1	NM_003246	1	22	8	+	39879548	39879721
299955405	chr15	39880795	39880967	39880818	39880944	THBS1	NM_003246	1	22	10	+	39880727	39880900
303249749	chr15	39881975	39882140	39881996	39882121	THBS1	NM_003246	1	22	13	+	39882006	39882224
300890987	chr15	39883313	39883451	39883339	39883425	THBS1	NM_003246	1	22	15	+	39883392	39883551
304331779	chr15	39884861	39885031	39884881	39885008	THBS1	NM_003246	1	22	17	+	39884769	39885003
301605301	chr15	39885524	39885690	39885550	39885667	THBS1	NM_003246	1	22	19	+	39885598	39885869
305984521	chr15	39886375	39886540	39886397	39886516	THBS1	NM_003246	1	22	21	+	39886502	39886641
305984521	chr15	39886375	39886540	39886397	39886516	THBS1	NM_003246	1	22	20	+	39886300	39886397
223296249	chr15	40457154	40457322	40457181	40457294	BUB1B	NM_001211	1	23	2	+	40457254	40457397
225143641	chr15	40462736	40462908	40462759	40462882	BUB1B	NM_001211	1	23	4	+	40462738	40462882
222284310	chr15	40475940	40476079	40475963	40476060	BUB1B	NM_001211	1	23	6	+	40475915	40476084
223710778	chr15	40477439	40477607	40477464	40477580	BUB1B	NM_001211	1	23	7	+	40477366	40477580
224129299	chr15	40488727	40488863	40488756	40488843	BUB1B	NM_001211	1	23	9	+	40488746	40488975
222937217	chr15	40491853	40492019	40491880	40491998	BUB1B	NM_001211	1	23	10	+	40491816	40491928
223191977	chr15	40494502	40494639	40494526	40494610	BUB1B	NM_001211	1	23	13	+	40494606	40494666
222383137	chr15	40498407	40498549	40498429	40498523	BUB1B	NM_001211	1	23	15	+	40498385	40498659
223374020	chr15	40501722	40501877	40501748	40501854	BUB1B	NM_001211	1	23	17	+	40501836	40501976
222846020	chr15	40504687	40504840	40504715	40504812	BUB1B	NM_001211	1	23	19	+	40504700	40504849
223916103	chr15	40509626	40509777	40509651	40509752	BUB1B	NM_001211	1	23	21	+	40509697	40509868
224958832	chr15	40512763	40512917	40512790	40512893	BUB1B	NM_001211	1	23	23	+	40512765	40513337
225668416	chr15	40897193	40897355	40897219	40897329	CASC5	NM_144508	1	26	3	+	40897308	40897347
225668416	chr15	40897193	40897355	40897219	40897329	CASC5	NM_170589	2	27	3	+	40897308	40897347
227036993	chr15	40900960	40901092	40900989	40901070	CASC5	NM_144508	1	26	5	+	40901045	40901106
227036993	chr15	40900960	40901092	40900989	40901070	CASC5	NM_170589	2	27	5	+	40901045	40901106
226512583	chr15	40911164	40911337	40911186	40911309	CASC5	NM_144508	1	26	9	+	40911157	40911209

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226512583	chr15	40911164	40911337	40911186	40911309	CASC5	NM_170589	2	27	10	+	40911157	40911209
225341622	chr15	40913027	40913162	40913049	40913137	CASC5	NM_144508	1	26	10	+	40912838	40917838
225341622	chr15	40913027	40913162	40913049	40913137	CASC5	NM_170589	2	27	11	+	40912838	40917838
226619980	chr15	40913339	40913505	40913363	40913477	CASC5	NM_144508	1	26	10	+	40912838	40917838
226619980	chr15	40913339	40913505	40913363	40913477	CASC5	NM_170589	2	27	11	+	40912838	40917838
226631415	chr15	40913681	40913826	40913709	40913798	CASC5	NM_144508	1	26	10	+	40912838	40917838
226631415	chr15	40913681	40913826	40913709	40913798	CASC5	NM_170589	2	27	11	+	40912838	40917838
226626071	chr15	40914002	40914126	40914026	40914104	CASC5	NM_144508	1	26	10	+	40912838	40917838
226626071	chr15	40914002	40914126	40914026	40914104	CASC5	NM_170589	2	27	11	+	40912838	40917838
226625742	chr15	40914418	40914579	40914446	40914551	CASC5	NM_144508	1	26	10	+	40912838	40917838
226625742	chr15	40914418	40914579	40914446	40914551	CASC5	NM_170589	2	27	11	+	40912838	40917838
226618259	chr15	40914748	40914872	40914772	40914844	CASC5	NM_144508	1	26	10	+	40912838	40917838
226618259	chr15	40914748	40914872	40914772	40914844	CASC5	NM_170589	2	27	11	+	40912838	40917838
226638922	chr15	40915220	40915384	40915248	40915356	CASC5	NM_144508	1	26	10	+	40912838	40917838
226638922	chr15	40915220	40915384	40915248	40915356	CASC5	NM_170589	2	27	11	+	40912838	40917838
225359204	chr15	40915598	40915771	40915626	40915747	CASC5	NM_144508	1	26	10	+	40912838	40917838
225359204	chr15	40915598	40915771	40915626	40915747	CASC5	NM_170589	2	27	11	+	40912838	40917838
225377843	chr15	40915951	40916124	40915974	40916103	CASC5	NM_144508	1	26	10	+	40912838	40917838
225377843	chr15	40915951	40916124	40915974	40916103	CASC5	NM_170589	2	27	11	+	40912838	40917838
226626951	chr15	40916341	40916501	40916367	40916475	CASC5	NM_144508	1	26	10	+	40912838	40917838
226626951	chr15	40916341	40916501	40916367	40916475	CASC5	NM_170589	2	27	11	+	40912838	40917838
226620608	chr15	40916784	40916951	40916806	40916923	CASC5	NM_144508	1	26	10	+	40912838	40917838
226620608	chr15	40916784	40916951	40916806	40916923	CASC5	NM_170589	2	27	11	+	40912838	40917838
226632595	chr15	40917080	40917248	40917104	40917219	CASC5	NM_144508	1	26	10	+	40912838	40917838
226632595	chr15	40917080	40917248	40917104	40917219	CASC5	NM_170589	2	27	11	+	40912838	40917838
226639252	chr15	40917449	40917573	40917475	40917548	CASC5	NM_144508	1	26	10	+	40912838	40917838
226639252	chr15	40917449	40917573	40917475	40917548	CASC5	NM_170589	2	27	11	+	40912838	40917838
225329345	chr15	40917809	40917953	40917836	40917926	CASC5	NM_144508	1	26	10	+	40912838	40917838
225329345	chr15	40917809	40917953	40917836	40917926	CASC5	NM_170589	2	27	11	+	40912838	40917838
225877579	chr15	40920704	40920872	40920726	40920843	CASC5	NM_144508	1	26	12	+	40920809	40920876
225877579	chr15	40920704	40920872	40920726	40920843	CASC5	NM_170589	2	27	13	+	40920809	40920876
226113858	chr15	40933151	40933283	40933180	40933257	CASC5	NM_144508	1	26	14	+	40933110	40933225
226113858	chr15	40933151	40933283	40933180	40933257	CASC5	NM_170589	2	27	15	+	40933110	40933225
253654556	chr15	40939105	40939278	40939129	40939252	CASC5	NM_144508	1	26	17	+	40939185	40939272
253654556	chr15	40939105	40939278	40939129	40939252	CASC5	NM_170589	2	27	18	+	40939185	40939272
226388747	chr15	40942736	40942873	40942762	40942851	CASC5	NM_144508	1	26	19	+	40942742	40942781
226388747	chr15	40942736	40942873	40942762	40942851	CASC5	NM_170589	2	27	20	+	40942742	40942781
225836854	chr15	40949489	40949633	40949514	40949604	CASC5	NM_144508	1	26	24	+	40949553	40949671
225836854	chr15	40949489	40949633	40949514	40949604	CASC5	NM_170589	2	27	25	+	40949553	40949671
270971933	chr15	41796287	41796451	41796308	41796430	LTK	NM_001135685	1	18	18	-	41795840	41796442
270971933	chr15	41796287	41796451	41796308	41796430	LTK	NM_002344	2	20	20	-	41795840	41796442

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270971933	chr15	41796287	41796451	41796308	41796430	LTK	NM_206961	3	19	19	-	41795840	41796442
271690212	chr15	41796772	41796928	41796790	41796905	LTK	NM_001135685	1	18	16	-	41796704	41796838
271690212	chr15	41796772	41796928	41796790	41796905	LTK	NM_002344	2	20	18	-	41796704	41796838
271690212	chr15	41796772	41796928	41796790	41796905	LTK	NM_206961	3	19	17	-	41796704	41796838
271076761	chr15	41797160	41797309	41797177	41797282	LTK	NM_001135685	1	18	14	-	41797170	41797262
271076761	chr15	41797160	41797309	41797177	41797282	LTK	NM_002344	2	20	16	-	41797170	41797262
271076761	chr15	41797160	41797309	41797177	41797282	LTK	NM_206961	3	19	15	-	41797170	41797262
270867194	chr15	41797834	41798003	41797856	41797981	LTK	NM_001135685	1	18	11	-	41797911	41797975
270867194	chr15	41797834	41798003	41797856	41797981	LTK	NM_002344	2	20	13	-	41797911	41797975
270867194	chr15	41797834	41798003	41797856	41797981	LTK	NM_206961	3	19	12	-	41797911	41797975
270809089	chr15	41799713	41799879	41799734	41799856	LTK	NM_001135685	1	18	9	-	41799760	41799855
270809089	chr15	41799713	41799879	41799734	41799856	LTK	NM_002344	2	20	10	-	41799760	41799855
270809089	chr15	41799713	41799879	41799734	41799856	LTK	NM_206961	3	19	9	-	41799760	41799855
272109932	chr15	41801261	41801407	41801287	41801387	LTK	NM_001135685	1	18	7	-	41801229	41801327
272109932	chr15	41801261	41801407	41801287	41801387	LTK	NM_002344	2	20	8	-	41801229	41801327
272109932	chr15	41801261	41801407	41801287	41801387	LTK	NM_206961	3	19	7	-	41801229	41801327
270161925	chr15	41804206	41804365	41804224	41804346	LTK	NM_001135685	1	18	4	-	41804313	41804463
270161925	chr15	41804206	41804365	41804224	41804346	LTK	NM_002344	2	20	4	-	41804313	41804463
270161925	chr15	41804206	41804365	41804224	41804346	LTK	NM_206961	3	19	4	-	41804313	41804463
272207334	chr15	41804933	41805068	41804950	41805046	LTK	NM_001135685	1	18	3	-	41804905	41805076
272207334	chr15	41804933	41805068	41804950	41805046	LTK	NM_002344	2	20	3	-	41804905	41805076
272207334	chr15	41804933	41805068	41804950	41805046	LTK	NM_206961	3	19	3	-	41804905	41805076
269946935	chr15	41805762	41805935	41805782	41805916	LTK	NM_001135685	1	18	1	-	41805865	41806085
269946935	chr15	41805762	41805935	41805782	41805916	LTK	NM_002344	2	20	1	-	41805865	41806085
269946935	chr15	41805762	41805935	41805782	41805916	LTK	NM_206961	3	19	1	-	41805865	41806085
294813189	chr15	43569117	43569260	43569140	43569238	TGM7	NM_052955	1	13	12	-	43569060	43569193
294899373	chr15	43571936	43572085	43571953	43572063	TGM7	NM_052955	1	13	10	-	43571823	43572149
294708383	chr15	43574172	43574315	43574193	43574293	TGM7	NM_052955	1	13	9	-	43574042	43574284
293998182	chr15	43579447	43579613	43579471	43579593	TGM7	NM_052955	1	13	6	-	43579478	43579655
294721639	chr15	43584149	43584320	43584170	43584296	TGM7	NM_052955	1	13	4	-	43584177	43584295
294131938	chr15	43585577	43585722	43585598	43585703	TGM7	NM_052955	1	13	2	-	43585647	43585829
242070584	chr15	57213138	57213310	57213162	57213284	TCF12	NM_207038	4	20	3	+	57213224	57213296
242070584	chr15	57213138	57213310	57213162	57213284	TCF12	NM_207036	2	21	3	+	57213224	57213296
242070584	chr15	57213138	57213310	57213162	57213284	TCF12	NM_003205	1	20	3	+	57213224	57213296
242070584	chr15	57213138	57213310	57213162	57213284	TCF12	NM_207037	3	21	3	+	57213224	57213296
239323860	chr15	57383967	57384120	57383990	57384092	TCF12	NM_207038	4	20	5	+	57383987	57384089
239323860	chr15	57383967	57384120	57383990	57384092	TCF12	NM_207036	2	21	5	+	57383987	57384089
239323860	chr15	57383967	57384120	57383990	57384092	TCF12	NM_003205	1	20	5	+	57383987	57384089
239323860	chr15	57383967	57384120	57383990	57384092	TCF12	NM_207037	3	21	5	+	57383987	57384089
241931093	chr15	57489845	57490009	57489870	57489988	TCF12	NM_207038	4	20	8	+	57489971	57490023
241931093	chr15	57489845	57490009	57489870	57489988	TCF12	NM_207036	2	21	8	+	57489971	57490023

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241931093	chr15	57489845	57490009	57489870	57489988	TCF12	NM_003205	1	20	8	+	57489971	57490023
241931093	chr15	57489845	57490009	57489870	57489988	TCF12	NM_207037	3	21	8	+	57489971	57490023
241342629	chr15	57523253	57523406	57523276	57523379	TCF12	NM_207038	4	20	9	+	57523350	57523455
241342629	chr15	57523253	57523406	57523276	57523379	TCF12	NM_207036	2	21	9	+	57523350	57523455
241342629	chr15	57523253	57523406	57523276	57523379	TCF12	NM_003205	1	20	9	+	57523350	57523455
241342629	chr15	57523253	57523406	57523276	57523379	TCF12	NM_207037	3	21	9	+	57523350	57523455
241342629	chr15	57523253	57523406	57523276	57523379	TCF12	NM_207040	5	13	2	+	57523350	57523455
238764877	chr15	57524796	57524950	57524824	57524924	TCF12	NM_207038	4	20	11	+	57524910	57525054
238764877	chr15	57524796	57524950	57524824	57524924	TCF12	NM_207036	2	21	11	+	57524910	57525054
238764877	chr15	57524796	57524950	57524824	57524924	TCF12	NM_003205	1	20	11	+	57524910	57525054
238764877	chr15	57524796	57524950	57524824	57524924	TCF12	NM_207037	3	21	11	+	57524910	57525054
238764877	chr15	57524796	57524950	57524824	57524924	TCF12	NM_207040	5	13	4	+	57524910	57525054
238433624	chr15	57535617	57535791	57535642	57535764	TCF12	NM_207038	4	20	13	+	57535670	57535748
238433624	chr15	57535617	57535791	57535642	57535764	TCF12	NM_207036	2	21	13	+	57535670	57535748
238433624	chr15	57535617	57535791	57535642	57535764	TCF12	NM_003205	1	20	13	+	57535670	57535748
238433624	chr15	57535617	57535791	57535642	57535764	TCF12	NM_207037	3	21	13	+	57535670	57535748
238433624	chr15	57535617	57535791	57535642	57535764	TCF12	NM_207040	5	13	6	+	57535670	57535748
261797703	chr15	57545408	57545549	57545434	57545529	TCF12	NM_207038	4	20	15	+	57545460	57545666
261797703	chr15	57545408	57545549	57545434	57545529	TCF12	NM_207036	2	21	16	+	57545460	57545666
261797703	chr15	57545408	57545549	57545434	57545529	TCF12	NM_003205	1	20	15	+	57545460	57545666
261797703	chr15	57545408	57545549	57545434	57545529	TCF12	NM_207037	3	21	16	+	57545460	57545666
261797703	chr15	57545408	57545549	57545434	57545529	TCF12	NM_207040	5	13	8	+	57545460	57545666
242194873	chr15	57554271	57554444	57554298	57554416	TCF12	NM_207038	4	20	16	+	57554292	57554406
242194873	chr15	57554271	57554444	57554298	57554416	TCF12	NM_207036	2	21	17	+	57554292	57554406
242194873	chr15	57554271	57554444	57554298	57554416	TCF12	NM_003205	1	20	16	+	57554292	57554406
242194873	chr15	57554271	57554444	57554298	57554416	TCF12	NM_207037	3	21	17	+	57554292	57554406
242194873	chr15	57554271	57554444	57554298	57554416	TCF12	NM_207040	5	13	9	+	57554292	57554406
264053729	chr15	57565128	57565287	57565155	57565260	TCF12	NM_207038	4	20	18	+	57565228	57565460
264053729	chr15	57565128	57565287	57565155	57565260	TCF12	NM_207036	2	21	19	+	57565228	57565460
264053729	chr15	57565128	57565287	57565155	57565260	TCF12	NM_003205	1	20	18	+	57565228	57565460
264053729	chr15	57565128	57565287	57565155	57565260	TCF12	NM_207037	3	21	19	+	57565228	57565460
264053729	chr15	57565128	57565287	57565155	57565260	TCF12	NM_207040	5	13	11	+	57565228	57565460
238864921	chr15	57574636	57574806	57574662	57574785	TCF12	NM_207038	4	20	19	+	57574643	57574796
238864921	chr15	57574636	57574806	57574662	57574785	TCF12	NM_207036	2	21	20	+	57574643	57574796
238864921	chr15	57574636	57574806	57574662	57574785	TCF12	NM_003205	1	20	19	+	57574643	57574796
238864921	chr15	57574636	57574806	57574662	57574785	TCF12	NM_207037	3	21	20	+	57574643	57574796
238864921	chr15	57574636	57574806	57574662	57574785	TCF12	NM_207040	5	13	12	+	57574643	57574796
231127821	chr15	66729016	66729186	66729043	66729165	MAP2K1	NM_002755	1	11	3	+	66729084	66729230
233571847	chr15	66736875	66737035	66736903	66737009	MAP2K1	NM_002755	1	11	5	+	66736994	66737045
233380037	chr15	66777281	66777435	66777304	66777413	MAP2K1	NM_002755	1	11	7	+	66777328	66777529
232253993	chr15	66782016	66782168	66782036	66782139	MAP2K1	NM_002755	1	11	10	+	66782056	66782101

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033250	9	7	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033249	8	7	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033247	7	5	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033246	6	6	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033244	5	8	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033240	4	7	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033239	3	8	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_033238	2	9	2	+	74290345	74290817
237947873	chr15	74290317	74290455	74290335	74290437	PML	NM_002675	1	8	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033250	9	7	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033249	8	7	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033247	7	5	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033246	6	6	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033244	5	8	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033240	4	7	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033239	3	8	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_033238	2	9	2	+	74290345	74290817
237961228	chr15	74290734	74290870	74290753	74290848	PML	NM_002675	1	8	2	+	74290345	74290817
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033250	9	7	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033249	8	7	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033247	7	5	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033246	6	6	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033244	5	8	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033240	4	7	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033239	3	8	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_033238	2	9	3	+	74315169	74315749
239374885	chr15	74315415	74315539	74315432	74315521	PML	NM_002675	1	8	3	+	74315169	74315749
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033250	9	7	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033249	8	7	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033247	7	5	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033246	6	6	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033244	5	8	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033240	4	7	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033239	3	8	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_033238	2	9	4	+	74317198	74317268
235984107	chr15	74317122	74317292	74317144	74317269	PML	NM_002675	1	8	4	+	74317198	74317268
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033250	9	7	5	+	74325497	74325755
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033249	8	7	5	+	74325497	74325755
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033240	4	7	6	+	74325497	74325755
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033239	3	8	6	+	74325497	74325755
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033238	2	9	6	+	74325497	74325755

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_002675	1	8	6	+	74325497	74325755
235483554	chr15	74325549	74325723	74325568	74325703	PML	NM_033244	5	8	6	+	74325497	74325763
235993981	chr15	74327588	74327723	74327605	74327705	PML	NM_033250	9	7	7	+	74327513	74328735
235993981	chr15	74327588	74327723	74327605	74327705	PML	NM_033244	5	8	8	+	74327513	74328735
235993981	chr15	74327588	74327723	74327605	74327705	PML	NM_033239	3	8	8	+	74327513	74328735
235993981	chr15	74327588	74327723	74327605	74327705	PML	NM_033240	4	7	7	+	74326819	74328735
234990716	chr15	74327919	74328090	74327939	74328070	PML	NM_033250	9	7	7	+	74327513	74328735
234990716	chr15	74327919	74328090	74327939	74328070	PML	NM_033244	5	8	8	+	74327513	74328735
234990716	chr15	74327919	74328090	74327939	74328070	PML	NM_033239	3	8	8	+	74327513	74328735
234990716	chr15	74327919	74328090	74327939	74328070	PML	NM_033240	4	7	7	+	74326819	74328735
236708352	chr15	74335303	74335447	74335325	74335426	PML	NM_033238	2	9	8	+	74335330	74335480
236708352	chr15	74335303	74335447	74335325	74335426	PML	NM_033249	8	7	7	+	74335330	74335717
236708352	chr15	74335303	74335447	74335325	74335426	PML	NM_033246	6	6	6	+	74335330	74335717
236708352	chr15	74335303	74335447	74335325	74335426	PML	NM_002675	1	8	8	+	74335330	74335717
239461955	chr15	74336744	74336917	74336765	74336896	PML	NM_033238	2	9	9	+	74336562	74340155
239458969	chr15	74337210	74337380	74337229	74337360	PML	NM_033238	2	9	9	+	74336562	74340155
236416748	chr15	88423518	88423684	88423539	88423659	NTRK3	NM_002530	4	19	18	-	88423501	88423659
236416748	chr15	88423518	88423684	88423539	88423659	NTRK3	NM_001012338	2	20	19	-	88423501	88423659
236416748	chr15	88423518	88423684	88423539	88423659	NTRK3	NM_001243101	3	18	17	-	88423501	88423659
238739778	chr15	88476190	88476347	88476208	88476327	NTRK3	NM_002530	4	19	16	-	88476243	88476415
238739778	chr15	88476190	88476347	88476208	88476327	NTRK3	NM_001012338	2	20	16	-	88476243	88476415
238739778	chr15	88476190	88476347	88476208	88476327	NTRK3	NM_001243101	3	18	15	-	88476243	88476415
237441721	chr15	88522487	88522658	88522512	88522637	NTRK3	NM_001007156	1	16	16	-	88520596	88522694
235129989	chr15	88669465	88669628	88669485	88669604	NTRK3	NM_002530	4	19	13	-	88669502	88669604
235129989	chr15	88669465	88669628	88669485	88669604	NTRK3	NM_001007156	1	16	13	-	88669502	88669604
235129989	chr15	88669465	88669628	88669485	88669604	NTRK3	NM_001012338	2	20	13	-	88669502	88669604
235129989	chr15	88669465	88669628	88669485	88669604	NTRK3	NM_001243101	3	18	12	-	88669502	88669604
239315061	chr15	88678382	88678536	88678403	88678518	NTRK3	NM_002530	4	19	10	-	88678332	88678628
239315061	chr15	88678382	88678536	88678403	88678518	NTRK3	NM_001007156	1	16	10	-	88678332	88678628
239315061	chr15	88678382	88678536	88678403	88678518	NTRK3	NM_001012338	2	20	10	-	88678332	88678628
239315061	chr15	88678382	88678536	88678403	88678518	NTRK3	NM_001243101	3	18	10	-	88678332	88678628
237552668	chr15	88679612	88679762	88679635	88679741	NTRK3	NM_002530	4	19	8	-	88679698	88679840
237552668	chr15	88679612	88679762	88679635	88679741	NTRK3	NM_001007156	1	16	8	-	88679698	88679840
237552668	chr15	88679612	88679762	88679635	88679741	NTRK3	NM_001012338	2	20	8	-	88679698	88679840
237552668	chr15	88679612	88679762	88679635	88679741	NTRK3	NM_001243101	3	18	8	-	88679698	88679840
236511584	chr15	88690517	88690691	88690540	88690663	NTRK3	NM_002530	4	19	6	-	88690566	88690634
236511584	chr15	88690517	88690691	88690540	88690663	NTRK3	NM_001007156	1	16	6	-	88690566	88690634
236511584	chr15	88690517	88690691	88690540	88690663	NTRK3	NM_001012338	2	20	6	-	88690566	88690634
236511584	chr15	88690517	88690691	88690540	88690663	NTRK3	NM_001243101	3	18	6	-	88690566	88690634
237387152	chr15	88799244	88799394	88799263	88799374	NTRK3	NM_002530	4	19	3	-	88799137	88799399
237387152	chr15	88799244	88799394	88799263	88799374	NTRK3	NM_001007156	1	16	3	-	88799137	88799399

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237387152	chr15	88799244	88799394	88799263	88799374	NTRK3	NM_001012338	2	20	3	-	88799137	88799399
237387152	chr15	88799244	88799394	88799263	88799374	NTRK3	NM_001243101	3	18	3	-	88799137	88799399
228405476	chr15	90628213	90628363	90628232	90628343	IDH2	NM_002168	1	11	9	-	90628233	90628330
227353866	chr15	90630357	90630526	90630377	90630499	IDH2	NM_002168	1	11	7	-	90630344	90630495
227884778	chr15	90631636	90631760	90631659	90631738	IDH2	NM_002168	1	11	5	-	90631591	90631734
227262516	chr15	90633735	90633862	90633756	90633835	IDH2	NM_002168	1	11	3	-	90633711	90633876
228890575	chr15	90645519	90645644	90645536	90645625	IDH2	NM_002168	1	11	1	-	90645508	90645708
222695036	chr15	91292826	91292970	91292849	91292942	BLM	NM_000057	1	22	3	+	91292597	91293297
224514773	chr15	91293220	91293374	91293241	91293348	BLM	NM_000057	1	22	3	+	91292597	91293297
222362633	chr15	91298064	91298188	91298091	91298160	BLM	NM_000057	1	22	5	+	91298041	91298168
225042649	chr15	91303760	91303925	91303781	91303905	BLM	NM_000057	1	22	7	+	91303824	91304485
225099443	chr15	91304184	91304338	91304212	91304312	BLM	NM_000057	1	22	7	+	91303824	91304485
222181900	chr15	91306200	91306374	91306228	91306348	BLM	NM_000057	1	22	8	+	91306196	91306387
223236603	chr15	91310025	91310180	91310058	91310155	BLM	NM_000057	1	22	10	+	91310140	91310253
223801498	chr15	91312670	91312841	91312696	91312816	BLM	NM_000057	1	22	12	+	91312668	91312816
223074051	chr15	91333822	91333990	91333848	91333966	BLM	NM_000057	1	22	15	+	91333879	91334074
223307258	chr15	91337530	91337680	91337558	91337652	BLM	NM_000057	1	22	16	+	91337397	91337587
222524420	chr15	91346635	91346809	91346662	91346781	BLM	NM_000057	1	22	18	+	91346751	91346950
223288157	chr15	91347461	91347635	91347483	91347612	BLM	NM_000057	1	22	19	+	91347397	91347589
223633960	chr15	91354525	91354685	91354551	91354657	BLM	NM_000057	1	22	21	+	91354435	91354636
271099486	chr15	99192794	99192922	99192822	99192905	IGF1R	NM_000875	1	21	1	+	99192761	99192904
269856497	chr15	99251015	99251177	99251035	99251157	IGF1R	NM_000875	1	21	2	+	99250791	99251336
270052805	chr15	99434642	99434807	99434661	99434786	IGF1R	NM_000875	1	21	3	+	99434554	99434866
269646455	chr15	99442661	99442832	99442683	99442809	IGF1R	NM_000875	1	21	5	+	99442706	99442850
269896136	chr15	99454475	99454618	99454496	99454598	IGF1R	NM_000875	1	21	7	+	99454544	99454670
270115037	chr15	99456443	99456606	99456462	99456583	IGF1R	NM_000875	1	21	8	+	99456273	99456511
272083197	chr15	99459941	99460093	99459964	99460069	IGF1R	NM_000875	1	21	10	+	99459901	99460105
271308173	chr15	99465547	99465682	99465570	99465661	IGF1R	NM_000875	1	21	11	+	99465377	99465660
272247687	chr15	99467843	99468010	99467866	99467983	IGF1R	NM_000875	1	21	13	+	99467754	99467913
269480384	chr15	99473480	99473644	99473501	99473617	IGF1R	NM_000875	1	21	15	+	99473464	99473534
269779186	chr15	99478610	99478776	99478633	99478753	IGF1R	NM_000875	1	21	17	+	99478545	99478655
272659444	chr15	99486132	99486306	99486153	99486281	IGF1R	NM_000875	1	21	19	+	99486152	99486281
272136807	chr15	99500289	99500428	99500311	99500407	IGF1R	NM_000875	1	21	21	+	99500290	99507759
241527099	chr16	2100365	2100517	2100387	2100489	TSC2	NM_000548	1	42	3	+	2100401	2100487
241527099	chr16	2100365	2100517	2100387	2100489	TSC2	NM_001077183	2	40	3	+	2100401	2100487
241527099	chr16	2100365	2100517	2100387	2100489	TSC2	NM_001114382	3	41	3	+	2100401	2100487
263000601	chr16	2105306	2105479	2105326	2105456	TSC2	NM_000548	1	42	6	+	2105403	2105520
263000601	chr16	2105306	2105479	2105326	2105456	TSC2	NM_001077183	2	40	6	+	2105403	2105520
263000601	chr16	2105306	2105479	2105326	2105456	TSC2	NM_001114382	3	41	6	+	2105403	2105520
240170798	chr16	2107079	2107251	2107097	2107232	TSC2	NM_000548	1	42	9	+	2107106	2107179
240170798	chr16	2107079	2107251	2107097	2107232	TSC2	NM_001077183	2	40	9	+	2107106	2107179

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240170798	chr16	2107079	2107251	2107097	2107232	TSC2	NM_001114382	3	41	9	+	2107106	2107179
240819467	chr16	2110678	2110806	2110697	2110787	TSC2	NM_000548	1	42	11	+	2110671	2110814
240819467	chr16	2110678	2110806	2110697	2110787	TSC2	NM_001077183	2	40	11	+	2110671	2110814
240819467	chr16	2110678	2110806	2110697	2110787	TSC2	NM_001114382	3	41	11	+	2110671	2110814
239566960	chr16	2112845	2113017	2112863	2113000	TSC2	NM_000548	1	42	14	+	2112973	2113054
239566960	chr16	2112845	2113017	2112863	2113000	TSC2	NM_001077183	2	40	14	+	2112973	2113054
239566960	chr16	2112845	2113017	2112863	2113000	TSC2	NM_001114382	3	41	14	+	2112973	2113054
264633381	chr16	2120386	2120542	2120407	2120521	TSC2	NM_000548	1	42	17	+	2120457	2120579
264633381	chr16	2120386	2120542	2120407	2120521	TSC2	NM_001077183	2	40	17	+	2120457	2120579
264633381	chr16	2120386	2120542	2120407	2120521	TSC2	NM_001114382	3	41	17	+	2120457	2120579
238409648	chr16	2121685	2121817	2121707	2121796	TSC2	NM_000548	1	42	19	+	2121785	2121935
238409648	chr16	2121685	2121817	2121707	2121796	TSC2	NM_001077183	2	40	19	+	2121785	2121935
238409648	chr16	2121685	2121817	2121707	2121796	TSC2	NM_001114382	3	41	19	+	2121785	2121935
241064397	chr16	2122294	2122435	2122321	2122415	TSC2	NM_000548	1	42	20	+	2122242	2122364
241064397	chr16	2122294	2122435	2122321	2122415	TSC2	NM_001077183	2	40	20	+	2122242	2122364
241064397	chr16	2122294	2122435	2122321	2122415	TSC2	NM_001114382	3	41	20	+	2122242	2122364
240330136	chr16	2124284	2124442	2124308	2124422	TSC2	NM_000548	1	42	22	+	2124201	2124390
240330136	chr16	2124284	2124442	2124308	2124422	TSC2	NM_001077183	2	40	22	+	2124201	2124390
240330136	chr16	2124284	2124442	2124308	2124422	TSC2	NM_001114382	3	41	22	+	2124201	2124390
241953402	chr16	2126462	2126593	2126482	2126573	TSC2	NM_000548	1	42	25	+	2126492	2126586
241953402	chr16	2126462	2126593	2126482	2126573	TSC2	NM_001077183	2	40	25	+	2126492	2126586
241953402	chr16	2126462	2126593	2126482	2126573	TSC2	NM_001114382	3	41	25	+	2126492	2126586
240061071	chr16	2128955	2129084	2128976	2129063	TSC2	NM_001077183	2	40	26	+	2129036	2129197
240061071	chr16	2128955	2129084	2128976	2129063	TSC2	NM_000548	1	42	27	+	2129033	2129197
240061071	chr16	2128955	2129084	2128976	2129063	TSC2	NM_001114382	3	41	27	+	2129033	2129197
239513718	chr16	2129283	2129451	2129302	2129430	TSC2	NM_000548	1	42	28	+	2129277	2129429
239513718	chr16	2129283	2129451	2129302	2129430	TSC2	NM_001077183	2	40	27	+	2129277	2129429
239513718	chr16	2129283	2129451	2129302	2129430	TSC2	NM_001114382	3	41	28	+	2129277	2129429
265786460	chr16	2130259	2130428	2130279	2130408	TSC2	NM_000548	1	42	30	+	2130166	2130378
265786460	chr16	2130259	2130428	2130279	2130408	TSC2	NM_001077183	2	40	29	+	2130166	2130378
265786460	chr16	2130259	2130428	2130279	2130408	TSC2	NM_001114382	3	41	30	+	2130166	2130378
240423762	chr16	2132370	2132527	2132389	2132506	TSC2	NM_000548	1	42	32	+	2132437	2132505
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_000548	1	42	34	+	2134229	2134716
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262611399	chr16	2134334	2134507	2134354	2134489	TSC2	NM_001114382	3	41	33	+	2134229	2134716
264929391	chr16	2134980	2135153	2134999	2135134	TSC2	NM_000548	1	42	35	+	2134952	2135027
264929391	chr16	2134980	2135153	2134999	2135134	TSC2	NM_001077183	2	40	33	+	2134952	2135027
264929391	chr16	2134980	2135153	2134999	2135134	TSC2	NM_001114382	3	41	34	+	2134952	2135027
242601234	chr16	2136292	2136451	2136310	2136431	TSC2	NM_000548	1	42	37	+	2136194	2136380
242601234	chr16	2136292	2136451	2136310	2136431	TSC2	NM_001077183	2	40	35	+	2136194	2136380
242601234	chr16	2136292	2136451	2136310	2136431	TSC2	NM_001114382	3	41	36	+	2136194	2136380

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262389934	chr16	2137878	2138015	2137897	2137998	TSC2	NM_000548	1	42	39	+	2137864	2137942
262389934	chr16	2137878	2138015	2137897	2137998	TSC2	NM_001077183	2	40	37	+	2137864	2137942
262389934	chr16	2137878	2138015	2137897	2137998	TSC2	NM_001114382	3	41	38	+	2137864	2137942
239350190	chr16	2138494	2138668	2138513	2138643	TSC2	NM_000548	1	42	42	+	2138447	2138713
239350190	chr16	2138494	2138668	2138513	2138643	TSC2	NM_001077183	2	40	40	+	2138447	2138713
239350190	chr16	2138494	2138668	2138513	2138643	TSC2	NM_001114382	3	41	41	+	2138447	2138713
225489391	chr16	3778008	3778171	3778025	3778153	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225489391	chr16	3778008	3778171	3778025	3778153	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225492496	chr16	3778385	3778544	3778402	3778522	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225492496	chr16	3778385	3778544	3778402	3778522	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226721283	chr16	3778815	3778946	3778832	3778929	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226721283	chr16	3778815	3778946	3778832	3778929	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226718611	chr16	3779283	3779446	3779300	3779427	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226718611	chr16	3779283	3779446	3779300	3779427	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226721978	chr16	3779757	3779899	3779776	3779879	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226721978	chr16	3779757	3779899	3779776	3779879	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225822526	chr16	3781713	3781840	3781732	3781820	CREBBP	NM_001079846	1	30	28	-	3781777	3781938
225822526	chr16	3781713	3781840	3781732	3781820	CREBBP	NM_004380	2	31	29	-	3781777	3781938
226450228	chr16	3786556	3786724	3786584	3786702	CREBBP	NM_001079846	1	30	26	-	3786651	3786816
226450228	chr16	3786556	3786724	3786584	3786702	CREBBP	NM_004380	2	31	27	-	3786651	3786816
225551071	chr16	3789522	3789692	3789545	3789668	CREBBP	NM_001079846	1	30	24	-	3789579	3789725
225551071	chr16	3789522	3789692	3789545	3789668	CREBBP	NM_004380	2	31	25	-	3789579	3789725
225982197	chr16	3794857	3795030	3794879	3795002	CREBBP	NM_001079846	1	30	22	-	3794895	3794962
225982197	chr16	3794857	3795030	3794879	3795002	CREBBP	NM_004380	2	31	23	-	3794895	3794962
225332696	chr16	3807238	3807383	3807258	3807360	CREBBP	NM_001079846	1	30	18	-	3807289	3807377
225332696	chr16	3807238	3807383	3807258	3807360	CREBBP	NM_004380	2	31	19	-	3807289	3807377
227018072	chr16	3808792	3808932	3808817	3808908	CREBBP	NM_001079846	1	30	16	-	3808855	3808973
227018072	chr16	3808792	3808932	3808817	3808908	CREBBP	NM_004380	2	31	17	-	3808855	3808973
226215586	chr16	3817836	3817970	3817861	3817946	CREBBP	NM_001079846	1	30	15	-	3817721	3817910
226215586	chr16	3817836	3817970	3817861	3817946	CREBBP	NM_004380	2	31	16	-	3817721	3817910
226568959	chr16	3820606	3820730	3820626	3820709	CREBBP	NM_001079846	1	30	13	-	3820571	3820987
226568959	chr16	3820606	3820730	3820626	3820709	CREBBP	NM_004380	2	31	14	-	3820571	3820987
225701836	chr16	3823703	3823853	3823730	3823834	CREBBP	NM_001079846	1	30	12	-	3823752	3823931
225701836	chr16	3823703	3823853	3823730	3823834	CREBBP	NM_004380	2	31	13	-	3823752	3823931
226137688	chr16	3827477	3827651	3827505	3827633	CREBBP	NM_001079846	1	30	10	-	3827614	3827658
226137688	chr16	3827477	3827651	3827505	3827633	CREBBP	NM_004380	2	31	11	-	3827614	3827658
225329957	chr16	3828590	3828764	3828616	3828739	CREBBP	NM_001079846	1	30	8	-	3828701	3828818
225329957	chr16	3828590	3828764	3828616	3828739	CREBBP	NM_004380	2	31	9	-	3828701	3828818
226534663	chr16	3831115	3831259	3831142	3831237	CREBBP	NM_001079846	1	30	6	-	3831205	3831307
226534663	chr16	3831115	3831259	3831142	3831237	CREBBP	NM_004380	2	31	7	-	3831205	3831307
253732414	chr16	3841870	3842013	3841890	3841990	CREBBP	NM_004380	2	31	5	-	3841982	3842095

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225710619	chr16	3843524	3843686	3843545	3843658	CREBBP	NM_001079846	1	30	4	-	3843387	3843627
225710619	chr16	3843524	3843686	3843545	3843658	CREBBP	NM_004380	2	31	4	-	3843387	3843627
226002581	chr16	3900357	3900531	3900378	3900505	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
226002581	chr16	3900357	3900531	3900378	3900505	CREBBP	NM_004380	2	31	2	-	3900298	3901010
227046797	chr16	3900826	3900959	3900849	3900932	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
227046797	chr16	3900826	3900959	3900849	3900932	CREBBP	NM_004380	2	31	2	-	3900298	3901010
264716282	chr16	11348723	11348892	11348741	11348874	SOCS1	NM_003745	1	2	2	-	11348274	11349385
264725010	chr16	11349131	11349268	11349148	11349246	SOCS1	NM_003745	1	2	2	-	11348274	11349385
229993934	chr16	14014010	14014181	14014031	14014161	ERCC4	NM_005236	1	11	1	+	14014014	14014229
231880586	chr16	14016012	14016170	14016039	14016142	ERCC4	NM_005236	1	11	2	+	14015888	14016068
232839964	chr16	14021763	14021928	14021789	14021900	ERCC4	NM_005236	1	11	4	+	14021885	14022092
233008945	chr16	14024603	14024753	14024630	14024729	ERCC4	NM_005236	1	11	5	+	14024567	14024747
229497753	chr16	14027970	14028142	14027998	14028114	ERCC4	NM_005236	1	11	7	+	14028049	14028159
232153993	chr16	14029151	14029311	14029180	14029286	ERCC4	NM_005236	1	11	8	+	14029003	14029600
228820941	chr16	14031527	14031656	14031547	14031627	ERCC4	NM_005236	1	11	9	+	14031623	14031715
232505733	chr16	14041508	14041672	14041533	14041647	ERCC4	NM_005236	1	11	11	+	14041471	14046205
230318142	chr16	14041936	14042099	14041958	14042077	ERCC4	NM_005236	1	11	11	+	14041471	14046205
241617783	chr16	15802595	15802747	15802617	15802722	MYH11	NM_022844	4	42	41	-	15802660	15802698
241617783	chr16	15802595	15802747	15802617	15802722	MYH11	NM_001040113	1	43	42	-	15802660	15802698
236876211	chr16	15809065	15809223	15809087	15809202	MYH11	NM_022844	4	42	39	-	15809021	15809129
236876211	chr16	15809065	15809223	15809087	15809202	MYH11	NM_002474	3	41	39	-	15809021	15809129
236876211	chr16	15809065	15809223	15809087	15809202	MYH11	NM_001040113	1	43	40	-	15809021	15809129
236876211	chr16	15809065	15809223	15809087	15809202	MYH11	NM_001040114	2	42	40	-	15809021	15809129
235710247	chr16	15812045	15812219	15812065	15812200	MYH11	NM_022844	4	42	37	-	15812172	15812295
235710247	chr16	15812045	15812219	15812065	15812200	MYH11	NM_002474	3	41	37	-	15812172	15812295
235710247	chr16	15812045	15812219	15812065	15812200	MYH11	NM_001040113	1	43	38	-	15812172	15812295
235710247	chr16	15812045	15812219	15812065	15812200	MYH11	NM_001040114	2	42	38	-	15812172	15812295
236507124	chr16	15813980	15814115	15813999	15814094	MYH11	NM_022844	4	42	34	-	15814008	15814169
236507124	chr16	15813980	15814115	15813999	15814094	MYH11	NM_002474	3	41	34	-	15814008	15814169
236507124	chr16	15813980	15814115	15813999	15814094	MYH11	NM_001040113	1	43	35	-	15814008	15814169
236507124	chr16	15813980	15814115	15813999	15814094	MYH11	NM_001040114	2	42	35	-	15814008	15814169
242178813	chr16	15814846	15814975	15814868	15814952	MYH11	NM_022844	4	42	33	-	15814696	15814908
242178813	chr16	15814846	15814975	15814868	15814952	MYH11	NM_002474	3	41	33	-	15814696	15814908
242178813	chr16	15814846	15814975	15814868	15814952	MYH11	NM_001040113	1	43	34	-	15814696	15814908
242178813	chr16	15814846	15814975	15814868	15814952	MYH11	NM_001040114	2	42	34	-	15814696	15814908
235092690	chr16	15818043	15818197	15818063	15818174	MYH11	NM_022844	4	42	31	-	15818018	15818266
235092690	chr16	15818043	15818197	15818063	15818174	MYH11	NM_002474	3	41	31	-	15818018	15818266
235092690	chr16	15818043	15818197	15818063	15818174	MYH11	NM_001040113	1	43	32	-	15818018	15818266
235092690	chr16	15818043	15818197	15818063	15818174	MYH11	NM_001040114	2	42	32	-	15818018	15818266
238728051	chr16	15818722	15818871	15818743	15818850	MYH11	NM_022844	4	42	29	-	15818745	15818849
238728051	chr16	15818722	15818871	15818743	15818850	MYH11	NM_002474	3	41	29	-	15818745	15818849

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238728051	chr16	15818722	15818871	15818743	15818850	MYH11	NM_001040113	1	43	30	-	15818745	15818849
238728051	chr16	15818722	15818871	15818743	15818850	MYH11	NM_001040114	2	42	30	-	15818745	15818849
235960673	chr16	15826362	15826533	15826384	15826512	MYH11	NM_022844	4	42	27	-	15826421	15826565
235960673	chr16	15826362	15826533	15826384	15826512	MYH11	NM_002474	3	41	27	-	15826421	15826565
235960673	chr16	15826362	15826533	15826384	15826512	MYH11	NM_001040113	1	43	28	-	15826421	15826565
235960673	chr16	15826362	15826533	15826384	15826512	MYH11	NM_001040114	2	42	28	-	15826421	15826565
236012826	chr16	15829354	15829526	15829375	15829502	MYH11	NM_022844	4	42	26	-	15829223	15829435
236012826	chr16	15829354	15829526	15829375	15829502	MYH11	NM_002474	3	41	26	-	15829223	15829435
236012826	chr16	15829354	15829526	15829375	15829502	MYH11	NM_001040113	1	43	27	-	15829223	15829435
236012826	chr16	15829354	15829526	15829375	15829502	MYH11	NM_001040114	2	42	27	-	15829223	15829435
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_022844	4	42	24	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_002474	3	41	24	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_001040113	1	43	25	-	15832422	15832545
235718920	chr16	15832414	15832563	15832441	15832539	MYH11	NM_001040114	2	42	25	-	15832422	15832545
235594750	chr16	15835300	15835473	15835319	15835451	MYH11	NM_022844	4	42	22	-	15835320	15835526
235594750	chr16	15835300	15835473	15835319	15835451	MYH11	NM_002474	3	41	22	-	15835320	15835526
235594750	chr16	15835300	15835473	15835319	15835451	MYH11	NM_001040113	1	43	23	-	15835320	15835526
235594750	chr16	15835300	15835473	15835319	15835451	MYH11	NM_001040114	2	42	23	-	15835320	15835526
236986781	chr16	15835613	15835787	15835634	15835763	MYH11	NM_022844	4	42	21	-	15835617	15835748
236986781	chr16	15835613	15835787	15835634	15835763	MYH11	NM_002474	3	41	21	-	15835617	15835748
236986781	chr16	15835613	15835787	15835634	15835763	MYH11	NM_001040113	1	43	22	-	15835617	15835748
236986781	chr16	15835613	15835787	15835634	15835763	MYH11	NM_001040114	2	42	22	-	15835617	15835748
235688412	chr16	15841458	15841616	15841479	15841593	MYH11	NM_022844	4	42	19	-	15841427	15841587
235688412	chr16	15841458	15841616	15841479	15841593	MYH11	NM_002474	3	41	19	-	15841427	15841587
235688412	chr16	15841458	15841616	15841479	15841593	MYH11	NM_001040113	1	43	20	-	15841427	15841587
235688412	chr16	15841458	15841616	15841479	15841593	MYH11	NM_001040114	2	42	20	-	15841427	15841587
238058943	chr16	15843990	15844163	15844010	15844143	MYH11	NM_022844	4	42	16	-	15843995	15844188
238058943	chr16	15843990	15844163	15844010	15844143	MYH11	NM_002474	3	41	16	-	15843995	15844188
238058943	chr16	15843990	15844163	15844010	15844143	MYH11	NM_001040113	1	43	17	-	15843995	15844188
238058943	chr16	15843990	15844163	15844010	15844143	MYH11	NM_001040114	2	42	17	-	15843995	15844188
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_022844	4	42	14	-	15850198	15850371
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_002474	3	41	14	-	15850198	15850371
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_001040113	1	43	15	-	15850198	15850371
239185226	chr16	15850109	15850238	15850131	15850214	MYH11	NM_001040114	2	42	15	-	15850198	15850371
237041724	chr16	15851753	15851920	15851771	15851897	MYH11	NM_022844	4	42	13	-	15851684	15851857
237041724	chr16	15851753	15851920	15851771	15851897	MYH11	NM_002474	3	41	13	-	15851684	15851857
237041724	chr16	15851753	15851920	15851771	15851897	MYH11	NM_001040113	1	43	14	-	15851684	15851857
237041724	chr16	15851753	15851920	15851771	15851897	MYH11	NM_001040114	2	42	14	-	15851684	15851857
237461314	chr16	15857617	15857791	15857644	15857768	MYH11	NM_022844	4	42	10	-	15857653	15857748
237461314	chr16	15857617	15857791	15857644	15857768	MYH11	NM_002474	3	41	10	-	15857653	15857748
237461314	chr16	15857617	15857791	15857644	15857768	MYH11	NM_001040113	1	43	11	-	15857653	15857748

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237461314	chr16	15857617	15857791	15857644	15857768	MYH11	NM_001040114	2	42	11	-	15857653	15857748
241656078	chr16	15872572	15872726	15872593	15872703	MYH11	NM_022844	4	42	7	-	15872637	15872700
241656078	chr16	15872572	15872726	15872593	15872703	MYH11	NM_002474	3	41	7	-	15872637	15872700
241656078	chr16	15872572	15872726	15872593	15872703	MYH11	NM_001040113	1	43	8	-	15872637	15872700
241656078	chr16	15872572	15872726	15872593	15872703	MYH11	NM_001040114	2	42	8	-	15872637	15872700
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_022844	4	42	4	-	15892517	15892544
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_002474	3	41	4	-	15892517	15892544
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_001040113	1	43	4	-	15892517	15892544
239276738	chr16	15892502	15892652	15892523	15892628	MYH11	NM_001040114	2	42	4	-	15892517	15892544
235107485	chr16	15931777	15931935	15931797	15931914	MYH11	NM_022844	4	42	2	-	15931765	15932126
235107485	chr16	15931777	15931935	15931797	15931914	MYH11	NM_002474	3	41	2	-	15931765	15932126
235107485	chr16	15931777	15931935	15931797	15931914	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235107485	chr16	15931777	15931935	15931797	15931914	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235975527	chr16	23614817	23614955	23614838	23614930	PALB2	NM_024675	1	13	13	-	23614483	23614990
238127121	chr16	23625300	23625458	23625321	23625429	PALB2	NM_024675	1	13	11	-	23625325	23625412
240212302	chr16	23635260	23635434	23635283	23635405	PALB2	NM_024675	1	13	8	-	23635330	23635415
238055908	chr16	23640486	23640660	23640510	23640637	PALB2	NM_024675	1	13	6	-	23640525	23640596
236586583	chr16	23641215	23641388	23641239	23641359	PALB2	NM_024675	1	13	5	-	23640961	23641790
239994214	chr16	23641673	23641847	23641701	23641818	PALB2	NM_024675	1	13	5	-	23640961	23641790
238268210	chr16	23646459	23646629	23646480	23646608	PALB2	NM_024675	1	13	4	-	23646183	23647655
235062549	chr16	23646851	23646979	23646879	23646951	PALB2	NM_024675	1	13	4	-	23646183	23647655
238231328	chr16	23647189	23647338	23647217	23647311	PALB2	NM_024675	1	13	4	-	23646183	23647655
237572719	chr16	23649142	23649293	23649167	23649270	PALB2	NM_024675	1	13	3	-	23649171	23649273
227410698	chr16	27414364	27414529	27414388	27414508	IL21R	NM_181079	3	10	2	+	27414401	27414541
228850312	chr16	27448783	27448938	27448802	27448917	IL21R	NM_181079	3	10	5	+	27448809	27449008
228850312	chr16	27448783	27448938	27448802	27448917	IL21R	NM_181078	2	9	4	+	27448809	27449008
228850312	chr16	27448783	27448938	27448802	27448917	IL21R	NM_021798	1	9	4	+	27448809	27449008
229414927	chr16	27455829	27455956	27455849	27455936	IL21R	NM_181079	3	10	7	+	27455863	27456040
229414927	chr16	27455829	27455956	27455849	27455936	IL21R	NM_181078	2	9	6	+	27455863	27456040
229414927	chr16	27455829	27455956	27455849	27455936	IL21R	NM_021798	1	9	6	+	27455863	27456040
227948622	chr16	27457284	27457443	27457304	27457424	IL21R	NM_181079	3	10	9	+	27457328	27457409
227948622	chr16	27457284	27457443	27457304	27457424	IL21R	NM_181078	2	9	8	+	27457328	27457409
227948622	chr16	27457284	27457443	27457304	27457424	IL21R	NM_021798	1	9	8	+	27457328	27457409
228964552	chr16	27460096	27460249	27460116	27460227	IL21R	NM_181079	3	10	10	+	27459855	27463363
228964552	chr16	27460096	27460249	27460116	27460227	IL21R	NM_181078	2	9	9	+	27459855	27463363
228964552	chr16	27460096	27460249	27460116	27460227	IL21R	NM_021798	1	9	9	+	27459855	27463363
228967394	chr16	27460550	27460696	27460570	27460675	IL21R	NM_181079	3	10	10	+	27459855	27463363
228967394	chr16	27460550	27460696	27460570	27460675	IL21R	NM_181078	2	9	9	+	27459855	27463363
228967394	chr16	27460550	27460696	27460570	27460675	IL21R	NM_021798	1	9	9	+	27459855	27463363
225430388	chr16	50783796	50783952	50783824	50783927	CYLD	NM_015247	3	20	4	+	50783487	50784113
225430388	chr16	50783796	50783952	50783824	50783927	CYLD	NM_001042355	1	18	3	+	50783487	50784113

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225430388	chr16	50783796	50783952	50783824	50783927	CYLD	NM_001042412	2	18	3	+	50783487	50784113
226588389	chr16	50785451	50785621	50785474	50785597	CYLD	NM_015247	3	20	5	+	50785515	50785817
226588389	chr16	50785451	50785621	50785474	50785597	CYLD	NM_001042355	1	18	4	+	50785515	50785817
226588389	chr16	50785451	50785621	50785474	50785597	CYLD	NM_001042412	2	18	4	+	50785515	50785817
225491507	chr16	50811792	50811966	50811815	50811939	CYLD	NM_015247	3	20	9	+	50811736	50811852
225491507	chr16	50811792	50811966	50811815	50811939	CYLD	NM_001042355	1	18	7	+	50811736	50811852
225491507	chr16	50811792	50811966	50811815	50811939	CYLD	NM_001042412	2	18	7	+	50811736	50811852
226588885	chr16	50813838	50814010	50813860	50813985	CYLD	NM_015247	3	20	10	+	50813576	50813955
226588885	chr16	50813838	50814010	50813860	50813985	CYLD	NM_001042355	1	18	8	+	50813576	50813955
226588885	chr16	50813838	50814010	50813860	50813985	CYLD	NM_001042412	2	18	8	+	50813576	50813955
225937169	chr16	50816226	50816350	50816251	50816326	CYLD	NM_015247	3	20	12	+	50816236	50816377
225937169	chr16	50816226	50816350	50816251	50816326	CYLD	NM_001042355	1	18	10	+	50816236	50816377
225937169	chr16	50816226	50816350	50816251	50816326	CYLD	NM_001042412	2	18	10	+	50816236	50816377
225736284	chr16	50818266	50818421	50818294	50818394	CYLD	NM_015247	3	20	13	+	50818240	50818362
225736284	chr16	50818266	50818421	50818294	50818394	CYLD	NM_001042355	1	18	11	+	50818240	50818362
225736284	chr16	50818266	50818421	50818294	50818394	CYLD	NM_001042412	2	18	11	+	50818240	50818362
225687463	chr16	50825473	50825646	50825501	50825618	CYLD	NM_015247	3	20	16	+	50825469	50825601
225687463	chr16	50825473	50825646	50825501	50825618	CYLD	NM_001042355	1	18	14	+	50825469	50825601
225687463	chr16	50825473	50825646	50825501	50825618	CYLD	NM_001042412	2	18	14	+	50825469	50825601
227037238	chr16	50828089	50828252	50828114	50828228	CYLD	NM_015247	3	20	19	+	50828123	50828339
227037238	chr16	50828089	50828252	50828114	50828228	CYLD	NM_001042355	1	18	17	+	50828123	50828339
227037238	chr16	50828089	50828252	50828114	50828228	CYLD	NM_001042412	2	18	17	+	50828123	50828339
292989818	chr16	55513377	55513542	55513395	55513520	MMP2	NM_004530	2	13	1	+	55513081	55513544
289244495	chr16	55516992	55517159	55517015	55517136	MMP2	NM_001127891	1	13	2	+	55516821	55517047
289244495	chr16	55516992	55517159	55517015	55517136	MMP2	NM_004530	2	13	2	+	55516821	55517047
290299138	chr16	55519287	55519448	55519309	55519426	MMP2	NM_001127891	1	13	4	+	55519211	55519339
290299138	chr16	55519287	55519448	55519309	55519426	MMP2	NM_004530	2	13	4	+	55519211	55519339
292512802	chr16	55522482	55522622	55522502	55522600	MMP2	NM_001127891	1	13	6	+	55522455	55522628
292512802	chr16	55522482	55522622	55522502	55522600	MMP2	NM_004530	2	13	6	+	55522455	55522628
290978553	chr16	55525656	55525828	55525682	55525806	MMP2	NM_001127891	1	13	8	+	55525713	55525868
290978553	chr16	55525656	55525828	55525682	55525806	MMP2	NM_004530	2	13	8	+	55525713	55525868
293210964	chr16	55530786	55530943	55530807	55530923	MMP2	NM_001127891	1	13	10	+	55530838	55530974
293210964	chr16	55530786	55530943	55530807	55530923	MMP2	NM_004530	2	13	10	+	55530838	55530974
291835844	chr16	55536660	55536833	55536681	55536811	MMP2	NM_001127891	1	13	12	+	55536691	55536800
291835844	chr16	55536660	55536833	55536681	55536811	MMP2	NM_004530	2	13	12	+	55536691	55536800
226967918	chr16	64981564	64981697	64981586	64981672	CDH11	NM_001797	1	13	13	-	64980683	64982002
226573464	chr16	64984585	64984759	64984609	64984741	CDH11	NM_001797	1	13	12	-	64984670	64984921
226463941	chr16	65005467	65005635	65005492	65005609	CDH11	NM_001797	1	13	11	-	65005482	65005599
225340594	chr16	65006848	65006991	65006876	65006968	CDH11	NM_001797	1	13	9	-	65006807	65006943
225596379	chr16	65021947	65022120	65021969	65022096	CDH11	NM_001797	1	13	7	-	65022060	65022247
225914479	chr16	65025704	65025863	65025725	65025841	CDH11	NM_001797	1	13	6	-	65025671	65025838

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
253667298	chr16	65032492	65032662	65032513	65032640	CDH11	NM_001797	1	13	4	-	65032465	65032759
225410451	chr16	65038620	65038794	65038637	65038773	CDH11	NM_001797	1	13	3	-	65038545	65038944
270821157	chr16	66420821	66420969	66420841	66420949	CDH5	NM_001795	1	12	3	+	66420712	66421000
270057810	chr16	66423321	66423494	66423339	66423475	CDH5	NM_001795	1	12	5	+	66423261	66423425
270138168	chr16	66426096	66426244	66426118	66426222	CDH5	NM_001795	1	12	7	+	66426039	66426286
272033280	chr16	66431769	66431940	66431790	66431913	CDH5	NM_001795	1	12	9	+	66431885	66432009
271424978	chr16	66434733	66434899	66434754	66434877	CDH5	NM_001795	1	12	11	+	66434674	66434919
271656348	chr16	66436755	66436925	66436773	66436907	CDH5	NM_001795	1	12	12	+	66436555	66438689
226420836	chr16	68772151	68772301	68772169	68772284	CDH1	NM_004360	1	16	2	+	68772200	68772314
226339152	chr16	68835651	68835824	68835676	68835796	CDH1	NM_004360	1	16	3	+	68835573	68835796
227056752	chr16	68842660	68842790	68842681	68842769	CDH1	NM_004360	1	16	5	+	68842596	68842751
225360840	chr16	68845655	68845823	68845677	68845797	CDH1	NM_004360	1	16	7	+	68845587	68845762
226237097	chr16	68847275	68847444	68847296	68847423	CDH1	NM_004360	1	16	9	+	68847216	68847398
225763808	chr16	68853146	68853312	68853171	68853291	CDH1	NM_004360	1	16	11	+	68853183	68853328
225507439	chr16	68855996	68856161	68856019	68856133	CDH1	NM_004360	1	16	12	+	68855904	68856128
226292480	chr16	68862073	68862238	68862095	68862213	CDH1	NM_004360	1	16	14	+	68862077	68862207
225388114	chr16	68867280	68867454	68867301	68867431	CDH1	NM_004360	1	16	16	+	68867193	68869444
232460433	chr16	79632715	79632857	79632735	79632836	MAF	NM_001031804	1	1	1	-	79627745	79634622
232460433	chr16	79632715	79632857	79632735	79632836	MAF	NM_005360	2	2	1	-	79632682	79634622
233797725	chr16	79633507	79633632	79633524	79633614	MAF	NM_001031804	1	1	1	-	79627745	79634622
233797725	chr16	79633507	79633632	79633524	79633614	MAF	NM_005360	2	2	1	-	79632682	79634622
228358514	chr16	89804878	89805047	89804903	89805029	FANCA	NM_000135	1	43	43	-	89803959	89805116
230584366	chr16	89805574	89805742	89805597	89805719	FANCA	NM_000135	1	43	41	-	89805541	89805697
228866715	chr16	89809133	89809268	89809156	89809243	FANCA	NM_000135	1	43	37	-	89809208	89809346
231484970	chr16	89812990	89813153	89813015	89813128	FANCA	NM_000135	1	43	35	-	89812992	89813096
230136099	chr16	89816209	89816336	89816228	89816314	FANCA	NM_000135	1	43	32	-	89816138	89816310
229832790	chr16	89828329	89828481	89828350	89828454	FANCA	NM_000135	1	43	29	-	89828357	89828430
228494752	chr16	89833482	89833633	89833500	89833605	FANCA	NM_000135	1	43	27	-	89833549	89833645
230712171	chr16	89836553	89836707	89836573	89836681	FANCA	NM_000135	1	43	25	-	89836574	89836667
230108947	chr16	89838113	89838247	89838134	89838223	FANCA	NM_000135	1	43	23	-	89838086	89838222
230799413	chr16	89845281	89845440	89845305	89845418	FANCA	NM_000135	1	43	19	-	89845351	89845411
228553361	chr16	89851220	89851383	89851242	89851365	FANCA	NM_000135	1	43	15	-	89851262	89851372
230591099	chr16	89858407	89858535	89858428	89858512	FANCA	NM_000135	1	43	13	-	89858335	89858476
232468843	chr16	89865362	89865530	89865383	89865502	FANCA	NM_001018112	2	11	11	-	89864767	89865487
229180702	chr16	89871658	89871829	89871679	89871808	FANCA	NM_000135	1	43	7	-	89871688	89871800
229180702	chr16	89871658	89871829	89871679	89871808	FANCA	NM_001018112	2	11	7	-	89871688	89871800
230343224	chr16	89877150	89877286	89877173	89877257	FANCA	NM_000135	1	43	5	-	89877115	89877210
230343224	chr16	89877150	89877286	89877173	89877257	FANCA	NM_001018112	2	11	5	-	89877115	89877210
227685428	chr16	89880935	89881074	89880963	89881052	FANCA	NM_000135	1	43	3	-	89880928	89881021
227685428	chr16	89880935	89881074	89880963	89881052	FANCA	NM_001018112	2	11	3	-	89880928	89881021
240340809	chr17	5418148	5418321	5418169	5418301	NLRP1	NM_014922	2	16	16	-	5417438	5418393

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240340809	chr17	5418148	5418321	5418169	5418301	NLRP1	NM_033007	5	15	15	-	5417438	5418393
240340809	chr17	5418148	5418321	5418169	5418301	NLRP1	NM_033006	4	16	16	-	5417438	5418393
240340809	chr17	5418148	5418321	5418169	5418301	NLRP1	NM_033004	3	17	17	-	5417438	5418393
241298434	chr17	5421131	5421263	5421151	5421238	NLRP1	NM_014922	2	16	14	-	5421066	5421207
241298434	chr17	5421131	5421263	5421151	5421238	NLRP1	NM_001033053	1	16	15	-	5421066	5421207
241298434	chr17	5421131	5421263	5421151	5421238	NLRP1	NM_033007	5	15	13	-	5421066	5421207
241298434	chr17	5421131	5421263	5421151	5421238	NLRP1	NM_033006	4	16	14	-	5421066	5421207
241298434	chr17	5421131	5421263	5421151	5421238	NLRP1	NM_033004	3	17	15	-	5421066	5421207
236763350	chr17	5424844	5425015	5424865	5424991	NLRP1	NM_014922	2	16	13	-	5424844	5425106
236763350	chr17	5424844	5425015	5424865	5424991	NLRP1	NM_001033053	1	16	13	-	5424844	5425106
236763350	chr17	5424844	5425015	5424865	5424991	NLRP1	NM_033007	5	15	12	-	5424844	5425106
236763350	chr17	5424844	5425015	5424865	5424991	NLRP1	NM_033006	4	16	12	-	5424844	5425106
236763350	chr17	5424844	5425015	5424865	5424991	NLRP1	NM_033004	3	17	13	-	5424844	5425106
235074202	chr17	5436028	5436185	5436049	5436163	NLRP1	NM_014922	2	16	11	-	5436142	5436304
235074202	chr17	5436028	5436185	5436049	5436163	NLRP1	NM_001033053	1	16	11	-	5436142	5436304
235074202	chr17	5436028	5436185	5436049	5436163	NLRP1	NM_033007	5	15	10	-	5436142	5436304
235074202	chr17	5436028	5436185	5436049	5436163	NLRP1	NM_033006	4	16	10	-	5436142	5436304
235074202	chr17	5436028	5436185	5436049	5436163	NLRP1	NM_033004	3	17	11	-	5436142	5436304
236835983	chr17	5440137	5440281	5440157	5440261	NLRP1	NM_014922	2	16	8	-	5440171	5440260
236835983	chr17	5440137	5440281	5440157	5440261	NLRP1	NM_001033053	1	16	8	-	5440171	5440260
236835983	chr17	5440137	5440281	5440157	5440261	NLRP1	NM_033004	3	17	8	-	5440171	5440260
237958497	chr17	5445211	5445385	5445232	5445362	NLRP1	NM_014922	2	16	6	-	5445177	5445347
237958497	chr17	5445211	5445385	5445232	5445362	NLRP1	NM_001033053	1	16	6	-	5445177	5445347
237958497	chr17	5445211	5445385	5445232	5445362	NLRP1	NM_033007	5	15	6	-	5445177	5445347
237958497	chr17	5445211	5445385	5445232	5445362	NLRP1	NM_033006	4	16	6	-	5445177	5445347
237958497	chr17	5445211	5445385	5445232	5445362	NLRP1	NM_033004	3	17	6	-	5445177	5445347
257578711	chr17	5461723	5461882	5461743	5461862	NLRP1	NM_014922	2	16	4	-	5461659	5463363
257578711	chr17	5461723	5461882	5461743	5461862	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
257578711	chr17	5461723	5461882	5461743	5461862	NLRP1	NM_033007	5	15	4	-	5461659	5463363
257578711	chr17	5461723	5461882	5461743	5461862	NLRP1	NM_033006	4	16	4	-	5461659	5463363
257578711	chr17	5461723	5461882	5461743	5461862	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237478406	chr17	5462222	5462392	5462243	5462370	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237478406	chr17	5462222	5462392	5462243	5462370	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237478406	chr17	5462222	5462392	5462243	5462370	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237478406	chr17	5462222	5462392	5462243	5462370	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237478406	chr17	5462222	5462392	5462243	5462370	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237700511	chr17	5462636	5462802	5462654	5462779	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237700511	chr17	5462636	5462802	5462654	5462779	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237700511	chr17	5462636	5462802	5462654	5462779	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237700511	chr17	5462636	5462802	5462654	5462779	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237700511	chr17	5462636	5462802	5462654	5462779	NLRP1	NM_033004	3	17	4	-	5461659	5463363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237679676	chr17	5463101	5463256	5463123	5463236	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237679676	chr17	5463101	5463256	5463123	5463236	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237679676	chr17	5463101	5463256	5463123	5463236	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237679676	chr17	5463101	5463256	5463123	5463236	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237679676	chr17	5463101	5463256	5463123	5463236	NLRP1	NM_033004	3	17	4	-	5461659	5463363
238251442	chr17	5485931	5486103	5485951	5486083	NLRP1	NM_014922	2	16	2	-	5485990	5486166
238251442	chr17	5485931	5486103	5485951	5486083	NLRP1	NM_001033053	1	16	2	-	5485990	5486166
238251442	chr17	5485931	5486103	5485951	5486083	NLRP1	NM_033007	5	15	2	-	5485990	5486166
238251442	chr17	5485931	5486103	5485951	5486083	NLRP1	NM_033006	4	16	2	-	5485990	5486166
238251442	chr17	5485931	5486103	5485951	5486083	NLRP1	NM_033004	3	17	2	-	5485990	5486166
235935639	chr17	5487205	5487350	5487227	5487328	NLRP1	NM_014922	2	16	1	-	5487007	5487832
235935639	chr17	5487205	5487350	5487227	5487328	NLRP1	NM_001033053	1	16	1	-	5487007	5487832
235935639	chr17	5487205	5487350	5487227	5487328	NLRP1	NM_033007	5	15	1	-	5487007	5487832
235935639	chr17	5487205	5487350	5487227	5487328	NLRP1	NM_033006	4	16	1	-	5487007	5487832
235935639	chr17	5487205	5487350	5487227	5487328	NLRP1	NM_033004	3	17	1	-	5487007	5487832
239556324	chr17	7576581	7576709	7576607	7576680	TP53	NM_001126116	6	8	6	-	7576525	7576657
239556324	chr17	7576581	7576709	7576607	7576680	TP53	NM_001126114	4	12	10	-	7576525	7576657
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126117	7	8	3	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126116	6	8	3	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126113	3	12	7	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_000546	1	11	7	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126118	8	10	6	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126114	4	12	7	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126112	2	11	7	-	7577499	7577608
261728092	chr17	7577372	7577532	7577393	7577509	TP53	NM_001126115	5	7	3	-	7577499	7577608
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126113	3	12	5	-	7578371	7578554
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_000546	1	11	5	-	7578371	7578554
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126118	8	10	4	-	7578371	7578554
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126114	4	12	5	-	7578371	7578554
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126112	2	11	5	-	7578371	7578554
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126117	7	8	1	-	7578371	7578811
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126116	6	8	1	-	7578371	7578811
262578967	chr17	7578283	7578450	7578305	7578428	TP53	NM_001126115	5	7	1	-	7578371	7578811
263779137	chr17	7579489	7579623	7579512	7579601	TP53	NM_001126113	3	12	4	-	7579312	7579590
263779137	chr17	7579489	7579623	7579512	7579601	TP53	NM_000546	1	11	4	-	7579312	7579590
263779137	chr17	7579489	7579623	7579512	7579601	TP53	NM_001126118	8	10	3	-	7579312	7579590
263779137	chr17	7579489	7579623	7579512	7579601	TP53	NM_001126114	4	12	4	-	7579312	7579590
263779137	chr17	7579489	7579623	7579512	7579601	TP53	NM_001126112	2	11	4	-	7579312	7579590
239261820	chr17	8044437	8044602	8044459	8044580	PER1	NM_002616	1	23	23	-	8043788	8044658
240574194	chr17	8045520	8045680	8045543	8045657	PER1	NM_002616	1	23	21	-	8045587	8045776
237920522	chr17	8046570	8046721	8046588	8046701	PER1	NM_002616	1	23	19	-	8046584	8047194

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237933219	chr17	8046872	8047028	8046896	8047010	PER1	NM_002616	1	23	19	-	8046584	8047194
237541503	chr17	8048084	8048221	8048104	8048204	PER1	NM_002616	1	23	18	-	8048069	8048311
236838687	chr17	8049667	8049821	8049689	8049801	PER1	NM_002616	1	23	16	-	8049690	8049820
236927713	chr17	8050179	8050351	8050202	8050331	PER1	NM_002616	1	23	14	-	8050215	8050320
236941231	chr17	8050866	8051031	8050887	8051011	PER1	NM_002616	1	23	12	-	8050788	8050896
236941231	chr17	8050866	8051031	8050887	8051011	PER1	NM_002616	1	23	11	-	8050992	8051145
239398075	chr17	8051299	8051449	8051320	8051429	PER1	NM_002616	1	23	10	-	8051315	8051421
237808863	chr17	8052544	8052697	8052565	8052674	PER1	NM_002616	1	23	7	-	8052577	8052628
237390027	chr17	8053006	8053133	8053029	8053111	PER1	NM_002616	1	23	5	-	8053073	8053194
235828506	chr17	8053466	8053634	8053494	8053613	PER1	NM_002616	1	23	3	-	8053537	8053635
236705068	chr17	8053954	8054122	8053975	8054101	PER1	NM_002616	1	23	2	-	8053750	8054163
272120561	chr17	8108536	8108677	8108554	8108656	AURKB	NM_004217	1	9	8	-	8108534	8108708
270119273	chr17	8109996	8110165	8110016	8110137	AURKB	NM_004217	1	9	6	-	8110068	8110206
269881635	chr17	8110574	8110740	8110595	8110713	AURKB	NM_004217	1	9	5	-	8110494	8110685
270885146	chr17	8113483	8113647	8113502	8113630	AURKB	NM_004217	1	9	2	-	8113495	8113567
230924464	chr17	11984550	11984724	11984576	11984698	MAP2K4	NM_003010	1	11	3	+	11984673	11984847
231246891	chr17	11998899	11999073	11998927	11999047	MAP2K4	NM_003010	1	11	4	+	11998892	11999011
233416676	chr17	12013690	12013831	12013718	12013802	MAP2K4	NM_003010	1	11	6	+	12013692	12013743
232225997	chr17	12032402	12032556	12032426	12032534	MAP2K4	NM_003010	1	11	9	+	12032456	12032604
234223086	chr17	12044368	12044532	12044391	12044506	MAP2K4	NM_003010	1	11	11	+	12044464	12047051
228701017	chr17	17118230	17118390	17118254	17118366	FLCN	NM_144997	2	14	13	-	17118299	17118404
229788422	chr17	17119612	17119784	17119635	17119764	FLCN	NM_144997	2	14	11	-	17119694	17119817
229337946	chr17	17122394	17122567	17122415	17122539	FLCN	NM_144997	2	14	9	-	17122333	17122523
227487033	chr17	17125779	17125942	17125805	17125920	FLCN	NM_144997	2	14	7	-	17125815	17125975
227487033	chr17	17125779	17125942	17125805	17125920	FLCN	NM_144606	1	8	7	-	17125815	17125975
227308615	chr17	17127386	17127553	17127408	17127532	FLCN	NM_144997	2	14	6	-	17127236	17127457
227308615	chr17	17127386	17127553	17127408	17127532	FLCN	NM_144606	1	8	6	-	17127236	17127457
227941325	chr17	17131273	17131435	17131293	17131416	FLCN	NM_144997	2	14	4	-	17131203	17131475
227941325	chr17	17131273	17131435	17131293	17131416	FLCN	NM_144606	1	8	4	-	17131203	17131475
237190476	chr17	29482907	29483071	29482934	29483045	NF1	NM_000267	1	57	2	+	29483001	29483144
237190476	chr17	29482907	29483071	29482934	29483045	NF1	NM_001128147	3	15	2	+	29483001	29483144
237190476	chr17	29482907	29483071	29482934	29483045	NF1	NM_001042492	2	58	2	+	29483001	29483144
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_000267	1	57	4	+	29490204	29490394
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_001128147	3	15	4	+	29490204	29490394
236487854	chr17	29490305	29490435	29490327	29490407	NF1	NM_001042492	2	58	4	+	29490204	29490394
238570345	chr17	29508762	29508936	29508790	29508909	NF1	NM_000267	1	57	7	+	29508728	29508803
238570345	chr17	29508762	29508936	29508790	29508909	NF1	NM_001128147	3	15	7	+	29508728	29508803
238570345	chr17	29508762	29508936	29508790	29508909	NF1	NM_001042492	2	58	7	+	29508728	29508803
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_000267	1	57	9	+	29527440	29527613
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_001128147	3	15	9	+	29527440	29527613
235101719	chr17	29527450	29527595	29527474	29527568	NF1	NM_001042492	2	58	9	+	29527440	29527613

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
258512573	chr17	29528057	29528192	29528084	29528167	NF1	NM_000267	1	57	10	+	29528055	29528177
258512573	chr17	29528057	29528192	29528084	29528167	NF1	NM_001128147	3	15	10	+	29528055	29528177
258512573	chr17	29528057	29528192	29528084	29528167	NF1	NM_001042492	2	58	10	+	29528055	29528177
236054430	chr17	29533131	29533305	29533157	29533280	NF1	NM_000267	1	57	12	+	29533258	29533389
236054430	chr17	29533131	29533305	29533157	29533280	NF1	NM_001128147	3	15	12	+	29533258	29533389
236054430	chr17	29533131	29533305	29533157	29533280	NF1	NM_001042492	2	58	12	+	29533258	29533389
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_000267	1	57	14	+	29546023	29546136
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_001128147	3	15	14	+	29546023	29546136
237168971	chr17	29546106	29546231	29546127	29546207	NF1	NM_001042492	2	58	14	+	29546023	29546136
237228343	chr17	29552118	29552292	29552146	29552265	NF1	NM_000267	1	57	17	+	29552113	29552268
237228343	chr17	29552118	29552292	29552146	29552265	NF1	NM_001042492	2	58	17	+	29552113	29552268
241790569	chr17	29554201	29554370	29554228	29554348	NF1	NM_000267	1	57	19	+	29554236	29554309
241790569	chr17	29554201	29554370	29554228	29554348	NF1	NM_001042492	2	58	19	+	29554236	29554309
236380415	chr17	29556138	29556301	29556161	29556278	NF1	NM_000267	1	57	21	+	29556043	29556483
236380415	chr17	29556138	29556301	29556161	29556278	NF1	NM_001042492	2	58	21	+	29556043	29556483
257904070	chr17	29556928	29557102	29556950	29557080	NF1	NM_000267	1	57	22	+	29556853	29556992
257904070	chr17	29556928	29557102	29556950	29557080	NF1	NM_001042492	2	58	22	+	29556853	29556992
236461297	chr17	29559024	29559196	29559051	29559171	NF1	NM_000267	1	57	25	+	29559091	29559207
236461297	chr17	29559024	29559196	29559051	29559171	NF1	NM_001042492	2	58	25	+	29559091	29559207
236252415	chr17	29559833	29559959	29559854	29559933	NF1	NM_000267	1	57	26	+	29559718	29559899
236252415	chr17	29559833	29559959	29559854	29559933	NF1	NM_001042492	2	58	26	+	29559718	29559899
239172883	chr17	29562682	29562835	29562706	29562811	NF1	NM_000267	1	57	28	+	29562629	29562790
239172883	chr17	29562682	29562835	29562706	29562811	NF1	NM_001042492	2	58	28	+	29562629	29562790
242714492	chr17	29576008	29576136	29576029	29576112	NF1	NM_000267	1	57	30	+	29576002	29576137
242714492	chr17	29576008	29576136	29576029	29576112	NF1	NM_001042492	2	58	30	+	29576002	29576137
235373297	chr17	29585383	29585520	29585404	29585495	NF1	NM_000267	1	57	31	+	29585362	29585520
235373297	chr17	29585383	29585520	29585404	29585495	NF1	NM_001042492	2	58	32	+	29585362	29585520
235093374	chr17	29587340	29587513	29587368	29587488	NF1	NM_000267	1	57	33	+	29587387	29587533
235093374	chr17	29587340	29587513	29587368	29587488	NF1	NM_001042492	2	58	34	+	29587387	29587533
235389989	chr17	29592193	29592318	29592222	29592292	NF1	NM_000267	1	57	35	+	29592247	29592357
235389989	chr17	29592193	29592318	29592222	29592292	NF1	NM_001042492	2	58	36	+	29592247	29592357
239275849	chr17	29652913	29653067	29652941	29653046	NF1	NM_000267	1	57	36	+	29652838	29653270
239275849	chr17	29652913	29653067	29652941	29653046	NF1	NM_001042492	2	58	37	+	29652838	29653270
239800737	chr17	29654603	29654738	29654630	29654718	NF1	NM_000267	1	57	37	+	29654517	29654857
239800737	chr17	29654603	29654738	29654630	29654718	NF1	NM_001042492	2	58	38	+	29654517	29654857
242447158	chr17	29657290	29657418	29657318	29657393	NF1	NM_000267	1	57	38	+	29657314	29657516
242447158	chr17	29657290	29657418	29657318	29657393	NF1	NM_001042492	2	58	39	+	29657314	29657516
258378481	chr17	29661890	29662063	29661914	29662041	NF1	NM_000267	1	57	39	+	29661856	29662049
258378481	chr17	29661890	29662063	29661914	29662041	NF1	NM_001042492	2	58	40	+	29661856	29662049
240002093	chr17	29663591	29663762	29663616	29663735	NF1	NM_000267	1	57	41	+	29663653	29663932
240002093	chr17	29663591	29663762	29663616	29663735	NF1	NM_001042492	2	58	42	+	29663653	29663932

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239213121	chr17	29664413	29664543	29664441	29664521	NF1	NM_000267	1	57	42	+	29664386	29664600
239213121	chr17	29664413	29664543	29664441	29664521	NF1	NM_001042492	2	58	43	+	29664386	29664600
241493432	chr17	29665047	29665177	29665074	29665158	NF1	NM_000267	1	57	44	+	29665043	29665157
241493432	chr17	29665047	29665177	29665074	29665158	NF1	NM_001042492	2	58	45	+	29665043	29665157
235871506	chr17	29669978	29670152	29670003	29670126	NF1	NM_000267	1	57	47	+	29670027	29670153
235871506	chr17	29669978	29670152	29670003	29670126	NF1	NM_001042492	2	58	48	+	29670027	29670153
235997411	chr17	29676246	29676385	29676264	29676364	NF1	NM_000267	1	57	48	+	29676138	29676269
235997411	chr17	29676246	29676385	29676264	29676364	NF1	NM_001042492	2	58	49	+	29676138	29676269
237993791	chr17	29679302	29679437	29679324	29679411	NF1	NM_000267	1	57	50	+	29679275	29679432
237993791	chr17	29679302	29679437	29679324	29679411	NF1	NM_001042492	2	58	51	+	29679275	29679432
235940833	chr17	29683537	29683661	29683560	29683636	NF1	NM_000267	1	57	51	+	29683478	29683600
235940833	chr17	29683537	29683661	29683560	29683636	NF1	NM_001042492	2	58	52	+	29683478	29683600
241703952	chr17	29684280	29684424	29684303	29684396	NF1	NM_000267	1	57	53	+	29684287	29684387
241703952	chr17	29684280	29684424	29684303	29684396	NF1	NM_001042492	2	58	54	+	29684287	29684387
235180806	chr17	29687492	29687660	29687520	29687638	NF1	NM_000267	1	57	56	+	29687505	29687721
235180806	chr17	29687492	29687660	29687520	29687638	NF1	NM_001042492	2	58	57	+	29687505	29687721
274601735	chr17	37618266	37618432	37618286	37618411	CDK12	NM_016507	2	14	1	+	37617739	37619370
274601735	chr17	37618266	37618432	37618286	37618411	CDK12	NM_015083	1	14	1	+	37617739	37619370
274621561	chr17	37618681	37618839	37618707	37618819	CDK12	NM_016507	2	14	1	+	37617739	37619370
274621561	chr17	37618681	37618839	37618707	37618819	CDK12	NM_015083	1	14	1	+	37617739	37619370
274610484	chr17	37619146	37619293	37619167	37619274	CDK12	NM_016507	2	14	1	+	37617739	37619370
274610484	chr17	37619146	37619293	37619167	37619274	CDK12	NM_015083	1	14	1	+	37617739	37619370
274413847	chr17	37627319	37627457	37627342	37627431	CDK12	NM_016507	2	14	2	+	37627132	37628016
274413847	chr17	37627319	37627457	37627342	37627431	CDK12	NM_015083	1	14	2	+	37627132	37628016
273512363	chr17	37627707	37627873	37627728	37627850	CDK12	NM_016507	2	14	2	+	37627132	37628016
273512363	chr17	37627707	37627873	37627728	37627850	CDK12	NM_015083	1	14	2	+	37627132	37628016
273621770	chr17	37646852	37647013	37646873	37646986	CDK12	NM_016507	2	14	3	+	37646810	37646986
273621770	chr17	37646852	37647013	37646873	37646986	CDK12	NM_015083	1	14	3	+	37646810	37646986
274467186	chr17	37650811	37650985	37650834	37650957	CDK12	NM_016507	2	14	5	+	37650777	37650947
274467186	chr17	37650811	37650985	37650834	37650957	CDK12	NM_015083	1	14	5	+	37650777	37650947
272809088	chr17	37665875	37666022	37665896	37665994	CDK12	NM_016507	2	14	7	+	37665958	37666014
272809088	chr17	37665875	37666022	37665896	37665994	CDK12	NM_015083	1	14	7	+	37665958	37666014
273223261	chr17	37671995	37672121	37672018	37672094	CDK12	NM_016507	2	14	9	+	37671984	37672061
273223261	chr17	37671995	37672121	37672018	37672094	CDK12	NM_015083	1	14	9	+	37671984	37672061
273049182	chr17	37680876	37681050	37680899	37681025	CDK12	NM_016507	2	14	12	+	37680927	37681138
273049182	chr17	37680876	37681050	37680899	37681025	CDK12	NM_015083	1	14	12	+	37680927	37681138
273936388	chr17	37682297	37682470	37682317	37682446	CDK12	NM_016507	2	14	13	+	37682117	37682569
273936388	chr17	37682297	37682470	37682317	37682446	CDK12	NM_015083	1	14	13	+	37682117	37682569
274036071	chr17	37686970	37687134	37686989	37687112	CDK12	NM_016507	2	14	14	+	37686857	37690800
274036071	chr17	37686970	37687134	37686989	37687112	CDK12	NM_015083	1	14	14	+	37686884	37690800
274053221	chr17	37687478	37687603	37687501	37687576	CDK12	NM_016507	2	14	14	+	37686857	37690800

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274053221	chr17	37687478	37687603	37687501	37687576	CDK12	NM_015083	1	14	14	+	37686884	37690800
298910341	chr17	37829382	37829552	37829401	37829531	PGAP3	NM_033419	1	8	7	-	37829304	37829508
299226761	chr17	37830777	37830941	37830798	37830919	PGAP3	NM_033419	1	8	4	-	37830870	37830932
299172421	chr17	37842131	37842304	37842154	37842283	PGAP3	NM_033419	1	8	2	-	37842175	37842272
232410644	chr17	37856521	37856680	37856539	37856660	ERBB2	NM_004448	2	27	1	+	37856254	37856564
229727395	chr17	37864665	37864837	37864688	37864812	ERBB2	NM_004448	2	27	3	+	37864574	37864787
229727395	chr17	37864665	37864837	37864688	37864812	ERBB2	NM_001005862	1	30	6	+	37864574	37864787
228631538	chr17	37866320	37866490	37866337	37866468	ERBB2	NM_004448	2	27	6	+	37866339	37866454
228631538	chr17	37866320	37866490	37866337	37866468	ERBB2	NM_001005862	1	30	9	+	37866339	37866454
230702380	chr17	37868237	37868399	37868259	37868376	ERBB2	NM_004448	2	27	8	+	37868181	37868300
230702380	chr17	37868237	37868399	37868259	37868376	ERBB2	NM_001005862	1	30	11	+	37868181	37868300
228410883	chr17	37871571	37871721	37871592	37871695	ERBB2	NM_004448	2	27	10	+	37871539	37871612
228410883	chr17	37871571	37871721	37871592	37871695	ERBB2	NM_001005862	1	30	13	+	37871539	37871612
228153452	chr17	37872531	37872705	37872550	37872686	ERBB2	NM_004448	2	27	13	+	37872554	37872686
228153452	chr17	37872531	37872705	37872550	37872686	ERBB2	NM_001005862	1	30	16	+	37872554	37872686
230680850	chr17	37875977	37876128	37875998	37876105	ERBB2	NM_004448	2	27	16	+	37876040	37876087
230680850	chr17	37875977	37876128	37875998	37876105	ERBB2	NM_001005862	1	30	19	+	37876040	37876087
229251007	chr17	37879795	37879930	37879813	37879913	ERBB2	NM_004448	2	27	18	+	37879791	37879913
229251007	chr17	37879795	37879930	37879813	37879913	ERBB2	NM_001005862	1	30	21	+	37879791	37879913
230479056	chr17	37881270	37881398	37881292	37881372	ERBB2	NM_004448	2	27	21	+	37881302	37881457
230479056	chr17	37881270	37881398	37881292	37881372	ERBB2	NM_001005862	1	30	24	+	37881302	37881457
229958107	chr17	37881833	37881987	37881854	37881965	ERBB2	NM_004448	2	27	23	+	37881960	37882106
229958107	chr17	37881833	37881987	37881854	37881965	ERBB2	NM_001005862	1	30	26	+	37881960	37882106
232158699	chr17	37882839	37882998	37882859	37882974	ERBB2	NM_004448	2	27	24	+	37882815	37882912
232158699	chr17	37882839	37882998	37882859	37882974	ERBB2	NM_001005862	1	30	27	+	37882815	37882912
230196134	chr17	37883627	37883773	37883645	37883751	ERBB2	NM_004448	2	27	26	+	37883548	37883800
230196134	chr17	37883627	37883773	37883645	37883751	ERBB2	NM_001005862	1	30	29	+	37883548	37883800
231068532	chr17	37884172	37884336	37884193	37884315	ERBB2	NM_004448	2	27	27	+	37883942	37884915
231068532	chr17	37884172	37884336	37884193	37884315	ERBB2	NM_001005862	1	30	30	+	37883942	37884915
242742426	chr17	38498990	38499154	38499014	38499132	RARA	NM_001024809	2	8	1	+	38498271	38499119
261007968	chr17	38506078	38506244	38506098	38506220	RARA	NM_001145301	3	9	4	+	38506036	38506177
261007968	chr17	38506078	38506244	38506098	38506220	RARA	NM_000964	1	9	4	+	38506036	38506177
261007968	chr17	38506078	38506244	38506098	38506220	RARA	NM_001024809	2	8	3	+	38506036	38506177
242295437	chr17	38508640	38508814	38508662	38508793	RARA	NM_001145302	4	7	4	+	38508583	38508759
242295437	chr17	38508640	38508814	38508662	38508793	RARA	NM_001145301	3	9	6	+	38508583	38508759
242295437	chr17	38508640	38508814	38508662	38508793	RARA	NM_000964	1	9	6	+	38508583	38508759
242295437	chr17	38508640	38508814	38508662	38508793	RARA	NM_001024809	2	8	5	+	38508583	38508759
263452725	chr17	38511616	38511772	38511640	38511750	RARA	NM_001145302	4	7	6	+	38511515	38511673
263452725	chr17	38511616	38511772	38511640	38511750	RARA	NM_001145301	3	9	8	+	38511515	38511673
263452725	chr17	38511616	38511772	38511640	38511750	RARA	NM_000964	1	9	8	+	38511515	38511673
263452725	chr17	38511616	38511772	38511640	38511750	RARA	NM_001024809	2	8	7	+	38511515	38511673

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232338668	chr17	41605960	41606134	41605981	41606112	ETV4	NM_001986	2	13	13	-	41605211	41606111
232338668	chr17	41605960	41606134	41605981	41606112	ETV4	NM_001079675	1	13	13	-	41605211	41606111
232157483	chr17	41607167	41607341	41607191	41607320	ETV4	NM_001986	2	13	10	-	41607252	41607320
232157483	chr17	41607167	41607341	41607191	41607320	ETV4	NM_001079675	1	13	10	-	41607252	41607320
229779601	chr17	41610165	41610334	41610190	41610311	ETV4	NM_001986	2	13	8	-	41610042	41610307
229779601	chr17	41610165	41610334	41610190	41610311	ETV4	NM_001079675	1	13	8	-	41610042	41610307
228708504	chr17	41611316	41611449	41611338	41611430	ETV4	NM_001986	2	13	6	-	41611227	41611353
228708504	chr17	41611316	41611449	41611338	41611430	ETV4	NM_001079675	1	13	6	-	41611227	41611353
230670910	chr17	41622800	41622966	41622818	41622946	ETV4	NM_001986	2	13	2	-	41622926	41623036
230670910	chr17	41622800	41622966	41622818	41622946	ETV4	NM_001079675	1	13	2	-	41622926	41623036
278747148	chr17	45360657	45360825	45360679	45360804	ITGB3	NM_000212	1	15	3	+	45360720	45360915
278095106	chr17	45361964	45362138	45361984	45362112	ITGB3	NM_000212	1	15	4	+	45361809	45362061
279902802	chr17	45364449	45364623	45364472	45364602	ITGB3	NM_000212	1	15	6	+	45364436	45364597
278463573	chr17	45368223	45368393	45368245	45368370	ITGB3	NM_000212	1	15	9	+	45368320	45368454
279365051	chr17	45369725	45369896	45369746	45369875	ITGB3	NM_000212	1	15	10	+	45369505	45369934
279730978	chr17	45377798	45377971	45377820	45377944	ITGB3	NM_000212	1	15	12	+	45377844	45377944
278026270	chr17	45384913	45385065	45384935	45385042	ITGB3	NM_000212	1	15	14	+	45384837	45385003
226699202	chr17	48263039	48263212	48263059	48263191	COL1A1	NM_000088	1	51	50	-	48263139	48263381
225529821	chr17	48263734	48263907	48263759	48263885	COL1A1	NM_000088	1	51	49	-	48263678	48263868
226986838	chr17	48264307	48264461	48264328	48264439	COL1A1	NM_000088	1	51	47	-	48264376	48264483
253634254	chr17	48265275	48265442	48265297	48265421	COL1A1	NM_000088	1	51	45	-	48265237	48265344
253781762	chr17	48266221	48266395	48266239	48266373	COL1A1	NM_000088	1	51	41	-	48266264	48266371
253976729	chr17	48266759	48266930	48266778	48266909	COL1A1	NM_000088	1	51	39	-	48266738	48266899
226609731	chr17	48267405	48267577	48267424	48267556	COL1A1	NM_000088	1	51	36	-	48267362	48267469
225779016	chr17	48268240	48268379	48268261	48268359	COL1A1	NM_000088	1	51	33	-	48268178	48268285
225655358	chr17	48269269	48269422	48269291	48269399	COL1A1	NM_000088	1	51	30	-	48269341	48269385
226282930	chr17	48270326	48270481	48270349	48270460	COL1A1	NM_000088	1	51	26	-	48270355	48270408
225661337	chr17	48271746	48271893	48271768	48271870	COL1A1	NM_000088	1	51	23	-	48271710	48271808
225766972	chr17	48272323	48272494	48272345	48272471	COL1A1	NM_000088	1	51	20	-	48272408	48272461
225417180	chr17	48273221	48273363	48273242	48273338	COL1A1	NM_000088	1	51	16	-	48273284	48273337
329218262	chr17	48273882	48274056	48273908	48274031	COL1A1	NM_000088	1	51	12	-	48273978	48274031
225678370	chr17	48275235	48275400	48275256	48275372	COL1A1	NM_000088	1	51	8	-	48275310	48275363
225644652	chr17	48276759	48276916	48276777	48276892	COL1A1	NM_000088	1	51	4	-	48276779	48276814
226083770	chr17	48278731	48278905	48278758	48278877	COL1A1	NM_000088	1	51	1	-	48278772	48279000
227379339	chr17	53345192	53345317	53345213	53345296	HLF	NM_002126	1	4	2	+	53345112	53345447
229428303	chr17	53392676	53392841	53392698	53392817	HLF	NM_002126	1	4	3	+	53392588	53392808
223434462	chr17	59760597	59760758	59760627	59760731	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223438922	chr17	59760839	59760966	59760863	59760940	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223454192	chr17	59761211	59761346	59761237	59761326	BRIP1	NM_032043	1	20	20	-	59756547	59761501
222191878	chr17	59763201	59763368	59763228	59763340	BRIP1	NM_032043	1	20	19	-	59763197	59763526
222789744	chr17	59793181	59793344	59793208	59793322	BRIP1	NM_032043	1	20	17	-	59793312	59793424

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223192411	chr17	59821764	59821893	59821790	59821868	BRIP1	NM_032043	1	20	15	-	59821793	59821952
222418050	chr17	59853827	59853979	59853853	59853952	BRIP1	NM_032043	1	20	14	-	59853762	59853923
224704972	chr17	59861570	59861743	59861595	59861716	BRIP1	NM_032043	1	20	11	-	59861631	59861785
222616774	chr17	59876422	59876592	59876450	59876566	BRIP1	NM_032043	1	20	9	-	59876461	59876660
223948400	chr17	59878763	59878936	59878788	59878909	BRIP1	NM_032043	1	20	8	-	59878614	59878835
223689434	chr17	59886020	59886192	59886047	59886164	BRIP1	NM_032043	1	20	7	-	59885828	59886118
223399585	chr17	59934384	59934537	59934406	59934512	BRIP1	NM_032043	1	20	4	-	59934419	59934592
222484306	chr17	59938684	59938853	59938712	59938826	BRIP1	NM_032043	1	20	2	-	59938808	59938930
226147485	chr17	62006748	62006874	62006766	62006849	CD79B	NM_000626	1	6	5	-	62006794	62006835
226147485	chr17	62006748	62006874	62006766	62006849	CD79B	NM_021602	3	5	4	-	62006794	62006835
226147485	chr17	62006748	62006874	62006766	62006849	CD79B	NM_001039933	2	6	5	-	62006794	62006835
227071677	chr17	62007465	62007626	62007486	62007605	CD79B	NM_000626	1	6	3	-	62007434	62007745
227071677	chr17	62007465	62007626	62007486	62007605	CD79B	NM_001039933	2	6	3	-	62007434	62007745
253992510	chr17	62009535	62009693	62009554	62009670	CD79B	NM_000626	1	6	1	-	62009555	62009704
253992510	chr17	62009535	62009693	62009554	62009670	CD79B	NM_021602	3	5	1	-	62009555	62009704
253992510	chr17	62009535	62009693	62009554	62009670	CD79B	NM_001039933	2	6	1	-	62009555	62009704
237601541	chr17	66518831	66518997	66518854	66518976	PRKAR1A	NM_002734	1	11	3	+	66518897	66519067
237601541	chr17	66518831	66518997	66518854	66518976	PRKAR1A	NM_212472	3	11	3	+	66518897	66519067
237601541	chr17	66518831	66518997	66518854	66518976	PRKAR1A	NM_212471	2	11	3	+	66518897	66519067
239613030	chr17	66520091	66520250	66520119	66520225	PRKAR1A	NM_002734	1	11	5	+	66520157	66520218
239613030	chr17	66520091	66520250	66520119	66520225	PRKAR1A	NM_212472	3	11	5	+	66520157	66520218
239613030	chr17	66520091	66520250	66520119	66520225	PRKAR1A	NM_212471	2	11	5	+	66520157	66520218
237751853	chr17	66521873	66522024	66521899	66522001	PRKAR1A	NM_002734	1	11	7	+	66521895	66522053
237751853	chr17	66521873	66522024	66521899	66522001	PRKAR1A	NM_212472	3	11	7	+	66521895	66522053
237751853	chr17	66521873	66522024	66521899	66522001	PRKAR1A	NM_212471	2	11	7	+	66521895	66522053
235359975	chr17	66525049	66525221	66525070	66525194	PRKAR1A	NM_002734	1	11	9	+	66525011	66525132
235359975	chr17	66525049	66525221	66525070	66525194	PRKAR1A	NM_212472	3	11	9	+	66525011	66525132
235359975	chr17	66525049	66525221	66525070	66525194	PRKAR1A	NM_212471	2	11	9	+	66525011	66525132
242511159	chr17	75277574	75277703	75277591	75277685	SEPT9	NM_001113491	1	12	1	+	75277492	75277636
264697035	chr17	75398094	75398233	75398117	75398214	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264697035	chr17	75398094	75398233	75398117	75398214	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264697035	chr17	75398094	75398233	75398117	75398214	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264697035	chr17	75398094	75398233	75398117	75398214	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264697035	chr17	75398094	75398233	75398117	75398214	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
264725705	chr17	75398513	75398654	75398535	75398636	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264725705	chr17	75398513	75398654	75398535	75398636	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264725705	chr17	75398513	75398654	75398535	75398636	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264725705	chr17	75398513	75398654	75398535	75398636	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264725705	chr17	75398513	75398654	75398535	75398636	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
242678647	chr17	75471585	75471751	75471603	75471728	SEPT9	NM_001113495	5	10	1	+	75471325	75471985
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_006640	7	11	3	+	75478226	75478417

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113496	6	10	2	+	75478226	75478417
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113495	5	10	2	+	75478226	75478417
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113494	4	11	3	+	75478226	75478417
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113493	3	11	3	+	75478226	75478417
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113492	2	12	4	+	75478226	75478417
240850314	chr17	75478298	75478459	75478318	75478439	SEPT9	NM_001113491	1	12	4	+	75478226	75478417
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_006640	7	11	5	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113496	6	10	4	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113495	5	10	4	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113494	4	11	5	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113493	3	11	5	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113492	2	12	6	+	75484322	75484403
239447841	chr17	75484330	75484486	75484350	75484465	SEPT9	NM_001113491	1	12	6	+	75484322	75484403
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_006640	7	11	8	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113496	6	10	7	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113495	5	10	7	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113494	4	11	8	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113493	3	11	8	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113492	2	12	9	+	75488703	75488798
241880803	chr17	75488676	75488831	75488698	75488809	SEPT9	NM_001113491	1	12	9	+	75488703	75488798
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_006640	7	11	11	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113496	6	10	10	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113495	5	10	10	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113494	4	11	11	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113493	3	11	11	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113492	2	12	12	+	75494605	75496678
241897440	chr17	75494566	75494729	75494583	75494710	SEPT9	NM_001113491	1	12	12	+	75494605	75496678
294265105	chr17	76210722	76210891	76210740	76210870	BIRC5	NM_001168	3	4	2	+	76210761	76210870
294265105	chr17	76210722	76210891	76210740	76210870	BIRC5	NM_001012271	2	5	2	+	76210761	76210870
294265105	chr17	76210722	76210891	76210740	76210870	BIRC5	NM_001012270	1	3	2	+	76210761	76210870
293731390	chr17	76219625	76219790	76219645	76219763	BIRC5	NM_001168	3	4	4	+	76219546	76221716
293731390	chr17	76219625	76219790	76219645	76219763	BIRC5	NM_001012271	2	5	5	+	76219546	76221716
293731390	chr17	76219625	76219790	76219645	76219763	BIRC5	NM_001012270	1	3	3	+	76219546	76221716
241012687	chr17	78247140	78247272	78247163	78247250	RNF213	NM_020954	2	17	3	+	78247040	78247203
241012687	chr17	78247140	78247272	78247163	78247250	RNF213	NM_001256071	1	68	3	+	78247040	78247203
263737237	chr17	78261593	78261740	78261621	78261722	RNF213	NM_020954	2	17	4	+	78261614	78262162
263737237	chr17	78261593	78261740	78261621	78261722	RNF213	NM_001256071	1	68	4	+	78261614	78262162
263741475	chr17	78262031	78262184	78262052	78262163	RNF213	NM_020954	2	17	4	+	78261614	78262162
263741475	chr17	78262031	78262184	78262052	78262163	RNF213	NM_001256071	1	68	4	+	78261614	78262162
237891453	chr17	78263599	78263760	78263622	78263735	RNF213	NM_020954	2	17	6	+	78263458	78263636
237891453	chr17	78263599	78263760	78263622	78263735	RNF213	NM_001256071	1	68	6	+	78263458	78263636

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238537993	chr17	78265435	78265587	78265454	78265567	RNF213	NM_020954	2	17	8	+	78265427	78265626
238537993	chr17	78265435	78265587	78265454	78265567	RNF213	NM_001256071	1	68	8	+	78265427	78265626
241642285	chr17	78268681	78268822	78268703	78268802	RNF213	NM_020954	2	17	9	+	78268519	78268802
241642285	chr17	78268681	78268822	78268703	78268802	RNF213	NM_001256071	1	68	9	+	78268519	78268802
238964042	chr17	78272089	78272250	78272110	78272230	RNF213	NM_020954	2	17	11	+	78272121	78272318
238964042	chr17	78272089	78272250	78272110	78272230	RNF213	NM_001256071	1	68	11	+	78272121	78272318
238635218	chr17	78280852	78281024	78280877	78281002	RNF213	NM_020954	2	17	13	+	78280928	78281001
238635218	chr17	78280852	78281024	78280877	78281002	RNF213	NM_001256071	1	68	13	+	78280928	78281001
241779987	chr17	78286887	78287012	78286908	78286990	RNF213	NM_020954	2	17	15	+	78286812	78286967
241779987	chr17	78286887	78287012	78286908	78286990	RNF213	NM_001256071	1	68	15	+	78286812	78286967
263597230	chr17	78293135	78293302	78293154	78293280	RNF213	NM_020954	2	17	17	+	78292990	78295262
239905868	chr17	78301662	78301812	78301682	78301792	RNF213	NM_001256071	1	68	19	+	78301616	78301789
263948069	chr17	78305807	78305980	78305828	78305958	RNF213	NM_001256071	1	68	21	+	78305806	78306431
263944337	chr17	78306293	78306456	78306315	78306432	RNF213	NM_001256071	1	68	21	+	78305806	78306431
264504908	chr17	78310009	78310147	78310032	78310125	RNF213	NM_001256071	1	68	23	+	78309961	78310178
238245429	chr17	78311587	78311752	78311608	78311725	RNF213	NM_001256071	1	68	25	+	78311633	78311797
263900655	chr17	78313218	78313383	78313242	78313362	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263865234	chr17	78313700	78313873	78313721	78313852	RNF213	NM_001256071	1	68	26	+	78313001	78314156
240500662	chr17	78316931	78317086	78316955	78317065	RNF213	NM_001256071	1	68	27	+	78316932	78317125
238951854	chr17	78318364	78318527	78318389	78318501	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239128751	chr17	78318845	78319005	78318869	78318982	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239081515	chr17	78319316	78319446	78319338	78319424	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262377757	chr17	78319743	78319915	78319764	78319892	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239125173	chr17	78320256	78320425	78320276	78320403	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262312386	chr17	78320761	78320932	78320781	78320911	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262352475	chr17	78321176	78321342	78321198	78321321	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262379084	chr17	78321636	78321804	78321656	78321783	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239925003	chr17	78323515	78323688	78323538	78323666	RNF213	NM_001256071	1	68	30	+	78323570	78323706
242274751	chr17	78325376	78325533	78325396	78325507	RNF213	NM_001256071	1	68	32	+	78325485	78325603
241560149	chr17	78327793	78327962	78327813	78327941	RNF213	NM_001256071	1	68	35	+	78327819	78327966
241601785	chr17	78332061	78332190	78332081	78332168	RNF213	NM_001256071	1	68	37	+	78332088	78332279
239683680	chr17	78335414	78335587	78335436	78335567	RNF213	NM_001256071	1	68	39	+	78335534	78335688
242667489	chr17	78337020	78337178	78337044	78337157	RNF213	NM_001256071	1	68	40	+	78336902	78337114
242588044	chr17	78341511	78341679	78341532	78341656	RNF213	NM_001256071	1	68	43	+	78341548	78341648
238924827	chr17	78343211	78343370	78343237	78343350	RNF213	NM_001256071	1	68	45	+	78343302	78343471
240043600	chr17	78345750	78345899	78345777	78345871	RNF213	NM_001256071	1	68	47	+	78345674	78345785
239766976	chr17	78346746	78346905	78346765	78346886	RNF213	NM_001256071	1	68	49	+	78346775	78346965
238404187	chr17	78349579	78349718	78349598	78349691	RNF213	NM_001256071	1	68	51	+	78349560	78349670
260795918	chr17	78350629	78350787	78350650	78350763	RNF213	NM_001256071	1	68	53	+	78350682	78350763
264542583	chr17	78354716	78354842	78354738	78354818	RNF213	NM_001256071	1	68	56	+	78354631	78354787
263421752	chr17	78357367	78357529	78357389	78357501	RNF213	NM_001256071	1	68	59	+	78357477	78357728

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239653958	chr17	78358869	78359029	78358891	78359007	RNF213	NM_001256071	1	68	60	+	78358839	78358971
241954369	chr17	78360377	78360551	78360399	78360529	RNF213	NM_001256071	1	68	63	+	78360490	78360691
261505861	chr17	78362911	78363063	78362932	78363041	RNF213	NM_001256071	1	68	65	+	78362973	78363167
241446669	chr17	78363723	78363892	78363745	78363866	RNF213	NM_001256071	1	68	67	+	78363812	78363996
263179203	chr18	22669424	22669588	22669446	22669559	ZNF521	NM_015461	1	8	7	-	22669429	22669544
266319755	chr18	22775137	22775310	22775161	22775284	ZNF521	NM_015461	1	8	5	-	22775124	22775208
241282020	chr18	22804608	22804765	22804631	22804742	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265120495	chr18	22805035	22805195	22805057	22805169	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265096247	chr18	22805505	22805651	22805528	22805622	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265070203	chr18	22805951	22806123	22805979	22806099	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265026366	chr18	22806392	22806519	22806414	22806494	ZNF521	NM_015461	1	8	4	-	22804309	22807661
264991937	chr18	22806772	22806943	22806793	22806917	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241212885	chr18	22807256	22807430	22807277	22807407	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241443488	chr18	22902000	22902125	22902023	22902100	ZNF521	NM_015461	1	8	3	-	22901972	22902151
271818011	chr18	25532117	25532289	25532140	25532264	CDH2	NM_001792	1	16	16	-	25530930	25532323
272085265	chr18	25562787	25562938	25562812	25562913	CDH2	NM_001792	1	16	14	-	25562908	25563047
271598774	chr18	25565024	25565162	25565046	25565135	CDH2	NM_001792	1	16	13	-	25564964	25565197
270730652	chr18	25568382	25568549	25568408	25568521	CDH2	NM_001792	1	16	11	-	25568488	25568630
270540787	chr18	25570132	25570272	25570157	25570251	CDH2	NM_001792	1	16	10	-	25570061	25570314
270213657	chr18	25573399	25573573	25573423	25573551	CDH2	NM_001792	1	16	8	-	25573464	25573601
272184623	chr18	25583057	25583184	25583083	25583163	CDH2	NM_001792	1	16	7	-	25582961	25583133
271542150	chr18	25589650	25589807	25589676	25589786	CDH2	NM_001792	1	16	5	-	25589681	25589836
271845993	chr18	25593617	25593756	25593640	25593733	CDH2	NM_001792	1	16	3	-	25593647	25593873
269977533	chr18	25756962	25757105	25756979	25757087	CDH2	NM_001792	1	16	1	-	25756927	25757445
271188905	chr18	45371713	45371843	45371735	45371817	SMAD2	NM_005901	3	11	10	-	45371711	45371855
271188905	chr18	45371713	45371843	45371735	45371817	SMAD2	NM_001135937	2	10	9	-	45371711	45371855
271188905	chr18	45371713	45371843	45371735	45371817	SMAD2	NM_001003652	1	11	10	-	45371711	45371855
271222952	chr18	45374740	45374914	45374763	45374889	SMAD2	NM_005901	3	11	8	-	45374846	45375058
271222952	chr18	45374740	45374914	45374763	45374889	SMAD2	NM_001135937	2	10	7	-	45374846	45375058
271222952	chr18	45374740	45374914	45374763	45374889	SMAD2	NM_001003652	1	11	8	-	45374846	45375058
272646247	chr18	45377636	45377772	45377663	45377739	SMAD2	NM_005901	3	11	7	-	45377645	45377698
272646247	chr18	45377636	45377772	45377663	45377739	SMAD2	NM_001135937	2	10	6	-	45377645	45377698
272646247	chr18	45377636	45377772	45377663	45377739	SMAD2	NM_001003652	1	11	7	-	45377645	45377698
269822068	chr18	45394740	45394866	45394769	45394838	SMAD2	NM_005901	3	11	5	-	45394694	45394828
269822068	chr18	45394740	45394866	45394769	45394838	SMAD2	NM_001135937	2	10	4	-	45394694	45394828
269822068	chr18	45394740	45394866	45394769	45394838	SMAD2	NM_001003652	1	11	5	-	45394694	45394828
271282002	chr18	45396815	45396984	45396838	45396957	SMAD2	NM_005901	3	11	3	-	45396846	45396935
271282002	chr18	45396815	45396984	45396838	45396957	SMAD2	NM_001003652	1	11	3	-	45396846	45396935
312213134	chr18	47796343	47796487	47796371	47796460	MBD1	NM_001204142	7	14	14	-	47795216	47796455
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_015846	13	17	13	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204137	2	17	14	-	47799704	47799841

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204136	1	16	13	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_015844	11	16	12	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_015847	14	16	12	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204141	6	15	12	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204140	5	16	13	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204139	4	17	13	-	47799704	47799841
312396246	chr18	47799618	47799778	47799642	47799758	MBD1	NM_001204138	3	17	14	-	47799704	47799841
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204138	3	17	13	-	47799934	47800230
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_015846	13	17	12	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204137	2	17	13	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204136	1	16	12	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_015845	12	14	11	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_015844	11	16	11	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_015847	14	16	11	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204151	9	13	10	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_002384	10	15	11	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204142	7	14	12	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204141	6	15	11	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204140	5	16	12	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204139	4	17	12	-	47799934	47800233
312428072	chr18	47800105	47800275	47800126	47800254	MBD1	NM_001204143	8	14	11	-	47799934	47800233
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_015846	13	17	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204137	2	17	10	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204136	1	16	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_015845	12	14	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_015844	11	16	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_015847	14	16	8	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204151	9	13	8	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_002384	10	15	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204142	7	14	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204141	6	15	8	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204140	5	16	10	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204139	4	17	9	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204138	3	17	10	-	47801499	47801615
312237680	chr18	47801471	47801645	47801489	47801621	MBD1	NM_001204143	8	14	9	-	47801499	47801615
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_015846	13	17	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204137	2	17	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204136	1	16	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_015845	12	14	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_015844	11	16	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204151	9	13	6	-	47802205	47802351

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_002384	10	15	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204142	7	14	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204140	5	16	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204139	4	17	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204138	3	17	7	-	47802205	47802351
312359759	chr18	47802180	47802325	47802200	47802303	MBD1	NM_001204143	8	14	7	-	47802205	47802351
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_015846	13	17	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204137	2	17	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204136	1	16	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_015845	12	14	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_015844	11	16	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_015847	14	16	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204151	9	13	3	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_002384	10	15	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204142	7	14	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204141	6	15	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204140	5	16	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204139	4	17	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204138	3	17	4	-	47803202	47803368
312234934	chr18	47803155	47803310	47803176	47803290	MBD1	NM_001204143	8	14	4	-	47803202	47803368
242717481	chr18	48573329	48573503	48573357	48573479	SMAD4	NM_005359	1	12	2	+	48573290	48573665
261794479	chr18	48575169	48575334	48575197	48575306	SMAD4	NM_005359	1	12	3	+	48575056	48575230
240170708	chr18	48581289	48581414	48581309	48581386	SMAD4	NM_005359	1	12	5	+	48581151	48581363
239527302	chr18	48586112	48586267	48586143	48586247	SMAD4	NM_005359	1	12	8	+	48586236	48586286
326977563	chr18	48591888	48592059	48591910	48592030	SMAD4	NM_005359	1	12	9	+	48591793	48591976
326795490	chr18	48603091	48603233	48603110	48603207	SMAD4	NM_005359	1	12	11	+	48603008	48603146
286447630	chr18	49867207	49867364	49867229	49867343	DCC	NM_005215	1	29	1	+	49866542	49867248
286119614	chr18	50432358	50432502	50432386	50432482	DCC	NM_005215	1	29	3	+	50432414	50432698
288733490	chr18	50450109	50450239	50450136	50450211	DCC	NM_005215	1	29	4	+	50450077	50450227
286997961	chr18	50589671	50589813	50589691	50589789	DCC	NM_005215	1	29	6	+	50589675	50589829
287249694	chr18	50683760	50683911	50683782	50683884	DCC	NM_005215	1	29	8	+	50683726	50683882
288777734	chr18	50733923	50734087	50733945	50734058	DCC	NM_005215	1	29	11	+	50734049	50734187
286812957	chr18	50831861	50832035	50831888	50832009	DCC	NM_005215	1	29	13	+	50831948	50832089
286485654	chr18	50866017	50866166	50866036	50866144	DCC	NM_005215	1	29	15	+	50866083	50866277
287842482	chr18	50912407	50912542	50912435	50912511	DCC	NM_005215	1	29	16	+	50912413	50912508
287549443	chr18	50923556	50923730	50923579	50923708	DCC	NM_005215	1	29	18	+	50923678	50923816
287049349	chr18	50936848	50937004	50936875	50936979	DCC	NM_005215	1	29	20	+	50936822	50937016
287769724	chr18	50976770	50976944	50976795	50976922	DCC	NM_005215	1	29	23	+	50976870	50977032
287053482	chr18	50985750	50985914	50985772	50985886	DCC	NM_005215	1	29	24	+	50985602	50985828
286070103	chr18	51013284	51013419	51013304	51013391	DCC	NM_005215	1	29	26	+	51013167	51013328
287732541	chr18	51052885	51053050	51052913	51053028	DCC	NM_005215	1	29	28	+	51052987	51053129

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232263253	chr18	56338869	56339015	56338886	56338996	MALT1	NM_173844	2	16	1	+	56338618	56339084
232263253	chr18	56338869	56339015	56338886	56338996	MALT1	NM_006785	1	17	1	+	56338618	56339084
232891998	chr18	56363669	56363843	56363692	56363815	MALT1	NM_173844	2	16	3	+	56363598	56363719
232891998	chr18	56363669	56363843	56363692	56363815	MALT1	NM_006785	1	17	3	+	56363598	56363719
233261900	chr18	56376604	56376735	56376628	56376712	MALT1	NM_173844	2	16	5	+	56376610	56376788
233261900	chr18	56376604	56376735	56376628	56376712	MALT1	NM_006785	1	17	5	+	56376610	56376788
233407222	chr18	56378087	56378226	56378107	56378202	MALT1	NM_006785	1	17	7	+	56378153	56378185
232171580	chr18	56390280	56390414	56390301	56390389	MALT1	NM_173844	2	16	9	+	56390280	56390483
232171580	chr18	56390280	56390414	56390301	56390389	MALT1	NM_006785	1	17	10	+	56390280	56390483
233957514	chr18	56400687	56400861	56400713	56400833	MALT1	NM_173844	2	16	10	+	56400629	56400806
233957514	chr18	56400687	56400861	56400713	56400833	MALT1	NM_006785	1	17	11	+	56400629	56400806
233149583	chr18	56409105	56409229	56409128	56409204	MALT1	NM_173844	2	16	13	+	56409097	56409246
233149583	chr18	56409105	56409229	56409128	56409204	MALT1	NM_006785	1	17	14	+	56409097	56409246
232728927	chr18	56412791	56412965	56412819	56412941	MALT1	NM_173844	2	16	15	+	56412898	56413023
232728927	chr18	56412791	56412965	56412819	56412941	MALT1	NM_006785	1	17	16	+	56412898	56413023
232741167	chr18	56414762	56414931	56414787	56414906	MALT1	NM_173844	2	16	16	+	56414637	56417370
232741167	chr18	56414762	56414931	56414787	56414906	MALT1	NM_006785	1	17	17	+	56414637	56417370
271386316	chr18	59157766	59157937	59157788	59157916	CDH20	NM_031891	1	11	1	+	59157775	59158032
271948043	chr18	59166611	59166735	59166633	59166713	CDH20	NM_031891	1	11	2	+	59166419	59166713
271268426	chr18	59170205	59170379	59170228	59170356	CDH20	NM_031891	1	11	4	+	59170186	59170353
271418601	chr18	59195250	59195382	59195273	59195362	CDH20	NM_031891	1	11	6	+	59195200	59195453
269609519	chr18	59206158	59206323	59206182	59206295	CDH20	NM_031891	1	11	8	+	59206257	59206378
269699203	chr18	59217320	59217484	59217339	59217464	CDH20	NM_031891	1	11	10	+	59217211	59217462
272636468	chr18	59221746	59221895	59221767	59221876	CDH20	NM_031891	1	11	11	+	59221423	59222365
222767728	chr18	60985181	60985337	60985202	60985316	BCL2	NM_000633	1	3	2	-	60985315	60986185
222767728	chr18	60985181	60985337	60985202	60985316	BCL2	NM_000657	2	2	2	-	60985187	60986185
222787394	chr18	60985606	60985768	60985623	60985751	BCL2	NM_000633	1	3	2	-	60985315	60986185
222787394	chr18	60985606	60985768	60985623	60985751	BCL2	NM_000657	2	2	2	-	60985187	60986185
261827469	chr19	1207079	1207223	1207098	1207202	STK11	NM_000455	1	10	1	+	1205798	1207202
260241491	chr19	1219358	1219532	1219377	1219507	STK11	NM_000455	1	10	3	+	1219323	1219412
238616560	chr19	1220667	1220838	1220687	1220820	STK11	NM_000455	1	10	5	+	1220580	1220716
240507914	chr19	1221936	1222084	1221956	1222067	STK11	NM_000455	1	10	7	+	1221948	1222005
240469438	chr19	1226347	1226521	1226366	1226502	STK11	NM_000455	1	10	9	+	1226453	1226662
241358173	chr19	1611751	1611908	1611772	1611886	TCF3	NM_003200	2	19	19	-	1609289	1611848
241358173	chr19	1611751	1611908	1611772	1611886	TCF3	NM_001136139	1	19	18	-	1611703	1611848
240574628	chr19	1615153	1615323	1615173	1615302	TCF3	NM_003200	2	19	18	-	1615284	1615519
239426118	chr19	1619041	1619195	1619063	1619176	TCF3	NM_001136139	1	19	15	-	1619110	1619233
239426118	chr19	1619041	1619195	1619063	1619176	TCF3	NM_003200	2	19	16	-	1619110	1619233
241561944	chr19	1619445	1619604	1619467	1619584	TCF3	NM_001136139	1	19	14	-	1619315	1619473
241561944	chr19	1619445	1619604	1619467	1619584	TCF3	NM_003200	2	19	15	-	1619315	1619473
264178054	chr19	1621042	1621215	1621061	1621196	TCF3	NM_001136139	1	19	11	-	1621132	1621190

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264178054	chr19	1621042	1621215	1621061	1621196	TCF3	NM_003200	2	19	12	-	1621132	1621190
242044200	chr19	1622084	1622256	1622102	1622239	TCF3	NM_001136139	1	19	9	-	1622053	1622222
242044200	chr19	1622084	1622256	1622102	1622239	TCF3	NM_003200	2	19	10	-	1622053	1622222
240440308	chr19	1625497	1625662	1625517	1625645	TCF3	NM_001136139	1	19	6	-	1625575	1625707
240440308	chr19	1625497	1625662	1625517	1625645	TCF3	NM_003200	2	19	7	-	1625575	1625707
262437218	chr19	1632288	1632438	1632309	1632415	TCF3	NM_001136139	1	19	3	-	1632331	1632404
262437218	chr19	1632288	1632438	1632309	1632415	TCF3	NM_003200	2	19	4	-	1632331	1632404
239733908	chr19	1650173	1650343	1650194	1650322	TCF3	NM_001136139	1	19	1	-	1650176	1650286
239733908	chr19	1650173	1650343	1650194	1650322	TCF3	NM_003200	2	19	2	-	1650176	1650286
273016031	chr19	3113293	3113451	3113311	3113433	GNA11	NM_002067	1	7	3	+	3113328	3113482
272884529	chr19	3118855	3118986	3118876	3118964	GNA11	NM_002067	1	7	5	+	3118922	3119051
274409819	chr19	3120924	3121094	3120941	3121076	GNA11	NM_002067	1	7	7	+	3120987	3121454
299170618	chr19	3525825	3525997	3525844	3525974	FZR1	NM_016263	3	14	3	+	3525866	3525991
299170618	chr19	3525825	3525997	3525844	3525974	FZR1	NM_001136197	1	11	2	+	3525866	3525991
299170618	chr19	3525825	3525997	3525844	3525974	FZR1	NM_001136198	2	13	2	+	3525866	3525991
298928334	chr19	3526890	3527041	3526907	3527019	FZR1	NM_016263	3	14	6	+	3526978	3527060
298928334	chr19	3526890	3527041	3526907	3527019	FZR1	NM_001136198	2	13	5	+	3526978	3527060
299226830	chr19	3531688	3531855	3531706	3531837	FZR1	NM_016263	3	14	9	+	3531712	3531814
299226830	chr19	3531688	3531855	3531706	3531837	FZR1	NM_001136197	1	11	6	+	3531712	3531814
299226830	chr19	3531688	3531855	3531706	3531837	FZR1	NM_001136198	2	13	8	+	3531712	3531814
299040875	chr19	3532347	3532472	3532365	3532453	FZR1	NM_016263	3	14	11	+	3532415	3532648
299040875	chr19	3532347	3532472	3532365	3532453	FZR1	NM_001136197	1	11	8	+	3532415	3532648
299040875	chr19	3532347	3532472	3532365	3532453	FZR1	NM_001136198	2	13	10	+	3532415	3532648
298919420	chr19	3534398	3534541	3534417	3534523	FZR1	NM_016263	3	14	13	+	3534419	3534511
298919420	chr19	3534398	3534541	3534417	3534523	FZR1	NM_001136197	1	11	10	+	3534419	3534511
298919420	chr19	3534398	3534541	3534417	3534523	FZR1	NM_001136198	2	13	12	+	3534419	3534520
269467294	chr19	4095326	4095468	4095345	4095448	MAP2K2	NM_030662	1	11	9	-	4095386	4095447
271294055	chr19	4100930	4101057	4100947	4101038	MAP2K2	NM_030662	1	11	6	-	4101017	4101141
271932773	chr19	4102316	4102473	4102335	4102452	MAP2K2	NM_030662	1	11	4	-	4102374	4102451
269999378	chr19	4117405	4117562	4117423	4117542	MAP2K2	NM_030662	1	11	2	-	4117417	4117627
294205160	chr19	10597406	10597578	10597426	10597555	KEAP1	NM_012289	1	6	6	-	10596796	10597494
294205160	chr19	10597406	10597578	10597426	10597555	KEAP1	NM_203500	2	6	6	-	10596796	10597494
293876579	chr19	10600329	10600455	10600350	10600432	KEAP1	NM_012289	1	6	4	-	10600324	10600529
293876579	chr19	10600329	10600455	10600350	10600432	KEAP1	NM_203500	2	6	4	-	10600324	10600529
294565194	chr19	10602423	10602580	10602441	10602561	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294565194	chr19	10602423	10602580	10602441	10602561	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294676979	chr19	10602879	10603004	10602900	10602986	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294676979	chr19	10602879	10603004	10602900	10602986	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294883767	chr19	10610364	10610536	10610383	10610515	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294883767	chr19	10610364	10610536	10610383	10610515	KEAP1	NM_203500	2	6	2	-	10610071	10610756
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128845	2	33	1	+	11094828	11095049

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128847	4	33	1	+	11094828	11095049
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128846	3	33	1	+	11094828	11095049
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128848	5	33	1	+	11094828	11095049
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128844	1	36	3	+	11094797	11095049
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_003072	7	35	2	+	11094797	11095049
262127475	chr19	11094891	11095059	11094908	11095037	SMARCA4	NM_001128849	6	36	2	+	11094797	11095049
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128844	1	36	5	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_003072	7	35	4	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128845	2	33	3	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128849	6	36	4	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128847	4	33	3	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128846	3	33	3	+	11096865	11097269
260467679	chr19	11096798	11096957	11096821	11096939	SMARCA4	NM_001128848	5	33	3	+	11096865	11097269
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128844	1	36	6	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_003072	7	35	5	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128845	2	33	4	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128849	6	36	5	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128847	4	33	4	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128846	3	33	4	+	11097581	11097679
241352636	chr19	11097532	11097702	11097553	11097680	SMARCA4	NM_001128848	5	33	4	+	11097581	11097679
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128844	1	36	7	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_003072	7	35	6	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128845	2	33	5	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128849	6	36	6	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128847	4	33	5	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128846	3	33	5	+	11098342	11098600
240434396	chr19	11098561	11098705	11098580	11098685	SMARCA4	NM_001128848	5	33	5	+	11098342	11098600
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128844	1	36	9	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_003072	7	35	8	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128845	2	33	7	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128849	6	36	8	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128847	4	33	7	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128846	3	33	7	+	11101826	11101999
238391369	chr19	11101932	11102103	11101954	11102080	SMARCA4	NM_001128848	5	33	7	+	11101826	11101999
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128844	1	36	11	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_003072	7	35	10	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128845	2	33	9	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128849	6	36	10	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128847	4	33	9	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128846	3	33	9	+	11106889	11107056
242421295	chr19	11106947	11107115	11106967	11107097	SMARCA4	NM_001128848	5	33	9	+	11106889	11107056

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128844	1	36	14	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_003072	7	35	13	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128845	2	33	12	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128849	6	36	13	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128847	4	33	12	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128846	3	33	12	+	11114016	11114073
238024164	chr19	11113930	11114097	11113951	11114073	SMARCA4	NM_001128848	5	33	12	+	11114016	11114073
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128844	1	36	17	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_003072	7	35	16	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128845	2	33	15	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128849	6	36	16	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128847	4	33	15	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128846	3	33	15	+	11123625	11123788
241730990	chr19	11123539	11123677	11123561	11123656	SMARCA4	NM_001128848	5	33	15	+	11123625	11123788
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128844	1	36	20	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_003072	7	35	19	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128845	2	33	18	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128849	6	36	19	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128847	4	33	18	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128846	3	33	18	+	11132401	11132643
261054286	chr19	11132365	11132535	11132382	11132516	SMARCA4	NM_001128848	5	33	18	+	11132401	11132643
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128844	1	36	22	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_003072	7	35	21	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128845	2	33	20	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128849	6	36	21	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128847	4	33	20	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128846	3	33	20	+	11135007	11135114
241393260	chr19	11134977	11135111	11134998	11135090	SMARCA4	NM_001128848	5	33	20	+	11135007	11135114
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128844	1	36	25	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_003072	7	35	24	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128845	2	33	23	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128849	6	36	24	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128847	4	33	23	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128846	3	33	23	+	11138460	11138626
264306922	chr19	11138401	11138525	11138422	11138499	SMARCA4	NM_001128848	5	33	23	+	11138460	11138626
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128844	1	36	27	+	11143966	11144193
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_003072	7	35	26	+	11143966	11144193
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128845	2	33	25	+	11143966	11144193
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128849	6	36	26	+	11143966	11144193
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128847	4	33	25	+	11143966	11144193
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128846	3	33	25	+	11143966	11144193

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239985141	chr19	11143940	11144111	11143959	11144091	SMARCA4	NM_001128848	5	33	25	+	11143966	11144193
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128844	1	36	30	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_003072	7	35	29	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128845	2	33	27	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128849	6	36	29	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128847	4	33	27	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128846	3	33	27	+	11145590	11145808
238628352	chr19	11145661	11145828	11145679	11145809	SMARCA4	NM_001128848	5	33	27	+	11145590	11145808
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128846	3	33	29	+	11168934	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128848	5	33	29	+	11168934	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128844	1	36	32	+	11168931	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_003072	7	35	31	+	11168931	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128845	2	33	29	+	11168931	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128849	6	36	32	+	11168931	11169039
241169387	chr19	11168904	11169061	11168922	11169039	SMARCA4	NM_001128847	4	33	29	+	11168931	11169039
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128844	1	36	34	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_003072	7	35	33	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128845	2	33	31	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128849	6	36	34	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128847	4	33	31	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128846	3	33	31	+	11170429	11170561
240225812	chr19	11170471	11170641	11170491	11170622	SMARCA4	NM_001128848	5	33	31	+	11170429	11170561
233312721	chr19	17937437	17937608	17937461	17937587	JAK3	NM_000215	1	24	24	-	17935593	17937719
233075863	chr19	17941205	17941363	17941225	17941342	JAK3	NM_000215	1	24	22	-	17941312	17941429
232255049	chr19	17942391	17942563	17942410	17942546	JAK3	NM_000215	1	24	20	-	17942483	17942607
231796494	chr19	17943522	17943668	17943542	17943648	JAK3	NM_000215	1	24	18	-	17943599	17943738
233510195	chr19	17945594	17945757	17945615	17945733	JAK3	NM_000215	1	24	16	-	17945661	17945812
234525335	chr19	17946758	17946930	17946778	17946909	JAK3	NM_000215	1	24	14	-	17946733	17946860
234724389	chr19	17950244	17950390	17950265	17950370	JAK3	NM_000215	1	24	10	-	17950286	17950472
232420265	chr19	17952221	17952382	17952239	17952364	JAK3	NM_000215	1	24	8	-	17952198	17952355
233107958	chr19	17953124	17953298	17953143	17953281	JAK3	NM_000215	1	24	6	-	17953125	17953419
233222267	chr19	17953911	17954044	17953931	17954020	JAK3	NM_000215	1	24	5	-	17953836	17953981
232610766	chr19	17954617	17954779	17954638	17954759	JAK3	NM_000215	1	24	3	-	17954586	17954709
293915654	chr19	18266710	18266861	18266727	18266844	PIK3R2	NM_005027	1	16	2	+	18266267	18267011
293770196	chr19	18271328	18271478	18271348	18271458	PIK3R2	NM_005027	1	16	3	+	18271281	18271373
294465760	chr19	18272748	18272894	18272767	18272870	PIK3R2	NM_005027	1	16	7	+	18272776	18272861
294691111	chr19	18273717	18273889	18273737	18273867	PIK3R2	NM_005027	1	16	10	+	18273777	18273957
294106689	chr19	18276901	18277063	18276920	18277039	PIK3R2	NM_005027	1	16	12	+	18276970	18277112
294995667	chr19	18279485	18279645	18279503	18279626	PIK3R2	NM_005027	1	16	15	+	18279536	18279706
225471531	chr19	18853630	18853800	18853653	18853782	CRTC1	NM_015321	2	14	2	+	18853720	18853836
225471531	chr19	18853630	18853800	18853653	18853782	CRTC1	NM_001098482	1	15	2	+	18853720	18853836

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226098551	chr19	18856602	18856776	18856626	18856756	CRTC1	NM_015321	2	14	3	+	18856633	18856770
226098551	chr19	18856602	18856776	18856626	18856756	CRTC1	NM_001098482	1	15	4	+	18856633	18856770
225769994	chr19	18864209	18864342	18864229	18864319	CRTC1	NM_015321	2	14	6	+	18864310	18864395
225769994	chr19	18864209	18864342	18864229	18864319	CRTC1	NM_001098482	1	15	7	+	18864310	18864395
226306973	chr19	18870893	18871057	18870915	18871039	CRTC1	NM_015321	2	14	8	+	18870818	18871038
226306973	chr19	18870893	18871057	18870915	18871039	CRTC1	NM_001098482	1	15	9	+	18870818	18871038
226064324	chr19	18879486	18879621	18879503	18879604	CRTC1	NM_015321	2	14	10	+	18879295	18879603
226064324	chr19	18879486	18879621	18879503	18879604	CRTC1	NM_001098482	1	15	11	+	18879295	18879603
226269921	chr19	18886429	18886601	18886447	18886583	CRTC1	NM_015321	2	14	13	+	18886451	18886631
226269921	chr19	18886429	18886601	18886447	18886583	CRTC1	NM_001098482	1	15	14	+	18886451	18886631
253993637	chr19	18888054	18888181	18888073	18888162	CRTC1	NM_015321	2	14	14	+	18887981	18893143
253993637	chr19	18888054	18888181	18888073	18888162	CRTC1	NM_001098482	1	15	15	+	18887981	18893143
270686370	chr19	30303774	30303912	30303794	30303887	CCNE1	NM_001238	1	12	4	+	30303876	30303944
271332965	chr19	30308248	30308419	30308272	30308397	CCNE1	NM_001238	1	12	6	+	30308313	30308448
270721147	chr19	30312580	30312749	30312605	30312728	CCNE1	NM_001238	1	12	8	+	30312629	30312724
271422510	chr19	30313259	30313423	30313281	30313400	CCNE1	NM_001238	1	12	11	+	30313353	30313510
226701748	chr19	33792119	33792289	33792139	33792271	CEBPA	NM_004364	1	1	1	-	33790840	33793430
226693890	chr19	33792684	33792851	33792703	33792831	CEBPA	NM_004364	1	1	1	-	33790840	33793430
223734461	chr19	40739748	40739907	40739765	40739889	AKT2	NM_001626	3	14	14	-	40736224	40739858
223734461	chr19	40739748	40739907	40739765	40739889	AKT2	NM_001243028	2	13	13	-	40736224	40739858
223734461	chr19	40739748	40739907	40739765	40739889	AKT2	NM_001243027	1	14	14	-	40736224	40739858
223880353	chr19	40741200	40741374	40741221	40741350	AKT2	NM_001626	3	14	12	-	40741170	40741257
223880353	chr19	40741200	40741374	40741221	40741350	AKT2	NM_001243028	2	13	11	-	40741170	40741257
223880353	chr19	40741200	40741374	40741221	40741350	AKT2	NM_001243027	1	14	12	-	40741170	40741257
222662947	chr19	40742125	40742291	40742145	40742269	AKT2	NM_001626	3	14	10	-	40742164	40742292
222662947	chr19	40742125	40742291	40742145	40742269	AKT2	NM_001243028	2	13	9	-	40742164	40742292
222662947	chr19	40742125	40742291	40742145	40742269	AKT2	NM_001243027	1	14	10	-	40742164	40742292
222639818	chr19	40744734	40744903	40744753	40744885	AKT2	NM_001626	3	14	8	-	40744812	40744880
222639818	chr19	40744734	40744903	40744753	40744885	AKT2	NM_001243028	2	13	7	-	40744812	40744880
222639818	chr19	40744734	40744903	40744753	40744885	AKT2	NM_001243027	1	14	8	-	40744812	40744880
223140553	chr19	40748341	40748500	40748362	40748480	AKT2	NM_001626	3	14	5	-	40748441	40748594
223140553	chr19	40748341	40748500	40748362	40748480	AKT2	NM_001243028	2	13	4	-	40748441	40748594
223140553	chr19	40748341	40748500	40748362	40748480	AKT2	NM_001243027	1	14	5	-	40748441	40748594
225085532	chr19	40762809	40762983	40762830	40762961	AKT2	NM_001626	3	14	3	-	40762833	40762961
225085532	chr19	40762809	40762983	40762830	40762961	AKT2	NM_001243028	2	13	2	-	40762833	40762961
225085532	chr19	40762809	40762983	40762830	40762961	AKT2	NM_001243027	1	14	3	-	40762833	40762961
281442216	chr19	41726620	41726751	41726640	41726726	AXL	NM_021913	2	20	2	+	41726541	41726763
281442216	chr19	41726620	41726751	41726640	41726726	AXL	NM_001699	1	19	2	+	41726541	41726763
282093342	chr19	41727716	41727889	41727738	41727871	AXL	NM_021913	2	20	4	+	41727785	41727961
282093342	chr19	41727716	41727889	41727738	41727871	AXL	NM_001699	1	19	4	+	41727785	41727961
281290144	chr19	41743787	41743957	41743810	41743938	AXL	NM_021913	2	20	7	+	41743849	41744059

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
281290144	chr19	41743787	41743957	41743810	41743938	AXL	NM_001699	1	19	7	+	41743849	41744059
281825518	chr19	41745002	41745148	41745024	41745125	AXL	NM_021913	2	20	9	+	41745069	41745219
281825518	chr19	41745002	41745148	41745024	41745125	AXL	NM_001699	1	19	9	+	41745069	41745219
283375389	chr19	41748863	41749029	41748886	41749001	AXL	NM_021913	2	20	11	+	41748788	41748920
283375389	chr19	41748863	41749029	41748886	41749001	AXL	NM_001699	1	19	10	+	41748788	41748920
281410162	chr19	41754574	41754748	41754600	41754725	AXL	NM_021913	2	20	14	+	41754648	41754725
281410162	chr19	41754574	41754748	41754600	41754725	AXL	NM_001699	1	19	13	+	41754648	41754725
282886729	chr19	41759547	41759706	41759569	41759684	AXL	NM_021913	2	20	17	+	41759504	41759613
282886729	chr19	41759547	41759706	41759569	41759684	AXL	NM_001699	1	19	16	+	41759504	41759613
281419625	chr19	41763456	41763580	41763479	41763556	AXL	NM_021913	2	20	19	+	41763398	41763534
281419625	chr19	41763456	41763580	41763479	41763556	AXL	NM_001699	1	19	18	+	41763398	41763534
253781261	chr19	42381334	42381472	42381355	42381453	CD79A	NM_001783	1	5	1	+	42381190	42381453
253781261	chr19	42381334	42381472	42381355	42381453	CD79A	NM_021601	2	5	1	+	42381190	42381453
226533895	chr19	42383578	42383752	42383601	42383733	CD79A	NM_001783	1	5	3	+	42383605	42383723
226533895	chr19	42383578	42383752	42383601	42383733	CD79A	NM_021601	2	5	3	+	42383605	42383723
226164949	chr19	42788845	42788977	42788862	42788958	CIC	NM_015125	1	20	1	+	42788817	42788923
225923404	chr19	42791231	42791405	42791248	42791384	CIC	NM_015125	1	20	3	+	42791158	42791392
227045723	chr19	42791672	42791817	42791693	42791798	CIC	NM_015125	1	20	5	+	42791697	42791879
226403739	chr19	42792082	42792254	42792099	42792232	CIC	NM_015125	1	20	6	+	42791962	42792127
225614923	chr19	42793227	42793384	42793248	42793361	CIC	NM_015125	1	20	8	+	42793333	42793558
225864443	chr19	42794337	42794510	42794356	42794489	CIC	NM_015125	1	20	10	+	42794385	42795618
225870293	chr19	42794723	42794896	42794742	42794877	CIC	NM_015125	1	20	10	+	42794385	42795618
225875386	chr19	42795187	42795321	42795205	42795303	CIC	NM_015125	1	20	10	+	42794385	42795618
226525022	chr19	42795658	42795814	42795680	42795795	CIC	NM_015125	1	20	11	+	42795710	42795897
226477007	chr19	42796541	42796687	42796559	42796668	CIC	NM_015125	1	20	13	+	42796452	42796618
226101558	chr19	42797075	42797229	42797094	42797210	CIC	NM_015125	1	20	15	+	42797108	42797433
227040672	chr19	42797717	42797883	42797735	42797866	CIC	NM_015125	1	20	16	+	42797744	42797988
225440403	chr19	42798104	42798259	42798124	42798241	CIC	NM_015125	1	20	17	+	42798087	42798241
226509452	chr19	42798745	42798919	42798764	42798900	CIC	NM_015125	1	20	19	+	42798756	42798887
223540041	chr19	45254456	45254608	45254478	45254587	BCL3	NM_005178	1	9	2	+	45254484	45254637
223261895	chr19	45260292	45260464	45260315	45260446	BCL3	NM_005178	1	9	4	+	45260274	45260478
222168421	chr19	45260810	45260973	45260827	45260956	BCL3	NM_005178	1	9	6	+	45260903	45260980
222729852	chr19	45261608	45261738	45261626	45261721	BCL3	NM_005178	1	9	7	+	45261503	45261670
290445150	chr19	45762200	45762343	45762220	45762323	MARK4	NM_031417	2	18	2	+	45762247	45762447
290445150	chr19	45762200	45762343	45762220	45762323	MARK4	NM_001199867	1	17	2	+	45762247	45762447
290583791	chr19	45767848	45768006	45767869	45767985	MARK4	NM_031417	2	18	5	+	45767942	45768007
290583791	chr19	45767848	45768006	45767869	45767985	MARK4	NM_001199867	1	17	5	+	45767942	45768007
290661675	chr19	45769409	45769541	45769430	45769519	MARK4	NM_031417	2	18	7	+	45769483	45769539
290661675	chr19	45769409	45769541	45769430	45769519	MARK4	NM_001199867	1	17	7	+	45769483	45769539
290511608	chr19	45774896	45775067	45774915	45775049	MARK4	NM_031417	2	18	8	+	45774730	45774966
290511608	chr19	45774896	45775067	45774915	45775049	MARK4	NM_001199867	1	17	8	+	45774730	45774966

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293650732	chr19	45783577	45783702	45783604	45783680	MARK4	NM_031417	2	18	11	+	45783632	45783741
293650732	chr19	45783577	45783702	45783604	45783680	MARK4	NM_001199867	1	17	11	+	45783632	45783741
289391907	chr19	45790840	45790987	45790857	45790969	MARK4	NM_031417	2	18	13	+	45790705	45790922
289391907	chr19	45790840	45790987	45790857	45790969	MARK4	NM_001199867	1	17	13	+	45790705	45790922
292309940	chr19	45801021	45801195	45801038	45801174	MARK4	NM_031417	2	18	15	+	45800934	45801212
292309940	chr19	45801021	45801195	45801038	45801174	MARK4	NM_001199867	1	17	15	+	45800934	45801212
291133822	chr19	45803017	45803180	45803039	45803160	MARK4	NM_031417	2	18	17	+	45803069	45803113
291133822	chr19	45803017	45803180	45803039	45803160	MARK4	NM_001199867	1	17	16	+	45803069	45803113
292531829	chr19	45805828	45805981	45805845	45805964	MARK4	NM_031417	2	18	18	+	45805632	45808541
292531829	chr19	45805828	45805981	45805845	45805964	MARK4	NM_001199867	1	17	17	+	45805632	45808541
227989378	chr19	45855494	45855655	45855515	45855635	ERCC2	NM_000400	1	23	22	-	45855467	45855610
230825291	chr19	45856290	45856461	45856311	45856440	ERCC2	NM_000400	1	23	19	-	45856341	45856413
230202484	chr19	45858014	45858187	45858036	45858159	ERCC2	NM_000400	1	23	17	-	45857988	45858109
228412673	chr19	45860851	45860992	45860872	45860972	ERCC2	NM_000400	1	23	13	-	45860888	45860957
230685164	chr19	45867061	45867194	45867080	45867177	ERCC2	NM_000400	1	23	11	-	45867001	45867169
230685164	chr19	45867061	45867194	45867080	45867177	ERCC2	NM_001130867	2	12	10	-	45867001	45867169
230583042	chr19	45867570	45867743	45867590	45867723	ERCC2	NM_000400	1	23	8	-	45867682	45867805
230583042	chr19	45867570	45867743	45867590	45867723	ERCC2	NM_001130867	2	12	7	-	45867682	45867805
228016994	chr19	45868295	45868452	45868319	45868431	ERCC2	NM_000400	1	23	6	-	45868300	45868416
228016994	chr19	45868295	45868452	45868319	45868431	ERCC2	NM_001130867	2	12	5	-	45868300	45868416
229429083	chr19	45872285	45872450	45872307	45872428	ERCC2	NM_000400	1	23	3	-	45872328	45872405
229429083	chr19	45872285	45872450	45872307	45872428	ERCC2	NM_001130867	2	12	2	-	45872328	45872405
295159371	chr19	45912878	45913029	45912898	45913001	ERCC1	NM_001983	2	10	10	-	45910591	45912983
295159371	chr19	45912878	45913029	45912898	45913001	ERCC1	NM_001166049	1	9	9	-	45910591	45912983
294680587	chr19	45918090	45918243	45918108	45918221	ERCC1	NM_202001	3	8	6	-	45918119	45918218
294680587	chr19	45918090	45918243	45918108	45918221	ERCC1	NM_001983	2	10	7	-	45918119	45918218
294680587	chr19	45918090	45918243	45918108	45918221	ERCC1	NM_001166049	1	9	7	-	45918119	45918218
293815620	chr19	45923486	45923657	45923511	45923636	ERCC1	NM_202001	3	8	3	-	45923582	45923685
293815620	chr19	45923486	45923657	45923511	45923636	ERCC1	NM_001983	2	10	4	-	45923582	45923685
293815620	chr19	45923486	45923657	45923511	45923636	ERCC1	NM_001166049	1	9	4	-	45923582	45923685
294509130	chr19	45924551	45924722	45924574	45924702	ERCC1	NM_202001	3	8	2	-	45924436	45924651
294509130	chr19	45924551	45924722	45924574	45924702	ERCC1	NM_001983	2	10	3	-	45924436	45924651
294509130	chr19	45924551	45924722	45924574	45924702	ERCC1	NM_001166049	1	9	3	-	45924436	45924651
236368953	chr19	52709167	52709340	52709189	52709320	PPP2R1A	NM_014225	1	15	3	+	52709216	52709316
238702010	chr19	52715903	52716044	52715920	52716023	PPP2R1A	NR_033500	2	14	4	+	52715939	52716086
238702010	chr19	52715903	52716044	52715920	52716023	PPP2R1A	NM_014225	1	15	5	+	52715939	52716086
237744065	chr19	52718936	52719108	52718960	52719084	PPP2R1A	NR_033500	2	14	6	+	52719032	52719146
237744065	chr19	52718936	52719108	52718960	52719084	PPP2R1A	NM_014225	1	15	7	+	52719032	52719146
241187681	chr19	52719824	52719948	52719846	52719927	PPP2R1A	NR_033500	2	14	8	+	52719782	52719916
241187681	chr19	52719824	52719948	52719846	52719927	PPP2R1A	NM_014225	1	15	9	+	52719782	52719916
236800513	chr19	52723353	52723524	52723374	52723503	PPP2R1A	NR_033500	2	14	10	+	52723442	52723502

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236800513	chr19	52723353	52723524	52723374	52723503	PPP2R1A	NM_014225	1	15	11	+	52723442	52723502
235755040	chr19	52725431	52725558	52725452	52725534	PPP2R1A	NR_033500	2	14	12	+	52725352	52725494
235755040	chr19	52725431	52725558	52725452	52725534	PPP2R1A	NM_014225	1	15	13	+	52725352	52725494
294331135	chr19	57742538	57742709	57742557	57742689	AURKC	NM_001015878	1	7	1	+	57742428	57742674
294985763	chr19	57743861	57743995	57743885	57743975	AURKC	NM_001015879	2	7	4	+	57743910	57744048
294985763	chr19	57743861	57743995	57743885	57743975	AURKC	NM_001015878	1	7	4	+	57743910	57744048
294985763	chr19	57743861	57743995	57743885	57743975	AURKC	NM_003160	3	7	4	+	57743910	57744048
294832211	chr19	57746151	57746325	57746172	57746298	AURKC	NM_001015879	2	7	6	+	57746252	57746426
294832211	chr19	57746151	57746325	57746172	57746298	AURKC	NM_001015878	1	7	6	+	57746252	57746426
294832211	chr19	57746151	57746325	57746172	57746298	AURKC	NM_003160	3	7	6	+	57746252	57746426
271636420	chr20	30309404	30309560	30309425	30309538	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
271675952	chr20	30309851	30309989	30309871	30309965	BCL2L1	NM_001191	1	3	2	-	30309647	30310151
271675952	chr20	30309851	30309989	30309871	30309965	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
223559778	chr20	30959882	30960041	30959904	30960012	ASXL1	NM_001164603	1	4	4	+	30959967	30960352
222662461	chr20	31017626	31017800	31017649	31017781	ASXL1	NM_015338	2	12	7	+	31017704	31017856
222869257	chr20	31019115	31019282	31019141	31019260	ASXL1	NM_015338	2	12	8	+	31019124	31019287
223288694	chr20	31020644	31020816	31020668	31020794	ASXL1	NM_015338	2	12	10	+	31020683	31020788
225157619	chr20	31021334	31021480	31021357	31021460	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223982077	chr20	31022130	31022285	31022154	31022264	ASXL1	NM_015338	2	12	12	+	31022235	31027122
224011664	chr20	31022599	31022747	31022622	31022726	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225307988	chr20	31023017	31023191	31023044	31023168	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225312048	chr20	31023500	31023662	31023520	31023640	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225297063	chr20	31023952	31024090	31023975	31024069	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225300064	chr20	31024386	31024544	31024410	31024522	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225295366	chr20	31024856	31025004	31024882	31024981	ASXL1	NM_015338	2	12	12	+	31022235	31027122
263422510	chr20	36014370	36014533	36014391	36014508	SRC	NM_198291	2	14	5	+	36014478	36014577
263422510	chr20	36014370	36014533	36014391	36014508	SRC	NM_005417	1	14	5	+	36014478	36014577
239926012	chr20	36024488	36024641	36024508	36024620	SRC	NM_198291	2	14	8	+	36024565	36024714
239926012	chr20	36024488	36024641	36024508	36024620	SRC	NM_005417	1	14	8	+	36024565	36024714
240361418	chr20	36028497	36028664	36028515	36028641	SRC	NM_198291	2	14	10	+	36028518	36028697
240361418	chr20	36028497	36028664	36028515	36028641	SRC	NM_005417	1	14	10	+	36028518	36028697
264595318	chr20	36030836	36030987	36030854	36030970	SRC	NM_198291	2	14	12	+	36030838	36030991
264595318	chr20	36030836	36030987	36030854	36030970	SRC	NM_005417	1	14	12	+	36030838	36030991
242076872	chr20	36031649	36031812	36031667	36031795	SRC	NM_198291	2	14	14	+	36031574	36033821
242076872	chr20	36031649	36031812	36031667	36031795	SRC	NM_005417	1	14	14	+	36031574	36033821
234397948	chr20	39316679	39316850	39316701	39316831	MAFB	NM_005461	1	1	1	-	39314517	39317876
232721538	chr20	39317105	39317247	39317122	39317225	MAFB	NM_005461	1	1	1	-	39314517	39317876
232731867	chr20	39317416	39317590	39317440	39317572	MAFB	NM_005461	1	1	1	-	39314517	39317876
239776746	chr20	39658033	39658203	39658059	39658182	TOP1	NM_003286	1	21	2	+	39658071	39658095
238697450	chr20	39706131	39706298	39706152	39706277	TOP1	NM_003286	1	21	5	+	39706222	39706277
242146499	chr20	39720981	39721137	39721003	39721114	TOP1	NM_003286	1	21	9	+	39721112	39721227

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264579210	chr20	39726767	39726939	39726791	39726917	TOP1	NM_003286	1	21	11	+	39726855	39726977
241252626	chr20	39729744	39729892	39729772	39729868	TOP1	NM_003286	1	21	13	+	39729849	39729993
261746947	chr20	39742545	39742716	39742573	39742692	TOP1	NM_003286	1	21	15	+	39742610	39742795
241945722	chr20	39746696	39746838	39746723	39746816	TOP1	NM_003286	1	21	18	+	39746809	39746936
265981573	chr20	39750647	39750818	39750673	39750796	TOP1	NM_003286	1	21	20	+	39750646	39750795
271119158	chr20	39788280	39788420	39788301	39788399	PLCG1	NM_002660	1	32	2	+	39788246	39788398
271119158	chr20	39788280	39788420	39788301	39788399	PLCG1	NM_182811	2	32	2	+	39788246	39788398
271562723	chr20	39791187	39791361	39791207	39791341	PLCG1	NM_002660	1	32	6	+	39791282	39791365
271562723	chr20	39791187	39791361	39791207	39791341	PLCG1	NM_182811	2	32	6	+	39791282	39791365
272514078	chr20	39791972	39792138	39791993	39792119	PLCG1	NM_002660	1	32	9	+	39792018	39792119
272514078	chr20	39791972	39792138	39791993	39792119	PLCG1	NM_182811	2	32	9	+	39792018	39792119
270127907	chr20	39792542	39792716	39792564	39792694	PLCG1	NM_002660	1	32	11	+	39792561	39792646
270127907	chr20	39792542	39792716	39792564	39792694	PLCG1	NM_182811	2	32	11	+	39792561	39792646
269683621	chr20	39793806	39793979	39793826	39793953	PLCG1	NM_002660	1	32	14	+	39793885	39794007
269683621	chr20	39793806	39793979	39793826	39793953	PLCG1	NM_182811	2	32	14	+	39793885	39794007
272123362	chr20	39794342	39794513	39794359	39794492	PLCG1	NM_002660	1	32	16	+	39794279	39794466
272123362	chr20	39794342	39794513	39794359	39794492	PLCG1	NM_182811	2	32	16	+	39794279	39794466
272684092	chr20	39795093	39795253	39795111	39795236	PLCG1	NM_002660	1	32	18	+	39795116	39795235
272684092	chr20	39795093	39795253	39795111	39795236	PLCG1	NM_182811	2	32	18	+	39795116	39795235
271822232	chr20	39797365	39797531	39797385	39797510	PLCG1	NM_002660	1	32	21	+	39797407	39797510
271822232	chr20	39797365	39797531	39797385	39797510	PLCG1	NM_182811	2	32	21	+	39797407	39797510
269469554	chr20	39798708	39798836	39798732	39798816	PLCG1	NM_002660	1	32	24	+	39798752	39798909
269469554	chr20	39798708	39798836	39798732	39798816	PLCG1	NM_182811	2	32	24	+	39798752	39798909
272215493	chr20	39800973	39801115	39800995	39801094	PLCG1	NM_002660	1	32	26	+	39801061	39801285
272215493	chr20	39800973	39801115	39800995	39801094	PLCG1	NM_182811	2	32	26	+	39801061	39801285
269990307	chr20	39801436	39801599	39801454	39801570	PLCG1	NM_002660	1	32	27	+	39801369	39801517
269990307	chr20	39801436	39801599	39801454	39801570	PLCG1	NM_182811	2	32	27	+	39801369	39801517
272674376	chr20	39802434	39802608	39802457	39802586	PLCG1	NM_002660	1	32	30	+	39802563	39802651
272674376	chr20	39802434	39802608	39802457	39802586	PLCG1	NM_182811	2	32	30	+	39802563	39802651
272246685	chr20	39803073	39803209	39803093	39803189	PLCG1	NM_002660	1	32	32	+	39803107	39804357
272246685	chr20	39803073	39803209	39803093	39803189	PLCG1	NM_182811	2	32	32	+	39803107	39804357
295529635	chr20	40713271	40713397	40713293	40713377	PTPRT	NM_007050	1	31	29	-	40713322	40713485
295529635	chr20	40713271	40713397	40713293	40713377	PTPRT	NM_133170	2	32	30	-	40713322	40713485
297893405	chr20	40727067	40727216	40727091	40727193	PTPRT	NM_007050	1	31	27	-	40727061	40727192
297893405	chr20	40727067	40727216	40727091	40727193	PTPRT	NM_133170	2	32	28	-	40727061	40727192
297938522	chr20	40733268	40733439	40733292	40733414	PTPRT	NM_007050	1	31	25	-	40733209	40733358
297938522	chr20	40733268	40733439	40733292	40733414	PTPRT	NM_133170	2	32	26	-	40733209	40733358
296757366	chr20	40739059	40739227	40739076	40739209	PTPRT	NM_007050	1	31	23	-	40738973	40739127
296757366	chr20	40739059	40739227	40739076	40739209	PTPRT	NM_133170	2	32	24	-	40738973	40739127
296201281	chr20	40748464	40748637	40748492	40748612	PTPRT	NM_007050	1	31	20	-	40748575	40748611
296201281	chr20	40748464	40748637	40748492	40748612	PTPRT	NM_133170	2	32	21	-	40748575	40748611

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
297258830	chr20	40790093	40790238	40790114	40790213	PTPRT	NM_007050	1	31	17	-	40789992	40790182
297258830	chr20	40790093	40790238	40790114	40790213	PTPRT	NM_133170	2	32	18	-	40789992	40790182
297693200	chr20	40877286	40877455	40877306	40877430	PTPRT	NM_007050	1	31	14	-	40877327	40877462
297693200	chr20	40877286	40877455	40877306	40877430	PTPRT	NM_133170	2	32	15	-	40877327	40877462
295653627	chr20	40944281	40944414	40944302	40944392	PTPRT	NM_007050	1	31	12	-	40944363	40944636
295653627	chr20	40944281	40944414	40944302	40944392	PTPRT	NM_133170	2	32	12	-	40944363	40944636
296968373	chr20	40980589	40980749	40980610	40980727	PTPRT	NM_007050	1	31	10	-	40980724	40980925
296968373	chr20	40980589	40980749	40980610	40980727	PTPRT	NM_133170	2	32	10	-	40980724	40980925
297195318	chr20	41100821	41100977	41100847	41100956	PTPRT	NM_007050	1	31	8	-	41100906	41101202
297195318	chr20	41100821	41100977	41100847	41100956	PTPRT	NM_133170	2	32	8	-	41100906	41101202
297693489	chr20	41306581	41306705	41306605	41306684	PTPRT	NM_007050	1	31	7	-	41306506	41306799
297693489	chr20	41306581	41306705	41306605	41306684	PTPRT	NM_133170	2	32	7	-	41306506	41306799
298654226	chr20	41400047	41400221	41400069	41400193	PTPRT	NM_007050	1	31	5	-	41400075	41400190
298654226	chr20	41400047	41400221	41400069	41400193	PTPRT	NM_133170	2	32	5	-	41400075	41400190
296507169	chr20	41419909	41420044	41419930	41420022	PTPRT	NM_007050	1	31	3	-	41419835	41420106
296507169	chr20	41419909	41420044	41419930	41420022	PTPRT	NM_133170	2	32	3	-	41419835	41420106
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_003600	1	9	9	-	54944445	54945396
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_198435	4	9	9	-	54944445	54945396
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_198436	5	10	10	-	54944445	54945396
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_198434	3	10	10	-	54944445	54945396
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_198433	2	11	11	-	54944445	54945396
271220154	chr20	54945148	54945288	54945176	54945267	AURKA	NM_198437	6	9	9	-	54944445	54945396
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_003600	1	9	8	-	54945541	54945715
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_198435	4	9	8	-	54945541	54945715
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_198436	5	10	9	-	54945541	54945715
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_198434	3	10	9	-	54945541	54945715
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_198433	2	11	10	-	54945541	54945715
270043233	chr20	54945581	54945755	54945605	54945733	AURKA	NM_198437	6	9	8	-	54945541	54945715
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_003600	1	9	6	-	54956489	54956627
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_198435	4	9	6	-	54956489	54956627
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_198436	5	10	7	-	54956489	54956627
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_198434	3	10	7	-	54956489	54956627
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_198433	2	11	8	-	54956489	54956627
269750987	chr20	54956541	54956668	54956565	54956640	AURKA	NM_198437	6	9	6	-	54956489	54956627
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_003600	1	9	4	-	54959326	54959380
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_198435	4	9	4	-	54959326	54959380
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_198436	5	10	5	-	54959326	54959380
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_198434	3	10	5	-	54959326	54959380
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_198433	2	11	6	-	54959326	54959380
269873391	chr20	54959244	54959371	54959268	54959348	AURKA	NM_198437	6	9	4	-	54959326	54959380
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_003600	1	9	3	-	54961313	54961589

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_198435	4	9	3	-	54961313	54961589
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_198436	5	10	4	-	54961313	54961589
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_198434	3	10	4	-	54961313	54961589
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_198433	2	11	5	-	54961313	54961589
270833925	chr20	54961559	54961715	54961580	54961687	AURKA	NM_198437	6	9	3	-	54961313	54961589
228097582	chr20	57415397	57415552	57415417	57415533	GNAS	NM_016592	5	13	1	+	57414795	57415941
227948598	chr20	57415810	57415962	57415827	57415941	GNAS	NM_016592	5	13	1	+	57414795	57415941
229426746	chr20	57428598	57428768	57428617	57428749	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229426746	chr20	57428598	57428768	57428617	57428749	GNAS	NM_080425	6	13	1	+	57428036	57430388
229429984	chr20	57429042	57429216	57429062	57429196	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229429984	chr20	57429042	57429216	57429062	57429196	GNAS	NM_080425	6	13	1	+	57428036	57430388
229439813	chr20	57429472	57429608	57429490	57429591	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229439813	chr20	57429472	57429608	57429490	57429591	GNAS	NM_080425	6	13	1	+	57428036	57430388
227519822	chr20	57430235	57430407	57430253	57430390	GNAS	NM_001077490	4	13	1	+	57428036	57430388
227519822	chr20	57430235	57430407	57430253	57430390	GNAS	NM_080425	6	13	1	+	57428036	57430388
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_016592	5	13	4	+	57478583	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_001077488	2	13	4	+	57478583	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_080426	7	12	3	+	57478583	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NR_003259	8	13	4	+	57478586	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_001077490	4	13	4	+	57478586	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_080425	6	13	4	+	57478586	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_001077489	3	12	3	+	57478586	57478640
227241495	chr20	57478593	57478736	57478614	57478708	GNAS	NM_000516	1	13	4	+	57478586	57478640
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_016592	5	13	7	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_001077488	2	13	7	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NR_003259	8	13	7	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_001077490	4	13	7	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_080426	7	12	6	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_080425	6	13	7	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_001077489	3	12	6	+	57484217	57484271
228773918	chr20	57484148	57484319	57484176	57484297	GNAS	NM_000516	1	13	7	+	57484217	57484271
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_016592	5	13	11	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_001077488	2	13	11	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NR_003259	8	13	11	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_001077490	4	13	11	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_080426	7	12	10	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_080425	6	13	11	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_001077489	3	12	10	+	57485006	57485136
227497817	chr20	57484986	57485158	57485005	57485136	GNAS	NM_000516	1	13	11	+	57485006	57485136
242436890	chr21	36164616	36164786	36164636	36164768	RUNX1	NM_001754	3	9	9	-	36160098	36164907
242436890	chr21	36164616	36164786	36164636	36164768	RUNX1	NM_001001890	1	6	6	-	36160098	36164907

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264733509	chr21	36171681	36171841	36171702	36171813	RUNX1	NM_001754	3	9	8	-	36171598	36171759
264733509	chr21	36171681	36171841	36171702	36171813	RUNX1	NM_001001890	1	6	5	-	36171598	36171759
240216090	chr21	36206819	36206992	36206839	36206968	RUNX1	NM_001754	3	9	7	-	36206707	36206898
240216090	chr21	36206819	36206992	36206839	36206968	RUNX1	NM_001122607	2	5	4	-	36206707	36206898
240216090	chr21	36206819	36206992	36206839	36206968	RUNX1	NM_001001890	1	6	4	-	36206707	36206898
241650333	chr21	36259122	36259267	36259139	36259250	RUNX1	NM_001122607	2	5	1	-	36259140	36260987
241650333	chr21	36259122	36259267	36259139	36259250	RUNX1	NM_001001890	1	6	1	-	36259140	36260987
241650333	chr21	36259122	36259267	36259139	36259250	RUNX1	NM_001754	3	9	4	-	36259140	36259393
238333128	chr21	36265216	36265390	36265239	36265362	RUNX1	NM_001754	3	9	3	-	36265222	36265260
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_001136154	1	12	12	-	39751950	39755845
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_001136155	2	9	9	-	39751950	39755845
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_004449	6	11	11	-	39751950	39755845
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_182918	7	10	10	-	39751950	39755845
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_001243429	4	9	9	-	39751950	39755845
232708234	chr21	39755499	39755664	39755520	39755641	ERG	NM_001243428	3	12	12	-	39751950	39755845
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_001136154	1	12	11	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_001136155	2	9	8	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_004449	6	11	10	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_182918	7	10	9	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_001243432	5	12	11	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_001243429	4	9	8	-	39762917	39762964
230134061	chr21	39762919	39763083	39762938	39763059	ERG	NM_001243428	3	12	11	-	39762917	39762964
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_001136154	1	12	7	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_001136155	2	9	4	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_004449	6	11	7	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_182918	7	10	5	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_001243432	5	12	7	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_001243429	4	9	5	-	39774479	39774559
227759808	chr21	39774397	39774557	39774419	39774531	ERG	NM_001243428	3	12	7	-	39774479	39774559
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_001136154	1	12	5	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_001136155	2	9	2	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_004449	6	11	5	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_182918	7	10	3	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_001243432	5	12	5	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_001243429	4	9	3	-	39795332	39795483
230685688	chr21	39795261	39795431	39795280	39795411	ERG	NM_001243428	3	12	5	-	39795332	39795483
228671793	chr21	39870209	39870383	39870236	39870355	ERG	NM_001136155	2	9	1	-	39870287	39870428
228671793	chr21	39870209	39870383	39870236	39870355	ERG	NM_182918	7	10	1	-	39870287	39870428
279764590	chr21	46306677	46306838	46306699	46306818	ITGB2	NM_000211	1	16	15	-	46306651	46306817
279764590	chr21	46306677	46306838	46306699	46306818	ITGB2	NM_001127491	2	16	15	-	46306651	46306817
279438743	chr21	46309088	46309212	46309107	46309193	ITGB2	NM_000211	1	16	13	-	46309191	46309410

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279438743	chr21	46309088	46309212	46309107	46309193	ITGB2	NM_001127491	2	16	13	-	46309191	46309410
279309689	chr21	46309933	46310079	46309954	46310059	ITGB2	NM_000211	1	16	12	-	46309893	46310137
279309689	chr21	46309933	46310079	46309954	46310059	ITGB2	NM_001127491	2	16	12	-	46309893	46310137
278406504	chr21	46311855	46312027	46311876	46312010	ITGB2	NM_000211	1	16	11	-	46311724	46311911
278406504	chr21	46311855	46312027	46311876	46312010	ITGB2	NM_001127491	2	16	11	-	46311724	46311911
278880619	chr21	46318944	46319103	46318962	46319083	ITGB2	NM_000211	1	16	8	-	46318982	46319077
278880619	chr21	46318944	46319103	46318962	46319083	ITGB2	NM_001127491	2	16	8	-	46318982	46319077
279984182	chr21	46321414	46321538	46321431	46321520	ITGB2	NM_000211	1	16	6	-	46321407	46321648
279984182	chr21	46321414	46321538	46321431	46321520	ITGB2	NM_001127491	2	16	6	-	46321407	46321648
280604259	chr21	46323321	46323482	46323340	46323460	ITGB2	NM_000211	1	16	5	-	46323280	46323450
280604259	chr21	46323321	46323482	46323340	46323460	ITGB2	NM_001127491	2	16	5	-	46323280	46323450
279722960	chr21	46330103	46330277	46330123	46330256	ITGB2	NM_000211	1	16	3	-	46330199	46330287
279722960	chr21	46330103	46330277	46330123	46330256	ITGB2	NM_001127491	2	16	3	-	46330199	46330287
269832760	chr22	21272408	21272582	21272427	21272563	CRKL	NM_005207	1	3	1	+	21271714	21272533
271561703	chr22	21288367	21288532	21288389	21288509	CRKL	NM_005207	1	3	2	+	21288067	21288532
293884057	chr22	22123445	22123588	22123466	22123563	MAPK1	NM_002745	1	9	8	-	22123484	22123609
293884057	chr22	22123445	22123588	22123466	22123563	MAPK1	NM_138957	2	8	8	-	22123319	22123609
294588030	chr22	22142570	22142733	22142592	22142705	MAPK1	NM_138957	2	8	6	-	22142546	22142677
294588030	chr22	22142570	22142733	22142592	22142705	MAPK1	NM_002745	1	9	6	-	22142546	22142677
294170750	chr22	22153361	22153535	22153383	22153507	MAPK1	NM_138957	2	8	4	-	22153301	22153417
294170750	chr22	22153361	22153535	22153383	22153507	MAPK1	NM_002745	1	9	4	-	22153301	22153417
294639707	chr22	22161906	22162058	22161929	22162030	MAPK1	NM_138957	2	8	2	-	22161953	22162135
294639707	chr22	22161906	22162058	22161929	22162030	MAPK1	NM_002745	1	9	2	-	22161953	22162135
224665546	chr22	23523176	23523311	23523193	23523294	BCR	NM_004327	1	23	1	+	23522552	23524426
224665546	chr22	23523176	23523311	23523193	23523294	BCR	NM_021574	2	22	1	+	23522552	23524426
223049351	chr22	23523505	23523644	23523524	23523627	BCR	NM_004327	1	23	1	+	23522552	23524426
223049351	chr22	23523505	23523644	23523524	23523627	BCR	NM_021574	2	22	1	+	23522552	23524426
223061250	chr22	23523905	23524078	23523924	23524059	BCR	NM_004327	1	23	1	+	23522552	23524426
223061250	chr22	23523905	23524078	23523924	23524059	BCR	NM_021574	2	22	1	+	23522552	23524426
224678216	chr22	23524380	23524553	23524400	23524530	BCR	NM_004327	1	23	1	+	23522552	23524426
224678216	chr22	23524380	23524553	23524400	23524530	BCR	NM_021574	2	22	1	+	23522552	23524426
224072838	chr22	23603509	23603663	23603530	23603637	BCR	NM_004327	1	23	4	+	23603542	23603727
224072838	chr22	23603509	23603663	23603530	23603637	BCR	NM_021574	2	22	4	+	23603542	23603727
222987957	chr22	23615184	23615335	23615202	23615315	BCR	NM_004327	1	23	7	+	23615268	23615320
222987957	chr22	23615184	23615335	23615202	23615315	BCR	NM_021574	2	22	7	+	23615268	23615320
222475686	chr22	23627183	23627343	23627204	23627323	BCR	NM_004327	1	23	10	+	23627220	23627388
222475686	chr22	23627183	23627343	23627204	23627323	BCR	NM_021574	2	22	10	+	23627220	23627388
222913496	chr22	23630246	23630384	23630267	23630362	BCR	NM_004327	1	23	12	+	23630284	23630359
222913496	chr22	23630246	23630384	23630267	23630362	BCR	NM_021574	2	22	12	+	23630284	23630359
222494797	chr22	23637139	23637288	23637161	23637260	BCR	NM_004327	1	23	16	+	23637211	23637342
222719902	chr22	23656106	23656279	23656125	23656260	BCR	NM_004327	1	23	21	+	23656155	23656260

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222719902	chr22	23656106	23656279	23656125	23656260	BCR	NM_021574	2	22	20	+	23656155	23656260
224341469	chr22	23657672	23657805	23657694	23657784	BCR	NM_004327	1	23	23	+	23657620	23660224
224341469	chr22	23657672	23657805	23657694	23657784	BCR	NM_021574	2	22	22	+	23657620	23660224
241541321	chr22	24135720	24135894	24135745	24135875	SMARCB1	NM_001007468	1	9	3	+	24135746	24135875
241541321	chr22	24135720	24135894	24135745	24135875	SMARCB1	NM_003073	2	9	3	+	24135746	24135875
241238070	chr22	24145557	24145721	24145579	24145701	SMARCB1	NM_001007468	1	9	5	+	24145482	24145609
241238070	chr22	24145557	24145721	24145579	24145701	SMARCB1	NM_003073	2	9	5	+	24145482	24145609
242161672	chr22	24167483	24167657	24167505	24167632	SMARCB1	NM_001007468	1	9	7	+	24167412	24167602
242161672	chr22	24167483	24167657	24167505	24167632	SMARCB1	NM_003073	2	9	7	+	24167412	24167602
240591948	chr22	28146791	28146953	28146813	28146927	MN1	NM_002430	1	2	2	-	28144265	28147084
235343396	chr22	28192832	28192997	28192851	28192977	MN1	NM_002430	1	2	1	-	28192751	28197486
240184627	chr22	28193304	28193440	28193322	28193422	MN1	NM_002430	1	2	1	-	28192751	28197486
240195941	chr22	28193739	28193913	28193758	28193894	MN1	NM_002430	1	2	1	-	28192751	28197486
240219591	chr22	28194149	28194304	28194168	28194287	MN1	NM_002430	1	2	1	-	28192751	28197486
240208065	chr22	28194667	28194815	28194685	28194797	MN1	NM_002430	1	2	1	-	28192751	28197486
240226383	chr22	28194962	28195099	28194980	28195079	MN1	NM_002430	1	2	1	-	28192751	28197486
235392346	chr22	28195405	28195557	28195424	28195539	MN1	NM_002430	1	2	1	-	28192751	28197486
240229741	chr22	28195743	28195898	28195762	28195878	MN1	NM_002430	1	2	1	-	28192751	28197486
235498907	chr22	28196290	28196449	28196307	28196425	MN1	NM_002430	1	2	1	-	28192751	28197486
226431181	chr22	29091769	29091900	29091790	29091873	CHEK2	NM_145862	3	14	10	-	29091698	29091861
226431181	chr22	29091769	29091900	29091790	29091873	CHEK2	NM_007194	2	15	11	-	29091698	29091861
226431181	chr22	29091769	29091900	29091790	29091873	CHEK2	NM_001005735	1	16	12	-	29091698	29091861
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_145862	3	14	7	-	29105994	29106047
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_007194	2	15	7	-	29105994	29106047
328931387	chr22	29106024	29106170	29106047	29106143	CHEK2	NM_001005735	1	16	8	-	29105994	29106047
226236166	chr22	29115381	29115542	29115409	29115515	CHEK2	NM_145862	3	14	5	-	29115383	29115473
226236166	chr22	29115381	29115542	29115409	29115515	CHEK2	NM_007194	2	15	5	-	29115383	29115473
226236166	chr22	29115381	29115542	29115409	29115515	CHEK2	NM_001005735	1	16	6	-	29115383	29115473
226111293	chr22	29121102	29121262	29121130	29121236	CHEK2	NM_145862	3	14	3	-	29121231	29121355
226111293	chr22	29121102	29121262	29121130	29121236	CHEK2	NM_007194	2	15	3	-	29121231	29121355
226111293	chr22	29121102	29121262	29121130	29121236	CHEK2	NM_001005735	1	16	4	-	29121231	29121355
226175883	chr22	29130565	29130734	29130585	29130710	CHEK2	NM_145862	3	14	2	-	29130391	29130715
226175883	chr22	29130565	29130734	29130585	29130710	CHEK2	NM_007194	2	15	2	-	29130391	29130715
226175883	chr22	29130565	29130734	29130585	29130710	CHEK2	NM_001005735	1	16	2	-	29130391	29130715
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_016418	2	17	2	+	30032740	30032865
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_000268	1	16	2	+	30032740	30032865
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_181833	9	5	2	+	30032740	30032865
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_181832	8	17	2	+	30032740	30032865
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_181825	3	16	2	+	30032740	30032865
240866038	chr22	30032717	30032889	30032742	30032865	NF2	NM_181829	5	16	2	+	30032740	30032865
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_016418	2	17	5	+	30050646	30050714

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_000268	1	16	5	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181832	8	17	5	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181828	4	16	4	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181825	3	16	5	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181831	7	15	3	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181830	6	15	3	+	30050646	30050714
236012201	chr22	30050579	30050751	30050601	30050724	NF2	NM_181829	5	16	4	+	30050646	30050714
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_016418	2	17	8	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_000268	1	16	8	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181832	8	17	8	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181828	4	16	7	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181825	3	16	8	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181831	7	15	6	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181830	6	15	6	+	30057194	30057328
237942000	chr22	30057153	30057319	30057173	30057294	NF2	NM_181829	5	16	7	+	30057194	30057328
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_016418	2	17	10	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_000268	1	16	10	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181832	8	17	10	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181828	4	16	9	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181825	3	16	10	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181831	7	15	8	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181830	6	15	8	+	30064322	30064435
236003797	chr22	30064193	30064362	30064218	30064333	NF2	NM_181829	5	16	9	+	30064322	30064435
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_016418	2	17	12	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_000268	1	16	12	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181832	8	17	12	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181828	4	16	11	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181825	3	16	12	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181831	7	15	10	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181830	6	15	10	+	30069258	30069475
238729811	chr22	30069355	30069510	30069375	30069492	NF2	NM_181829	5	16	11	+	30069258	30069475
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_016418	2	17	14	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_000268	1	16	14	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181832	8	17	14	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181828	4	16	13	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181825	3	16	14	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181831	7	15	12	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181830	6	15	12	+	30074185	30074312
239338049	chr22	30074207	30074369	30074229	30074345	NF2	NM_181829	5	16	13	+	30074185	30074312
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_016418	2	17	17	+	30090741	30094589
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_000268	1	16	16	+	30090741	30094589

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_181833	9	5	5	+	30090741	30094589
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_181832	8	17	17	+	30090741	30094589
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_181828	4	16	16	+	30090741	30094589
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_181830	6	15	15	+	30090741	30094589
239408094	chr22	30090711	30090867	30090734	30090843	NF2	NM_181829	5	16	16	+	30090741	30094589
321906834	chr22	33253974	33254145	33254000	33254125	TIMP3	NM_000362	1	5	4	+	33254004	33254125
236698582	chr22	36678707	36678860	36678729	36678838	MYH9	NM_002473	1	41	41	-	36677323	36678831
237843874	chr22	36681077	36681240	36681097	36681219	MYH9	NM_002473	1	41	38	-	36681167	36681375
236883988	chr22	36681705	36681875	36681724	36681857	MYH9	NM_002473	1	41	37	-	36681704	36681827
237896052	chr22	36684225	36684356	36684246	36684336	MYH9	NM_002473	1	41	34	-	36684298	36684459
237940466	chr22	36684874	36685034	36684893	36685014	MYH9	NM_002473	1	41	33	-	36684773	36684985
236544179	chr22	36687985	36688159	36688008	36688142	MYH9	NM_002473	1	41	31	-	36688032	36688280
242402961	chr22	36689397	36689546	36689417	36689527	MYH9	NM_002473	1	41	30	-	36689375	36689527
240857828	chr22	36690300	36690441	36690322	36690420	MYH9	NM_002473	1	41	28	-	36690138	36690344
241518871	chr22	36691630	36691788	36691652	36691767	MYH9	NM_002473	1	41	26	-	36691551	36691763
236352665	chr22	36694958	36695124	36694979	36695101	MYH9	NM_002473	1	41	24	-	36694965	36695088
237092059	chr22	36696902	36697065	36696927	36697046	MYH9	NM_002473	1	41	22	-	36696897	36697103
238373365	chr22	36698596	36698744	36698613	36698723	MYH9	NM_002473	1	41	20	-	36698614	36698722
239245378	chr22	36701873	36702043	36701891	36702023	MYH9	NM_002473	1	41	17	-	36701976	36702097
241147907	chr22	36702533	36702684	36702553	36702664	MYH9	NM_002473	1	41	16	-	36702460	36702653
238437323	chr22	36708093	36708238	36708113	36708219	MYH9	NM_002473	1	41	14	-	36708094	36708267
238899873	chr22	36712463	36712637	36712484	36712616	MYH9	NM_002473	1	41	12	-	36712562	36712714
257630711	chr22	36715539	36715711	36715560	36715689	MYH9	NM_002473	1	41	10	-	36715585	36715680
239364419	chr22	36717724	36717897	36717746	36717868	MYH9	NM_002473	1	41	7	-	36717803	36717866
235680989	chr22	36723421	36723565	36723443	36723536	MYH9	NM_002473	1	41	4	-	36723506	36723533
236935865	chr22	36744943	36745098	36744968	36745076	MYH9	NM_002473	1	41	2	-	36744949	36745300
237764564	chr22	39626067	39626240	39626088	39626217	PDGFB	NM_033016	2	7	5	-	39626089	39626233
237764564	chr22	39626067	39626240	39626088	39626217	PDGFB	NM_002608	1	7	5	-	39626089	39626233
235468355	chr22	39627788	39627945	39627807	39627925	PDGFB	NM_033016	2	7	4	-	39627627	39627832
235468355	chr22	39627788	39627945	39627807	39627925	PDGFB	NM_002608	1	7	4	-	39627627	39627832
235310012	chr22	39636832	39636993	39636855	39636970	PDGFB	NM_033016	2	7	1	-	39636860	39636914
231316189	chr22	41513254	41513395	41513278	41513374	EP300	NM_001429	1	31	2	+	41513191	41513825
228133392	chr22	41513703	41513870	41513727	41513850	EP300	NM_001429	1	31	2	+	41513191	41513825
233021250	chr22	41523483	41523631	41523503	41523607	EP300	NM_001429	1	31	4	+	41523491	41523752
229870056	chr22	41525970	41526100	41525993	41526074	EP300	NM_001429	1	31	5	+	41525894	41526007
230996229	chr22	41531768	41531940	41531795	41531913	EP300	NM_001429	1	31	7	+	41531817	41531910
229847973	chr22	41536177	41536311	41536202	41536283	EP300	NM_001429	1	31	9	+	41536144	41536261
230538832	chr22	41542776	41542907	41542796	41542885	EP300	NM_001429	1	31	11	+	41542743	41542820
229410421	chr22	41545086	41545260	41545109	41545232	EP300	NM_001429	1	31	13	+	41545042	41545179
229965806	chr22	41546054	41546211	41546077	41546188	EP300	NM_001429	1	31	14	+	41545765	41546202
227908584	chr22	41548129	41548301	41548152	41548277	EP300	NM_001429	1	31	16	+	41548210	41548354

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230505350	chr22	41553104	41553257	41553129	41553237	EP300	NM_001429	1	31	18	+	41553173	41553412
229040206	chr22	41556608	41556774	41556628	41556745	EP300	NM_001429	1	31	20	+	41556646	41556726
230422213	chr22	41564385	41564511	41564413	41564484	EP300	NM_001429	1	31	24	+	41564453	41564603
230722952	chr22	41565409	41565572	41565431	41565550	EP300	NM_001429	1	31	26	+	41565507	41565620
228833383	chr22	41568410	41568579	41568434	41568558	EP300	NM_001429	1	31	28	+	41568503	41568667
227866508	chr22	41572231	41572398	41572257	41572376	EP300	NM_001429	1	31	30	+	41572251	41572532
231259522	chr22	41572783	41572950	41572810	41572929	EP300	NM_001429	1	31	31	+	41572777	41576081
227964014	chr22	41573221	41573391	41573239	41573372	EP300	NM_001429	1	31	31	+	41572777	41576081
228026211	chr22	41573728	41573893	41573750	41573873	EP300	NM_001429	1	31	31	+	41572777	41576081
228074384	chr22	41574205	41574353	41574227	41574331	EP300	NM_001429	1	31	31	+	41572777	41576081
228162393	chr22	41574602	41574775	41574624	41574754	EP300	NM_001429	1	31	31	+	41572777	41576081
289125118	chr22	42523462	42523636	42523484	42523617	CYP2D6	NM_000106	1	9	7	-	42523449	42523636
289125118	chr22	42523462	42523636	42523484	42523617	CYP2D6	NM_001025161	2	8	6	-	42523449	42523636
287891289	chr22	42524164	42524304	42524184	42524282	CYP2D6	NM_000106	1	9	5	-	42524176	42524352
287891289	chr22	42524164	42524304	42524184	42524282	CYP2D6	NM_001025161	2	8	4	-	42524176	42524352
288330494	chr22	42525114	42525257	42525132	42525238	CYP2D6	NM_000106	1	9	3	-	42525035	42525187
286249533	chr22	42526639	42526812	42526659	42526789	CYP2D6	NM_000106	1	9	1	-	42526614	42526883
286249533	chr22	42526639	42526812	42526659	42526789	CYP2D6	NM_001025161	2	8	1	-	42526614	42526883
269551133	chrX	40988277	40988447	40988297	40988424	USP9X	NM_001039590	1	45	3	+	40988253	40988398
269551133	chrX	40988277	40988447	40988297	40988424	USP9X	NM_001039591	2	45	3	+	40988253	40988398
271066316	chrX	40993986	40994144	40994010	40994116	USP9X	NM_001039590	1	45	5	+	40993978	40994090
271066316	chrX	40993986	40994144	40994010	40994116	USP9X	NM_001039591	2	45	5	+	40993978	40994090
270206351	chrX	40999768	40999941	40999792	40999916	USP9X	NM_001039590	1	45	7	+	40999909	41000024
270206351	chrX	40999768	40999941	40999792	40999916	USP9X	NM_001039591	2	45	7	+	40999909	41000024
270259261	chrX	41000227	41000374	41000252	41000347	USP9X	NM_001039590	1	45	8	+	41000219	41000470
270259261	chrX	41000227	41000374	41000252	41000347	USP9X	NM_001039591	2	45	8	+	41000219	41000470
271529589	chrX	41000571	41000712	41000598	41000683	USP9X	NM_001039590	1	45	9	+	41000546	41000684
271529589	chrX	41000571	41000712	41000598	41000683	USP9X	NM_001039591	2	45	9	+	41000546	41000684
271937803	chrX	41003826	41004000	41003849	41003972	USP9X	NM_001039590	1	45	11	+	41003775	41003879
271937803	chrX	41003826	41004000	41003849	41003972	USP9X	NM_001039591	2	45	11	+	41003775	41003879
270294657	chrX	41010161	41010297	41010188	41010271	USP9X	NM_001039590	1	45	13	+	41010174	41010310
270294657	chrX	41010161	41010297	41010188	41010271	USP9X	NM_001039591	2	45	13	+	41010174	41010310
270979883	chrX	41021960	41022094	41021986	41022068	USP9X	NM_001039590	1	45	15	+	41022043	41022130
270979883	chrX	41021960	41022094	41021986	41022068	USP9X	NM_001039591	2	45	15	+	41022043	41022130
272443262	chrX	41025256	41025407	41025284	41025379	USP9X	NM_001039590	1	45	16	+	41025125	41025467
272443262	chrX	41025256	41025407	41025284	41025379	USP9X	NM_001039591	2	45	16	+	41025125	41025467
271849889	chrX	41027247	41027390	41027275	41027369	USP9X	NM_001039590	1	45	18	+	41027260	41027471
271849889	chrX	41027247	41027390	41027275	41027369	USP9X	NM_001039591	2	45	18	+	41027260	41027471
270084018	chrX	41029719	41029892	41029746	41029865	USP9X	NM_001039590	1	45	20	+	41029723	41029872
270084018	chrX	41029719	41029892	41029746	41029865	USP9X	NM_001039591	2	45	20	+	41029723	41029872
271311334	chrX	41043126	41043298	41043149	41043269	USP9X	NM_001039590	1	45	22	+	41043251	41043381

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271311334	chrX	41043126	41043298	41043149	41043269	USP9X	NM_001039591	2	45	22	+	41043251	41043381
269635376	chrX	41043740	41043912	41043764	41043891	USP9X	NM_001039590	1	45	23	+	41043650	41043928
269635376	chrX	41043740	41043912	41043764	41043891	USP9X	NM_001039591	2	45	23	+	41043650	41043928
271520970	chrX	41047300	41047431	41047318	41047403	USP9X	NM_001039590	1	45	25	+	41047245	41047370
271520970	chrX	41047300	41047431	41047318	41047403	USP9X	NM_001039591	2	45	25	+	41047245	41047370
270699044	chrX	41055428	41055566	41055455	41055545	USP9X	NM_001039590	1	45	27	+	41055504	41055612
270699044	chrX	41055428	41055566	41055455	41055545	USP9X	NM_001039591	2	45	27	+	41055504	41055612
272579288	chrX	41056669	41056799	41056689	41056770	USP9X	NM_001039590	1	45	29	+	41056617	41056763
272579288	chrX	41056669	41056799	41056689	41056770	USP9X	NM_001039591	2	45	29	+	41056617	41056763
270026210	chrX	41060270	41060444	41060291	41060416	USP9X	NM_001039590	1	45	31	+	41060313	41060533
270026210	chrX	41060270	41060444	41060291	41060416	USP9X	NM_001039591	2	45	31	+	41060313	41060533
271395109	chrX	41064558	41064723	41064582	41064700	USP9X	NM_001039590	1	45	32	+	41064556	41064746
271395109	chrX	41064558	41064723	41064582	41064700	USP9X	NM_001039591	2	45	32	+	41064556	41064746
271945806	chrX	41069787	41069941	41069811	41069920	USP9X	NM_001039590	1	45	33	+	41069762	41069935
271945806	chrX	41069787	41069941	41069811	41069920	USP9X	NM_001039591	2	45	33	+	41069762	41069935
270916338	chrX	41075155	41075315	41075176	41075293	USP9X	NM_001039590	1	45	35	+	41075152	41075905
270916338	chrX	41075155	41075315	41075176	41075293	USP9X	NM_001039591	2	45	35	+	41075152	41075905
272443264	chrX	41075606	41075779	41075633	41075752	USP9X	NM_001039590	1	45	35	+	41075152	41075905
272443264	chrX	41075606	41075779	41075633	41075752	USP9X	NM_001039591	2	45	35	+	41075152	41075905
271657569	chrX	41076474	41076621	41076495	41076594	USP9X	NM_001039590	1	45	36	+	41076473	41076596
271657569	chrX	41076474	41076621	41076495	41076594	USP9X	NM_001039591	2	45	36	+	41076473	41076596
272495457	chrX	41078315	41078468	41078341	41078441	USP9X	NM_001039590	1	45	38	+	41078355	41078484
272495457	chrX	41078315	41078468	41078341	41078441	USP9X	NM_001039591	2	45	38	+	41078355	41078484
269698278	chrX	41084005	41084177	41084029	41084157	USP9X	NM_001039590	1	45	40	+	41083995	41084215
269698278	chrX	41084005	41084177	41084029	41084157	USP9X	NM_001039591	2	45	40	+	41083995	41084215
269630797	chrX	41088509	41088664	41088536	41088643	USP9X	NM_001039590	1	45	42	+	41088506	41088662
269630797	chrX	41088509	41088664	41088536	41088643	USP9X	NM_001039591	2	45	42	+	41088506	41088662
271018508	chrX	41088901	41089074	41088929	41089049	USP9X	NM_001039591	2	45	43	+	41088820	41089032
271018508	chrX	41088901	41089074	41088929	41089049	USP9X	NM_001039590	1	45	43	+	41088820	41089080
270069802	chrX	41091555	41091695	41091581	41091673	USP9X	NM_001039590	1	45	45	+	41091640	41095832
270069802	chrX	41091555	41091695	41091581	41091673	USP9X	NM_001039591	2	45	45	+	41091640	41095832
233621867	chrX	44733128	44733252	44733152	44733233	KDM6A	NM_021140	1	29	2	+	44733170	44733233
233151787	chrX	44870185	44870322	44870212	44870294	KDM6A	NM_021140	1	29	5	+	44870206	44870264
232659486	chrX	44894113	44894283	44894141	44894255	KDM6A	NM_021140	1	29	7	+	44894176	44894230
233442258	chrX	44913061	44913185	44913088	44913163	KDM6A	NM_021140	1	29	10	+	44913074	44913200
233654913	chrX	44918297	44918424	44918325	44918393	KDM6A	NM_021140	1	29	11	+	44918251	44918349
233034073	chrX	44919188	44919357	44919216	44919338	KDM6A	NM_021140	1	29	13	+	44919267	44919401
232193218	chrX	44921881	44922016	44921907	44921988	KDM6A	NM_021140	1	29	15	+	44921892	44921993
231316630	chrX	44922836	44922991	44922858	44922970	KDM6A	NM_021140	1	29	16	+	44922667	44923062
232840039	chrX	44929031	44929205	44929057	44929180	KDM6A	NM_021140	1	29	17	+	44928824	44929602
234437533	chrX	44929494	44929630	44929519	44929605	KDM6A	NM_021140	1	29	17	+	44928824	44929602

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234693025	chrX	44937603	44937735	44937630	44937712	KDM6A	NM_021140	1	29	19	+	44937645	44937750
230952414	chrX	44938461	44938601	44938481	44938573	KDM6A	NM_021140	1	29	20	+	44938391	44938596
231360905	chrX	44942654	44942802	44942680	44942775	KDM6A	NM_021140	1	29	23	+	44942705	44942853
231826108	chrX	44948919	44949091	44948946	44949068	KDM6A	NM_021140	1	29	25	+	44948988	44949175
232083633	chrX	44949973	44950142	44949997	44950115	KDM6A	NM_021140	1	29	26	+	44949968	44950109
232869692	chrX	44969335	44969467	44969363	44969442	KDM6A	NM_021140	1	29	28	+	44969324	44969494
238571478	chrX	48117136	48117302	48117162	48117276	SSX1	NM_005635	1	8	3	+	48117181	48117295
261007470	chrX	48125677	48125848	48125699	48125826	SSX1	NM_005635	1	8	7	+	48125722	48125826
239125971	chrX	48542760	48542909	48542781	48542885	WAS	NM_000377	1	12	2	+	48542672	48542812
239505349	chrX	48544280	48544409	48544304	48544383	WAS	NM_000377	1	12	5	+	48544335	48544376
239908628	chrX	48546364	48546511	48546386	48546485	WAS	NM_000377	1	12	8	+	48546443	48546485
262402238	chrX	48547117	48547259	48547138	48547238	WAS	NM_000377	1	12	10	+	48547049	48547455
264820706	chrX	48549431	48549578	48549451	48549557	WAS	NM_000377	1	12	12	+	48549498	48549817
227550127	chrX	48650252	48650426	48650275	48650406	GATA1	NM_002049	1	6	3	+	48650251	48650628
228793209	chrX	48650789	48650961	48650810	48650933	GATA1	NM_002049	1	6	4	+	48650730	48650875
227650148	chrX	48652321	48652473	48652341	48652452	GATA1	NM_002049	1	6	6	+	48652200	48652717
265471474	chrX	48887815	48887978	48887837	48887958	TFE3	NM_006521	1	10	10	-	48886242	48888112
239317146	chrX	48888992	48889118	48889012	48889095	TFE3	NM_006521	1	10	9	-	48888912	48889059
261996895	chrX	48895437	48895611	48895459	48895588	TFE3	NM_006521	1	10	5	-	48895535	48895639
242133132	chrX	48895858	48896028	48895876	48896007	TFE3	NM_006521	1	10	4	-	48895722	48895967
241277623	chrX	48896832	48897004	48896855	48896982	TFE3	NM_006521	1	10	3	-	48896632	48896935
262448152	chrX	48900632	48900761	48900649	48900743	TFE3	NM_006521	1	10	1	-	48900637	48900990
232719190	chrX	53222071	53222218	53222093	53222197	KDM5C	NM_004187	2	26	26	-	53220503	53222514
233394266	chrX	53222538	53222712	53222556	53222693	KDM5C	NM_004187	2	26	25	-	53222619	53222818
233394266	chrX	53222538	53222712	53222556	53222693	KDM5C	NM_001146702	1	24	23	-	53222680	53222818
233916305	chrX	53223378	53223518	53223400	53223498	KDM5C	NM_004187	2	26	23	-	53223321	53223920
233916305	chrX	53223378	53223518	53223400	53223498	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
231227168	chrX	53223782	53223947	53223803	53223926	KDM5C	NM_004187	2	26	23	-	53223321	53223920
231227168	chrX	53223782	53223947	53223803	53223926	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
233295506	chrX	53224476	53224632	53224497	53224611	KDM5C	NM_004187	2	26	21	-	53224413	53224592
233295506	chrX	53224476	53224632	53224497	53224611	KDM5C	NM_001146702	1	24	19	-	53224413	53224592
232602474	chrX	53225905	53226056	53225927	53226035	KDM5C	NM_004187	2	26	19	-	53225868	53226226
232602474	chrX	53225905	53226056	53225927	53226035	KDM5C	NM_001146702	1	24	17	-	53225868	53226226
234203278	chrX	53227634	53227776	53227656	53227751	KDM5C	NM_004187	2	26	17	-	53227672	53227819
234203278	chrX	53227634	53227776	53227656	53227751	KDM5C	NM_001146702	1	24	15	-	53227672	53227819
232116379	chrX	53228133	53228288	53228153	53228266	KDM5C	NM_004187	2	26	15	-	53228159	53228340
232116379	chrX	53228133	53228288	53228153	53228266	KDM5C	NM_001146702	1	24	13	-	53228159	53228340
233714380	chrX	53231008	53231178	53231029	53231155	KDM5C	NM_004187	2	26	13	-	53231036	53231155
233714380	chrX	53231008	53231178	53231029	53231155	KDM5C	NM_001146702	1	24	11	-	53231036	53231155
233561851	chrX	53239942	53240094	53239964	53240069	KDM5C	NM_004187	2	26	11	-	53239858	53240039
233561851	chrX	53239942	53240094	53239964	53240069	KDM5C	NM_001146702	1	24	9	-	53239858	53240039

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232616920	chrX	53243798	53243970	53243819	53243948	KDM5C	NM_004187	2	26	8	-	53243871	53244029
232616920	chrX	53243798	53243970	53243819	53243948	KDM5C	NM_001146702	1	24	6	-	53243871	53244029
233677585	chrX	53245236	53245408	53245255	53245380	KDM5C	NM_004187	2	26	6	-	53245256	53245379
233677585	chrX	53245236	53245408	53245255	53245380	KDM5C	NM_001146702	1	24	4	-	53245256	53245379
234219370	chrX	53247036	53247181	53247057	53247153	KDM5C	NM_004187	2	26	4	-	53246978	53247148
234219370	chrX	53247036	53247181	53247057	53247153	KDM5C	NM_001146702	1	24	2	-	53246978	53247148
234167778	chrX	53253964	53254126	53253985	53254107	KDM5C	NM_004187	2	26	1	-	53253922	53254604
234167778	chrX	53253964	53254126	53253985	53254107	KDM5C	NM_001146702	1	24	1	-	53253922	53254604
231974862	chrX	63410059	63410220	63410080	63410197	FAM123B	NM_152424	1	2	2	-	63404997	63413264
228871697	chrX	63410464	63410635	63410484	63410608	FAM123B	NM_152424	1	2	2	-	63404997	63413264
228966707	chrX	63410887	63411056	63410910	63411032	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232010741	chrX	63411334	63411490	63411352	63411469	FAM123B	NM_152424	1	2	2	-	63404997	63413264
229466346	chrX	63411789	63411928	63411812	63411907	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232034043	chrX	63412155	63412327	63412181	63412307	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232011782	chrX	63412609	63412754	63412629	63412730	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232036327	chrX	63413070	63413196	63413093	63413175	FAM123B	NM_152424	1	2	2	-	63404997	63413264
264307250	chrX	66765318	66765485	66765340	66765467	AR	NM_000044	1	8	1	+	66763874	66766604
264308558	chrX	66765785	66765954	66765804	66765933	AR	NM_000044	1	8	1	+	66763874	66766604
264319593	chrX	66766274	66766445	66766292	66766428	AR	NM_000044	1	8	1	+	66763874	66766604
264905162	chrX	66863034	66863174	66863059	66863154	AR	NM_001011645	2	8	2	+	66863098	66863249
264905162	chrX	66863034	66863174	66863059	66863154	AR	NM_000044	1	8	2	+	66863098	66863249
257481829	chrX	66931212	66931374	66931240	66931351	AR	NM_001011645	2	8	4	+	66931244	66931531
257481829	chrX	66931212	66931374	66931240	66931351	AR	NM_000044	1	8	4	+	66931244	66931531
254496744	chrX	66937400	66937555	66937421	66937534	AR	NM_001011645	2	8	5	+	66937320	66937464
254496744	chrX	66937400	66937555	66937421	66937534	AR	NM_000044	1	8	5	+	66937320	66937464
266958813	chrX	66942764	66942934	66942786	66942913	AR	NM_001011645	2	8	7	+	66942669	66942826
266958813	chrX	66942764	66942934	66942786	66942913	AR	NM_000044	1	8	7	+	66942669	66942826
303257213	chrX	70586143	70586307	70586170	70586284	TAF1	NM_138923	2	38	1	+	70586114	70586344
303257213	chrX	70586143	70586307	70586170	70586284	TAF1	NM_004606	1	38	1	+	70586114	70586344
305593567	chrX	70594951	70595077	70594972	70595054	TAF1	NM_138923	2	38	4	+	70595017	70595136
305593567	chrX	70594951	70595077	70594972	70595054	TAF1	NM_004606	1	38	4	+	70595017	70595136
300429944	chrX	70596902	70597071	70596922	70597048	TAF1	NM_004606	1	38	5	+	70596800	70597041
300429944	chrX	70596902	70597071	70596922	70597048	TAF1	NM_138923	2	38	5	+	70596863	70597041
303984230	chrX	70598167	70598333	70598186	70598306	TAF1	NM_138923	2	38	7	+	70598085	70598303
303984230	chrX	70598167	70598333	70598186	70598306	TAF1	NM_004606	1	38	7	+	70598085	70598303
304901761	chrX	70601657	70601829	70601678	70601801	TAF1	NM_138923	2	38	9	+	70601593	70601769
304901761	chrX	70601657	70601829	70601678	70601801	TAF1	NM_004606	1	38	9	+	70601593	70601769
304844842	chrX	70602630	70602784	70602657	70602760	TAF1	NM_138923	2	38	11	+	70602611	70602718
304844842	chrX	70602630	70602784	70602657	70602760	TAF1	NM_004606	1	38	11	+	70602611	70602718
305892028	chrX	70603834	70603996	70603855	70603967	TAF1	NM_138923	2	38	13	+	70603812	70603985
305892028	chrX	70603834	70603996	70603855	70603967	TAF1	NM_004606	1	38	13	+	70603812	70603985

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300418453	chrX	70607029	70607196	70607054	70607172	TAF1	NM_138923	2	38	15	+	70607111	70607311
300418453	chrX	70607029	70607196	70607054	70607172	TAF1	NM_004606	1	38	15	+	70607111	70607311
305661436	chrX	70608082	70608256	70608106	70608228	TAF1	NM_138923	2	38	16	+	70608087	70608228
305661436	chrX	70608082	70608256	70608106	70608228	TAF1	NM_004606	1	38	16	+	70608087	70608228
299810576	chrX	70612512	70612644	70612535	70612620	TAF1	NM_138923	2	38	19	+	70612419	70612568
299810576	chrX	70612512	70612644	70612535	70612620	TAF1	NM_004606	1	38	19	+	70612419	70612568
302867481	chrX	70613177	70613341	70613198	70613315	TAF1	NM_138923	2	38	21	+	70613151	70613326
302867481	chrX	70613177	70613341	70613198	70613315	TAF1	NM_004606	1	38	21	+	70613151	70613326
303445556	chrX	70617070	70617223	70617098	70617197	TAF1	NM_138923	2	38	23	+	70617103	70617316
303445556	chrX	70617070	70617223	70617098	70617197	TAF1	NM_004606	1	38	23	+	70617103	70617316
304787258	chrX	70621335	70621509	70621358	70621485	TAF1	NM_138923	2	38	25	+	70621378	70621589
304787258	chrX	70621335	70621509	70621358	70621485	TAF1	NM_004606	1	38	25	+	70621378	70621589
302920015	chrX	70627767	70627919	70627790	70627897	TAF1	NM_138923	2	38	28	+	70627824	70628001
302920015	chrX	70627767	70627919	70627790	70627897	TAF1	NM_004606	1	38	28	+	70627824	70628001
300555819	chrX	70642992	70643141	70643015	70643120	TAF1	NM_138923	2	38	30	+	70642967	70643089
300555819	chrX	70642992	70643141	70643015	70643120	TAF1	NM_004606	1	38	30	+	70642967	70643089
305755393	chrX	70673940	70674114	70673961	70674088	TAF1	NM_138923	2	38	33	+	70674020	70674087
305755393	chrX	70673940	70674114	70673961	70674088	TAF1	NM_004606	1	38	33	+	70674020	70674087
303051272	chrX	70679336	70679460	70679358	70679437	TAF1	NM_138923	2	38	36	+	70679402	70679558
303051272	chrX	70679336	70679460	70679358	70679437	TAF1	NM_004606	1	38	36	+	70679402	70679558
300057107	chrX	70683589	70683733	70683610	70683712	TAF1	NM_138923	2	38	38	+	70683674	70685855
300057107	chrX	70683589	70683733	70683610	70683712	TAF1	NM_004606	1	38	38	+	70683674	70685855
274078084	chrX	76763852	76763987	76763877	76763960	ATRX	NM_000489	1	35	35	-	76760356	76764107
274078084	chrX	76763852	76763987	76763877	76763960	ATRX	NM_138270	2	34	34	-	76760356	76764107
273008867	chrX	76776250	76776396	76776278	76776370	ATRX	NM_000489	1	35	34	-	76776266	76776394
273008867	chrX	76776250	76776396	76776278	76776370	ATRX	NM_138270	2	34	33	-	76776266	76776394
274250697	chrX	76777733	76777867	76777755	76777846	ATRX	NM_000489	1	35	32	-	76777741	76777866
274250697	chrX	76777733	76777867	76777755	76777846	ATRX	NM_138270	2	34	31	-	76777741	76777866
273138417	chrX	76812865	76813038	76812893	76813011	ATRX	NM_000489	1	35	30	-	76812922	76813116
273138417	chrX	76812865	76813038	76812893	76813011	ATRX	NM_138270	2	34	29	-	76812922	76813116
273198390	chrX	76814167	76814294	76814193	76814264	ATRX	NM_000489	1	35	29	-	76814140	76814317
273198390	chrX	76814167	76814294	76814193	76814264	ATRX	NM_138270	2	34	28	-	76814140	76814317
274051097	chrX	76845193	76845359	76845219	76845330	ATRX	NM_000489	1	35	27	-	76845304	76845410
274051097	chrX	76845193	76845359	76845219	76845330	ATRX	NM_138270	2	34	26	-	76845304	76845410
273714387	chrX	76849236	76849382	76849258	76849354	ATRX	NM_000489	1	35	26	-	76849166	76849319
273714387	chrX	76849236	76849382	76849258	76849354	ATRX	NM_138270	2	34	25	-	76849166	76849319
274364891	chrX	76855081	76855252	76855109	76855228	ATRX	NM_000489	1	35	24	-	76855201	76855289
274364891	chrX	76855081	76855252	76855109	76855228	ATRX	NM_138270	2	34	23	-	76855201	76855289
273069004	chrX	76871964	76872121	76871995	76872093	ATRX	NM_000489	1	35	22	-	76872081	76872198
273069004	chrX	76871964	76872121	76871995	76872093	ATRX	NM_138270	2	34	21	-	76872081	76872198
273185319	chrX	76874390	76874545	76874416	76874519	ATRX	NM_000489	1	35	21	-	76874274	76874449

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273185319	chrX	76874390	76874545	76874416	76874519	ATRX	NM_138270	2	34	20	-	76874274	76874449
272768781	chrX	76888745	76888881	76888773	76888853	ATRX	NM_000489	1	35	19	-	76888695	76888872
272768781	chrX	76888745	76888881	76888773	76888853	ATRX	NM_138270	2	34	18	-	76888695	76888872
273002949	chrX	76889152	76889318	76889180	76889292	ATRX	NM_000489	1	35	18	-	76889054	76889200
273002949	chrX	76889152	76889318	76889180	76889292	ATRX	NM_138270	2	34	17	-	76889054	76889200
273217867	chrX	76891450	76891602	76891474	76891574	ATRX	NM_000489	1	35	16	-	76891406	76891547
273217867	chrX	76891450	76891602	76891474	76891574	ATRX	NM_138270	2	34	15	-	76891406	76891547
273452724	chrX	76909615	76909789	76909643	76909761	ATRX	NM_000489	1	35	14	-	76909588	76909690
273452724	chrX	76909615	76909789	76909643	76909761	ATRX	NM_138270	2	34	13	-	76909588	76909690
273176949	chrX	76918927	76919097	76918950	76919069	ATRX	NM_000489	1	35	12	-	76918871	76919047
273176949	chrX	76918927	76919097	76918950	76919069	ATRX	NM_138270	2	34	11	-	76918871	76919047
273276259	chrX	76931737	76931911	76931761	76931885	ATRX	NM_000489	1	35	10	-	76931721	76931793
273276259	chrX	76931737	76931911	76931761	76931885	ATRX	NM_138270	2	34	9	-	76931721	76931793
274012212	chrX	76937172	76937309	76937200	76937282	ATRX	NM_000489	1	35	9	-	76937012	76940085
274012212	chrX	76937172	76937309	76937200	76937282	ATRX	NM_138270	2	34	8	-	76937012	76940085
273992345	chrX	76937473	76937637	76937501	76937609	ATRX	NM_000489	1	35	9	-	76937012	76940085
273992345	chrX	76937473	76937637	76937501	76937609	ATRX	NM_138270	2	34	8	-	76937012	76940085
274014805	chrX	76937854	76938002	76937882	76937980	ATRX	NM_000489	1	35	9	-	76937012	76940085
274014805	chrX	76937854	76938002	76937882	76937980	ATRX	NM_138270	2	34	8	-	76937012	76940085
274000677	chrX	76938435	76938561	76938463	76938534	ATRX	NM_000489	1	35	9	-	76937012	76940085
274000677	chrX	76938435	76938561	76938463	76938534	ATRX	NM_138270	2	34	8	-	76937012	76940085
274016450	chrX	76938854	76938979	76938877	76938953	ATRX	NM_000489	1	35	9	-	76937012	76940085
274016450	chrX	76938854	76938979	76938877	76938953	ATRX	NM_138270	2	34	8	-	76937012	76940085
272801828	chrX	76939274	76939404	76939302	76939376	ATRX	NM_000489	1	35	9	-	76937012	76940085
272801828	chrX	76939274	76939404	76939302	76939376	ATRX	NM_138270	2	34	8	-	76937012	76940085
274022360	chrX	76939599	76939761	76939626	76939733	ATRX	NM_000489	1	35	9	-	76937012	76940085
274022360	chrX	76939599	76939761	76939626	76939733	ATRX	NM_138270	2	34	8	-	76937012	76940085
272892384	chrX	76939953	76940091	76939980	76940072	ATRX	NM_000489	1	35	9	-	76937012	76940085
272892384	chrX	76939953	76940091	76939980	76940072	ATRX	NM_138270	2	34	8	-	76937012	76940085
273138387	chrX	76951948	76952096	76951972	76952068	ATRX	NM_000489	1	35	5	-	76952065	76952192
273138387	chrX	76951948	76952096	76951972	76952068	ATRX	NM_138270	2	34	5	-	76952065	76952192
273522366	chrX	76954055	76954201	76954080	76954172	ATRX	NM_000489	1	35	3	-	76954062	76954117
273522366	chrX	76954055	76954201	76954080	76954172	ATRX	NM_138270	2	34	3	-	76954062	76954117
270176290	chrX	79277738	79277899	79277759	79277878	TBX22	NM_016954	3	8	1	+	79277742	79277943
270176290	chrX	79277738	79277899	79277759	79277878	TBX22	NM_001109879	2	9	2	+	79277767	79277943
270176290	chrX	79277738	79277899	79277759	79277878	TBX22	NM_001109878	1	9	2	+	79277767	79277943
270984879	chrX	79279527	79279700	79279552	79279676	TBX22	NM_016954	3	8	3	+	79279562	79279663
270984879	chrX	79279527	79279700	79279552	79279676	TBX22	NM_001109879	2	9	4	+	79279562	79279663
270984879	chrX	79279527	79279700	79279552	79279676	TBX22	NM_001109878	1	9	4	+	79279562	79279663
272553983	chrX	79282266	79282436	79282289	79282412	TBX22	NM_016954	3	8	5	+	79282203	79282367
272553983	chrX	79282266	79282436	79282289	79282412	TBX22	NM_001109879	2	9	6	+	79282203	79282367

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272553983	chrX	79282266	79282436	79282289	79282412	TBX22	NM_001109878	1	9	6	+	79282203	79282367
271639407	chrX	79285943	79286110	79285968	79286082	TBX22	NM_016954	3	8	8	+	79285997	79287268
271639407	chrX	79285943	79286110	79285968	79286082	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271639407	chrX	79285943	79286110	79285968	79286082	TBX22	NM_001109878	1	9	9	+	79285997	79287268
271637613	chrX	79286420	79286592	79286442	79286565	TBX22	NM_016954	3	8	8	+	79285997	79287268
271637613	chrX	79286420	79286592	79286442	79286565	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271637613	chrX	79286420	79286592	79286442	79286565	TBX22	NM_001109878	1	9	9	+	79285997	79287268
253972931	chrX	100608231	100608401	100608252	100608379	BTK	NM_000061	1	19	18	-	100608182	100608339
265681463	chrX	100611012	100611185	100611035	100611164	BTK	NM_000061	1	19	15	-	100611040	100611256
262478576	chrX	100612431	100612595	100612452	100612572	BTK	NM_000061	1	19	13	-	100612497	100612571
266705515	chrX	100614209	100614377	100614230	100614354	BTK	NM_000061	1	19	10	-	100614281	100614335
265958773	chrX	100615621	100615772	100615644	100615744	BTK	NM_000061	1	19	8	-	100615556	100615743
257231228	chrX	100624983	100625108	100625005	100625083	BTK	NM_000061	1	19	5	-	100624986	100625067
253829947	chrX	100630125	100630299	100630149	100630274	BTK	NM_000061	1	19	2	-	100630132	100630302
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_001128172	4	15	2	+	110385324	110385424
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_001128168	3	16	2	+	110385324	110385424
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_001128173	5	15	2	+	110385324	110385424
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_001128166	1	16	4	+	110385324	110385424
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_001128167	2	15	3	+	110385324	110385424
270390579	chrX	110385353	110385505	110385380	110385477	PAK3	NM_002578	6	18	6	+	110385324	110385424
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_001128172	4	15	4	+	110390965	110391118
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_001128168	3	16	5	+	110390965	110391118
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_001128173	5	15	4	+	110390965	110391118
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_001128166	1	16	5	+	110390965	110391118
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_001128167	2	15	4	+	110390965	110391118
269585238	chrX	110390972	110391145	110390993	110391118	PAK3	NM_002578	6	18	7	+	110390965	110391118
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_001128172	4	15	6	+	110406143	110406274
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_001128168	3	16	7	+	110406143	110406274
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_001128173	5	15	6	+	110406143	110406274
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_001128166	1	16	7	+	110406143	110406274
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_001128167	2	15	6	+	110406143	110406274
269564100	chrX	110406173	110406335	110406193	110406307	PAK3	NM_002578	6	18	9	+	110406143	110406274
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_001128172	4	15	9	+	110435355	110435403
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_001128168	3	16	10	+	110435355	110435403
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_001128173	5	15	9	+	110435355	110435403
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_001128166	1	16	10	+	110435355	110435403
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_001128167	2	15	9	+	110435355	110435403
270238911	chrX	110435249	110435396	110435274	110435370	PAK3	NM_002578	6	18	12	+	110435355	110435403
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_001128172	4	15	11	+	110437529	110437646
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_001128168	3	16	12	+	110437529	110437646
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_001128173	5	15	11	+	110437529	110437646

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_001128166	1	16	12	+	110437529	110437646
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_001128167	2	15	11	+	110437529	110437646
270506588	chrX	110437410	110437571	110437434	110437543	PAK3	NM_002578	6	18	14	+	110437529	110437646
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_001128172	4	15	13	+	110439672	110439868
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_001128168	3	16	14	+	110439672	110439868
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_001128173	5	15	13	+	110439672	110439868
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_001128166	1	16	14	+	110439672	110439868
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_001128167	2	15	13	+	110439672	110439868
270748461	chrX	110439638	110439801	110439666	110439777	PAK3	NM_002578	6	18	16	+	110439672	110439868
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_001128172	4	15	15	+	110463586	110464173
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_001128168	3	16	16	+	110463586	110464173
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_001128173	5	15	15	+	110463586	110464173
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_001128166	1	16	16	+	110463586	110464173
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_001128167	2	15	15	+	110463586	110464173
272588651	chrX	110463483	110463620	110463516	110463595	PAK3	NM_002578	6	18	18	+	110463586	110464173
299175013	chrX	123499593	123499737	123499621	123499709	SH2D1A	NM_001114937	1	4	2	+	123499611	123499674
299175013	chrX	123499593	123499737	123499621	123499709	SH2D1A	NM_002351	2	4	2	+	123499611	123499674
295127668	chrX	152482060	152482195	152482077	152482170	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
295133034	chrX	152482463	152482604	152482484	152482579	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
295172446	chrX	152482850	152483010	152482871	152482987	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
298906482	chrX	153760331	153760482	153760351	153760462	G6PD	NM_001042351	2	13	12	-	153760403	153760495
298906482	chrX	153760331	153760482	153760351	153760462	G6PD	NM_000402	1	13	12	-	153760403	153760495
299024987	chrX	153760863	153761035	153760881	153761018	G6PD	NM_001042351	2	13	10	-	153760782	153761017
299024987	chrX	153760863	153761035	153760881	153761018	G6PD	NM_000402	1	13	10	-	153760782	153761017
299121238	chrX	153761803	153761946	153761824	153761925	G6PD	NM_001042351	2	13	8	-	153761791	153761884
299121238	chrX	153761803	153761946	153761824	153761925	G6PD	NM_000402	1	13	8	-	153761791	153761884
299087229	chrX	153762608	153762780	153762629	153762759	G6PD	NM_001042351	2	13	6	-	153762553	153762711
299087229	chrX	153762608	153762780	153762629	153762759	G6PD	NM_000402	1	13	6	-	153762553	153762711
299072574	chrX	153764102	153764244	153764122	153764225	G6PD	NM_001042351	2	13	4	-	153764152	153764260
299072574	chrX	153764102	153764244	153764122	153764225	G6PD	NM_000402	1	13	4	-	153764152	153764260
298916908	chrX	153774246	153774405	153774266	153774381	G6PD	NM_001042351	2	13	2	-	153774251	153774378
298916908	chrX	153774246	153774405	153774266	153774381	G6PD	NM_000402	1	13	2	-	153774251	153774378
242158034	chr1	2491222	2491351	2491242	2491331	TNFRSF14	NM_003820	1	8	4	+	2491262	2491417
239720969	chr1	2493159	2493316	2493182	2493295	TNFRSF14	NM_003820	1	8	6	+	2493112	2493254
294866890	chr1	6527510	6527674	6527530	6527653	PLEKHG5	NM_001042664	2	21	21	-	6526152	6527632
294866890	chr1	6527510	6527674	6527530	6527653	PLEKHG5	NM_001042665	3	21	21	-	6526152	6527632
294866890	chr1	6527510	6527674	6527530	6527653	PLEKHG5	NM_020631	4	21	21	-	6526152	6527632
294866890	chr1	6527510	6527674	6527530	6527653	PLEKHG5	NM_001042663	1	22	22	-	6526152	6527632
294866890	chr1	6527510	6527674	6527530	6527653	PLEKHG5	NM_198681	5	22	22	-	6526152	6527632
294026880	chr1	6528140	6528311	6528162	6528293	PLEKHG5	NM_001042664	2	21	20	-	6527885	6528646
294026880	chr1	6528140	6528311	6528162	6528293	PLEKHG5	NM_001042665	3	21	20	-	6527885	6528646

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294026880	chr1	6528140	6528311	6528162	6528293	PLEKHG5	NM_020631	4	21	20	-	6527885	6528646
294026880	chr1	6528140	6528311	6528162	6528293	PLEKHG5	NM_001042663	1	22	21	-	6527885	6528646
294026880	chr1	6528140	6528311	6528162	6528293	PLEKHG5	NM_198681	5	22	21	-	6527885	6528646
294260986	chr1	6529081	6529252	6529101	6529234	PLEKHG5	NM_001042664	2	21	19	-	6529102	6529301
294260986	chr1	6529081	6529252	6529101	6529234	PLEKHG5	NM_001042665	3	21	19	-	6529102	6529301
294260986	chr1	6529081	6529252	6529101	6529234	PLEKHG5	NM_020631	4	21	19	-	6529102	6529301
294260986	chr1	6529081	6529252	6529101	6529234	PLEKHG5	NM_001042663	1	22	20	-	6529102	6529301
294260986	chr1	6529081	6529252	6529101	6529234	PLEKHG5	NM_198681	5	22	20	-	6529102	6529301
295379979	chr1	6529596	6529737	6529616	6529712	PLEKHG5	NM_001042664	2	21	17	-	6529604	6529736
295379979	chr1	6529596	6529737	6529616	6529712	PLEKHG5	NM_001042665	3	21	17	-	6529604	6529736
295379979	chr1	6529596	6529737	6529616	6529712	PLEKHG5	NM_020631	4	21	17	-	6529604	6529736
295379979	chr1	6529596	6529737	6529616	6529712	PLEKHG5	NM_001042663	1	22	18	-	6529604	6529736
295379979	chr1	6529596	6529737	6529616	6529712	PLEKHG5	NM_198681	5	22	18	-	6529604	6529736
294989499	chr1	6530450	6530624	6530473	6530607	PLEKHG5	NM_001042664	2	21	15	-	6530566	6530703
294989499	chr1	6530450	6530624	6530473	6530607	PLEKHG5	NM_001042665	3	21	15	-	6530566	6530703
294989499	chr1	6530450	6530624	6530473	6530607	PLEKHG5	NM_020631	4	21	15	-	6530566	6530703
294989499	chr1	6530450	6530624	6530473	6530607	PLEKHG5	NM_001042663	1	22	16	-	6530566	6530703
294989499	chr1	6530450	6530624	6530473	6530607	PLEKHG5	NM_198681	5	22	16	-	6530566	6530703
294267858	chr1	6530893	6531064	6530912	6531047	PLEKHG5	NM_001042664	2	21	14	-	6530795	6530944
294267858	chr1	6530893	6531064	6530912	6531047	PLEKHG5	NM_001042665	3	21	14	-	6530795	6530944
294267858	chr1	6530893	6531064	6530912	6531047	PLEKHG5	NM_020631	4	21	14	-	6530795	6530944
294267858	chr1	6530893	6531064	6530912	6531047	PLEKHG5	NM_001042663	1	22	15	-	6530795	6530944
294267858	chr1	6530893	6531064	6530912	6531047	PLEKHG5	NM_198681	5	22	15	-	6530795	6530944
293957501	chr1	6531542	6531680	6531565	6531660	PLEKHG5	NM_001042664	2	21	12	-	6531548	6531697
293957501	chr1	6531542	6531680	6531565	6531660	PLEKHG5	NM_001042665	3	21	12	-	6531548	6531697
293957501	chr1	6531542	6531680	6531565	6531660	PLEKHG5	NM_020631	4	21	12	-	6531548	6531697
293957501	chr1	6531542	6531680	6531565	6531660	PLEKHG5	NM_001042663	1	22	13	-	6531548	6531697
293957501	chr1	6531542	6531680	6531565	6531660	PLEKHG5	NM_198681	5	22	13	-	6531548	6531697
295279645	chr1	6532576	6532716	6532599	6532696	PLEKHG5	NM_001042664	2	21	10	-	6532587	6532682
295279645	chr1	6532576	6532716	6532599	6532696	PLEKHG5	NM_001042665	3	21	10	-	6532587	6532682
295279645	chr1	6532576	6532716	6532599	6532696	PLEKHG5	NM_020631	4	21	10	-	6532587	6532682
295279645	chr1	6532576	6532716	6532599	6532696	PLEKHG5	NM_001042663	1	22	11	-	6532587	6532682
295279645	chr1	6532576	6532716	6532599	6532696	PLEKHG5	NM_198681	5	22	11	-	6532587	6532682
294478924	chr1	6533370	6533498	6533388	6533476	PLEKHG5	NM_001042664	2	21	8	-	6533311	6533514
294478924	chr1	6533370	6533498	6533388	6533476	PLEKHG5	NM_001042665	3	21	8	-	6533311	6533514
294478924	chr1	6533370	6533498	6533388	6533476	PLEKHG5	NM_020631	4	21	8	-	6533311	6533514
294478924	chr1	6533370	6533498	6533388	6533476	PLEKHG5	NM_001042663	1	22	9	-	6533311	6533514
294478924	chr1	6533370	6533498	6533388	6533476	PLEKHG5	NM_198681	5	22	9	-	6533311	6533514
293934686	chr1	6534417	6534590	6534437	6534569	PLEKHG5	NM_001042664	2	21	6	-	6534511	6534647
293934686	chr1	6534417	6534590	6534437	6534569	PLEKHG5	NM_001042665	3	21	6	-	6534511	6534647
293934686	chr1	6534417	6534590	6534437	6534569	PLEKHG5	NM_020631	4	21	6	-	6534511	6534647

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293934686	chr1	6534417	6534590	6534437	6534569	PLEKHG5	NM_001042663	1	22	7	-	6534511	6534647
293934686	chr1	6534417	6534590	6534437	6534569	PLEKHG5	NM_198681	5	22	7	-	6534511	6534647
294092006	chr1	6535956	6536123	6535977	6536101	PLEKHG5	NM_001042664	2	21	3	-	6535991	6536096
294092006	chr1	6535956	6536123	6535977	6536101	PLEKHG5	NM_001042665	3	21	3	-	6535991	6536096
294092006	chr1	6535956	6536123	6535977	6536101	PLEKHG5	NM_020631	4	21	3	-	6535991	6536096
294092006	chr1	6535956	6536123	6535977	6536101	PLEKHG5	NM_001042663	1	22	4	-	6535991	6536096
294092006	chr1	6535956	6536123	6535977	6536101	PLEKHG5	NM_198681	5	22	4	-	6535991	6536096
295246033	chr1	6579443	6579577	6579467	6579552	PLEKHG5	NM_198681	5	22	1	-	6579505	6580069
294696370	chr1	9775574	9775699	9775591	9775682	PIK3CD	NM_005026	1	24	4	+	9775599	9775827
294135873	chr1	9775908	9776039	9775929	9776019	PIK3CD	NM_005026	1	24	5	+	9775907	9776136
294163015	chr1	9776562	9776705	9776582	9776687	PIK3CD	NM_005026	1	24	6	+	9776498	9776677
294159274	chr1	9778649	9778822	9778670	9778804	PIK3CD	NM_005026	1	24	9	+	9778752	9778973
294985593	chr1	9780108	9780261	9780128	9780243	PIK3CD	NM_005026	1	24	11	+	9780170	9780300
295272242	chr1	9780857	9781025	9780877	9781006	PIK3CD	NM_005026	1	24	13	+	9780800	9780967
294705339	chr1	9781734	9781878	9781751	9781858	PIK3CD	NM_005026	1	24	16	+	9781819	9781918
295388887	chr1	9782202	9782370	9782222	9782350	PIK3CD	NM_005026	1	24	18	+	9782302	9782414
294689592	chr1	9783246	9783405	9783267	9783383	PIK3CD	NM_005026	1	24	20	+	9783183	9783350
294705199	chr1	9784367	9784497	9784395	9784480	PIK3CD	NM_005026	1	24	22	+	9784334	9784479
242442006	chr1	11167449	11167580	11167475	11167554	MTOR	NM_004958	1	58	58	-	11166588	11167557
236088874	chr1	11172837	11172981	11172856	11172958	MTOR	NM_004958	1	58	54	-	11172909	11172974
236401551	chr1	11175400	11175552	11175421	11175525	MTOR	NM_004958	1	58	51	-	11175453	11175525
235637180	chr1	11181367	11181493	11181387	11181468	MTOR	NM_004958	1	58	49	-	11181303	11181425
237502624	chr1	11184639	11184774	11184660	11184751	MTOR	NM_004958	1	58	47	-	11184555	11184690
237250850	chr1	11187078	11187235	11187100	11187210	MTOR	NM_004958	1	58	45	-	11187067	11187201
237538587	chr1	11188085	11188255	11188106	11188228	MTOR	NM_004958	1	58	43	-	11188061	11188183
235538631	chr1	11188889	11189062	11188913	11189039	MTOR	NM_004958	1	58	41	-	11188912	11189008
236794546	chr1	11190642	11190805	11190662	11190780	MTOR	NM_004958	1	58	39	-	11190586	11190834
237951564	chr1	11194359	11194523	11194382	11194503	MTOR	NM_004958	1	58	37	-	11194408	11194523
239338431	chr1	11199563	11199725	11199581	11199707	MTOR	NM_004958	1	58	35	-	11199590	11199715
237328549	chr1	11206702	11206876	11206723	11206848	MTOR	NM_004958	1	58	32	-	11206733	11206848
238172418	chr1	11217252	11217376	11217272	11217351	MTOR	NM_004958	1	58	30	-	11217209	11217348
236950519	chr1	11259510	11259659	11259533	11259637	MTOR	NM_004958	1	58	27	-	11259598	11259760
237505475	chr1	11269334	11269492	11269356	11269466	MTOR	NM_004958	1	58	25	-	11269369	11269515
242201305	chr1	11272459	11272583	11272481	11272554	MTOR	NM_004958	1	58	23	-	11272369	11272531
238986358	chr1	11276143	11276317	11276165	11276294	MTOR	NM_004958	1	58	20	-	11276205	11276291
238532025	chr1	11290899	11291069	11290924	11291046	MTOR	NM_004958	1	58	18	-	11290982	11291111
237628281	chr1	11292455	11292615	11292476	11292591	MTOR	NM_004958	1	58	16	-	11292493	11292585
237141662	chr1	11297880	11298021	11297899	11297999	MTOR	NM_004958	1	58	13	-	11297900	11298105
238753363	chr1	11298644	11298770	11298664	11298742	MTOR	NM_004958	1	58	12	-	11298459	11298674
238992850	chr1	11301577	11301751	11301598	11301727	MTOR	NM_004958	1	58	10	-	11301610	11301738
236058540	chr1	11307644	11307817	11307669	11307793	MTOR	NM_004958	1	58	8	-	11307682	11307790

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236286849	chr1	11313863	11314000	11313881	11313977	MTOR	NM_004958	1	58	6	-	11313896	11314030
241166866	chr1	11316968	11317133	11316989	11317110	MTOR	NM_004958	1	58	4	-	11316990	11317222
258783469	chr1	11319263	11319421	11319284	11319400	MTOR	NM_004958	1	58	2	-	11319305	11319480
262033805	chr1	17348973	17349135	17348994	17349113	SDHB	NM_003000	1	8	7	-	17349103	17349225
242031628	chr1	17354280	17354421	17354302	17354394	SDHB	NM_003000	1	8	5	-	17354244	17354360
238784852	chr1	17371152	17371326	17371180	17371304	SDHB	NM_003000	1	8	2	-	17371256	17371383
237553879	chr1	18960733	18960904	18960754	18960884	PAX7	NM_002584	2	8	2	+	18960797	18961032
237553879	chr1	18960733	18960904	18960754	18960884	PAX7	NM_001135254	1	9	2	+	18960797	18961032
237553879	chr1	18960733	18960904	18960754	18960884	PAX7	NM_013945	3	8	2	+	18960797	18961032
240303735	chr1	18962611	18962754	18962638	18962733	PAX7	NM_002584	2	8	4	+	18962731	18962865
240303735	chr1	18962611	18962754	18962638	18962733	PAX7	NM_001135254	1	9	4	+	18962731	18962865
239386296	chr1	19018283	19018408	19018303	19018387	PAX7	NM_002584	2	8	5	+	19018248	19018447
239386296	chr1	19018283	19018408	19018303	19018387	PAX7	NM_001135254	1	9	5	+	19018248	19018447
239386296	chr1	19018283	19018408	19018303	19018387	PAX7	NM_013945	3	8	5	+	19018248	19018447
235304633	chr1	19029552	19029723	19029574	19029701	PAX7	NM_002584	2	8	7	+	19029588	19029790
235304633	chr1	19029552	19029723	19029574	19029701	PAX7	NM_001135254	1	9	7	+	19029588	19029790
235304633	chr1	19029552	19029723	19029574	19029701	PAX7	NM_013945	3	8	7	+	19029588	19029790
237308552	chr1	19062292	19062455	19062311	19062431	PAX7	NM_001135254	1	9	8	+	19062126	19062372
237308552	chr1	19062292	19062455	19062311	19062431	PAX7	NM_002584	2	8	8	+	19062126	19062632
237308552	chr1	19062292	19062455	19062311	19062431	PAX7	NM_013945	3	8	8	+	19062126	19062632
225015835	chr1	27023183	27023352	27023203	27023335	ARID1A	NM_139135	2	20	1	+	27022522	27024031
225015835	chr1	27023183	27023352	27023203	27023335	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223545729	chr1	27023485	27023612	27023503	27023595	ARID1A	NM_139135	2	20	1	+	27022522	27024031
223545729	chr1	27023485	27023612	27023503	27023595	ARID1A	NM_006015	1	20	1	+	27022522	27024031
223547643	chr1	27023886	27024053	27023904	27024035	ARID1A	NM_139135	2	20	1	+	27022522	27024031
223547643	chr1	27023886	27024053	27023904	27024035	ARID1A	NM_006015	1	20	1	+	27022522	27024031
222713071	chr1	27057682	27057852	27057704	27057831	ARID1A	NM_139135	2	20	3	+	27057643	27058095
222713071	chr1	27057682	27057852	27057704	27057831	ARID1A	NM_006015	1	20	3	+	27057643	27058095
222482150	chr1	27087229	27087403	27087255	27087381	ARID1A	NM_139135	2	20	5	+	27087347	27087587
222482150	chr1	27087229	27087403	27087255	27087381	ARID1A	NM_006015	1	20	5	+	27087347	27087587
222566968	chr1	27087908	27088051	27087929	27088027	ARID1A	NM_139135	2	20	6	+	27087875	27087964
222566968	chr1	27087908	27088051	27087929	27088027	ARID1A	NM_006015	1	20	6	+	27087875	27087964
224713333	chr1	27089525	27089698	27089545	27089678	ARID1A	NM_139135	2	20	8	+	27089464	27089776
224713333	chr1	27089525	27089698	27089545	27089678	ARID1A	NM_006015	1	20	8	+	27089464	27089776
222728323	chr1	27092855	27093029	27092880	27093004	ARID1A	NM_139135	2	20	10	+	27092948	27093057
222728323	chr1	27092855	27093029	27092880	27093004	ARID1A	NM_006015	1	20	10	+	27092948	27093057
223507169	chr1	27094403	27094564	27094425	27094538	ARID1A	NM_139135	2	20	11	+	27094281	27094490
223507169	chr1	27094403	27094564	27094425	27094538	ARID1A	NM_006015	1	20	11	+	27094281	27094490
223141663	chr1	27099017	27099189	27099037	27099164	ARID1A	NM_139135	2	20	13	+	27098991	27099123
223141663	chr1	27099017	27099189	27099037	27099164	ARID1A	NM_006015	1	20	13	+	27098991	27099123
222666532	chr1	27099890	27100056	27099909	27100033	ARID1A	NM_139135	2	20	15	+	27099837	27099987

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222666532	chr1	27099890	27100056	27099909	27100033	ARID1A	NM_006015	1	20	15	+	27099837	27099987
225144662	chr1	27100765	27100933	27100790	27100915	ARID1A	NM_006015	1	20	18	+	27100820	27101711
225173327	chr1	27101170	27101332	27101192	27101310	ARID1A	NM_006015	1	20	18	+	27100820	27101711
222573315	chr1	27101574	27101748	27101595	27101726	ARID1A	NM_006015	1	20	18	+	27100820	27101711
222573315	chr1	27101574	27101748	27101595	27101726	ARID1A	NM_139135	2	20	18	+	27101471	27101711
223518210	chr1	27105519	27105662	27105541	27105641	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223518210	chr1	27105519	27105662	27105541	27105641	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223518218	chr1	27105942	27106070	27105963	27106049	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223518218	chr1	27105942	27106070	27105963	27106049	ARID1A	NM_006015	1	20	20	+	27105514	27108601
223579249	chr1	27106341	27106514	27106364	27106494	ARID1A	NM_139135	2	20	20	+	27105514	27108601
223579249	chr1	27106341	27106514	27106364	27106494	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224997894	chr1	27106740	27106872	27106762	27106852	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224997894	chr1	27106740	27106872	27106762	27106852	ARID1A	NM_006015	1	20	20	+	27105514	27108601
224995126	chr1	27107165	27107311	27107186	27107285	ARID1A	NM_139135	2	20	20	+	27105514	27108601
224995126	chr1	27107165	27107311	27107186	27107285	ARID1A	NM_006015	1	20	20	+	27105514	27108601
231004130	chr1	32740570	32740704	32740591	32740684	LCK	NM_005356	2	13	4	+	32740594	32740684
231004130	chr1	32740570	32740704	32740591	32740684	LCK	NM_001042771	1	13	4	+	32740594	32740684
233365503	chr1	32741466	32741636	32741487	32741616	LCK	NM_005356	2	13	7	+	32741515	32741664
233365503	chr1	32741466	32741636	32741487	32741616	LCK	NM_001042771	1	13	7	+	32741515	32741664
232550196	chr1	32742176	32742348	32742197	32742329	LCK	NM_005356	2	13	9	+	32742208	32742387
232550196	chr1	32742176	32742348	32742197	32742329	LCK	NM_001042771	1	13	9	+	32742208	32742387
233184959	chr1	32745499	32745625	32745520	32745603	LCK	NM_005356	2	13	11	+	32745442	32745595
233184959	chr1	32745499	32745625	32745520	32745603	LCK	NM_001042771	1	13	11	+	32745442	32745595
233340159	chr1	32751197	32751368	32751217	32751346	LCK	NM_005356	2	13	13	+	32751115	32751766
233340159	chr1	32751197	32751368	32751217	32751346	LCK	NM_001042771	1	13	13	+	32751115	32751766
241509966	chr1	40363266	40363439	40363286	40363414	MYCL1	NM_001033082	2	3	3	-	40361096	40363642
241509966	chr1	40363266	40363439	40363286	40363414	MYCL1	NM_001033081	1	2	2	-	40361096	40363642
241869507	chr1	40366470	40366622	40366489	40366603	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235129035	chr1	40366880	40367033	40366898	40367014	MYCL1	NM_005376	3	2	2	-	40365284	40367115
235129035	chr1	40366880	40367033	40366898	40367014	MYCL1	NM_001033082	2	3	2	-	40366611	40367115
235129035	chr1	40366880	40367033	40366898	40367014	MYCL1	NM_001033081	1	2	1	-	40366611	40367687
237301619	chr1	43803747	43803921	43803769	43803902	MPL	NM_005373	1	12	2	+	43803770	43803902
238538049	chr1	43804958	43805130	43804980	43805109	MPL	NM_005373	1	12	4	+	43804942	43805240
237648822	chr1	43805935	43806089	43805962	43806067	MPL	NM_005373	1	12	6	+	43806058	43806184
242031286	chr1	43812371	43812523	43812392	43812502	MPL	NM_005373	1	12	8	+	43812463	43812605
235664696	chr1	43814908	43815081	43814933	43815063	MPL	NM_005373	1	12	10	+	43814934	43815030
241711920	chr1	43818394	43818518	43818416	43818493	MPL	NM_005373	1	12	12	+	43818189	43820135
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_012222	6	16	14	-	45796854	45797006
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_001048171	1	16	14	-	45796854	45797006
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_001128425	5	16	14	-	45796854	45797006
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_001048174	4	16	14	-	45796854	45797006

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_001048173	3	16	14	-	45796854	45797006
235636895	chr1	45796799	45796934	45796827	45796915	MUTYH	NM_001048172	2	16	14	-	45796854	45797006
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_012222	6	16	12	-	45797333	45797521
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_001048171	1	16	12	-	45797333	45797521
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_001128425	5	16	12	-	45797333	45797521
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_001048174	4	16	12	-	45797333	45797521
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_001048173	3	16	12	-	45797333	45797521
237481091	chr1	45797312	45797464	45797332	45797444	MUTYH	NM_001048172	2	16	12	-	45797333	45797521
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_012222	6	16	10	-	45797838	45797982
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_001048171	1	16	10	-	45797838	45797982
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_001128425	5	16	10	-	45797838	45797982
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_001048174	4	16	10	-	45797838	45797982
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_001048173	3	16	10	-	45797838	45797982
237750565	chr1	45797853	45798024	45797871	45798004	MUTYH	NM_001048172	2	16	10	-	45797838	45797982
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_012222	6	16	6	-	45798590	45798631
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_001048171	1	16	6	-	45798590	45798631
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_001128425	5	16	6	-	45798590	45798631
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_001048174	4	16	6	-	45798590	45798631
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_001048173	3	16	6	-	45798590	45798631
240281327	chr1	45798498	45798668	45798520	45798645	MUTYH	NM_001048172	2	16	6	-	45798590	45798631
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_001048172	2	16	3	-	45799085	45799236
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_001048171	1	16	3	-	45799085	45799233
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_001048174	4	16	3	-	45799085	45799233
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_001048173	3	16	3	-	45799085	45799233
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_012222	6	16	3	-	45799085	45799266
237691345	chr1	45799093	45799267	45799114	45799245	MUTYH	NM_001128425	5	16	3	-	45799085	45799275
265217081	chr1	47685359	47685515	47685377	47685498	TAL1	NM_003189	1	4	4	-	47681963	47685846
265159899	chr1	47685705	47685877	47685730	47685849	TAL1	NM_003189	1	4	4	-	47681963	47685846
240388042	chr1	47691133	47691292	47691150	47691274	TAL1	NM_003189	1	4	2	-	47691115	47691561
321949430	chr1	47799583	47799728	47799600	47799709	CMPK1	NM_016308	2	6	1	+	47799469	47799788
321949430	chr1	47799583	47799728	47799600	47799709	CMPK1	NM_001136140	1	5	1	+	47799469	47799788
321877815	chr1	47838619	47838763	47838646	47838735	CMPK1	NM_016308	2	6	3	+	47838627	47838779
321877815	chr1	47838619	47838763	47838646	47838735	CMPK1	NM_001136140	1	5	2	+	47838627	47838779
321844825	chr1	47840881	47841038	47840908	47841011	CMPK1	NM_016308	2	6	5	+	47840869	47840965
321844825	chr1	47840881	47841038	47840908	47841011	CMPK1	NM_001136140	1	5	4	+	47840869	47840965
225596011	chr1	51439514	51439650	51439541	51439628	CDKN2C	NM_001262	1	3	3	+	51439565	51440306
225596011	chr1	51439514	51439650	51439541	51439628	CDKN2C	NM_078626	2	2	2	+	51439565	51440309
232147392	chr1	59247604	59247774	59247626	59247753	JUN	NM_002228	1	1	1	-	59246463	59249785
232187510	chr1	59248356	59248520	59248373	59248503	JUN	NM_002228	1	1	1	-	59246463	59249785
232058500	chr1	65301157	65301313	65301175	65301284	JAK1	NM_002227	1	25	24	-	65301079	65301189
233098213	chr1	65303643	65303815	65303669	65303788	JAK1	NM_002227	1	25	22	-	65303615	65303787

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233536088	chr1	65305331	65305503	65305358	65305482	JAK1	NM_002227	1	25	20	-	65305286	65305478
231115990	chr1	65309671	65309805	65309691	65309782	JAK1	NM_002227	1	25	17	-	65309747	65309898
233715676	chr1	65311153	65311277	65311175	65311257	JAK1	NM_002227	1	25	15	-	65311196	65311323
231766843	chr1	65313266	65313419	65313292	65313398	JAK1	NM_002227	1	25	13	-	65313215	65313358
233062564	chr1	65321250	65321411	65321271	65321383	JAK1	NM_002227	1	25	11	-	65321192	65321381
232038781	chr1	65330398	65330570	65330420	65330546	JAK1	NM_002227	1	25	8	-	65330470	65330655
232932404	chr1	65332689	65332858	65332715	65332835	JAK1	NM_002227	1	25	7	-	65332549	65332891
233337251	chr1	65339032	65339206	65339052	65339180	JAK1	NM_002227	1	25	5	-	65339053	65339206
233757513	chr1	65348901	65349051	65348928	65349027	JAK1	NM_002227	1	25	3	-	65348960	65349158
224739952	chr1	85733189	85733344	85733219	85733317	BCL10	NM_003921	1	3	3	-	85731460	85733665
223216196	chr1	85733593	85733743	85733620	85733716	BCL10	NM_003921	1	3	3	-	85731460	85733665
222969030	chr1	85736517	85736663	85736544	85736635	BCL10	NM_003921	1	3	2	-	85736301	85736589
299199908	chr1	97544562	97544736	97544587	97544708	DPYD	NM_000110	1	23	23	-	97543300	97544702
298938594	chr1	97564070	97564242	97564098	97564214	DPYD	NM_000110	1	23	21	-	97564045	97564188
298925596	chr1	97700416	97700588	97700439	97700560	DPYD	NM_000110	1	23	19	-	97700408	97700550
329751229	chr1	97839021	97839191	97839044	97839163	DPYD	NM_000110	1	23	16	-	97839117	97839200
299080416	chr1	97915562	97915704	97915590	97915676	DPYD	NM_000110	1	23	14	-	97915615	97915779
298978017	chr1	97981371	97981500	97981394	97981477	DPYD	NM_000110	1	23	13	-	97981282	97981497
329739921	chr1	98039226	98039372	98039254	98039351	DPYD	NM_000110	1	23	11	-	98039316	98039526
299042374	chr1	98058841	98059003	98058863	98058980	DPYD	NM_000110	1	23	10	-	98058774	98058943
299202090	chr1	98144712	98144848	98144734	98144820	DPYD	NM_000110	1	23	8	-	98144651	98144738
299255022	chr1	98186389	98186561	98186413	98186535	DPYD	NM_001160301	2	6	6	-	98185314	98186482
299019950	chr1	98205865	98206039	98205890	98206015	DPYD	NM_001160301	2	6	4	-	98205948	98206035
299019950	chr1	98205865	98206039	98205890	98206015	DPYD	NM_000110	1	23	4	-	98205948	98206035
299037641	chr1	98348770	98348942	98348795	98348918	DPYD	NM_001160301	2	6	2	-	98348820	98348930
299037641	chr1	98348770	98348942	98348795	98348918	DPYD	NM_000110	1	23	2	-	98348820	98348930
261992705	chr1	114940402	114940534	114940429	114940506	TRIM33	NM_015906	1	20	20	-	114935399	114940482
261992705	chr1	114940402	114940534	114940429	114940506	TRIM33	NM_033020	2	19	19	-	114935399	114940482
238693151	chr1	114943976	114944114	114943996	114944090	TRIM33	NM_015906	1	20	17	-	114944011	114944085
238693151	chr1	114943976	114944114	114943996	114944090	TRIM33	NM_033020	2	19	17	-	114944011	114944085
264707391	chr1	114948023	114948169	114948047	114948144	TRIM33	NM_015906	1	20	15	-	114948032	114948381
264707391	chr1	114948023	114948169	114948047	114948144	TRIM33	NM_033020	2	19	15	-	114948032	114948381
241101424	chr1	114949599	114949738	114949626	114949711	TRIM33	NM_015906	1	20	14	-	114949563	114949722
241101424	chr1	114949599	114949738	114949626	114949711	TRIM33	NM_033020	2	19	14	-	114949563	114949722
266405516	chr1	114967271	114967395	114967293	114967367	TRIM33	NM_015906	1	20	10	-	114967213	114967377
266405516	chr1	114967271	114967395	114967293	114967367	TRIM33	NM_033020	2	19	10	-	114967213	114967377
239397856	chr1	114968275	114968425	114968296	114968396	TRIM33	NM_015906	1	20	9	-	114968071	114968345
239397856	chr1	114968275	114968425	114968296	114968396	TRIM33	NM_033020	2	19	9	-	114968071	114968345
241374390	chr1	114970357	114970492	114970378	114970466	TRIM33	NM_015906	1	20	7	-	114970370	114970516
241374390	chr1	114970357	114970492	114970378	114970466	TRIM33	NM_033020	2	19	7	-	114970370	114970516
266291585	chr1	114976281	114976446	114976307	114976417	TRIM33	NM_015906	1	20	5	-	114976239	114976355

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
266291585	chr1	114976281	114976446	114976307	114976417	TRIM33	NM_033020	2	19	5	-	114976239	114976355
240054812	chr1	115005977	115006106	115006004	115006078	TRIM33	NM_015906	1	20	3	-	115006034	115006178
240054812	chr1	115005977	115006106	115006004	115006078	TRIM33	NM_033020	2	19	3	-	115006034	115006178
238824990	chr1	115006901	115007075	115006927	115007047	TRIM33	NM_015906	1	20	2	-	115006892	115007010
238824990	chr1	115006901	115007075	115006927	115007047	TRIM33	NM_033020	2	19	2	-	115006892	115007010
266355648	chr1	115053324	115053476	115053341	115053459	TRIM33	NM_015906	1	20	1	-	115053172	115053781
266355648	chr1	115053324	115053476	115053341	115053459	TRIM33	NM_033020	2	19	1	-	115053172	115053781
237243672	chr1	115252239	115252402	115252258	115252374	NRAS	NM_002524	1	7	4	-	115252190	115252349
237248971	chr1	115258677	115258802	115258705	115258781	NRAS	NM_002524	1	7	2	-	115258671	115258798
242103129	chr1	120458212	120458338	120458233	120458317	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
242089236	chr1	120458639	120458764	120458660	120458743	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237121169	chr1	120459087	120459260	120459109	120459235	NOTCH2	NM_024408	2	34	34	-	120454176	120459317
237669460	chr1	120460910	120461082	120460937	120461060	NOTCH2	NM_024408	2	34	32	-	120461029	120461176
238375387	chr1	120462116	120462290	120462137	120462263	NOTCH2	NM_024408	2	34	31	-	120461935	120462236
237122141	chr1	120464357	120464509	120464377	120464485	NOTCH2	NM_024408	2	34	29	-	120464336	120464432
239289337	chr1	120465330	120465467	120465351	120465443	NOTCH2	NM_024408	2	34	27	-	120465259	120465401
235165652	chr1	120466558	120466702	120466580	120466674	NOTCH2	NM_024408	2	34	26	-	120466260	120466607
257692662	chr1	120468210	120468343	120468228	120468326	NOTCH2	NM_024408	2	34	25	-	120467928	120468433
241526442	chr1	120471498	120471639	120471521	120471615	NOTCH2	NM_024408	2	34	23	-	120471599	120471835
235731344	chr1	120478018	120478153	120478043	120478131	NOTCH2	NM_001200001	1	22	22	-	120477736	120478227
235731344	chr1	120478018	120478153	120478043	120478131	NOTCH2	NM_024408	2	34	22	-	120478095	120478227
238476825	chr1	120480363	120480530	120480385	120480509	NOTCH2	NM_001200001	1	22	20	-	120480480	120480633
238476825	chr1	120480363	120480530	120480385	120480509	NOTCH2	NM_024408	2	34	20	-	120480480	120480633
235816422	chr1	120484033	120484191	120484055	120484166	NOTCH2	NM_001200001	1	22	18	-	120484149	120484377
235816422	chr1	120484033	120484191	120484055	120484166	NOTCH2	NM_024408	2	34	18	-	120484149	120484377
240752289	chr1	120491043	120491215	120491065	120491190	NOTCH2	NM_001200001	1	22	17	-	120491037	120491189
240752289	chr1	120491043	120491215	120491065	120491190	NOTCH2	NM_024408	2	34	17	-	120491037	120491189
236400355	chr1	120493358	120493511	120493379	120493484	NOTCH2	NM_001200001	1	22	15	-	120493347	120493460
236400355	chr1	120493358	120493511	120493379	120493484	NOTCH2	NM_024408	2	34	15	-	120493347	120493460
235611339	chr1	120497709	120497883	120497730	120497861	NOTCH2	NM_001200001	1	22	13	-	120497663	120497855
235611339	chr1	120497709	120497883	120497730	120497861	NOTCH2	NM_024408	2	34	13	-	120497663	120497855
237644417	chr1	120506327	120506473	120506350	120506450	NOTCH2	NM_001200001	1	22	11	-	120506197	120506430
237644417	chr1	120506327	120506473	120506350	120506450	NOTCH2	NM_024408	2	34	11	-	120506197	120506430
237328237	chr1	120509989	120510160	120510014	120510138	NOTCH2	NM_001200001	1	22	8	-	120510056	120510244
237328237	chr1	120509989	120510160	120510014	120510138	NOTCH2	NM_024408	2	34	8	-	120510056	120510244
237636363	chr1	120512109	120512282	120512132	120512260	NOTCH2	NM_001200001	1	22	6	-	120512134	120512367
237636363	chr1	120512109	120512282	120512132	120512260	NOTCH2	NM_024408	2	34	6	-	120512134	120512367
238056291	chr1	120539526	120539700	120539550	120539681	NOTCH2	NM_001200001	1	22	4	-	120539620	120539955
238056291	chr1	120539526	120539700	120539550	120539681	NOTCH2	NM_024408	2	34	4	-	120539620	120539955
238089891	chr1	120539918	120540043	120539937	120540021	NOTCH2	NM_001200001	1	22	4	-	120539620	120539955
238089891	chr1	120539918	120540043	120539937	120540021	NOTCH2	NM_024408	2	34	4	-	120539620	120539955

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237645114	chr1	144854089	144854252	144854113	144854230	PDE4DIP	NM_001198832	6	46	45	-	144854165	144854211
237645114	chr1	144854089	144854252	144854113	144854230	PDE4DIP	NM_001198834	7	44	43	-	144854165	144854211
237645114	chr1	144854089	144854252	144854113	144854230	PDE4DIP	NM_014644	8	44	43	-	144854165	144854211
235292280	chr1	144855844	144855970	144855862	144855945	PDE4DIP	NM_001198832	6	46	43	-	144855740	144855883
235292280	chr1	144855844	144855970	144855862	144855945	PDE4DIP	NM_001198834	7	44	41	-	144855740	144855883
235292280	chr1	144855844	144855970	144855862	144855945	PDE4DIP	NM_014644	8	44	41	-	144855740	144855883
241118515	chr1	144857592	144857764	144857620	144857744	PDE4DIP	NM_001198832	6	46	41	-	144857612	144857728
241118515	chr1	144857592	144857764	144857620	144857744	PDE4DIP	NM_001198834	7	44	39	-	144857612	144857728
241118515	chr1	144857592	144857764	144857620	144857744	PDE4DIP	NM_014644	8	44	39	-	144857612	144857728
236403266	chr1	144863207	144863377	144863230	144863352	PDE4DIP	NM_001198832	6	46	39	-	144863318	144863442
236403266	chr1	144863207	144863377	144863230	144863352	PDE4DIP	NM_001198834	7	44	37	-	144863318	144863442
236403266	chr1	144863207	144863377	144863230	144863352	PDE4DIP	NM_014644	8	44	37	-	144863318	144863442
236869106	chr1	144865744	144865888	144865767	144865865	PDE4DIP	NM_001198832	6	46	37	-	144865810	144865929
236869106	chr1	144865744	144865888	144865767	144865865	PDE4DIP	NM_001198834	7	44	35	-	144865810	144865929
236869106	chr1	144865744	144865888	144865767	144865865	PDE4DIP	NM_014644	8	44	35	-	144865810	144865929
235811629	chr1	144867844	144868014	144867865	144867993	PDE4DIP	NM_001198832	6	46	35	-	144867921	144868172
235811629	chr1	144867844	144868014	144867865	144867993	PDE4DIP	NM_001198834	7	44	33	-	144867921	144868172
235811629	chr1	144867844	144868014	144867865	144867993	PDE4DIP	NM_014644	8	44	33	-	144867921	144868172
236842413	chr1	144871749	144871886	144871769	144871859	PDE4DIP	NM_001198834	7	44	32	-	144871696	144871881
236842413	chr1	144871749	144871886	144871769	144871859	PDE4DIP	NM_014644	8	44	32	-	144871696	144871881
237069981	chr1	144874597	144874738	144874618	144874715	PDE4DIP	NM_001198832	6	46	33	-	144874681	144874904
237069981	chr1	144874597	144874738	144874618	144874715	PDE4DIP	NM_001198834	7	44	30	-	144874681	144874904
237069981	chr1	144874597	144874738	144874618	144874715	PDE4DIP	NM_014644	8	44	30	-	144874681	144874904
236548237	chr1	144876915	144877062	144876943	144877042	PDE4DIP	NM_001198832	6	46	31	-	144877036	144877271
236548237	chr1	144876915	144877062	144876943	144877042	PDE4DIP	NM_001198834	7	44	28	-	144877036	144877271
236548237	chr1	144876915	144877062	144876943	144877042	PDE4DIP	NM_014644	8	44	28	-	144877036	144877271
235378816	chr1	144879151	144879308	144879174	144879281	PDE4DIP	NM_001198832	6	46	30	-	144879035	144879563
235378816	chr1	144879151	144879308	144879174	144879281	PDE4DIP	NM_001198834	7	44	27	-	144879035	144879563
235378816	chr1	144879151	144879308	144879174	144879281	PDE4DIP	NM_014644	8	44	27	-	144879035	144879563
237629333	chr1	144881434	144881597	144881460	144881580	PDE4DIP	NM_001198832	6	46	28	-	144881430	144881622
237629333	chr1	144881434	144881597	144881460	144881580	PDE4DIP	NM_001198834	7	44	25	-	144881430	144881622
237629333	chr1	144881434	144881597	144881460	144881580	PDE4DIP	NM_014644	8	44	25	-	144881430	144881622
237736320	chr1	144882631	144882776	144882654	144882753	PDE4DIP	NM_001198834	7	44	24	-	144882446	144882881
237736320	chr1	144882631	144882776	144882654	144882753	PDE4DIP	NM_014644	8	44	24	-	144882446	144882881
235048587	chr1	144886106	144886247	144886128	144886225	PDE4DIP	NM_001198832	6	46	26	-	144886097	144886329
235048587	chr1	144886106	144886247	144886128	144886225	PDE4DIP	NM_001198834	7	44	23	-	144886097	144886329
235048587	chr1	144886106	144886247	144886128	144886225	PDE4DIP	NM_014644	8	44	23	-	144886097	144886329
236879263	chr1	144902983	144903155	144903006	144903133	PDE4DIP	NM_001198832	6	46	24	-	144903077	144903204
236879263	chr1	144902983	144903155	144903006	144903133	PDE4DIP	NM_001198834	7	44	21	-	144903077	144903204
236879263	chr1	144902983	144903155	144903006	144903133	PDE4DIP	NM_014644	8	44	21	-	144903077	144903204
236879263	chr1	144902983	144903155	144903006	144903133	PDE4DIP	NM_001002812	3	23	21	-	144903077	144903204

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236879263	chr1	144902983	144903155	144903006	144903133	PDE4DIP	NM_001002811	2	19	17	-	144903077	144903204
236605072	chr1	144906109	144906279	144906136	144906256	PDE4DIP	NM_001198832	6	46	22	-	144906059	144906196
236605072	chr1	144906109	144906279	144906136	144906256	PDE4DIP	NM_001198834	7	44	19	-	144906059	144906196
236605072	chr1	144906109	144906279	144906136	144906256	PDE4DIP	NM_014644	8	44	19	-	144906059	144906196
236605072	chr1	144906109	144906279	144906136	144906256	PDE4DIP	NM_001002812	3	23	19	-	144906059	144906196
236605072	chr1	144906109	144906279	144906136	144906256	PDE4DIP	NM_001002811	2	19	15	-	144906059	144906196
237026902	chr1	144911882	144912016	144911906	144911988	PDE4DIP	NM_001198832	6	46	19	-	144911882	144911963
237026902	chr1	144911882	144912016	144911906	144911988	PDE4DIP	NM_001198834	7	44	16	-	144911882	144911963
237026902	chr1	144911882	144912016	144911906	144911988	PDE4DIP	NM_014644	8	44	16	-	144911882	144911963
237026902	chr1	144911882	144912016	144911906	144911988	PDE4DIP	NM_001002812	3	23	16	-	144911882	144911963
237026902	chr1	144911882	144912016	144911906	144911988	PDE4DIP	NM_001002811	2	19	12	-	144911882	144911963
234950438	chr1	144915392	144915552	144915421	144915531	PDE4DIP	NM_001198832	6	46	17	-	144915445	144915639
234950438	chr1	144915392	144915552	144915421	144915531	PDE4DIP	NM_001198834	7	44	14	-	144915445	144915639
234950438	chr1	144915392	144915552	144915421	144915531	PDE4DIP	NM_014644	8	44	14	-	144915445	144915639
234950438	chr1	144915392	144915552	144915421	144915531	PDE4DIP	NM_001002812	3	23	14	-	144915445	144915639
234950438	chr1	144915392	144915552	144915421	144915531	PDE4DIP	NM_001002811	2	19	10	-	144915445	144915639
237742914	chr1	144917434	144917583	144917456	144917563	PDE4DIP	NM_001198832	6	46	15	-	144917499	144917636
237742914	chr1	144917434	144917583	144917456	144917563	PDE4DIP	NM_001198834	7	44	12	-	144917499	144917636
237742914	chr1	144917434	144917583	144917456	144917563	PDE4DIP	NM_014644	8	44	12	-	144917499	144917636
237742914	chr1	144917434	144917583	144917456	144917563	PDE4DIP	NM_001002812	3	23	12	-	144917499	144917636
237742914	chr1	144917434	144917583	144917456	144917563	PDE4DIP	NM_001002811	2	19	8	-	144917499	144917636
235552029	chr1	144918927	144919057	144918948	144919028	PDE4DIP	NM_001198832	6	46	13	-	144918833	144918991
235552029	chr1	144918927	144919057	144918948	144919028	PDE4DIP	NM_001198834	7	44	10	-	144918833	144918991
235552029	chr1	144918927	144919057	144918948	144919028	PDE4DIP	NM_014644	8	44	10	-	144918833	144918991
235552029	chr1	144918927	144919057	144918948	144919028	PDE4DIP	NM_001002812	3	23	10	-	144918833	144918991
235552029	chr1	144918927	144919057	144918948	144919028	PDE4DIP	NM_001002811	2	19	6	-	144918833	144918991
237596265	chr1	144922147	144922296	144922171	144922272	PDE4DIP	NM_001198832	6	46	11	-	144922187	144922279
237596265	chr1	144922147	144922296	144922171	144922272	PDE4DIP	NM_001198834	7	44	8	-	144922187	144922279
237596265	chr1	144922147	144922296	144922171	144922272	PDE4DIP	NM_014644	8	44	8	-	144922187	144922279
237596265	chr1	144922147	144922296	144922171	144922272	PDE4DIP	NM_001002812	3	23	8	-	144922187	144922279
237596265	chr1	144922147	144922296	144922171	144922272	PDE4DIP	NM_001002811	2	19	4	-	144922187	144922279
236296853	chr1	144923698	144923846	144923720	144923822	PDE4DIP	NM_001198832	6	46	9	-	144923690	144923821
236296853	chr1	144923698	144923846	144923720	144923822	PDE4DIP	NM_001198834	7	44	6	-	144923690	144923821
236296853	chr1	144923698	144923846	144923720	144923822	PDE4DIP	NM_014644	8	44	6	-	144923690	144923821
236296853	chr1	144923698	144923846	144923720	144923822	PDE4DIP	NM_001002812	3	23	6	-	144923690	144923821
236296853	chr1	144923698	144923846	144923720	144923822	PDE4DIP	NM_001002811	2	19	2	-	144923690	144923821
240430143	chr1	144930884	144931050	144930909	144931027	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
236949929	chr1	144931355	144931517	144931376	144931496	PDE4DIP	NM_001002811	2	19	1	-	144930584	144932032
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001198832	6	46	5	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001198834	7	44	2	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_014644	8	44	2	-	144955216	144955292

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001195261	5	5	3	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001195260	4	5	3	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_022359	9	7	5	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001002812	3	23	2	-	144955216	144955292
235068746	chr1	144955266	144955391	144955289	144955371	PDE4DIP	NM_001002810	1	4	2	-	144955216	144955292
234945360	chr1	145015767	145015906	145015788	145015885	PDE4DIP	NM_001198832	6	46	3	-	145015860	145016011
234945360	chr1	145015767	145015906	145015788	145015885	PDE4DIP	NM_022359	9	7	3	-	145015860	145016011
236986582	chr1	145039499	145039634	145039519	145039609	PDE4DIP	NM_001198832	6	46	1	-	145039590	145039992
232687558	chr1	145525023	145525162	145525044	145525138	ITGA10	NM_003637	1	30	1	+	145524990	145525117
231127428	chr1	145528215	145528385	145528239	145528365	ITGA10	NM_003637	1	30	4	+	145528254	145528345
231462672	chr1	145530782	145530954	145530805	145530933	ITGA10	NM_003637	1	30	7	+	145530878	145531026
234433011	chr1	145532377	145532536	145532398	145532507	ITGA10	NM_003637	1	30	9	+	145532457	145532622
233640920	chr1	145533100	145533264	145533122	145533243	ITGA10	NM_003637	1	30	11	+	145533055	145533199
231547396	chr1	145533846	145534020	145533873	145533996	ITGA10	NM_003637	1	30	13	+	145533798	145533941
233556313	chr1	145535674	145535844	145535696	145535822	ITGA10	NM_003637	1	30	16	+	145535735	145535901
233709944	chr1	145536835	145537006	145536862	145536987	ITGA10	NM_003637	1	30	18	+	145536853	145536966
231161228	chr1	145537698	145537857	145537719	145537833	ITGA10	NM_003637	1	30	21	+	145537737	145537829
231945161	chr1	145538944	145539116	145538967	145539096	ITGA10	NM_003637	1	30	25	+	145538980	145539093
232999948	chr1	145541422	145541584	145541446	145541556	ITGA10	NM_003637	1	30	28	+	145541441	145541536
222493828	chr1	147084618	147084788	147084643	147084767	BCL9	NM_004326	1	10	5	+	147084682	147084998
223743505	chr1	147086142	147086306	147086165	147086286	BCL9	NM_004326	1	10	6	+	147086226	147086415
224752671	chr1	147090559	147090733	147090584	147090712	BCL9	NM_004326	1	10	8	+	147090622	147092863
224769868	chr1	147090984	147091116	147091004	147091090	BCL9	NM_004326	1	10	8	+	147090622	147092863
223249581	chr1	147091424	147091595	147091445	147091571	BCL9	NM_004326	1	10	8	+	147090622	147092863
224771570	chr1	147091825	147091984	147091846	147091963	BCL9	NM_004326	1	10	8	+	147090622	147092863
224789312	chr1	147092306	147092475	147092329	147092454	BCL9	NM_004326	1	10	8	+	147090622	147092863
223271587	chr1	147092773	147092919	147092794	147092897	BCL9	NM_004326	1	10	8	+	147090622	147092863
224484489	chr1	147095541	147095711	147095569	147095692	BCL9	NM_004326	1	10	10	+	147095643	147098015
224506289	chr1	147096021	147096154	147096041	147096134	BCL9	NM_004326	1	10	10	+	147095643	147098015
224510214	chr1	147096424	147096568	147096445	147096547	BCL9	NM_004326	1	10	10	+	147095643	147098015
270685211	chr1	150549911	150550044	150549934	150550015	MCL1	NM_021960	2	3	3	-	150547027	150549967
270685211	chr1	150549911	150550044	150549934	150550015	MCL1	NM_001197320	1	4	4	-	150547027	150549967
270685211	chr1	150549911	150550044	150549934	150550015	MCL1	NM_182763	3	2	2	-	150547027	150549967
271046844	chr1	150551204	150551376	150551228	150551356	MCL1	NM_001197320	1	4	2	-	150551319	150551439
271046844	chr1	150551204	150551376	150551228	150551356	MCL1	NM_021960	2	3	1	-	150551319	150552214
271046844	chr1	150551204	150551376	150551228	150551356	MCL1	NM_182763	3	2	1	-	150551319	150552214
271816086	chr1	150551634	150551806	150551653	150551788	MCL1	NM_021960	2	3	1	-	150551319	150552214
271816086	chr1	150551634	150551806	150551653	150551788	MCL1	NM_182763	3	2	1	-	150551319	150552214
223250648	chr1	150784472	150784622	150784494	150784594	ARNT	NM_001668	2	22	22	-	150782181	150784586
223250648	chr1	150784472	150784622	150784494	150784594	ARNT	NM_178427	3	21	21	-	150782181	150784586
223250648	chr1	150784472	150784622	150784494	150784594	ARNT	NM_001197325	1	21	21	-	150782181	150784586

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222534318	chr1	150786641	150786806	150786663	150786779	ARNT	NM_001197325	1	21	19	-	150786553	150786712
222534318	chr1	150786641	150786806	150786663	150786779	ARNT	NM_001668	2	22	20	-	150786553	150786715
222534318	chr1	150786641	150786806	150786663	150786779	ARNT	NM_178427	3	21	19	-	150786553	150786715
224112676	chr1	150789462	150789607	150789489	150789579	ARNT	NM_001668	2	22	17	-	150789558	150789678
224112676	chr1	150789462	150789607	150789489	150789579	ARNT	NM_178427	3	21	16	-	150789558	150789678
224112676	chr1	150789462	150789607	150789489	150789579	ARNT	NM_001197325	1	21	16	-	150789558	150789678
222479079	chr1	150790363	150790537	150790391	150790511	ARNT	NM_001668	2	22	15	-	150790396	150790506
222479079	chr1	150790363	150790537	150790391	150790511	ARNT	NM_178427	3	21	14	-	150790396	150790506
222479079	chr1	150790363	150790537	150790391	150790511	ARNT	NM_001197325	1	21	14	-	150790396	150790506
225121006	chr1	150801482	150801652	150801509	150801630	ARNT	NM_001668	2	22	12	-	150801569	150801703
225121006	chr1	150801482	150801652	150801509	150801630	ARNT	NM_178427	3	21	11	-	150801569	150801703
225121006	chr1	150801482	150801652	150801509	150801630	ARNT	NM_001197325	1	21	11	-	150801569	150801703
222206251	chr1	150804337	150804511	150804358	150804486	ARNT	NM_001668	2	22	10	-	150804294	150804379
222206251	chr1	150804337	150804511	150804358	150804486	ARNT	NM_178427	3	21	9	-	150804294	150804379
222206251	chr1	150804337	150804511	150804358	150804486	ARNT	NM_001197325	1	21	9	-	150804294	150804379
223119828	chr1	150808785	150808959	150808809	150808936	ARNT	NM_001668	2	22	7	-	150808756	150808969
223119828	chr1	150808785	150808959	150808809	150808936	ARNT	NM_178427	3	21	6	-	150808756	150808969
223119828	chr1	150808785	150808959	150808809	150808936	ARNT	NM_001197325	1	21	6	-	150808756	150808969
222529352	chr1	150814773	150814929	150814797	150814906	ARNT	NM_001668	2	22	5	-	150814900	150814944
225177733	chr1	150830711	150830876	150830738	150830853	ARNT	NM_001668	2	22	2	-	150830825	150830936
225177733	chr1	150830711	150830876	150830738	150830853	ARNT	NM_178427	3	21	2	-	150830825	150830936
225177733	chr1	150830711	150830876	150830738	150830853	ARNT	NM_001197325	1	21	2	-	150830825	150830936
294885571	chr1	154950366	154950524	154950392	154950498	CKS1B	NM_001826	1	3	2	+	154950463	154950590
294885571	chr1	154950366	154950524	154950392	154950498	CKS1B	NR_024163	2	3	2	+	154950463	154950590
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001044391	4	5	4	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001044390	3	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204290	12	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204289	11	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204288	10	8	7	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_002456	20	8	7	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204286	8	9	8	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204294	16	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204293	15	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001044392	5	5	4	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001018017	2	8	7	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001044393	6	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204292	14	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204297	19	5	4	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204296	18	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204295	17	6	5	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204287	9	8	7	-	155159701	155159850

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204285	7	9	8	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001204291	13	7	6	-	155159701	155159850
238672207	chr1	155159598	155159772	155159622	155159752	MUC1	NM_001018016	1	8	7	-	155159701	155159850
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204290	12	7	4	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204289	11	7	4	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204288	10	8	5	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_002456	20	8	5	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204286	8	9	6	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204294	16	7	4	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204293	15	7	5	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001018017	2	8	5	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204292	14	7	4	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204287	9	8	5	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204285	7	9	6	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001204291	13	7	4	-	155160198	155160334
237825634	chr1	155160105	155160242	155160127	155160222	MUC1	NM_001018016	1	8	5	-	155160198	155160334
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_001204286	8	9	4	-	155160639	155161063
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_001204285	7	9	4	-	155160639	155161063
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_002456	20	8	3	-	155160639	155160761
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_001204293	15	7	3	-	155160639	155160761
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_001204297	19	5	3	-	155160639	155160761
236140634	chr1	155160711	155160880	155160738	155160857	MUC1	NM_001204287	9	8	3	-	155160639	155160761
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204286	8	9	2	-	155161699	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204285	7	9	2	-	155161699	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204289	11	7	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204288	10	8	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001044392	5	5	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204292	14	7	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204297	19	5	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204296	18	7	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204295	17	6	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204287	9	8	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204291	13	7	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001018016	1	8	2	-	155161974	155162101
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001044391	4	5	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001044390	3	7	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_002456	20	8	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204294	16	7	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001204293	15	7	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001018017	2	8	2	-	155161974	155162074
237036970	chr1	155162017	155162182	155162039	155162157	MUC1	NM_001044393	6	7	2	-	155161974	155162074

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235682733	chr1	156830615	156830771	156830633	156830754	NTRK1	NM_002529	3	17	1	+	156830671	156830938
235682733	chr1	156830615	156830771	156830633	156830754	NTRK1	NM_001012331	2	16	1	+	156830671	156830938
235690796	chr1	156834491	156834657	156834510	156834637	NTRK1	NM_002529	3	17	3	+	156834520	156834591
235690796	chr1	156834491	156834657	156834510	156834637	NTRK1	NM_001012331	2	16	3	+	156834520	156834591
235690796	chr1	156834491	156834657	156834510	156834637	NTRK1	NM_001007792	1	17	4	+	156834520	156834591
236801740	chr1	156838192	156838344	156838212	156838325	NTRK1	NM_002529	3	17	6	+	156838297	156838439
236801740	chr1	156838192	156838344	156838212	156838325	NTRK1	NM_001012331	2	16	6	+	156838297	156838439
236801740	chr1	156838192	156838344	156838212	156838325	NTRK1	NM_001007792	1	17	7	+	156838297	156838439
236920537	chr1	156843393	156843567	156843413	156843543	NTRK1	NM_002529	3	17	8	+	156843425	156843751
236920537	chr1	156843393	156843567	156843413	156843543	NTRK1	NM_001012331	2	16	8	+	156843425	156843751
236920537	chr1	156843393	156843567	156843413	156843543	NTRK1	NM_001007792	1	17	9	+	156843425	156843751
236775892	chr1	156844303	156844446	156844324	156844421	NTRK1	NM_002529	3	17	10	+	156844363	156844418
236775892	chr1	156844303	156844446	156844324	156844421	NTRK1	NM_001012331	2	16	9	+	156844363	156844418
236775892	chr1	156844303	156844446	156844324	156844421	NTRK1	NM_001007792	1	17	10	+	156844363	156844418
235273681	chr1	156845421	156845564	156845442	156845542	NTRK1	NM_002529	3	17	12	+	156845312	156845458
235273681	chr1	156845421	156845564	156845442	156845542	NTRK1	NM_001012331	2	16	11	+	156845312	156845458
235273681	chr1	156845421	156845564	156845442	156845542	NTRK1	NM_001007792	1	17	12	+	156845312	156845458
237549836	chr1	156846310	156846439	156846331	156846415	NTRK1	NM_002529	3	17	14	+	156846192	156846364
237549836	chr1	156846310	156846439	156846331	156846415	NTRK1	NM_001012331	2	16	13	+	156846192	156846364
237549836	chr1	156846310	156846439	156846331	156846415	NTRK1	NM_001007792	1	17	14	+	156846192	156846364
241831145	chr1	156849751	156849925	156849768	156849908	NTRK1	NM_002529	3	17	16	+	156849791	156849949
241831145	chr1	156849751	156849925	156849768	156849908	NTRK1	NM_001012331	2	16	15	+	156849791	156849949
241831145	chr1	156849751	156849925	156849768	156849908	NTRK1	NM_001007792	1	17	16	+	156849791	156849949
239130126	chr1	161284066	161284240	161284091	161284219	SDHC	NM_003001	4	6	1	+	161284166	161284215
239130126	chr1	161284066	161284240	161284091	161284219	SDHC	NM_001035512	2	5	1	+	161284166	161284215
239130126	chr1	161284066	161284240	161284091	161284219	SDHC	NM_001035513	3	4	1	+	161284166	161284215
239130126	chr1	161284066	161284240	161284091	161284219	SDHC	NM_001035511	1	5	1	+	161284166	161284215
241473524	chr1	161310323	161310450	161310351	161310426	SDHC	NM_003001	4	6	4	+	161310384	161310445
241473524	chr1	161310323	161310450	161310351	161310426	SDHC	NM_001035512	2	5	3	+	161310384	161310445
241473524	chr1	161310323	161310450	161310351	161310426	SDHC	NM_001035513	3	4	2	+	161310384	161310445
241473524	chr1	161310323	161310450	161310351	161310426	SDHC	NM_001035511	1	5	4	+	161310384	161310445
262831543	chr1	161332051	161332205	161332078	161332179	SDHC	NM_003001	4	6	6	+	161332119	161334535
262831543	chr1	161332051	161332205	161332078	161332179	SDHC	NM_001035512	2	5	5	+	161332119	161334535
262831543	chr1	161332051	161332205	161332078	161332179	SDHC	NM_001035513	3	4	4	+	161332119	161334535
262831543	chr1	161332051	161332205	161332078	161332179	SDHC	NM_001035511	1	5	5	+	161332119	161334535
230138524	chr1	162724339	162724490	162724360	162724466	DDR2	NM_006182	2	18	5	+	162724414	162724645
230138524	chr1	162724339	162724490	162724360	162724466	DDR2	NM_001014796	1	19	6	+	162724414	162724645
227934283	chr1	162724944	162725115	162724968	162725094	DDR2	NM_006182	2	18	6	+	162724946	162725093
227934283	chr1	162724944	162725115	162724968	162725094	DDR2	NM_001014796	1	19	7	+	162724946	162725093
230471658	chr1	162730954	162731128	162730974	162731107	DDR2	NM_006182	2	18	9	+	162731001	162731244
230471658	chr1	162730954	162731128	162730974	162731107	DDR2	NM_001014796	1	19	10	+	162731001	162731244

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227835801	chr1	162736920	162737052	162736942	162737029	DDR2	NM_006182	2	18	11	+	162737019	162737149
227835801	chr1	162736920	162737052	162736942	162737029	DDR2	NM_001014796	1	19	12	+	162737019	162737149
231010473	chr1	162741735	162741909	162741757	162741887	DDR2	NM_006182	2	18	13	+	162741814	162742037
231010473	chr1	162741735	162741909	162741757	162741887	DDR2	NM_001014796	1	19	14	+	162741814	162742037
229442557	chr1	162743275	162743449	162743302	162743421	DDR2	NM_006182	2	18	14	+	162743259	162743386
229442557	chr1	162743275	162743449	162743302	162743421	DDR2	NM_001014796	1	19	15	+	162743259	162743386
232596737	chr1	162746016	162746188	162746042	162746161	DDR2	NM_006182	2	18	16	+	162745926	162746160
232596737	chr1	162746016	162746188	162746042	162746161	DDR2	NM_001014796	1	19	17	+	162745926	162746160
229589418	chr1	162749956	162750088	162749978	162750066	DDR2	NM_006182	2	18	18	+	162749902	162750247
229589418	chr1	162749956	162750088	162749978	162750066	DDR2	NM_001014796	1	19	19	+	162749902	162750247
235113886	chr1	164532413	164532587	164532439	164532559	PBX1	NM_002585	3	9	2	+	164532475	164532548
235113886	chr1	164532413	164532587	164532439	164532559	PBX1	NM_001204963	2	9	2	+	164532475	164532548
235113886	chr1	164532413	164532587	164532439	164532559	PBX1	NM_001204961	1	8	2	+	164532475	164532548
240097273	chr1	164768877	164769051	164768898	164769030	PBX1	NM_002585	3	9	4	+	164768936	164769126
240097273	chr1	164768877	164769051	164768898	164769030	PBX1	NM_001204963	2	9	4	+	164768936	164769126
240097273	chr1	164768877	164769051	164768898	164769030	PBX1	NM_001204961	1	8	4	+	164768936	164769126
237463193	chr1	164781164	164781333	164781190	164781311	PBX1	NM_002585	3	9	6	+	164781227	164781386
237463193	chr1	164781164	164781333	164781190	164781311	PBX1	NM_001204963	2	9	6	+	164781227	164781386
237463193	chr1	164781164	164781333	164781190	164781311	PBX1	NM_001204961	1	8	6	+	164781227	164781386
237986190	chr1	164790783	164790936	164790805	164790908	PBX1	NM_002585	3	9	8	+	164790774	164790863
237986190	chr1	164790783	164790936	164790805	164790908	PBX1	NM_001204963	2	9	8	+	164790774	164790863
237986190	chr1	164790783	164790936	164790805	164790908	PBX1	NM_001204961	1	8	7	+	164790774	164790863
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_001168239	6	12	12	-	179068462	179078033
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_001168238	5	12	12	-	179068462	179078033
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_001136000	1	13	13	-	179068462	179078033
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_001168237	4	13	13	-	179068462	179078033
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_005158	7	12	12	-	179068462	179078576
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_007314	8	12	12	-	179068462	179078576
224190541	chr1	179076938	179077064	179076960	179077043	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_005158	7	12	12	-	179068462	179078576
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_007314	8	12	12	-	179068462	179078576
223423206	chr1	179077371	179077528	179077392	179077503	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_001168239	6	12	12	-	179068462	179078033
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_001168238	5	12	12	-	179068462	179078033
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_001136000	1	13	13	-	179068462	179078033
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_001168237	4	13	13	-	179068462	179078033
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_005158	7	12	12	-	179068462	179078576

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_007314	8	12	12	-	179068462	179078576
223459586	chr1	179077783	179077918	179077807	179077896	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_005158	7	12	12	-	179068462	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_007314	8	12	12	-	179068462	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_001168236	3	11	11	-	179068462	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_001168239	6	12	11	-	179078343	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_001168238	5	12	11	-	179078343	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_001136000	1	13	12	-	179078343	179078576
223118898	chr1	179078222	179078384	179078243	179078360	ABL2	NM_001168237	4	13	12	-	179078343	179078576
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_005158	7	12	11	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_001168239	6	12	10	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_001168238	5	12	10	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_001136000	1	13	11	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_007314	8	12	11	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_001168237	4	13	11	-	179079417	179079590
222202160	chr1	179079452	179079619	179079475	179079594	ABL2	NM_001168236	3	11	10	-	179079417	179079590
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_005158	7	12	8	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001168239	6	12	7	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001168238	5	12	7	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001136001	2	10	7	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001136000	1	13	8	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_007314	8	12	8	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001168237	4	13	8	-	179086467	179086651
223787473	chr1	179086378	179086552	179086406	179086528	ABL2	NM_001168236	3	11	7	-	179086467	179086651
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_005158	7	12	6	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001168239	6	12	5	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001168238	5	12	5	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001136001	2	10	5	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001136000	1	13	6	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_007314	8	12	6	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001168237	4	13	6	-	179089325	179089409
222851068	chr1	179089278	179089448	179089302	179089420	ABL2	NM_001168236	3	11	5	-	179089325	179089409
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_005158	7	12	4	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001168239	6	12	3	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001168238	5	12	3	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001136001	2	10	3	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001136000	1	13	4	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_007314	8	12	4	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001168237	4	13	4	-	179095512	179095807
222775082	chr1	179095490	179095662	179095511	179095642	ABL2	NM_001168236	3	11	3	-	179095512	179095807
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_005158	7	12	3	-	179100446	179100616

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001168239	6	12	2	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001168238	5	12	2	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001136001	2	10	2	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001136000	1	13	3	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_007314	8	12	3	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001168237	4	13	3	-	179100446	179100616
222885161	chr1	179100475	179100644	179100503	179100616	ABL2	NM_001168236	3	11	2	-	179100446	179100616
321979748	chr1	182544505	182544663	182544528	182544635	RNASEL	NM_021133	1	7	7	-	182542769	182544713
321814406	chr1	182550256	182550402	182550277	182550374	RNASEL	NM_021133	1	7	5	-	182550360	182550492
321733811	chr1	182553177	182553325	182553205	182553301	RNASEL	NM_021133	1	7	3	-	182553216	182553301
322088606	chr1	182554720	182554876	182554740	182554849	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322101092	chr1	182555116	182555285	182555138	182555264	RNASEL	NM_021133	1	7	2	-	182554462	182556105
322089461	chr1	182555580	182555739	182555608	182555717	RNASEL	NM_021133	1	7	2	-	182554462	182556105
312326593	chr1	185060695	185060856	185060722	185060834	RNF2	NM_007212	1	7	3	+	185060711	185060871
312225628	chr1	185062330	185062454	185062355	185062427	RNF2	NM_007212	1	7	4	+	185062193	185062408
312499430	chr1	185067390	185067544	185067414	185067516	RNF2	NM_007212	1	7	5	+	185067204	185067476
312256721	chr1	185069281	185069437	185069309	185069415	RNF2	NM_007212	1	7	7	+	185069332	185071740
264029419	chr1	186283826	186283981	186283853	186283948	TPR	NM_003292	1	51	50	-	186283761	186283856
242025027	chr1	186287579	186287732	186287601	186287707	TPR	NM_003292	1	51	48	-	186287579	186287735
239686636	chr1	186289478	186289651	186289506	186289623	TPR	NM_003292	1	51	46	-	186289444	186289550
264703299	chr1	186291668	186291810	186291688	186291782	TPR	NM_003292	1	51	44	-	186291650	186291718
242753058	chr1	186292941	186293110	186292966	186293086	TPR	NM_003292	1	51	43	-	186292818	186293002
241949775	chr1	186296746	186296909	186296774	186296879	TPR	NM_003292	1	51	40	-	186296592	186296792
242721006	chr1	186301417	186301574	186301441	186301546	TPR	NM_003292	1	51	38	-	186301327	186301475
242286369	chr1	186303331	186303498	186303357	186303476	TPR	NM_003292	1	51	36	-	186303457	186303665
239176080	chr1	186304191	186304318	186304218	186304292	TPR	NM_003292	1	51	35	-	186304200	186304261
262019467	chr1	186305497	186305668	186305524	186305642	TPR	NM_003292	1	51	33	-	186305628	186305826
239362747	chr1	186306145	186306305	186306173	186306277	TPR	NM_003292	1	51	32	-	186306145	186306288
239501093	chr1	186307286	186307442	186307314	186307412	TPR	NM_003292	1	51	31	-	186307165	186307375
241459122	chr1	186310242	186310374	186310268	186310346	TPR	NM_003292	1	51	29	-	186310160	186310291
265010091	chr1	186312475	186312599	186312502	186312572	TPR	NM_003292	1	51	27	-	186312458	186312605
262965872	chr1	186313507	186313662	186313534	186313641	TPR	NM_003292	1	51	25	-	186313507	186313710
242257244	chr1	186315250	186315393	186315277	186315365	TPR	NM_003292	1	51	23	-	186315267	186315419
240999353	chr1	186319261	186319395	186319292	186319371	TPR	NM_003292	1	51	21	-	186319355	186319520
242459536	chr1	186320547	186320714	186320574	186320687	TPR	NM_003292	1	51	20	-	186320462	186320602
242573832	chr1	186322831	186322986	186322857	186322958	TPR	NM_003292	1	51	18	-	186322820	186322982
262310223	chr1	186324807	186324952	186324831	186324924	TPR	NM_003292	1	51	16	-	186324767	186324900
239075894	chr1	186326588	186326752	186326616	186326725	TPR	NM_003292	1	51	14	-	186326529	186326755
262890925	chr1	186328884	186329049	186328912	186329022	TPR	NM_003292	1	51	12	-	186328931	186329128
239783045	chr1	186329865	186330020	186329893	186329994	TPR	NM_003292	1	51	10	-	186329897	186330037
241381215	chr1	186330825	186330996	186330846	186330975	TPR	NM_003292	1	51	8	-	186330921	186331001

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263414015	chr1	186332442	186332586	186332473	186332559	TPR	NM_003292	1	51	5	-	186332474	186332577
239860841	chr1	186339993	186340166	186340020	186340138	TPR	NM_003292	1	51	3	-	186340102	186340175
266351742	chr1	186343984	186344110	186344006	186344089	TPR	NM_003292	1	51	1	-	186344010	186344457
296658907	chr1	186643561	186643691	186643588	186643666	PTGS2	NM_000963	1	10	10	-	186640944	186643894
297104433	chr1	186644467	186644600	186644490	186644572	PTGS2	NM_000963	1	10	9	-	186644381	186644528
296109707	chr1	186645220	186645374	186645248	186645346	PTGS2	NM_000963	1	10	8	-	186645030	186645316
297550913	chr1	186645794	186645967	186645819	186645938	PTGS2	NM_000963	1	10	7	-	186645599	186645845
297705057	chr1	186647338	186647509	186647359	186647482	PTGS2	NM_000963	1	10	4	-	186647393	186647536
295421755	chr1	186648322	186648496	186648346	186648474	PTGS2	NM_000963	1	10	2	-	186648454	186648570
226606215	chr1	193091328	193091480	193091347	193091461	CDC73	NM_024529	1	17	1	+	193091088	193091461
225467306	chr1	193104656	193104808	193104683	193104781	CDC73	NM_024529	1	17	5	+	193104667	193104719
225916488	chr1	193111016	193111182	193111043	193111156	CDC73	NM_024529	1	17	7	+	193110980	193111196
226762818	chr1	193121392	193121548	193121421	193121520	CDC73	NM_024529	1	17	10	+	193121510	193121574
225625657	chr1	193202152	193202296	193202179	193202268	CDC73	NM_024529	1	17	14	+	193202123	193202284
227035892	chr1	193218766	193218914	193218792	193218889	CDC73	NM_024529	1	17	16	+	193218860	193219001
295031204	chr1	204393891	204394064	204393913	204394046	PIK3C2B	NM_002646	1	34	34	-	204391758	204394168
295398054	chr1	204396669	204396841	204396693	204396817	PIK3C2B	NM_002646	1	34	32	-	204396776	204396882
294542636	chr1	204399068	204399223	204399088	204399198	PIK3C2B	NM_002646	1	34	30	-	204399049	204399166
294366601	chr1	204401380	204401554	204401400	204401530	PIK3C2B	NM_002646	1	34	28	-	204401328	204401529
294456422	chr1	204403489	204403649	204403510	204403628	PIK3C2B	NM_002646	1	34	25	-	204403567	204403736
294344662	chr1	204409299	204409471	204409319	204409450	PIK3C2B	NM_002646	1	34	23	-	204409320	204409449
293918415	chr1	204412656	204412785	204412677	204412763	PIK3C2B	NM_002646	1	34	20	-	204412545	204412725
294002756	chr1	204415125	204415273	204415146	204415251	PIK3C2B	NM_002646	1	34	17	-	204415084	204415272
294718913	chr1	204418292	204418447	204418312	204418424	PIK3C2B	NM_002646	1	34	15	-	204418313	204418424
294016796	chr1	204423807	204423945	204423829	204423919	PIK3C2B	NM_002646	1	34	13	-	204423797	204423919
295267816	chr1	204426054	204426222	204426074	204426198	PIK3C2B	NM_002646	1	34	11	-	204426165	204426198
294833769	chr1	204429389	204429563	204429410	204429540	PIK3C2B	NM_002646	1	34	8	-	204429452	204429531
294763999	chr1	204433485	204433641	204433507	204433618	PIK3C2B	NM_002646	1	34	5	-	204433578	204433732
294269056	chr1	204437932	204438099	204437956	204438079	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
294297094	chr1	204438309	204438448	204438331	204438426	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
295200186	chr1	204438725	204438878	204438747	204438858	PIK3C2B	NM_002646	1	34	3	-	204437998	204439014
233684563	chr1	204499714	204499851	204499746	204499824	MDM4	NM_002393	3	11	4	+	204499812	204499945
233684563	chr1	204499714	204499851	204499746	204499824	MDM4	NR_024171	4	10	4	+	204499812	204499945
233684563	chr1	204499714	204499851	204499746	204499824	MDM4	NM_001204171	1	10	4	+	204499812	204499945
232901363	chr1	204507256	204507427	204507277	204507399	MDM4	NM_002393	3	11	7	+	204507337	204507436
232901363	chr1	204507256	204507427	204507277	204507399	MDM4	NR_024171	4	10	6	+	204507337	204507436
232901363	chr1	204507256	204507427	204507277	204507399	MDM4	NM_001204171	1	10	7	+	204507337	204507436
231478046	chr1	204513564	204513738	204513589	204513709	MDM4	NM_002393	3	11	9	+	204513663	204513812
231478046	chr1	204513564	204513738	204513589	204513709	MDM4	NR_024171	4	10	8	+	204513663	204513812
231890033	chr1	204518123	204518296	204518148	204518268	MDM4	NM_002393	3	11	11	+	204518241	204527248
231890033	chr1	204518123	204518296	204518148	204518268	MDM4	NR_024171	4	10	10	+	204518241	204527248

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231890033	chr1	204518123	204518296	204518148	204518268	MDM4	NM_001204171	1	10	10	+	204518241	204527248
232037661	chr1	204518614	204518788	204518637	204518763	MDM4	NM_001204172	2	3	3	+	204518394	204527248
232037661	chr1	204518614	204518788	204518637	204518763	MDM4	NM_002393	3	11	11	+	204518241	204527248
232037661	chr1	204518614	204518788	204518637	204518763	MDM4	NR_024171	4	10	10	+	204518241	204527248
232037661	chr1	204518614	204518788	204518637	204518763	MDM4	NM_001204171	1	10	10	+	204518241	204527248
272138685	chr1	206647743	206647899	206647764	206647872	IKBKE	NM_014002	3	22	4	+	206647674	206647814
272138685	chr1	206647743	206647899	206647764	206647872	IKBKE	NM_001193322	2	21	4	+	206647674	206647814
272138685	chr1	206647743	206647899	206647764	206647872	IKBKE	NM_001193321	1	21	3	+	206647674	206647814
270053136	chr1	206649556	206649706	206649577	206649685	IKBKE	NM_014002	3	22	6	+	206649524	206649705
270053136	chr1	206649556	206649706	206649577	206649685	IKBKE	NM_001193322	2	21	6	+	206649524	206649705
270053136	chr1	206649556	206649706	206649577	206649685	IKBKE	NM_001193321	1	21	5	+	206649524	206649705
271659990	chr1	206651067	206651220	206651084	206651202	IKBKE	NM_014002	3	22	8	+	206651092	206651202
271659990	chr1	206651067	206651220	206651084	206651202	IKBKE	NM_001193322	2	21	8	+	206651092	206651202
271659990	chr1	206651067	206651220	206651084	206651202	IKBKE	NM_001193321	1	21	7	+	206651092	206651202
271442592	chr1	206652334	206652495	206652355	206652476	IKBKE	NM_014002	3	22	10	+	206652286	206652476
271442592	chr1	206652334	206652495	206652355	206652476	IKBKE	NM_001193322	2	21	10	+	206652286	206652476
271442592	chr1	206652334	206652495	206652355	206652476	IKBKE	NM_001193321	1	21	9	+	206652286	206652476
270549085	chr1	206658302	206658452	206658325	206658431	IKBKE	NM_014002	3	22	14	+	206658334	206658409
270549085	chr1	206658302	206658452	206658325	206658431	IKBKE	NM_001193322	2	21	14	+	206658334	206658409
270549085	chr1	206658302	206658452	206658325	206658431	IKBKE	NM_001193321	1	21	13	+	206658334	206658409
272422175	chr1	206661267	206661408	206661292	206661385	IKBKE	NM_014002	3	22	16	+	206661251	206661327
272422175	chr1	206661267	206661408	206661292	206661385	IKBKE	NM_001193322	2	21	16	+	206661251	206661327
272422175	chr1	206661267	206661408	206661292	206661385	IKBKE	NM_001193321	1	21	15	+	206661251	206661327
270266331	chr1	206666310	206666480	206666332	206666458	IKBKE	NM_014002	3	22	19	+	206666356	206666452
270266331	chr1	206666310	206666480	206666332	206666458	IKBKE	NM_001193322	2	21	19	+	206666356	206666452
270266331	chr1	206666310	206666480	206666332	206666458	IKBKE	NM_001193321	1	21	18	+	206666356	206666452
292065172	chr1	220702079	220702235	220702096	220702216	MARK1	NM_018650	1	18	1	+	220701568	220702215
291413278	chr1	220754310	220754457	220754340	220754430	MARK1	NM_018650	1	18	3	+	220754407	220754460
328491218	chr1	220789185	220789330	220789218	220789303	MARK1	NM_018650	1	18	7	+	220789281	220789337
289877403	chr1	220791838	220792000	220791865	220791978	MARK1	NM_018650	1	18	9	+	220791978	220792097
289877403	chr1	220791838	220792000	220791865	220791978	MARK1	NM_018650	1	18	8	+	220791652	220791888
292888944	chr1	220805457	220805589	220805479	220805563	MARK1	NM_018650	1	18	11	+	220805543	220805655
289645278	chr1	220808742	220808913	220808765	220808893	MARK1	NM_018650	1	18	12	+	220808718	220808871
292895216	chr1	220823972	220824126	220823994	220824105	MARK1	NM_018650	1	18	14	+	220823962	220824062
290907869	chr1	220826466	220826624	220826487	220826604	MARK1	NM_018650	1	18	16	+	220826443	220826694
289989503	chr1	220835019	220835183	220835040	220835158	MARK1	NM_018650	1	18	18	+	220835154	220837799
289432624	chr1	226549103	226549265	226549124	226549242	PARP1	NM_001618	1	23	23	-	226548392	226549242
291760028	chr1	226552633	226552804	226552659	226552781	PARP1	NM_001618	1	23	19	-	226552703	226552855
289297575	chr1	226555160	226555330	226555180	226555309	PARP1	NM_001618	1	23	17	-	226555181	226555309
290681866	chr1	226561792	226561966	226561814	226561940	PARP1	NM_001618	1	23	14	-	226561927	226562055
293013878	chr1	226566746	226566914	226566765	226566891	PARP1	NM_001618	1	23	12	-	226566843	226566975

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
290420800	chr1	226567663	226567830	226567682	226567807	PARP1	NM_001618	1	23	10	-	226567623	226567865
292104380	chr1	226568822	226568946	226568845	226568924	PARP1	NM_001618	1	23	9	-	226568769	226568909
290060530	chr1	226573157	226573314	226573180	226573293	PARP1	NM_001618	1	23	7	-	226573205	226573381
291719875	chr1	226577984	226578158	226578005	226578134	PARP1	NM_001618	1	23	4	-	226578111	226578325
291101263	chr1	226579900	226580047	226579928	226580022	PARP1	NM_001618	1	23	3	-	226579900	226580015
291570020	chr1	226595547	226595689	226595569	226595669	PARP1	NM_001618	1	23	1	-	226595511	226595801
291617219	chr1	236966832	236966967	236966854	236966942	MTR	NM_000254	1	33	2	+	236966728	236966942
291640055	chr1	236976006	236976180	236976032	236976159	MTR	NM_000254	1	33	6	+	236976038	236976144
291838754	chr1	236987278	236987448	236987306	236987428	MTR	NM_000254	1	33	9	+	236987419	236987519
289301233	chr1	236990037	236990196	236990065	236990172	MTR	NM_000254	1	33	11	+	236990129	236990196
291449323	chr1	236998757	236998929	236998781	236998906	MTR	NM_000254	1	33	14	+	236998847	236998987
290140384	chr1	237013501	237013675	237013526	237013647	MTR	NM_000254	1	33	16	+	237013644	237013823
290507409	chr1	237015820	237015964	237015842	237015938	MTR	NM_000254	1	33	17	+	237015821	237015937
290941878	chr1	237024342	237024477	237024363	237024453	MTR	NM_000254	1	33	20	+	237024425	237024577
289554230	chr1	237037014	237037167	237037040	237037141	MTR	NM_000254	1	33	23	+	237037073	237037140
290663779	chr1	237048390	237048545	237048416	237048517	MTR	NM_000254	1	33	26	+	237048421	237048519
289933703	chr1	237052527	237052662	237052548	237052636	MTR	NM_000254	1	33	28	+	237052481	237052636
290647478	chr1	237057563	237057721	237057586	237057701	MTR	NM_000254	1	33	30	+	237057657	237057857
291511143	chr1	237058675	237058840	237058697	237058820	MTR	NM_000254	1	33	31	+	237058658	237058850
293474182	chr1	237060842	237061004	237060867	237060977	MTR	NM_000254	1	33	33	+	237060858	237067281
227255223	chr1	241663731	241663856	241663759	241663831	FH	NM_000143	1	10	9	-	241663737	241663890
227629815	chr1	241667239	241667413	241667263	241667394	FH	NM_000143	1	10	7	-	241667342	241667545
229377639	chr1	241669315	241669472	241669338	241669442	FH	NM_000143	1	10	6	-	241669303	241669468
227991413	chr1	241671975	241672148	241672000	241672120	FH	NM_000143	1	10	5	-	241671903	241672085
227650454	chr1	241676849	241677013	241676870	241676988	FH	NM_000143	1	10	3	-	241676903	241677013
227280469	chr1	241682796	241682928	241682815	241682911	FH	NM_000143	1	10	1	-	241682891	241683085
271504750	chr1	243668513	243668663	243668541	243668635	AKT3	NM_005465	2	13	13	-	243663021	243668636
270357700	chr1	243716077	243716239	243716104	243716215	AKT3	NM_005465	2	13	10	-	243716031	243716245
270357700	chr1	243716077	243716239	243716104	243716215	AKT3	NM_181690	3	14	10	-	243716031	243716245
270357700	chr1	243716077	243716239	243716104	243716215	AKT3	NM_001206729	1	14	11	-	243716031	243716245
271730421	chr1	243727119	243727250	243727138	243727222	AKT3	NM_005465	2	13	9	-	243727022	243727150
271730421	chr1	243727119	243727250	243727138	243727222	AKT3	NM_181690	3	14	9	-	243727022	243727150
271730421	chr1	243727119	243727250	243727138	243727222	AKT3	NM_001206729	1	14	10	-	243727022	243727150
269977056	chr1	243777007	243777156	243777030	243777124	AKT3	NM_005465	2	13	7	-	243776973	243777041
269977056	chr1	243777007	243777156	243777030	243777124	AKT3	NM_181690	3	14	7	-	243776973	243777041
269977056	chr1	243777007	243777156	243777030	243777124	AKT3	NM_001206729	1	14	8	-	243776973	243777041
270901439	chr1	243809159	243809330	243809182	243809307	AKT3	NM_005465	2	13	4	-	243809195	243809339
270901439	chr1	243809159	243809330	243809182	243809307	AKT3	NM_181690	3	14	4	-	243809195	243809339
270901439	chr1	243809159	243809330	243809182	243809307	AKT3	NM_001206729	1	14	5	-	243809195	243809339
270059854	chr1	243858888	243859040	243858914	243859018	AKT3	NM_005465	2	13	2	-	243858893	243859018
270059854	chr1	243858888	243859040	243858914	243859018	AKT3	NM_181690	3	14	2	-	243858893	243859018

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270059854	chr1	243858888	243859040	243858914	243859018	AKT3	NM_001206729	1	14	3	-	243858893	243859018
297483440	chr2	5833015	5833142	5833036	5833120	SOX11	NM_003108	1	1	1	+	5832799	5841517
297473348	chr2	5833345	5833515	5833366	5833496	SOX11	NM_003108	1	1	1	+	5832799	5841517
297481480	chr2	5833779	5833948	5833798	5833927	SOX11	NM_003108	1	1	1	+	5832799	5841517
297503942	chr2	5834082	5834251	5834103	5834229	SOX11	NM_003108	1	1	1	+	5832799	5841517
241283727	chr2	16082147	16082303	16082167	16082282	MYCN	NM_005378	1	3	2	+	16082070	16082976
236528386	chr2	16082503	16082633	16082520	16082616	MYCN	NM_005378	1	3	2	+	16082070	16082976
239187339	chr2	16085695	16085820	16085716	16085799	MYCN	NM_005378	1	3	3	+	16085615	16087129
239198234	chr2	16086075	16086241	16086097	16086219	MYCN	NM_005378	1	3	3	+	16085615	16087129
235885514	chr2	24888681	24888817	24888705	24888794	NCOA1	NM_147233	3	21	4	+	24888618	24888784
235885514	chr2	24888681	24888817	24888705	24888794	NCOA1	NM_147223	2	22	4	+	24888618	24888784
235885514	chr2	24888681	24888817	24888705	24888794	NCOA1	NM_003743	1	21	4	+	24888618	24888784
241658901	chr2	24905890	24906054	24905918	24906022	NCOA1	NM_147233	3	21	6	+	24905820	24905997
241658901	chr2	24905890	24906054	24905918	24906022	NCOA1	NM_147223	2	22	6	+	24905820	24905997
241658901	chr2	24905890	24906054	24905918	24906022	NCOA1	NM_003743	1	21	6	+	24905820	24905997
235258061	chr2	24916085	24916217	24916110	24916189	NCOA1	NM_147233	3	21	8	+	24916121	24916216
235258061	chr2	24916085	24916217	24916110	24916189	NCOA1	NM_147223	2	22	8	+	24916121	24916216
235258061	chr2	24916085	24916217	24916110	24916189	NCOA1	NM_003743	1	21	8	+	24916121	24916216
239949488	chr2	24927850	24928022	24927874	24927994	NCOA1	NM_147233	3	21	10	+	24927955	24928102
239949488	chr2	24927850	24928022	24927874	24927994	NCOA1	NM_147223	2	22	10	+	24927955	24928102
239949488	chr2	24927850	24928022	24927874	24927994	NCOA1	NM_003743	1	21	10	+	24927955	24928102
237981708	chr2	24929431	24929598	24929449	24929572	NCOA1	NM_147233	3	21	11	+	24929437	24930757
237981708	chr2	24929431	24929598	24929449	24929572	NCOA1	NM_147223	2	22	11	+	24929437	24930757
237981708	chr2	24929431	24929598	24929449	24929572	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238030869	chr2	24929897	24930052	24929925	24930027	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238030869	chr2	24929897	24930052	24929925	24930027	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238030869	chr2	24929897	24930052	24929925	24930027	NCOA1	NM_003743	1	21	11	+	24929437	24930757
238177503	chr2	24930356	24930522	24930379	24930499	NCOA1	NM_147233	3	21	11	+	24929437	24930757
238177503	chr2	24930356	24930522	24930379	24930499	NCOA1	NM_147223	2	22	11	+	24929437	24930757
238177503	chr2	24930356	24930522	24930379	24930499	NCOA1	NM_003743	1	21	11	+	24929437	24930757
236638986	chr2	24933738	24933895	24933763	24933873	NCOA1	NM_147233	3	21	12	+	24933800	24933980
236638986	chr2	24933738	24933895	24933763	24933873	NCOA1	NM_147223	2	22	12	+	24933800	24933980
236638986	chr2	24933738	24933895	24933763	24933873	NCOA1	NM_003743	1	21	12	+	24933800	24933980
236912127	chr2	24951135	24951265	24951162	24951242	NCOA1	NM_147233	3	21	14	+	24951177	24951345
236912127	chr2	24951135	24951265	24951162	24951242	NCOA1	NM_147223	2	22	14	+	24951177	24951345
236912127	chr2	24951135	24951265	24951162	24951242	NCOA1	NM_003743	1	21	14	+	24951177	24951345
237674806	chr2	24952540	24952713	24952563	24952686	NCOA1	NM_147233	3	21	15	+	24952370	24952684
237674806	chr2	24952540	24952713	24952563	24952686	NCOA1	NM_147223	2	22	15	+	24952370	24952684
237674806	chr2	24952540	24952713	24952563	24952686	NCOA1	NM_003743	1	21	15	+	24952370	24952684
237537191	chr2	24964680	24964814	24964700	24964792	NCOA1	NM_147233	3	21	17	+	24964653	24965055
237537191	chr2	24964680	24964814	24964700	24964792	NCOA1	NM_147223	2	22	17	+	24964653	24965055

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237537191	chr2	24964680	24964814	24964700	24964792	NCOA1	NM_003743	1	21	17	+	24964653	24965055
236813210	chr2	24974837	24975003	24974862	24974985	NCOA1	NM_147233	3	21	18	+	24974851	24975025
236813210	chr2	24974837	24975003	24974862	24974985	NCOA1	NM_147223	2	22	18	+	24974851	24975025
236813210	chr2	24974837	24975003	24974862	24974985	NCOA1	NM_003743	1	21	18	+	24974851	24975025
236317926	chr2	24985435	24985605	24985461	24985584	NCOA1	NM_147233	3	21	20	+	24985556	24985645
236317926	chr2	24985435	24985605	24985461	24985584	NCOA1	NM_147223	2	22	20	+	24985556	24985645
236317926	chr2	24985435	24985605	24985461	24985584	NCOA1	NM_003743	1	21	20	+	24985556	24985645
240776088	chr2	24991115	24991262	24991137	24991236	NCOA1	NM_147223	2	22	22	+	24991090	24993570
240776088	chr2	24991115	24991262	24991137	24991236	NCOA1	NM_003743	1	21	21	+	24991090	24993570
240776088	chr2	24991115	24991262	24991137	24991236	NCOA1	NM_147233	3	21	21	+	24991093	24993570
229276928	chr2	25458459	25458604	25458479	25458579	DNMT3A	NM_022552	1	23	22	-	25458576	25458694
229276928	chr2	25458459	25458604	25458479	25458579	DNMT3A	NM_153759	2	19	18	-	25458576	25458694
229276928	chr2	25458459	25458604	25458479	25458579	DNMT3A	NM_175629	3	23	22	-	25458576	25458694
230331827	chr2	25461981	25462114	25462002	25462090	DNMT3A	NM_022552	1	23	20	-	25461999	25462084
230331827	chr2	25461981	25462114	25462002	25462090	DNMT3A	NM_153759	2	19	16	-	25461999	25462084
230331827	chr2	25461981	25462114	25462002	25462090	DNMT3A	NM_175629	3	23	20	-	25461999	25462084
228880608	chr2	25464411	25464573	25464430	25464553	DNMT3A	NM_022552	1	23	17	-	25464431	25464576
228880608	chr2	25464411	25464573	25464430	25464553	DNMT3A	NM_153759	2	19	13	-	25464431	25464576
228880608	chr2	25464411	25464573	25464430	25464553	DNMT3A	NM_175629	3	23	17	-	25464431	25464576
230814901	chr2	25467014	25467141	25467036	25467120	DNMT3A	NM_022552	1	23	15	-	25467024	25467207
230814901	chr2	25467014	25467141	25467036	25467120	DNMT3A	NM_153759	2	19	11	-	25467024	25467207
230814901	chr2	25467014	25467141	25467036	25467120	DNMT3A	NM_175629	3	23	15	-	25467024	25467207
229059179	chr2	25468051	25468224	25468070	25468205	DNMT3A	NM_022552	1	23	13	-	25468122	25468201
229059179	chr2	25468051	25468224	25468070	25468205	DNMT3A	NM_153759	2	19	9	-	25468122	25468201
229059179	chr2	25468051	25468224	25468070	25468205	DNMT3A	NM_175629	3	23	13	-	25468122	25468201
232229960	chr2	25469139	25469292	25469165	25469271	DNMT3A	NM_022552	1	23	11	-	25469029	25469178
232229960	chr2	25469139	25469292	25469165	25469271	DNMT3A	NM_153759	2	19	7	-	25469029	25469178
232229960	chr2	25469139	25469292	25469165	25469271	DNMT3A	NM_175629	3	23	11	-	25469029	25469178
229121332	chr2	25470403	25470548	25470424	25470526	DNMT3A	NM_022552	1	23	8	-	25470460	25470618
229121332	chr2	25470403	25470548	25470424	25470526	DNMT3A	NM_153759	2	19	4	-	25470460	25470618
229121332	chr2	25470403	25470548	25470424	25470526	DNMT3A	NM_175629	3	23	8	-	25470460	25470618
227756646	chr2	25471067	25471202	25471090	25471180	DNMT3A	NM_022552	1	23	7	-	25470906	25471121
227756646	chr2	25471067	25471202	25471090	25471180	DNMT3A	NM_153759	2	19	3	-	25470906	25471121
227756646	chr2	25471067	25471202	25471090	25471180	DNMT3A	NM_175629	3	23	7	-	25470906	25471121
230795000	chr2	25497830	25498002	25497847	25497982	DNMT3A	NM_022552	1	23	6	-	25497810	25497956
230795000	chr2	25497830	25498002	25497847	25497982	DNMT3A	NM_175629	3	23	6	-	25497810	25497956
228732352	chr2	25505471	25505614	25505492	25505586	DNMT3A	NM_175630	4	4	4	-	25504321	25505580
228732352	chr2	25505471	25505614	25505492	25505586	DNMT3A	NM_022552	1	23	4	-	25505310	25505580
228732352	chr2	25505471	25505614	25505492	25505586	DNMT3A	NM_175629	3	23	4	-	25505310	25505580
222625425	chr2	29416185	29416350	29416205	29416329	ALK	NM_004304	1	29	29	-	29415640	29416788
224411115	chr2	29416653	29416813	29416673	29416786	ALK	NM_004304	1	29	29	-	29415640	29416788

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222194209	chr2	29420461	29420585	29420482	29420559	ALK	NM_004304	1	29	27	-	29420408	29420542
224021488	chr2	29443544	29443710	29443566	29443688	ALK	NM_004304	1	29	23	-	29443572	29443701
223041857	chr2	29446116	29446255	29446138	29446233	ALK	NM_004304	1	29	20	-	29446208	29446394
223281376	chr2	29448325	29448498	29448348	29448476	ALK	NM_004304	1	29	19	-	29448327	29448431
223305399	chr2	29451718	29451889	29451740	29451867	ALK	NM_004304	1	29	16	-	29451750	29451932
222811857	chr2	29456391	29456525	29456413	29456497	ALK	NM_004304	1	29	14	-	29456431	29456562
222222770	chr2	29473902	29474076	29473923	29474057	ALK	NM_004304	1	29	12	-	29473971	29474133
223911986	chr2	29498133	29498304	29498158	29498280	ALK	NM_004304	1	29	10	-	29498268	29498362
225124762	chr2	29541124	29541297	29541149	29541271	ALK	NM_004304	1	29	8	-	29541170	29541270
222232757	chr2	29551221	29551385	29551243	29551362	ALK	NM_004304	1	29	6	-	29551216	29551347
222664325	chr2	29754810	29754971	29754831	29754948	ALK	NM_004304	1	29	4	-	29754781	29754982
222439364	chr2	29917836	29917999	29917857	29917978	ALK	NM_004304	1	29	3	-	29917716	29917880
224308442	chr2	30142858	30143026	30142880	30143005	ALK	NM_004304	1	29	1	-	30142859	30144477
224313424	chr2	30143241	30143405	30143259	30143386	ALK	NM_004304	1	29	1	-	30142859	30144477
228012459	chr2	42472528	42472698	42472555	42472678	EML4	NM_019063	2	23	2	+	42472645	42472827
228012459	chr2	42472528	42472698	42472555	42472678	EML4	NM_001145076	1	22	2	+	42472645	42472827
229093790	chr2	42483646	42483807	42483667	42483779	EML4	NM_019063	2	23	3	+	42483641	42483770
229093790	chr2	42483646	42483807	42483667	42483779	EML4	NM_001145076	1	22	3	+	42483641	42483770
230513775	chr2	42490390	42490534	42490417	42490506	EML4	NM_019063	2	23	5	+	42490318	42490446
230513775	chr2	42490390	42490534	42490417	42490506	EML4	NM_001145076	1	22	4	+	42490318	42490446
231128360	chr2	42509855	42510016	42509882	42509994	EML4	NM_019063	2	23	8	+	42509963	42510112
231128360	chr2	42509855	42510016	42509882	42509994	EML4	NM_001145076	1	22	7	+	42509963	42510112
232287439	chr2	42513343	42513469	42513370	42513440	EML4	NM_019063	2	23	10	+	42513409	42513519
232287439	chr2	42513343	42513469	42513370	42513440	EML4	NM_001145076	1	22	9	+	42513409	42513519
230703444	chr2	42522152	42522319	42522178	42522294	EML4	NM_019063	2	23	12	+	42522265	42522399
230703444	chr2	42522152	42522319	42522178	42522294	EML4	NM_001145076	1	22	11	+	42522265	42522399
230331325	chr2	42522563	42522718	42522588	42522690	EML4	NM_019063	2	23	13	+	42522521	42522656
230331325	chr2	42522563	42522718	42522588	42522690	EML4	NM_001145076	1	22	12	+	42522521	42522656
227784576	chr2	42530239	42530399	42530263	42530371	EML4	NM_019063	2	23	15	+	42530244	42530369
227784576	chr2	42530239	42530399	42530263	42530371	EML4	NM_001145076	1	22	14	+	42530244	42530369
228414528	chr2	42543090	42543247	42543116	42543223	EML4	NM_019063	2	23	18	+	42543102	42543190
228414528	chr2	42543090	42543247	42543116	42543223	EML4	NM_001145076	1	22	17	+	42543102	42543190
230564142	chr2	42553212	42553344	42553238	42553320	EML4	NM_019063	2	23	21	+	42553294	42553392
230564142	chr2	42553212	42553344	42553238	42553320	EML4	NM_001145076	1	22	20	+	42553294	42553392
228751448	chr2	42556806	42556979	42556830	42556955	EML4	NM_019063	2	23	23	+	42556874	42559688
228751448	chr2	42556806	42556979	42556830	42556955	EML4	NM_001145076	1	22	22	+	42556874	42559688
228834071	chr2	42557241	42557387	42557263	42557363	EML4	NM_019063	2	23	23	+	42556874	42559688
228834071	chr2	42557241	42557387	42557263	42557363	EML4	NM_001145076	1	22	22	+	42556874	42559688
237655143	chr2	47635534	47635687	47635560	47635660	MSH2	NM_000251	1	16	2	+	47635540	47635694
235692106	chr2	47639424	47639583	47639456	47639556	MSH2	NM_000251	1	16	4	+	47639553	47639699
239680434	chr2	47641290	47641451	47641314	47641423	MSH2	NM_000251	1	16	5	+	47641408	47641557

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235555845	chr2	47643368	47643527	47643393	47643502	MSH2	NM_000251	1	16	6	+	47643435	47643568
239524898	chr2	47656991	47657148	47657018	47657120	MSH2	NM_000251	1	16	7	+	47656881	47657080
257444649	chr2	47693796	47693959	47693813	47693939	MSH2	NM_000251	1	16	10	+	47693797	47693947
236818060	chr2	47702221	47702351	47702242	47702323	MSH2	NM_000251	1	16	12	+	47702164	47702409
240388592	chr2	47705306	47705464	47705330	47705436	MSH2	NM_000251	1	16	14	+	47705411	47705658
235406697	chr2	47707809	47707957	47707831	47707929	MSH2	NM_000251	1	16	15	+	47707835	47708010
237703486	chr2	47709963	47710112	47709990	47710084	MSH2	NM_000251	1	16	16	+	47709918	47710360
236885923	chr2	48018131	48018286	48018153	48018262	MSH6	NM_000179	1	10	2	+	48018066	48018262
257765576	chr2	48025839	48025983	48025861	48025962	MSH6	NM_000179	1	10	4	+	48025750	48028294
257752696	chr2	48026286	48026458	48026310	48026434	MSH6	NM_000179	1	10	4	+	48025750	48028294
238006007	chr2	48026752	48026882	48026780	48026856	MSH6	NM_000179	1	10	4	+	48025750	48028294
238076498	chr2	48027145	48027314	48027169	48027289	MSH6	NM_000179	1	10	4	+	48025750	48028294
257789735	chr2	48027537	48027662	48027564	48027635	MSH6	NM_000179	1	10	4	+	48025750	48028294
257855790	chr2	48027924	48028094	48027949	48028072	MSH6	NM_000179	1	10	4	+	48025750	48028294
238228637	chr2	48030621	48030792	48030643	48030770	MSH6	NM_000179	1	10	5	+	48030559	48030824
236903470	chr2	48032646	48032819	48032678	48032796	MSH6	NM_000179	1	10	7	+	48032757	48032846
241845298	chr2	48033384	48033555	48033412	48033534	MSH6	NM_000179	1	10	8	+	48033343	48033497
235583861	chr2	48033855	48034025	48033876	48033999	MSH6	NM_000179	1	10	10	+	48033918	48034092
224676149	chr2	60687611	60687742	60687638	60687719	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224602906	chr2	60687990	60688157	60688011	60688135	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224602906	chr2	60687990	60688157	60688011	60688135	BCL11A	NM_018014	1	5	4	-	60687817	60689559
224593002	chr2	60688455	60688627	60688472	60688608	BCL11A	NM_022893	2	4	4	-	60684329	60689559
224593002	chr2	60688455	60688627	60688472	60688608	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223029675	chr2	60688866	60689037	60688887	60689014	BCL11A	NM_022893	2	4	4	-	60684329	60689559
223029675	chr2	60688866	60689037	60688887	60689014	BCL11A	NM_018014	1	5	4	-	60687817	60689559
222820600	chr2	60689310	60689484	60689338	60689463	BCL11A	NM_022893	2	4	4	-	60684329	60689559
222820600	chr2	60689310	60689484	60689338	60689463	BCL11A	NM_138559	3	5	4	-	60689417	60689559
222820600	chr2	60689310	60689484	60689338	60689463	BCL11A	NM_018014	1	5	4	-	60687817	60689559
223738516	chr2	60773104	60773277	60773127	60773255	BCL11A	NM_018014	1	5	2	-	60773106	60773435
223738516	chr2	60773104	60773277	60773127	60773255	BCL11A	NM_022893	2	4	2	-	60773106	60773435
223738516	chr2	60773104	60773277	60773127	60773255	BCL11A	NM_138559	3	5	2	-	60773106	60773435
238557550	chr2	61108896	61109039	61108916	61109017	REL	NM_002908	1	11	1	+	61108752	61108985
264038785	chr2	61127990	61128154	61128011	61128128	REL	NM_002908	1	11	4	+	61128127	61128218
239630595	chr2	61145405	61145568	61145433	61145544	REL	NM_002908	1	11	7	+	61145529	61145741
263772589	chr2	61147709	61147834	61147736	61147808	REL	NM_002908	1	11	10	+	61147709	61147777
241945435	chr2	61149088	61149261	61149114	61149235	REL	NM_002908	1	11	11	+	61148898	61150178
264255626	chr2	61149566	61149723	61149592	61149695	REL	NM_002908	1	11	11	+	61148898	61150178
273534040	chr2	61709474	61709600	61709496	61709574	XPO1	NM_003400	1	25	23	-	61709515	61709674
274002624	chr2	61711132	61711294	61711159	61711267	XPO1	NM_003400	1	25	21	-	61711072	61711240
272966064	chr2	61715239	61715373	61715267	61715346	XPO1	NM_003400	1	25	19	-	61715300	61715406
273465242	chr2	61715828	61715961	61715853	61715934	XPO1	NM_003400	1	25	18	-	61715723	61715906

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273147446	chr2	61719173	61719317	61719202	61719290	XPO1	NM_003400	1	25	16	-	61719170	61719333
273457021	chr2	61719675	61719840	61719704	61719815	XPO1	NM_003400	1	25	14	-	61719702	61719883
273620428	chr2	61721054	61721226	61721076	61721198	XPO1	NM_003400	1	25	12	-	61721029	61721226
273190949	chr2	61722654	61722782	61722682	61722758	XPO1	NM_003400	1	25	11	-	61722590	61722748
274160800	chr2	61725857	61726018	61725883	61725991	XPO1	NM_003400	1	25	9	-	61725808	61725927
273469372	chr2	61726964	61727136	61726991	61727107	XPO1	NM_003400	1	25	7	-	61726848	61727029
274234535	chr2	61753465	61753603	61753498	61753577	XPO1	NM_003400	1	25	3	-	61753555	61753656
273426769	chr2	61760919	61761083	61760947	61761059	XPO1	NM_003400	1	25	2	-	61760907	61761038
299007962	chr2	85361528	85361681	85361546	85361664	TCF7L1	NM_031283	1	12	3	+	85361446	85361573
299076224	chr2	85530980	85531142	85531002	85531121	TCF7L1	NM_031283	1	12	6	+	85531018	85531120
299031333	chr2	85533283	85533425	85533304	85533400	TCF7L1	NM_031283	1	12	9	+	85533329	85533488
299255290	chr2	85536041	85536196	85536063	85536175	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
299264572	chr2	85536429	85536590	85536446	85536569	TCF7L1	NM_031283	1	12	12	+	85536152	85537511
222917470	chr2	100170759	100170884	100170776	100170867	AFF3	NM_002285	2	24	23	-	100170773	100170996
222917470	chr2	100170759	100170884	100170776	100170867	AFF3	NM_001025108	1	24	23	-	100170773	100170996
223283109	chr2	100175305	100175461	100175332	100175438	AFF3	NM_002285	2	24	21	-	100175337	100175430
223283109	chr2	100175305	100175461	100175332	100175438	AFF3	NM_001025108	1	24	21	-	100175337	100175430
223240815	chr2	100185251	100185424	100185274	100185397	AFF3	NM_002285	2	24	18	-	100185314	100185377
223240815	chr2	100185251	100185424	100185274	100185397	AFF3	NM_001025108	1	24	18	-	100185314	100185377
223292186	chr2	100199343	100199502	100199365	100199474	AFF3	NM_002285	2	24	16	-	100199260	100199461
223292186	chr2	100199343	100199502	100199365	100199474	AFF3	NM_001025108	1	24	16	-	100199260	100199461
225170060	chr2	100209669	100209839	100209694	100209817	AFF3	NM_002285	2	24	14	-	100209657	100210751
225170060	chr2	100209669	100209839	100209694	100209817	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223845412	chr2	100210113	100210250	100210137	100210231	AFF3	NM_002285	2	24	14	-	100209657	100210751
223845412	chr2	100210113	100210250	100210137	100210231	AFF3	NM_001025108	1	24	14	-	100209657	100210751
223862141	chr2	100210548	100210701	100210573	100210677	AFF3	NM_002285	2	24	14	-	100209657	100210751
223862141	chr2	100210548	100210701	100210573	100210677	AFF3	NM_001025108	1	24	14	-	100209657	100210751
222789201	chr2	100265981	100266153	100266009	100266129	AFF3	NM_002285	2	24	12	-	100266088	100266128
222789201	chr2	100265981	100266153	100266009	100266129	AFF3	NM_001025108	1	24	12	-	100266088	100266128
223818723	chr2	100368624	100368794	100368646	100368766	AFF3	NM_002285	2	24	8	-	100368683	100368763
223818723	chr2	100368624	100368794	100368646	100368766	AFF3	NM_001025108	1	24	8	-	100368683	100368763
223088530	chr2	100623297	100623470	100623321	100623449	AFF3	NM_002285	2	24	6	-	100623094	100623479
223088530	chr2	100623297	100623470	100623321	100623449	AFF3	NM_001025108	1	24	6	-	100623094	100623479
225102835	chr2	100623788	100623953	100623809	100623925	AFF3	NM_002285	2	24	5	-	100623610	100623922
225102835	chr2	100623788	100623953	100623809	100623925	AFF3	NM_001025108	1	24	5	-	100623610	100623922
240211846	chr2	113976067	113976230	113976088	113976206	PAX8	NM_003466	1	12	12	-	113973574	113976186
240211846	chr2	113976067	113976230	113976088	113976206	PAX8	NM_013992	4	9	9	-	113973574	113976186
240211846	chr2	113976067	113976230	113976088	113976206	PAX8	NM_013952	2	12	12	-	113973574	113976186
240211846	chr2	113976067	113976230	113976088	113976206	PAX8	NM_013953	3	10	10	-	113973574	113976186
237168735	chr2	113992952	113993105	113992970	113993083	PAX8	NM_003466	1	12	9	-	113992971	113993159
237168735	chr2	113992952	113993105	113992970	113993083	PAX8	NM_013952	2	12	9	-	113992971	113993080

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234913890	chr2	113999030	113999201	113999052	113999182	PAX8	NM_003466	1	12	7	-	113999128	113999303
234913890	chr2	113999030	113999201	113999052	113999182	PAX8	NM_013992	4	9	7	-	113999128	113999303
234913890	chr2	113999030	113999201	113999052	113999182	PAX8	NM_013952	2	12	7	-	113999128	113999303
234913890	chr2	113999030	113999201	113999052	113999182	PAX8	NM_013953	3	10	7	-	113999128	113999303
239086549	chr2	113999634	113999800	113999655	113999777	PAX8	NM_003466	1	12	6	-	113999585	113999707
239086549	chr2	113999634	113999800	113999655	113999777	PAX8	NM_013992	4	9	6	-	113999585	113999707
239086549	chr2	113999634	113999800	113999655	113999777	PAX8	NM_013952	2	12	6	-	113999585	113999707
239086549	chr2	113999634	113999800	113999655	113999777	PAX8	NM_013953	3	10	6	-	113999585	113999707
236410744	chr2	114004265	114004429	114004287	114004410	PAX8	NM_003466	1	12	3	-	114004331	114004496
236410744	chr2	114004265	114004429	114004287	114004410	PAX8	NM_013992	4	9	3	-	114004331	114004496
236410744	chr2	114004265	114004429	114004287	114004410	PAX8	NM_013952	2	12	3	-	114004331	114004496
236410744	chr2	114004265	114004429	114004287	114004410	PAX8	NM_013953	3	10	3	-	114004331	114004496
229824988	chr2	128015169	128015339	128015192	128015318	ERCC3	NM_000122	1	15	15	-	128014866	128015303
230751341	chr2	128018832	128018960	128018852	128018931	ERCC3	NM_000122	1	15	13	-	128018804	128018922
232198762	chr2	128036707	128036881	128036728	128036854	ERCC3	NM_000122	1	15	10	-	128036749	128036951
230993793	chr2	128044234	128044408	128044257	128044385	ERCC3	NM_000122	1	15	8	-	128044279	128044593
232996915	chr2	128046324	128046485	128046348	128046457	ERCC3	NM_000122	1	15	7	-	128046236	128046440
229381883	chr2	128047305	128047479	128047328	128047451	ERCC3	NM_000122	1	15	5	-	128047265	128047400
230385903	chr2	128051067	128051196	128051088	128051176	ERCC3	NM_000122	1	15	2	-	128051089	128051294
271150687	chr2	140990759	140990892	140990788	140990864	LRP1B	NM_018557	1	91	91	-	140988996	140990895
270489206	chr2	141004523	141004688	141004546	141004664	LRP1B	NM_018557	1	91	87	-	141004655	141004731
270946346	chr2	141031937	141032081	141031959	141032057	LRP1B	NM_018557	1	91	85	-	141031993	141032167
269855758	chr2	141055412	141055546	141055432	141055525	LRP1B	NM_018557	1	91	84	-	141055377	141055538
272548323	chr2	141079403	141079577	141079428	141079548	LRP1B	NM_018557	1	91	82	-	141079532	141079657
271367815	chr2	141083308	141083472	141083334	141083447	LRP1B	NM_018557	1	91	80	-	141083331	141083447
271117121	chr2	141093261	141093433	141093283	141093407	LRP1B	NM_018557	1	91	78	-	141093184	141093407
269899785	chr2	141110517	141110678	141110543	141110650	LRP1B	NM_018557	1	91	76	-	141110522	141110641
271922030	chr2	141115569	141115736	141115589	141115708	LRP1B	NM_018557	1	91	74	-	141115548	141115685
270941167	chr2	141122243	141122401	141122265	141122373	LRP1B	NM_018557	1	91	72	-	141122230	141122352
270000980	chr2	141130491	141130656	141130515	141130628	LRP1B	NM_018557	1	91	69	-	141130577	141130706
270182346	chr2	141143513	141143637	141143534	141143612	LRP1B	NM_018557	1	91	67	-	141143462	141143578
271540817	chr2	141201928	141202055	141201956	141202027	LRP1B	NM_018557	1	91	65	-	141201899	141202018
269716739	chr2	141208122	141208287	141208145	141208258	LRP1B	NM_018557	1	91	63	-	141208137	141208230
270026459	chr2	141215057	141215198	141215080	141215171	LRP1B	NM_018557	1	91	61	-	141215032	141215220
270753588	chr2	141242789	141242951	141242815	141242924	LRP1B	NM_018557	1	91	59	-	141242912	141243093
269533978	chr2	141245221	141245395	141245238	141245367	LRP1B	NM_018557	1	91	58	-	141245186	141245308
271989311	chr2	141253185	141253337	141253208	141253312	LRP1B	NM_018557	1	91	56	-	141253134	141253317
272613081	chr2	141259340	141259484	141259361	141259461	LRP1B	NM_018557	1	91	55	-	141259256	141259443
270015907	chr2	141264262	141264431	141264289	141264407	LRP1B	NM_018557	1	91	53	-	141264365	141264487
269998767	chr2	141272190	141272355	141272218	141272326	LRP1B	NM_018557	1	91	51	-	141272222	141272341
270202245	chr2	141283344	141283492	141283369	141283471	LRP1B	NM_018557	1	91	49	-	141283413	141283562

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269503718	chr2	141283805	141283955	141283830	141283927	LRP1B	NM_018557	1	91	48	-	141283806	141283919
271801927	chr2	141294149	141294322	141294175	141294296	LRP1B	NM_018557	1	91	46	-	141294150	141294278
270025021	chr2	141299346	141299512	141299368	141299484	LRP1B	NM_018557	1	91	44	-	141299348	141299540
270997674	chr2	141356315	141356489	141356336	141356462	LRP1B	NM_018557	1	91	43	-	141356200	141356404
270639785	chr2	141457814	141457953	141457845	141457928	LRP1B	NM_018557	1	91	41	-	141457819	141458190
269657676	chr2	141459267	141459411	141459294	141459391	LRP1B	NM_018557	1	91	40	-	141459290	141459414
271062752	chr2	141459829	141460003	141459847	141459975	LRP1B	NM_018557	1	91	39	-	141459710	141459861
270361981	chr2	141473543	141473676	141473564	141473645	LRP1B	NM_018557	1	91	37	-	141473542	141473671
271163955	chr2	141526786	141526935	141526809	141526913	LRP1B	NM_018557	1	91	35	-	141526782	141526913
270088150	chr2	141571175	141571338	141571199	141571311	LRP1B	NM_018557	1	91	32	-	141571226	141571375
269717300	chr2	141598483	141598636	141598502	141598612	LRP1B	NM_018557	1	91	30	-	141598487	141598661
270459807	chr2	141607814	141607943	141607841	141607915	LRP1B	NM_018557	1	91	29	-	141607671	141607898
272203665	chr2	141625206	141625344	141625231	141625319	LRP1B	NM_018557	1	91	27	-	141625159	141625403
270745251	chr2	141641267	141641441	141641293	141641418	LRP1B	NM_018557	1	91	25	-	141641386	141641590
270164267	chr2	141660463	141660599	141660491	141660576	LRP1B	NM_018557	1	91	23	-	141660489	141660734
271179076	chr2	141665435	141665605	141665459	141665578	LRP1B	NM_018557	1	91	22	-	141665446	141665646
269615805	chr2	141707674	141707840	141707700	141707815	LRP1B	NM_018557	1	91	20	-	141707804	141707971
272679257	chr2	141739604	141739757	141739629	141739733	LRP1B	NM_018557	1	91	18	-	141739729	141739845
271816452	chr2	141751478	141751640	141751503	141751618	LRP1B	NM_018557	1	91	16	-	141751564	141751704
270828722	chr2	141770995	141771169	141771021	141771146	LRP1B	NM_018557	1	91	14	-	141771125	141771314
270934637	chr2	141773303	141773430	141773327	141773408	LRP1B	NM_018557	1	91	13	-	141773265	141773484
271500441	chr2	141806453	141806610	141806481	141806589	LRP1B	NM_018557	1	91	11	-	141806555	141806791
270194607	chr2	141812729	141812866	141812750	141812840	LRP1B	NM_018557	1	91	10	-	141812685	141812828
270059944	chr2	141819624	141819786	141819649	141819760	LRP1B	NM_018557	1	91	8	-	141819620	141819842
269715626	chr2	141986646	141986820	141986668	141986794	LRP1B	NM_018557	1	91	6	-	141986752	141987009
270482101	chr2	142004674	142004839	142004702	142004817	LRP1B	NM_018557	1	91	5	-	142004795	142004923
269520344	chr2	142012175	142012316	142012197	142012288	LRP1B	NM_018557	1	91	4	-	142012091	142012210
271352298	chr2	142888116	142888290	142888140	142888267	LRP1B	NM_018557	1	91	1	-	142888217	142889270
281669088	chr2	148653791	148653940	148653818	148653913	ACVR2A	NM_001616	1	11	2	+	148653870	148654077
282039668	chr2	148657198	148657343	148657224	148657320	ACVR2A	NM_001616	1	11	4	+	148657313	148657467
282119945	chr2	148672831	148672988	148672854	148672960	ACVR2A	NM_001616	1	11	5	+	148672760	148672903
281929773	chr2	148676016	148676150	148676044	148676131	ACVR2A	NM_001616	1	11	7	+	148676016	148676161
283677332	chr2	148680439	148680582	148680464	148680559	ACVR2A	NM_001616	1	11	9	+	148680542	148680680
284552408	chr2	148683608	148683750	148683635	148683722	ACVR2A	NM_001616	1	11	10	+	148683600	148683730
235196344	chr2	178095435	178095578	178095460	178095553	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235196344	chr2	178095435	178095578	178095460	178095553	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235196344	chr2	178095435	178095578	178095460	178095553	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235218925	chr2	178095796	178095942	178095820	178095914	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235218925	chr2	178095796	178095942	178095820	178095914	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235218925	chr2	178095796	178095942	178095820	178095914	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
239872671	chr2	178096269	178096432	178096292	178096409	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239872671	chr2	178096269	178096432	178096292	178096409	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
239872671	chr2	178096269	178096432	178096292	178096409	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
235101088	chr2	178096677	178096841	178096698	178096814	NFE2L2	NM_001145412	1	5	5	-	178095031	178096736
235101088	chr2	178096677	178096841	178096698	178096814	NFE2L2	NM_001145413	2	5	5	-	178095031	178096736
235101088	chr2	178096677	178096841	178096698	178096814	NFE2L2	NM_006164	3	5	5	-	178095031	178096736
241785959	chr2	178097888	178098062	178097915	178098038	NFE2L2	NM_001145412	1	5	3	-	178097978	178098067
241785959	chr2	178097888	178098062	178097915	178098038	NFE2L2	NM_001145413	2	5	3	-	178097978	178098067
241785959	chr2	178097888	178098062	178097915	178098038	NFE2L2	NM_006164	3	5	3	-	178097978	178098067
238582189	chr2	178098857	178098991	178098885	178098962	NFE2L2	NM_001145412	1	5	2	-	178098733	178098999
238582189	chr2	178098857	178098991	178098885	178098962	NFE2L2	NM_001145413	2	5	2	-	178098733	178098999
238582189	chr2	178098857	178098991	178098885	178098962	NFE2L2	NM_006164	3	5	2	-	178098733	178098999
238003298	chr2	190656549	190656693	190656567	190656668	PMS1	NM_001128144	3	12	2	+	190656516	190656667
238003298	chr2	190656549	190656693	190656567	190656668	PMS1	NM_000534	1	13	2	+	190656516	190656667
238003298	chr2	190656549	190656693	190656567	190656668	PMS1	NM_001128143	2	12	2	+	190656516	190656667
235900009	chr2	190660633	190660763	190660654	190660736	PMS1	NM_001128144	3	12	3	+	190660495	190660677
235900009	chr2	190660633	190660763	190660654	190660736	PMS1	NM_000534	1	13	3	+	190660495	190660677
235900009	chr2	190660633	190660763	190660654	190660736	PMS1	NM_001128143	2	12	3	+	190660495	190660677
237943523	chr2	190682738	190682869	190682766	190682844	PMS1	NM_001128144	3	12	5	+	190682743	190682906
237943523	chr2	190682738	190682869	190682766	190682844	PMS1	NM_000534	1	13	5	+	190682743	190682906
237943523	chr2	190682738	190682869	190682766	190682844	PMS1	NM_001128143	2	12	5	+	190682743	190682906
238526316	chr2	190717400	190717572	190717422	190717547	PMS1	NM_001128144	3	12	7	+	190717381	190717503
238526316	chr2	190717400	190717572	190717422	190717547	PMS1	NM_000534	1	13	7	+	190717381	190717503
238526316	chr2	190717400	190717572	190717422	190717547	PMS1	NM_001128143	2	12	6	+	190717381	190717503
241084245	chr2	190719223	190719349	190719250	190719321	PMS1	NM_001128144	3	12	9	+	190718965	190719854
241084245	chr2	190719223	190719349	190719250	190719321	PMS1	NM_000534	1	13	9	+	190718965	190719854
241084245	chr2	190719223	190719349	190719250	190719321	PMS1	NM_001128143	2	12	8	+	190718965	190719854
237601009	chr2	190719693	190719837	190719721	190719811	PMS1	NM_001128144	3	12	9	+	190718965	190719854
237601009	chr2	190719693	190719837	190719721	190719811	PMS1	NM_000534	1	13	9	+	190718965	190719854
237601009	chr2	190719693	190719837	190719721	190719811	PMS1	NM_001128143	2	12	8	+	190718965	190719854
238272444	chr2	190728634	190728808	190728661	190728784	PMS1	NM_000534	1	13	10	+	190728469	190728954
238272444	chr2	190728634	190728808	190728661	190728784	PMS1	NM_001128143	2	12	9	+	190728469	190728954
235206860	chr2	190732570	190732728	190732594	190732701	PMS1	NM_001128144	3	12	10	+	190732525	190732655
235206860	chr2	190732570	190732728	190732594	190732701	PMS1	NM_000534	1	13	11	+	190732525	190732655
235206860	chr2	190732570	190732728	190732594	190732701	PMS1	NM_001128143	2	12	10	+	190732525	190732655
273515136	chr2	198256979	198257139	198257004	198257112	SF3B1	NM_012433	2	25	25	-	198256698	198257185
272791781	chr2	198260715	198260882	198260744	198260854	SF3B1	NM_012433	2	25	23	-	198260780	198261052
273368146	chr2	198262706	198262840	198262728	198262816	SF3B1	NM_012433	2	25	22	-	198262709	198262840
273481492	chr2	198264673	198264833	198264698	198264811	SF3B1	NM_012433	2	25	20	-	198264779	198264890
273891216	chr2	198265351	198265519	198265380	198265491	SF3B1	NM_012433	2	25	18	-	198265439	198265660
273458782	chr2	198266119	198266247	198266147	198266222	SF3B1	NM_012433	2	25	17	-	198266124	198266249
273792945	chr2	198266634	198266786	198266666	198266758	SF3B1	NM_012433	2	25	15	-	198266709	198266854

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272959310	chr2	198267448	198267588	198267471	198267562	SF3B1	NM_012433	2	25	14	-	198267280	198267550
272989313	chr2	198268298	198268449	198268325	198268422	SF3B1	NM_012433	2	25	12	-	198268309	198268488
273565067	chr2	198270047	198270194	198270072	198270172	SF3B1	NM_012433	2	25	10	-	198269999	198270196
274403466	chr2	198272802	198272942	198272821	198272909	SF3B1	NM_012433	2	25	9	-	198272722	198272843
272910209	chr2	198274450	198274595	198274473	198274574	SF3B1	NM_012433	2	25	7	-	198274494	198274731
273982179	chr2	198281567	198281704	198281588	198281676	SF3B1	NM_012433	2	25	6	-	198281465	198281635
272958936	chr2	198285136	198285263	198285161	198285241	SF3B1	NM_012433	2	25	4	-	198285152	198285266
272958936	chr2	198285136	198285263	198285161	198285241	SF3B1	NM_001005526	1	5	4	-	198285152	198285266
273830269	chr2	198288440	198288579	198288464	198288555	SF3B1	NM_012433	2	25	2	-	198288532	198288698
273830269	chr2	198288440	198288579	198288464	198288555	SF3B1	NM_001005526	1	5	2	-	198288532	198288698
226043318	chr2	208420288	208420436	208420312	208420410	CREB1	NM_134442	2	9	2	+	208420352	208420473
226043318	chr2	208420288	208420436	208420312	208420410	CREB1	NM_004379	1	8	2	+	208420352	208420473
226576715	chr2	208425783	208425910	208425806	208425885	CREB1	NM_134442	2	9	4	+	208425843	208425884
225336186	chr2	208434909	208435051	208434937	208435024	CREB1	NM_134442	2	9	6	+	208434903	208435045
225336186	chr2	208434909	208435051	208434937	208435024	CREB1	NM_004379	1	8	5	+	208434903	208435045
225566072	chr2	208442185	208442311	208442211	208442288	CREB1	NM_134442	2	9	8	+	208442229	208442379
225566072	chr2	208442185	208442311	208442211	208442288	CREB1	NM_004379	1	8	7	+	208442229	208442379
229584337	chr2	209101749	209101891	209101777	209101864	IDH1	NM_005896	1	10	10	-	209100953	209101893
228829961	chr2	209104491	209104633	209104514	209104611	IDH1	NM_005896	1	10	8	-	209104587	209104727
229308600	chr2	209108059	209108233	209108087	209108208	IDH1	NM_005896	1	10	6	-	209108151	209108328
227335193	chr2	209110120	209110254	209110144	209110227	IDH1	NM_005896	1	10	5	-	209110043	209110148
227234030	chr2	209113297	209113466	209113325	209113442	IDH1	NM_005896	1	10	4	-	209113093	209113384
230963303	chr2	212248325	212248493	212248348	212248468	ERBB4	NM_001042599	1	27	27	-	212240442	212248785
230963303	chr2	212248325	212248493	212248348	212248468	ERBB4	NM_005235	2	28	28	-	212240442	212248785
229591568	chr2	212251536	212251707	212251557	212251685	ERBB4	NM_001042599	1	27	26	-	212251578	212251875
229591568	chr2	212251536	212251707	212251557	212251685	ERBB4	NM_005235	2	28	27	-	212251578	212251875
231905807	chr2	212252654	212252809	212252682	212252783	ERBB4	NM_005235	2	28	26	-	212252670	212252717
232490403	chr2	212286791	212286962	212286820	212286934	ERBB4	NM_001042599	1	27	24	-	212286732	212286829
232490403	chr2	212286791	212286962	212286820	212286934	ERBB4	NM_005235	2	28	24	-	212286732	212286829
230496898	chr2	212295639	212295767	212295667	212295739	ERBB4	NM_001042599	1	27	21	-	212295670	212295825
230496898	chr2	212295639	212295767	212295667	212295739	ERBB4	NM_005235	2	28	21	-	212295670	212295825
230765484	chr2	212426738	212426902	212426758	212426874	ERBB4	NM_001042599	1	27	20	-	212426628	212426813
230765484	chr2	212426738	212426902	212426758	212426874	ERBB4	NM_005235	2	28	20	-	212426628	212426813
232287458	chr2	212495138	212495276	212495162	212495254	ERBB4	NM_001042599	1	27	17	-	212495187	212495319
232287458	chr2	212495138	212495276	212495162	212495254	ERBB4	NM_005235	2	28	17	-	212495187	212495319
231416259	chr2	212530096	212530261	212530123	212530236	ERBB4	NM_001042599	1	27	15	-	212530048	212530202
231416259	chr2	212530096	212530261	212530123	212530236	ERBB4	NM_005235	2	28	15	-	212530048	212530202
231158942	chr2	212566575	212566749	212566597	212566723	ERBB4	NM_001042599	1	27	12	-	212566692	212566891
231158942	chr2	212566575	212566749	212566597	212566723	ERBB4	NM_005235	2	28	12	-	212566692	212566891
230582892	chr2	212568846	212569017	212568871	212568989	ERBB4	NM_001042599	1	27	11	-	212568829	212568919
230582892	chr2	212568846	212569017	212568871	212568989	ERBB4	NM_005235	2	28	11	-	212568829	212568919

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228397738	chr2	212576773	212576928	212576800	212576901	ERBB4	NM_001042599	1	27	9	-	212576775	212576901
228397738	chr2	212576773	212576928	212576800	212576901	ERBB4	NM_005235	2	28	9	-	212576775	212576901
227703162	chr2	212587189	212587334	212587214	212587313	ERBB4	NM_001042599	1	27	7	-	212587118	212587259
227703162	chr2	212587189	212587334	212587214	212587313	ERBB4	NM_005235	2	28	7	-	212587118	212587259
232311534	chr2	212652682	212652819	212652706	212652796	ERBB4	NM_001042599	1	27	4	-	212652750	212652884
232311534	chr2	212652682	212652819	212652706	212652796	ERBB4	NM_005235	2	28	4	-	212652750	212652884
229768853	chr2	212812248	212812379	212812273	212812352	ERBB4	NM_001042599	1	27	3	-	212812155	212812341
229768853	chr2	212812248	212812379	212812273	212812352	ERBB4	NM_005235	2	28	3	-	212812155	212812341
232530475	chr2	213403169	213403309	213403189	213403286	ERBB4	NM_001042599	1	27	1	-	213403173	213403352
232530475	chr2	213403169	213403309	213403189	213403286	ERBB4	NM_005235	2	28	1	-	213403173	213403352
280611711	chr2	216229581	216229737	216229601	216229712	FN1	NM_212476	4	44	42	-	216229602	216229708
280611711	chr2	216229581	216229737	216229601	216229712	FN1	NM_212478	5	46	44	-	216229602	216229708
280611711	chr2	216229581	216229737	216229601	216229712	FN1	NM_212482	6	46	44	-	216229602	216229708
280611711	chr2	216229581	216229737	216229601	216229712	FN1	NM_212474	3	44	42	-	216229602	216229708
280611711	chr2	216229581	216229737	216229601	216229712	FN1	NM_002026	1	46	44	-	216229602	216229708
280711609	chr2	216232655	216232828	216232678	216232799	FN1	NM_212476	4	44	40	-	216232586	216232750
280711609	chr2	216232655	216232828	216232678	216232799	FN1	NM_212478	5	46	42	-	216232586	216232750
280711609	chr2	216232655	216232828	216232678	216232799	FN1	NM_212482	6	46	42	-	216232586	216232750
280711609	chr2	216232655	216232828	216232678	216232799	FN1	NM_212474	3	44	40	-	216232586	216232750
280711609	chr2	216232655	216232828	216232678	216232799	FN1	NM_002026	1	46	42	-	216232586	216232750
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_212478	5	46	39	-	216236832	216237023
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_002026	1	46	39	-	216236832	216237098
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_212476	4	44	38	-	216236632	216237098
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_212482	6	46	40	-	216236632	216237098
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_212478	5	46	40	-	216236632	216236738
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_212474	3	44	38	-	216236632	216236738
280030316	chr2	216236703	216236869	216236727	216236847	FN1	NM_002026	1	46	40	-	216236632	216236738
279229108	chr2	216239898	216240072	216239926	216240049	FN1	NM_212476	4	44	36	-	216239937	216240116
279229108	chr2	216239898	216240072	216239926	216240049	FN1	NM_212478	5	46	37	-	216239937	216240116
279229108	chr2	216239898	216240072	216239926	216240049	FN1	NM_212482	6	46	38	-	216239937	216240116
279229108	chr2	216239898	216240072	216239926	216240049	FN1	NM_212474	3	44	36	-	216239937	216240116
279229108	chr2	216239898	216240072	216239926	216240049	FN1	NM_002026	1	46	37	-	216239937	216240116
280790829	chr2	216241160	216241324	216241183	216241302	FN1	NM_212476	4	44	34	-	216241221	216241397
280790829	chr2	216241160	216241324	216241183	216241302	FN1	NM_212478	5	46	35	-	216241221	216241397
280790829	chr2	216241160	216241324	216241183	216241302	FN1	NM_212482	6	46	36	-	216241221	216241397
280790829	chr2	216241160	216241324	216241183	216241302	FN1	NM_212474	3	44	34	-	216241221	216241397
280790829	chr2	216241160	216241324	216241183	216241302	FN1	NM_002026	1	46	35	-	216241221	216241397
279837730	chr2	216243827	216243973	216243850	216243952	FN1	NM_212476	4	44	32	-	216243853	216244040
279837730	chr2	216243827	216243973	216243850	216243952	FN1	NM_212478	5	46	33	-	216243853	216244040
279837730	chr2	216243827	216243973	216243850	216243952	FN1	NM_212482	6	46	34	-	216243853	216244040
279837730	chr2	216243827	216243973	216243850	216243952	FN1	NM_212474	3	44	32	-	216243853	216244040

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279837730	chr2	216243827	216243973	216243850	216243952	FN1	NM_002026	1	46	33	-	216243853	216244040
278604434	chr2	216245732	216245860	216245756	216245832	FN1	NM_212478	5	46	32	-	216245534	216245803
278604434	chr2	216245732	216245860	216245756	216245832	FN1	NM_212482	6	46	33	-	216245534	216245803
278604434	chr2	216245732	216245860	216245756	216245832	FN1	NM_002026	1	46	32	-	216245534	216245803
278075537	chr2	216248134	216248268	216248155	216248244	FN1	NM_212476	4	44	30	-	216248051	216248206
278075537	chr2	216248134	216248268	216248155	216248244	FN1	NM_212478	5	46	30	-	216248051	216248206
278075537	chr2	216248134	216248268	216248155	216248244	FN1	NM_212482	6	46	31	-	216248051	216248206
278075537	chr2	216248134	216248268	216248155	216248244	FN1	NM_212474	3	44	30	-	216248051	216248206
278075537	chr2	216248134	216248268	216248155	216248244	FN1	NM_002026	1	46	30	-	216248051	216248206
279036829	chr2	216251360	216251522	216251384	216251499	FN1	NM_212476	4	44	27	-	216251412	216251681
279036829	chr2	216251360	216251522	216251384	216251499	FN1	NM_212478	5	46	27	-	216251412	216251681
279036829	chr2	216251360	216251522	216251384	216251499	FN1	NM_212482	6	46	28	-	216251412	216251681
279036829	chr2	216251360	216251522	216251384	216251499	FN1	NM_212474	3	44	27	-	216251412	216251681
279036829	chr2	216251360	216251522	216251384	216251499	FN1	NM_002026	1	46	27	-	216251412	216251681
277875628	chr2	216256262	216256436	216256286	216256412	FN1	NM_212476	4	44	25	-	216256355	216256537
277875628	chr2	216256262	216256436	216256286	216256412	FN1	NM_212478	5	46	25	-	216256355	216256537
277875628	chr2	216256262	216256436	216256286	216256412	FN1	NM_212482	6	46	26	-	216256355	216256537
277875628	chr2	216256262	216256436	216256286	216256412	FN1	NM_212474	3	44	25	-	216256355	216256537
277875628	chr2	216256262	216256436	216256286	216256412	FN1	NM_002026	1	46	25	-	216256355	216256537
278776869	chr2	216257755	216257917	216257782	216257889	FN1	NM_212482	6	46	25	-	216257654	216257926
277994181	chr2	216261819	216261992	216261844	216261968	FN1	NM_212476	4	44	23	-	216261860	216261946
277994181	chr2	216261819	216261992	216261844	216261968	FN1	NM_212478	5	46	23	-	216261860	216261946
277994181	chr2	216261819	216261992	216261844	216261968	FN1	NM_212482	6	46	23	-	216261860	216261946
277994181	chr2	216261819	216261992	216261844	216261968	FN1	NM_212474	3	44	23	-	216261860	216261946
277994181	chr2	216261819	216261992	216261844	216261968	FN1	NM_002026	1	46	23	-	216261860	216261946
281125072	chr2	216264026	216264178	216264046	216264152	FN1	NM_212476	4	44	21	-	216263980	216264074
281125072	chr2	216264026	216264178	216264046	216264152	FN1	NM_212478	5	46	21	-	216263980	216264074
281125072	chr2	216264026	216264178	216264046	216264152	FN1	NM_212482	6	46	21	-	216263980	216264074
281125072	chr2	216264026	216264178	216264046	216264152	FN1	NM_212474	3	44	21	-	216263980	216264074
281125072	chr2	216264026	216264178	216264046	216264152	FN1	NM_002026	1	46	21	-	216263980	216264074
278603657	chr2	216270910	216271083	216270932	216271062	FN1	NM_212476	4	44	19	-	216270961	216271233
278603657	chr2	216270910	216271083	216270932	216271062	FN1	NM_212478	5	46	19	-	216270961	216271233
278603657	chr2	216270910	216271083	216270932	216271062	FN1	NM_212482	6	46	19	-	216270961	216271233
278603657	chr2	216270910	216271083	216270932	216271062	FN1	NM_212474	3	44	19	-	216270961	216271233
278603657	chr2	216270910	216271083	216270932	216271062	FN1	NM_002026	1	46	19	-	216270961	216271233
279161711	chr2	216271861	216272007	216271883	216271986	FN1	NM_212476	4	44	18	-	216271850	216272044
279161711	chr2	216271861	216272007	216271883	216271986	FN1	NM_212478	5	46	18	-	216271850	216272044
279161711	chr2	216271861	216272007	216271883	216271986	FN1	NM_212482	6	46	18	-	216271850	216272044
279161711	chr2	216271861	216272007	216271883	216271986	FN1	NM_212474	3	44	18	-	216271850	216272044
279161711	chr2	216271861	216272007	216271883	216271986	FN1	NM_002026	1	46	18	-	216271850	216272044
279155326	chr2	216272941	216273105	216272963	216273078	FN1	NM_212476	4	44	16	-	216273021	216273149

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279155326	chr2	216272941	216273105	216272963	216273078	FN1	NM_212478	5	46	16	-	216273021	216273149
279155326	chr2	216272941	216273105	216272963	216273078	FN1	NM_212482	6	46	16	-	216273021	216273149
279155326	chr2	216272941	216273105	216272963	216273078	FN1	NM_212474	3	44	16	-	216273021	216273149
279155326	chr2	216272941	216273105	216272963	216273078	FN1	NM_002026	1	46	16	-	216273021	216273149
278401592	chr2	216274551	216274722	216274572	216274702	FN1	NM_212476	4	44	14	-	216274657	216274837
278401592	chr2	216274551	216274722	216274572	216274702	FN1	NM_212478	5	46	14	-	216274657	216274837
278401592	chr2	216274551	216274722	216274572	216274702	FN1	NM_212482	6	46	14	-	216274657	216274837
278401592	chr2	216274551	216274722	216274572	216274702	FN1	NM_212474	3	44	14	-	216274657	216274837
278401592	chr2	216274551	216274722	216274572	216274702	FN1	NM_002026	1	46	14	-	216274657	216274837
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_212476	4	44	13	-	216279560	216279681
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_212478	5	46	13	-	216279560	216279681
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_212482	6	46	13	-	216279560	216279681
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_212474	3	44	13	-	216279560	216279681
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_002026	1	46	13	-	216279560	216279681
278049465	chr2	216279548	216279681	216279569	216279661	FN1	NM_054034	2	13	13	-	216279384	216279681
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_054034	2	13	11	-	216285396	216285524
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_212476	4	44	11	-	216285396	216285524
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_212478	5	46	11	-	216285396	216285524
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_212482	6	46	11	-	216285396	216285524
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_212474	3	44	11	-	216285396	216285524
279970946	chr2	216285359	216285507	216285383	216285481	FN1	NM_002026	1	46	11	-	216285396	216285524
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_054034	2	13	9	-	216288073	216288249
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_212476	4	44	9	-	216288073	216288249
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_212478	5	46	9	-	216288073	216288249
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_212482	6	46	9	-	216288073	216288249
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_212474	3	44	9	-	216288073	216288249
278136247	chr2	216288048	216288184	216288069	216288158	FN1	NM_002026	1	46	9	-	216288073	216288249
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_054034	2	13	7	-	216289817	216290008
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_212476	4	44	7	-	216289817	216290008
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_212478	5	46	7	-	216289817	216290008
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_212482	6	46	7	-	216289817	216290008
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_212474	3	44	7	-	216289817	216290008
279450306	chr2	216289805	216289947	216289830	216289928	FN1	NM_002026	1	46	7	-	216289817	216290008
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_054034	2	13	5	-	216295438	216295575
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_212476	4	44	5	-	216295438	216295575
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_212478	5	46	5	-	216295438	216295575
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_212482	6	46	5	-	216295438	216295575
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_212474	3	44	5	-	216295438	216295575
279650790	chr2	216295365	216295511	216295393	216295490	FN1	NM_002026	1	46	5	-	216295438	216295575
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_054034	2	13	3	-	216298047	216298184
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_212476	4	44	3	-	216298047	216298184

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_212478	5	46	3	-	216298047	216298184
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_212482	6	46	3	-	216298047	216298184
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_212474	3	44	3	-	216298047	216298184
280221803	chr2	216297963	216298132	216297991	216298107	FN1	NM_002026	1	46	3	-	216298047	216298184
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_054034	2	13	1	-	216300378	216300791
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_212476	4	44	1	-	216300378	216300791
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_212478	5	46	1	-	216300378	216300791
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_212482	6	46	1	-	216300378	216300791
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_212474	3	44	1	-	216300378	216300791
279464888	chr2	216300296	216300432	216300319	216300412	FN1	NM_002026	1	46	1	-	216300378	216300791
237807561	chr2	219538393	219538548	219538414	219538526	STK36	NM_015690	2	27	3	+	219538348	219538488
237807561	chr2	219538393	219538548	219538414	219538526	STK36	NM_001243313	1	27	3	+	219538348	219538488
261072067	chr2	219540657	219540827	219540678	219540802	STK36	NM_015690	2	27	6	+	219540752	219541001
261072067	chr2	219540657	219540827	219540678	219540802	STK36	NM_001243313	1	27	6	+	219540752	219541001
239917344	chr2	219544221	219544374	219544242	219544353	STK36	NM_015690	2	27	8	+	219544283	219544452
239917344	chr2	219544221	219544374	219544242	219544353	STK36	NM_001243313	1	27	8	+	219544283	219544452
261131852	chr2	219545281	219545447	219545304	219545425	STK36	NM_015690	2	27	10	+	219545326	219545425
261131852	chr2	219545281	219545447	219545304	219545425	STK36	NM_001243313	1	27	10	+	219545326	219545425
240344964	chr2	219553489	219553619	219553510	219553599	STK36	NM_015690	2	27	12	+	219553420	219553599
240344964	chr2	219553489	219553619	219553510	219553599	STK36	NM_001243313	1	27	12	+	219553420	219553599
242095150	chr2	219556819	219556965	219556840	219556944	STK36	NM_015690	2	27	15	+	219556866	219557016
242095150	chr2	219556819	219556965	219556840	219556944	STK36	NM_001243313	1	27	15	+	219556866	219557016
264790777	chr2	219557919	219558093	219557946	219558069	STK36	NM_015690	2	27	17	+	219557963	219558067
264790777	chr2	219557919	219558093	219557946	219558069	STK36	NM_001243313	1	27	17	+	219557963	219558067
240349234	chr2	219559133	219559304	219559157	219559284	STK36	NM_015690	2	27	21	+	219559248	219559358
240349234	chr2	219559133	219559304	219559157	219559284	STK36	NM_001243313	1	27	21	+	219559248	219559358
238263939	chr2	219561813	219561983	219561833	219561960	STK36	NM_015690	2	27	23	+	219561762	219561936
238263939	chr2	219561813	219561983	219561833	219561960	STK36	NM_001243313	1	27	23	+	219561762	219561936
240832073	chr2	219562647	219562799	219562668	219562772	STK36	NM_015690	2	27	25	+	219562577	219562724
240832073	chr2	219562647	219562799	219562668	219562772	STK36	NM_001243313	1	27	25	+	219562577	219562724
240866303	chr2	219563641	219563795	219563661	219563776	STK36	NM_015690	2	27	26	+	219563325	219564071
240866303	chr2	219563641	219563795	219563661	219563776	STK36	NM_001243313	1	27	26	+	219563325	219564071
262633509	chr2	219566485	219566651	219566507	219566629	STK36	NM_015690	2	27	27	+	219566589	219567440
262633509	chr2	219566485	219566651	219566507	219566629	STK36	NM_001243313	1	27	27	+	219566589	219567440
235189467	chr2	223066562	223066713	223066587	223066690	PAX3	NM_001127366	2	9	8	-	223066663	223066909
235189467	chr2	223066562	223066713	223066587	223066690	PAX3	NM_181459	6	10	8	-	223066663	223066909
235189467	chr2	223066562	223066713	223066587	223066690	PAX3	NM_181458	5	9	8	-	223066663	223066909
235189467	chr2	223066562	223066713	223066587	223066690	PAX3	NM_181457	4	8	8	-	223066432	223066909
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_001127366	2	9	7	-	223084859	223085073
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_181461	8	8	7	-	223084859	223085073
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_181459	6	10	7	-	223084859	223085073

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_181460	7	9	7	-	223084859	223085073
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_181458	5	9	7	-	223084859	223085073
236053466	chr2	223084968	223085130	223084988	223085105	PAX3	NM_181457	4	8	7	-	223084859	223085073
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_001127366	2	9	5	-	223096797	223097002
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_181461	8	8	5	-	223096797	223097002
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_181459	6	10	5	-	223096797	223097002
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_181460	7	9	5	-	223096797	223097002
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_181458	5	9	5	-	223096797	223097002
239888601	chr2	223096743	223096914	223096767	223096893	PAX3	NM_181457	4	8	5	-	223096797	223097002
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_000438	1	4	4	-	223158349	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_001127366	2	9	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_181461	8	8	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_181459	6	10	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_013942	3	5	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_181460	7	9	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_181458	5	9	4	-	223158886	223159020
237357763	chr2	223158841	223158997	223158861	223158970	PAX3	NM_181457	4	8	4	-	223158886	223159020
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_001127366	2	9	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_000438	1	4	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_181461	8	8	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_181459	6	10	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_013942	3	5	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_181460	7	9	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_181458	5	9	2	-	223161697	223161932
235289799	chr2	223161724	223161895	223161744	223161874	PAX3	NM_181457	4	8	2	-	223161697	223161932
304779296	chr2	234669017	234669182	234669042	234669162	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
304784711	chr2	234669468	234669617	234669490	234669595	UGT1A1	NM_000463	1	5	1	+	234668919	234669797
300042335	chr2	234675672	234675801	234675696	234675778	UGT1A1	NM_000463	1	5	2	+	234675680	234675811
304630651	chr2	234676951	234677125	234676973	234677099	UGT1A1	NM_000463	1	5	4	+	234676866	234677085
294774274	chr3	3194058	3194221	3194081	3194194	CRBN	NM_016302	2	11	10	-	3194140	3194271
294774274	chr3	3194058	3194221	3194081	3194194	CRBN	NM_001173482	1	11	10	-	3194140	3194271
294164839	chr3	3195573	3195741	3195594	3195712	CRBN	NM_016302	2	11	8	-	3195644	3195759
294164839	chr3	3195573	3195741	3195594	3195712	CRBN	NM_001173482	1	11	8	-	3195644	3195759
293810449	chr3	3197925	3198059	3197947	3198031	CRBN	NM_016302	2	11	6	-	3197903	3197965
293810449	chr3	3197925	3198059	3197947	3198031	CRBN	NM_001173482	1	11	6	-	3197903	3197965
294172724	chr3	3214376	3214501	3214404	3214476	CRBN	NM_016302	2	11	4	-	3214460	3214609
294172724	chr3	3214376	3214501	3214404	3214476	CRBN	NM_001173482	1	11	4	-	3214460	3214609
294826414	chr3	3215774	3215940	3215801	3215913	CRBN	NM_016302	2	11	3	-	3215743	3215945
294826414	chr3	3215774	3215940	3215801	3215913	CRBN	NM_001173482	1	11	3	-	3215743	3215945
294853263	chr3	3221269	3221395	3221289	3221375	CRBN	NM_016302	2	11	1	-	3221305	3221401
294853263	chr3	3221269	3221395	3221289	3221375	CRBN	NM_001173482	1	11	1	-	3221305	3221401

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227864954	chr3	10076098	10076266	10076126	10076244	FANCD2	NM_033084	2	43	4	+	10076153	10076220
227864954	chr3	10076098	10076266	10076126	10076244	FANCD2	NM_001018115	1	44	4	+	10076153	10076220
228471147	chr3	10077932	10078066	10077960	10078038	FANCD2	NM_033084	2	43	7	+	10077971	10078023
228471147	chr3	10077932	10078066	10077960	10078038	FANCD2	NM_001018115	1	44	7	+	10077971	10078023
229483363	chr3	10081412	10081558	10081433	10081530	FANCD2	NM_033084	2	43	9	+	10081405	10081529
229483363	chr3	10081412	10081558	10081433	10081530	FANCD2	NM_001018115	1	44	9	+	10081405	10081529
231508584	chr3	10084685	10084858	10084710	10084834	FANCD2	NM_033084	2	43	12	+	10084734	10084834
231508584	chr3	10084685	10084858	10084710	10084834	FANCD2	NM_001018115	1	44	12	+	10084734	10084834
228282140	chr3	10088263	10088392	10088285	10088370	FANCD2	NM_033084	2	43	15	+	10088264	10088407
228282140	chr3	10088263	10088392	10088285	10088370	FANCD2	NM_001018115	1	44	15	+	10088264	10088407
230354183	chr3	10094028	10094172	10094052	10094150	FANCD2	NM_033084	2	43	18	+	10094071	10094181
230354183	chr3	10094028	10094172	10094052	10094150	FANCD2	NM_001018115	1	44	18	+	10094071	10094181
231802329	chr3	10106367	10106494	10106387	10106473	FANCD2	NM_033084	2	43	23	+	10106413	10106559
231802329	chr3	10106367	10106494	10106387	10106473	FANCD2	NM_001018115	1	44	23	+	10106413	10106559
227982794	chr3	10107493	10107664	10107517	10107642	FANCD2	NM_033084	2	43	25	+	10107548	10107663
227982794	chr3	10107493	10107664	10107517	10107642	FANCD2	NM_001018115	1	44	25	+	10107548	10107663
229952504	chr3	10114473	10114640	10114498	10114613	FANCD2	NM_033084	2	43	27	+	10114555	10114665
229952504	chr3	10114473	10114640	10114498	10114613	FANCD2	NM_001018115	1	44	27	+	10114555	10114665
228534174	chr3	10116276	10116448	10116299	10116423	FANCD2	NM_033084	2	43	29	+	10116214	10116357
228534174	chr3	10116276	10116448	10116299	10116423	FANCD2	NM_001018115	1	44	29	+	10116214	10116357
231617288	chr3	10122907	10123078	10122933	10123053	FANCD2	NM_033084	2	43	32	+	10123030	10123148
231617288	chr3	10122907	10123078	10122933	10123053	FANCD2	NM_001018115	1	44	32	+	10123030	10123148
231187713	chr3	10128870	10129039	10128898	10129018	FANCD2	NM_033084	2	43	34	+	10128818	10128948
231187713	chr3	10128870	10129039	10128898	10129018	FANCD2	NM_001018115	1	44	34	+	10128818	10128948
232799444	chr3	10131953	10132113	10131975	10132085	FANCD2	NM_033084	2	43	37	+	10131976	10132069
232799444	chr3	10131953	10132113	10131975	10132085	FANCD2	NM_001018115	1	44	37	+	10131976	10132069
230005614	chr3	10136758	10136928	10136784	10136906	FANCD2	NM_033084	2	43	41	+	10136884	10136958
230005614	chr3	10136758	10136928	10136784	10136906	FANCD2	NM_001018115	1	44	41	+	10136884	10136958
228399992	chr3	10140309	10140457	10140337	10140436	FANCD2	NM_001018115	1	44	43	+	10140404	10140499
228399992	chr3	10140309	10140457	10140337	10140436	FANCD2	NM_033084	2	43	43	+	10140404	10141344
264379712	chr3	10183398	10183572	10183417	10183555	VHL	NM_000551	1	3	1	+	10183319	10183871
264379712	chr3	10183398	10183572	10183417	10183555	VHL	NM_198156	2	2	1	+	10183319	10183871
261850969	chr3	10188157	10188293	10188177	10188271	VHL	NM_000551	1	3	2	+	10188198	10188320
235985044	chr3	12393055	12393200	12393080	12393173	PPARG	NM_015869	2	7	1	+	12393001	12393173
235893903	chr3	12422723	12422886	12422751	12422860	PPARG	NM_138711	3	8	4	+	12422821	12422990
235893903	chr3	12422723	12422886	12422751	12422860	PPARG	NM_015869	2	7	3	+	12422821	12422990
235893903	chr3	12422723	12422886	12422751	12422860	PPARG	NM_138712	4	8	4	+	12422821	12422990
235893903	chr3	12422723	12422886	12422751	12422860	PPARG	NM_005037	1	7	3	+	12422821	12422990
235035972	chr3	12447352	12447526	12447379	12447501	PPARG	NM_138711	3	8	6	+	12447381	12447580
235035972	chr3	12447352	12447526	12447379	12447501	PPARG	NM_015869	2	7	5	+	12447381	12447580
235035972	chr3	12447352	12447526	12447379	12447501	PPARG	NM_138712	4	8	6	+	12447381	12447580

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235035972	chr3	12447352	12447526	12447379	12447501	PPARG	NM_005037	1	7	5	+	12447381	12447580
234966282	chr3	12458419	12458572	12458446	12458548	PPARG	NM_138711	3	8	7	+	12458203	12458653
234966282	chr3	12458419	12458572	12458446	12458548	PPARG	NM_015869	2	7	6	+	12458203	12458653
234966282	chr3	12458419	12458572	12458446	12458548	PPARG	NM_138712	4	8	7	+	12458203	12458653
234966282	chr3	12458419	12458572	12458446	12458548	PPARG	NM_005037	1	7	6	+	12458203	12458653
236626272	chr3	12475510	12475683	12475533	12475660	PPARG	NM_138711	3	8	8	+	12475397	12475855
236626272	chr3	12475510	12475683	12475533	12475660	PPARG	NM_015869	2	7	7	+	12475397	12475855
236626272	chr3	12475510	12475683	12475533	12475660	PPARG	NM_138712	4	8	8	+	12475397	12475855
236626272	chr3	12475510	12475683	12475533	12475660	PPARG	NM_005037	1	7	7	+	12475397	12475855
236255129	chr3	12626360	12626505	12626386	12626480	RAF1	NM_002880	1	17	16	-	12626346	12626480
237675781	chr3	12627186	12627323	12627207	12627298	RAF1	NM_002880	1	17	14	-	12627180	12627298
235594429	chr3	12633145	12633319	12633166	12633294	RAF1	NM_002880	1	17	11	-	12633207	12633291
237431039	chr3	12641731	12641905	12641752	12641883	RAF1	NM_002880	1	17	9	-	12641651	12641778
237933606	chr3	12647602	12647737	12647625	12647717	RAF1	NM_002880	1	17	6	-	12647700	12647798
236823376	chr3	12650667	12650830	12650691	12650804	RAF1	NM_002880	1	17	4	-	12650732	12650834
236788686	chr3	12660016	12660147	12660038	12660125	RAF1	NM_002880	1	17	2	-	12660014	12660246
238403967	chr3	14188740	14188909	14188762	14188884	XPC	NR_027299	3	15	14	-	14188790	14188879
238403967	chr3	14188740	14188909	14188762	14188884	XPC	NM_001145769	1	16	15	-	14188790	14188879
238403967	chr3	14188740	14188909	14188762	14188884	XPC	NM_004628	2	16	15	-	14188790	14188879
239508301	chr3	14190240	14190386	14190261	14190364	XPC	NR_027299	3	15	11	-	14190314	14190448
239508301	chr3	14190240	14190386	14190261	14190364	XPC	NM_001145769	1	16	12	-	14190314	14190448
239508301	chr3	14190240	14190386	14190261	14190364	XPC	NM_004628	2	16	12	-	14190314	14190448
239567874	chr3	14197756	14197923	14197777	14197900	XPC	NR_027299	3	15	9	-	14197835	14197995
239567874	chr3	14197756	14197923	14197777	14197900	XPC	NM_001145769	1	16	10	-	14197835	14197995
239567874	chr3	14197756	14197923	14197777	14197900	XPC	NM_004628	2	16	10	-	14197835	14197995
266264558	chr3	14199735	14199908	14199758	14199888	XPC	NR_027299	3	15	8	-	14199511	14200392
266264558	chr3	14199735	14199908	14199758	14199888	XPC	NM_001145769	1	16	9	-	14199511	14200392
266264558	chr3	14199735	14199908	14199758	14199888	XPC	NM_004628	2	16	9	-	14199511	14200392
262314705	chr3	14200145	14200274	14200166	14200253	XPC	NR_027299	3	15	8	-	14199511	14200392
262314705	chr3	14200145	14200274	14200166	14200253	XPC	NM_001145769	1	16	9	-	14199511	14200392
262314705	chr3	14200145	14200274	14200166	14200253	XPC	NM_004628	2	16	9	-	14199511	14200392
263355930	chr3	14206246	14206375	14206271	14206347	XPC	NR_027299	3	15	6	-	14206313	14206433
263355930	chr3	14206246	14206375	14206271	14206347	XPC	NM_001145769	1	16	7	-	14206313	14206433
263355930	chr3	14206246	14206375	14206271	14206347	XPC	NM_004628	2	16	7	-	14206313	14206433
262185555	chr3	14208615	14208789	14208635	14208762	XPC	NR_027299	3	15	4	-	14208669	14208753
262185555	chr3	14208615	14208789	14208635	14208762	XPC	NM_001145769	1	16	5	-	14208669	14208753
262185555	chr3	14208615	14208789	14208635	14208762	XPC	NM_004628	2	16	5	-	14208669	14208753
239488196	chr3	14211918	14212077	14211946	14212052	XPC	NM_001145769	1	16	3	-	14211945	14212050
239488196	chr3	14211918	14212077	14211946	14212052	XPC	NR_027299	3	15	3	-	14211938	14212050
239488196	chr3	14211918	14212077	14211946	14212052	XPC	NM_004628	2	16	3	-	14211938	14212050
239503310	chr3	14219959	14220107	14219979	14220090	XPC	NR_027299	3	15	1	-	14219966	14220172

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239503310	chr3	14219959	14220107	14219979	14220090	XPC	NM_001145769	1	16	1	-	14219966	14220172
239503310	chr3	14219959	14220107	14219979	14220090	XPC	NM_004628	2	16	1	-	14219966	14220172
270337583	chr3	30686115	30686275	30686142	30686253	TGFBR2	NM_001024847	1	8	3	+	30686239	30686407
270337583	chr3	30686115	30686275	30686142	30686253	TGFBR2	NM_003242	2	7	2	+	30686239	30686407
271962815	chr3	30691810	30691979	30691831	30691953	TGFBR2	NM_001024847	1	8	4	+	30691762	30691952
271962815	chr3	30691810	30691979	30691831	30691953	TGFBR2	NM_003242	2	7	3	+	30691762	30691952
272371485	chr3	30713443	30713601	30713467	30713577	TGFBR2	NM_001024847	1	8	5	+	30713130	30713929
272371485	chr3	30713443	30713601	30713467	30713577	TGFBR2	NM_003242	2	7	4	+	30713130	30713929
269560786	chr3	30715517	30715651	30715538	30715624	TGFBR2	NM_001024847	1	8	6	+	30715597	30715738
269560786	chr3	30715517	30715651	30715538	30715624	TGFBR2	NM_003242	2	7	5	+	30715597	30715738
272493639	chr3	30732888	30733061	30732911	30733040	TGFBR2	NM_001024847	1	8	8	+	30732912	30735633
272493639	chr3	30732888	30733061	30732911	30733040	TGFBR2	NM_003242	2	7	7	+	30732912	30735633
233155726	chr3	37038105	37038230	37038129	37038202	MLH1	NM_001167618	3	19	2	+	37038115	37038200
233155726	chr3	37038105	37038230	37038129	37038202	MLH1	NM_001167619	4	18	2	+	37038110	37038200
233155726	chr3	37038105	37038230	37038129	37038202	MLH1	NM_001167617	2	19	2	+	37038110	37038200
233155726	chr3	37038105	37038230	37038129	37038202	MLH1	NM_000249	1	19	2	+	37038110	37038200
233511006	chr3	37045903	37046052	37045925	37046027	MLH1	NM_001167619	4	18	4	+	37045892	37045965
233511006	chr3	37045903	37046052	37045925	37046027	MLH1	NM_001167618	3	19	4	+	37045892	37045965
233511006	chr3	37045903	37046052	37045925	37046027	MLH1	NM_001167617	2	19	4	+	37045892	37045965
233511006	chr3	37045903	37046052	37045925	37046027	MLH1	NM_000249	1	19	4	+	37045892	37045965
231631651	chr3	37053247	37053379	37053269	37053354	MLH1	NM_001167619	4	18	6	+	37053311	37053353
231631651	chr3	37053247	37053379	37053269	37053354	MLH1	NM_001167618	3	19	7	+	37053311	37053353
231631651	chr3	37053247	37053379	37053269	37053354	MLH1	NM_001167617	2	19	7	+	37053311	37053353
231631651	chr3	37053247	37053379	37053269	37053354	MLH1	NM_000249	1	19	7	+	37053311	37053353
232268177	chr3	37055922	37056066	37055950	37056038	MLH1	NM_001167619	4	18	8	+	37055923	37056035
232268177	chr3	37055922	37056066	37055950	37056038	MLH1	NM_001167618	3	19	9	+	37055923	37056035
232268177	chr3	37055922	37056066	37055950	37056038	MLH1	NM_001167617	2	19	9	+	37055923	37056035
232268177	chr3	37055922	37056066	37055950	37056038	MLH1	NM_000249	1	19	9	+	37055923	37056035
233218407	chr3	37067005	37067177	37067032	37067153	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233218407	chr3	37067005	37067177	37067032	37067153	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233218407	chr3	37067005	37067177	37067032	37067153	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233218407	chr3	37067005	37067177	37067032	37067153	MLH1	NM_000249	1	19	12	+	37067128	37067498
233230073	chr3	37067402	37067531	37067424	37067506	MLH1	NM_001167619	4	18	11	+	37067128	37067498
233230073	chr3	37067402	37067531	37067424	37067506	MLH1	NM_001167618	3	19	12	+	37067128	37067498
233230073	chr3	37067402	37067531	37067424	37067506	MLH1	NM_001167617	2	19	12	+	37067128	37067498
233230073	chr3	37067402	37067531	37067424	37067506	MLH1	NM_000249	1	19	12	+	37067128	37067498
232050300	chr3	37081668	37081811	37081690	37081785	MLH1	NM_001167619	4	18	13	+	37081677	37081785
232050300	chr3	37081668	37081811	37081690	37081785	MLH1	NM_001167618	3	19	14	+	37081677	37081785
232050300	chr3	37081668	37081811	37081690	37081785	MLH1	NM_001167617	2	19	14	+	37081677	37081785
232050300	chr3	37081668	37081811	37081690	37081785	MLH1	NM_000249	1	19	14	+	37081677	37081785
232951523	chr3	37089069	37089203	37089092	37089175	MLH1	NM_001167619	4	18	15	+	37089010	37089174

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232951523	chr3	37089069	37089203	37089092	37089175	MLH1	NM_001167618	3	19	16	+	37089010	37089174
232951523	chr3	37089069	37089203	37089092	37089175	MLH1	NM_001167617	2	19	16	+	37089010	37089174
232951523	chr3	37089069	37089203	37089092	37089175	MLH1	NM_000249	1	19	16	+	37089010	37089174
233389980	chr3	37091912	37092046	37091932	37092019	MLH1	NM_001167619	4	18	18	+	37091977	37092337
233389980	chr3	37091912	37092046	37091932	37092019	MLH1	NM_001167618	3	19	19	+	37091977	37092337
233389980	chr3	37091912	37092046	37091932	37092019	MLH1	NM_001167617	2	19	19	+	37091977	37092337
233389980	chr3	37091912	37092046	37091932	37092019	MLH1	NM_000249	1	19	19	+	37091977	37092337
234115582	chr3	37512512	37512686	37512537	37512659	ITGA9	NM_002207	1	28	2	+	37512498	37512625
231275066	chr3	37522978	37523127	37522999	37523101	ITGA9	NM_002207	1	28	4	+	37522975	37523098
234247736	chr3	37547440	37547606	37547463	37547581	ITGA9	NM_002207	1	28	7	+	37547491	37547576
234431668	chr3	37555343	37555515	37555365	37555487	ITGA9	NM_002207	1	28	9	+	37555254	37555391
233424149	chr3	37564963	37565132	37564986	37565104	ITGA9	NM_002207	1	28	12	+	37565012	37565102
231171217	chr3	37583879	37584053	37583905	37584031	ITGA9	NM_002207	1	28	15	+	37583916	37584076
233550165	chr3	37695132	37695305	37695155	37695281	ITGA9	NM_002207	1	28	17	+	37695205	37695281
233753022	chr3	37778354	37778527	37778375	37778499	ITGA9	NM_002207	1	28	20	+	37778395	37778474
232933928	chr3	37791981	37792105	37792002	37792081	ITGA9	NM_002207	1	28	23	+	37791953	37792060
232971250	chr3	37821374	37821535	37821400	37821513	ITGA9	NM_002207	1	28	25	+	37821393	37821512
233462484	chr3	37860335	37860507	37860361	37860485	ITGA9	NM_002207	1	28	28	+	37860382	37861281
274104583	chr3	38180347	38180481	38180374	38180461	MYD88	NM_002468	5	5	1	+	38179969	38180519
274104583	chr3	38180347	38180481	38180374	38180461	MYD88	NM_001172569	4	4	1	+	38179969	38180519
274104583	chr3	38180347	38180481	38180374	38180461	MYD88	NM_001172568	3	4	1	+	38179969	38180519
274104583	chr3	38180347	38180481	38180374	38180461	MYD88	NM_001172567	2	5	1	+	38179969	38180519
274104583	chr3	38180347	38180481	38180374	38180461	MYD88	NM_001172566	1	3	1	+	38179969	38180519
273447121	chr3	38181834	38181964	38181854	38181943	MYD88	NM_001172567	2	5	3	+	38181879	38182083
273447121	chr3	38181834	38181964	38181854	38181943	MYD88	NM_002468	5	5	3	+	38181879	38182059
273447121	chr3	38181834	38181964	38181854	38181943	MYD88	NM_001172568	3	4	2	+	38181879	38182059
273941488	chr3	38182552	38182707	38182572	38182685	MYD88	NM_002468	5	5	5	+	38182623	38184512
273941488	chr3	38182552	38182707	38182572	38182685	MYD88	NM_001172569	4	4	4	+	38182623	38184512
273941488	chr3	38182552	38182707	38182572	38182685	MYD88	NM_001172568	3	4	4	+	38182623	38184512
273941488	chr3	38182552	38182707	38182572	38182685	MYD88	NM_001172567	2	5	5	+	38182623	38184512
273941488	chr3	38182552	38182707	38182572	38182685	MYD88	NM_001172566	1	3	3	+	38182623	38184512
326932763	chr3	41266051	41266180	41266073	41266157	CTNNB1	NM_001904	3	15	3	+	41266017	41266244
326932763	chr3	41266051	41266180	41266073	41266157	CTNNB1	NM_001098209	1	16	3	+	41266017	41266244
326932763	chr3	41266051	41266180	41266073	41266157	CTNNB1	NM_001098210	2	16	3	+	41266017	41266244
226818035	chr3	41266573	41266731	41266595	41266703	CTNNB1	NM_001904	3	15	4	+	41266445	41266698
226818035	chr3	41266573	41266731	41266595	41266703	CTNNB1	NM_001098209	1	16	4	+	41266445	41266698
226818035	chr3	41266573	41266731	41266595	41266703	CTNNB1	NM_001098210	2	16	4	+	41266445	41266698
226532029	chr3	41267055	41267200	41267080	41267175	CTNNB1	NM_001904	3	15	6	+	41267151	41267352
226532029	chr3	41267055	41267200	41267080	41267175	CTNNB1	NM_001098209	1	16	6	+	41267151	41267352
226532029	chr3	41267055	41267200	41267080	41267175	CTNNB1	NM_001098210	2	16	6	+	41267151	41267352
226484528	chr3	41268761	41268898	41268785	41268870	CTNNB1	NM_001904	3	15	7	+	41268699	41268843

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226484528	chr3	41268761	41268898	41268785	41268870	CTNNB1	NM_001098209	1	16	7	+	41268699	41268843
226484528	chr3	41268761	41268898	41268785	41268870	CTNNB1	NM_001098210	2	16	7	+	41268699	41268843
226048551	chr3	41275175	41275322	41275194	41275295	CTNNB1	NM_001904	3	15	9	+	41275020	41275358
226048551	chr3	41275175	41275322	41275194	41275295	CTNNB1	NM_001098209	1	16	9	+	41275020	41275358
226048551	chr3	41275175	41275322	41275194	41275295	CTNNB1	NM_001098210	2	16	9	+	41275020	41275358
225873270	chr3	41277183	41277356	41277207	41277328	CTNNB1	NM_001904	3	15	11	+	41277215	41277334
225873270	chr3	41277183	41277356	41277207	41277328	CTNNB1	NM_001098209	1	16	11	+	41277215	41277334
225873270	chr3	41277183	41277356	41277207	41277328	CTNNB1	NM_001098210	2	16	11	+	41277215	41277334
253680963	chr3	41278079	41278231	41278100	41278203	CTNNB1	NM_001904	3	15	13	+	41278079	41278200
253680963	chr3	41278079	41278231	41278100	41278203	CTNNB1	NM_001098209	1	16	13	+	41278079	41278200
253680963	chr3	41278079	41278231	41278100	41278203	CTNNB1	NM_001098210	2	16	13	+	41278079	41278200
226052050	chr3	41280786	41280958	41280807	41280931	CTNNB1	NM_001098209	1	16	15	+	41280625	41280845
226052050	chr3	41280786	41280958	41280807	41280931	CTNNB1	NM_001098210	2	16	15	+	41280625	41280845
226052050	chr3	41280786	41280958	41280807	41280931	CTNNB1	NM_001904	3	15	15	+	41280625	41281939
280465168	chr3	46480731	46480905	46480752	46480885	LTF	NM_002343	2	17	15	-	46480787	46480971
280465168	chr3	46480731	46480905	46480752	46480885	LTF	NM_001199149	1	17	15	-	46480787	46480971
280610934	chr3	46484949	46485117	46484970	46485094	LTF	NM_002343	2	17	13	-	46484932	46485073
280610934	chr3	46484949	46485117	46484970	46485094	LTF	NM_001199149	1	17	13	-	46484932	46485073
279807173	chr3	46488751	46488915	46488773	46488892	LTF	NM_002343	2	17	10	-	46488799	46488889
279807173	chr3	46488751	46488915	46488773	46488892	LTF	NM_001199149	1	17	10	-	46488799	46488889
279159679	chr3	46491332	46491461	46491354	46491437	LTF	NM_002343	2	17	8	-	46491344	46491518
279159679	chr3	46491332	46491461	46491354	46491437	LTF	NM_001199149	1	17	8	-	46491344	46491518
278977111	chr3	46495723	46495875	46495748	46495850	LTF	NM_002343	2	17	6	-	46495795	46495850
278977111	chr3	46495723	46495875	46495748	46495850	LTF	NM_001199149	1	17	6	-	46495795	46495850
278503690	chr3	46497375	46497513	46497395	46497486	LTF	NM_002343	2	17	4	-	46497286	46497468
278503690	chr3	46497375	46497513	46497395	46497486	LTF	NM_001199149	1	17	4	-	46497286	46497468
280568621	chr3	46501201	46501349	46501222	46501324	LTF	NM_002343	2	17	2	-	46501146	46501309
280568621	chr3	46501201	46501349	46501222	46501324	LTF	NM_001199149	1	17	2	-	46501146	46501309
239569560	chr3	47061200	47061357	47061225	47061330	SETD2	NM_014159	1	21	19	-	47061250	47061330
240498687	chr3	47087915	47088077	47087943	47088055	SETD2	NM_014159	1	21	16	-	47087977	47088111
261230442	chr3	47098511	47098679	47098532	47098655	SETD2	NM_014159	1	21	15	-	47098311	47098980
242049018	chr3	47103585	47103753	47103613	47103725	SETD2	NM_014159	1	21	14	-	47103653	47103836
264168458	chr3	47125178	47125324	47125207	47125302	SETD2	NM_014159	1	21	12	-	47125210	47125872
264368162	chr3	47125594	47125763	47125622	47125738	SETD2	NM_014159	1	21	12	-	47125210	47125872
264253301	chr3	47129617	47129760	47129642	47129732	SETD2	NM_014159	1	21	10	-	47129603	47129737
264447142	chr3	47142988	47143144	47143011	47143116	SETD2	NM_014159	1	21	8	-	47142948	47143045
242038760	chr3	47147489	47147654	47147517	47147628	SETD2	NM_014159	1	21	6	-	47147487	47147610
262430759	chr3	47161561	47161734	47161589	47161712	SETD2	NM_014159	1	21	3	-	47161672	47166038
262505892	chr3	47161977	47162151	47162005	47162124	SETD2	NM_014159	1	21	3	-	47161672	47166038
239150870	chr3	47162437	47162584	47162462	47162563	SETD2	NM_014159	1	21	3	-	47161672	47166038
239092654	chr3	47162851	47162980	47162873	47162952	SETD2	NM_014159	1	21	3	-	47161672	47166038

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239164556	chr3	47163266	47163405	47163289	47163378	SETD2	NM_014159	1	21	3	-	47161672	47166038
262433061	chr3	47163627	47163772	47163654	47163748	SETD2	NM_014159	1	21	3	-	47161672	47166038
262516899	chr3	47164081	47164214	47164102	47164185	SETD2	NM_014159	1	21	3	-	47161672	47166038
262468359	chr3	47164453	47164624	47164481	47164596	SETD2	NM_014159	1	21	3	-	47161672	47166038
238809746	chr3	47164822	47164967	47164846	47164941	SETD2	NM_014159	1	21	3	-	47161672	47166038
239079411	chr3	47165178	47165313	47165206	47165285	SETD2	NM_014159	1	21	3	-	47161672	47166038
239111343	chr3	47165465	47165629	47165489	47165608	SETD2	NM_014159	1	21	3	-	47161672	47166038
262597430	chr3	47165952	47166104	47165976	47166076	SETD2	NM_014159	1	21	3	-	47161672	47166038
223442538	chr3	52436298	52436468	52436316	52436447	BAP1	NM_004656	1	17	17	-	52435025	52436437
223707208	chr3	52437196	52437360	52437216	52437336	BAP1	NM_004656	1	17	14	-	52437154	52437314
222347971	chr3	52437776	52437945	52437799	52437922	BAP1	NM_004656	1	17	13	-	52437432	52437910
223808364	chr3	52439203	52439368	52439222	52439343	BAP1	NM_004656	1	17	11	-	52439126	52439310
223270696	chr3	52440294	52440467	52440314	52440446	BAP1	NM_004656	1	17	9	-	52440269	52440392
222243185	chr3	52441360	52441496	52441384	52441471	BAP1	NM_004656	1	17	6	-	52441415	52441476
223177753	chr3	52442493	52442667	52442519	52442645	BAP1	NM_004656	1	17	4	-	52442490	52442622
222165518	chr3	52443862	52444013	52443880	52443996	BAP1	NM_004656	1	17	1	-	52443858	52444009
237240658	chr3	52584383	52584555	52584409	52584534	PBRM1	NM_018165	1	28	27	-	52584437	52584653
237240658	chr3	52584383	52584555	52584409	52584534	PBRM1	NM_018313	2	30	29	-	52584437	52584653
237240658	chr3	52584383	52584555	52584409	52584534	PBRM1	NM_181042	3	28	27	-	52584437	52584653
235080783	chr3	52588803	52588967	52588822	52588942	PBRM1	NM_018165	1	28	25	-	52588740	52588895
235080783	chr3	52588803	52588967	52588822	52588942	PBRM1	NM_018313	2	30	27	-	52588740	52588895
235388069	chr3	52597345	52597479	52597368	52597455	PBRM1	NM_018165	1	28	23	-	52597299	52597509
235388069	chr3	52597345	52597479	52597368	52597455	PBRM1	NM_181042	3	28	24	-	52597299	52597509
235388069	chr3	52597345	52597479	52597368	52597455	PBRM1	NM_018313	2	30	25	-	52597380	52597509
237326341	chr3	52610539	52610667	52610567	52610642	PBRM1	NM_018165	1	28	21	-	52610557	52610714
237326341	chr3	52610539	52610667	52610567	52610642	PBRM1	NM_018313	2	30	23	-	52610557	52610714
237326341	chr3	52610539	52610667	52610567	52610642	PBRM1	NM_181042	3	28	22	-	52610557	52610714
235589069	chr3	52613103	52613243	52613125	52613215	PBRM1	NM_018165	1	28	20	-	52613070	52613215
235589069	chr3	52613103	52613243	52613125	52613215	PBRM1	NM_018313	2	30	22	-	52613070	52613215
235589069	chr3	52613103	52613243	52613125	52613215	PBRM1	NM_181042	3	28	21	-	52613070	52613215
237565516	chr3	52620565	52620708	52620586	52620680	PBRM1	NM_018165	1	28	19	-	52620441	52620704
237565516	chr3	52620565	52620708	52620586	52620680	PBRM1	NM_018313	2	30	21	-	52620441	52620704
237565516	chr3	52620565	52620708	52620586	52620680	PBRM1	NM_181042	3	28	20	-	52620441	52620704
238835635	chr3	52623025	52623199	52623052	52623171	PBRM1	NM_018165	1	28	17	-	52623086	52623271
238835635	chr3	52623025	52623199	52623052	52623171	PBRM1	NM_018313	2	30	19	-	52623086	52623271
238835635	chr3	52623025	52623199	52623052	52623171	PBRM1	NM_181042	3	28	18	-	52623086	52623271
239414678	chr3	52643207	52643369	52643231	52643341	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239414678	chr3	52643207	52643369	52643231	52643341	PBRM1	NM_018313	2	30	17	-	52643329	52643971
239414678	chr3	52643207	52643369	52643231	52643341	PBRM1	NM_181042	3	28	16	-	52643329	52643971
239471359	chr3	52643606	52643753	52643627	52643726	PBRM1	NM_018165	1	28	15	-	52643329	52643971
239471359	chr3	52643606	52643753	52643627	52643726	PBRM1	NM_018313	2	30	17	-	52643329	52643971

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239471359	chr3	52643606	52643753	52643627	52643726	PBRM1	NM_181042	3	28	16	-	52643329	52643971
236028696	chr3	52649340	52649466	52649366	52649438	PBRM1	NM_018165	1	28	14	-	52649367	52649472
236028696	chr3	52649340	52649466	52649366	52649438	PBRM1	NM_018313	2	30	16	-	52649367	52649472
236028696	chr3	52649340	52649466	52649366	52649438	PBRM1	NM_181042	3	28	15	-	52649367	52649472
237760425	chr3	52661251	52661413	52661273	52661388	PBRM1	NM_018165	1	28	12	-	52661289	52661386
237760425	chr3	52661251	52661413	52661273	52661388	PBRM1	NM_018313	2	30	14	-	52661289	52661386
237760425	chr3	52661251	52661413	52661273	52661388	PBRM1	NM_181042	3	28	13	-	52661289	52661386
237519695	chr3	52668631	52668758	52668660	52668731	PBRM1	NM_018165	1	28	10	-	52668618	52668831
237519695	chr3	52668631	52668758	52668660	52668731	PBRM1	NM_018313	2	30	12	-	52668618	52668831
237519695	chr3	52668631	52668758	52668660	52668731	PBRM1	NM_181042	3	28	11	-	52668618	52668831
236170473	chr3	52677264	52677413	52677291	52677384	PBRM1	NM_018313	2	30	10	-	52677264	52677359
236170473	chr3	52677264	52677413	52677291	52677384	PBRM1	NM_181042	3	28	9	-	52677264	52677359
240589498	chr3	52692180	52692345	52692208	52692321	PBRM1	NM_018165	1	28	5	-	52692215	52692331
240589498	chr3	52692180	52692345	52692208	52692321	PBRM1	NM_018313	2	30	6	-	52692215	52692331
240589498	chr3	52692180	52692345	52692208	52692321	PBRM1	NM_181042	3	28	5	-	52692215	52692331
237329729	chr3	52702601	52702765	52702628	52702741	PBRM1	NM_018165	1	28	3	-	52702514	52702661
237329729	chr3	52702601	52702765	52702628	52702741	PBRM1	NM_018313	2	30	4	-	52702514	52702661
237329729	chr3	52702601	52702765	52702628	52702741	PBRM1	NM_181042	3	28	3	-	52702514	52702661
236085027	chr3	52713664	52713817	52713685	52713796	PBRM1	NM_018165	1	28	1	-	52713590	52713739
236085027	chr3	52713664	52713817	52713685	52713796	PBRM1	NM_018313	2	30	2	-	52713590	52713739
236085027	chr3	52713664	52713817	52713685	52713796	PBRM1	NM_181042	3	28	1	-	52713590	52713739
312301746	chr3	65342584	65342712	65342605	65342692	MAGI1	NM_015520	3	25	25	-	65339906	65342807
312301746	chr3	65342584	65342712	65342605	65342692	MAGI1	NM_001033057	1	23	23	-	65339906	65342807
312167073	chr3	65346866	65347040	65346890	65347013	MAGI1	NM_015520	3	25	23	-	65346874	65347012
312167073	chr3	65346866	65347040	65346890	65347013	MAGI1	NM_001033057	1	23	22	-	65346874	65347012
312167073	chr3	65346866	65347040	65346890	65347013	MAGI1	NM_004742	2	23	23	-	65344944	65347012
312568784	chr3	65350500	65350654	65350527	65350626	MAGI1	NM_004742	2	23	20	-	65350528	65350621
312568784	chr3	65350500	65350654	65350527	65350626	MAGI1	NM_015520	3	25	20	-	65350528	65350621
312568784	chr3	65350500	65350654	65350527	65350626	MAGI1	NM_001033057	1	23	19	-	65350528	65350621
312395471	chr3	65364848	65364987	65364871	65364967	MAGI1	NM_004742	2	23	18	-	65364936	65365229
312395471	chr3	65364848	65364987	65364871	65364967	MAGI1	NM_015520	3	25	18	-	65364936	65365229
312395471	chr3	65364848	65364987	65364871	65364967	MAGI1	NM_001033057	1	23	17	-	65364936	65365229
312516097	chr3	65367486	65367653	65367509	65367627	MAGI1	NM_004742	2	23	17	-	65367552	65367744
312516097	chr3	65367486	65367653	65367509	65367627	MAGI1	NM_015520	3	25	17	-	65367552	65367744
312516097	chr3	65367486	65367653	65367509	65367627	MAGI1	NM_001033057	1	23	16	-	65367552	65367744
312308822	chr3	65372770	65372943	65372796	65372915	MAGI1	NM_004742	2	23	15	-	65372818	65372901
312308822	chr3	65372770	65372943	65372796	65372915	MAGI1	NM_015520	3	25	15	-	65372818	65372901
312331201	chr3	65415174	65415334	65415200	65415315	MAGI1	NM_004742	2	23	12	-	65415195	65415815
312331201	chr3	65415174	65415334	65415200	65415315	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312331201	chr3	65415174	65415334	65415200	65415315	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312413777	chr3	65415547	65415715	65415569	65415692	MAGI1	NM_004742	2	23	12	-	65415195	65415815

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312413777	chr3	65415547	65415715	65415569	65415692	MAGI1	NM_015520	3	25	12	-	65415195	65415815
312413777	chr3	65415547	65415715	65415569	65415692	MAGI1	NM_001033057	1	23	12	-	65415195	65415815
312269277	chr3	65422734	65422901	65422758	65422879	MAGI1	NM_004742	2	23	10	-	65422830	65422922
312269277	chr3	65422734	65422901	65422758	65422879	MAGI1	NM_015520	3	25	10	-	65422830	65422922
312269277	chr3	65422734	65422901	65422758	65422879	MAGI1	NM_001033057	1	23	10	-	65422830	65422922
312316809	chr3	65428386	65428560	65428413	65428534	MAGI1	NM_004742	2	23	8	-	65428467	65428524
312316809	chr3	65428386	65428560	65428413	65428534	MAGI1	NM_015520	3	25	8	-	65428467	65428524
312316809	chr3	65428386	65428560	65428413	65428534	MAGI1	NM_001033057	1	23	8	-	65428467	65428524
312326580	chr3	65455969	65456116	65455996	65456088	MAGI1	NM_004742	2	23	5	-	65455958	65456159
312326580	chr3	65455969	65456116	65455996	65456088	MAGI1	NM_015520	3	25	5	-	65455958	65456159
312326580	chr3	65455969	65456116	65455996	65456088	MAGI1	NM_001033057	1	23	5	-	65455958	65456159
312466883	chr3	65479124	65479265	65479145	65479237	MAGI1	NM_004742	2	23	3	-	65479187	65479306
312466883	chr3	65479124	65479265	65479145	65479237	MAGI1	NM_015520	3	25	3	-	65479187	65479306
312466883	chr3	65479124	65479265	65479145	65479237	MAGI1	NM_001033057	1	23	3	-	65479187	65479306
312517356	chr3	66023616	66023783	66023637	66023765	MAGI1	NM_004742	2	23	1	-	66023671	66024509
312517356	chr3	66023616	66023783	66023637	66023765	MAGI1	NM_015520	3	25	1	-	66023671	66024509
312517356	chr3	66023616	66023783	66023637	66023765	MAGI1	NM_001033057	1	23	1	-	66023671	66024509
234237766	chr3	69812957	69813131	69812981	69813103	MITF	NM_006722	4	10	1	+	69812962	69813093
231573509	chr3	69928429	69928602	69928451	69928575	MITF	NM_001184967	2	10	2	+	69928285	69928534
231573509	chr3	69928429	69928602	69928451	69928575	MITF	NM_006722	4	10	2	+	69928285	69928534
231573509	chr3	69928429	69928602	69928451	69928575	MITF	NM_198177	7	10	2	+	69928285	69928534
231573509	chr3	69928429	69928602	69928451	69928575	MITF	NM_198159	6	10	2	+	69928285	69928534
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_001184968	3	3	2	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_001184967	2	10	3	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_006722	4	10	3	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_000248	1	9	2	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_198177	7	10	3	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_198159	6	10	3	+	69986973	69987200
232620064	chr3	69987059	69987223	69987084	69987197	MITF	NM_198158	5	9	2	+	69986973	69987200
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_001184967	2	10	5	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_006722	4	10	5	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_000248	1	9	4	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_198177	7	10	5	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_198159	6	10	5	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_198178	8	9	4	+	69990387	69990482
231495698	chr3	69990356	69990530	69990383	69990503	MITF	NM_198158	5	9	4	+	69990387	69990482
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_001184967	2	10	7	+	70000981	70001037
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_006722	4	10	7	+	70000981	70001037
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_198177	7	10	7	+	70000981	70001037
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_198159	6	10	7	+	70000981	70001037
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_198178	8	9	6	+	70000981	70001037

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_198158	5	9	6	+	70000981	70001037
231457109	chr3	70000953	70001126	70000975	70001098	MITF	NM_000248	1	9	6	+	70000963	70001037
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_001184967	2	10	10	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_006722	4	10	10	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_000248	1	9	9	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_198177	7	10	10	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_198159	6	10	10	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_198178	8	9	9	+	70013998	70017488
233934055	chr3	70014005	70014172	70014024	70014150	MITF	NM_198158	5	9	9	+	70013998	70017488
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244816	8	20	20	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244815	7	16	16	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244814	6	17	17	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244813	5	15	15	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_032682	9	21	21	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244812	4	16	16	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244808	2	21	21	-	71003865	71008542
228687797	chr3	71008399	71008573	71008422	71008547	FOXP1	NM_001244810	3	21	21	-	71003865	71008542
227756753	chr3	71021092	71021266	71021114	71021238	FOXP1	NM_001244810	3	21	18	-	71021162	71021331
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244816	8	20	16	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244815	7	16	12	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244814	6	17	13	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244813	5	15	11	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_032682	9	21	17	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244812	4	16	12	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244808	2	21	17	-	71026092	71026193
227829164	chr3	71026000	71026143	71026026	71026121	FOXP1	NM_001244810	3	21	17	-	71026092	71026193
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244816	8	20	14	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244815	7	16	10	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244814	6	17	11	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244813	5	15	9	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_032682	9	21	15	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244812	4	16	10	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244808	2	21	15	-	71026979	71027180
229385729	chr3	71026855	71027020	71026876	71026999	FOXP1	NM_001244810	3	21	15	-	71026979	71027180
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244816	8	20	13	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244815	7	16	9	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244814	6	17	10	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244813	5	15	8	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_032682	9	21	14	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244812	4	16	9	-	71037145	71037228
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244808	2	21	14	-	71037145	71037228

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227826863	chr3	71037156	71037280	71037177	71037252	FOXP1	NM_001244810	3	21	14	-	71037145	71037228
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244816	8	20	11	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244815	7	16	7	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244814	6	17	8	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244813	5	15	6	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_032682	9	21	12	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244812	4	16	7	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244808	2	21	12	-	71064700	71064804
229251688	chr3	71064743	71064870	71064764	71064850	FOXP1	NM_001244810	3	21	12	-	71064700	71064804
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244816	8	20	9	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244815	7	16	5	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244814	6	17	6	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244813	5	15	4	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_032682	9	21	10	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244812	4	16	5	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244808	2	21	10	-	71096093	71096246
229352887	chr3	71096177	71096307	71096198	71096279	FOXP1	NM_001244810	3	21	10	-	71096093	71096246
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244816	8	20	6	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244815	7	16	2	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244814	6	17	3	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_032682	9	21	7	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244812	4	16	4	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244808	2	21	7	-	71161687	71161788
230140959	chr3	71161552	71161725	71161576	71161699	FOXP1	NM_001244810	3	21	7	-	71161687	71161788
229038654	chr3	71247012	71247169	71247034	71247145	FOXP1	NM_001012505	1	7	7	-	71247034	71247219
269963333	chr3	89156796	89156967	89156817	89156946	EPHA3	NM_005233	1	17	1	+	89156674	89156986
269963333	chr3	89156796	89156967	89156817	89156946	EPHA3	NM_182644	2	7	1	+	89156674	89156986
271498581	chr3	89258975	89259146	89258999	89259119	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271498581	chr3	89258975	89259146	89258999	89259119	EPHA3	NM_182644	2	7	3	+	89259010	89259670
271500457	chr3	89259457	89259630	89259483	89259608	EPHA3	NM_005233	1	17	3	+	89259010	89259670
271500457	chr3	89259457	89259630	89259483	89259608	EPHA3	NM_182644	2	7	3	+	89259010	89259670
272667913	chr3	89390130	89390262	89390156	89390240	EPHA3	NM_005233	1	17	4	+	89390066	89390221
272667913	chr3	89390130	89390262	89390156	89390240	EPHA3	NM_182644	2	7	4	+	89390066	89390221
270744867	chr3	89391141	89391313	89391168	89391290	EPHA3	NM_005233	1	17	5	+	89390905	89391240
270744867	chr3	89391141	89391313	89391168	89391290	EPHA3	NM_182644	2	7	5	+	89390905	89391240
271504069	chr3	89448501	89448663	89448523	89448636	EPHA3	NM_182644	2	7	7	+	89448468	89449495
271504069	chr3	89448501	89448663	89448523	89448636	EPHA3	NM_005233	1	17	7	+	89448468	89448630
271729435	chr3	89457180	89457327	89457205	89457301	EPHA3	NM_005233	1	17	9	+	89457217	89457281
269688668	chr3	89468407	89468573	89468431	89468546	EPHA3	NM_005233	1	17	11	+	89468355	89468540
272705412	chr3	89480297	89480421	89480320	89480402	EPHA3	NM_005233	1	17	13	+	89480300	89480509
271433293	chr3	89498389	89498523	89498412	89498499	EPHA3	NM_005233	1	17	14	+	89498375	89498524

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271714114	chr3	89521526	89521695	89521548	89521672	EPHA3	NM_005233	1	17	16	+	89521614	89521769
229858420	chr3	128199840	128200004	128199859	128199985	GATA2	NM_032638	3	6	6	-	128198265	128200161
229858420	chr3	128199840	128200004	128199859	128199985	GATA2	NM_001145661	1	7	7	-	128198265	128200161
229858420	chr3	128199840	128200004	128199859	128199985	GATA2	NM_001145662	2	6	6	-	128198265	128200161
227636588	chr3	128200723	128200892	128200743	128200872	GATA2	NM_001145662	2	6	5	-	128200662	128200745
227636588	chr3	128200723	128200892	128200743	128200872	GATA2	NM_032638	3	6	5	-	128200662	128200787
227636588	chr3	128200723	128200892	128200743	128200872	GATA2	NM_001145661	1	7	6	-	128200662	128200787
229075496	chr3	128204646	128204798	128204667	128204778	GATA2	NM_032638	3	6	3	-	128204570	128205211
229075496	chr3	128204646	128204798	128204667	128204778	GATA2	NM_001145661	1	7	4	-	128204570	128205211
229075496	chr3	128204646	128204798	128204667	128204778	GATA2	NM_001145662	2	6	3	-	128204570	128205211
227232177	chr3	128205121	128205272	128205139	128205253	GATA2	NM_032638	3	6	3	-	128204570	128205211
227232177	chr3	128205121	128205272	128205139	128205253	GATA2	NM_001145661	1	7	4	-	128204570	128205211
227232177	chr3	128205121	128205272	128205139	128205253	GATA2	NM_001145662	2	6	3	-	128204570	128205211
271519793	chr3	134644581	134644749	134644602	134644722	EPHB1	NM_004441	1	16	2	+	134644658	134644722
271002316	chr3	134670441	134670602	134670463	134670580	EPHB1	NM_004441	1	16	3	+	134670213	134670894
271944066	chr3	134825242	134825410	134825263	134825389	EPHB1	NM_004441	1	16	4	+	134825290	134825445
270596087	chr3	134851765	134851913	134851784	134851893	EPHB1	NM_004441	1	16	5	+	134851556	134851891
270678291	chr3	134880937	134881111	134880959	134881088	EPHB1	NM_004441	1	16	7	+	134880860	134881022
270063110	chr3	134898711	134898873	134898736	134898850	EPHB1	NM_004441	1	16	10	+	134898702	134898824
269819689	chr3	134920286	134920460	134920312	134920438	EPHB1	NM_004441	1	16	12	+	134920316	134920531
269526427	chr3	134967117	134967291	134967140	134967269	EPHB1	NM_004441	1	16	14	+	134967158	134967351
271633856	chr3	134977818	134977991	134977846	134977969	EPHB1	NM_004441	1	16	16	+	134977854	134979307
294197818	chr3	138375031	138375156	138375053	138375132	PIK3CB	NM_001256045	1	13	12	-	138374984	138375116
294197818	chr3	138375031	138375156	138375053	138375132	PIK3CB	NM_006219	2	22	21	-	138374984	138375116
294723502	chr3	138382762	138382921	138382788	138382900	PIK3CB	NM_001256045	1	13	10	-	138382748	138382871
294723502	chr3	138382762	138382921	138382788	138382900	PIK3CB	NM_006219	2	22	19	-	138382748	138382871
294661112	chr3	138400817	138400943	138400844	138400917	PIK3CB	NM_001256045	1	13	8	-	138400809	138400887
294661112	chr3	138400817	138400943	138400844	138400917	PIK3CB	NM_006219	2	22	17	-	138400809	138400887
293816619	chr3	138403562	138403734	138403584	138403706	PIK3CB	NM_001256045	1	13	6	-	138403467	138403645
293816619	chr3	138403562	138403734	138403584	138403706	PIK3CB	NM_006219	2	22	15	-	138403467	138403645
294637665	chr3	138409900	138410030	138409925	138410007	PIK3CB	NM_001256045	1	13	4	-	138409842	138409985
294637665	chr3	138409900	138410030	138409925	138410007	PIK3CB	NM_006219	2	22	13	-	138409842	138409985
293919516	chr3	138417782	138417912	138417807	138417884	PIK3CB	NM_001256045	1	13	2	-	138417749	138417937
293919516	chr3	138417782	138417912	138417807	138417884	PIK3CB	NM_006219	2	22	11	-	138417749	138417937
294795751	chr3	138425957	138426111	138425985	138426083	PIK3CB	NM_006219	2	22	9	-	138426001	138426131
294795751	chr3	138425957	138426111	138425985	138426083	PIK3CB	NM_001256045	1	13	1	-	138426001	138426463
294663219	chr3	138433263	138433411	138433296	138433384	PIK3CB	NM_006219	2	22	7	-	138433310	138433561
293782019	chr3	138452232	138452357	138452258	138452330	PIK3CB	NM_006219	2	22	6	-	138452203	138452280
294584322	chr3	138456624	138456748	138456649	138456728	PIK3CB	NM_006219	2	22	4	-	138456549	138456728
294179051	chr3	138461589	138461733	138461617	138461708	PIK3CB	NM_006219	2	22	3	-	138461400	138461623
293769976	chr3	138478070	138478243	138478092	138478214	PIK3CB	NM_006219	2	22	1	-	138478015	138478201

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229746342	chr3	138665073	138665198	138665090	138665179	FOXL2	NM_023067	1	1	1	-	138663066	138665982
227673797	chr3	138665485	138665642	138665503	138665624	FOXL2	NM_023067	1	1	1	-	138663066	138665982
282984326	chr3	142168194	142168346	142168222	142168318	ATR	NM_001184	1	47	47	-	142168077	142168444
284008048	chr3	142172012	142172175	142172036	142172145	ATR	NM_001184	1	47	46	-	142171970	142172075
281323794	chr3	142177717	142177880	142177744	142177852	ATR	NM_001184	1	47	44	-	142177800	142177953
284429991	chr3	142178069	142178198	142178095	142178175	ATR	NM_001184	1	47	43	-	142178069	142178225
282579012	chr3	142180812	142180936	142180835	142180910	ATR	NM_001184	1	47	42	-	142180782	142180932
282268377	chr3	142183968	142184095	142183996	142184066	ATR	NM_001184	1	47	41	-	142183939	142184082
281332426	chr3	142185305	142185479	142185333	142185454	ATR	NM_001184	1	47	40	-	142185166	142185375
283079514	chr3	142188188	142188312	142188211	142188284	ATR	NM_001184	1	47	38	-	142188179	142188411
283168724	chr3	142188964	142189123	142188990	142189095	ATR	NM_001184	1	47	37	-	142188928	142189025
282758133	chr3	142212022	142212151	142212048	142212127	ATR	NM_001184	1	47	35	-	142211974	142212153
281383356	chr3	142215938	142216066	142215966	142216034	ATR	NM_001184	1	47	33	-	142215855	142216034
284238766	chr3	142218488	142218629	142218512	142218601	ATR	NM_001184	1	47	31	-	142218469	142218560
283605102	chr3	142224112	142224239	142224135	142224208	ATR	NM_001184	1	47	29	-	142223981	142224145
282729136	chr3	142231119	142231276	142231144	142231248	ATR	NM_001184	1	47	27	-	142231102	142231312
281788185	chr3	142234156	142234330	142234180	142234304	ATR	NM_001184	1	47	25	-	142234237	142234357
284679529	chr3	142241623	142241758	142241651	142241730	ATR	NM_001184	1	47	23	-	142241570	142241683
285744066	chr3	142253854	142253996	142253882	142253970	ATR	NM_001184	1	47	21	-	142253922	142254047
283730043	chr3	142257340	142257474	142257363	142257453	ATR	NM_001184	1	47	19	-	142257324	142257467
282602113	chr3	142266462	142266608	142266485	142266586	ATR	NM_001184	1	47	16	-	142266567	142266752
282013144	chr3	142268322	142268493	142268350	142268473	ATR	NM_001184	1	47	15	-	142268321	142268515
284346107	chr3	142272016	142272172	142272042	142272149	ATR	NM_001184	1	47	13	-	142272069	142272240
282320404	chr3	142272493	142272645	142272520	142272617	ATR	NM_001184	1	47	12	-	142272482	142272582
284567672	chr3	142274714	142274864	142274742	142274843	ATR	NM_001184	1	47	10	-	142274719	142274981
285720114	chr3	142275248	142275415	142275276	142275395	ATR	NM_001184	1	47	9	-	142275225	142275417
282754619	chr3	142278124	142278273	142278146	142278245	ATR	NM_001184	1	47	7	-	142278093	142278283
282184631	chr3	142280051	142280182	142280079	142280154	ATR	NM_001184	1	47	5	-	142280085	142280263
281394192	chr3	142281165	142281294	142281189	142281266	ATR	NM_001184	1	47	4	-	142281074	142281951
283765127	chr3	142281499	142281671	142281528	142281647	ATR	NM_001184	1	47	4	-	142281074	142281951
283788728	chr3	142281811	142281936	142281836	142281912	ATR	NM_001184	1	47	4	-	142281074	142281951
282896541	chr3	142286927	142287101	142286953	142287073	ATR	NM_001184	1	47	2	-	142286905	142286996
237452875	chr3	178916784	178916936	178916812	178916911	PIK3CA	NM_006218	1	21	2	+	178916538	178916965
236856970	chr3	178917574	178917742	178917597	178917713	PIK3CA	NM_006218	1	21	3	+	178917478	178917687
235927943	chr3	178921308	178921442	178921328	178921414	PIK3CA	NM_006218	1	21	5	+	178921332	178921577
240029004	chr3	178927374	178927547	178927401	178927519	PIK3CA	NM_006218	1	21	7	+	178927383	178927488
236070143	chr3	178928247	178928372	178928269	178928348	PIK3CA	NM_006218	1	21	9	+	178928219	178928353
235349704	chr3	178936910	178937071	178936938	178937043	PIK3CA	NM_006218	1	21	11	+	178936984	178937065
236374135	chr3	178938842	178938972	178938869	178938945	PIK3CA	NM_006218	1	21	14	+	178938774	178938945
236987977	chr3	178942552	178942702	178942580	178942676	PIK3CA	NM_006218	1	21	16	+	178942488	178942609
235023347	chr3	178947187	178947317	178947210	178947289	PIK3CA	NM_006218	1	21	18	+	178947060	178947230

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237322555	chr3	178948025	178948176	178948053	178948154	PIK3CA	NM_006218	1	21	20	+	178948013	178948164
235602326	chr3	178952011	178952185	178952039	178952157	PIK3CA	NM_006218	1	21	21	+	178951882	178952497
263678611	chr3	181430374	181430532	181430392	181430510	SOX2	NM_003106	1	1	1	+	181429712	181432223
263680581	chr3	181430780	181430929	181430799	181430908	SOX2	NM_003106	1	1	1	+	181429712	181432223
223500187	chr3	187442728	187442900	187442752	187442879	BCL6	NM_001706	3	10	9	-	187442729	187442866
223500187	chr3	187442728	187442900	187442752	187442879	BCL6	NM_001134738	2	8	7	-	187442729	187442866
223500187	chr3	187442728	187442900	187442752	187442879	BCL6	NM_001130845	1	10	9	-	187442729	187442866
222799918	chr3	187444574	187444731	187444594	187444710	BCL6	NM_001706	3	10	7	-	187444519	187444686
222799918	chr3	187444574	187444731	187444594	187444710	BCL6	NM_001130845	1	10	7	-	187444519	187444686
225160732	chr3	187446921	187447083	187446942	187447058	BCL6	NM_001706	3	10	5	-	187446838	187447809
225160732	chr3	187446921	187447083	187446942	187447058	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225160732	chr3	187446921	187447083	187446942	187447058	BCL6	NM_001130845	1	10	5	-	187446838	187447809
225157523	chr3	187447373	187447507	187447396	187447486	BCL6	NM_001706	3	10	5	-	187446838	187447809
225157523	chr3	187447373	187447507	187447396	187447486	BCL6	NM_001134738	2	8	4	-	187446838	187447809
225157523	chr3	187447373	187447507	187447396	187447486	BCL6	NM_001130845	1	10	5	-	187446838	187447809
223603221	chr3	187449365	187449527	187449388	187449505	BCL6	NM_001706	3	10	4	-	187449497	187449718
223603221	chr3	187449365	187449527	187449388	187449505	BCL6	NM_001134738	2	8	3	-	187449497	187449718
223603221	chr3	187449365	187449527	187449388	187449505	BCL6	NM_001130845	1	10	4	-	187449497	187449718
223198077	chr3	187451358	187451523	187451378	187451497	BCL6	NM_001706	3	10	3	-	187451321	187451491
223198077	chr3	187451358	187451523	187451378	187451497	BCL6	NM_001134738	2	8	2	-	187451321	187451491
223198077	chr3	187451358	187451523	187451378	187451497	BCL6	NM_001130845	1	10	3	-	187451321	187451491
232743949	chr3	188202407	188202564	188202430	188202537	LPP	NM_001167672	2	10	3	+	188202380	188202492
232743949	chr3	188202407	188202564	188202430	188202537	LPP	NM_001167671	1	11	4	+	188202380	188202492
232743949	chr3	188202407	188202564	188202430	188202537	LPP	NM_005578	3	11	4	+	188202380	188202492
233636458	chr3	188327157	188327321	188327178	188327300	LPP	NM_001167671	1	11	6	+	188326949	188327632
233636458	chr3	188327157	188327321	188327178	188327300	LPP	NM_005578	3	11	6	+	188326949	188327632
233636458	chr3	188327157	188327321	188327178	188327300	LPP	NM_001167672	2	10	5	+	188326949	188327191
234446488	chr3	188425995	188426166	188426017	188426141	LPP	NM_001167672	2	10	6	+	188426055	188426181
234446488	chr3	188425995	188426166	188426017	188426141	LPP	NM_001167671	1	11	7	+	188426055	188426181
234446488	chr3	188425995	188426166	188426017	188426141	LPP	NM_005578	3	11	7	+	188426055	188426181
233722694	chr3	188583914	188584087	188583939	188584066	LPP	NM_001167672	2	10	8	+	188583988	188584166
233722694	chr3	188583914	188584087	188583939	188584066	LPP	NM_001167671	1	11	9	+	188583988	188584166
233722694	chr3	188583914	188584087	188583939	188584066	LPP	NM_005578	3	11	9	+	188583988	188584166
233483284	chr3	188592164	188592318	188592186	188592290	LPP	NM_001167672	2	10	10	+	188592139	188608460
233483284	chr3	188592164	188592318	188592186	188592290	LPP	NM_001167671	1	11	11	+	188592139	188608460
233483284	chr3	188592164	188592318	188592186	188592290	LPP	NM_005578	3	11	11	+	188592139	188608460
303385073	chr3	195594002	195594170	195594021	195594152	TNK2	NM_005781	2	15	13	-	195594040	195594129
304438287	chr3	195594542	195594704	195594565	195594683	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304438287	chr3	195594542	195594704	195594565	195594683	TNK2	NM_005781	2	15	12	-	195594232	195595580
300731148	chr3	195594851	195595011	195594869	195594990	TNK2	NM_001010938	1	15	13	-	195594232	195595580
300731148	chr3	195594851	195595011	195594869	195594990	TNK2	NM_005781	2	15	12	-	195594232	195595580

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
304440057	chr3	195595181	195595347	195595206	195595330	TNK2	NM_001010938	1	15	13	-	195594232	195595580
304440057	chr3	195595181	195595347	195595206	195595330	TNK2	NM_005781	2	15	12	-	195594232	195595580
303410005	chr3	195596933	195597106	195596955	195597085	TNK2	NM_001010938	1	15	11	-	195596985	195597076
303410005	chr3	195596933	195597106	195596955	195597085	TNK2	NM_005781	2	15	11	-	195596985	195597076
302217250	chr3	195605264	195605415	195605284	195605394	TNK2	NM_001010938	1	15	8	-	195605317	195605463
302217250	chr3	195605264	195605415	195605284	195605394	TNK2	NM_005781	2	15	8	-	195605317	195605463
301181163	chr3	195608879	195609041	195608898	195609021	TNK2	NM_001010938	1	15	6	-	195608922	195609199
301181163	chr3	195608879	195609041	195608898	195609021	TNK2	NM_005781	2	15	6	-	195608922	195609199
302436617	chr3	195610054	195610214	195610072	195610192	TNK2	NM_001010938	1	15	5	-	195610028	195610180
302436617	chr3	195610054	195610214	195610072	195610192	TNK2	NM_005781	2	15	5	-	195610028	195610180
304390514	chr3	195613844	195613983	195613865	195613966	TNK2	NM_001010938	1	15	3	-	195613848	195613918
304390514	chr3	195613844	195613983	195613865	195613966	TNK2	NM_005781	2	15	3	-	195613848	195613918
302254754	chr3	195622141	195622306	195622160	195622288	TNK2	NM_001010938	1	15	1	-	195622117	195622432
227587050	chr4	1801434	1801565	1801452	1801547	FGFR3	NM_000142	1	18	4	+	1801474	1801539
227587050	chr4	1801434	1801565	1801452	1801547	FGFR3	NM_022965	3	16	4	+	1801474	1801539
227587050	chr4	1801434	1801565	1801452	1801547	FGFR3	NM_001163213	2	18	4	+	1801474	1801539
227974391	chr4	1803411	1803555	1803429	1803537	FGFR3	NM_000142	1	18	6	+	1803347	1803470
227974391	chr4	1803411	1803555	1803429	1803537	FGFR3	NM_022965	3	16	6	+	1803347	1803470
227974391	chr4	1803411	1803555	1803429	1803537	FGFR3	NM_001163213	2	18	6	+	1803347	1803470
227468833	chr4	1804542	1804705	1804562	1804687	FGFR3	NM_001163213	2	18	8	+	1804641	1804791
227640499	chr4	1806032	1806205	1806049	1806186	FGFR3	NM_000142	1	18	9	+	1806057	1806247
227640499	chr4	1806032	1806205	1806049	1806186	FGFR3	NM_001163213	2	18	9	+	1806057	1806247
227874069	chr4	1807039	1807213	1807058	1807192	FGFR3	NM_000142	1	18	11	+	1807082	1807203
227874069	chr4	1807039	1807213	1807058	1807192	FGFR3	NM_022965	3	16	9	+	1807082	1807203
227874069	chr4	1807039	1807213	1807058	1807192	FGFR3	NM_001163213	2	18	11	+	1807082	1807203
228568810	chr4	1807454	1807578	1807472	1807557	FGFR3	NM_000142	1	18	13	+	1807477	1807667
228568810	chr4	1807454	1807578	1807472	1807557	FGFR3	NM_022965	3	16	11	+	1807477	1807667
228568810	chr4	1807454	1807578	1807472	1807557	FGFR3	NM_001163213	2	18	13	+	1807477	1807667
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_000142	1	18	15	+	1807984	1808054
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_022965	3	16	13	+	1807984	1808054
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_001163213	2	18	15	+	1807984	1808054
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_000142	1	18	14	+	1807778	1807900
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_022965	3	16	12	+	1807778	1807900
227627830	chr4	1807862	1808032	1807882	1808012	FGFR3	NM_001163213	2	18	14	+	1807778	1807900
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_000142	1	18	17	+	1808556	1808661
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_022965	3	16	15	+	1808556	1808661
229322652	chr4	1808491	1808659	1808514	1808640	FGFR3	NM_001163213	2	18	17	+	1808556	1808661
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_007331	2	11	4	+	1902353	1902978
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_133330	3	24	4	+	1902353	1902978
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_133335	6	22	2	+	1902353	1902978
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_133334	5	9	1	+	1902353	1902978

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_133331	4	23	3	+	1902353	1902978
294585035	chr4	1902347	1902517	1902373	1902498	WHSC1	NM_001042424	1	22	2	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_007331	2	11	4	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_133330	3	24	4	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_133335	6	22	2	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_133334	5	9	1	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_133331	4	23	3	+	1902353	1902978
295366735	chr4	1902836	1903008	1902864	1902986	WHSC1	NM_001042424	1	22	2	+	1902353	1902978
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_007331	2	11	6	+	1918598	1918764
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_133330	3	24	6	+	1918598	1918764
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_133335	6	22	4	+	1918598	1918764
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_133334	5	9	3	+	1918598	1918764
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_133331	4	23	5	+	1918598	1918764
293964537	chr4	1918645	1918797	1918667	1918769	WHSC1	NM_001042424	1	22	4	+	1918598	1918764
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_007331	2	11	7	+	1919868	1920350
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_133330	3	24	7	+	1919868	1920350
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_133335	6	22	5	+	1919868	1920350
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_133334	5	9	4	+	1919868	1920350
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_133331	4	23	6	+	1919868	1920350
294421359	chr4	1920114	1920282	1920139	1920260	WHSC1	NM_001042424	1	22	5	+	1919868	1920350
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_007331	2	11	9	+	1936871	1936989
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_133330	3	24	9	+	1936871	1936989
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_133335	6	22	7	+	1936871	1936989
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_133334	5	9	6	+	1936871	1936989
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_133331	4	23	8	+	1936871	1936989
293773695	chr4	1936841	1937015	1936865	1936989	WHSC1	NM_001042424	1	22	7	+	1936871	1936989
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_133330	3	24	11	+	1941381	1941505
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_133335	6	22	9	+	1941381	1941505
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_133334	5	9	8	+	1941381	1941505
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_133331	4	23	10	+	1941381	1941505
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_001042424	1	22	9	+	1941381	1941505
294072966	chr4	1941381	1941547	1941407	1941520	WHSC1	NM_007331	2	11	11	+	1941381	1944302
294955758	chr4	1953761	1953928	1953780	1953909	WHSC1	NM_133330	3	24	13	+	1953835	1953958
294955758	chr4	1953761	1953928	1953780	1953909	WHSC1	NM_133335	6	22	11	+	1953835	1953958
294955758	chr4	1953761	1953928	1953780	1953909	WHSC1	NM_133331	4	23	12	+	1953835	1953958
294955758	chr4	1953761	1953928	1953780	1953909	WHSC1	NM_001042424	1	22	11	+	1953835	1953958
294754558	chr4	1956826	1956999	1956852	1956979	WHSC1	NM_133330	3	24	15	+	1956888	1957067
294754558	chr4	1956826	1956999	1956852	1956979	WHSC1	NM_133335	6	22	13	+	1956888	1957067
294754558	chr4	1956826	1956999	1956852	1956979	WHSC1	NM_133331	4	23	14	+	1956888	1957067
294754558	chr4	1956826	1956999	1956852	1956979	WHSC1	NM_001042424	1	22	13	+	1956888	1957067
294333337	chr4	1957654	1957828	1957681	1957800	WHSC1	NM_133330	3	24	17	+	1957710	1957915

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294333337	chr4	1957654	1957828	1957681	1957800	WHSC1	NM_133335	6	22	15	+	1957710	1957915
294333337	chr4	1957654	1957828	1957681	1957800	WHSC1	NM_133331	4	23	16	+	1957710	1957915
294333337	chr4	1957654	1957828	1957681	1957800	WHSC1	NM_001042424	1	22	15	+	1957710	1957915
294298181	chr4	1961134	1961308	1961155	1961286	WHSC1	NM_133330	3	24	19	+	1961198	1961467
294298181	chr4	1961134	1961308	1961155	1961286	WHSC1	NM_133335	6	22	17	+	1961198	1961467
294298181	chr4	1961134	1961308	1961155	1961286	WHSC1	NM_133331	4	23	18	+	1961198	1961467
294298181	chr4	1961134	1961308	1961155	1961286	WHSC1	NM_001042424	1	22	17	+	1961198	1961467
294758238	chr4	1976489	1976654	1976514	1976633	WHSC1	NM_133330	3	24	21	+	1976590	1976731
294758238	chr4	1976489	1976654	1976514	1976633	WHSC1	NM_133335	6	22	19	+	1976590	1976731
294758238	chr4	1976489	1976654	1976514	1976633	WHSC1	NM_133331	4	23	20	+	1976590	1976731
294758238	chr4	1976489	1976654	1976514	1976633	WHSC1	NM_001042424	1	22	19	+	1976590	1976731
294949645	chr4	1978102	1978241	1978125	1978216	WHSC1	NM_133330	3	24	23	+	1978202	1978406
294949645	chr4	1978102	1978241	1978125	1978216	WHSC1	NM_133335	6	22	21	+	1978202	1978406
294949645	chr4	1978102	1978241	1978125	1978216	WHSC1	NM_133331	4	23	22	+	1978202	1978406
294949645	chr4	1978102	1978241	1978125	1978216	WHSC1	NM_001042424	1	22	21	+	1978202	1978406
294949939	chr4	1980389	1980551	1980410	1980530	WHSC1	NM_133335	6	22	22	+	1980365	1983934
294949939	chr4	1980389	1980551	1980410	1980530	WHSC1	NM_001042424	1	22	22	+	1980365	1983934
294949939	chr4	1980389	1980551	1980410	1980530	WHSC1	NM_133330	3	24	24	+	1980365	1983930
294949939	chr4	1980389	1980551	1980410	1980530	WHSC1	NM_133331	4	23	23	+	1980365	1983930
238635270	chr4	40245192	40245332	40245212	40245311	RHOH	NM_004310	1	3	3	+	40244798	40246281
239026460	chr4	41748298	41748451	41748318	41748427	PHOX2B	NM_003924	1	3	3	-	41746099	41748339
238127313	chr4	41750363	41750534	41750386	41750514	PHOX2B	NM_003924	1	3	1	-	41750387	41750987
240008519	chr4	55127339	55127511	55127365	55127490	PDGFRA	NM_006206	1	23	3	+	55127262	55127579
235202208	chr4	55129984	55130154	55130006	55130131	PDGFRA	NM_006206	1	23	4	+	55129834	55130094
238736337	chr4	55133547	55133721	55133571	55133696	PDGFRA	NM_006206	1	23	6	+	55133456	55133627
236410986	chr4	55136819	55136964	55136842	55136936	PDGFRA	NM_006206	1	23	8	+	55136800	55136915
235239707	chr4	55139747	55139921	55139771	55139898	PDGFRA	NM_006206	1	23	10	+	55139704	55139897
237541513	chr4	55143513	55143677	55143534	55143656	PDGFRA	NM_006206	1	23	13	+	55143555	55143659
236510920	chr4	55144597	55144727	55144618	55144699	PDGFRA	NM_006206	1	23	15	+	55144529	55144682
237932366	chr4	55151562	55151686	55151590	55151661	PDGFRA	NM_006206	1	23	17	+	55151538	55151653
239394432	chr4	55154937	55155111	55154963	55155090	PDGFRA	NM_006206	1	23	20	+	55154966	55155065
235011344	chr4	55156612	55156786	55156631	55156765	PDGFRA	NM_006206	1	23	22	+	55156480	55156721
233143073	chr4	55561589	55561761	55561615	55561739	KIT	NM_000222	1	21	2	+	55561678	55561947
233143073	chr4	55561589	55561761	55561615	55561739	KIT	NM_001093772	2	21	2	+	55561678	55561947
233647608	chr4	55564521	55564686	55564542	55564664	KIT	NM_000222	1	21	3	+	55564450	55564731
233647608	chr4	55564521	55564686	55564542	55564664	KIT	NM_001093772	2	21	3	+	55564450	55564731
233220649	chr4	55569775	55569929	55569807	55569902	KIT	NM_000222	1	21	5	+	55569890	55570058
233220649	chr4	55569775	55569929	55569807	55569902	KIT	NM_001093772	2	21	5	+	55569890	55570058
234331842	chr4	55575500	55575674	55575526	55575649	KIT	NM_000222	1	21	7	+	55575590	55575705
234331842	chr4	55575500	55575674	55575526	55575649	KIT	NM_001093772	2	21	7	+	55575590	55575705
232611153	chr4	55591984	55592136	55592007	55592108	KIT	NM_001093772	2	21	9	+	55592023	55592204

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232611153	chr4	55591984	55592136	55592007	55592108	KIT	NM_000222	1	21	9	+	55592023	55592216
234674208	chr4	55593574	55593733	55593598	55593710	KIT	NM_000222	1	21	11	+	55593582	55593708
234674208	chr4	55593574	55593733	55593598	55593710	KIT	NM_001093772	2	21	11	+	55593582	55593708
234737858	chr4	55595582	55595727	55595606	55595703	KIT	NM_000222	1	21	14	+	55595501	55595651
234737858	chr4	55595582	55595727	55595606	55595703	KIT	NM_001093772	2	21	14	+	55595501	55595651
233305581	chr4	55599205	55599367	55599233	55599339	KIT	NM_000222	1	21	17	+	55599236	55599358
233305581	chr4	55599205	55599367	55599233	55599339	KIT	NM_001093772	2	21	17	+	55599236	55599358
232472076	chr4	55602774	55602948	55602800	55602921	KIT	NM_000222	1	21	19	+	55602887	55602986
232472076	chr4	55602774	55602948	55602800	55602921	KIT	NM_001093772	2	21	19	+	55602887	55602986
233961810	chr4	55604495	55604621	55604523	55604596	KIT	NM_000222	1	21	21	+	55604595	55606881
233961810	chr4	55604495	55604621	55604523	55604596	KIT	NM_001093772	2	21	21	+	55604595	55606881
231409323	chr4	55948000	55948166	55948024	55948138	KDR	NM_002253	1	30	29	-	55948123	55948208
233949246	chr4	55953682	55953852	55953707	55953828	KDR	NM_002253	1	30	27	-	55953774	55953925
233714392	chr4	55955563	55955735	55955586	55955709	KDR	NM_002253	1	30	25	-	55955541	55955640
232979344	chr4	55958753	55958919	55958777	55958894	KDR	NM_002253	1	30	22	-	55958784	55958881
232551113	chr4	55962273	55962446	55962300	55962423	KDR	NM_002253	1	30	19	-	55962396	55962509
232264321	chr4	55964204	55964370	55964232	55964345	KDR	NM_002253	1	30	17	-	55964304	55964439
231256663	chr4	55968060	55968214	55968088	55968187	KDR	NM_002253	1	30	15	-	55968064	55968195
232816140	chr4	55970712	55970870	55970739	55970848	KDR	NM_002253	1	30	13	-	55970810	55971151
232152723	chr4	55971971	55972145	55971994	55972121	KDR	NM_002253	1	30	12	-	55971999	55972107
231576131	chr4	55973971	55974100	55973995	55974072	KDR	NM_002253	1	30	10	-	55973904	55974060
232837566	chr4	55976889	55977044	55976910	55977023	KDR	NM_002253	1	30	8	-	55976821	55976935
234387582	chr4	55980314	55980479	55980341	55980451	KDR	NM_002253	1	30	6	-	55980293	55980432
233401480	chr4	55981412	55981537	55981440	55981510	KDR	NM_002253	1	30	4	-	55981448	55981578
232279141	chr4	55987242	55987404	55987270	55987380	KDR	NM_002253	1	30	2	-	55987264	55987357
294436151	chr4	62452980	62453137	62453002	62453116	LPHN3	NM_015236	1	23	2	+	62452945	62453158
330026444	chr4	62596323	62596494	62596350	62596467	LPHN3	NM_015236	1	23	4	+	62596340	62596354
294474736	chr4	62598703	62598867	62598730	62598844	LPHN3	NM_015236	1	23	5	+	62598472	62599272
295347043	chr4	62599129	62599301	62599153	62599274	LPHN3	NM_015236	1	23	5	+	62598472	62599272
294192709	chr4	62761389	62761527	62761419	62761502	LPHN3	NM_015236	1	23	8	+	62761449	62761552
294970276	chr4	62775415	62775572	62775437	62775545	LPHN3	NM_015236	1	23	9	+	62775278	62775463
293704792	chr4	62801592	62801763	62801619	62801736	LPHN3	NM_015236	1	23	12	+	62801641	62801763
293984448	chr4	62813809	62813950	62813829	62813923	LPHN3	NM_015236	1	23	14	+	62813818	62813994
294772722	chr4	62849039	62849170	62849063	62849149	LPHN3	NM_015236	1	23	16	+	62849101	62849321
294869337	chr4	62863802	62863972	62863830	62863949	LPHN3	NM_015236	1	23	18	+	62863892	62863983
294347028	chr4	62897157	62897288	62897180	62897260	LPHN3	NM_015236	1	23	20	+	62897160	62897328
294315773	chr4	62910108	62910254	62910136	62910226	LPHN3	NM_015236	1	23	22	+	62910171	62910267
294710065	chr4	62935994	62936152	62936022	62936131	LPHN3	NM_015236	1	23	23	+	62935827	62938168
294704489	chr4	62936437	62936574	62936462	62936550	LPHN3	NM_015236	1	23	23	+	62935827	62938168
223834985	chr4	87967183	87967345	87967207	87967321	AFF1	NM_005935	2	20	2	+	87967318	87967438
223834985	chr4	87967183	87967345	87967207	87967321	AFF1	NM_001166693	1	21	3	+	87967318	87967438

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
223637505	chr4	87968016	87968160	87968037	87968138	AFF1	NM_005935	2	20	3	+	87967847	87968746
223637505	chr4	87968016	87968160	87968037	87968138	AFF1	NM_001166693	1	21	4	+	87967847	87968746
225048191	chr4	87968437	87968602	87968459	87968582	AFF1	NM_005935	2	20	3	+	87967847	87968746
225048191	chr4	87968437	87968602	87968459	87968582	AFF1	NM_001166693	1	21	4	+	87967847	87968746
224778196	chr4	88011145	88011283	88011163	88011259	AFF1	NM_005935	2	20	5	+	88011136	88011222
224778196	chr4	88011145	88011283	88011163	88011259	AFF1	NM_001166693	1	21	6	+	88011136	88011222
222621410	chr4	88026739	88026908	88026767	88026883	AFF1	NM_005935	2	20	8	+	88026780	88026834
222621410	chr4	88026739	88026908	88026767	88026883	AFF1	NM_001166693	1	21	9	+	88026780	88026834
224101720	chr4	88029361	88029507	88029383	88029487	AFF1	NM_005935	2	20	10	+	88029311	88029467
224101720	chr4	88029361	88029507	88029383	88029487	AFF1	NM_001166693	1	21	11	+	88029311	88029467
225161815	chr4	88035765	88035939	88035783	88035917	AFF1	NM_005935	2	20	11	+	88035519	88036451
225161815	chr4	88035765	88035939	88035783	88035917	AFF1	NM_001166693	1	21	12	+	88035519	88036451
223722248	chr4	88036208	88036377	88036229	88036351	AFF1	NM_005935	2	20	11	+	88035519	88036451
223722248	chr4	88036208	88036377	88036229	88036351	AFF1	NM_001166693	1	21	12	+	88035519	88036451
222308689	chr4	88046193	88046332	88046221	88046308	AFF1	NM_005935	2	20	12	+	88046189	88046295
222308689	chr4	88046193	88046332	88046221	88046308	AFF1	NM_001166693	1	21	13	+	88046189	88046295
222809429	chr4	88048094	88048222	88048119	88048196	AFF1	NM_005935	2	20	14	+	88048178	88048269
222809429	chr4	88048094	88048222	88048119	88048196	AFF1	NM_001166693	1	21	15	+	88048178	88048269
225219362	chr4	88052237	88052392	88052258	88052371	AFF1	NM_005935	2	20	16	+	88052235	88052371
225219362	chr4	88052237	88052392	88052258	88052371	AFF1	NM_001166693	1	21	17	+	88052235	88052371
223061572	chr4	88053507	88053662	88053532	88053634	AFF1	NM_005935	2	20	18	+	88053423	88053560
223061572	chr4	88053507	88053662	88053532	88053634	AFF1	NM_001166693	1	21	19	+	88053423	88053560
222734835	chr4	88056635	88056809	88056658	88056788	AFF1	NM_005935	2	20	20	+	88056732	88062191
222734835	chr4	88056635	88056809	88056658	88056788	AFF1	NM_001166693	1	21	21	+	88056732	88062206
290156214	chr4	103450994	103451127	103451022	103451098	NFKB1	NM_001165412	1	24	3	+	103450993	103451071
290156214	chr4	103450994	103451127	103451022	103451098	NFKB1	NM_003998	2	24	3	+	103450993	103451071
293300191	chr4	103488171	103488318	103488198	103488292	NFKB1	NM_001165412	1	24	6	+	103488144	103488292
293300191	chr4	103488171	103488318	103488198	103488292	NFKB1	NM_003998	2	24	6	+	103488144	103488292
292514635	chr4	103500099	103500223	103500119	103500203	NFKB1	NM_001165412	1	24	8	+	103500038	103500196
292514635	chr4	103500099	103500223	103500119	103500203	NFKB1	NM_003998	2	24	8	+	103500038	103500196
293545975	chr4	103505842	103505991	103505869	103505963	NFKB1	NM_001165412	1	24	11	+	103505839	103505977
293545975	chr4	103505842	103505991	103505869	103505963	NFKB1	NM_003998	2	24	11	+	103505839	103505977
290086475	chr4	103515975	103516149	103515999	103516124	NFKB1	NM_001165412	1	24	13	+	103516049	103516138
290086475	chr4	103515975	103516149	103515999	103516124	NFKB1	NM_003998	2	24	13	+	103516049	103516138
290230726	chr4	103518570	103518726	103518594	103518705	NFKB1	NM_001165412	1	24	15	+	103518677	103518818
290230726	chr4	103518570	103518726	103518594	103518705	NFKB1	NM_003998	2	24	15	+	103518677	103518818
292343085	chr4	103527614	103527771	103527635	103527749	NFKB1	NM_001165412	1	24	17	+	103527653	103527854
292343085	chr4	103527614	103527771	103527635	103527749	NFKB1	NM_003998	2	24	17	+	103527653	103527854
291533322	chr4	103528755	103528929	103528779	103528908	NFKB1	NM_001165412	1	24	19	+	103528806	103528908
291533322	chr4	103528755	103528929	103528779	103528908	NFKB1	NM_003998	2	24	19	+	103528806	103528908
292225273	chr4	103533543	103533717	103533569	103533689	NFKB1	NM_001165412	1	24	22	+	103533591	103533763

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
292225273	chr4	103533543	103533717	103533569	103533689	NFKB1	NM_003998	2	24	22	+	103533591	103533763
291945238	chr4	103537508	103537672	103537530	103537649	NFKB1	NM_001165412	1	24	24	+	103537591	103538459
291945238	chr4	103537508	103537672	103537530	103537649	NFKB1	NM_003998	2	24	24	+	103537591	103538459
242202824	chr4	106155254	106155427	106155280	106155406	TET2	NM_001127208	1	11	3	+	106155054	106158508
242202824	chr4	106155254	106155427	106155280	106155406	TET2	NM_017628	2	3	3	+	106155054	106163928
265694111	chr4	106155729	106155881	106155751	106155855	TET2	NM_001127208	1	11	3	+	106155054	106158508
265694111	chr4	106155729	106155881	106155751	106155855	TET2	NM_017628	2	3	3	+	106155054	106163928
265719730	chr4	106156123	106156283	106156144	106156258	TET2	NM_001127208	1	11	3	+	106155054	106158508
265719730	chr4	106156123	106156283	106156144	106156258	TET2	NM_017628	2	3	3	+	106155054	106163928
242152677	chr4	106156564	106156729	106156587	106156705	TET2	NM_001127208	1	11	3	+	106155054	106158508
242152677	chr4	106156564	106156729	106156587	106156705	TET2	NM_017628	2	3	3	+	106155054	106163928
242654504	chr4	106157028	106157187	106157049	106157159	TET2	NM_001127208	1	11	3	+	106155054	106158508
242654504	chr4	106157028	106157187	106157049	106157159	TET2	NM_017628	2	3	3	+	106155054	106163928
242115218	chr4	106157468	106157593	106157495	106157566	TET2	NM_001127208	1	11	3	+	106155054	106158508
242115218	chr4	106157468	106157593	106157495	106157566	TET2	NM_017628	2	3	3	+	106155054	106163928
242202654	chr4	106157840	106157976	106157866	106157950	TET2	NM_001127208	1	11	3	+	106155054	106158508
242202654	chr4	106157840	106157976	106157866	106157950	TET2	NM_017628	2	3	3	+	106155054	106163928
242223332	chr4	106158225	106158390	106158252	106158367	TET2	NM_001127208	1	11	3	+	106155054	106158508
242223332	chr4	106158225	106158390	106158252	106158367	TET2	NM_017628	2	3	3	+	106155054	106163928
242653825	chr4	106162477	106162605	106162510	106162580	TET2	NM_001127208	1	11	4	+	106162496	106162586
242653825	chr4	106162477	106162605	106162510	106162580	TET2	NM_017628	2	3	3	+	106155054	106163928
262977071	chr4	106164696	106164867	106164719	106164843	TET2	NM_001127208	1	11	6	+	106164727	106164935
241020386	chr4	106182796	106182963	106182821	106182939	TET2	NM_001127208	1	11	8	+	106182916	106183005
240599405	chr4	106193668	106193810	106193691	106193783	TET2	NM_001127208	1	11	10	+	106193721	106194075
241665505	chr4	106196074	106196236	106196101	106196215	TET2	NM_001127208	1	11	11	+	106196205	106200960
241749424	chr4	106196517	106196686	106196544	106196662	TET2	NM_001127208	1	11	11	+	106196205	106200960
265285371	chr4	106196991	106197165	106197012	106197143	TET2	NM_001127208	1	11	11	+	106196205	106200960
265253714	chr4	106197431	106197591	106197454	106197568	TET2	NM_001127208	1	11	11	+	106196205	106200960
233788764	chr4	123374835	123375009	123374861	123374986	IL2	NM_000586	1	4	3	-	123374865	123375008
233255448	chr4	123377334	123377508	123377361	123377485	IL2	NM_000586	1	4	1	-	123377449	123377650
231818832	chr4	153244018	153244185	153244045	153244161	FBXW7	NM_033632	3	12	12	-	153242410	153244301
231818832	chr4	153244018	153244185	153244045	153244161	FBXW7	NM_001013415	1	11	11	-	153242410	153244301
231818832	chr4	153244018	153244185	153244045	153244161	FBXW7	NM_018315	2	11	11	-	153242410	153244301
232201046	chr4	153245353	153245516	153245380	153245491	FBXW7	NM_033632	3	12	11	-	153245336	153245546
232201046	chr4	153245353	153245516	153245380	153245491	FBXW7	NM_001013415	1	11	10	-	153245336	153245546
232201046	chr4	153245353	153245516	153245380	153245491	FBXW7	NM_018315	2	11	10	-	153245336	153245546
229675987	chr4	153249263	153249434	153249290	153249406	FBXW7	NM_033632	3	12	9	-	153249360	153249541
229675987	chr4	153249263	153249434	153249290	153249406	FBXW7	NM_001013415	1	11	8	-	153249360	153249541
229675987	chr4	153249263	153249434	153249290	153249406	FBXW7	NM_018315	2	11	8	-	153249360	153249541
230235757	chr4	153250858	153251018	153250885	153250990	FBXW7	NM_033632	3	12	8	-	153250824	153250937
230235757	chr4	153250858	153251018	153250885	153250990	FBXW7	NM_001013415	1	11	7	-	153250824	153250937

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230235757	chr4	153250858	153251018	153250885	153250990	FBXW7	NM_018315	2	11	7	-	153250824	153250937
230790029	chr4	153253743	153253880	153253770	153253854	FBXW7	NM_033632	3	12	6	-	153253748	153253871
230790029	chr4	153253743	153253880	153253770	153253854	FBXW7	NM_001013415	1	11	5	-	153253748	153253871
230790029	chr4	153253743	153253880	153253770	153253854	FBXW7	NM_018315	2	11	5	-	153253748	153253871
228993942	chr4	153268032	153268178	153268057	153268158	FBXW7	NM_033632	3	12	4	-	153268082	153268223
228993942	chr4	153268032	153268178	153268057	153268158	FBXW7	NM_001013415	1	11	3	-	153268082	153268223
228993942	chr4	153268032	153268178	153268057	153268158	FBXW7	NM_018315	2	11	3	-	153268082	153268223
231761491	chr4	153271204	153271347	153271229	153271319	FBXW7	NM_033632	3	12	3	-	153271194	153271276
231761491	chr4	153271204	153271347	153271229	153271319	FBXW7	NM_001013415	1	11	2	-	153271194	153271276
231761491	chr4	153271204	153271347	153271229	153271319	FBXW7	NM_018315	2	11	2	-	153271194	153271276
229300131	chr4	153303277	153303418	153303302	153303393	FBXW7	NM_001013415	1	11	1	-	153303341	153303664
228125907	chr4	153332587	153332761	153332608	153332739	FBXW7	NM_033632	3	12	2	-	153332455	153333024
294349993	chr5	224560	224705	224581	224685	SDHA	NM_004168	1	15	3	+	224475	224636
294358109	chr5	225940	226088	225968	226065	SDHA	NM_004168	1	15	5	+	225998	226162
294624815	chr5	228411	228565	228435	228544	SDHA	NM_004168	1	15	6	+	228300	228448
293724426	chr5	233601	233773	233622	233751	SDHA	NM_004168	1	15	8	+	233592	233760
294318125	chr5	235427	235585	235448	235552	SDHA	NM_004168	1	15	9	+	235259	235454
294149955	chr5	251421	251585	251440	251564	SDHA	NM_004168	1	15	13	+	251453	251583
290552761	chr5	7870890	7871063	7870915	7871036	MTRR	NM_002454	1	15	2	+	7870883	7871036
290552761	chr5	7870890	7871063	7870915	7871036	MTRR	NM_024010	2	15	2	+	7870883	7871036
289669704	chr5	7875360	7875513	7875383	7875488	MTRR	NM_002454	1	15	4	+	7875371	7875488
289669704	chr5	7875360	7875513	7875383	7875488	MTRR	NM_024010	2	15	4	+	7875371	7875488
293630941	chr5	7878347	7878494	7878367	7878470	MTRR	NM_002454	1	15	5	+	7878057	7878435
293630941	chr5	7878347	7878494	7878367	7878470	MTRR	NM_024010	2	15	5	+	7878057	7878435
290018871	chr5	7885867	7886040	7885892	7886019	MTRR	NM_002454	1	15	7	+	7885814	7885967
290018871	chr5	7885867	7886040	7885892	7886019	MTRR	NM_024010	2	15	7	+	7885814	7885967
291670311	chr5	7891484	7891642	7891511	7891614	MTRR	NM_002454	1	15	10	+	7891485	7891527
291670311	chr5	7891484	7891642	7891511	7891614	MTRR	NM_024010	2	15	10	+	7891485	7891527
290255112	chr5	7895882	7896013	7895905	7895987	MTRR	NM_002454	1	15	12	+	7895847	7895965
290255112	chr5	7895882	7896013	7895905	7895987	MTRR	NM_024010	2	15	12	+	7895847	7895965
292380461	chr5	7897233	7897390	7897256	7897370	MTRR	NM_002454	1	15	14	+	7897178	7897360
292380461	chr5	7897233	7897390	7897256	7897370	MTRR	NM_024010	2	15	14	+	7897178	7897360
274227048	chr5	35857084	35857247	35857111	35857224	IL7R	NM_002185	1	8	1	+	35856991	35857161
272992621	chr5	35867417	35867544	35867439	35867517	IL7R	NM_002185	1	8	3	+	35867408	35867565
274243448	chr5	35873532	35873675	35873554	35873647	IL7R	NM_002185	1	8	5	+	35873582	35873750
274627094	chr5	35876037	35876211	35876060	35876183	IL7R	NM_002185	1	8	8	+	35876085	35876923
274618756	chr5	35876514	35876664	35876538	35876636	IL7R	NM_002185	1	8	8	+	35876085	35876923
299020477	chr5	37815992	37816154	37816016	37816130	GDNF	NM_199231	4	3	3	-	37812779	37816237
299020477	chr5	37815992	37816154	37816016	37816130	GDNF	NM_001190468	2	3	3	-	37812779	37816237
299020477	chr5	37815992	37816154	37816016	37816130	GDNF	NM_001190469	3	3	3	-	37812779	37816237
299020477	chr5	37815992	37816154	37816016	37816130	GDNF	NM_000514	1	3	3	-	37812779	37816237

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299023057	chr5	37834808	37834981	37834826	37834961	GDNF	NM_199231	4	3	2	-	37834826	37834924
299023057	chr5	37834808	37834981	37834826	37834961	GDNF	NM_001190469	3	3	2	-	37834826	37834924
299023057	chr5	37834808	37834981	37834826	37834961	GDNF	NM_001190468	2	3	2	-	37834748	37834924
299023057	chr5	37834808	37834981	37834826	37834961	GDNF	NM_000514	1	3	2	-	37834748	37834924
233052193	chr5	38481900	38482051	38481923	38482028	LIFR	NM_001127671	1	20	20	-	38475065	38482320
233052193	chr5	38481900	38482051	38481923	38482028	LIFR	NM_002310	2	20	20	-	38475065	38482320
231672364	chr5	38482733	38482893	38482760	38482862	LIFR	NM_001127671	1	20	19	-	38482691	38482769
231672364	chr5	38482733	38482893	38482760	38482862	LIFR	NM_002310	2	20	19	-	38482691	38482769
231796369	chr5	38485982	38486132	38486002	38486105	LIFR	NM_001127671	1	20	17	-	38485921	38486082
231796369	chr5	38485982	38486132	38486002	38486105	LIFR	NM_002310	2	20	17	-	38485921	38486082
234711282	chr5	38490336	38490495	38490362	38490462	LIFR	NM_001127671	1	20	15	-	38490292	38490393
234711282	chr5	38490336	38490495	38490362	38490462	LIFR	NM_002310	2	20	15	-	38490292	38490393
233098930	chr5	38496470	38496634	38496495	38496611	LIFR	NM_001127671	1	20	13	-	38496484	38496697
233098930	chr5	38496470	38496634	38496495	38496611	LIFR	NM_002310	2	20	13	-	38496484	38496697
232115560	chr5	38502734	38502862	38502762	38502836	LIFR	NM_001127671	1	20	11	-	38502739	38502901
232115560	chr5	38502734	38502862	38502762	38502836	LIFR	NM_002310	2	20	11	-	38502739	38502901
233689870	chr5	38505937	38506061	38505967	38506042	LIFR	NM_001127671	1	20	9	-	38506007	38506176
233689870	chr5	38505937	38506061	38505967	38506042	LIFR	NM_002310	2	20	9	-	38506007	38506176
230831118	chr5	38510484	38510637	38510507	38510609	LIFR	NM_001127671	1	20	7	-	38510566	38510820
230831118	chr5	38510484	38510637	38510507	38510609	LIFR	NM_002310	2	20	7	-	38510566	38510820
233380365	chr5	38511895	38512054	38511917	38512027	LIFR	NM_001127671	1	20	6	-	38511892	38512066
233380365	chr5	38511895	38512054	38511917	38512027	LIFR	NM_002310	2	20	6	-	38511892	38512066
233530736	chr5	38523569	38523701	38523594	38523670	LIFR	NM_001127671	1	20	5	-	38523521	38523684
233530736	chr5	38523569	38523701	38523594	38523670	LIFR	NM_002310	2	20	5	-	38523521	38523684
232609526	chr5	38530652	38530778	38530680	38530754	LIFR	NM_001127671	1	20	2	-	38530608	38530768
232609526	chr5	38530652	38530778	38530680	38530754	LIFR	NM_002310	2	20	2	-	38530608	38530768
231688652	chr5	55237141	55237266	55237168	55237244	IL6ST	NM_175767	3	16	16	-	55230925	55237647
231688652	chr5	55237141	55237266	55237168	55237244	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
231688652	chr5	55237141	55237266	55237168	55237244	IL6ST	NM_002184	2	17	17	-	55230925	55237647
234057208	chr5	55237559	55237698	55237587	55237672	IL6ST	NM_175767	3	16	16	-	55230925	55237647
234057208	chr5	55237559	55237698	55237587	55237672	IL6ST	NM_001190981	1	16	16	-	55230925	55237647
234057208	chr5	55237559	55237698	55237587	55237672	IL6ST	NM_002184	2	17	17	-	55230925	55237647
233350281	chr5	55247301	55247474	55247328	55247447	IL6ST	NM_175767	3	16	13	-	55247292	55247432
233350281	chr5	55247301	55247474	55247328	55247447	IL6ST	NM_001190981	1	16	13	-	55247292	55247432
233350281	chr5	55247301	55247474	55247328	55247447	IL6ST	NM_002184	2	17	14	-	55247292	55247432
233691452	chr5	55250533	55250694	55250556	55250670	IL6ST	NM_175767	3	16	10	-	55250638	55250820
233691452	chr5	55250533	55250694	55250556	55250670	IL6ST	NM_002184	2	17	11	-	55250638	55250820
232579292	chr5	55251892	55252064	55251920	55252042	IL6ST	NM_175767	3	16	9	-	55251853	55252063
232579292	chr5	55251892	55252064	55251920	55252042	IL6ST	NM_001190981	1	16	10	-	55251853	55252063
232579292	chr5	55251892	55252064	55251920	55252042	IL6ST	NM_002184	2	17	10	-	55251853	55252063
231588069	chr5	55259109	55259262	55259141	55259234	IL6ST	NM_175767	3	16	7	-	55259180	55259334

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231588069	chr5	55259109	55259262	55259141	55259234	IL6ST	NM_001190981	1	16	7	-	55259180	55259334
231588069	chr5	55259109	55259262	55259141	55259234	IL6ST	NM_002184	2	17	7	-	55259180	55259334
234381385	chr5	55264117	55264242	55264142	55264214	IL6ST	NM_175767	3	16	5	-	55264104	55264224
234381385	chr5	55264117	55264242	55264142	55264214	IL6ST	NM_001190981	1	16	5	-	55264104	55264224
234381385	chr5	55264117	55264242	55264142	55264214	IL6ST	NM_002184	2	17	5	-	55264104	55264224
241120916	chr5	67522473	67522646	67522496	67522623	PIK3R1	NM_181523	3	16	2	+	67522118	67522837
236354637	chr5	67569710	67569866	67569732	67569842	PIK3R1	NM_181523	3	16	4	+	67569767	67569841
234931385	chr5	67576425	67576588	67576453	67576560	PIK3R1	NM_181523	3	16	6	+	67576356	67576557
236184850	chr5	67586493	67586663	67586517	67586634	PIK3R1	NM_181504	2	10	1	+	67586467	67586662
237433713	chr5	67588882	67589056	67588910	67589028	PIK3R1	NM_181523	3	16	9	+	67588929	67589027
237433713	chr5	67588882	67589056	67588910	67589028	PIK3R1	NM_001242466	1	9	2	+	67588929	67589027
237433713	chr5	67588882	67589056	67588910	67589028	PIK3R1	NM_181524	4	10	3	+	67588929	67589027
237433713	chr5	67588882	67589056	67588910	67589028	PIK3R1	NM_181504	2	10	3	+	67588929	67589027
235877850	chr5	67590380	67590551	67590409	67590523	PIK3R1	NM_181523	3	16	12	+	67590364	67590506
235877850	chr5	67590380	67590551	67590409	67590523	PIK3R1	NM_001242466	1	9	5	+	67590364	67590506
235877850	chr5	67590380	67590551	67590409	67590523	PIK3R1	NM_181524	4	10	6	+	67590364	67590506
235877850	chr5	67590380	67590551	67590409	67590523	PIK3R1	NM_181504	2	10	6	+	67590364	67590506
236474903	chr5	67591219	67591388	67591247	67591360	PIK3R1	NM_181523	3	16	14	+	67591248	67591316
236474903	chr5	67591219	67591388	67591247	67591360	PIK3R1	NM_001242466	1	9	7	+	67591248	67591316
236474903	chr5	67591219	67591388	67591247	67591360	PIK3R1	NM_181524	4	10	8	+	67591248	67591316
236474903	chr5	67591219	67591388	67591247	67591360	PIK3R1	NM_181504	2	10	8	+	67591248	67591316
240318884	chr5	67593292	67593462	67593311	67593436	PIK3R1	NM_181523	3	16	16	+	67593240	67597649
240318884	chr5	67593292	67593462	67593311	67593436	PIK3R1	NM_001242466	1	9	9	+	67593240	67597649
240318884	chr5	67593292	67593462	67593311	67593436	PIK3R1	NM_181524	4	10	10	+	67593240	67597649
240318884	chr5	67593292	67593462	67593311	67593436	PIK3R1	NM_181504	2	10	10	+	67593240	67597649
223861114	chr5	112090621	112090792	112090644	112090764	APC	NM_000038	1	16	2	+	112090570	112090722
223861114	chr5	112090621	112090792	112090644	112090764	APC	NM_001127510	2	17	3	+	112090570	112090722
225050967	chr5	112102913	112103043	112102936	112103017	APC	NM_000038	1	16	4	+	112102886	112103087
225050967	chr5	112102913	112103043	112102936	112103017	APC	NM_001127510	2	17	5	+	112102886	112103087
225050967	chr5	112102913	112103043	112102936	112103017	APC	NM_001127511	3	14	3	+	112102886	112103087
223189535	chr5	112116368	112116538	112116391	112116514	APC	NM_000038	1	16	6	+	112116487	112116600
223189535	chr5	112116368	112116538	112116391	112116514	APC	NM_001127510	2	17	7	+	112116487	112116600
223189535	chr5	112116368	112116538	112116391	112116514	APC	NM_001127511	3	14	5	+	112116487	112116600
223264351	chr5	112137034	112137208	112137058	112137179	APC	NM_000038	1	16	8	+	112136976	112137080
223264351	chr5	112137034	112137208	112137058	112137179	APC	NM_001127510	2	17	9	+	112136976	112137080
223264351	chr5	112137034	112137208	112137058	112137179	APC	NM_001127511	3	14	6	+	112136976	112137080
222856433	chr5	112154682	112154849	112154708	112154822	APC	NM_000038	1	16	10	+	112154663	112155041
222856433	chr5	112154682	112154849	112154708	112154822	APC	NM_001127510	2	17	11	+	112154663	112155041
222856433	chr5	112154682	112154849	112154708	112154822	APC	NM_001127511	3	14	8	+	112154663	112155041
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_000038	1	16	12	+	112162805	112162944
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_001127510	2	17	13	+	112162805	112162944

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224043938	chr5	112162771	112162906	112162797	112162878	APC	NM_001127511	3	14	10	+	112162805	112162944
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_000038	1	16	14	+	112164553	112164669
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_001127510	2	17	15	+	112164553	112164669
223604539	chr5	112164540	112164675	112164568	112164647	APC	NM_001127511	3	14	12	+	112164553	112164669
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_000038	1	16	15	+	112170648	112170862
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_001127510	2	17	16	+	112170648	112170862
222414448	chr5	112170727	112170863	112170752	112170839	APC	NM_001127511	3	14	13	+	112170648	112170862
224562476	chr5	112173528	112173668	112173549	112173644	APC	NM_000038	1	16	16	+	112173250	112181936
224562476	chr5	112173528	112173668	112173549	112173644	APC	NM_001127510	2	17	17	+	112173250	112181936
224562476	chr5	112173528	112173668	112173549	112173644	APC	NM_001127511	3	14	14	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_000038	1	16	16	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_001127510	2	17	17	+	112173250	112181936
224566238	chr5	112173965	112174134	112173990	112174105	APC	NM_001127511	3	14	14	+	112173250	112181936
222812353	chr5	112174395	112174566	112174419	112174543	APC	NM_000038	1	16	16	+	112173250	112181936
222812353	chr5	112174395	112174566	112174419	112174543	APC	NM_001127510	2	17	17	+	112173250	112181936
222812353	chr5	112174395	112174566	112174419	112174543	APC	NM_001127511	3	14	14	+	112173250	112181936
222770598	chr5	112174802	112174951	112174830	112174928	APC	NM_000038	1	16	16	+	112173250	112181936
222770598	chr5	112174802	112174951	112174830	112174928	APC	NM_001127510	2	17	17	+	112173250	112181936
222770598	chr5	112174802	112174951	112174830	112174928	APC	NM_001127511	3	14	14	+	112173250	112181936
222748274	chr5	112175177	112175341	112175205	112175320	APC	NM_000038	1	16	16	+	112173250	112181936
222748274	chr5	112175177	112175341	112175205	112175320	APC	NM_001127510	2	17	17	+	112173250	112181936
222748274	chr5	112175177	112175341	112175205	112175320	APC	NM_001127511	3	14	14	+	112173250	112181936
222847417	chr5	112175661	112175835	112175685	112175815	APC	NM_000038	1	16	16	+	112173250	112181936
222847417	chr5	112175661	112175835	112175685	112175815	APC	NM_001127510	2	17	17	+	112173250	112181936
222847417	chr5	112175661	112175835	112175685	112175815	APC	NM_001127511	3	14	14	+	112173250	112181936
224598520	chr5	112176113	112176284	112176133	112176256	APC	NM_000038	1	16	16	+	112173250	112181936
224598520	chr5	112176113	112176284	112176133	112176256	APC	NM_001127510	2	17	17	+	112173250	112181936
224598520	chr5	112176113	112176284	112176133	112176256	APC	NM_001127511	3	14	14	+	112173250	112181936
224582559	chr5	112176600	112176773	112176626	112176748	APC	NM_000038	1	16	16	+	112173250	112181936
224582559	chr5	112176600	112176773	112176626	112176748	APC	NM_001127510	2	17	17	+	112173250	112181936
224582559	chr5	112176600	112176773	112176626	112176748	APC	NM_001127511	3	14	14	+	112173250	112181936
222829506	chr5	112177040	112177177	112177066	112177149	APC	NM_000038	1	16	16	+	112173250	112181936
222829506	chr5	112177040	112177177	112177066	112177149	APC	NM_001127510	2	17	17	+	112173250	112181936
222829506	chr5	112177040	112177177	112177066	112177149	APC	NM_001127511	3	14	14	+	112173250	112181936
224555286	chr5	112177448	112177612	112177476	112177584	APC	NM_000038	1	16	16	+	112173250	112181936
224555286	chr5	112177448	112177612	112177476	112177584	APC	NM_001127510	2	17	17	+	112173250	112181936
224555286	chr5	112177448	112177612	112177476	112177584	APC	NM_001127511	3	14	14	+	112173250	112181936
224533629	chr5	112177923	112178095	112177943	112178073	APC	NM_000038	1	16	16	+	112173250	112181936
224533629	chr5	112177923	112178095	112177943	112178073	APC	NM_001127510	2	17	17	+	112173250	112181936
224533629	chr5	112177923	112178095	112177943	112178073	APC	NM_001127511	3	14	14	+	112173250	112181936
224564759	chr5	112178398	112178536	112178421	112178508	APC	NM_000038	1	16	16	+	112173250	112181936

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224564759	chr5	112178398	112178536	112178421	112178508	APC	NM_001127510	2	17	17	+	112173250	112181936
224564759	chr5	112178398	112178536	112178421	112178508	APC	NM_001127511	3	14	14	+	112173250	112181936
222796899	chr5	112178814	112178971	112178843	112178946	APC	NM_000038	1	16	16	+	112173250	112181936
222796899	chr5	112178814	112178971	112178843	112178946	APC	NM_001127510	2	17	17	+	112173250	112181936
222796899	chr5	112178814	112178971	112178843	112178946	APC	NM_001127511	3	14	14	+	112173250	112181936
224549064	chr5	112179248	112179411	112179274	112179383	APC	NM_000038	1	16	16	+	112173250	112181936
224549064	chr5	112179248	112179411	112179274	112179383	APC	NM_001127510	2	17	17	+	112173250	112181936
224549064	chr5	112179248	112179411	112179274	112179383	APC	NM_001127511	3	14	14	+	112173250	112181936
224537542	chr5	112179693	112179832	112179713	112179804	APC	NM_000038	1	16	16	+	112173250	112181936
224537542	chr5	112179693	112179832	112179713	112179804	APC	NM_001127510	2	17	17	+	112173250	112181936
224537542	chr5	112179693	112179832	112179713	112179804	APC	NM_001127511	3	14	14	+	112173250	112181936
236544422	chr5	131894921	131895066	131894950	131895041	RAD50	NM_005732	1	25	2	+	131894976	131895059
236513480	chr5	131914990	131915164	131915018	131915139	RAD50	NM_005732	1	25	4	+	131915009	131915194
241350429	chr5	131923182	131923348	131923210	131923324	RAD50	NM_005732	1	25	6	+	131923254	131923382
235112686	chr5	131924374	131924498	131924396	131924477	RAD50	NM_005732	1	25	8	+	131924379	131924572
235878631	chr5	131925424	131925548	131925452	131925515	RAD50	NM_005732	1	25	9	+	131925323	131925529
239915118	chr5	131927469	131927626	131927502	131927598	RAD50	NM_005732	1	25	11	+	131927569	131927726
237565403	chr5	131930564	131930700	131930592	131930672	RAD50	NM_005732	1	25	12	+	131930561	131930736
235156026	chr5	131931337	131931477	131931360	131931455	RAD50	NM_005732	1	25	13	+	131931265	131931502
235629082	chr5	131939627	131939774	131939654	131939747	RAD50	NM_005732	1	25	15	+	131939612	131939738
237093681	chr5	131944748	131944903	131944770	131944876	RAD50	NM_005732	1	25	18	+	131944809	131944901
235665606	chr5	131953684	131953832	131953714	131953810	RAD50	NM_005732	1	25	21	+	131953762	131953986
239913450	chr5	131972773	131972902	131972805	131972879	RAD50	NM_005732	1	25	22	+	131972807	131972892
236387002	chr5	131976281	131976435	131976306	131976415	RAD50	NM_005732	1	25	24	+	131976364	131976497
234932132	chr5	131977979	131978104	131978007	131978076	RAD50	NM_005732	1	25	25	+	131977870	131980313
273193763	chr5	138118882	138119034	138118905	138119011	CTNNA1	NM_001903	1	18	3	+	138118866	138119061
272853118	chr5	138147793	138147961	138147821	138147933	CTNNA1	NM_001903	1	18	5	+	138147872	138147991
273797969	chr5	138160347	138160514	138160371	138160488	CTNNA1	NM_001903	1	18	6	+	138160219	138160488
272908084	chr5	138221959	138222099	138221979	138222071	CTNNA1	NM_001903	1	18	8	+	138221901	138221981
272780381	chr5	138239933	138240094	138239956	138240066	CTNNA1	NM_001903	1	18	10	+	138240038	138240130
273414536	chr5	138253528	138253668	138253551	138253640	CTNNA1	NM_001903	1	18	11	+	138253431	138253587
273674748	chr5	138261006	138261135	138261027	138261107	CTNNA1	NM_001903	1	18	13	+	138260945	138261096
273653487	chr5	138266476	138266646	138266502	138266624	CTNNA1	NM_001903	1	18	16	+	138266519	138266624
273974839	chr5	138269523	138269673	138269547	138269648	CTNNA1	NM_001903	1	18	18	+	138269491	138270723
226694375	chr5	149433667	149433831	149433686	149433808	CSF1R	NM_005211	1	22	22	-	149432854	149433787
225525840	chr5	149435632	149435794	149435653	149435772	CSF1R	NM_005211	1	22	19	-	149435589	149435700
226091160	chr5	149437008	149437178	149437030	149437156	CSF1R	NM_005211	1	22	16	-	149437067	149437155
227025256	chr5	149440417	149440565	149440438	149440542	CSF1R	NM_005211	1	22	14	-	149440425	149440535
225692713	chr5	149441343	149441479	149441368	149441456	CSF1R	NM_005211	1	22	12	-	149441286	149441412
225525002	chr5	149449512	149449660	149449536	149449639	CSF1R	NM_005211	1	22	10	-	149449436	149449626
226532812	chr5	149452803	149452957	149452825	149452935	CSF1R	NM_005211	1	22	7	-	149452864	149453056

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226281759	chr5	149457565	149457715	149457586	149457687	CSF1R	NM_005211	1	22	5	-	149457675	149457811
225571638	chr5	149459801	149459926	149459818	149459905	CSF1R	NM_005211	1	22	4	-	149459615	149459899
226206526	chr5	149465890	149466064	149465911	149466042	CSF1R	NM_005211	1	22	2	-	149465942	149466170
240137361	chr5	149497137	149497277	149497160	149497252	PDGFRB	NM_002609	1	23	22	-	149497181	149497413
235073014	chr5	149499008	149499152	149499032	149499131	PDGFRB	NM_002609	1	23	20	-	149499030	149499129
236311842	chr5	149500450	149500623	149500473	149500602	PDGFRB	NM_002609	1	23	18	-	149500451	149500573
236570762	chr5	149501470	149501629	149501492	149501607	PDGFRB	NM_002609	1	23	16	-	149501443	149501603
236520959	chr5	149503830	149504003	149503850	149503981	PDGFRB	NM_002609	1	23	14	-	149503813	149503923
236372734	chr5	149506032	149506206	149506058	149506185	PDGFRB	NM_002609	1	23	11	-	149506083	149506177
236561258	chr5	149509976	149510138	149509997	149510117	PDGFRB	NM_002609	1	23	9	-	149510102	149510225
236937241	chr5	149512258	149512432	149512281	149512411	PDGFRB	NM_002609	1	23	7	-	149512313	149512505
235211354	chr5	149513374	149513501	149513394	149513479	PDGFRB	NM_002609	1	23	5	-	149513444	149513571
236118403	chr5	149514484	149514610	149514505	149514586	PDGFRB	NM_002609	1	23	4	-	149514313	149514579
238241534	chr5	149516542	149516683	149516565	149516663	PDGFRB	NM_002609	1	23	2	-	149516571	149516616
257845858	chr5	170818253	170818377	170818281	170818354	NPM1	NM_002520	2	11	3	+	170818309	170818428
257845858	chr5	170818253	170818377	170818281	170818354	NPM1	NM_001037738	1	10	3	+	170818309	170818428
257845858	chr5	170818253	170818377	170818281	170818354	NPM1	NM_199185	3	10	3	+	170818309	170818428
237086719	chr5	170819662	170819788	170819685	170819759	NPM1	NM_002520	2	11	5	+	170819714	170819820
237086719	chr5	170819662	170819788	170819685	170819759	NPM1	NM_001037738	1	10	5	+	170819714	170819820
237086719	chr5	170819662	170819788	170819685	170819759	NPM1	NM_199185	3	10	5	+	170819714	170819820
237277788	chr5	170833276	170833438	170833301	170833411	NPM1	NM_001037738	1	10	10	+	170833401	170833731
270013737	chr5	176517365	176517513	176517383	176517494	FGFR4	NM_022963	2	16	2	+	176517391	176517654
270013737	chr5	176517365	176517513	176517383	176517494	FGFR4	NM_002011	1	18	3	+	176517391	176517654
270013737	chr5	176517365	176517513	176517383	176517494	FGFR4	NM_213647	3	18	3	+	176517391	176517654
272538031	chr5	176517895	176518065	176517916	176518045	FGFR4	NM_022963	2	16	4	+	176517939	176518105
272538031	chr5	176517895	176518065	176517916	176518045	FGFR4	NM_002011	1	18	5	+	176517939	176518105
272538031	chr5	176517895	176518065	176517916	176518045	FGFR4	NM_213647	3	18	5	+	176517939	176518105
271359854	chr5	176519288	176519453	176519308	176519433	FGFR4	NM_022963	2	16	6	+	176519322	176519512
271359854	chr5	176519288	176519453	176519308	176519433	FGFR4	NM_002011	1	18	7	+	176519322	176519512
271359854	chr5	176519288	176519453	176519308	176519433	FGFR4	NM_213647	3	18	7	+	176519322	176519512
269924505	chr5	176520049	176520208	176520070	176520190	FGFR4	NM_002011	1	18	9	+	176520139	176520332
269924505	chr5	176520049	176520208	176520070	176520190	FGFR4	NM_213647	3	18	9	+	176520139	176520332
271304540	chr5	176520497	176520647	176520520	176520626	FGFR4	NM_002011	1	18	10	+	176520407	176520552
271304540	chr5	176520497	176520647	176520520	176520626	FGFR4	NM_213647	3	18	10	+	176520407	176520552
271304540	chr5	176520497	176520647	176520520	176520626	FGFR4	NM_022963	2	16	8	+	176520333	176520552
270157245	chr5	176522570	176522724	176522589	176522703	FGFR4	NM_022963	2	16	11	+	176522534	176522724
270157245	chr5	176522570	176522724	176522589	176522703	FGFR4	NM_002011	1	18	13	+	176522534	176522724
270157245	chr5	176522570	176522724	176522589	176522703	FGFR4	NM_213647	3	18	13	+	176522534	176522724
270155146	chr5	176523247	176523411	176523266	176523392	FGFR4	NM_022963	2	16	13	+	176523288	176523358
270155146	chr5	176523247	176523411	176523266	176523392	FGFR4	NM_002011	1	18	15	+	176523288	176523358
270155146	chr5	176523247	176523411	176523266	176523392	FGFR4	NM_213647	3	18	15	+	176523288	176523358

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270071303	chr5	176524298	176524466	176524316	176524449	FGFR4	NM_022963	2	16	15	+	176524293	176524398
270071303	chr5	176524298	176524466	176524316	176524449	FGFR4	NM_002011	1	18	17	+	176524293	176524398
270071303	chr5	176524298	176524466	176524316	176524449	FGFR4	NM_213647	3	18	17	+	176524293	176524398
240492380	chr5	176562185	176562350	176562205	176562326	NSD1	NM_022455	1	23	2	+	176562088	176563031
235784652	chr5	176562620	176562793	176562643	176562771	NSD1	NM_022455	1	23	2	+	176562088	176563031
238369458	chr5	176618794	176618942	176618822	176618915	NSD1	NM_022455	1	23	3	+	176618885	176619020
238369458	chr5	176618794	176618942	176618822	176618915	NSD1	NM_172349	2	24	4	+	176618885	176619020
242511282	chr5	176636560	176636711	176636586	176636688	NSD1	NM_022455	1	23	5	+	176636637	176639196
242511282	chr5	176636560	176636711	176636586	176636688	NSD1	NM_172349	2	24	6	+	176636637	176639196
257633669	chr5	176637020	176637180	176637045	176637155	NSD1	NM_022455	1	23	5	+	176636637	176639196
257633669	chr5	176637020	176637180	176637045	176637155	NSD1	NM_172349	2	24	6	+	176636637	176639196
237653717	chr5	176637452	176637620	176637477	176637595	NSD1	NM_022455	1	23	5	+	176636637	176639196
237653717	chr5	176637452	176637620	176637477	176637595	NSD1	NM_172349	2	24	6	+	176636637	176639196
257626179	chr5	176637864	176638023	176637888	176637997	NSD1	NM_022455	1	23	5	+	176636637	176639196
257626179	chr5	176637864	176638023	176637888	176637997	NSD1	NM_172349	2	24	6	+	176636637	176639196
257549696	chr5	176638276	176638408	176638298	176638387	NSD1	NM_022455	1	23	5	+	176636637	176639196
257549696	chr5	176638276	176638408	176638298	176638387	NSD1	NM_172349	2	24	6	+	176636637	176639196
257556167	chr5	176638687	176638849	176638715	176638822	NSD1	NM_022455	1	23	5	+	176636637	176639196
257556167	chr5	176638687	176638849	176638715	176638822	NSD1	NM_172349	2	24	6	+	176636637	176639196
242571562	chr5	176639089	176639257	176639110	176639229	NSD1	NM_022455	1	23	5	+	176636637	176639196
242571562	chr5	176639089	176639257	176639110	176639229	NSD1	NM_172349	2	24	6	+	176636637	176639196
236190837	chr5	176665276	176665421	176665299	176665400	NSD1	NM_022455	1	23	7	+	176665238	176665508
236190837	chr5	176665276	176665421	176665299	176665400	NSD1	NM_172349	2	24	8	+	176665238	176665508
235728187	chr5	176671160	176671327	176671187	176671299	NSD1	NM_022455	1	23	9	+	176671196	176671271
235728187	chr5	176671160	176671327	176671187	176671299	NSD1	NM_172349	2	24	10	+	176671196	176671271
238156385	chr5	176675216	176675351	176675238	176675326	NSD1	NM_022455	1	23	11	+	176675182	176675325
238156385	chr5	176675216	176675351	176675238	176675326	NSD1	NM_172349	2	24	12	+	176675182	176675325
240355595	chr5	176684027	176684184	176684053	176684155	NSD1	NM_022455	1	23	13	+	176683952	176684152
240355595	chr5	176684027	176684184	176684053	176684155	NSD1	NM_172349	2	24	14	+	176683952	176684152
237703933	chr5	176694514	176694641	176694540	176694614	NSD1	NM_022455	1	23	15	+	176694563	176694719
237703933	chr5	176694514	176694641	176694540	176694614	NSD1	NM_172349	2	24	16	+	176694563	176694719
236737901	chr5	176696732	176696872	176696754	176696847	NSD1	NM_022455	1	23	16	+	176696603	176696808
236737901	chr5	176696732	176696872	176696754	176696847	NSD1	NM_172349	2	24	17	+	176696603	176696808
235851738	chr5	176707731	176707884	176707754	176707856	NSD1	NM_022455	1	23	18	+	176707566	176707835
235851738	chr5	176707731	176707884	176707754	176707856	NSD1	NM_172349	2	24	19	+	176707566	176707835
235240300	chr5	176710789	176710961	176710810	176710938	NSD1	NM_022455	1	23	20	+	176710788	176710929
235240300	chr5	176710789	176710961	176710810	176710938	NSD1	NM_172349	2	24	21	+	176710788	176710929
240628014	chr5	176719027	176719192	176719050	176719167	NSD1	NM_022455	1	23	22	+	176718955	176719159
240628014	chr5	176719027	176719192	176719050	176719167	NSD1	NM_172349	2	24	23	+	176718955	176719159
239856763	chr5	176721086	176721230	176721107	176721204	NSD1	NM_022455	1	23	23	+	176720833	176727214
239856763	chr5	176721086	176721230	176721107	176721204	NSD1	NM_172349	2	24	24	+	176720833	176727214

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235285964	chr5	176721452	176721626	176721475	176721605	NSD1	NM_022455	1	23	23	+	176720833	176727214
235285964	chr5	176721452	176721626	176721475	176721605	NSD1	NM_172349	2	24	24	+	176720833	176727214
239780501	chr5	176721880	176722054	176721903	176722033	NSD1	NM_022455	1	23	23	+	176720833	176727214
239780501	chr5	176721880	176722054	176721903	176722033	NSD1	NM_172349	2	24	24	+	176720833	176727214
235243339	chr5	176722358	176722494	176722380	176722472	NSD1	NM_022455	1	23	23	+	176720833	176727214
235243339	chr5	176722358	176722494	176722380	176722472	NSD1	NM_172349	2	24	24	+	176720833	176727214
271660081	chr5	180035918	180036083	180035938	180036065	FLT4	NM_182925	2	30	29	-	180035968	180036053
271660081	chr5	180035918	180036083	180035938	180036065	FLT4	NM_002020	1	30	29	-	180035968	180036053
271309736	chr5	180039464	180039632	180039484	180039615	FLT4	NM_182925	2	30	26	-	180039506	180039611
271309736	chr5	180039464	180039632	180039484	180039615	FLT4	NM_002020	1	30	26	-	180039506	180039611
270290062	chr5	180043416	180043560	180043439	180043539	FLT4	NM_182925	2	30	23	-	180043367	180043489
270290062	chr5	180043416	180043560	180043439	180043539	FLT4	NM_002020	1	30	23	-	180043367	180043489
271191504	chr5	180045919	180046090	180045936	180046069	FLT4	NM_182925	2	30	20	-	180046021	180046109
271191504	chr5	180045919	180046090	180045936	180046069	FLT4	NM_002020	1	30	20	-	180046021	180046109
272405912	chr5	180047077	180047241	180047103	180047219	FLT4	NM_182925	2	30	17	-	180047173	180047308
272405912	chr5	180047077	180047241	180047103	180047219	FLT4	NM_002020	1	30	17	-	180047173	180047308
272200093	chr5	180047785	180047954	180047804	180047935	FLT4	NM_182925	2	30	15	-	180047876	180048007
272200093	chr5	180047785	180047954	180047804	180047935	FLT4	NM_002020	1	30	15	-	180047876	180048007
270128547	chr5	180048193	180048366	180048212	180048345	FLT4	NM_182925	2	30	14	-	180048106	180048252
270128547	chr5	180048193	180048366	180048212	180048345	FLT4	NM_002020	1	30	14	-	180048106	180048252
271360552	chr5	180048806	180048935	180048827	180048916	FLT4	NM_182925	2	30	13	-	180048542	180048904
271360552	chr5	180048806	180048935	180048827	180048916	FLT4	NM_002020	1	30	13	-	180048542	180048904
271140763	chr5	180050931	180051101	180050959	180051081	FLT4	NM_182925	2	30	11	-	180050935	180051061
271140763	chr5	180050931	180051101	180050959	180051081	FLT4	NM_002020	1	30	11	-	180050935	180051061
272537513	chr5	180053196	180053362	180053216	180053340	FLT4	NM_182925	2	30	9	-	180053111	180053265
272537513	chr5	180053196	180053362	180053216	180053340	FLT4	NM_002020	1	30	9	-	180053111	180053265
269689358	chr5	180056337	180056500	180056356	180056483	FLT4	NM_182925	2	30	7	-	180056259	180056427
269689358	chr5	180056337	180056500	180056356	180056483	FLT4	NM_002020	1	30	7	-	180056259	180056427
271914870	chr5	180056964	180057132	180056985	180057112	FLT4	NM_182925	2	30	5	-	180056943	180057105
271914870	chr5	180056964	180057132	180056985	180057112	FLT4	NM_002020	1	30	5	-	180056943	180057105
271661205	chr5	180058635	180058807	180058653	180058790	FLT4	NM_182925	2	30	2	-	180058682	180058778
271661205	chr5	180058635	180058807	180058653	180058790	FLT4	NM_002020	1	30	2	-	180058682	180058778
233269954	chr6	394789	394941	394816	394918	IRF4	NM_001195286	1	9	3	+	394821	395007
233269954	chr6	394789	394941	394816	394918	IRF4	NR_046000	4	10	3	+	394821	395007
233269954	chr6	394789	394941	394816	394918	IRF4	NM_002460	2	9	3	+	394821	395007
233269954	chr6	394789	394941	394816	394918	IRF4	NR_036585	3	8	2	+	394821	395007
232061773	chr6	397089	397214	397110	397192	IRF4	NM_002460	2	9	5	+	397108	397252
232061773	chr6	397089	397214	397110	397192	IRF4	NM_001195286	1	9	5	+	397111	397252
232061773	chr6	397089	397214	397110	397192	IRF4	NR_046000	4	10	5	+	397111	397252
232061773	chr6	397089	397214	397110	397192	IRF4	NR_036585	3	8	4	+	397111	397252
234179932	chr6	401347	401474	401367	401453	IRF4	NM_001195286	1	9	7	+	401424	401777

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234179932	chr6	401347	401474	401367	401453	IRF4	NR_046000	4	10	7	+	401424	401777
234179932	chr6	401347	401474	401367	401453	IRF4	NM_002460	2	9	7	+	401424	401777
234179932	chr6	401347	401474	401367	401453	IRF4	NR_036585	3	8	6	+	401424	401777
233282033	chr6	404990	405163	405012	405138	IRF4	NM_001195286	1	9	8	+	405018	405130
233282033	chr6	404990	405163	405012	405138	IRF4	NR_046000	4	10	8	+	405018	405130
233282033	chr6	404990	405163	405012	405138	IRF4	NM_002460	2	9	8	+	405018	405130
233282033	chr6	404990	405163	405012	405138	IRF4	NR_036585	3	8	7	+	405018	405130
228009593	chr6	18236688	18236830	18236716	18236802	DEK	NM_003472	2	11	9	-	18236683	18236831
228009593	chr6	18236688	18236830	18236716	18236802	DEK	NM_001134709	1	10	8	-	18236683	18236831
227713919	chr6	18249902	18250074	18249929	18250051	DEK	NM_003472	2	11	7	-	18249882	18250070
227713919	chr6	18249902	18250074	18249929	18250051	DEK	NM_001134709	1	10	6	-	18249882	18250070
230482361	chr6	18256512	18256682	18256535	18256655	DEK	NM_003472	2	11	5	-	18256592	18256686
230482361	chr6	18256512	18256682	18256535	18256655	DEK	NM_001134709	1	10	4	-	18256592	18256686
232657919	chr6	18264130	18264257	18264147	18264237	DEK	NM_003472	2	11	2	-	18264074	18264227
232657919	chr6	18264130	18264257	18264147	18264237	DEK	NM_001134709	1	10	2	-	18264074	18264227
235513636	chr6	31133226	31133384	31133248	31133364	POU5F1	NM_002701	2	5	3	-	31133348	31133478
235513636	chr6	31133226	31133384	31133248	31133364	POU5F1	NM_203289	3	4	2	-	31133348	31133478
235513636	chr6	31133226	31133384	31133248	31133364	POU5F1	NM_001173531	1	5	3	-	31133348	31133478
237537220	chr6	31137881	31138035	31137899	31138014	POU5F1	NM_002701	2	5	1	-	31137993	31138451
290130224	chr6	32163321	32163487	32163340	32163466	NOTCH4	NM_004557	1	30	30	-	32162620	32163927
292645477	chr6	32163776	32163948	32163795	32163930	NOTCH4	NM_004557	1	30	30	-	32162620	32163927
290765366	chr6	32165037	32165201	32165055	32165183	NOTCH4	NM_004557	1	30	27	-	32165076	32165371
289638280	chr6	32166222	32166384	32166243	32166361	NOTCH4	NM_004557	1	30	26	-	32166198	32166336
290451239	chr6	32168536	32168706	32168557	32168685	NOTCH4	NM_004557	1	30	23	-	32168608	32168783
293606970	chr6	32169057	32169231	32169078	32169210	NOTCH4	NM_004557	1	30	22	-	32168894	32169277
292912887	chr6	32170043	32170202	32170060	32170181	NOTCH4	NM_004557	1	30	21	-	32169853	32170376
291428262	chr6	32171830	32171962	32171850	32171942	NOTCH4	NM_004557	1	30	19	-	32171914	32172166
289593479	chr6	32178583	32178755	32178604	32178728	NOTCH4	NM_004557	1	30	18	-	32178529	32178713
289948189	chr6	32180572	32180717	32180592	32180693	NOTCH4	NM_004557	1	30	16	-	32180601	32180688
290957729	chr6	32181850	32182021	32181872	32182002	NOTCH4	NM_004557	1	30	13	-	32181887	32182032
289786277	chr6	32184661	32184829	32184682	32184806	NOTCH4	NM_004557	1	30	11	-	32184722	32184844
290909291	chr6	32187304	32187470	32187328	32187450	NOTCH4	NM_004557	1	30	8	-	32187369	32187563
293003093	chr6	32188158	32188332	32188181	32188311	NOTCH4	NM_004557	1	30	6	-	32188182	32188418
290050469	chr6	32188730	32188876	32188747	32188858	NOTCH4	NM_004557	1	30	4	-	32188755	32189102
291657011	chr6	32190198	32190372	32190224	32190350	NOTCH4	NM_004557	1	30	3	-	32190288	32190583
292388317	chr6	32191585	32191759	32191604	32191741	NOTCH4	NM_004557	1	30	1	-	32191633	32191844
273037727	chr6	33287130	33287286	33287153	33287264	DAXX	NM_001254717	3	7	5	-	33287157	33287631
273037727	chr6	33287130	33287286	33287153	33287264	DAXX	NM_001350	4	8	6	-	33287157	33287631
273037727	chr6	33287130	33287286	33287153	33287264	DAXX	NM_001141969	1	8	6	-	33287157	33287631
273037727	chr6	33287130	33287286	33287153	33287264	DAXX	NM_001141970	2	8	6	-	33287157	33287631
273117672	chr6	33287571	33287703	33287597	33287677	DAXX	NM_001254717	3	7	5	-	33287157	33287631

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273117672	chr6	33287571	33287703	33287597	33287677	DAXX	NM_001350	4	8	6	-	33287157	33287631
273117672	chr6	33287571	33287703	33287597	33287677	DAXX	NM_001141969	1	8	6	-	33287157	33287631
273117672	chr6	33287571	33287703	33287597	33287677	DAXX	NM_001141970	2	8	6	-	33287157	33287631
273225455	chr6	33288121	33288292	33288144	33288265	DAXX	NM_001254717	3	7	3	-	33288157	33288368
273225455	chr6	33288121	33288292	33288144	33288265	DAXX	NM_001350	4	8	4	-	33288157	33288368
273225455	chr6	33288121	33288292	33288144	33288265	DAXX	NM_001141969	1	8	4	-	33288157	33288368
273225455	chr6	33288121	33288292	33288144	33288265	DAXX	NM_001141970	2	8	4	-	33288157	33288368
274339719	chr6	33288690	33288850	33288714	33288828	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274339719	chr6	33288690	33288850	33288714	33288828	DAXX	NM_001350	4	8	3	-	33288513	33289344
274339719	chr6	33288690	33288850	33288714	33288828	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274339719	chr6	33288690	33288850	33288714	33288828	DAXX	NM_001141970	2	8	3	-	33288513	33289344
274328061	chr6	33289144	33289271	33289164	33289250	DAXX	NM_001254717	3	7	2	-	33288513	33289344
274328061	chr6	33289144	33289271	33289164	33289250	DAXX	NM_001350	4	8	3	-	33288513	33289344
274328061	chr6	33289144	33289271	33289164	33289250	DAXX	NM_001141969	1	8	3	-	33288513	33289344
274328061	chr6	33289144	33289271	33289164	33289250	DAXX	NM_001141970	2	8	3	-	33288513	33289344
272978391	chr6	33289543	33289696	33289564	33289676	DAXX	NM_001141970	2	8	2	-	33289496	33289685
272978391	chr6	33289543	33289696	33289564	33289676	DAXX	NM_001350	4	8	2	-	33289496	33289751
272978391	chr6	33289543	33289696	33289564	33289676	DAXX	NM_001141969	1	8	2	-	33289496	33289754
237815087	chr6	37138262	37138386	37138280	37138369	PIM1	NM_002648	2	6	1	+	37137922	37138433
237815087	chr6	37138262	37138386	37138280	37138369	PIM1	NM_001243186	1	6	1	+	37137922	37138433
238237165	chr6	37138862	37138987	37138879	37138966	PIM1	NM_002648	2	6	4	+	37138901	37139267
238237165	chr6	37138862	37138987	37138879	37138966	PIM1	NM_001243186	1	6	4	+	37138901	37139267
236670853	chr6	37140747	37140895	37140771	37140871	PIM1	NM_002648	2	6	5	+	37140772	37140948
236670853	chr6	37140747	37140895	37140771	37140871	PIM1	NM_001243186	1	6	5	+	37140772	37140948
269482576	chr6	41533464	41533618	41533486	41533598	FOXP4	NM_138457	3	17	2	+	41533483	41533702
269482576	chr6	41533464	41533618	41533486	41533598	FOXP4	NM_001012427	2	17	2	+	41533483	41533702
269482576	chr6	41533464	41533618	41533486	41533598	FOXP4	NM_001012426	1	17	2	+	41533483	41533702
270151252	chr6	41552420	41552575	41552438	41552556	FOXP4	NM_138457	3	17	4	+	41552507	41552629
270151252	chr6	41552420	41552575	41552438	41552556	FOXP4	NM_001012427	2	17	4	+	41552507	41552629
270151252	chr6	41552420	41552575	41552438	41552556	FOXP4	NM_001012426	1	17	4	+	41552507	41552629
270350449	chr6	41554782	41554950	41554803	41554932	FOXP4	NM_138457	3	17	6	+	41554747	41554894
270350449	chr6	41554782	41554950	41554803	41554932	FOXP4	NM_001012427	2	17	6	+	41554747	41554894
270350449	chr6	41554782	41554950	41554803	41554932	FOXP4	NM_001012426	1	17	6	+	41554747	41554894
271022150	chr6	41555497	41555648	41555514	41555624	FOXP4	NM_138457	3	17	8	+	41555531	41555635
271022150	chr6	41555497	41555648	41555514	41555624	FOXP4	NM_001012427	2	17	8	+	41555531	41555635
271022150	chr6	41555497	41555648	41555514	41555624	FOXP4	NM_001012426	1	17	8	+	41555531	41555635
270273188	chr6	41557618	41557778	41557637	41557756	FOXP4	NM_138457	3	17	11	+	41557737	41557908
270273188	chr6	41557618	41557778	41557637	41557756	FOXP4	NM_001012427	2	17	11	+	41557701	41557908
270273188	chr6	41557618	41557778	41557637	41557756	FOXP4	NM_001012426	1	17	11	+	41557701	41557908
271936106	chr6	41558925	41559050	41558944	41559028	FOXP4	NM_138457	3	17	13	+	41558959	41559060
271936106	chr6	41558925	41559050	41558944	41559028	FOXP4	NM_001012427	2	17	13	+	41558959	41559060

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271936106	chr6	41558925	41559050	41558944	41559028	FOXP4	NM_001012426	1	17	13	+	41558959	41559060
271424033	chr6	41564921	41565048	41564945	41565023	FOXP4	NM_138457	3	17	15	+	41564914	41564980
271424033	chr6	41564921	41565048	41564945	41565023	FOXP4	NM_001012427	2	17	15	+	41564914	41564980
271424033	chr6	41564921	41565048	41564945	41565023	FOXP4	NM_001012426	1	17	15	+	41564914	41564980
271758520	chr6	41566527	41566696	41566546	41566679	FOXP4	NM_138457	3	17	17	+	41566527	41570122
271758520	chr6	41566527	41566696	41566546	41566679	FOXP4	NM_001012427	2	17	17	+	41566527	41570122
271758520	chr6	41566527	41566696	41566546	41566679	FOXP4	NM_001012426	1	17	17	+	41566527	41570122
228043861	chr6	44217180	44217351	44217204	44217323	HSP90AB1	NM_007355	1	12	3	+	44217114	44217320
227818293	chr6	44217774	44217936	44217800	44217910	HSP90AB1	NM_007355	1	12	5	+	44217758	44217891
229313295	chr6	44219052	44219214	44219075	44219191	HSP90AB1	NM_007355	1	12	8	+	44219155	44219345
228543907	chr6	44219608	44219777	44219633	44219756	HSP90AB1	NM_007355	1	12	10	+	44219736	44220004
227197215	chr6	44220714	44220856	44220737	44220835	HSP90AB1	NM_007355	1	12	11	+	44220782	44221115
228018196	chr6	44221191	44221365	44221216	44221337	HSP90AB1	NM_007355	1	12	12	+	44221226	44221614
270535909	chr6	51484109	51484278	51484131	51484257	PKHD1	NM_138694	1	67	67	-	51480145	51484318
271522846	chr6	51497249	51497405	51497277	51497386	PKHD1	NM_138694	1	67	65	-	51497363	51497521
271001588	chr6	51503675	51503823	51503696	51503795	PKHD1	NM_138694	1	67	64	-	51503647	51503754
271075402	chr6	51523709	51523853	51523733	51523830	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271143895	chr6	51524114	51524270	51524134	51524247	PKHD1	NM_138694	1	67	61	-	51523750	51524767
271132830	chr6	51524566	51524727	51524591	51524702	PKHD1	NM_138694	1	67	61	-	51523750	51524767
269839453	chr6	51609200	51609367	51609223	51609341	PKHD1	NM_138694	1	67	60	-	51609183	51609340
269839453	chr6	51609200	51609367	51609223	51609341	PKHD1	NM_170724	2	61	60	-	51609183	51609340
272267886	chr6	51612642	51612794	51612663	51612772	PKHD1	NM_138694	1	67	58	-	51612585	51613463
272267886	chr6	51612642	51612794	51612663	51612772	PKHD1	NM_170724	2	61	58	-	51612585	51613463
270536047	chr6	51613110	51613277	51613132	51613257	PKHD1	NM_138694	1	67	58	-	51612585	51613463
270536047	chr6	51613110	51613277	51613132	51613257	PKHD1	NM_170724	2	61	58	-	51612585	51613463
272658426	chr6	51618049	51618215	51618071	51618187	PKHD1	NM_138694	1	67	57	-	51617999	51618151
272658426	chr6	51618049	51618215	51618071	51618187	PKHD1	NM_170724	2	61	57	-	51617999	51618151
270895374	chr6	51640549	51640707	51640573	51640679	PKHD1	NM_138694	1	67	54	-	51640606	51640719
270895374	chr6	51640549	51640707	51640573	51640679	PKHD1	NM_170724	2	61	54	-	51640606	51640719
271898868	chr6	51695615	51695780	51695638	51695757	PKHD1	NM_138694	1	67	52	-	51695659	51695787
271898868	chr6	51695615	51695780	51695638	51695757	PKHD1	NM_170724	2	61	52	-	51695659	51695787
271364883	chr6	51712662	51712814	51712682	51712785	PKHD1	NM_138694	1	67	50	-	51712573	51712768
271364883	chr6	51712662	51712814	51712682	51712785	PKHD1	NM_170724	2	61	50	-	51712573	51712768
272232188	chr6	51732716	51732844	51732738	51732819	PKHD1	NM_138694	1	67	48	-	51732661	51732907
272232188	chr6	51732716	51732844	51732738	51732819	PKHD1	NM_170724	2	61	48	-	51732661	51732907
269789333	chr6	51747829	51747954	51747851	51747926	PKHD1	NM_138694	1	67	46	-	51747891	51748025
269789333	chr6	51747829	51747954	51747851	51747926	PKHD1	NM_170724	2	61	46	-	51747891	51748025
270522336	chr6	51751813	51751977	51751836	51751955	PKHD1	NM_138694	1	67	44	-	51751931	51752043
270522336	chr6	51751813	51751977	51751836	51751955	PKHD1	NM_170724	2	61	44	-	51751931	51752043
270619718	chr6	51768686	51768840	51768714	51768817	PKHD1	NM_138694	1	67	42	-	51768784	51768840
270619718	chr6	51768686	51768840	51768714	51768817	PKHD1	NM_170724	2	61	42	-	51768784	51768840

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271102763	chr6	51774039	51774199	51774067	51774177	PKHD1	NM_138694	1	67	40	-	51774081	51774272
271102763	chr6	51774039	51774199	51774067	51774177	PKHD1	NM_170724	2	61	40	-	51774081	51774272
271333904	chr6	51777094	51777267	51777119	51777243	PKHD1	NM_138694	1	67	38	-	51777164	51777374
271333904	chr6	51777094	51777267	51777119	51777243	PKHD1	NM_170724	2	61	38	-	51777164	51777374
269482545	chr6	51824586	51824718	51824609	51824696	PKHD1	NM_138694	1	67	36	-	51824668	51824824
269482545	chr6	51824586	51824718	51824609	51824696	PKHD1	NM_170724	2	61	36	-	51824668	51824824
269709359	chr6	51882078	51882250	51882100	51882227	PKHD1	NM_138694	1	67	34	-	51882208	51882427
269709359	chr6	51882078	51882250	51882100	51882227	PKHD1	NM_170724	2	61	34	-	51882208	51882427
270334089	chr6	51887582	51887716	51887605	51887694	PKHD1	NM_138694	1	67	33	-	51887599	51887742
270334089	chr6	51887582	51887716	51887605	51887694	PKHD1	NM_170724	2	61	33	-	51887599	51887742
271907684	chr6	51889527	51889685	51889551	51889659	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271907684	chr6	51889527	51889685	51889551	51889659	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271886519	chr6	51889996	51890140	51890020	51890119	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271886519	chr6	51889996	51890140	51890020	51890119	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271895544	chr6	51890362	51890536	51890384	51890515	PKHD1	NM_138694	1	67	32	-	51889372	51890979
271895544	chr6	51890362	51890536	51890384	51890515	PKHD1	NM_170724	2	61	32	-	51889372	51890979
270072350	chr6	51890865	51891000	51890885	51890973	PKHD1	NM_138694	1	67	32	-	51889372	51890979
270072350	chr6	51890865	51891000	51890885	51890973	PKHD1	NM_170724	2	61	32	-	51889372	51890979
271384077	chr6	51892958	51893122	51892980	51893099	PKHD1	NM_138694	1	67	30	-	51892954	51893149
271384077	chr6	51892958	51893122	51892980	51893099	PKHD1	NM_170724	2	61	30	-	51892954	51893149
272127989	chr6	51897913	51898037	51897938	51898012	PKHD1	NM_138694	1	67	29	-	51897828	51897963
272127989	chr6	51897913	51898037	51897938	51898012	PKHD1	NM_170724	2	61	29	-	51897828	51897963
271967993	chr6	51907745	51907893	51907766	51907870	PKHD1	NM_138694	1	67	27	-	51907657	51907932
271967993	chr6	51907745	51907893	51907766	51907870	PKHD1	NM_170724	2	61	27	-	51907657	51907932
269692076	chr6	51909739	51909894	51909759	51909868	PKHD1	NM_138694	1	67	25	-	51909764	51909886
269692076	chr6	51909739	51909894	51909759	51909868	PKHD1	NM_170724	2	61	25	-	51909764	51909886
269582769	chr6	51913268	51913439	51913289	51913417	PKHD1	NM_138694	1	67	23	-	51913290	51913417
269582769	chr6	51913268	51913439	51913289	51913417	PKHD1	NM_170724	2	61	23	-	51913290	51913417
269606739	chr6	51917908	51918075	51917928	51918052	PKHD1	NM_138694	1	67	21	-	51917874	51918049
269606739	chr6	51917908	51918075	51917928	51918052	PKHD1	NM_170724	2	61	21	-	51917874	51918049
272735411	chr6	51920395	51920561	51920417	51920534	PKHD1	NM_138694	1	67	19	-	51920385	51920527
272735411	chr6	51920395	51920561	51920417	51920534	PKHD1	NM_170724	2	61	19	-	51920385	51920527
271451531	chr6	51923054	51923199	51923075	51923177	PKHD1	NM_138694	1	67	16	-	51923121	51923399
271451531	chr6	51923054	51923199	51923075	51923177	PKHD1	NM_170724	2	61	16	-	51923121	51923399
270979447	chr6	51924707	51924876	51924735	51924849	PKHD1	NM_138694	1	67	15	-	51924726	51924840
270979447	chr6	51924707	51924876	51924735	51924849	PKHD1	NM_170724	2	61	15	-	51924726	51924840
270169017	chr6	51930693	51930860	51930716	51930839	PKHD1	NM_138694	1	67	12	-	51930774	51930875
270169017	chr6	51930693	51930860	51930716	51930839	PKHD1	NM_170724	2	61	12	-	51930774	51930875
272038150	chr6	51935127	51935275	51935156	51935247	PKHD1	NM_138694	1	67	10	-	51935204	51935243
272038150	chr6	51935127	51935275	51935156	51935247	PKHD1	NM_170724	2	61	10	-	51935204	51935243
270751543	chr6	51938288	51938450	51938317	51938425	PKHD1	NM_138694	1	67	7	-	51938261	51938339

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270751543	chr6	51938288	51938450	51938317	51938425	PKHD1	NM_170724	2	61	7	-	51938261	51938339
272547623	chr6	51947199	51947367	51947220	51947341	PKHD1	NM_138694	1	67	4	-	51947190	51947340
272547623	chr6	51947199	51947367	51947220	51947341	PKHD1	NM_170724	2	61	4	-	51947190	51947340
280726094	chr6	52870017	52870151	52870039	52870128	ICK	NM_016513	2	15	15	-	52866098	52870101
280726094	chr6	52870017	52870151	52870039	52870128	ICK	NM_014920	1	14	14	-	52866098	52870101
277968558	chr6	52876455	52876608	52876477	52876587	ICK	NM_016513	2	15	12	-	52876567	52876715
277968558	chr6	52876455	52876608	52876477	52876587	ICK	NM_014920	1	14	11	-	52876567	52876715
279463868	chr6	52878404	52878577	52878429	52878554	ICK	NM_016513	2	15	10	-	52878460	52878780
279463868	chr6	52878404	52878577	52878429	52878554	ICK	NM_014920	1	14	9	-	52878460	52878780
278324282	chr6	52880947	52881089	52880970	52881062	ICK	NM_016513	2	15	9	-	52880881	52881048
278324282	chr6	52880947	52881089	52880970	52881062	ICK	NM_014920	1	14	8	-	52880881	52881048
279987498	chr6	52884058	52884189	52884081	52884161	ICK	NM_016513	2	15	7	-	52884025	52884157
279987498	chr6	52884058	52884189	52884081	52884161	ICK	NM_014920	1	14	6	-	52884025	52884157
277963588	chr6	52902742	52902874	52902763	52902844	ICK	NM_016513	2	15	4	-	52902737	52902791
277963588	chr6	52902742	52902874	52902763	52902844	ICK	NM_014920	1	14	3	-	52902737	52902791
286504551	chr6	56323926	56324092	56323948	56324068	DST	NM_015548	2	84	84	-	56322785	56324065
288403406	chr6	56327856	56327987	56327876	56327959	DST	NM_015548	2	84	82	-	56327844	56327954
284763569	chr6	56330905	56331066	56330927	56331039	DST	NM_015548	2	84	80	-	56330876	56330993
287588762	chr6	56334864	56335030	56334886	56335002	DST	NM_015548	2	84	77	-	56334926	56335080
288176885	chr6	56336024	56336182	56336052	56336154	DST	NM_015548	2	84	76	-	56335904	56336066
286733791	chr6	56338674	56338818	56338696	56338789	DST	NM_015548	2	84	74	-	56338671	56338800
287915445	chr6	56341086	56341259	56341108	56341235	DST	NM_015548	2	84	73	-	56340947	56341135
286818393	chr6	56346858	56347001	56346880	56346977	DST	NM_015548	2	84	71	-	56346848	56346976
286887046	chr6	56350120	56350258	56350148	56350234	DST	NM_015548	2	84	69	-	56350110	56350269
287538480	chr6	56354165	56354339	56354187	56354311	DST	NM_015548	2	84	67	-	56354288	56354407
286264620	chr6	56357049	56357222	56357076	56357194	DST	NM_015548	2	84	66	-	56357025	56357231
285849174	chr6	56358728	56358853	56358753	56358828	DST	NM_015548	2	84	64	-	56358808	56358978
288192409	chr6	56362195	56362333	56362215	56362305	DST	NM_015548	2	84	63	-	56362177	56362305
288686174	chr6	56365812	56365943	56365841	56365919	DST	NM_015548	2	84	61	-	56365878	56366033
285230145	chr6	56366303	56366437	56366331	56366409	DST	NM_015548	2	84	60	-	56366318	56366491
286027699	chr6	56371161	56371335	56371187	56371307	DST	NM_015548	2	84	58	-	56371241	56371342
289153538	chr6	56373248	56373380	56373275	56373352	DST	NM_015548	2	84	56	-	56373327	56373553
286577714	chr6	56374469	56374596	56374495	56374573	DST	NM_015548	2	84	55	-	56374440	56374671
284768320	chr6	56376030	56376155	56376053	56376133	DST	NM_015548	2	84	54	-	56375995	56376198
285200215	chr6	56380329	56380503	56380349	56380476	DST	NM_015548	2	84	53	-	56380248	56380466
286947879	chr6	56382310	56382456	56382331	56382433	DST	NM_015548	2	84	51	-	56382299	56382418
289064462	chr6	56392261	56392410	56392289	56392390	DST	NM_015548	2	84	49	-	56392291	56392532
287495943	chr6	56394134	56394274	56394165	56394254	DST	NM_015548	2	84	47	-	56394246	56394572
287522692	chr6	56394526	56394679	56394554	56394649	DST	NM_015548	2	84	47	-	56394246	56394572
288837825	chr6	56397177	56397321	56397202	56397295	DST	NM_015548	2	84	45	-	56397142	56397308
285302550	chr6	56401496	56401628	56401523	56401606	DST	NM_015548	2	84	43	-	56401577	56401738

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
285780764	chr6	56416995	56417165	56417020	56417145	DST	NM_015548	2	84	42	-	56416982	56418453
288131384	chr6	56417443	56417596	56417470	56417572	DST	NM_015548	2	84	42	-	56416982	56418453
288115832	chr6	56417904	56418067	56417932	56418043	DST	NM_015548	2	84	42	-	56416982	56418453
288154313	chr6	56418322	56418458	56418350	56418434	DST	NM_015548	2	84	42	-	56416982	56418453
287269078	chr6	56420281	56420453	56420307	56420429	DST	NM_015548	2	84	41	-	56420143	56420638
286187363	chr6	56422125	56422276	56422149	56422249	DST	NM_015548	2	84	40	-	56422117	56422316
285144333	chr6	56426076	56426214	56426096	56426190	DST	NM_015548	2	84	38	-	56426106	56426347
287626514	chr6	56426954	56427079	56426977	56427051	DST	NM_015548	2	84	37	-	56426936	56426998
287151388	chr6	56434673	56434805	56434699	56434778	DST	NM_015548	2	84	35	-	56434654	56434810
285779038	chr6	56437520	56437682	56437544	56437654	DST	NM_015548	2	84	33	-	56437545	56437862
287233376	chr6	56438348	56438522	56438376	56438496	DST	NM_015548	2	84	32	-	56438477	56438685
287565568	chr6	56443584	56443708	56443612	56443682	DST	NM_015548	2	84	31	-	56443612	56443735
288798199	chr6	56458377	56458551	56458402	56458528	DST	NM_015548	2	84	29	-	56458461	56458991
288791019	chr6	56458861	56459035	56458889	56459009	DST	NM_015548	2	84	29	-	56458461	56458991
286385670	chr6	56463236	56463408	56463260	56463379	DST	NM_015548	2	84	27	-	56463274	56463507
288491911	chr6	56464851	56464978	56464878	56464950	DST	NM_015548	2	84	26	-	56464867	56465019
286957052	chr6	56476232	56476386	56476258	56476358	DST	NM_015548	2	84	24	-	56476306	56476394
287144219	chr6	56480279	56480450	56480299	56480424	DST	NM_001723	1	24	24	-	56479375	56482216
287181011	chr6	56480721	56480884	56480741	56480859	DST	NM_001723	1	24	24	-	56479375	56482216
289088345	chr6	56481148	56481321	56481176	56481298	DST	NM_001723	1	24	24	-	56479375	56482216
289076840	chr6	56481603	56481777	56481628	56481755	DST	NM_001723	1	24	24	-	56479375	56482216
287488869	chr6	56482060	56482226	56482087	56482199	DST	NM_001723	1	24	24	-	56479375	56482216
288282014	chr6	56482961	56483108	56482984	56483086	DST	NM_001723	1	24	23	-	56482784	56485513
288273391	chr6	56483405	56483548	56483432	56483521	DST	NM_001723	1	24	23	-	56482784	56485513
286188723	chr6	56483824	56483995	56483852	56483972	DST	NM_001723	1	24	23	-	56482784	56485513
286218676	chr6	56484214	56484383	56484243	56484356	DST	NM_001723	1	24	23	-	56482784	56485513
288316383	chr6	56484649	56484805	56484675	56484782	DST	NM_001723	1	24	23	-	56482784	56485513
286166607	chr6	56485068	56485240	56485092	56485216	DST	NM_001723	1	24	23	-	56482784	56485513
287166234	chr6	56489270	56489428	56489296	56489403	DST	NM_015548	2	84	22	-	56489328	56489426
287166234	chr6	56489270	56489428	56489296	56489403	DST	NM_001723	1	24	22	-	56489328	56489426
288335376	chr6	56491910	56492078	56491934	56492050	DST	NM_015548	2	84	20	-	56492002	56492085
288335376	chr6	56491910	56492078	56491934	56492050	DST	NM_001723	1	24	20	-	56492002	56492085
284774584	chr6	56494038	56494185	56494065	56494162	DST	NM_015548	2	84	18	-	56494048	56494241
284774584	chr6	56494038	56494185	56494065	56494162	DST	NM_001723	1	24	18	-	56494048	56494241
288580845	chr6	56496108	56496233	56496136	56496211	DST	NM_015548	2	84	16	-	56496009	56496187
288580845	chr6	56496108	56496233	56496136	56496211	DST	NM_001723	1	24	16	-	56496009	56496187
286256827	chr6	56497629	56497763	56497651	56497739	DST	NM_015548	2	84	14	-	56497652	56497835
286256827	chr6	56497629	56497763	56497651	56497739	DST	NM_001723	1	24	14	-	56497652	56497835
285873003	chr6	56499218	56499355	56499242	56499329	DST	NM_015548	2	84	12	-	56499260	56499414
285873003	chr6	56499218	56499355	56499242	56499329	DST	NM_001723	1	24	12	-	56499260	56499414
288040426	chr6	56500385	56500543	56500411	56500514	DST	NM_015548	2	84	10	-	56500387	56500512

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288040426	chr6	56500385	56500543	56500411	56500514	DST	NM_001723	1	24	10	-	56500387	56500512
284846222	chr6	56504057	56504227	56504079	56504199	DST	NM_015548	2	84	8	-	56504057	56504161
284846222	chr6	56504057	56504227	56504079	56504199	DST	NM_001723	1	24	8	-	56504057	56504161
286677984	chr6	56504447	56504612	56504476	56504587	DST	NM_015548	2	84	6	-	56504494	56504571
286677984	chr6	56504447	56504612	56504476	56504587	DST	NM_001723	1	24	6	-	56504494	56504571
287187111	chr6	56504844	56504985	56504870	56504955	DST	NM_015548	2	84	4	-	56504941	56505403
287187111	chr6	56504844	56504985	56504870	56504955	DST	NM_001723	1	24	4	-	56504941	56505403
287046095	chr6	56505236	56505406	56505260	56505387	DST	NM_015548	2	84	4	-	56504941	56505403
287046095	chr6	56505236	56505406	56505260	56505387	DST	NM_001723	1	24	4	-	56504941	56505403
288659801	chr6	56507210	56507359	56507233	56507335	DST	NM_015548	2	84	2	-	56507208	56507301
288659801	chr6	56507210	56507359	56507233	56507335	DST	NM_001723	1	24	2	-	56507208	56507301
284129794	chr6	69348573	69348738	69348600	69348710	BAI3	NM_001704	1	32	3	+	69348553	69349324
284145573	chr6	69348908	69349053	69348935	69349026	BAI3	NM_001704	1	32	3	+	69348553	69349324
283073007	chr6	69640400	69640531	69640427	69640510	BAI3	NM_001704	1	32	4	+	69640451	69640561
281793725	chr6	69653670	69653811	69653698	69653787	BAI3	NM_001704	1	32	6	+	69653722	69653886
281416215	chr6	69666498	69666672	69666525	69666652	BAI3	NM_001704	1	32	8	+	69666537	69666701
284234024	chr6	69703619	69703776	69703646	69703749	BAI3	NM_001704	1	32	11	+	69703660	69703854
283542865	chr6	69757994	69758149	69758021	69758127	BAI3	NM_001704	1	32	14	+	69758077	69758226
284094978	chr6	69772745	69772888	69772772	69772863	BAI3	NM_001704	1	32	16	+	69772826	69772928
283323898	chr6	69943069	69943224	69943096	69943202	BAI3	NM_001704	1	32	18	+	69943182	69943308
282576160	chr6	69948928	69949075	69948952	69949047	BAI3	NM_001704	1	32	20	+	69949016	69949118
282259218	chr6	70034782	70034956	70034808	70034928	BAI3	NM_001704	1	32	21	+	70034764	70034914
283281688	chr6	70042758	70042925	70042780	70042900	BAI3	NM_001704	1	32	24	+	70042815	70042900
281812746	chr6	70049296	70049452	70049324	70049427	BAI3	NM_001704	1	32	26	+	70049225	70049396
284250516	chr6	70070663	70070793	70070692	70070773	BAI3	NM_001704	1	32	29	+	70070761	70071404
284276577	chr6	70071078	70071213	70071105	70071185	BAI3	NM_001704	1	32	29	+	70070761	70071404
283476185	chr6	70082171	70082334	70082202	70082308	BAI3	NM_001704	1	32	30	+	70082298	70082333
283503083	chr6	70098688	70098857	70098710	70098834	BAI3	NM_001704	1	32	32	+	70098595	70099403
294843999	chr6	91228191	91228357	91228221	91228329	MAP3K7	NM_145331	2	17	16	-	91228166	91228281
294843999	chr6	91228191	91228357	91228221	91228329	MAP3K7	NM_003188	1	16	15	-	91228166	91228281
294300955	chr6	91233374	91233529	91233399	91233503	MAP3K7	NM_145333	4	15	13	-	91233397	91233502
294300955	chr6	91233374	91233529	91233399	91233503	MAP3K7	NM_145332	3	16	14	-	91233397	91233502
294300955	chr6	91233374	91233529	91233399	91233503	MAP3K7	NM_145331	2	17	14	-	91233397	91233502
294300955	chr6	91233374	91233529	91233399	91233503	MAP3K7	NM_003188	1	16	13	-	91233397	91233502
294822323	chr6	91257027	91257195	91257047	91257170	MAP3K7	NM_145333	4	15	11	-	91256977	91257106
294822323	chr6	91257027	91257195	91257047	91257170	MAP3K7	NM_145332	3	16	11	-	91256977	91257106
294822323	chr6	91257027	91257195	91257047	91257170	MAP3K7	NM_145331	2	17	11	-	91256977	91257106
294822323	chr6	91257027	91257195	91257047	91257170	MAP3K7	NM_003188	1	16	11	-	91256977	91257106
294263913	chr6	91261819	91261975	91261844	91261947	MAP3K7	NM_145333	4	15	8	-	91261768	91261898
294263913	chr6	91261819	91261975	91261844	91261947	MAP3K7	NM_145332	3	16	8	-	91261768	91261898
294263913	chr6	91261819	91261975	91261844	91261947	MAP3K7	NM_145331	2	17	8	-	91261768	91261898

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294263913	chr6	91261819	91261975	91261844	91261947	MAP3K7	NM_003188	1	16	8	-	91261768	91261898
294790341	chr6	91266242	91266388	91266263	91266360	MAP3K7	NM_145333	4	15	6	-	91266219	91266343
294790341	chr6	91266242	91266388	91266263	91266360	MAP3K7	NM_145332	3	16	6	-	91266219	91266343
294790341	chr6	91266242	91266388	91266263	91266360	MAP3K7	NM_145331	2	17	6	-	91266219	91266343
294790341	chr6	91266242	91266388	91266263	91266360	MAP3K7	NM_003188	1	16	6	-	91266219	91266343
294535709	chr6	91271314	91271440	91271342	91271418	MAP3K7	NM_145333	4	15	4	-	91271341	91271386
294535709	chr6	91271314	91271440	91271342	91271418	MAP3K7	NM_145332	3	16	4	-	91271341	91271386
294535709	chr6	91271314	91271440	91271342	91271418	MAP3K7	NM_145331	2	17	4	-	91271341	91271386
294535709	chr6	91271314	91271440	91271342	91271418	MAP3K7	NM_003188	1	16	4	-	91271341	91271386
293704544	chr6	91296371	91296535	91296390	91296512	MAP3K7	NM_145331	2	17	1	-	91296483	91296764
293704544	chr6	91296371	91296535	91296390	91296512	MAP3K7	NM_145333	4	15	1	-	91296483	91296907
293704544	chr6	91296371	91296535	91296390	91296512	MAP3K7	NM_145332	3	16	1	-	91296483	91296907
293704544	chr6	91296371	91296535	91296390	91296512	MAP3K7	NM_003188	1	16	1	-	91296483	91296907
270551230	chr6	93955010	93955145	93955034	93955117	EPHA7	NM_004440	1	17	16	-	93955016	93955171
270969962	chr6	93964280	93964423	93964308	93964395	EPHA7	NM_004440	1	17	14	-	93964365	93964514
269624201	chr6	93965552	93965698	93965578	93965670	EPHA7	NM_004440	1	17	13	-	93965546	93965755
270121094	chr6	93967807	93967945	93967835	93967919	EPHA7	NM_004440	1	17	11	-	93967817	93968002
269940465	chr6	93973493	93973663	93973518	93973634	EPHA7	NM_004440	1	17	9	-	93973578	93973633
270682186	chr6	93979266	93979434	93979288	93979408	EPHA7	NM_004440	1	17	7	-	93979195	93979378
270908173	chr6	94066491	94066663	94066519	94066638	EPHA7	NM_004440	1	17	5	-	94066435	94066770
271447687	chr6	94067995	94068169	94068016	94068141	EPHA7	NM_004440	1	17	4	-	94067974	94068129
270626492	chr6	94120430	94120574	94120454	94120546	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270585182	chr6	94120802	94120960	94120823	94120932	EPHA7	NM_004440	1	17	3	-	94120219	94120888
270665964	chr6	94129002	94129126	94129023	94129098	EPHA7	NM_004440	1	17	1	-	94128963	94129300
273825037	chr6	106543385	106543530	106543416	106543502	PRDM1	NM_001198	1	7	3	+	106543490	106543609
274584780	chr6	106547092	106547266	106547116	106547245	PRDM1	NM_182907	2	5	2	+	106547175	106547427
274584780	chr6	106547092	106547266	106547116	106547245	PRDM1	NM_001198	1	7	4	+	106547175	106547427
272783145	chr6	106552732	106552900	106552757	106552878	PRDM1	NM_182907	2	5	3	+	106552700	106553808
272783145	chr6	106552732	106552900	106552757	106552878	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273916896	chr6	106553226	106553352	106553245	106553331	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273916896	chr6	106553226	106553352	106553245	106553331	PRDM1	NM_001198	1	7	5	+	106552700	106553808
273926165	chr6	106553628	106553762	106553648	106553739	PRDM1	NM_182907	2	5	3	+	106552700	106553808
273926165	chr6	106553628	106553762	106553648	106553739	PRDM1	NM_001198	1	7	5	+	106552700	106553808
272969485	chr6	106554712	106554875	106554733	106554853	PRDM1	NM_182907	2	5	5	+	106554786	106557814
272969485	chr6	106554712	106554875	106554733	106554853	PRDM1	NM_001198	1	7	7	+	106554786	106557814
273046282	chr6	106555163	106555319	106555184	106555297	PRDM1	NM_182907	2	5	5	+	106554786	106557814
273046282	chr6	106555163	106555319	106555184	106555297	PRDM1	NM_001198	1	7	7	+	106554786	106557814
229530828	chr6	108984601	108984775	108984621	108984757	FOXO3	NM_001455	1	3	2	+	108984658	108986092
229530828	chr6	108984601	108984775	108984621	108984757	FOXO3	NM_201559	2	4	3	+	108984658	108986092
227540757	chr6	108985467	108985640	108985488	108985617	FOXO3	NM_001455	1	3	2	+	108984658	108986092
227540757	chr6	108985467	108985640	108985488	108985617	FOXO3	NM_201559	2	4	3	+	108984658	108986092

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242615893	chr6	117609727	117609896	117609752	117609868	ROS1	NM_002944	1	43	43	-	117609530	117609965
241740937	chr6	117622253	117622411	117622275	117622383	ROS1	NM_002944	1	43	42	-	117622137	117622300
262632891	chr6	117631314	117631438	117631342	117631416	ROS1	NM_002944	1	43	40	-	117631244	117631444
263887680	chr6	117638311	117638468	117638333	117638444	ROS1	NM_002944	1	43	38	-	117638306	117638435
260933423	chr6	117642364	117642515	117642385	117642490	ROS1	NM_002944	1	43	35	-	117642422	117642557
264095394	chr6	117647356	117647495	117647380	117647467	ROS1	NM_002944	1	43	33	-	117647387	117647577
240783064	chr6	117650569	117650729	117650596	117650701	ROS1	NM_002944	1	43	32	-	117650492	117650609
241292336	chr6	117662225	117662392	117662251	117662365	ROS1	NM_002944	1	43	30	-	117662298	117662474
240372757	chr6	117662669	117662843	117662693	117662821	ROS1	NM_002944	1	43	29	-	117662563	117662795
242663757	chr6	117665389	117665513	117665412	117665480	ROS1	NM_002944	1	43	27	-	117665223	117665425
238495867	chr6	117677792	117677963	117677813	117677934	ROS1	NM_002944	1	43	25	-	117677792	117678078
239482916	chr6	117679110	117679284	117679138	117679256	ROS1	NM_002944	1	43	24	-	117678967	117679172
237953328	chr6	117681457	117681615	117681485	117681594	ROS1	NM_002944	1	43	22	-	117681505	117681568
261842869	chr6	117686089	117686261	117686118	117686238	ROS1	NM_002944	1	43	20	-	117686223	117686367
240985825	chr6	117686805	117686977	117686832	117686944	ROS1	NM_002944	1	43	19	-	117686744	117686904
264285123	chr6	117700177	117700302	117700206	117700280	ROS1	NM_002944	1	43	17	-	117700222	117700322
238485366	chr6	117704581	117704705	117704603	117704677	ROS1	NM_002944	1	43	16	-	117704480	117704671
241715498	chr6	117708882	117709042	117708903	117709017	ROS1	NM_002944	1	43	13	-	117708943	117709197
242282859	chr6	117710507	117710669	117710527	117710642	ROS1	NM_002944	1	43	12	-	117710513	117711009
241005601	chr6	117714274	117714435	117714301	117714411	ROS1	NM_002944	1	43	11	-	117714387	117714484
262212932	chr6	117715792	117715934	117715816	117715908	ROS1	NM_002944	1	43	9	-	117715779	117715901
262143308	chr6	117724288	117724438	117724307	117724417	ROS1	NM_002944	1	43	6	-	117724302	117724440
241239949	chr6	117730695	117730868	117730716	117730840	ROS1	NM_002944	1	43	4	-	117730745	117730805
241828787	chr6	117746690	117746847	117746718	117746819	ROS1	NM_002944	1	43	1	-	117746697	117747018
293930921	chr6	134492089	134492262	134492110	134492234	SGK1	NM_001143676	1	14	12	-	134492161	134492316
293930921	chr6	134492089	134492262	134492110	134492234	SGK1	NM_001143677	2	12	10	-	134492161	134492316
293930921	chr6	134492089	134492262	134492110	134492234	SGK1	NM_005627	4	12	10	-	134492161	134492316
293930921	chr6	134492089	134492262	134492110	134492234	SGK1	NM_001143678	3	12	10	-	134492161	134492316
294373144	chr6	134493387	134493560	134493411	134493532	SGK1	NM_001143676	1	14	10	-	134493331	134493454
294373144	chr6	134493387	134493560	134493411	134493532	SGK1	NM_001143677	2	12	8	-	134493331	134493454
294373144	chr6	134493387	134493560	134493411	134493532	SGK1	NM_005627	4	12	8	-	134493331	134493454
294373144	chr6	134493387	134493560	134493411	134493532	SGK1	NM_001143678	3	12	8	-	134493331	134493454
293799534	chr6	134494389	134494543	134494409	134494515	SGK1	NM_001143676	1	14	7	-	134494412	134494495
293799534	chr6	134494389	134494543	134494409	134494515	SGK1	NM_001143677	2	12	5	-	134494412	134494495
293799534	chr6	134494389	134494543	134494409	134494515	SGK1	NM_005627	4	12	5	-	134494412	134494495
293799534	chr6	134494389	134494543	134494409	134494515	SGK1	NM_001143678	3	12	5	-	134494412	134494495
294044403	chr6	134495583	134495755	134495604	134495727	SGK1	NM_001143676	1	14	4	-	134495649	134495724
294044403	chr6	134495583	134495755	134495604	134495727	SGK1	NM_001143677	2	12	2	-	134495649	134495724
294044403	chr6	134495583	134495755	134495604	134495727	SGK1	NM_005627	4	12	2	-	134495649	134495724
294044403	chr6	134495583	134495755	134495604	134495727	SGK1	NM_001143678	3	12	2	-	134495649	134495724
294773538	chr6	134498883	134499040	134498905	134499011	SGK1	NM_001143677	2	12	1	-	134498801	134499010

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294791334	chr6	134583119	134583277	134583141	134583256	SGK1	NM_001143676	1	14	2	-	134583071	134583286
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001130173	2	16	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001130172	1	15	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001161657	4	14	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001161656	3	16	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_005375	8	15	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001161658	5	16	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001161660	7	14	2	+	135507041	135507158
236130391	chr6	135507088	135507248	135507110	135507220	MYB	NM_001161659	6	14	2	+	135507041	135507158
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001130173	2	16	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001130172	1	15	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001161657	4	14	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001161656	3	16	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_005375	8	15	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001161658	5	16	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001161660	7	14	4	+	135510929	135511021
239641660	chr6	135510950	135511111	135510971	135511084	MYB	NM_001161659	6	14	4	+	135510929	135511021
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001130173	2	16	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001130172	1	15	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001161657	4	14	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001161656	3	16	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_005375	8	15	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001161658	5	16	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001161660	7	14	6	+	135513462	135513696
235767608	chr6	135513346	135513513	135513371	135513491	MYB	NM_001161659	6	14	6	+	135513462	135513696
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001130173	2	16	8	+	135515494	135515598
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001161657	4	14	8	+	135515494	135515598
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_005375	8	15	8	+	135515494	135515598
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001161658	5	16	8	+	135515494	135515598
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001161659	6	14	8	+	135515494	135515598
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001130172	1	15	8	+	135515494	135515589
238260775	chr6	135515403	135515568	135515423	135515541	MYB	NM_001161656	3	16	8	+	135515494	135515589
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_001130173	2	16	9	+	135516886	135517140
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_001130172	1	15	9	+	135516886	135517140
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_001161656	3	16	9	+	135516886	135517140
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_005375	8	15	9	+	135516886	135517140
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_001161660	7	14	8	+	135516886	135517140
237151736	chr6	135517072	135517230	135517097	135517202	MYB	NM_001161659	6	14	9	+	135516886	135517140
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001130173	2	16	11	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001130172	1	15	10	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001161657	4	14	9	+	135520046	135520188

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001161656	3	16	11	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_005375	8	15	10	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001161658	5	16	11	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001161660	7	14	9	+	135520046	135520188
237803449	chr6	135519941	135520109	135519966	135520087	MYB	NM_001161659	6	14	10	+	135520046	135520188
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001130173	2	16	13	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001130172	1	15	12	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001161657	4	14	11	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001161656	3	16	13	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_005375	8	15	12	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001161658	5	16	13	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001161660	7	14	11	+	135521428	135521553
236652232	chr6	135521321	135521460	135521348	135521432	MYB	NM_001161659	6	14	12	+	135521428	135521553
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001130173	2	16	15	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001130172	1	15	14	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001161657	4	14	13	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001161656	3	16	15	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_005375	8	15	14	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001161658	5	16	15	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001161660	7	14	13	+	135524355	135524462
236530876	chr6	135524393	135524523	135524421	135524495	MYB	NM_001161659	6	14	13	+	135524355	135524462
238880401	chr6	138192402	138192574	138192425	138192553	TNFAIP3	NM_006290	1	9	2	+	138192350	138192659
264817832	chr6	138196777	138196945	138196803	138196919	TNFAIP3	NM_006290	1	9	4	+	138196825	138196972
241400582	chr6	138198143	138198305	138198170	138198276	TNFAIP3	NM_006290	1	9	6	+	138198213	138198393
263771837	chr6	138199636	138199794	138199662	138199772	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
263783514	chr6	138200038	138200209	138200059	138200184	TNFAIP3	NM_006290	1	9	7	+	138199569	138200488
240709322	chr6	138201164	138201336	138201186	138201311	TNFAIP3	NM_006290	1	9	8	+	138201208	138201389
240213014	chr6	138202384	138202529	138202408	138202505	TNFAIP3	NM_006290	1	9	9	+	138202172	138204449
272095991	chr6	152129218	152129387	152129236	152129368	ESR1	NM_000125	1	8	1	+	152128814	152129499
272095991	chr6	152129218	152129387	152129236	152129368	ESR1	NM_001122740	2	9	2	+	152128978	152129499
272095991	chr6	152129218	152129387	152129236	152129368	ESR1	NM_001122742	4	10	3	+	152128978	152129499
272095991	chr6	152129218	152129387	152129236	152129368	ESR1	NM_001122741	3	9	2	+	152128978	152129499
272587052	chr6	152163760	152163885	152163782	152163860	ESR1	NM_000125	1	8	2	+	152163732	152163922
272587052	chr6	152163760	152163885	152163782	152163860	ESR1	NM_001122740	2	9	3	+	152163732	152163922
272587052	chr6	152163760	152163885	152163782	152163860	ESR1	NM_001122742	4	10	4	+	152163732	152163922
272587052	chr6	152163760	152163885	152163782	152163860	ESR1	NM_001122741	3	9	3	+	152163732	152163922
269914831	chr6	152265185	152265337	152265211	152265315	ESR1	NM_000125	1	8	4	+	152265308	152265643
269914831	chr6	152265185	152265337	152265211	152265315	ESR1	NM_001122740	2	9	5	+	152265308	152265643
269914831	chr6	152265185	152265337	152265211	152265315	ESR1	NM_001122742	4	10	6	+	152265308	152265643
269914831	chr6	152265185	152265337	152265211	152265315	ESR1	NM_001122741	3	9	5	+	152265308	152265643
270051480	chr6	152332701	152332838	152332725	152332815	ESR1	NM_000125	1	8	5	+	152332791	152332929

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270051480	chr6	152332701	152332838	152332725	152332815	ESR1	NM_001122740	2	9	6	+	152332791	152332929
270051480	chr6	152332701	152332838	152332725	152332815	ESR1	NM_001122742	4	10	7	+	152332791	152332929
270051480	chr6	152332701	152332838	152332725	152332815	ESR1	NM_001122741	3	9	6	+	152332791	152332929
269783908	chr6	152415465	152415618	152415490	152415595	ESR1	NM_000125	1	8	7	+	152415520	152415703
269783908	chr6	152415465	152415618	152415490	152415595	ESR1	NM_001122740	2	9	8	+	152415520	152415703
269783908	chr6	152415465	152415618	152415490	152415595	ESR1	NM_001122742	4	10	9	+	152415520	152415703
269783908	chr6	152415465	152415618	152415490	152415595	ESR1	NM_001122741	3	9	8	+	152415520	152415703
272100855	chr6	152420033	152420159	152420057	152420135	ESR1	NM_000125	1	8	8	+	152419867	152424408
272100855	chr6	152420033	152420159	152420057	152420135	ESR1	NM_001122740	2	9	9	+	152419867	152424408
272100855	chr6	152420033	152420159	152420057	152420135	ESR1	NM_001122742	4	10	10	+	152419867	152424408
272100855	chr6	152420033	152420159	152420057	152420135	ESR1	NM_001122741	3	9	9	+	152419867	152424408
300577608	chr6	152451763	152451935	152451789	152451914	SYNE1	NM_033071	1	146	145	-	152451855	152451913
300577608	chr6	152451763	152451935	152451789	152451914	SYNE1	NM_182961	2	146	145	-	152451855	152451913
302875798	chr6	152454516	152454690	152454541	152454664	SYNE1	NM_033071	1	146	143	-	152454411	152454623
302875798	chr6	152454516	152454690	152454541	152454664	SYNE1	NM_182961	2	146	143	-	152454411	152454623
302297080	chr6	152457824	152457968	152457844	152457943	SYNE1	NM_033071	1	146	141	-	152457753	152457953
302297080	chr6	152457824	152457968	152457844	152457943	SYNE1	NM_182961	2	146	141	-	152457753	152457953
299325664	chr6	152461205	152461377	152461227	152461349	SYNE1	NM_033071	1	146	140	-	152461085	152461296
299325664	chr6	152461205	152461377	152461227	152461349	SYNE1	NM_182961	2	146	140	-	152461085	152461296
304814428	chr6	152466550	152466721	152466573	152466696	SYNE1	NM_033071	1	146	137	-	152466622	152466690
299883195	chr6	152470545	152470709	152470567	152470690	SYNE1	NM_033071	1	146	135	-	152470612	152470803
299883195	chr6	152470545	152470709	152470567	152470690	SYNE1	NM_182961	2	146	136	-	152470612	152470803
300891121	chr6	152473016	152473182	152473040	152473158	SYNE1	NM_033071	1	146	133	-	152473094	152473276
300891121	chr6	152473016	152473182	152473040	152473158	SYNE1	NM_182961	2	146	134	-	152473094	152473276
304455941	chr6	152476965	152477139	152476988	152477117	SYNE1	NM_033071	1	146	131	-	152477045	152477232
304455941	chr6	152476965	152477139	152476988	152477117	SYNE1	NM_182961	2	146	132	-	152477045	152477232
301016851	chr6	152497453	152497606	152497475	152497578	SYNE1	NM_033071	1	146	129	-	152497529	152497695
301016851	chr6	152497453	152497606	152497475	152497578	SYNE1	NM_182961	2	146	130	-	152497529	152497695
300471160	chr6	152510309	152510475	152510331	152510449	SYNE1	NM_033071	1	146	127	-	152510387	152510542
300471160	chr6	152510309	152510475	152510331	152510449	SYNE1	NM_182961	2	146	128	-	152510387	152510542
301943150	chr6	152527236	152527387	152527261	152527364	SYNE1	NM_033071	1	146	125	-	152527303	152527497
301943150	chr6	152527236	152527387	152527261	152527364	SYNE1	NM_182961	2	146	126	-	152527303	152527497
301455509	chr6	152529178	152529332	152529203	152529304	SYNE1	NM_033071	1	146	124	-	152529107	152529341
301455509	chr6	152529178	152529332	152529203	152529304	SYNE1	NM_182961	2	146	125	-	152529107	152529341
304004750	chr6	152534654	152534821	152534679	152534793	SYNE1	NM_033071	1	146	122	-	152534747	152534894
304004750	chr6	152534654	152534821	152534679	152534793	SYNE1	NM_182961	2	146	123	-	152534747	152534894
300936034	chr6	152539365	152539534	152539389	152539506	SYNE1	NM_033071	1	146	120	-	152539392	152539538
300936034	chr6	152539365	152539534	152539389	152539506	SYNE1	NM_182961	2	146	121	-	152539392	152539538
300410761	chr6	152541949	152542109	152541972	152542083	SYNE1	NM_033071	1	146	118	-	152541977	152542181
300410761	chr6	152541949	152542109	152541972	152542083	SYNE1	NM_182961	2	146	119	-	152541977	152542181
305426153	chr6	152545537	152545669	152545563	152545647	SYNE1	NM_033071	1	146	116	-	152545629	152545799

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305426153	chr6	152545537	152545669	152545563	152545647	SYNE1	NM_182961	2	146	117	-	152545629	152545799
305367500	chr6	152546904	152547067	152546929	152547041	SYNE1	NM_033071	1	146	115	-	152546856	152547011
305367500	chr6	152546904	152547067	152546929	152547041	SYNE1	NM_182961	2	146	116	-	152546856	152547011
300512286	chr6	152552483	152552646	152552508	152552624	SYNE1	NM_033071	1	146	113	-	152552526	152552702
300512286	chr6	152552483	152552646	152552508	152552624	SYNE1	NM_182961	2	146	114	-	152552526	152552702
300851420	chr6	152554971	152555129	152554991	152555103	SYNE1	NM_033071	1	146	111	-	152554916	152555098
300851420	chr6	152554971	152555129	152554991	152555103	SYNE1	NM_182961	2	146	112	-	152554916	152555098
299710819	chr6	152557260	152557426	152557286	152557398	SYNE1	NM_033071	1	146	109	-	152557242	152557438
299710819	chr6	152557260	152557426	152557286	152557398	SYNE1	NM_182961	2	146	110	-	152557242	152557438
303857764	chr6	152560626	152560778	152560650	152560755	SYNE1	NM_033071	1	146	107	-	152560668	152560841
303857764	chr6	152560626	152560778	152560650	152560755	SYNE1	NM_182961	2	146	108	-	152560668	152560841
299805726	chr6	152565630	152565780	152565651	152565754	SYNE1	NM_033071	1	146	105	-	152565672	152565791
299805726	chr6	152565630	152565780	152565651	152565754	SYNE1	NM_182961	2	146	106	-	152565672	152565791
305966286	chr6	152575919	152576085	152575945	152576059	SYNE1	NM_033071	1	146	103	-	152576015	152576224
305966286	chr6	152575919	152576085	152575945	152576059	SYNE1	NM_182961	2	146	104	-	152576015	152576224
305349186	chr6	152576788	152576953	152576811	152576925	SYNE1	NM_033071	1	146	102	-	152576726	152576881
305349186	chr6	152576788	152576953	152576811	152576925	SYNE1	NM_182961	2	146	103	-	152576726	152576881
305198456	chr6	152583169	152583316	152583192	152583292	SYNE1	NM_033071	1	146	100	-	152583167	152583323
305198456	chr6	152583169	152583316	152583192	152583292	SYNE1	NM_182961	2	146	101	-	152583167	152583323
299401901	chr6	152590388	152590534	152590410	152590509	SYNE1	NM_033071	1	146	98	-	152590290	152590421
299401901	chr6	152590388	152590534	152590410	152590509	SYNE1	NM_182961	2	146	99	-	152590290	152590421
302968032	chr6	152602898	152603026	152602926	152603004	SYNE1	NM_033071	1	146	96	-	152602942	152603115
302968032	chr6	152602898	152603026	152602926	152603004	SYNE1	NM_182961	2	146	97	-	152602942	152603115
302716872	chr6	152614662	152614823	152614684	152614800	SYNE1	NM_033071	1	146	94	-	152614723	152614884
302716872	chr6	152614662	152614823	152614684	152614800	SYNE1	NM_182961	2	146	95	-	152614723	152614884
301781847	chr6	152621647	152621810	152621671	152621787	SYNE1	NM_033071	1	146	92	-	152621776	152621916
301781847	chr6	152621647	152621810	152621671	152621787	SYNE1	NM_182961	2	146	93	-	152621776	152621916
300122718	chr6	152623112	152623277	152623133	152623254	SYNE1	NM_033071	1	146	91	-	152623004	152623198
300122718	chr6	152623112	152623277	152623133	152623254	SYNE1	NM_182961	2	146	92	-	152623004	152623198
302628740	chr6	152631034	152631168	152631056	152631140	SYNE1	NM_182961	2	146	90	-	152630970	152631152
302628740	chr6	152631034	152631168	152631056	152631140	SYNE1	NM_033071	1	146	89	-	152630966	152631152
305972948	chr6	152631832	152631971	152631854	152631944	SYNE1	NM_033071	1	146	87	-	152631823	152632008
305972948	chr6	152631832	152631971	152631854	152631944	SYNE1	NM_182961	2	146	88	-	152631823	152632008
301865505	chr6	152639172	152639346	152639198	152639320	SYNE1	NM_033071	1	146	85	-	152639216	152639398
301865505	chr6	152639172	152639346	152639198	152639320	SYNE1	NM_182961	2	146	86	-	152639216	152639398
305624700	chr6	152642309	152642473	152642332	152642445	SYNE1	NM_033071	1	146	83	-	152642373	152642525
305624700	chr6	152642309	152642473	152642332	152642445	SYNE1	NM_182961	2	146	84	-	152642373	152642525
305536618	chr6	152644602	152644775	152644625	152644753	SYNE1	NM_033071	1	146	81	-	152644613	152644872
305536618	chr6	152644602	152644775	152644625	152644753	SYNE1	NM_182961	2	146	82	-	152644613	152644872
304752189	chr6	152646315	152646484	152646335	152646460	SYNE1	NM_033071	1	146	80	-	152646219	152646437
304752189	chr6	152646315	152646484	152646335	152646460	SYNE1	NM_182961	2	146	81	-	152646219	152646437

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
303822219	chr6	152647424	152647552	152647449	152647532	SYNE1	NM_033071	1	146	78	-	152647431	152647768
303822219	chr6	152647424	152647552	152647449	152647532	SYNE1	NM_182961	2	146	79	-	152647431	152647768
305399730	chr6	152650913	152651064	152650934	152651036	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305399730	chr6	152650913	152651064	152650934	152651036	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305396438	chr6	152651348	152651517	152651369	152651490	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305396438	chr6	152651348	152651517	152651369	152651490	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305395790	chr6	152651787	152651941	152651810	152651915	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305395790	chr6	152651787	152651941	152651810	152651915	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305438622	chr6	152652199	152652362	152652221	152652335	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305438622	chr6	152652199	152652362	152652221	152652335	SYNE1	NM_182961	2	146	78	-	152650865	152653025
305472088	chr6	152652664	152652834	152652685	152652806	SYNE1	NM_033071	1	146	77	-	152650865	152653025
305472088	chr6	152652664	152652834	152652685	152652806	SYNE1	NM_182961	2	146	78	-	152650865	152653025
299879931	chr6	152655241	152655374	152655264	152655346	SYNE1	NM_033071	1	146	76	-	152655143	152655408
299879931	chr6	152655241	152655374	152655264	152655346	SYNE1	NM_182961	2	146	77	-	152655143	152655408
304425230	chr6	152658062	152658234	152658085	152658206	SYNE1	NM_033071	1	146	75	-	152657976	152658152
304425230	chr6	152658062	152658234	152658085	152658206	SYNE1	NM_182961	2	146	76	-	152657976	152658152
305189078	chr6	152665320	152665467	152665341	152665441	SYNE1	NM_033071	1	146	73	-	152665216	152665362
305189078	chr6	152665320	152665467	152665341	152665441	SYNE1	NM_182961	2	146	74	-	152665216	152665362
305179455	chr6	152671388	152671559	152671408	152671533	SYNE1	NM_182961	2	146	72	-	152671303	152671470
301059023	chr6	152673232	152673394	152673256	152673365	SYNE1	NM_033071	1	146	70	-	152673162	152673488
301059023	chr6	152673232	152673394	152673256	152673365	SYNE1	NM_182961	2	146	70	-	152673162	152673488
300813580	chr6	152674667	152674838	152674688	152674817	SYNE1	NM_033071	1	146	68	-	152674724	152674879
300813580	chr6	152674667	152674838	152674688	152674817	SYNE1	NM_182961	2	146	68	-	152674724	152674879
302460437	chr6	152676001	152676175	152676021	152676153	SYNE1	NM_033071	1	146	67	-	152675860	152676111
302460437	chr6	152676001	152676175	152676021	152676153	SYNE1	NM_182961	2	146	67	-	152675794	152676111
300319950	chr6	152680342	152680507	152680364	152680482	SYNE1	NM_033071	1	146	65	-	152680450	152680593
300319950	chr6	152680342	152680507	152680364	152680482	SYNE1	NM_182961	2	146	65	-	152680450	152680593
304374767	chr6	152685937	152686098	152685964	152686070	SYNE1	NM_033071	1	146	63	-	152685982	152686154
304374767	chr6	152685937	152686098	152685964	152686070	SYNE1	NM_182961	2	146	63	-	152685982	152686154
304701890	chr6	152690065	152690239	152690090	152690218	SYNE1	NM_033071	1	146	61	-	152690107	152690262
304701890	chr6	152690065	152690239	152690090	152690218	SYNE1	NM_182961	2	146	61	-	152690107	152690262
301677427	chr6	152694138	152694282	152694161	152694260	SYNE1	NM_033071	1	146	59	-	152694172	152694354
301677427	chr6	152694138	152694282	152694161	152694260	SYNE1	NM_182961	2	146	59	-	152694172	152694354
302021927	chr6	152697784	152697947	152697817	152697919	SYNE1	NM_033071	1	146	57	-	152697911	152698047
302021927	chr6	152697784	152697947	152697817	152697919	SYNE1	NM_182961	2	146	57	-	152697911	152698047
304661152	chr6	152702199	152702348	152702220	152702324	SYNE1	NM_033071	1	146	56	-	152702141	152702497
304661152	chr6	152702199	152702348	152702220	152702324	SYNE1	NM_182961	2	146	56	-	152702141	152702497
302795534	chr6	152706834	152707008	152706857	152706980	SYNE1	NM_033071	1	146	55	-	152706809	152706973
302795534	chr6	152706834	152707008	152706857	152706980	SYNE1	NM_182961	2	146	55	-	152706809	152706973
304636065	chr6	152708448	152708585	152708469	152708556	SYNE1	NM_033071	1	146	54	-	152708207	152708516
304636065	chr6	152708448	152708585	152708469	152708556	SYNE1	NM_182961	2	146	54	-	152708207	152708516

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
300491726	chr6	152712478	152712605	152712499	152712580	SYNE1	NM_033071	1	146	52	-	152712412	152712703
300491726	chr6	152712478	152712605	152712499	152712580	SYNE1	NM_182961	2	146	52	-	152712412	152712703
304098327	chr6	152716707	152716849	152716732	152716821	SYNE1	NM_033071	1	146	51	-	152716651	152716806
304098327	chr6	152716707	152716849	152716732	152716821	SYNE1	NM_182961	2	146	51	-	152716651	152716806
303761911	chr6	152719642	152719808	152719665	152719789	SYNE1	NM_033071	1	146	49	-	152719754	152719866
303761911	chr6	152719642	152719808	152719665	152719789	SYNE1	NM_182961	2	146	49	-	152719754	152719866
305768974	chr6	152722170	152722342	152722191	152722315	SYNE1	NM_033071	1	146	47	-	152722273	152722476
305768974	chr6	152722170	152722342	152722191	152722315	SYNE1	NM_182961	2	146	47	-	152722273	152722476
302372548	chr6	152728097	152728224	152728120	152728202	SYNE1	NM_033071	1	146	45	-	152728149	152728331
302372548	chr6	152728097	152728224	152728120	152728202	SYNE1	NM_182961	2	146	45	-	152728149	152728331
304609638	chr6	152730282	152730424	152730310	152730393	SYNE1	NM_033071	1	146	44	-	152730203	152730361
304609638	chr6	152730282	152730424	152730310	152730393	SYNE1	NM_182961	2	146	44	-	152730203	152730361
302640770	chr6	152734400	152734559	152734425	152734537	SYNE1	NM_033071	1	146	42	-	152734487	152734666
302640770	chr6	152734400	152734559	152734425	152734537	SYNE1	NM_182961	2	146	42	-	152734487	152734666
305273589	chr6	152737607	152737767	152737630	152737744	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305273589	chr6	152737607	152737767	152737630	152737744	SYNE1	NM_182961	2	146	41	-	152737522	152738150
305256527	chr6	152738021	152738178	152738042	152738151	SYNE1	NM_033071	1	146	41	-	152737522	152738150
305256527	chr6	152738021	152738178	152738042	152738151	SYNE1	NM_182961	2	146	41	-	152737522	152738150
301379783	chr6	152746510	152746643	152746538	152746616	SYNE1	NM_033071	1	146	39	-	152746516	152746682
301379783	chr6	152746510	152746643	152746538	152746616	SYNE1	NM_182961	2	146	39	-	152746516	152746682
303406398	chr6	152749378	152749552	152749399	152749529	SYNE1	NM_033071	1	146	37	-	152749340	152749527
303406398	chr6	152749378	152749552	152749399	152749529	SYNE1	NM_182961	2	146	37	-	152749340	152749527
304740983	chr6	152751721	152751883	152751748	152751855	SYNE1	NM_033071	1	146	35	-	152751617	152751844
304740983	chr6	152751721	152751883	152751748	152751855	SYNE1	NM_182961	2	146	35	-	152751617	152751844
302776730	chr6	152757039	152757206	152757067	152757184	SYNE1	NM_033071	1	146	33	-	152757076	152757236
302776730	chr6	152757039	152757206	152757067	152757184	SYNE1	NM_182961	2	146	33	-	152757076	152757236
301999504	chr6	152763189	152763351	152763209	152763330	SYNE1	NM_033071	1	146	31	-	152763210	152763380
301999504	chr6	152763189	152763351	152763209	152763330	SYNE1	NM_182961	2	146	31	-	152763210	152763380
301402785	chr6	152768548	152768675	152768572	152768652	SYNE1	NM_033071	1	146	29	-	152768593	152768757
301402785	chr6	152768548	152768675	152768572	152768652	SYNE1	NM_182961	2	146	29	-	152768593	152768757
300630768	chr6	152771637	152771804	152771663	152771782	SYNE1	NM_033071	1	146	27	-	152771760	152771968
300630768	chr6	152771637	152771804	152771663	152771782	SYNE1	NM_182961	2	146	27	-	152771760	152771968
302318531	chr6	152772250	152772412	152772276	152772384	SYNE1	NM_033071	1	146	26	-	152772182	152772340
302318531	chr6	152772250	152772412	152772276	152772384	SYNE1	NM_182961	2	146	26	-	152772182	152772340
304582756	chr6	152776609	152776765	152776629	152776737	SYNE1	NM_033071	1	146	24	-	152776561	152776725
304582756	chr6	152776609	152776765	152776629	152776737	SYNE1	NM_182961	2	146	24	-	152776561	152776725
302805685	chr6	152779901	152780029	152779927	152780008	SYNE1	NM_033071	1	146	22	-	152779892	152780065
302805685	chr6	152779901	152780029	152779927	152780008	SYNE1	NM_182961	2	146	22	-	152779892	152780065
305236647	chr6	152783806	152783978	152783834	152783956	SYNE1	NM_033071	1	146	20	-	152783873	152784025
305236647	chr6	152783806	152783978	152783834	152783956	SYNE1	NM_182961	2	146	20	-	152783873	152784025
304020444	chr6	152784595	152784730	152784617	152784699	SYNE1	NM_033071	1	146	19	-	152784488	152784652

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
304020444	chr6	152784595	152784730	152784617	152784699	SYNE1	NM_182961	2	146	19	-	152784488	152784652
302032757	chr6	152787076	152787243	152787097	152787215	SYNE1	NM_033071	1	146	17	-	152787117	152787213
302032757	chr6	152787076	152787243	152787097	152787215	SYNE1	NM_182961	2	146	17	-	152787117	152787213
301579164	chr6	152793447	152793610	152793470	152793586	SYNE1	NM_033071	1	146	15	-	152793436	152793548
301579164	chr6	152793447	152793610	152793470	152793586	SYNE1	NM_182961	2	146	15	-	152793436	152793548
301011774	chr6	152805977	152806137	152806004	152806114	SYNE1	NM_033071	1	146	13	-	152805970	152806107
301011774	chr6	152805977	152806137	152806004	152806114	SYNE1	NM_182961	2	146	13	-	152805970	152806107
302335621	chr6	152823789	152823963	152823811	152823936	SYNE1	NM_033071	1	146	10	-	152823768	152823877
302335621	chr6	152823789	152823963	152823811	152823936	SYNE1	NM_182961	2	146	10	-	152823768	152823877
300586938	chr6	152831232	152831406	152831260	152831385	SYNE1	NM_033071	1	146	8	-	152831328	152831506
300586938	chr6	152831232	152831406	152831260	152831385	SYNE1	NM_182961	2	146	8	-	152831328	152831506
301083336	chr6	152832588	152832747	152832616	152832721	SYNE1	NM_033071	1	146	6	-	152832706	152832726
300169265	chr6	152847173	152847338	152847202	152847310	SYNE1	NM_033071	1	146	4	-	152847215	152847310
300169265	chr6	152847173	152847338	152847202	152847310	SYNE1	NM_182961	2	146	5	-	152847215	152847310
270247605	chr6	160412110	160412284	160412138	160412256	IGF2R	NM_000876	1	48	2	+	160412216	160412355
272694587	chr6	160431718	160431866	160431744	160431837	IGF2R	NM_000876	1	48	4	+	160431719	160431817
271090433	chr6	160448219	160448390	160448240	160448367	IGF2R	NM_000876	1	48	6	+	160448217	160448346
270755081	chr6	160453943	160454076	160453969	160454054	IGF2R	NM_000876	1	48	9	+	160453974	160454139
271348519	chr6	160461636	160461805	160461658	160461781	IGF2R	NM_000876	1	48	11	+	160461592	160461756
271173197	chr6	160465588	160465754	160465616	160465729	IGF2R	NM_000876	1	48	13	+	160465546	160465689
271511024	chr6	160467529	160467689	160467557	160467667	IGF2R	NM_000876	1	48	15	+	160467530	160467677
272408618	chr6	160468686	160468854	160468708	160468830	IGF2R	NM_000876	1	48	17	+	160468824	160468939
271148576	chr6	160471472	160471635	160471496	160471617	IGF2R	NM_000876	1	48	19	+	160471505	160471684
270302007	chr6	160479014	160479183	160479035	160479156	IGF2R	NM_000876	1	48	21	+	160479055	160479156
270216458	chr6	160481623	160481785	160481643	160481764	IGF2R	NM_000876	1	48	23	+	160481579	160481749
270315047	chr6	160482863	160482988	160482884	160482964	IGF2R	NM_000876	1	48	25	+	160482785	160482960
270837606	chr6	160484639	160484764	160484660	160484738	IGF2R	NM_000876	1	48	27	+	160484447	160484662
271084482	chr6	160485900	160486024	160485921	160486003	IGF2R	NM_000876	1	48	29	+	160485836	160485933
270397215	chr6	160492815	160492964	160492839	160492944	IGF2R	NM_000876	1	48	32	+	160492942	160493068
270556299	chr6	160494207	160494376	160494230	160494353	IGF2R	NM_000876	1	48	34	+	160494245	160494501
271049732	chr6	160494860	160495034	160494885	160495008	IGF2R	NM_000876	1	48	35	+	160494789	160495007
271290182	chr6	160499271	160499413	160499293	160499394	IGF2R	NM_000876	1	48	37	+	160499233	160499394
270392693	chr6	160501074	160501246	160501095	160501224	IGF2R	NM_000876	1	48	39	+	160501161	160501307
270677970	chr6	160505995	160506169	160506016	160506145	IGF2R	NM_000876	1	48	41	+	160506027	160506163
270795576	chr6	160510103	160510267	160510124	160510242	IGF2R	NM_000876	1	48	43	+	160510139	160510285
272663909	chr6	160517383	160517555	160517410	160517530	IGF2R	NM_000876	1	48	45	+	160517471	160517657
271347101	chr6	160524729	160524873	160524750	160524847	IGF2R	NM_000876	1	48	47	+	160524778	160524847
272105274	chr6	160526048	160526195	160526069	160526168	IGF2R	NM_000876	1	48	48	+	160525706	160527583
238222715	chr6	166827326	166827481	166827348	166827460	RPS6KA2	NM_001006932	1	22	21	-	166827282	166827419
238222715	chr6	166827326	166827481	166827348	166827460	RPS6KA2	NM_021135	2	21	20	-	166827282	166827419
237972800	chr6	166836690	166836833	166836711	166836814	RPS6KA2	NM_001006932	1	22	18	-	166836744	166836905

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237972800	chr6	166836690	166836833	166836711	166836814	RPS6KA2	NM_021135	2	21	17	-	166836744	166836905
241969549	chr6	166843952	166844103	166843974	166844079	RPS6KA2	NM_001006932	1	22	17	-	166843941	166844099
241969549	chr6	166843952	166844103	166843974	166844079	RPS6KA2	NM_021135	2	21	16	-	166843941	166844099
262625807	chr6	166862252	166862417	166862273	166862396	RPS6KA2	NM_001006932	1	22	15	-	166862212	166862337
262625807	chr6	166862252	166862417	166862273	166862396	RPS6KA2	NM_021135	2	21	14	-	166862212	166862337
240549107	chr6	166883264	166883424	166883286	166883395	RPS6KA2	NM_001006932	1	22	12	-	166883329	166883393
240549107	chr6	166883264	166883424	166883286	166883395	RPS6KA2	NM_021135	2	21	11	-	166883329	166883393
242589314	chr6	166911910	166912084	166911931	166912065	RPS6KA2	NM_001006932	1	22	9	-	166911996	166912138
242589314	chr6	166911910	166912084	166911931	166912065	RPS6KA2	NM_021135	2	21	8	-	166911996	166912138
240395542	chr6	166918011	166918174	166918032	166918146	RPS6KA2	NM_001006932	1	22	7	-	166917994	166918100
240395542	chr6	166918011	166918174	166918032	166918146	RPS6KA2	NM_021135	2	21	6	-	166917994	166918100
237790388	chr6	166952092	166952259	166952113	166952233	RPS6KA2	NM_001006932	1	22	3	-	166952156	166952272
237790388	chr6	166952092	166952259	166952113	166952233	RPS6KA2	NM_021135	2	21	2	-	166952156	166952272
240819645	chr6	167275534	167275699	167275554	167275671	RPS6KA2	NM_001006932	1	22	1	-	167275596	167275771
223184524	chr7	2949670	2949824	2949689	2949806	CARD11	NM_032415	1	25	24	-	2949684	2949799
223190183	chr7	2952968	2953131	2952986	2953114	CARD11	NM_032415	1	25	22	-	2952921	2953100
222349353	chr7	2958103	2958272	2958121	2958253	CARD11	NM_032415	1	25	19	-	2958125	2958221
223793663	chr7	2962249	2962413	2962267	2962394	CARD11	NM_032415	1	25	17	-	2962268	2962394
223055961	chr7	2963742	2963908	2963766	2963888	CARD11	NM_032415	1	25	15	-	2963867	2963999
222436285	chr7	2969533	2969682	2969551	2969665	CARD11	NM_032415	1	25	12	-	2969626	2969708
222347361	chr7	2974132	2974297	2974156	2974277	CARD11	NM_032415	1	25	10	-	2974087	2974263
225105839	chr7	2977522	2977695	2977539	2977669	CARD11	NM_032415	1	25	8	-	2977541	2977666
223897475	chr7	2979399	2979544	2979422	2979520	CARD11	NM_032415	1	25	6	-	2979383	2979562
222298895	chr7	2983990	2984153	2984011	2984133	CARD11	NM_032415	1	25	5	-	2983846	2984171
222957374	chr7	2987186	2987347	2987207	2987327	CARD11	NM_032415	1	25	3	-	2987209	2987421
240528309	chr7	6026480	6026607	6026506	6026586	PMS2	NM_000535	1	15	11	-	6026390	6027251
240528309	chr7	6026480	6026607	6026506	6026586	PMS2	NR_003085	2	15	11	-	6026390	6027251
240504125	chr7	6026826	6026954	6026843	6026934	PMS2	NM_000535	1	15	11	-	6026390	6027251
240504125	chr7	6026826	6026954	6026843	6026934	PMS2	NR_003085	2	15	11	-	6026390	6027251
240542727	chr7	6027136	6027304	6027159	6027280	PMS2	NM_000535	1	15	11	-	6026390	6027251
240542727	chr7	6027136	6027304	6027159	6027280	PMS2	NR_003085	2	15	11	-	6026390	6027251
235084924	chr7	6035183	6035316	6035206	6035290	PMS2	NM_000535	1	15	8	-	6035165	6035264
235084924	chr7	6035183	6035316	6035206	6035290	PMS2	NR_003085	2	15	8	-	6035165	6035264
235004173	chr7	6038811	6038980	6038834	6038953	PMS2	NM_000535	1	15	6	-	6038739	6038906
235004173	chr7	6038811	6038980	6038834	6038953	PMS2	NR_003085	2	15	6	-	6038739	6038906
234913839	chr7	6043288	6043428	6043316	6043403	PMS2	NM_000535	1	15	4	-	6043321	6043423
234913839	chr7	6043288	6043428	6043316	6043403	PMS2	NR_003085	2	15	4	-	6043321	6043423
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163151	5	9	9	-	13930856	13935712
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163150	4	10	10	-	13930856	13935712
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163149	3	12	12	-	13930856	13935712
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163148	2	13	13	-	13930856	13935712

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163147	1	12	12	-	13930856	13935712
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_004956	7	14	14	-	13930856	13935712
232297927	chr7	13935460	13935624	13935480	13935601	ETV1	NM_001163152	6	9	9	-	13930856	13935712
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163151	5	9	7	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163150	4	10	8	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163149	3	12	10	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163148	2	13	11	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163147	1	12	10	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_004956	7	14	12	-	13946055	13946224
227941641	chr7	13946050	13946203	13946074	13946182	ETV1	NM_001163152	6	9	7	-	13946055	13946224
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163151	5	9	4	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163150	4	10	5	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163149	3	12	7	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163148	2	13	8	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163147	1	12	8	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_004956	7	14	9	-	13971127	13971374
230167957	chr7	13971068	13971241	13971092	13971222	ETV1	NM_001163152	6	9	4	-	13971127	13971374
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_001163151	5	9	3	-	13975333	13975521
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_001163150	4	10	4	-	13975333	13975521
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_001163149	3	12	6	-	13975333	13975521
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_001163148	2	13	7	-	13975333	13975521
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_001163147	1	12	7	-	13975333	13975521
228498071	chr7	13975398	13975544	13975417	13975521	ETV1	NM_004956	7	14	8	-	13975333	13975521
233023862	chr7	14017051	14017215	14017075	14017192	ETV1	NM_001163150	4	10	2	-	14017052	14017105
233023862	chr7	14017051	14017215	14017075	14017192	ETV1	NM_001163147	1	12	5	-	14017052	14017105
233023862	chr7	14017051	14017215	14017075	14017192	ETV1	NM_004956	7	14	6	-	14017052	14017105
233023862	chr7	14017051	14017215	14017075	14017192	ETV1	NM_001163152	6	9	2	-	14017052	14017105
228806351	chr7	14027649	14027812	14027671	14027789	ETV1	NM_001163149	3	12	3	-	14027711	14027798
228806351	chr7	14027649	14027812	14027671	14027789	ETV1	NM_001163148	2	13	4	-	14027711	14027798
228806351	chr7	14027649	14027812	14027671	14027789	ETV1	NM_001163147	1	12	3	-	14027711	14027798
228806351	chr7	14027649	14027812	14027671	14027789	ETV1	NM_004956	7	14	4	-	14027711	14027798
227676098	chr7	50444198	50444335	50444218	50444313	IKZF1	NM_006060	13	8	4	+	50444231	50444491
227676098	chr7	50444198	50444335	50444218	50444313	IKZF1	NM_001220771	7	5	4	+	50444231	50444491
227676098	chr7	50444198	50444335	50444218	50444313	IKZF1	NM_001220768	4	6	4	+	50444231	50444491
227676098	chr7	50444198	50444335	50444218	50444313	IKZF1	NM_001220765	1	7	4	+	50444231	50444491
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_006060	13	8	5	+	50450238	50450405
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220770	6	6	4	+	50450238	50450405
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220769	5	6	4	+	50450238	50450405
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220768	4	6	5	+	50450238	50450405
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220767	3	7	4	+	50450238	50450405
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220766	2	7	4	+	50450238	50450405

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227833011	chr7	50450300	50450467	50450320	50450448	IKZF1	NM_001220765	1	7	5	+	50450238	50450405
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220770	6	6	5	+	50459427	50459531
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220774	10	5	4	+	50459427	50459531
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220767	3	7	6	+	50459427	50459531
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220776	12	4	3	+	50459427	50459531
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_006060	13	8	7	+	50459427	50459561
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220773	9	5	4	+	50459427	50459561
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220769	5	6	5	+	50459427	50459561
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220766	2	7	6	+	50459427	50459561
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220765	1	7	6	+	50459427	50459561
227319244	chr7	50459448	50459622	50459470	50459594	IKZF1	NM_001220775	11	4	3	+	50459427	50459561
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_006060	13	8	8	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220771	7	5	5	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220770	6	6	6	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220774	10	5	5	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220773	9	5	5	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220772	8	3	3	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220769	5	6	6	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220768	4	6	6	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220767	3	7	7	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220766	2	7	7	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220765	1	7	7	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220776	12	4	4	+	50467616	50472798
228281272	chr7	50467891	50468051	50467911	50468034	IKZF1	NM_001220775	11	4	4	+	50467616	50472798
231493149	chr7	55086912	55087074	55086933	55087055	EGFR	NM_005228	1	28	1	+	55086725	55087058
231493149	chr7	55086912	55087074	55086933	55087055	EGFR	NM_201284	4	16	1	+	55086725	55087058
231493149	chr7	55086912	55087074	55086933	55087055	EGFR	NM_201283	3	10	1	+	55086725	55087058
231493149	chr7	55086912	55087074	55086933	55087055	EGFR	NM_201282	2	16	1	+	55086725	55087058
229630617	chr7	55211061	55211230	55211089	55211207	EGFR	NM_005228	1	28	3	+	55210998	55211181
229630617	chr7	55211061	55211230	55211089	55211207	EGFR	NM_201284	4	16	3	+	55210998	55211181
229630617	chr7	55211061	55211230	55211089	55211207	EGFR	NM_201283	3	10	3	+	55210998	55211181
229630617	chr7	55211061	55211230	55211089	55211207	EGFR	NM_201282	2	16	3	+	55210998	55211181
229052979	chr7	55220204	55220365	55220225	55220345	EGFR	NM_005228	1	28	6	+	55220239	55220357
229052979	chr7	55220204	55220365	55220225	55220345	EGFR	NM_201284	4	16	6	+	55220239	55220357
229052979	chr7	55220204	55220365	55220225	55220345	EGFR	NM_201283	3	10	6	+	55220239	55220357
229052979	chr7	55220204	55220365	55220225	55220345	EGFR	NM_201282	2	16	6	+	55220239	55220357
230392156	chr7	55223485	55223626	55223506	55223604	EGFR	NM_005228	1	28	8	+	55223523	55223639
230392156	chr7	55223485	55223626	55223506	55223604	EGFR	NM_201284	4	16	8	+	55223523	55223639
230392156	chr7	55223485	55223626	55223506	55223604	EGFR	NM_201283	3	10	8	+	55223523	55223639
230392156	chr7	55223485	55223626	55223506	55223604	EGFR	NM_201282	2	16	8	+	55223523	55223639
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_005228	1	28	10	+	55224452	55224525

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201284	4	16	10	+	55224452	55224525
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201282	2	16	10	+	55224452	55224525
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201283	3	10	10	+	55224452	55224644
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_005228	1	28	9	+	55224226	55224352
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201284	4	16	9	+	55224226	55224352
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201283	3	10	9	+	55224226	55224352
230683680	chr7	55224306	55224479	55224326	55224455	EGFR	NM_201282	2	16	9	+	55224226	55224352
230187475	chr7	55227833	55227987	55227856	55227965	EGFR	NM_005228	1	28	12	+	55227832	55228031
230187475	chr7	55227833	55227987	55227856	55227965	EGFR	NM_201284	4	16	12	+	55227832	55228031
230187475	chr7	55227833	55227987	55227856	55227965	EGFR	NM_201282	2	16	12	+	55227832	55228031
228709018	chr7	55231396	55231548	55231416	55231527	EGFR	NM_005228	1	28	14	+	55231426	55231516
228709018	chr7	55231396	55231548	55231416	55231527	EGFR	NM_201284	4	16	14	+	55231426	55231516
228709018	chr7	55231396	55231548	55231416	55231527	EGFR	NM_201282	2	16	14	+	55231426	55231516
230628101	chr7	55237863	55238037	55237892	55238012	EGFR	NM_201284	4	16	16	+	55238000	55238738
227716821	chr7	55240623	55240789	55240645	55240771	EGFR	NM_005228	1	28	17	+	55240676	55240817
227830783	chr7	55242389	55242560	55242412	55242539	EGFR	NM_005228	1	28	19	+	55242415	55242513
232260099	chr7	55259462	55259604	55259485	55259582	EGFR	NM_005228	1	28	21	+	55259412	55259567
230075336	chr7	55267958	55268131	55267986	55268107	EGFR	NM_005228	1	28	24	+	55268009	55268106
231314233	chr7	55270172	55270340	55270191	55270318	EGFR	NM_005228	1	28	27	+	55270210	55270318
231239581	chr7	55273188	55273337	55273211	55273312	EGFR	NM_005228	1	28	28	+	55272949	55275031
261471365	chr7	66458120	66458244	66458145	66458219	SBDS	NM_016038	1	5	3	-	66458204	66458404
238818575	chr7	66459177	66459350	66459198	66459328	SBDS	NM_016038	1	5	2	-	66459199	66459328
224090430	chr7	91602942	91603068	91602964	91603049	AKAP9	NM_005751	1	50	2	+	91603025	91603282
224090430	chr7	91602942	91603068	91602964	91603049	AKAP9	NM_147185	2	50	2	+	91603025	91603282
224642519	chr7	91609489	91609637	91609522	91609613	AKAP9	NM_005751	1	50	3	+	91609603	91609647
224642519	chr7	91609489	91609637	91609522	91609613	AKAP9	NM_147185	2	50	3	+	91609603	91609647
223433067	chr7	91622136	91622286	91622164	91622259	AKAP9	NM_005751	1	50	5	+	91622199	91622369
223433067	chr7	91622136	91622286	91622164	91622259	AKAP9	NM_147185	2	50	5	+	91622199	91622369
223420540	chr7	91623982	91624107	91624007	91624074	AKAP9	NM_005751	1	50	6	+	91623935	91624090
223420540	chr7	91623982	91624107	91624007	91624074	AKAP9	NM_147185	2	50	6	+	91623935	91624090
222723458	chr7	91630518	91630644	91630539	91630620	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222723458	chr7	91630518	91630644	91630539	91630620	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224473632	chr7	91630822	91630964	91630850	91630936	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224473632	chr7	91630822	91630964	91630850	91630936	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224469873	chr7	91631138	91631296	91631166	91631269	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224469873	chr7	91631138	91631296	91631166	91631269	AKAP9	NM_147185	2	50	8	+	91630162	91632549
224477574	chr7	91631615	91631777	91631643	91631748	AKAP9	NM_005751	1	50	8	+	91630162	91632549
224477574	chr7	91631615	91631777	91631643	91631748	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222658515	chr7	91632183	91632314	91632211	91632286	AKAP9	NM_005751	1	50	8	+	91630162	91632549
222658515	chr7	91632183	91632314	91632211	91632286	AKAP9	NM_147185	2	50	8	+	91630162	91632549
222262238	chr7	91641634	91641780	91641667	91641760	AKAP9	NM_005751	1	50	9	+	91641743	91641956

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222262238	chr7	91641634	91641780	91641667	91641760	AKAP9	NM_147185	2	50	9	+	91641743	91641956
222233508	chr7	91643474	91643635	91643495	91643607	AKAP9	NM_005751	1	50	10	+	91643563	91643642
222233508	chr7	91643474	91643635	91643495	91643607	AKAP9	NM_147185	2	50	10	+	91643563	91643642
223291112	chr7	91651489	91651662	91651517	91651635	AKAP9	NM_005751	1	50	13	+	91651552	91651666
223291112	chr7	91651489	91651662	91651517	91651635	AKAP9	NM_147185	2	50	13	+	91651552	91651666
223043830	chr7	91659133	91659298	91659158	91659266	AKAP9	NM_005751	1	50	15	+	91659209	91659305
223043830	chr7	91659133	91659298	91659158	91659266	AKAP9	NM_147185	2	50	15	+	91659209	91659305
222551487	chr7	91667830	91667974	91667858	91667945	AKAP9	NM_005751	1	50	17	+	91667733	91668086
222551487	chr7	91667830	91667974	91667858	91667945	AKAP9	NM_147185	2	50	17	+	91667733	91668086
222165273	chr7	91669990	91670151	91670016	91670129	AKAP9	NM_005751	1	50	18	+	91669988	91670212
222165273	chr7	91669990	91670151	91670016	91670129	AKAP9	NM_147185	2	50	18	+	91669988	91670212
223547092	chr7	91671903	91672058	91671929	91672029	AKAP9	NM_005751	1	50	20	+	91671982	91672085
223547092	chr7	91671903	91672058	91671929	91672029	AKAP9	NM_147185	2	50	20	+	91671982	91672085
222669308	chr7	91681932	91682104	91681960	91682076	AKAP9	NM_005751	1	50	22	+	91682040	91682272
222669308	chr7	91681932	91682104	91681960	91682076	AKAP9	NM_147185	2	50	22	+	91682040	91682272
222892556	chr7	91690562	91690687	91690587	91690667	AKAP9	NM_005751	1	50	23	+	91690574	91690736
222892556	chr7	91690562	91690687	91690587	91690667	AKAP9	NM_147185	2	50	23	+	91690574	91690736
224492689	chr7	91694444	91694618	91694472	91694591	AKAP9	NM_005751	1	50	25	+	91694545	91694777
224492689	chr7	91694444	91694618	91694472	91694591	AKAP9	NM_147185	2	50	25	+	91694545	91694777
223782434	chr7	91695726	91695888	91695754	91695862	AKAP9	NM_005751	1	50	26	+	91695741	91695860
223782434	chr7	91695726	91695888	91695754	91695862	AKAP9	NM_147185	2	50	26	+	91695741	91695860
223211645	chr7	91700226	91700361	91700249	91700334	AKAP9	NM_005751	1	50	28	+	91700219	91700323
223211645	chr7	91700226	91700361	91700249	91700334	AKAP9	NM_147185	2	50	28	+	91700219	91700323
223483934	chr7	91708298	91708437	91708323	91708410	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223483934	chr7	91708298	91708437	91708323	91708410	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223512051	chr7	91708718	91708867	91708746	91708840	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223512051	chr7	91708718	91708867	91708746	91708840	AKAP9	NM_147185	2	50	31	+	91708393	91709466
223514492	chr7	91709079	91709244	91709107	91709219	AKAP9	NM_005751	1	50	31	+	91708393	91709466
223514492	chr7	91709079	91709244	91709107	91709219	AKAP9	NM_147185	2	50	31	+	91708393	91709466
222334565	chr7	91711809	91711970	91711831	91711942	AKAP9	NM_005751	1	50	32	+	91711836	91711976
222334565	chr7	91711809	91711970	91711831	91711942	AKAP9	NM_147185	2	50	32	+	91711836	91711976
224052491	chr7	91712616	91712772	91712638	91712744	AKAP9	NM_005751	1	50	33	+	91712484	91712969
224052491	chr7	91712616	91712772	91712638	91712744	AKAP9	NM_147185	2	50	33	+	91712484	91712969
224318535	chr7	91713854	91714022	91713880	91713994	AKAP9	NM_005751	1	50	34	+	91713954	91714017
224318535	chr7	91713854	91714022	91713880	91713994	AKAP9	NM_147185	2	50	34	+	91713954	91714017
222342358	chr7	91714765	91714897	91714793	91714871	AKAP9	NM_005751	1	50	36	+	91714809	91715000
222342358	chr7	91714765	91714897	91714793	91714871	AKAP9	NM_147185	2	50	36	+	91714809	91715000
222613119	chr7	91715674	91715846	91715702	91715813	AKAP9	NM_005751	1	50	37	+	91715542	91715730
222613119	chr7	91715674	91715846	91715702	91715813	AKAP9	NM_147185	2	50	37	+	91715542	91715730
224432586	chr7	91722519	91722656	91722543	91722630	AKAP9	NM_005751	1	50	39	+	91722411	91722630
224432586	chr7	91722519	91722656	91722543	91722630	AKAP9	NM_147185	2	50	39	+	91722411	91722630

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224232526	chr7	91726077	91726233	91726102	91726212	AKAP9	NM_005751	1	50	41	+	91726003	91726671
224232526	chr7	91726077	91726233	91726102	91726212	AKAP9	NM_147185	2	50	41	+	91726003	91726671
222173340	chr7	91726494	91726624	91726516	91726599	AKAP9	NM_005751	1	50	41	+	91726003	91726671
222173340	chr7	91726494	91726624	91726516	91726599	AKAP9	NM_147185	2	50	41	+	91726003	91726671
225163228	chr7	91727017	91727142	91727045	91727117	AKAP9	NM_005751	1	50	42	+	91726900	91727108
225163228	chr7	91727017	91727142	91727045	91727117	AKAP9	NM_147185	2	50	42	+	91726900	91727108
223224502	chr7	91730114	91730286	91730142	91730264	AKAP9	NM_005751	1	50	45	+	91730170	91730370
223224502	chr7	91730114	91730286	91730142	91730264	AKAP9	NM_147185	2	50	45	+	91730170	91730370
223672356	chr7	91732070	91732226	91732091	91732201	AKAP9	NM_005751	1	50	46	+	91731908	91732140
223672356	chr7	91732070	91732226	91732091	91732201	AKAP9	NM_147185	2	50	46	+	91731908	91732140
222683971	chr7	91737690	91737862	91737718	91737837	AKAP9	NM_005751	1	50	49	+	91737808	91737947
222683971	chr7	91737690	91737862	91737718	91737837	AKAP9	NM_147185	2	50	49	+	91737808	91737947
225817173	chr7	92244532	92244703	92244554	92244677	CDK6	NM_001145306	1	8	8	-	92234235	92244600
225817173	chr7	92244532	92244703	92244554	92244677	CDK6	NM_001259	2	8	8	-	92234235	92244600
253699548	chr7	92252367	92252491	92252392	92252463	CDK6	NM_001145306	1	8	6	-	92252350	92252400
253699548	chr7	92252367	92252491	92252392	92252463	CDK6	NM_001259	2	8	6	-	92252350	92252400
253671035	chr7	92403939	92404075	92403965	92404049	CDK6	NM_001145306	1	8	3	-	92404010	92404145
253671035	chr7	92403939	92404075	92403965	92404049	CDK6	NM_001259	2	8	3	-	92404010	92404145
227041516	chr7	92462548	92462706	92462569	92462689	CDK6	NM_001145306	1	8	2	-	92462405	92463004
227041516	chr7	92462548	92462706	92462569	92462689	CDK6	NM_001259	2	8	2	-	92462405	92463004
294120449	chr7	92730960	92731091	92730988	92731063	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294120449	chr7	92730960	92731091	92730988	92731063	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294035378	chr7	92731325	92731463	92731353	92731438	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294035378	chr7	92731325	92731463	92731353	92731438	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294078714	chr7	92731771	92731944	92731795	92731923	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294078714	chr7	92731771	92731944	92731795	92731923	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294107291	chr7	92732206	92732363	92732234	92732335	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294107291	chr7	92732206	92732363	92732234	92732335	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295077533	chr7	92732563	92732707	92732590	92732682	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295077533	chr7	92732563	92732707	92732590	92732682	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295047038	chr7	92732919	92733090	92732947	92733062	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295047038	chr7	92732919	92733090	92732947	92733062	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294127471	chr7	92733315	92733440	92733341	92733412	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294127471	chr7	92733315	92733440	92733341	92733412	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294149872	chr7	92733671	92733806	92733695	92733779	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294149872	chr7	92733671	92733806	92733695	92733779	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294092717	chr7	92734081	92734247	92734109	92734220	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294092717	chr7	92734081	92734247	92734109	92734220	SAMD9	NM_017654	2	3	3	-	92728826	92735418
295054327	chr7	92734371	92734513	92734394	92734484	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
295054327	chr7	92734371	92734513	92734394	92734484	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294123642	chr7	92734775	92734947	92734797	92734920	SAMD9	NM_001193307	1	2	2	-	92728826	92735418

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294123642	chr7	92734775	92734947	92734797	92734920	SAMD9	NM_017654	2	3	3	-	92728826	92735418
294164548	chr7	92735178	92735312	92735205	92735286	SAMD9	NM_001193307	1	2	2	-	92728826	92735418
294164548	chr7	92735178	92735312	92735205	92735286	SAMD9	NM_017654	2	3	3	-	92728826	92735418
300630684	chr7	98487833	98487984	98487861	98487959	TRRAP	NM_003496	2	71	4	+	98487958	98488068
300630684	chr7	98487833	98487984	98487861	98487959	TRRAP	NM_001244580	1	72	4	+	98487958	98488068
301514509	chr7	98491329	98491499	98491352	98491481	TRRAP	NM_003496	2	71	6	+	98491421	98491504
301514509	chr7	98491329	98491499	98491352	98491481	TRRAP	NM_001244580	1	72	6	+	98491421	98491504
302042720	chr7	98495356	98495517	98495383	98495489	TRRAP	NM_003496	2	71	8	+	98495364	98495489
302042720	chr7	98495356	98495517	98495383	98495489	TRRAP	NM_001244580	1	72	8	+	98495364	98495489
305443079	chr7	98498132	98498294	98498155	98498270	TRRAP	NM_003496	2	71	11	+	98498247	98498343
305443079	chr7	98498132	98498294	98498155	98498270	TRRAP	NM_001244580	1	72	11	+	98498247	98498343
300550073	chr7	98503757	98503923	98503784	98503897	TRRAP	NM_003496	2	71	13	+	98503800	98503878
300550073	chr7	98503757	98503923	98503784	98503897	TRRAP	NM_001244580	1	72	13	+	98503800	98503878
301107212	chr7	98507752	98507923	98507772	98507902	TRRAP	NM_003496	2	71	15	+	98507679	98508042
301107212	chr7	98507752	98507923	98507772	98507902	TRRAP	NM_001244580	1	72	15	+	98507679	98508042
301949789	chr7	98508027	98508175	98508048	98508151	TRRAP	NM_003496	2	71	16	+	98508133	98508230
301949789	chr7	98508027	98508175	98508048	98508151	TRRAP	NM_001244580	1	72	16	+	98508133	98508230
299910055	chr7	98508839	98509012	98508864	98508984	TRRAP	NM_003496	2	71	17	+	98508700	98508894
299910055	chr7	98508839	98509012	98508864	98508984	TRRAP	NM_001244580	1	72	17	+	98508700	98508894
302649094	chr7	98513388	98513547	98513408	98513521	TRRAP	NM_003496	2	71	19	+	98513346	98513511
302649094	chr7	98513388	98513547	98513408	98513521	TRRAP	NM_001244580	1	72	19	+	98513346	98513511
303543103	chr7	98519308	98519479	98519331	98519457	TRRAP	NM_003496	2	71	21	+	98519376	98519576
303543103	chr7	98519308	98519479	98519331	98519457	TRRAP	NM_001244580	1	72	21	+	98519376	98519576
305970013	chr7	98524713	98524879	98524742	98524858	TRRAP	NM_003496	2	71	23	+	98524790	98524989
305970013	chr7	98524713	98524879	98524742	98524858	TRRAP	NM_001244580	1	72	23	+	98524790	98524989
300555003	chr7	98527683	98527853	98527704	98527830	TRRAP	NM_003496	2	71	24	+	98527612	98527829
300555003	chr7	98527683	98527853	98527704	98527830	TRRAP	NM_001244580	1	72	24	+	98527612	98527829
300077631	chr7	98529084	98529213	98529105	98529191	TRRAP	NM_003496	2	71	26	+	98529028	98529288
300077631	chr7	98529084	98529213	98529105	98529191	TRRAP	NM_001244580	1	72	26	+	98529028	98529288
303583139	chr7	98533113	98533284	98533139	98533262	TRRAP	NM_003496	2	71	28	+	98533202	98533298
303583139	chr7	98533113	98533284	98533139	98533262	TRRAP	NM_001244580	1	72	28	+	98533202	98533298
301753883	chr7	98535162	98535336	98535189	98535313	TRRAP	NM_003496	2	71	30	+	98535273	98535443
301753883	chr7	98535162	98535336	98535189	98535313	TRRAP	NM_001244580	1	72	30	+	98535273	98535443
300900046	chr7	98543354	98543480	98543373	98543452	TRRAP	NM_001244580	1	72	32	+	98543370	98543423
301466556	chr7	98546992	98547116	98547020	98547095	TRRAP	NM_003496	2	71	34	+	98547040	98547204
301466556	chr7	98546992	98547116	98547020	98547095	TRRAP	NM_001244580	1	72	35	+	98547040	98547204
299979189	chr7	98547349	98547521	98547366	98547501	TRRAP	NM_003496	2	71	35	+	98547283	98547464
299979189	chr7	98547349	98547521	98547366	98547501	TRRAP	NM_001244580	1	72	36	+	98547283	98547464
299367199	chr7	98548491	98548651	98548518	98548628	TRRAP	NM_003496	2	71	37	+	98548499	98548627
299367199	chr7	98548491	98548651	98548518	98548628	TRRAP	NM_001244580	1	72	38	+	98548499	98548627
299822840	chr7	98552624	98552749	98552651	98552728	TRRAP	NM_003496	2	71	39	+	98552721	98552927

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
299822840	chr7	98552624	98552749	98552651	98552728	TRRAP	NM_001244580	1	72	40	+	98552721	98552927
301168999	chr7	98553840	98554010	98553861	98553989	TRRAP	NM_003496	2	71	40	+	98553769	98553927
301168999	chr7	98553840	98554010	98553861	98553989	TRRAP	NM_001244580	1	72	41	+	98553769	98553927
300623133	chr7	98556940	98557107	98556960	98557087	TRRAP	NM_003496	2	71	43	+	98556967	98557113
300623133	chr7	98556940	98557107	98556960	98557087	TRRAP	NM_001244580	1	72	44	+	98556967	98557113
301188197	chr7	98559875	98560030	98559894	98560011	TRRAP	NM_003496	2	71	45	+	98559925	98560050
301188197	chr7	98559875	98560030	98559894	98560011	TRRAP	NM_001244580	1	72	46	+	98559925	98560050
305288711	chr7	98563283	98563455	98563303	98563431	TRRAP	NM_003496	2	71	47	+	98563319	98563518
305288711	chr7	98563283	98563455	98563303	98563431	TRRAP	NM_001244580	1	72	48	+	98563319	98563518
301681571	chr7	98565071	98565228	98565091	98565203	TRRAP	NM_003496	2	71	49	+	98565108	98565321
301681571	chr7	98565071	98565228	98565091	98565203	TRRAP	NM_001244580	1	72	50	+	98565108	98565321
300604967	chr7	98569375	98569545	98569399	98569524	TRRAP	NM_003496	2	71	51	+	98569422	98569568
300604967	chr7	98569375	98569545	98569399	98569524	TRRAP	NM_001244580	1	72	52	+	98569422	98569568
301224072	chr7	98574078	98574252	98574102	98574233	TRRAP	NM_003496	2	71	53	+	98574106	98574393
301224072	chr7	98574078	98574252	98574102	98574233	TRRAP	NM_001244580	1	72	54	+	98574106	98574393
305827655	chr7	98574571	98574744	98574592	98574720	TRRAP	NM_003496	2	71	54	+	98574562	98574699
305827655	chr7	98574571	98574744	98574592	98574720	TRRAP	NM_001244580	1	72	55	+	98574562	98574699
299825413	chr7	98579311	98579461	98579337	98579442	TRRAP	NM_003496	2	71	57	+	98579392	98579583
299825413	chr7	98579311	98579461	98579337	98579442	TRRAP	NM_001244580	1	72	58	+	98579392	98579583
300291622	chr7	98580920	98581083	98580941	98581063	TRRAP	NM_003496	2	71	58	+	98580887	98581082
300291622	chr7	98580920	98581083	98580941	98581063	TRRAP	NM_001244580	1	72	59	+	98580887	98581115
300975360	chr7	98581868	98582014	98581895	98581992	TRRAP	NM_003496	2	71	59	+	98581716	98581981
300975360	chr7	98581868	98582014	98581895	98581992	TRRAP	NM_001244580	1	72	60	+	98581716	98581981
304240388	chr7	98586463	98586622	98586482	98586601	TRRAP	NM_003496	2	71	61	+	98586388	98586589
304240388	chr7	98586463	98586622	98586482	98586601	TRRAP	NM_001244580	1	72	62	+	98586388	98586589
303756423	chr7	98589802	98589972	98589823	98589952	TRRAP	NM_003496	2	71	63	+	98589760	98589850
303756423	chr7	98589802	98589972	98589823	98589952	TRRAP	NM_001244580	1	72	64	+	98589760	98589850
299795551	chr7	98592296	98592467	98592318	98592446	TRRAP	NM_003496	2	71	65	+	98592210	98592471
299795551	chr7	98592296	98592467	98592318	98592446	TRRAP	NM_001244580	1	72	66	+	98592210	98592471
300497635	chr7	98601925	98602076	98601948	98602056	TRRAP	NM_003496	2	71	66	+	98601813	98602038
300497635	chr7	98601925	98602076	98601948	98602056	TRRAP	NM_001244580	1	72	67	+	98601813	98602038
299986029	chr7	98605969	98606142	98605987	98606120	TRRAP	NM_003496	2	71	68	+	98606000	98606184
299986029	chr7	98605969	98606142	98605987	98606120	TRRAP	NM_001244580	1	72	69	+	98606000	98606184
304648248	chr7	98608928	98609090	98608952	98609066	TRRAP	NM_003496	2	71	70	+	98608964	98609158
304648248	chr7	98608928	98609090	98608952	98609066	TRRAP	NM_001244580	1	72	71	+	98608964	98609158
306012731	chr7	98609865	98610019	98609883	98610001	TRRAP	NM_003496	2	71	71	+	98609694	98610866
306012731	chr7	98609865	98610019	98609883	98610001	TRRAP	NM_001244580	1	72	72	+	98609694	98610866
272031576	chr7	100402893	100403066	100402915	100403043	EPHB4	NM_004444	1	17	16	-	100402788	100402943
270065220	chr7	100404076	100404220	100404098	100404195	EPHB4	NM_004444	1	17	14	-	100404042	100404191
271674055	chr7	100410392	100410558	100410415	100410536	EPHB4	NM_004444	1	17	12	-	100410369	100410616
271859326	chr7	100411238	100411364	100411260	100411341	EPHB4	NM_004444	1	17	10	-	100411274	100411338

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271682755	chr7	100416078	100416230	100416096	100416212	EPHB4	NM_004444	1	17	7	-	100416142	100416266
271322846	chr7	100417415	100417589	100417432	100417571	EPHB4	NM_004444	1	17	6	-	100417179	100417511
270688615	chr7	100419973	100420135	100419993	100420111	EPHB4	NM_004444	1	17	4	-	100419893	100420289
269700785	chr7	100421313	100421461	100421335	100421443	EPHB4	NM_004444	1	17	3	-	100421266	100421553
294971180	chr7	106507986	106508158	106508003	106508140	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294971293	chr7	106508440	106508604	106508459	106508585	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294997269	chr7	106508890	106509062	106508911	106509042	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294034002	chr7	106509347	106509488	106509368	106509464	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294058203	chr7	106509752	106509896	106509777	106509874	PIK3CG	NM_002649	1	11	2	+	106507995	106510001
294535797	chr7	106513167	106513318	106513195	106513293	PIK3CG	NM_002649	1	11	4	+	106513158	106513383
293941175	chr7	106520034	106520187	106520061	106520160	PIK3CG	NM_002649	1	11	6	+	106519964	106520110
293766834	chr7	106523488	106523640	106523509	106523617	PIK3CG	NM_002649	1	11	8	+	106523478	106523608
294121214	chr7	106526603	106526759	106526627	106526737	PIK3CG	NM_002649	1	11	10	+	106526580	106526737
294638268	chr7	106545730	106545904	106545755	106545876	PIK3CG	NM_002649	1	11	11	+	106545554	106547592
234562684	chr7	116339445	116339610	116339469	116339587	MET	NM_001127500	2	21	2	+	116339125	116340338
234562684	chr7	116339445	116339610	116339469	116339587	MET	NM_000245	1	21	2	+	116339125	116340338
234567815	chr7	116339854	116339987	116339880	116339959	MET	NM_001127500	2	21	2	+	116339125	116340338
234567815	chr7	116339854	116339987	116339880	116339959	MET	NM_000245	1	21	2	+	116339125	116340338
233164695	chr7	116340250	116340420	116340275	116340392	MET	NM_001127500	2	21	2	+	116339125	116340338
233164695	chr7	116340250	116340420	116340275	116340392	MET	NM_000245	1	21	2	+	116339125	116340338
233372842	chr7	116380011	116380183	116380034	116380157	MET	NM_001127500	2	21	4	+	116380004	116380138
233372842	chr7	116380011	116380183	116380034	116380157	MET	NM_000245	1	21	4	+	116380004	116380138
230837406	chr7	116395464	116395621	116395491	116395595	MET	NM_001127500	2	21	6	+	116395409	116395569
230837406	chr7	116395464	116395621	116395491	116395595	MET	NM_000245	1	21	6	+	116395409	116395569
231232247	chr7	116397769	116397915	116397795	116397887	MET	NM_001127500	2	21	8	+	116397692	116397828
231232247	chr7	116397769	116397915	116397795	116397887	MET	NM_000245	1	21	8	+	116397692	116397828
233132382	chr7	116399398	116399572	116399423	116399545	MET	NM_001127500	2	21	10	+	116399391	116399544
233132382	chr7	116399398	116399572	116399423	116399545	MET	NM_000245	1	21	10	+	116399445	116399544
232292902	chr7	116409627	116409796	116409651	116409768	MET	NM_001127500	2	21	12	+	116409699	116409845
232292902	chr7	116409627	116409796	116409651	116409768	MET	NM_000245	1	21	12	+	116409699	116409845
233290267	chr7	116411647	116411790	116411675	116411762	MET	NM_001127500	2	21	13	+	116411552	116411708
233290267	chr7	116411647	116411790	116411675	116411762	MET	NM_000245	1	21	13	+	116411552	116411708
230881645	chr7	116414962	116415099	116414982	116415077	MET	NM_001127500	2	21	15	+	116414935	116415165
230881645	chr7	116414962	116415099	116414982	116415077	MET	NM_000245	1	21	15	+	116414935	116415165
234187817	chr7	116418899	116419063	116418919	116419041	MET	NM_001127500	2	21	17	+	116418830	116419011
234187817	chr7	116418899	116419063	116418919	116419041	MET	NM_000245	1	21	17	+	116418830	116419011
233314485	chr7	116435660	116435810	116435684	116435783	MET	NM_001127500	2	21	20	+	116435709	116435845
233314485	chr7	116435660	116435810	116435684	116435783	MET	NM_000245	1	21	20	+	116435709	116435845
234563384	chr7	116436055	116436205	116436080	116436178	MET	NM_001127500	2	21	21	+	116435941	116438440
234563384	chr7	116436055	116436205	116436080	116436178	MET	NM_000245	1	21	21	+	116435941	116438440
294848776	chr7	124467262	124467403	124467290	124467375	POT1	NR_003103	4	18	16	-	124467268	124467359

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294848776	chr7	124467262	124467403	124467290	124467375	POT1	NR_003104	5	20	18	-	124467268	124467359
294848776	chr7	124467262	124467403	124467290	124467375	POT1	NR_003102	3	20	18	-	124467268	124467359
294848776	chr7	124467262	124467403	124467290	124467375	POT1	NM_001042594	1	18	16	-	124467268	124467359
294848776	chr7	124467262	124467403	124467290	124467375	POT1	NM_015450	2	19	17	-	124467268	124467359
293933059	chr7	124481041	124481173	124481065	124481146	POT1	NR_003103	4	18	14	-	124481027	124481232
293933059	chr7	124481041	124481173	124481065	124481146	POT1	NR_003104	5	20	14	-	124481027	124481232
293933059	chr7	124481041	124481173	124481065	124481146	POT1	NR_003102	3	20	15	-	124481027	124481232
293933059	chr7	124481041	124481173	124481065	124481146	POT1	NM_001042594	1	18	13	-	124481027	124481232
293933059	chr7	124481041	124481173	124481065	124481146	POT1	NM_015450	2	19	14	-	124481027	124481232
294180913	chr7	124482936	124483089	124482957	124483066	POT1	NR_003103	4	18	13	-	124482861	124483017
294180913	chr7	124482936	124483089	124482957	124483066	POT1	NR_003104	5	20	13	-	124482861	124483017
294180913	chr7	124482936	124483089	124482957	124483066	POT1	NR_003102	3	20	14	-	124482861	124483017
294180913	chr7	124482936	124483089	124482957	124483066	POT1	NM_001042594	1	18	12	-	124482861	124483017
294180913	chr7	124482936	124483089	124482957	124483066	POT1	NM_015450	2	19	13	-	124482861	124483017
294422316	chr7	124493041	124493168	124493067	124493140	POT1	NR_003103	4	18	10	-	124493026	124493192
294422316	chr7	124493041	124493168	124493067	124493140	POT1	NR_003104	5	20	10	-	124493026	124493192
294422316	chr7	124493041	124493168	124493067	124493140	POT1	NR_003102	3	20	10	-	124493026	124493192
294422316	chr7	124493041	124493168	124493067	124493140	POT1	NM_001042594	1	18	9	-	124493026	124493192
294422316	chr7	124493041	124493168	124493067	124493140	POT1	NM_015450	2	19	10	-	124493026	124493192
293861257	chr7	124503347	124503513	124503375	124503485	POT1	NR_003103	4	18	8	-	124503404	124503694
293861257	chr7	124503347	124503513	124503375	124503485	POT1	NR_003104	5	20	8	-	124503404	124503694
293861257	chr7	124503347	124503513	124503375	124503485	POT1	NR_003102	3	20	8	-	124503404	124503694
293861257	chr7	124503347	124503513	124503375	124503485	POT1	NM_001042594	1	18	7	-	124503404	124503694
293861257	chr7	124503347	124503513	124503375	124503485	POT1	NM_015450	2	19	8	-	124503404	124503694
294000233	chr7	124510972	124511106	124511000	124511079	POT1	NR_003103	4	18	7	-	124510965	124511095
294000233	chr7	124510972	124511106	124511000	124511079	POT1	NR_003104	5	20	7	-	124510965	124511095
294000233	chr7	124510972	124511106	124511000	124511079	POT1	NR_003102	3	20	7	-	124510965	124511095
294000233	chr7	124510972	124511106	124511000	124511079	POT1	NM_015450	2	19	7	-	124510965	124511095
294118650	chr7	124532375	124532536	124532403	124532506	POT1	NR_003103	4	18	6	-	124532320	124532434
294118650	chr7	124532375	124532536	124532403	124532506	POT1	NR_003104	5	20	6	-	124532320	124532434
294118650	chr7	124532375	124532536	124532403	124532506	POT1	NR_003102	3	20	6	-	124532320	124532434
294118650	chr7	124532375	124532536	124532403	124532506	POT1	NM_001042594	1	18	6	-	124532320	124532434
294118650	chr7	124532375	124532536	124532403	124532506	POT1	NM_015450	2	19	6	-	124532320	124532434
294589882	chr7	126086145	126086300	126086167	126086279	GRM8	NR_028041	3	11	10	-	126086180	126086426
294589882	chr7	126086145	126086300	126086167	126086279	GRM8	NM_000845	1	10	9	-	126086180	126086426
294589882	chr7	126086145	126086300	126086167	126086279	GRM8	NM_001127323	2	11	10	-	126086125	126086426
293760490	chr7	126173013	126173158	126173034	126173132	GRM8	NR_028041	3	11	9	-	126173006	126173941
293760490	chr7	126173013	126173158	126173034	126173132	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293760490	chr7	126173013	126173158	126173034	126173132	GRM8	NM_000845	1	10	8	-	126173006	126173941
293797228	chr7	126173459	126173633	126173481	126173611	GRM8	NR_028041	3	11	9	-	126173006	126173941
293797228	chr7	126173459	126173633	126173481	126173611	GRM8	NM_001127323	2	11	9	-	126173006	126173941

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293797228	chr7	126173459	126173633	126173481	126173611	GRM8	NM_000845	1	10	8	-	126173006	126173941
293838190	chr7	126173893	126174019	126173912	126173994	GRM8	NR_028041	3	11	9	-	126173006	126173941
293838190	chr7	126173893	126174019	126173912	126173994	GRM8	NM_001127323	2	11	9	-	126173006	126173941
293838190	chr7	126173893	126174019	126173912	126173994	GRM8	NM_000845	1	10	8	-	126173006	126173941
293844588	chr7	126409946	126410110	126409972	126410083	GRM8	NR_028041	3	11	6	-	126409919	126410119
293844588	chr7	126409946	126410110	126409972	126410083	GRM8	NM_001127323	2	11	7	-	126409919	126410119
293844588	chr7	126409946	126410110	126409972	126410083	GRM8	NM_000845	1	10	6	-	126409919	126410119
294597046	chr7	126544121	126544284	126544143	126544257	GRM8	NR_028041	3	11	4	-	126544026	126544180
294597046	chr7	126544121	126544284	126544143	126544257	GRM8	NM_001127323	2	11	5	-	126544026	126544180
294597046	chr7	126544121	126544284	126544143	126544257	GRM8	NM_000845	1	10	4	-	126544026	126544180
293914297	chr7	126746686	126746819	126746710	126746793	GRM8	NR_028041	3	11	2	-	126746550	126746766
293914297	chr7	126746686	126746819	126746710	126746793	GRM8	NM_001127323	2	11	3	-	126746550	126746766
293914297	chr7	126746686	126746819	126746710	126746793	GRM8	NM_000845	1	10	2	-	126746550	126746766
295256038	chr7	126882987	126883160	126883011	126883138	GRM8	NR_028041	3	11	1	-	126882749	126883569
295256038	chr7	126882987	126883160	126883011	126883138	GRM8	NM_001127323	2	11	2	-	126882749	126883569
295256038	chr7	126882987	126883160	126883011	126883138	GRM8	NM_000845	1	10	1	-	126882749	126883569
238670567	chr7	128843166	128843338	128843184	128843321	SMO	NM_005631	1	12	2	+	128843225	128843430
262603904	chr7	128845167	128845322	128845187	128845302	SMO	NM_005631	1	12	3	+	128845044	128845253
238195566	chr7	128846060	128846234	128846083	128846212	SMO	NM_005631	1	12	5	+	128845991	128846210
239725368	chr7	128849091	128849257	128849110	128849239	SMO	NM_005631	1	12	8	+	128849130	128849238
242210853	chr7	128850853	128851022	128850875	128851002	SMO	NM_005631	1	12	10	+	128850806	128850954
241167943	chr7	128851874	128852043	128851894	128852022	SMO	NM_005631	1	12	12	+	128851865	128853385
273201713	chr7	138145435	138145571	138145452	138145553	TRIM24	NM_015905	2	19	1	+	138145079	138145657
273201713	chr7	138145435	138145571	138145452	138145553	TRIM24	NM_003852	1	19	1	+	138145079	138145657
273446829	chr7	138199879	138200053	138199903	138200030	TRIM24	NM_015905	2	19	3	+	138199957	138200104
273446829	chr7	138199879	138200053	138199903	138200030	TRIM24	NM_003852	1	19	3	+	138199957	138200104
273159061	chr7	138213827	138213998	138213850	138213975	TRIM24	NM_015905	2	19	6	+	138213861	138213975
273159061	chr7	138213827	138213998	138213850	138213975	TRIM24	NM_003852	1	19	6	+	138213861	138213975
273238145	chr7	138235847	138235974	138235867	138235946	TRIM24	NM_015905	2	19	8	+	138235808	138235925
273238145	chr7	138235847	138235974	138235867	138235946	TRIM24	NM_003852	1	19	8	+	138235808	138235925
273663154	chr7	138252116	138252287	138252144	138252265	TRIM24	NM_015905	2	19	10	+	138252226	138252399
273663154	chr7	138252116	138252287	138252144	138252265	TRIM24	NM_003852	1	19	10	+	138252226	138252399
273630597	chr7	138255632	138255794	138255652	138255766	TRIM24	NM_015905	2	19	11	+	138255575	138255748
273630597	chr7	138255632	138255794	138255652	138255766	TRIM24	NM_003852	1	19	11	+	138255575	138255748
272913141	chr7	138262144	138262272	138262171	138262251	TRIM24	NM_015905	2	19	14	+	138262165	138262333
272913141	chr7	138262144	138262272	138262171	138262251	TRIM24	NM_003852	1	19	14	+	138262165	138262333
273611626	chr7	138264064	138264207	138264088	138264186	TRIM24	NM_015905	2	19	15	+	138263949	138264277
273611626	chr7	138264064	138264207	138264088	138264186	TRIM24	NM_003852	1	19	15	+	138263949	138264277
273674754	chr7	138266343	138266488	138266365	138266462	TRIM24	NM_015905	2	19	17	+	138266442	138266516
273674754	chr7	138266343	138266488	138266365	138266462	TRIM24	NM_003852	1	19	17	+	138266442	138266516
273270976	chr7	138269386	138269512	138269415	138269488	TRIM24	NM_015905	2	19	19	+	138269487	138270332

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273270976	chr7	138269386	138269512	138269415	138269488	TRIM24	NM_003852	1	19	19	+	138269487	138270332
222635553	chr7	140434425	140434574	140434445	140434549	BRAF	NM_004333	1	18	18	-	140433813	140434570
223177865	chr7	140449163	140449303	140449191	140449274	BRAF	NM_004333	1	18	16	-	140449087	140449218
223960162	chr7	140476622	140476791	140476647	140476763	BRAF	NM_004333	1	18	13	-	140476712	140476888
326889377	chr7	140481273	140481418	140481298	140481391	BRAF	NM_004333	1	18	11	-	140481376	140481493
223588249	chr7	140487269	140487440	140487296	140487412	BRAF	NM_004333	1	18	9	-	140487348	140487384
223708886	chr7	140500192	140500321	140500215	140500294	BRAF	NM_004333	1	18	7	-	140500162	140500281
222259284	chr7	140507759	140507892	140507785	140507865	BRAF	NM_004333	1	18	5	-	140507760	140507862
222903910	chr7	140534401	140534551	140534422	140534524	BRAF	NM_004333	1	18	3	-	140534409	140534672
223104608	chr7	140549929	140550103	140549952	140550074	BRAF	NM_004333	1	18	2	-	140549911	140550012
269890290	chr7	142561359	142561491	142561382	142561468	EPHB6	NM_004445	1	20	6	+	142561389	142561453
271212458	chr7	142561930	142562056	142561951	142562036	EPHB6	NM_004445	1	20	7	+	142561724	142562504
272599539	chr7	142562357	142562531	142562378	142562512	EPHB6	NM_004445	1	20	7	+	142561724	142562504
271798176	chr7	142563809	142563952	142563830	142563930	EPHB6	NM_004445	1	20	9	+	142563715	142564071
271524137	chr7	142564279	142564418	142564298	142564397	EPHB6	NM_004445	1	20	10	+	142564236	142564360
269654623	chr7	142565378	142565533	142565399	142565510	EPHB6	NM_004445	1	20	12	+	142565363	142565477
270712427	chr7	142566218	142566392	142566239	142566373	EPHB6	NM_004445	1	20	15	+	142566247	142566494
269938245	chr7	142567563	142567687	142567580	142567662	EPHB6	NM_004445	1	20	17	+	142567570	142567719
272256598	chr7	142568090	142568231	142568111	142568204	EPHB6	NM_004445	1	20	18	+	142567967	142568160
227858973	chr7	148504649	148504823	148504676	148504798	EZH2	NM_001203248	2	20	20	-	148504464	148504798
227858973	chr7	148504649	148504823	148504676	148504798	EZH2	NM_152998	5	19	19	-	148504464	148504798
227858973	chr7	148504649	148504823	148504676	148504798	EZH2	NM_001203247	1	20	20	-	148504464	148504798
227858973	chr7	148504649	148504823	148504676	148504798	EZH2	NM_001203249	3	19	19	-	148504464	148504798
227858973	chr7	148504649	148504823	148504676	148504798	EZH2	NM_004456	4	20	20	-	148504464	148504798
228766607	chr7	148508686	148508812	148508710	148508789	EZH2	NM_001203248	2	20	16	-	148508717	148508812
228766607	chr7	148508686	148508812	148508710	148508789	EZH2	NM_152998	5	19	15	-	148508717	148508812
228766607	chr7	148508686	148508812	148508710	148508789	EZH2	NM_001203247	1	20	16	-	148508717	148508812
228766607	chr7	148508686	148508812	148508710	148508789	EZH2	NM_001203249	3	19	15	-	148508717	148508812
228766607	chr7	148508686	148508812	148508710	148508789	EZH2	NM_004456	4	20	16	-	148508717	148508812
231493730	chr7	148511977	148512129	148512002	148512102	EZH2	NM_001203248	2	20	14	-	148512006	148512131
231493730	chr7	148511977	148512129	148512002	148512102	EZH2	NM_152998	5	19	13	-	148512006	148512131
231493730	chr7	148511977	148512129	148512002	148512102	EZH2	NM_001203247	1	20	14	-	148512006	148512131
231493730	chr7	148511977	148512129	148512002	148512102	EZH2	NM_004456	4	20	14	-	148512006	148512131
228394031	chr7	148514241	148514392	148514269	148514363	EZH2	NM_001203248	2	20	11	-	148514314	148514483
228394031	chr7	148514241	148514392	148514269	148514363	EZH2	NM_152998	5	19	10	-	148514314	148514483
228394031	chr7	148514241	148514392	148514269	148514363	EZH2	NM_001203247	1	20	11	-	148514314	148514483
228394031	chr7	148514241	148514392	148514269	148514363	EZH2	NM_001203249	3	19	11	-	148514314	148514483
228394031	chr7	148514241	148514392	148514269	148514363	EZH2	NM_004456	4	20	11	-	148514314	148514483
228995216	chr7	148515064	148515238	148515090	148515211	EZH2	NM_001203248	2	20	10	-	148514969	148515209
228995216	chr7	148515064	148515238	148515090	148515211	EZH2	NM_152998	5	19	9	-	148514969	148515209
228995216	chr7	148515064	148515238	148515090	148515211	EZH2	NM_001203247	1	20	10	-	148514969	148515209

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228995216	chr7	148515064	148515238	148515090	148515211	EZH2	NM_001203249	3	19	10	-	148514969	148515209
228995216	chr7	148515064	148515238	148515090	148515211	EZH2	NM_004456	4	20	10	-	148514969	148515209
230199961	chr7	148523570	148523731	148523598	148523702	EZH2	NM_001203248	2	20	8	-	148523561	148523724
230199961	chr7	148523570	148523731	148523598	148523702	EZH2	NM_152998	5	19	7	-	148523561	148523724
230199961	chr7	148523570	148523731	148523598	148523702	EZH2	NM_001203247	1	20	8	-	148523561	148523724
230199961	chr7	148523570	148523731	148523598	148523702	EZH2	NM_001203249	3	19	8	-	148523561	148523724
230199961	chr7	148523570	148523731	148523598	148523702	EZH2	NM_004456	4	20	8	-	148523546	148523724
230544561	chr7	148525870	148526025	148525896	148525997	EZH2	NM_001203248	2	20	6	-	148525832	148525972
230544561	chr7	148525870	148526025	148525896	148525997	EZH2	NM_152998	5	19	5	-	148525832	148525972
230544561	chr7	148525870	148526025	148525896	148525997	EZH2	NM_001203247	1	20	6	-	148525832	148525972
230544561	chr7	148525870	148526025	148525896	148525997	EZH2	NM_001203249	3	19	6	-	148525832	148525972
230544561	chr7	148525870	148526025	148525896	148525997	EZH2	NM_004456	4	20	6	-	148525832	148525972
231128421	chr7	148529744	148529906	148529769	148529882	EZH2	NM_001203248	2	20	4	-	148529726	148529842
231128421	chr7	148529744	148529906	148529769	148529882	EZH2	NM_001203247	1	20	4	-	148529726	148529842
231128421	chr7	148529744	148529906	148529769	148529882	EZH2	NM_001203249	3	19	4	-	148529726	148529842
231128421	chr7	148529744	148529906	148529769	148529882	EZH2	NM_004456	4	20	4	-	148529726	148529842
230779586	chr7	148544356	148544481	148544379	148544455	EZH2	NM_001203248	2	20	2	-	148544274	148544397
230779586	chr7	148544356	148544481	148544379	148544455	EZH2	NM_152998	5	19	2	-	148544274	148544397
230779586	chr7	148544356	148544481	148544379	148544455	EZH2	NM_001203247	1	20	2	-	148544274	148544397
230779586	chr7	148544356	148544481	148544379	148544455	EZH2	NM_001203249	3	19	2	-	148544274	148544397
230779586	chr7	148544356	148544481	148544379	148544455	EZH2	NM_004456	4	20	2	-	148544274	148544397
273241257	chr7	151836661	151836832	151836686	151836807	MLL3	NM_170606	1	59	56	-	151836760	151836876
273208773	chr7	151842136	151842286	151842157	151842262	MLL3	NM_170606	1	59	54	-	151842238	151842380
273050992	chr7	151845077	151845250	151845100	151845229	MLL3	NM_170606	1	59	52	-	151845118	151846237
273129202	chr7	151845535	151845709	151845557	151845688	MLL3	NM_170606	1	59	52	-	151845118	151846237
274197231	chr7	151846005	151846178	151846025	151846154	MLL3	NM_170606	1	59	52	-	151845118	151846237
273581285	chr7	151848437	151848606	151848461	151848581	MLL3	NM_170606	1	59	50	-	151848527	151848666
274052725	chr7	151849916	151850076	151849939	151850049	MLL3	NM_170606	1	59	49	-	151849790	151850039
273092002	chr7	151851307	151851449	151851335	151851426	MLL3	NM_170606	1	59	47	-	151851352	151851530
274369973	chr7	151853104	151853241	151853126	151853215	MLL3	NM_170606	1	59	46	-	151852995	151853142
273395823	chr7	151856054	151856226	151856073	151856198	MLL3	NM_170606	1	59	44	-	151855948	151856157
274542821	chr7	151859414	151859581	151859439	151859553	MLL3	NM_170606	1	59	43	-	151859202	151860911
274547317	chr7	151859804	151859976	151859828	151859951	MLL3	NM_170606	1	59	43	-	151859202	151860911
274567805	chr7	151860258	151860409	151860283	151860383	MLL3	NM_170606	1	59	43	-	151859202	151860911
273625285	chr7	151860658	151860795	151860681	151860774	MLL3	NM_170606	1	59	43	-	151859202	151860911
273808856	chr7	151864281	151864452	151864305	151864429	MLL3	NM_170606	1	59	42	-	151864231	151864463
273353908	chr7	151871164	151871294	151871191	151871267	MLL3	NM_170606	1	59	39	-	151871216	151871327
274290898	chr7	151873454	151873617	151873476	151873589	MLL3	NM_170606	1	59	38	-	151873276	151875095
273348830	chr7	151873843	151873968	151873867	151873943	MLL3	NM_170606	1	59	38	-	151873276	151875095
273367532	chr7	151874122	151874289	151874150	151874261	MLL3	NM_170606	1	59	38	-	151873276	151875095
273327612	chr7	151874516	151874680	151874541	151874659	MLL3	NM_170606	1	59	38	-	151873276	151875095

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274294288	chr7	151874949	151875096	151874978	151875070	MLL3	NM_170606	1	59	38	-	151873276	151875095
273003937	chr7	151877084	151877258	151877106	151877230	MLL3	NM_170606	1	59	37	-	151876919	151877211
273864900	chr7	151878079	151878253	151878103	151878227	MLL3	NM_170606	1	59	36	-	151877796	151879679
273865504	chr7	151878486	151878645	151878509	151878623	MLL3	NM_170606	1	59	36	-	151877796	151879679
273872082	chr7	151878929	151879080	151878950	151879054	MLL3	NM_170606	1	59	36	-	151877796	151879679
273860266	chr7	151879390	151879531	151879415	151879509	MLL3	NM_170606	1	59	36	-	151877796	151879679
273834567	chr7	151880077	151880235	151880106	151880213	MLL3	NM_170606	1	59	35	-	151880059	151880241
273702065	chr7	151884435	151884568	151884456	151884543	MLL3	NM_170606	1	59	33	-	151884347	151884561
273254136	chr7	151884871	151884996	151884893	151884967	MLL3	NM_170606	1	59	32	-	151884800	151884932
273010461	chr7	151891535	151891667	151891562	151891638	MLL3	NM_170606	1	59	29	-	151891525	151891653
272911558	chr7	151896355	151896479	151896382	151896456	MLL3	NM_170606	1	59	27	-	151896364	151896544
273303014	chr7	151900029	151900174	151900055	151900146	MLL3	NM_170606	1	59	26	-	151900019	151900149
273264587	chr7	151917607	151917734	151917631	151917706	MLL3	NM_170606	1	59	23	-	151917608	151917820
273648404	chr7	151927239	151927378	151927265	151927350	MLL3	NM_170606	1	59	17	-	151927305	151927406
273461041	chr7	151945029	151945153	151945052	151945133	MLL3	NM_170606	1	59	14	-	151944987	151945705
274351964	chr7	151945486	151945641	151945512	151945613	MLL3	NM_170606	1	59	14	-	151944987	151945705
274570497	chr7	151947977	151948151	151948002	151948123	MLL3	NM_170606	1	59	12	-	151947938	151948051
272928598	chr7	151949671	151949800	151949696	151949772	MLL3	NM_170606	1	59	10	-	151949631	151949800
273752064	chr7	151962165	151962296	151962190	151962274	MLL3	NM_170606	1	59	8	-	151962123	151962294
273715183	chr7	152008838	152008971	152008864	152008946	MLL3	NM_170606	1	59	5	-	152008883	152009031
274407104	chr7	152027659	152027828	152027682	152027801	MLL3	NM_170606	1	59	3	-	152027686	152027824
293853803	chr7	152345690	152345864	152345712	152345839	XRCC2	NM_005431	1	3	3	-	152343587	152346448
294972858	chr7	152346143	152346308	152346172	152346282	XRCC2	NM_005431	1	3	3	-	152343587	152346448
294669874	chr7	152373085	152373239	152373107	152373219	XRCC2	NM_005431	1	3	1	-	152373126	152373250
241445317	chr8	30921795	30921926	30921823	30921899	WRN	NM_000553	1	35	4	+	30921805	30921950
239084035	chr8	30922505	30922662	30922533	30922629	WRN	NM_000553	1	35	5	+	30922431	30922579
265753258	chr8	30925661	30925832	30925683	30925808	WRN	NM_000553	1	35	7	+	30925774	30925843
240004731	chr8	30938307	30938475	30938335	30938450	WRN	NM_000553	1	35	9	+	30938383	30938812
240029170	chr8	30938704	30938834	30938733	30938806	WRN	NM_000553	1	35	9	+	30938383	30938812
262093424	chr8	30946419	30946555	30946441	30946530	WRN	NM_000553	1	35	13	+	30946406	30946481
239542949	chr8	30954172	30954329	30954205	30954301	WRN	NM_000553	1	35	17	+	30954284	30954366
264527360	chr8	30969176	30969312	30969204	30969288	WRN	NM_000553	1	35	19	+	30969131	30969315
262271608	chr8	30977645	30977818	30977668	30977794	WRN	NM_000553	1	35	21	+	30977759	30977940
238920328	chr8	30982036	30982210	30982063	30982182	WRN	NM_000553	1	35	22	+	30982038	30982139
264616739	chr8	30989926	30990097	30989951	30990069	WRN	NM_000553	1	35	24	+	30989881	30990022
262577279	chr8	30999124	30999275	30999146	30999246	WRN	NM_000553	1	35	26	+	30999197	30999291
242324749	chr8	31001053	31001222	31001082	31001194	WRN	NM_000553	1	35	28	+	31001066	31001139
264785472	chr8	31004924	31005090	31004950	31005062	WRN	NM_000553	1	35	30	+	31004880	31004992
241851452	chr8	31014782	31014956	31014809	31014935	WRN	NM_000553	1	35	33	+	31014884	31015046
239411065	chr8	31024640	31024802	31024666	31024774	WRN	NM_000553	1	35	34	+	31024538	31024746
228266355	chr8	37654774	37654923	37654792	37654906	GPR124	NM_032777	1	19	1	+	37654401	37655052

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227240187	chr8	37686284	37686439	37686306	37686417	GPR124	NM_032777	1	19	3	+	37686406	37686477
229776979	chr8	37687331	37687474	37687350	37687453	GPR124	NM_032777	1	19	6	+	37687369	37687532
228123523	chr8	37688897	37689058	37688914	37689040	GPR124	NM_032777	1	19	8	+	37688941	37689105
227673321	chr8	37690668	37690799	37690691	37690779	GPR124	NM_032777	1	19	9	+	37690528	37690726
229082232	chr8	37691499	37691666	37691517	37691646	GPR124	NM_032777	1	19	11	+	37691485	37691646
227129353	chr8	37693034	37693203	37693054	37693185	GPR124	NM_032777	1	19	13	+	37693072	37693288
229081028	chr8	37695287	37695457	37695304	37695439	GPR124	NM_032777	1	19	14	+	37695249	37695457
228837269	chr8	37696986	37697160	37697010	37697140	GPR124	NM_032777	1	19	16	+	37697017	37697140
227505112	chr8	37698575	37698729	37698597	37698711	GPR124	NM_032777	1	19	19	+	37698604	37701504
227508959	chr8	37699045	37699178	37699067	37699161	GPR124	NM_032777	1	19	19	+	37698604	37701504
227560128	chr8	37699681	37699805	37699698	37699786	GPR124	NM_032777	1	19	19	+	37698604	37701504
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_001174066	4	17	17	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_001174065	3	18	18	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_001174063	1	18	18	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_023110	9	18	18	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_023106	8	17	17	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_023105	7	17	17	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_015850	6	18	18	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_001174067	5	19	19	-	38268656	38271322
230396934	chr8	38271216	38271342	38271238	38271322	FGFR1	NM_001174064	2	19	19	-	38268656	38271322
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_001174066	4	17	14	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_001174065	3	18	15	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_001174063	1	18	15	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_023110	9	18	15	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_023106	8	17	14	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_023105	7	17	14	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_015850	6	18	15	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_001174067	5	19	16	-	38272077	38272147
230095797	chr8	38271977	38272144	38271999	38272123	FGFR1	NM_001174064	2	19	16	-	38272077	38272147
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_001174066	4	17	12	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_001174065	3	18	13	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_001174063	1	18	13	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_023110	9	18	13	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_023106	8	17	12	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_023105	7	17	12	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_015850	6	18	13	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_001174067	5	19	14	-	38273388	38273578
228261037	chr8	38273342	38273503	38273362	38273481	FGFR1	NM_001174064	2	19	14	-	38273388	38273578
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_001174066	4	17	10	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_001174065	3	18	11	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_001174063	1	18	11	-	38275388	38275509

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_023110	9	18	11	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_023106	8	17	10	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_023105	7	17	10	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_015850	6	18	11	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_001174067	5	19	12	-	38275388	38275509
231772711	chr8	38275333	38275466	38275354	38275446	FGFR1	NM_001174064	2	19	12	-	38275388	38275509
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_001174063	1	18	9	-	38277057	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_001174064	2	19	10	-	38277057	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_001174066	4	17	8	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_001174065	3	18	9	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_023110	9	18	9	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_023106	8	17	8	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_023105	7	17	8	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_015850	6	18	9	-	38277051	38277253
229700862	chr8	38277024	38277161	38277046	38277140	FGFR1	NM_001174067	5	19	10	-	38277051	38277253
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_001174066	4	17	6	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_001174065	3	18	7	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_001174063	1	18	7	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_023110	9	18	7	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_023106	8	17	6	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_023105	7	17	6	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_015850	6	18	7	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_001174067	5	19	8	-	38282027	38282217
229184746	chr8	38281991	38282154	38282011	38282132	FGFR1	NM_001174064	2	19	8	-	38282027	38282217
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_001174066	4	17	4	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_001174065	3	18	5	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_001174063	1	18	5	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_023110	9	18	5	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_023106	8	17	4	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_023105	7	17	4	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_015850	6	18	5	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_001174067	5	19	6	-	38285439	38285611
228278153	chr8	38285392	38285538	38285415	38285515	FGFR1	NM_001174064	2	19	6	-	38285439	38285611
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_001174065	3	18	3	-	38287200	38287466
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_001174063	1	18	3	-	38287200	38287466
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_023110	9	18	3	-	38287200	38287466
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_015850	6	18	3	-	38287200	38287466
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_001174067	5	19	4	-	38287200	38287466
227977149	chr8	38287212	38287382	38287234	38287361	FGFR1	NM_001174064	2	19	4	-	38287200	38287466
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_001174066	4	17	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_001174065	3	18	2	-	38314874	38315052

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_001174063	1	18	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_023110	9	18	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_023106	8	17	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_023105	7	17	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_015850	6	18	2	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_001174067	5	19	3	-	38314874	38315052
329435470	chr8	38314784	38314956	38314804	38314935	FGFR1	NM_001174064	2	19	2	-	38314874	38315052
312166422	chr8	41789640	41789792	41789665	41789770	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312166422	chr8	41789640	41789792	41789665	41789770	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312166422	chr8	41789640	41789792	41789665	41789770	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312183495	chr8	41790016	41790176	41790039	41790154	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312183495	chr8	41790016	41790176	41790039	41790154	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312183495	chr8	41790016	41790176	41790039	41790154	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312625899	chr8	41790472	41790638	41790492	41790619	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312625899	chr8	41790472	41790638	41790492	41790619	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312625899	chr8	41790472	41790638	41790492	41790619	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312350980	chr8	41791104	41791230	41791125	41791210	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312350980	chr8	41791104	41791230	41791125	41791210	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312350980	chr8	41791104	41791230	41791125	41791210	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312629215	chr8	41791545	41791707	41791565	41791683	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312629215	chr8	41791545	41791707	41791565	41791683	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312629215	chr8	41791545	41791707	41791565	41791683	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312316549	chr8	41791928	41792089	41791948	41792072	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312316549	chr8	41791928	41792089	41791948	41792072	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312316549	chr8	41791928	41792089	41791948	41792072	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312381093	chr8	41792304	41792460	41792327	41792434	KAT6A	NM_001099412	1	18	18	-	41786997	41792385
312381093	chr8	41792304	41792460	41792327	41792434	KAT6A	NM_006766	3	17	17	-	41786997	41792385
312381093	chr8	41792304	41792460	41792327	41792434	KAT6A	NM_001099413	2	18	18	-	41786997	41792385
312364906	chr8	41794984	41795135	41795010	41795102	KAT6A	NM_001099412	1	18	17	-	41794774	41795086
312364906	chr8	41794984	41795135	41795010	41795102	KAT6A	NM_006766	3	17	16	-	41794774	41795086
312364906	chr8	41794984	41795135	41795010	41795102	KAT6A	NM_001099413	2	18	17	-	41794774	41795086
312418056	chr8	41798565	41798732	41798586	41798711	KAT6A	NM_001099412	1	18	16	-	41798360	41798962
312418056	chr8	41798565	41798732	41798586	41798711	KAT6A	NM_006766	3	17	15	-	41798360	41798962
312418056	chr8	41798565	41798732	41798586	41798711	KAT6A	NM_001099413	2	18	16	-	41798360	41798962
312448965	chr8	41800290	41800464	41800316	41800441	KAT6A	NM_001099412	1	18	15	-	41800311	41800518
312448965	chr8	41800290	41800464	41800316	41800441	KAT6A	NM_006766	3	17	14	-	41800311	41800518
312448965	chr8	41800290	41800464	41800316	41800441	KAT6A	NM_001099413	2	18	15	-	41800311	41800518
312378979	chr8	41801410	41801542	41801435	41801516	KAT6A	NM_001099412	1	18	14	-	41801266	41801497
312378979	chr8	41801410	41801542	41801435	41801516	KAT6A	NM_006766	3	17	13	-	41801266	41801497
312378979	chr8	41801410	41801542	41801435	41801516	KAT6A	NM_001099413	2	18	14	-	41801266	41801497
312351544	chr8	41806686	41806815	41806709	41806791	KAT6A	NM_001099412	1	18	11	-	41806740	41806881

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312351544	chr8	41806686	41806815	41806709	41806791	KAT6A	NM_006766	3	17	10	-	41806740	41806881
312351544	chr8	41806686	41806815	41806709	41806791	KAT6A	NM_001099413	2	18	11	-	41806740	41806881
312465149	chr8	41832134	41832286	41832164	41832258	KAT6A	NM_001099412	1	18	9	-	41832222	41832340
312465149	chr8	41832134	41832286	41832164	41832258	KAT6A	NM_006766	3	17	8	-	41832222	41832340
312465149	chr8	41832134	41832286	41832164	41832258	KAT6A	NM_001099413	2	18	9	-	41832222	41832340
312439552	chr8	41834648	41834775	41834670	41834751	KAT6A	NM_001099412	1	18	8	-	41834526	41834845
312439552	chr8	41834648	41834775	41834670	41834751	KAT6A	NM_006766	3	17	7	-	41834526	41834845
312439552	chr8	41834648	41834775	41834670	41834751	KAT6A	NM_001099413	2	18	8	-	41834526	41834845
312255016	chr8	41838302	41838427	41838328	41838403	KAT6A	NM_001099412	1	18	6	-	41838364	41838445
312255016	chr8	41838302	41838427	41838328	41838403	KAT6A	NM_006766	3	17	5	-	41838364	41838445
312255016	chr8	41838302	41838427	41838328	41838403	KAT6A	NM_001099413	2	18	6	-	41838364	41838445
312477388	chr8	41905860	41906029	41905884	41906008	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312477388	chr8	41905860	41906029	41905884	41906008	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312477388	chr8	41905860	41906029	41905884	41906008	KAT6A	NM_001099413	2	18	3	-	41905896	41906820
312478655	chr8	41906322	41906464	41906350	41906441	KAT6A	NM_001099412	1	18	3	-	41905896	41906820
312478655	chr8	41906322	41906464	41906350	41906441	KAT6A	NM_006766	3	17	2	-	41905896	41906820
312478655	chr8	41906322	41906464	41906350	41906441	KAT6A	NM_001099413	2	18	3	-	41905896	41906820
280911485	chr8	42129662	42129804	42129683	42129782	IKBKB	NM_001242778	2	21	2	+	42129601	42129723
280911485	chr8	42129662	42129804	42129683	42129782	IKBKB	NR_033819	5	21	2	+	42129601	42129723
280911485	chr8	42129662	42129804	42129683	42129782	IKBKB	NR_033818	4	22	2	+	42129601	42129723
280911485	chr8	42129662	42129804	42129683	42129782	IKBKB	NM_001556	3	22	2	+	42129601	42129723
280911485	chr8	42129662	42129804	42129683	42129782	IKBKB	NR_040009	6	22	2	+	42129601	42129723
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NR_033818	4	22	5	+	42150961	42151086
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NM_001242778	2	21	4	+	42150961	42151030
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NR_033819	5	21	5	+	42150961	42151030
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NM_001556	3	22	5	+	42150961	42151030
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NM_001190720	1	21	4	+	42150961	42151030
279972545	chr8	42150881	42151054	42150903	42151031	IKBKB	NR_040009	6	22	5	+	42150961	42151030
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NM_001242778	2	21	7	+	42166419	42166543
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NR_033819	5	21	8	+	42166419	42166543
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NR_033818	4	22	8	+	42166419	42166543
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NM_001556	3	22	8	+	42166419	42166543
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NM_001190720	1	21	7	+	42166419	42166543
279298323	chr8	42166309	42166480	42166329	42166460	IKBKB	NR_040009	6	22	8	+	42166419	42166543
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NM_001242778	2	21	10	+	42174228	42174422
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NR_033819	5	21	11	+	42174228	42174422
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NR_033818	4	22	11	+	42174228	42174422
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NM_001556	3	22	11	+	42174228	42174422
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NM_001190720	1	21	10	+	42174228	42174422
279935289	chr8	42174158	42174325	42174182	42174304	IKBKB	NR_040009	6	22	11	+	42174228	42174422
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NM_001242778	2	21	12	+	42176070	42176193

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NR_033819	5	21	13	+	42176070	42176193
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NR_033818	4	22	13	+	42176070	42176193
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NM_001556	3	22	13	+	42176070	42176193
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NM_001190720	1	21	12	+	42176070	42176193
278490458	chr8	42176030	42176170	42176058	42176151	IKBKB	NR_040009	6	22	13	+	42176070	42176193
280290434	chr8	42177028	42177189	42177056	42177165	IKBKB	NM_001242778	2	21	14	+	42177103	42177164
280290434	chr8	42177028	42177189	42177056	42177165	IKBKB	NR_033818	4	22	15	+	42177103	42177164
280290434	chr8	42177028	42177189	42177056	42177165	IKBKB	NM_001556	3	22	15	+	42177103	42177164
280290434	chr8	42177028	42177189	42177056	42177165	IKBKB	NM_001190720	1	21	14	+	42177103	42177164
280290434	chr8	42177028	42177189	42177056	42177165	IKBKB	NR_040009	6	22	15	+	42177103	42177164
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NM_001242778	2	21	18	+	42179865	42180012
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NR_033819	5	21	18	+	42179865	42180012
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NR_033818	4	22	19	+	42179865	42180012
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NM_001556	3	22	19	+	42179865	42180012
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NM_001190720	1	21	18	+	42179865	42180012
277925179	chr8	42179812	42179958	42179833	42179932	IKBKB	NR_040009	6	22	19	+	42179865	42180012
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NM_001242778	2	21	20	+	42186642	42186732
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NR_033819	5	21	20	+	42186642	42186732
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NR_033818	4	22	21	+	42186642	42186732
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NM_001556	3	22	21	+	42186642	42186732
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NM_001190720	1	21	20	+	42186642	42186732
278780757	chr8	42186636	42186785	42186660	42186758	IKBKB	NR_040009	6	22	21	+	42186642	42186732
227483565	chr8	42761349	42761520	42761373	42761497	HOOK3	NM_032410	1	22	2	+	42761316	42761401
228152251	chr8	42798347	42798514	42798369	42798491	HOOK3	NM_032410	1	22	5	+	42798456	42798588
227127621	chr8	42812146	42812282	42812174	42812258	HOOK3	NM_032410	1	22	7	+	42812237	42812299
227463777	chr8	42819379	42819511	42819406	42819483	HOOK3	NM_032410	1	22	9	+	42819454	42819617
229791820	chr8	42823092	42823256	42823119	42823232	HOOK3	NM_032410	1	22	11	+	42823156	42823357
227963366	chr8	42828455	42828580	42828482	42828552	HOOK3	NM_032410	1	22	12	+	42828432	42828542
227223206	chr8	42841809	42841963	42841837	42841938	HOOK3	NM_032410	1	22	15	+	42841798	42841938
227232251	chr8	42868231	42868381	42868258	42868350	HOOK3	NM_032410	1	22	20	+	42868194	42868298
230353202	chr8	42873502	42873663	42873525	42873642	HOOK3	NM_032410	1	22	22	+	42873501	42885682
269838560	chr8	48689418	48689573	48689439	48689545	PRKDC	NM_001081640	1	85	84	-	48689405	48689544
269838560	chr8	48689418	48689573	48689439	48689545	PRKDC	NM_006904	2	86	85	-	48689405	48689544
269482531	chr8	48691075	48691232	48691097	48691212	PRKDC	NM_001081640	1	85	82	-	48691020	48691221
269482531	chr8	48691075	48691232	48691097	48691212	PRKDC	NM_006904	2	86	83	-	48691020	48691221
270176645	chr8	48691584	48691730	48691609	48691704	PRKDC	NM_001081640	1	85	80	-	48691565	48691654
270176645	chr8	48691584	48691730	48691609	48691704	PRKDC	NM_006904	2	86	81	-	48691565	48691654
270331990	chr8	48695013	48695187	48695037	48695159	PRKDC	NM_001081640	1	85	79	-	48694939	48695159
270331990	chr8	48695013	48695187	48695037	48695159	PRKDC	NM_006904	2	86	79	-	48694939	48695159
270802411	chr8	48697786	48697931	48697812	48697903	PRKDC	NM_001081640	1	85	77	-	48697674	48697878
270802411	chr8	48697786	48697931	48697812	48697903	PRKDC	NM_006904	2	86	77	-	48697674	48697878

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270920472	chr8	48701710	48701854	48701738	48701821	PRKDC	NM_001081640	1	85	75	-	48701712	48701799
270920472	chr8	48701710	48701854	48701738	48701821	PRKDC	NM_006904	2	86	75	-	48701712	48701799
272562597	chr8	48710710	48710879	48710730	48710850	PRKDC	NM_001081640	1	85	73	-	48710798	48710958
272562597	chr8	48710710	48710879	48710730	48710850	PRKDC	NM_006904	2	86	73	-	48710798	48710958
271684678	chr8	48713290	48713463	48713311	48713441	PRKDC	NM_001081640	1	85	71	-	48713354	48713547
271684678	chr8	48713290	48713463	48713311	48713441	PRKDC	NM_006904	2	86	71	-	48713354	48713547
269846173	chr8	48715969	48716109	48715988	48716082	PRKDC	NM_001081640	1	85	70	-	48715867	48716041
269846173	chr8	48715969	48716109	48715988	48716082	PRKDC	NM_006904	2	86	70	-	48715867	48716041
270246100	chr8	48731855	48732027	48731882	48732002	PRKDC	NM_001081640	1	85	67	-	48731963	48732071
270246100	chr8	48731855	48732027	48731882	48732002	PRKDC	NM_006904	2	86	67	-	48731963	48732071
270317423	chr8	48734059	48734233	48734086	48734206	PRKDC	NM_001081640	1	85	65	-	48734165	48734353
270317423	chr8	48734059	48734233	48734086	48734206	PRKDC	NM_006904	2	86	65	-	48734165	48734353
271587765	chr8	48736460	48736595	48736487	48736567	PRKDC	NM_001081640	1	85	64	-	48736419	48736557
271587765	chr8	48736460	48736595	48736487	48736567	PRKDC	NM_006904	2	86	64	-	48736419	48736557
272000202	chr8	48740748	48740909	48740771	48740884	PRKDC	NM_001081640	1	85	62	-	48740729	48740908
272000202	chr8	48740748	48740909	48740771	48740884	PRKDC	NM_006904	2	86	62	-	48740729	48740908
271535753	chr8	48744263	48744437	48744284	48744414	PRKDC	NM_001081640	1	85	60	-	48744375	48744487
271535753	chr8	48744263	48744437	48744284	48744414	PRKDC	NM_006904	2	86	60	-	48744375	48744487
271198532	chr8	48748801	48748962	48748826	48748942	PRKDC	NM_001081640	1	85	58	-	48748899	48749088
271198532	chr8	48748801	48748962	48748826	48748942	PRKDC	NM_006904	2	86	58	-	48748899	48749088
270216500	chr8	48749810	48749960	48749833	48749936	PRKDC	NM_001081640	1	85	57	-	48749773	48749980
270216500	chr8	48749810	48749960	48749833	48749936	PRKDC	NM_006904	2	86	57	-	48749773	48749980
269654586	chr8	48761688	48761840	48761709	48761816	PRKDC	NM_001081640	1	85	54	-	48761715	48761864
269654586	chr8	48761688	48761840	48761709	48761816	PRKDC	NM_006904	2	86	54	-	48761715	48761864
270374843	chr8	48765169	48765338	48765198	48765310	PRKDC	NM_001081640	1	85	52	-	48765234	48765345
270374843	chr8	48765169	48765338	48765198	48765310	PRKDC	NM_006904	2	86	52	-	48765234	48765345
270042634	chr8	48767677	48767819	48767710	48767794	PRKDC	NM_001081640	1	85	50	-	48767783	48767934
270042634	chr8	48767677	48767819	48767710	48767794	PRKDC	NM_006904	2	86	50	-	48767783	48767934
272503520	chr8	48769703	48769869	48769728	48769846	PRKDC	NM_001081640	1	85	49	-	48769717	48769860
272503520	chr8	48769703	48769869	48769728	48769846	PRKDC	NM_006904	2	86	49	-	48769717	48769860
272660778	chr8	48771487	48771645	48771509	48771621	PRKDC	NM_001081640	1	85	47	-	48771410	48771547
272660778	chr8	48771487	48771645	48771509	48771621	PRKDC	NM_006904	2	86	47	-	48771410	48771547
270507494	chr8	48773414	48773540	48773440	48773512	PRKDC	NM_001081640	1	85	45	-	48773460	48773532
270507494	chr8	48773414	48773540	48773440	48773512	PRKDC	NM_006904	2	86	45	-	48773460	48773532
270423296	chr8	48774978	48775150	48775003	48775123	PRKDC	NM_001081640	1	85	43	-	48774934	48775102
270423296	chr8	48774978	48775150	48775003	48775123	PRKDC	NM_006904	2	86	43	-	48774934	48775102
270567417	chr8	48777039	48777185	48777060	48777158	PRKDC	NM_001081640	1	85	41	-	48777117	48777324
270567417	chr8	48777039	48777185	48777060	48777158	PRKDC	NM_006904	2	86	41	-	48777117	48777324
269697698	chr8	48791930	48792094	48791956	48792071	PRKDC	NM_001081640	1	85	39	-	48792052	48792219
269697698	chr8	48791930	48792094	48791956	48792071	PRKDC	NM_006904	2	86	39	-	48792052	48792219
271837888	chr8	48794392	48794566	48794420	48794542	PRKDC	NM_001081640	1	85	37	-	48794473	48794658

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271837888	chr8	48794392	48794566	48794420	48794542	PRKDC	NM_006904	2	86	37	-	48794473	48794658
271287802	chr8	48800038	48800192	48800063	48800171	PRKDC	NM_001081640	1	85	35	-	48800108	48800266
271287802	chr8	48800038	48800192	48800063	48800171	PRKDC	NM_006904	2	86	35	-	48800108	48800266
271681153	chr8	48801525	48801693	48801547	48801673	PRKDC	NM_001081640	1	85	33	-	48801575	48801783
271681153	chr8	48801525	48801693	48801547	48801673	PRKDC	NM_006904	2	86	33	-	48801575	48801783
269952645	chr8	48802948	48803100	48802970	48803072	PRKDC	NM_001081640	1	85	32	-	48802818	48803041
269952645	chr8	48802948	48803100	48802970	48803072	PRKDC	NM_006904	2	86	32	-	48802818	48803041
271940050	chr8	48809617	48809771	48809644	48809742	PRKDC	NM_001081640	1	85	30	-	48809721	48809854
271940050	chr8	48809617	48809771	48809644	48809742	PRKDC	NM_006904	2	86	30	-	48809721	48809854
272254024	chr8	48812899	48813073	48812921	48813044	PRKDC	NM_001081640	1	85	28	-	48812933	48813027
272254024	chr8	48812899	48813073	48812921	48813044	PRKDC	NM_006904	2	86	28	-	48812933	48813027
272419258	chr8	48817382	48817529	48817408	48817503	PRKDC	NM_001081640	1	85	26	-	48817429	48817536
272419258	chr8	48817382	48817529	48817408	48817503	PRKDC	NM_006904	2	86	26	-	48817429	48817536
271151827	chr8	48826367	48826520	48826391	48826500	PRKDC	NM_001081640	1	85	24	-	48826461	48826624
271151827	chr8	48826367	48826520	48826391	48826500	PRKDC	NM_006904	2	86	24	-	48826461	48826624
270249605	chr8	48827910	48828068	48827933	48828046	PRKDC	NM_001081640	1	85	23	-	48827888	48827978
270249605	chr8	48827910	48828068	48827933	48828046	PRKDC	NM_006904	2	86	23	-	48827888	48827978
271286903	chr8	48839740	48839866	48839767	48839840	PRKDC	NM_001081640	1	85	21	-	48839754	48839913
271286903	chr8	48839740	48839866	48839767	48839840	PRKDC	NM_006904	2	86	21	-	48839754	48839913
271316757	chr8	48841678	48841812	48841705	48841786	PRKDC	NM_001081640	1	85	19	-	48841652	48841738
271316757	chr8	48841678	48841812	48841705	48841786	PRKDC	NM_006904	2	86	19	-	48841652	48841738
271056252	chr8	48843124	48843292	48843153	48843264	PRKDC	NM_001081640	1	85	17	-	48843232	48843347
271056252	chr8	48843124	48843292	48843153	48843264	PRKDC	NM_006904	2	86	17	-	48843232	48843347
271550600	chr8	48845666	48845831	48845694	48845808	PRKDC	NM_001081640	1	85	16	-	48845580	48845732
271550600	chr8	48845666	48845831	48845694	48845808	PRKDC	NM_006904	2	86	16	-	48845580	48845732
271326655	chr8	48847573	48847731	48847596	48847705	PRKDC	NM_001081640	1	85	14	-	48847569	48847618
271326655	chr8	48847573	48847731	48847596	48847705	PRKDC	NM_006904	2	86	14	-	48847569	48847618
272419976	chr8	48848810	48848983	48848833	48848960	PRKDC	NM_001081640	1	85	12	-	48848913	48849077
272419976	chr8	48848810	48848983	48848833	48848960	PRKDC	NM_006904	2	86	12	-	48848913	48849077
270049771	chr8	48852133	48852261	48852161	48852237	PRKDC	NM_001081640	1	85	11	-	48852111	48852257
270049771	chr8	48852133	48852261	48852161	48852237	PRKDC	NM_006904	2	86	11	-	48852111	48852257
272552769	chr8	48856272	48856435	48856297	48856413	PRKDC	NM_001081640	1	85	9	-	48856413	48856443
272552769	chr8	48856272	48856435	48856297	48856413	PRKDC	NM_006904	2	86	9	-	48856413	48856443
270723984	chr8	48866208	48866339	48866229	48866311	PRKDC	NM_001081640	1	85	7	-	48866180	48866279
270723984	chr8	48866208	48866339	48866229	48866311	PRKDC	NM_006904	2	86	7	-	48866180	48866279
270303677	chr8	48868319	48868471	48868346	48868445	PRKDC	NM_001081640	1	85	4	-	48868434	48868508
270303677	chr8	48868319	48868471	48868346	48868445	PRKDC	NM_006904	2	86	4	-	48868434	48868508
270799056	chr8	48869862	48870034	48869889	48870006	PRKDC	NM_001081640	1	85	2	-	48869915	48869991
270799056	chr8	48869862	48870034	48869889	48870006	PRKDC	NM_006904	2	86	2	-	48869915	48869991
240812979	chr8	57078937	57079094	57078960	57079070	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240812979	chr8	57078937	57079094	57078960	57079070	PLAG1	NM_001114634	1	4	4	-	57073468	57080062

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240812979	chr8	57078937	57079094	57078960	57079070	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
240924785	chr8	57079402	57079567	57079422	57079544	PLAG1	NM_002655	3	5	5	-	57073468	57080062
240924785	chr8	57079402	57079567	57079422	57079544	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
240924785	chr8	57079402	57079567	57079422	57079544	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
237196610	chr8	57079882	57080016	57079906	57079990	PLAG1	NM_002655	3	5	5	-	57073468	57080062
237196610	chr8	57079882	57080016	57079906	57079990	PLAG1	NM_001114634	1	4	4	-	57073468	57080062
237196610	chr8	57079882	57080016	57079906	57079990	PLAG1	NM_001114635	2	3	3	-	57073468	57080062
238303733	chr8	57080711	57080857	57080733	57080834	PLAG1	NM_002655	3	5	4	-	57080587	57080945
238303733	chr8	57080711	57080857	57080733	57080834	PLAG1	NM_001114634	1	4	3	-	57080587	57080945
236427857	chr8	71036072	71036240	71036094	71036221	NCOA2	NM_006540	1	23	21	-	71036119	71036317
237342173	chr8	71038919	71039078	71038940	71039056	NCOA2	NM_006540	1	23	19	-	71039048	71039282
258729776	chr8	71040654	71040827	71040677	71040804	NCOA2	NM_006540	1	23	18	-	71040668	71040745
237616127	chr8	71043983	71044147	71044004	71044124	NCOA2	NM_006540	1	23	16	-	71044072	71044237
237245300	chr8	71053376	71053548	71053404	71053527	NCOA2	NM_006540	1	23	14	-	71053419	71053634
236836287	chr8	71056999	71057167	71057021	71057139	NCOA2	NM_006540	1	23	13	-	71056877	71057083
240141288	chr8	71068136	71068309	71068160	71068283	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240248972	chr8	71068584	71068716	71068608	71068696	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240215552	chr8	71068979	71069140	71068999	71069121	NCOA2	NM_006540	1	23	11	-	71068206	71069475
240222052	chr8	71069422	71069577	71069443	71069549	NCOA2	NM_006540	1	23	11	-	71068206	71069475
237986575	chr8	71074948	71075122	71074974	71075094	NCOA2	NM_006540	1	23	9	-	71074946	71075089
235759170	chr8	71078839	71079013	71078861	71078989	NCOA2	NM_006540	1	23	7	-	71078801	71078989
236707970	chr8	71086967	71087130	71086993	71087102	NCOA2	NM_006540	1	23	5	-	71086991	71087094
235600121	chr8	71128835	71128973	71128859	71128949	NCOA2	NM_006540	1	23	3	-	71128895	71128999
239131541	chr8	90955407	90955574	90955429	90955549	NBN	NM_002485	1	16	14	-	90955481	90955594
235145652	chr8	90959923	90960097	90959948	90960074	NBN	NM_002485	1	16	12	-	90960052	90960120
258728496	chr8	90965646	90965817	90965669	90965789	NBN	NM_002485	1	16	11	-	90965472	90965919
235645223	chr8	90967528	90967696	90967555	90967668	NBN	NM_002485	1	16	10	-	90967511	90967783
238099926	chr8	90970947	90971120	90970973	90971091	NBN	NM_002485	1	16	9	-	90970953	90971082
236516677	chr8	90982660	90982785	90982688	90982758	NBN	NM_002485	1	16	7	-	90982592	90982785
237180090	chr8	90990525	90990649	90990547	90990622	NBN	NM_002485	1	16	5	-	90990448	90990551
235146310	chr8	90993625	90993749	90993650	90993721	NBN	NM_002485	1	16	3	-	90993603	90993751
238352888	chr8	90996704	90996860	90996724	90996842	NBN	NM_002485	1	16	1	-	90996753	90996899
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_004349	12	11	10	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198625	1	15	14	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198626	2	13	12	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198627	3	14	13	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198679	11	12	11	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_175636	15	10	9	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198630	6	13	12	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_175635	14	11	10	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_175634	13	12	11	-	92982886	92983076

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198633	9	11	10	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198632	8	12	11	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198631	7	12	11	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198634	10	11	10	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198629	5	12	11	-	92982886	92983076
240868327	chr8	92982847	92983006	92982875	92982985	RUNX1T1	NM_001198628	4	12	11	-	92982886	92983076
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_004349	12	11	8	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198625	1	15	12	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198626	2	13	10	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198627	3	14	11	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198679	11	12	9	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_175636	15	10	7	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198630	6	13	10	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_175635	14	11	8	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_175634	13	12	9	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198633	9	11	8	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198632	8	12	9	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198631	7	12	9	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198634	10	11	8	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198629	5	12	9	-	92998352	92998553
241679980	chr8	92998461	92998585	92998484	92998562	RUNX1T1	NM_001198628	4	12	9	-	92998352	92998553
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_004349	12	11	6	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198625	1	15	10	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198626	2	13	8	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198627	3	14	9	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198679	11	12	7	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_175636	15	10	5	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198630	6	13	8	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_175635	14	11	6	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_175634	13	12	7	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198633	9	11	6	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198632	8	12	7	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198631	7	12	7	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198634	10	11	6	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198629	5	12	7	-	93003867	93004117
242734403	chr8	93003933	93004096	93003955	93004074	RUNX1T1	NM_001198628	4	12	7	-	93003867	93004117
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_004349	12	11	4	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198625	1	15	8	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198626	2	13	6	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198627	3	14	7	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198679	11	12	5	-	93023230	93023319

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_175636	15	10	3	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198630	6	13	6	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_175635	14	11	4	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_175634	13	12	5	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198633	9	11	4	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198632	8	12	5	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198631	7	12	5	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198634	10	11	4	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198629	5	12	5	-	93023230	93023319
242061294	chr8	93023159	93023327	93023184	93023299	RUNX1T1	NM_001198628	4	12	5	-	93023230	93023319
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_004349	12	11	3	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198625	1	15	7	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198626	2	13	5	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198627	3	14	6	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198679	11	12	4	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_175636	15	10	2	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198630	6	13	5	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_175635	14	11	3	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_175634	13	12	4	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198633	9	11	3	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198632	8	12	4	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198631	7	12	4	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198634	10	11	3	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198629	5	12	4	-	93026807	93027048
240978961	chr8	93026937	93027077	93026960	93027051	RUNX1T1	NM_001198628	4	12	4	-	93026807	93027048
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198625	1	15	4	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198626	2	13	3	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198627	3	14	4	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198630	6	13	3	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_175634	13	12	2	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198631	7	12	2	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198629	5	12	2	-	93088193	93088365
242523472	chr8	93088176	93088308	93088204	93088285	RUNX1T1	NM_001198628	4	12	2	-	93088193	93088365
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198625	1	15	1	-	93107575	93107882
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198626	2	13	1	-	93107575	93107882
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198627	3	14	1	-	93107575	93107882
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198679	11	12	1	-	93107575	93107882
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198631	7	12	1	-	93107575	93107882
238988956	chr8	93107626	93107753	93107650	93107733	RUNX1T1	NM_001198634	10	11	1	-	93107575	93107882
303480444	chr8	103266630	103266804	103266657	103266776	UBR5	NM_015902	1	59	59	-	103264502	103266742
302822257	chr8	103271285	103271443	103271314	103271417	UBR5	NM_015902	1	59	57	-	103271213	103271357

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
305633496	chr8	103274136	103274305	103274157	103274277	UBR5	NM_015902	1	59	55	-	103274143	103274298
303205548	chr8	103279078	103279244	103279106	103279216	UBR5	NM_015902	1	59	52	-	103279175	103279235
302616103	chr8	103282233	103282403	103282261	103282379	UBR5	NM_015902	1	59	50	-	103282267	103282411
300352930	chr8	103284749	103284914	103284772	103284887	UBR5	NM_015902	1	59	48	-	103284757	103285000
299304410	chr8	103287920	103288082	103287946	103288057	UBR5	NM_015902	1	59	46	-	103287936	103288056
302178770	chr8	103290995	103291168	103291022	103291143	UBR5	NM_015902	1	59	44	-	103291054	103291167
303850764	chr8	103291351	103291513	103291373	103291486	UBR5	NM_015902	1	59	43	-	103291264	103291436
299338747	chr8	103293627	103293766	103293653	103293740	UBR5	NM_015902	1	59	41	-	103293517	103293747
300464541	chr8	103297735	103297908	103297763	103297887	UBR5	NM_015902	1	59	39	-	103297741	103298009
299301887	chr8	103299568	103299741	103299596	103299717	UBR5	NM_015902	1	59	37	-	103299661	103299792
302795636	chr8	103301575	103301718	103301602	103301690	UBR5	NM_015902	1	59	35	-	103301681	103301804
302142779	chr8	103305950	103306077	103305972	103306052	UBR5	NM_015902	1	59	34	-	103305833	103306072
300347106	chr8	103306201	103306332	103306228	103306303	UBR5	NM_015902	1	59	33	-	103306183	103306343
301949562	chr8	103307446	103307620	103307474	103307592	UBR5	NM_015902	1	59	31	-	103307432	103307558
305551647	chr8	103307872	103308009	103307897	103307987	UBR5	NM_015902	1	59	29	-	103307864	103308010
302054590	chr8	103309708	103309877	103309736	103309851	UBR5	NM_015902	1	59	27	-	103309686	103309834
302766250	chr8	103311107	103311248	103311134	103311220	UBR5	NM_015902	1	59	25	-	103311076	103311199
302044698	chr8	103312291	103312425	103312312	103312396	UBR5	NM_015902	1	59	23	-	103312228	103312379
301654997	chr8	103317275	103317402	103317304	103317374	UBR5	NM_015902	1	59	21	-	103317313	103317523
301806449	chr8	103323534	103323693	103323559	103323671	UBR5	NM_015902	1	59	20	-	103323527	103323724
299468427	chr8	103324044	103324208	103324069	103324180	UBR5	NM_015902	1	59	19	-	103323963	103324117
300640549	chr8	103324608	103324733	103324631	103324707	UBR5	NM_015902	1	59	17	-	103324570	103324713
300172750	chr8	103326918	103327079	103326939	103327057	UBR5	NM_015902	1	59	15	-	103326972	103327081
302572142	chr8	103338763	103338937	103338786	103338909	UBR5	NM_015902	1	59	13	-	103338774	103338891
303222067	chr8	103341357	103341529	103341382	103341501	UBR5	NM_015902	1	59	11	-	103341318	103341428
302661673	chr8	103354693	103354834	103354716	103354808	UBR5	NM_015902	1	59	9	-	103354701	103354912
305651721	chr8	103358435	103358609	103358459	103358581	UBR5	NM_015902	1	59	7	-	103358464	103358623
300479646	chr8	103372222	103372360	103372245	103372337	UBR5	NM_015902	1	59	5	-	103372299	103372418
299741860	chr8	103373276	103373429	103373304	103373405	UBR5	NM_015902	1	59	3	-	103373353	103373434
286577285	chr8	113237051	113237220	113237071	113237195	CSMD3	NM_052900	1	69	69	-	113235159	113237159
286577285	chr8	113237051	113237220	113237071	113237195	CSMD3	NM_198123	2	71	71	-	113235159	113237159
286577285	chr8	113237051	113237220	113237071	113237195	CSMD3	NM_198124	3	72	72	-	113235159	113237159
287558469	chr8	113246524	113246694	113246547	113246677	CSMD3	NM_052900	1	69	66	-	113246594	113246706
287558469	chr8	113246524	113246694	113246547	113246677	CSMD3	NM_198123	2	71	68	-	113246594	113246706
287558469	chr8	113246524	113246694	113246547	113246677	CSMD3	NM_198124	3	72	69	-	113246594	113246706
287421386	chr8	113253955	113254127	113253973	113254100	CSMD3	NM_052900	1	69	64	-	113253949	113254014
287421386	chr8	113253955	113254127	113253973	113254100	CSMD3	NM_198123	2	71	66	-	113253949	113254014
287421386	chr8	113253955	113254127	113253973	113254100	CSMD3	NM_198124	3	72	67	-	113253949	113254014
288968248	chr8	113259310	113259477	113259333	113259449	CSMD3	NM_052900	1	69	62	-	113259249	113259360
288968248	chr8	113259310	113259477	113259333	113259449	CSMD3	NM_198123	2	71	64	-	113259249	113259360
288968248	chr8	113259310	113259477	113259333	113259449	CSMD3	NM_198124	3	72	65	-	113259249	113259360

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
288645827	chr8	113267555	113267719	113267582	113267690	CSMD3	NM_052900	1	69	60	-	113267483	113267656
288645827	chr8	113267555	113267719	113267582	113267690	CSMD3	NM_198123	2	71	62	-	113267483	113267656
288645827	chr8	113267555	113267719	113267582	113267690	CSMD3	NM_198124	3	72	63	-	113267483	113267656
286439285	chr8	113277635	113277773	113277662	113277746	CSMD3	NM_052900	1	69	58	-	113277640	113277819
286439285	chr8	113277635	113277773	113277662	113277746	CSMD3	NM_198123	2	71	60	-	113277640	113277819
286439285	chr8	113277635	113277773	113277662	113277746	CSMD3	NM_198124	3	72	61	-	113277640	113277819
289041610	chr8	113293464	113293596	113293488	113293569	CSMD3	NM_052900	1	69	57	-	113293403	113293579
289041610	chr8	113293464	113293596	113293488	113293569	CSMD3	NM_198123	2	71	59	-	113293403	113293579
289041610	chr8	113293464	113293596	113293488	113293569	CSMD3	NM_198124	3	72	60	-	113293403	113293579
287332829	chr8	113301561	113301730	113301589	113301707	CSMD3	NM_052900	1	69	55	-	113301594	113301767
287332829	chr8	113301561	113301730	113301589	113301707	CSMD3	NM_198123	2	71	57	-	113301594	113301767
287332829	chr8	113301561	113301730	113301589	113301707	CSMD3	NM_198124	3	72	58	-	113301594	113301767
286339231	chr8	113303816	113303940	113303841	113303911	CSMD3	NM_052900	1	69	54	-	113303739	113303924
286339231	chr8	113303816	113303940	113303841	113303911	CSMD3	NM_198123	2	71	56	-	113303739	113303924
286339231	chr8	113303816	113303940	113303841	113303911	CSMD3	NM_198124	3	72	57	-	113303739	113303924
287190402	chr8	113307987	113308122	113308020	113308095	CSMD3	NM_052900	1	69	52	-	113308062	113308235
287190402	chr8	113307987	113308122	113308020	113308095	CSMD3	NM_198123	2	71	54	-	113308062	113308235
287190402	chr8	113307987	113308122	113308020	113308095	CSMD3	NM_198124	3	72	55	-	113308062	113308235
288078950	chr8	113314043	113314172	113314066	113314144	CSMD3	NM_052900	1	69	51	-	113314022	113314195
288078950	chr8	113314043	113314172	113314066	113314144	CSMD3	NM_198123	2	71	53	-	113314022	113314195
288078950	chr8	113314043	113314172	113314066	113314144	CSMD3	NM_198124	3	72	54	-	113314022	113314195
286336627	chr8	113317060	113317225	113317088	113317198	CSMD3	NM_198123	2	71	52	-	113316950	113317144
286336627	chr8	113317060	113317225	113317088	113317198	CSMD3	NM_198124	3	72	53	-	113316950	113317144
287833854	chr8	113323227	113323378	113323251	113323353	CSMD3	NM_052900	1	69	49	-	113323207	113323395
287833854	chr8	113323227	113323378	113323251	113323353	CSMD3	NM_198123	2	71	50	-	113323207	113323395
287833854	chr8	113323227	113323378	113323251	113323353	CSMD3	NM_198124	3	72	51	-	113323207	113323395
286390498	chr8	113326646	113326789	113326670	113326761	CSMD3	NM_052900	1	69	47	-	113326658	113326846
286390498	chr8	113326646	113326789	113326670	113326761	CSMD3	NM_198123	2	71	48	-	113326658	113326846
286390498	chr8	113326646	113326789	113326670	113326761	CSMD3	NM_198124	3	72	49	-	113326658	113326846
285548535	chr8	113332076	113332250	113332100	113332222	CSMD3	NM_052900	1	69	45	-	113332130	113332210
285548535	chr8	113332076	113332250	113332100	113332222	CSMD3	NM_198123	2	71	46	-	113332130	113332210
285548535	chr8	113332076	113332250	113332100	113332222	CSMD3	NM_198124	3	72	47	-	113332130	113332210
284878493	chr8	113348953	113349127	113348981	113349104	CSMD3	NM_052900	1	69	43	-	113348881	113349058
284878493	chr8	113348953	113349127	113348981	113349104	CSMD3	NM_198123	2	71	44	-	113348881	113349058
284878493	chr8	113348953	113349127	113348981	113349104	CSMD3	NM_198124	3	72	45	-	113348881	113349058
287943066	chr8	113353705	113353832	113353735	113353810	CSMD3	NM_052900	1	69	41	-	113353706	113353915
287943066	chr8	113353705	113353832	113353735	113353810	CSMD3	NM_198123	2	71	42	-	113353706	113353915
287943066	chr8	113353705	113353832	113353735	113353810	CSMD3	NM_198124	3	72	43	-	113353706	113353915
285910178	chr8	113358414	113358541	113358436	113358518	CSMD3	NM_052900	1	69	40	-	113358326	113358442
285910178	chr8	113358414	113358541	113358436	113358518	CSMD3	NM_198123	2	71	41	-	113358326	113358442
285910178	chr8	113358414	113358541	113358436	113358518	CSMD3	NM_198124	3	72	42	-	113358326	113358442

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
284768236	chr8	113364728	113364865	113364751	113364833	CSMD3	NM_052900	1	69	38	-	113364645	113364763
284768236	chr8	113364728	113364865	113364751	113364833	CSMD3	NM_198123	2	71	39	-	113364645	113364763
284768236	chr8	113364728	113364865	113364751	113364833	CSMD3	NM_198124	3	72	40	-	113364645	113364763
287938976	chr8	113395828	113395964	113395852	113395936	CSMD3	NM_052900	1	69	36	-	113395796	113395892
287938976	chr8	113395828	113395964	113395852	113395936	CSMD3	NM_198123	2	71	37	-	113395796	113395892
287938976	chr8	113395828	113395964	113395852	113395936	CSMD3	NM_198124	3	72	38	-	113395796	113395892
288474451	chr8	113418800	113418960	113418827	113418934	CSMD3	NM_052900	1	69	34	-	113418753	113418956
288474451	chr8	113418800	113418960	113418827	113418934	CSMD3	NM_198123	2	71	35	-	113418753	113418956
288474451	chr8	113418800	113418960	113418827	113418934	CSMD3	NM_198124	3	72	36	-	113418753	113418956
286988319	chr8	113421113	113421286	113421136	113421266	CSMD3	NM_052900	1	69	32	-	113421148	113421261
286988319	chr8	113421113	113421286	113421136	113421266	CSMD3	NM_198123	2	71	33	-	113421148	113421261
286988319	chr8	113421113	113421286	113421136	113421266	CSMD3	NM_198124	3	72	34	-	113421148	113421261
286756890	chr8	113504719	113504868	113504742	113504839	CSMD3	NM_052900	1	69	30	-	113504718	113504912
286756890	chr8	113504719	113504868	113504742	113504839	CSMD3	NM_198123	2	71	31	-	113504718	113504912
286756890	chr8	113504719	113504868	113504742	113504839	CSMD3	NM_198124	3	72	32	-	113504718	113504912
284766633	chr8	113516144	113516275	113516170	113516242	CSMD3	NM_052900	1	69	29	-	113516019	113516206
284766633	chr8	113516144	113516275	113516170	113516242	CSMD3	NM_198123	2	71	30	-	113516019	113516206
284766633	chr8	113516144	113516275	113516170	113516242	CSMD3	NM_198124	3	72	31	-	113516019	113516206
286887226	chr8	113529278	113529452	113529295	113529434	CSMD3	NM_052900	1	69	27	-	113529263	113529454
286887226	chr8	113529278	113529452	113529295	113529434	CSMD3	NM_198123	2	71	28	-	113529263	113529454
286887226	chr8	113529278	113529452	113529295	113529434	CSMD3	NM_198124	3	72	29	-	113529263	113529454
288873798	chr8	113562973	113563113	113563001	113563093	CSMD3	NM_052900	1	69	26	-	113562900	113563102
288873798	chr8	113562973	113563113	113563001	113563093	CSMD3	NM_198123	2	71	27	-	113562900	113563102
288873798	chr8	113562973	113563113	113563001	113563093	CSMD3	NM_198124	3	72	28	-	113562900	113563102
286255377	chr8	113568987	113569116	113569010	113569095	CSMD3	NM_052900	1	69	24	-	113568992	113569183
286255377	chr8	113568987	113569116	113569010	113569095	CSMD3	NM_198123	2	71	25	-	113568992	113569183
286255377	chr8	113568987	113569116	113569010	113569095	CSMD3	NM_198124	3	72	26	-	113568992	113569183
287545749	chr8	113585748	113585872	113585772	113585844	CSMD3	NM_052900	1	69	23	-	113585730	113585886
287545749	chr8	113585748	113585872	113585772	113585844	CSMD3	NM_198123	2	71	24	-	113585730	113585886
287545749	chr8	113585748	113585872	113585772	113585844	CSMD3	NM_198124	3	72	25	-	113585730	113585886
286426780	chr8	113599383	113599549	113599411	113599520	CSMD3	NM_052900	1	69	22	-	113599295	113599464
286426780	chr8	113599383	113599549	113599411	113599520	CSMD3	NM_198123	2	71	23	-	113599295	113599464
286426780	chr8	113599383	113599549	113599411	113599520	CSMD3	NM_198124	3	72	24	-	113599295	113599464
288126393	chr8	113650816	113650990	113650845	113650967	CSMD3	NM_052900	1	69	20	-	113650925	113651140
288126393	chr8	113650816	113650990	113650845	113650967	CSMD3	NM_198123	2	71	21	-	113650925	113651140
288126393	chr8	113650816	113650990	113650845	113650967	CSMD3	NM_198124	3	72	22	-	113650925	113651140
285180096	chr8	113657326	113657489	113657350	113657463	CSMD3	NM_052900	1	69	19	-	113657338	113657454
285180096	chr8	113657326	113657489	113657350	113657463	CSMD3	NM_198123	2	71	20	-	113657338	113657454
285180096	chr8	113657326	113657489	113657350	113657463	CSMD3	NM_198124	3	72	21	-	113657338	113657454
284964077	chr8	113668411	113668567	113668439	113668538	CSMD3	NM_052900	1	69	17	-	113668383	113668570
284964077	chr8	113668411	113668567	113668439	113668538	CSMD3	NM_198123	2	71	18	-	113668383	113668570

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
284964077	chr8	113668411	113668567	113668439	113668538	CSMD3	NM_198124	3	72	19	-	113668383	113668570
286458248	chr8	113678587	113678757	113678608	113678725	CSMD3	NM_052900	1	69	16	-	113678506	113678644
286458248	chr8	113678587	113678757	113678608	113678725	CSMD3	NM_198123	2	71	17	-	113678506	113678644
286458248	chr8	113678587	113678757	113678608	113678725	CSMD3	NM_198124	3	72	18	-	113678506	113678644
286418467	chr8	113694790	113694929	113694815	113694903	CSMD3	NM_052900	1	69	15	-	113694671	113694865
286418467	chr8	113694790	113694929	113694815	113694903	CSMD3	NM_198123	2	71	16	-	113694671	113694865
286418467	chr8	113694790	113694929	113694815	113694903	CSMD3	NM_198124	3	72	17	-	113694671	113694865
285145171	chr8	113697855	113697990	113697883	113697959	CSMD3	NM_052900	1	69	14	-	113697635	113697961
285145171	chr8	113697855	113697990	113697883	113697959	CSMD3	NM_198123	2	71	15	-	113697635	113697961
285145171	chr8	113697855	113697990	113697883	113697959	CSMD3	NM_198124	3	72	16	-	113697635	113697961
287683597	chr8	113812390	113812532	113812418	113812504	CSMD3	NM_052900	1	69	12	-	113812391	113812503
287683597	chr8	113812390	113812532	113812418	113812504	CSMD3	NM_198123	2	71	13	-	113812391	113812503
287683597	chr8	113812390	113812532	113812418	113812504	CSMD3	NM_198124	3	72	14	-	113812391	113812503
286416149	chr8	113933735	113933891	113933768	113933870	CSMD3	NM_052900	1	69	9	-	113933856	113933980
286416149	chr8	113933735	113933891	113933768	113933870	CSMD3	NM_198123	2	71	10	-	113933856	113933980
286416149	chr8	113933735	113933891	113933768	113933870	CSMD3	NM_198124	3	72	11	-	113933856	113933980
286128378	chr8	113966920	113967094	113966944	113967066	CSMD3	NM_052900	1	69	7	-	113966913	113966990
286128378	chr8	113966920	113967094	113966944	113967066	CSMD3	NM_198123	2	71	8	-	113966913	113966990
286128378	chr8	113966920	113967094	113966944	113967066	CSMD3	NM_198124	3	72	9	-	113966913	113966990
288555471	chr8	114031263	114031389	114031292	114031364	CSMD3	NM_052900	1	69	6	-	114031296	114031408
288555471	chr8	114031263	114031389	114031292	114031364	CSMD3	NM_198123	2	71	6	-	114031296	114031408
288555471	chr8	114031263	114031389	114031292	114031364	CSMD3	NM_198124	3	72	7	-	114031296	114031408
285134453	chr8	114111142	114111313	114111165	114111287	CSMD3	NM_052900	1	69	5	-	114110985	114111192
285134453	chr8	114111142	114111313	114111165	114111287	CSMD3	NM_198123	2	71	5	-	114110985	114111192
285134453	chr8	114111142	114111313	114111165	114111287	CSMD3	NM_198124	3	72	6	-	114110985	114111192
287425402	chr8	114290771	114290934	114290799	114290911	CSMD3	NM_052900	1	69	3	-	114290821	114290933
287425402	chr8	114290771	114290934	114290799	114290911	CSMD3	NM_198123	2	71	3	-	114290821	114290933
287425402	chr8	114290771	114290934	114290799	114290911	CSMD3	NM_198124	3	72	4	-	114290821	114290933
288176354	chr8	114326966	114327130	114326993	114327100	CSMD3	NM_052900	1	69	2	-	114326800	114327022
288176354	chr8	114326966	114327130	114326993	114327100	CSMD3	NM_198123	2	71	2	-	114326800	114327022
288176354	chr8	114326966	114327130	114326993	114327100	CSMD3	NM_198124	3	72	3	-	114326800	114327022
288970582	chr8	114448937	114449108	114448965	114449087	CSMD3	NM_052900	1	69	1	-	114448906	114449242
288970582	chr8	114448937	114449108	114448965	114449087	CSMD3	NM_198123	2	71	1	-	114448906	114449242
227719938	chr8	118817011	118817173	118817033	118817151	EXT1	NM_000127	1	11	10	-	118816961	118817132
232204972	chr8	118830632	118830792	118830654	118830769	EXT1	NM_000127	1	11	7	-	118830674	118830769
227907248	chr8	118842444	118842614	118842464	118842588	EXT1	NM_000127	1	11	4	-	118842469	118842588
231369649	chr8	119122415	119122573	119122437	119122550	EXT1	NM_000127	1	11	1	-	119122324	119124058
231381127	chr8	119122868	119123016	119122887	119122992	EXT1	NM_000127	1	11	1	-	119122324	119124058
238812706	chr8	128748752	128748891	128748774	128748870	MYC	NM_002467	1	3	1	+	128748315	128748869
240731575	chr8	128750723	128750861	128750742	128750838	MYC	NM_002467	1	3	2	+	128750494	128751265
240724714	chr8	128751156	128751330	128751177	128751304	MYC	NM_002467	1	3	2	+	128750494	128751265

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242627940	chr8	128752871	128752999	128752894	128752977	MYC	NM_002467	1	3	3	+	128752642	128753680
238882536	chr8	145736785	145736958	145736805	145736938	RECQL4	NM_004260	1	22	22	-	145736667	145736938
238913142	chr8	145737346	145737486	145737369	145737466	RECQL4	NM_004260	1	22	20	-	145737294	145737450
238599629	chr8	145737842	145737978	145737862	145737957	RECQL4	NM_004260	1	22	18	-	145737775	145737944
264243674	chr8	145738320	145738464	145738340	145738444	RECQL4	NM_004260	1	22	16	-	145738230	145738521
240947865	chr8	145738781	145738907	145738801	145738887	RECQL4	NM_004260	1	22	14	-	145738769	145738864
238537438	chr8	145739346	145739473	145739365	145739456	RECQL4	NM_004260	1	22	12	-	145739312	145739491
238179129	chr8	145739741	145739876	145739763	145739856	RECQL4	NM_004260	1	22	10	-	145739826	145739909
260973611	chr8	145740469	145740621	145740487	145740604	RECQL4	NM_004260	1	22	8	-	145740534	145740626
238508169	chr8	145741053	145741219	145741075	145741196	RECQL4	NM_004260	1	22	6	-	145741148	145741274
264073738	chr8	145741506	145741659	145741524	145741642	RECQL4	NM_004260	1	22	5	-	145741372	145742148
264063961	chr8	145741904	145742063	145741925	145742043	RECQL4	NM_004260	1	22	5	-	145741372	145742148
241400507	chr8	145742663	145742836	145742681	145742819	RECQL4	NM_004260	1	22	3	-	145742798	145742892
234596971	chr9	5029760	5029884	5029789	5029857	JAK2	NM_004972	1	25	4	+	5029783	5029906
232445874	chr9	5050671	5050804	5050695	5050776	JAK2	NM_004972	1	25	6	+	5050686	5050831
233551762	chr9	5054649	5054782	5054677	5054756	JAK2	NM_004972	1	25	7	+	5054563	5054884
233182078	chr9	5064831	5064973	5064859	5064945	JAK2	NM_004972	1	25	9	+	5064883	5065040
234421554	chr9	5066665	5066802	5066693	5066778	JAK2	NM_004972	1	25	10	+	5066678	5066789
232041027	chr9	5069990	5070132	5070016	5070100	JAK2	NM_004972	1	25	12	+	5069925	5070052
233377865	chr9	5077338	5077483	5077371	5077455	JAK2	NM_004972	1	25	15	+	5077453	5077580
231876115	chr9	5078370	5078495	5078394	5078467	JAK2	NM_004972	1	25	16	+	5078306	5078444
230836387	chr9	5080621	5080795	5080645	5080769	JAK2	NM_004972	1	25	18	+	5080533	5080683
234405587	chr9	5089772	5089918	5089796	5089895	JAK2	NM_004972	1	25	20	+	5089674	5089863
233275646	chr9	5090788	5090916	5090816	5090891	JAK2	NM_004972	1	25	22	+	5090739	5090911
233701248	chr9	5126332	5126487	5126359	5126459	JAK2	NM_004972	1	25	24	+	5126333	5126446
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_001040712	1	30	29	-	8319831	8319966
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_001171025	2	29	28	-	8319831	8319966
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_130393	6	29	28	-	8319831	8319966
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_130392	5	31	30	-	8319831	8319966
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_130391	4	31	30	-	8319831	8319966
272602707	chr9	8319712	8319883	8319735	8319855	PTPRD	NM_002839	3	46	45	-	8319831	8319966
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_001040712	1	30	27	-	8338922	8339047
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_001171025	2	29	26	-	8338922	8339047
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_130393	6	29	26	-	8338922	8339047
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_130392	5	31	28	-	8338922	8339047
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_130391	4	31	28	-	8338922	8339047
270943687	chr9	8338805	8338963	8338831	8338935	PTPRD	NM_002839	3	46	43	-	8338922	8339047
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_001040712	1	30	25	-	8341090	8341268
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_001171025	2	29	24	-	8341090	8341268
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_130393	6	29	24	-	8341090	8341268
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_130392	5	31	26	-	8341090	8341268

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_130391	4	31	26	-	8341090	8341268
271886243	chr9	8341036	8341177	8341062	8341152	PTPRD	NM_002839	3	46	41	-	8341090	8341268
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_001040712	1	30	24	-	8341693	8341978
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_001171025	2	29	23	-	8341693	8341978
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_130393	6	29	23	-	8341693	8341978
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_130392	5	31	25	-	8341693	8341978
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_130391	4	31	25	-	8341693	8341978
271254430	chr9	8341729	8341891	8341757	8341865	PTPRD	NM_002839	3	46	40	-	8341693	8341978
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_001040712	1	30	22	-	8376607	8376726
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_001171025	2	29	21	-	8376607	8376726
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_130393	6	29	21	-	8376607	8376726
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_130392	5	31	23	-	8376607	8376726
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_130391	4	31	23	-	8376607	8376726
270638702	chr9	8376482	8376648	8376508	8376626	PTPRD	NM_002839	3	46	38	-	8376607	8376726
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_001040712	1	30	20	-	8404537	8404660
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_001171025	2	29	19	-	8404537	8404660
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_130393	6	29	19	-	8404537	8404660
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_130392	5	31	21	-	8404537	8404660
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_130391	4	31	21	-	8404537	8404660
270940170	chr9	8404508	8404636	8404533	8404608	PTPRD	NM_002839	3	46	36	-	8404537	8404660
271170233	chr9	8437214	8437380	8437236	8437352	PTPRD	NM_001171025	2	29	17	-	8437198	8437239
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_001040712	1	30	16	-	8460411	8460571
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_001171025	2	29	15	-	8460411	8460571
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_130393	6	29	16	-	8460411	8460571
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_130392	5	31	17	-	8460411	8460571
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_130391	4	31	17	-	8460411	8460571
271195694	chr9	8460327	8460476	8460351	8460455	PTPRD	NM_002839	3	46	33	-	8460411	8460571
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_001040712	1	30	15	-	8465466	8465675
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_001171025	2	29	14	-	8465466	8465675
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_130393	6	29	15	-	8465466	8465675
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_130392	5	31	16	-	8465466	8465675
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_130391	4	31	16	-	8465466	8465675
270227492	chr9	8465499	8465667	8465527	8465643	PTPRD	NM_002839	3	46	32	-	8465466	8465675
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_001040712	1	30	13	-	8484119	8484378
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_001171025	2	29	12	-	8484119	8484378
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_130393	6	29	13	-	8484119	8484378
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_130392	5	31	14	-	8484119	8484378
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_130391	4	31	14	-	8484119	8484378
270030547	chr9	8484190	8484363	8484211	8484337	PTPRD	NM_002839	3	46	30	-	8484119	8484378
272546777	chr9	8485739	8485906	8485761	8485883	PTPRD	NM_002839	3	46	28	-	8485762	8486349
271121051	chr9	8486219	8486378	8486239	8486355	PTPRD	NM_002839	3	46	28	-	8485762	8486349

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272584604	chr9	8499620	8499787	8499648	8499765	PTPRD	NM_002839	3	46	25	-	8499647	8499840
270853646	chr9	8500931	8501105	8500959	8501077	PTPRD	NM_002839	3	46	24	-	8500754	8501059
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_001040712	1	30	10	-	8507301	8507434
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_001171025	2	29	9	-	8507301	8507434
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_130393	6	29	10	-	8507301	8507434
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_130392	5	31	11	-	8507301	8507434
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_130391	4	31	11	-	8507301	8507434
270630900	chr9	8507293	8507461	8507316	8507439	PTPRD	NM_002839	3	46	22	-	8507301	8507434
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_001040712	1	30	9	-	8517848	8518429
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_001171025	2	29	8	-	8517848	8518429
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_130393	6	29	9	-	8517848	8518429
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_130392	5	31	10	-	8517848	8518429
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_130391	4	31	10	-	8517848	8518429
269901119	chr9	8518185	8518321	8518205	8518293	PTPRD	NM_002839	3	46	21	-	8517848	8518429
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_001040712	1	30	8	-	8521277	8521546
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_001171025	2	29	7	-	8521277	8521546
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_130393	6	29	8	-	8521277	8521546
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_130392	5	31	9	-	8521277	8521546
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_130391	4	31	9	-	8521277	8521546
271228660	chr9	8521282	8521455	8521306	8521430	PTPRD	NM_002839	3	46	20	-	8521277	8521546
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_001040712	1	30	6	-	8524925	8525035
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_001171025	2	29	6	-	8524925	8525035
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_130393	6	29	6	-	8524925	8525035
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_130392	5	31	7	-	8524925	8525035
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_130391	4	31	7	-	8524925	8525035
270598958	chr9	8524970	8525133	8524991	8525105	PTPRD	NM_002839	3	46	18	-	8524925	8525035
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_001040712	1	30	4	-	8528591	8528779
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_001171025	2	29	4	-	8528591	8528779
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_130393	6	29	4	-	8528591	8528779
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_130392	5	31	4	-	8528591	8528779
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_130391	4	31	4	-	8528591	8528779
270405220	chr9	8528713	8528886	8528735	8528860	PTPRD	NM_002839	3	46	15	-	8528591	8528779
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_001040712	1	30	2	-	8636699	8636844
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_001171025	2	29	2	-	8636699	8636844
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_130393	6	29	2	-	8636699	8636844
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_130392	5	31	2	-	8636699	8636844
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_130391	4	31	2	-	8636699	8636844
271798691	chr9	8636747	8636919	8636769	8636896	PTPRD	NM_002839	3	46	13	-	8636699	8636844
235576359	chr9	15468569	15468733	15468591	15468705	PSIP1	NM_001128217	1	16	14	-	15468628	15468841
235576359	chr9	15468569	15468733	15468591	15468705	PSIP1	NM_033222	3	16	14	-	15468628	15468841
237829691	chr9	15469910	15470059	15469942	15470034	PSIP1	NM_001128217	1	16	11	-	15469936	15469991

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237829691	chr9	15469910	15470059	15469942	15470034	PSIP1	NM_033222	3	16	11	-	15469936	15469991
235618914	chr9	15474015	15474187	15474043	15474161	PSIP1	NM_001128217	1	16	9	-	15474007	15474235
235618914	chr9	15474015	15474187	15474043	15474161	PSIP1	NM_033222	3	16	9	-	15474007	15474235
235618914	chr9	15474015	15474187	15474043	15474161	PSIP1	NM_021144	2	10	8	-	15474007	15474235
236220075	chr9	15479596	15479750	15479624	15479722	PSIP1	NM_001128217	1	16	7	-	15479589	15479685
236220075	chr9	15479596	15479750	15479624	15479722	PSIP1	NM_033222	3	16	7	-	15479589	15479685
236220075	chr9	15479596	15479750	15479624	15479722	PSIP1	NM_021144	2	10	6	-	15479589	15479685
236434332	chr9	15486816	15486953	15486841	15486926	PSIP1	NM_001128217	1	16	5	-	15486825	15486929
236434332	chr9	15486816	15486953	15486841	15486926	PSIP1	NM_033222	3	16	5	-	15486825	15486929
236434332	chr9	15486816	15486953	15486841	15486926	PSIP1	NM_021144	2	10	4	-	15486825	15486929
235272916	chr9	15510064	15510202	15510084	15510185	PSIP1	NM_001128217	1	16	2	-	15510115	15510324
235272916	chr9	15510064	15510202	15510084	15510185	PSIP1	NM_033222	3	16	2	-	15510115	15510327
235272916	chr9	15510064	15510202	15510084	15510185	PSIP1	NM_021144	2	10	1	-	15510115	15510287
225942695	chr9	21970967	21971138	21970985	21971121	CDKN2A	NM_058195	3	3	2	-	21970901	21971207
225942695	chr9	21970967	21971138	21970985	21971121	CDKN2A	NM_058197	4	3	2	-	21970901	21971207
225942695	chr9	21970967	21971138	21970985	21971121	CDKN2A	NM_001195132	2	4	2	-	21970901	21971207
225942695	chr9	21970967	21971138	21970985	21971121	CDKN2A	NM_000077	1	3	2	-	21970901	21971207
225530996	chr9	21974655	21974810	21974673	21974792	CDKN2A	NM_058197	4	3	1	-	21974403	21974826
225530996	chr9	21974655	21974810	21974673	21974792	CDKN2A	NM_001195132	2	4	1	-	21974677	21975132
225530996	chr9	21974655	21974810	21974673	21974792	CDKN2A	NM_000077	1	3	1	-	21974677	21975132
226280984	chr9	22005974	22006130	22005991	22006112	CDKN2B	NM_004936	1	2	2	-	22002902	22006246
226280984	chr9	22005974	22006130	22005991	22006112	CDKN2B	NM_078487	2	2	2	-	22002902	22006246
226594583	chr9	22008786	22008916	22008803	22008898	CDKN2B	NM_078487	2	2	1	-	22008674	22009312
226594583	chr9	22008786	22008916	22008803	22008898	CDKN2B	NM_004936	1	2	1	-	22008797	22009312
261420334	chr9	32630205	32630340	32630229	32630314	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261293654	chr9	32630565	32630734	32630592	32630709	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237778006	chr9	32630931	32631103	32630955	32631075	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237912034	chr9	32631307	32631448	32631334	32631422	TAF1L	NM_153809	1	1	1	-	32629452	32635667
238036994	chr9	32631719	32631847	32631741	32631824	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237857203	chr9	32632087	32632211	32632110	32632183	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261212029	chr9	32632425	32632598	32632446	32632573	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261403500	chr9	32632815	32632985	32632835	32632964	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261356293	chr9	32633170	32633310	32633196	32633287	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237833804	chr9	32633603	32633773	32633624	32633746	TAF1L	NM_153809	1	1	1	-	32629452	32635667
237881176	chr9	32634059	32634184	32634084	32634161	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261265676	chr9	32634458	32634602	32634481	32634577	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261281126	chr9	32634905	32635070	32634927	32635045	TAF1L	NM_153809	1	1	1	-	32629452	32635667
261541258	chr9	32635334	32635492	32635356	32635471	TAF1L	NM_153809	1	1	1	-	32629452	32635667
230665536	chr9	35074235	35074409	35074257	35074389	FANCG	NM_004629	1	14	13	-	35074368	35074491
230002338	chr9	35075171	35075345	35075195	35075322	FANCG	NM_004629	1	14	11	-	35075276	35075322
231411694	chr9	35075908	35076049	35075927	35076026	FANCG	NM_004629	1	14	9	-	35075959	35076025

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
328673846	chr9	35076823	35076988	35076844	35076967	FANCG	NM_004629	1	14	7	-	35076721	35076867
228468412	chr9	35077349	35077474	35077374	35077448	FANCG	NM_004629	1	14	5	-	35077261	35077396
227735291	chr9	35078527	35078698	35078549	35078676	FANCG	NM_004629	1	14	3	-	35078602	35078733
235542358	chr9	36840511	36840669	36840533	36840649	PAX5	NM_016734	1	10	10	-	36838531	36840633
237646732	chr9	36923383	36923551	36923402	36923530	PAX5	NM_016734	1	10	7	-	36923352	36923481
236643006	chr9	37002634	37002800	37002658	37002782	PAX5	NM_016734	1	10	5	-	37002645	37002773
235299806	chr9	37015057	37015230	37015077	37015208	PAX5	NM_016734	1	10	3	-	37014994	37015191
227229650	chr9	80336219	80336374	80336238	80336347	GNAQ	NM_002072	1	7	7	-	80335191	80336429
228784339	chr9	80409348	80409514	80409376	80409492	GNAQ	NM_002072	1	7	5	-	80409379	80409508
229842797	chr9	80430509	80430681	80430530	80430654	GNAQ	NM_002072	1	7	3	-	80430532	80430686
227583556	chr9	80645998	80646142	80646015	80646123	GNAQ	NM_002072	1	7	1	-	80646016	80646219
238001198	chr9	93606279	93606404	93606303	93606384	SYK	NM_001135052	1	13	2	+	93606140	93606597
238001198	chr9	93606279	93606404	93606303	93606384	SYK	NM_001174167	2	14	2	+	93606140	93606597
238001198	chr9	93606279	93606404	93606303	93606384	SYK	NM_001174168	3	13	2	+	93606140	93606597
238001198	chr9	93606279	93606404	93606303	93606384	SYK	NM_003177	4	14	2	+	93606140	93606597
240544696	chr9	93607679	93607853	93607703	93607826	SYK	NM_001135052	1	13	3	+	93607716	93607876
240544696	chr9	93607679	93607853	93607703	93607826	SYK	NM_001174167	2	14	3	+	93607716	93607876
240544696	chr9	93607679	93607853	93607703	93607826	SYK	NM_001174168	3	13	3	+	93607716	93607876
240544696	chr9	93607679	93607853	93607703	93607826	SYK	NM_003177	4	14	3	+	93607716	93607876
263560236	chr9	93626802	93626972	93626830	93626950	SYK	NM_001135052	1	13	5	+	93626871	93626949
263560236	chr9	93626802	93626972	93626830	93626950	SYK	NM_001174167	2	14	5	+	93626871	93626949
263560236	chr9	93626802	93626972	93626830	93626950	SYK	NM_001174168	3	13	5	+	93626871	93626949
263560236	chr9	93626802	93626972	93626830	93626950	SYK	NM_003177	4	14	5	+	93626871	93626949
260579401	chr9	93636920	93637080	93636941	93637057	SYK	NM_001135052	1	13	8	+	93636954	93637131
260579401	chr9	93636920	93637080	93636941	93637057	SYK	NM_001174167	2	14	9	+	93636954	93637131
260579401	chr9	93636920	93637080	93636941	93637057	SYK	NM_001174168	3	13	8	+	93636954	93637131
260579401	chr9	93636920	93637080	93636941	93637057	SYK	NM_003177	4	14	9	+	93636954	93637131
237833444	chr9	93640022	93640156	93640043	93640135	SYK	NM_001135052	1	13	9	+	93639853	93640062
237833444	chr9	93640022	93640156	93640043	93640135	SYK	NM_001174167	2	14	10	+	93639853	93640062
237833444	chr9	93640022	93640156	93640043	93640135	SYK	NM_001174168	3	13	9	+	93639853	93640062
237833444	chr9	93640022	93640156	93640043	93640135	SYK	NM_003177	4	14	10	+	93639853	93640062
239240505	chr9	93650058	93650196	93650078	93650174	SYK	NM_001135052	1	13	11	+	93650031	93650171
239240505	chr9	93650058	93650196	93650078	93650174	SYK	NM_001174167	2	14	12	+	93650031	93650171
239240505	chr9	93650058	93650196	93650078	93650174	SYK	NM_001174168	3	13	11	+	93650031	93650171
239240505	chr9	93650058	93650196	93650078	93650174	SYK	NM_003177	4	14	12	+	93650031	93650171
232197002	chr9	97863884	97864041	97863905	97864019	FANCC	NM_001243743	2	15	15	-	97861336	97864132
232197002	chr9	97863884	97864041	97863905	97864019	FANCC	NM_000136	1	15	15	-	97861336	97864132
232432173	chr9	97873450	97873596	97873473	97873576	FANCC	NM_001243744	3	14	14	-	97872508	97873627
230601886	chr9	97876848	97877022	97876871	97877000	FANCC	NM_001243744	3	14	12	-	97876911	97876992
230601886	chr9	97876848	97877022	97876871	97877000	FANCC	NM_001243743	2	15	12	-	97876911	97876992
230601886	chr9	97876848	97877022	97876871	97877000	FANCC	NM_000136	1	15	12	-	97876911	97876992

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228758323	chr9	97897515	97897672	97897544	97897644	FANCC	NM_001243744	3	14	8	-	97897628	97897784
228758323	chr9	97897515	97897672	97897544	97897644	FANCC	NM_001243743	2	15	8	-	97897628	97897784
228758323	chr9	97897515	97897672	97897544	97897644	FANCC	NM_000136	1	15	8	-	97897628	97897784
232139723	chr9	97912249	97912415	97912271	97912389	FANCC	NM_001243744	3	14	7	-	97912205	97912369
232139723	chr9	97912249	97912415	97912271	97912389	FANCC	NM_001243743	2	15	7	-	97912205	97912369
232139723	chr9	97912249	97912415	97912271	97912389	FANCC	NM_000136	1	15	7	-	97912205	97912369
228877049	chr9	98002793	98002961	98002820	98002934	FANCC	NM_001243744	3	14	4	-	98002931	98003025
228877049	chr9	98002793	98002961	98002820	98002934	FANCC	NM_001243743	2	15	4	-	98002931	98003025
228877049	chr9	98002793	98002961	98002820	98002934	FANCC	NM_000136	1	15	4	-	98002931	98003025
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237358820	chr9	98209143	98209293	98209163	98209274	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083605	5	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083602	2	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_000264	1	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083604	4	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083606	6	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083607	7	24	23	-	98209193	98209733
237380984	chr9	98209553	98209726	98209581	98209706	PTCH1	NM_001083603	3	24	23	-	98209193	98209733
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083605	5	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083602	2	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_000264	1	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083604	4	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083606	6	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083607	7	24	22	-	98211351	98211605
235198390	chr9	98211577	98211703	98211594	98211680	PTCH1	NM_001083603	3	24	22	-	98211351	98211605
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083605	5	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083602	2	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_000264	1	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083604	4	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083606	6	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083607	7	24	19	-	98218558	98218695
236568832	chr9	98218501	98218668	98218523	98218649	PTCH1	NM_001083603	3	24	19	-	98218558	98218695
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083605	5	24	18	-	98220295	98220575
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083602	2	24	18	-	98220295	98220575
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_000264	1	24	18	-	98220295	98220575
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083604	4	24	18	-	98220295	98220575

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083606	6	24	18	-	98220295	98220575
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083607	7	24	18	-	98220295	98220575
234960414	chr9	98220465	98220600	98220488	98220578	PTCH1	NM_001083603	3	24	18	-	98220295	98220575
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083605	5	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083602	2	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_000264	1	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083604	4	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083606	6	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083607	7	24	16	-	98224138	98224280
236793103	chr9	98224179	98224321	98224200	98224293	PTCH1	NM_001083603	3	24	16	-	98224138	98224280
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083605	5	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083602	2	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_000264	1	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083604	4	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083606	6	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083607	7	24	14	-	98231033	98231435
235315006	chr9	98230952	98231106	98230980	98231084	PTCH1	NM_001083603	3	24	14	-	98231033	98231435
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083605	5	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083602	2	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_000264	1	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083604	4	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083606	6	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083607	7	24	13	-	98232095	98232213
237938149	chr9	98231999	98232166	98232027	98232141	PTCH1	NM_001083603	3	24	13	-	98232095	98232213
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083605	5	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083602	2	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_000264	1	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083604	4	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083606	6	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083607	7	24	11	-	98239041	98239139
237906436	chr9	98238994	98239163	98239015	98239139	PTCH1	NM_001083603	3	24	11	-	98239041	98239139
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083605	5	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083602	2	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_000264	1	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083604	4	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083606	6	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083607	7	24	9	-	98240337	98240468
236686923	chr9	98240412	98240552	98240433	98240530	PTCH1	NM_001083603	3	24	9	-	98240337	98240468
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083605	5	24	7	-	98242251	98242372
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083602	2	24	7	-	98242251	98242372
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_000264	1	24	7	-	98242251	98242372

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083604	4	24	7	-	98242251	98242372
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083606	6	24	7	-	98242251	98242372
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083607	7	24	7	-	98242251	98242372
237894790	chr9	98242289	98242422	98242310	98242395	PTCH1	NM_001083603	3	24	7	-	98242251	98242372
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083605	5	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083602	2	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_000264	1	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083604	4	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083606	6	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083607	7	24	4	-	98244416	98244485
235884867	chr9	98244338	98244504	98244358	98244476	PTCH1	NM_001083603	3	24	4	-	98244416	98244485
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083605	5	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083602	2	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_000264	1	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083604	4	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083606	6	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083607	7	24	2	-	98268689	98268881
237793618	chr9	98268776	98268907	98268798	98268887	PTCH1	NM_001083603	3	24	2	-	98268689	98268881
237341087	chr9	98278886	98279058	98278904	98279041	PTCH1	NM_001083603	3	24	1	-	98278905	98279247
237341087	chr9	98278886	98279058	98278904	98279041	PTCH1	NM_001083602	2	24	1	-	98278751	98279247
264430561	chr9	100437821	100437959	100437844	100437936	XPA	NR_027302	2	7	7	-	100437191	100437869
264430561	chr9	100437821	100437959	100437844	100437936	XPA	NM_000380	1	6	6	-	100437191	100437869
241658590	chr9	100449390	100449545	100449417	100449517	XPA	NR_027302	2	7	4	-	100449378	100449543
241658590	chr9	100449390	100449545	100449417	100449517	XPA	NM_000380	1	6	4	-	100449378	100449543
241031717	chr9	100451873	100452045	100451900	100452012	XPA	NR_027302	2	7	3	-	100451816	100451921
241031717	chr9	100451873	100452045	100451900	100452012	XPA	NM_000380	1	6	3	-	100451816	100451921
238374676	chr9	100459454	100459607	100459471	100459588	XPA	NR_027302	2	7	1	-	100459403	100459691
238374676	chr9	100459454	100459607	100459471	100459588	XPA	NM_000380	1	6	1	-	100459403	100459691
295047540	chr9	120474532	120474706	120474554	120474681	TLR4	NM_003266	1	4	4	+	120474667	120479769
295047540	chr9	120474532	120474706	120474554	120474681	TLR4	NM_138554	2	3	3	+	120474667	120479769
295047540	chr9	120474532	120474706	120474554	120474681	TLR4	NM_138557	3	2	2	+	120474667	120479769
295047540	chr9	120474532	120474706	120474554	120474681	TLR4	NR_024169	5	2	2	+	120474667	120479766
295047540	chr9	120474532	120474706	120474554	120474681	TLR4	NR_024168	4	4	4	+	120474667	120479766
295092326	chr9	120474944	120475071	120474966	120475045	TLR4	NM_003266	1	4	4	+	120474667	120479769
295092326	chr9	120474944	120475071	120474966	120475045	TLR4	NM_138554	2	3	3	+	120474667	120479769
295092326	chr9	120474944	120475071	120474966	120475045	TLR4	NM_138557	3	2	2	+	120474667	120479769
295092326	chr9	120474944	120475071	120474966	120475045	TLR4	NR_024169	5	2	2	+	120474667	120479766
295092326	chr9	120474944	120475071	120474966	120475045	TLR4	NR_024168	4	4	4	+	120474667	120479766
294055743	chr9	120475333	120475500	120475358	120475477	TLR4	NM_003266	1	4	4	+	120474667	120479769
294055743	chr9	120475333	120475500	120475358	120475477	TLR4	NM_138554	2	3	3	+	120474667	120479769
294055743	chr9	120475333	120475500	120475358	120475477	TLR4	NM_138557	3	2	2	+	120474667	120479769

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294055743	chr9	120475333	120475500	120475358	120475477	TLR4	NR_024169	5	2	2	+	120474667	120479766
294055743	chr9	120475333	120475500	120475358	120475477	TLR4	NR_024168	4	4	4	+	120474667	120479766
295083633	chr9	120475759	120475915	120475785	120475892	TLR4	NM_003266	1	4	4	+	120474667	120479769
295083633	chr9	120475759	120475915	120475785	120475892	TLR4	NM_138554	2	3	3	+	120474667	120479769
295083633	chr9	120475759	120475915	120475785	120475892	TLR4	NM_138557	3	2	2	+	120474667	120479769
295083633	chr9	120475759	120475915	120475785	120475892	TLR4	NR_024169	5	2	2	+	120474667	120479766
295083633	chr9	120475759	120475915	120475785	120475892	TLR4	NR_024168	4	4	4	+	120474667	120479766
294133164	chr9	120476213	120476366	120476238	120476338	TLR4	NM_003266	1	4	4	+	120474667	120479769
294133164	chr9	120476213	120476366	120476238	120476338	TLR4	NM_138554	2	3	3	+	120474667	120479769
294133164	chr9	120476213	120476366	120476238	120476338	TLR4	NM_138557	3	2	2	+	120474667	120479769
294133164	chr9	120476213	120476366	120476238	120476338	TLR4	NR_024169	5	2	2	+	120474667	120479766
294133164	chr9	120476213	120476366	120476238	120476338	TLR4	NR_024168	4	4	4	+	120474667	120479766
295085960	chr9	120476688	120476858	120476710	120476837	TLR4	NM_003266	1	4	4	+	120474667	120479769
295085960	chr9	120476688	120476858	120476710	120476837	TLR4	NM_138554	2	3	3	+	120474667	120479769
295085960	chr9	120476688	120476858	120476710	120476837	TLR4	NM_138557	3	2	2	+	120474667	120479769
295085960	chr9	120476688	120476858	120476710	120476837	TLR4	NR_024169	5	2	2	+	120474667	120479766
295085960	chr9	120476688	120476858	120476710	120476837	TLR4	NR_024168	4	4	4	+	120474667	120479766
222419902	chr9	133710821	133710948	133710838	133710930	ABL1	NM_005157	1	11	1	+	133710831	133710912
222596754	chr9	133730278	133730452	133730299	133730430	ABL1	NM_005157	1	11	3	+	133730188	133730483
222596754	chr9	133730278	133730452	133730299	133730430	ABL1	NM_007313	2	11	3	+	133730188	133730483
224091517	chr9	133738282	133738430	133738303	133738408	ABL1	NM_005157	1	11	4	+	133738150	133738422
224091517	chr9	133738282	133738430	133738303	133738408	ABL1	NM_007313	2	11	4	+	133738150	133738422
223927302	chr9	133748139	133748300	133748161	133748276	ABL1	NM_005157	1	11	6	+	133748247	133748424
223927302	chr9	133748139	133748300	133748161	133748276	ABL1	NM_007313	2	11	6	+	133748247	133748424
223605569	chr9	133750317	133750483	133750338	133750460	ABL1	NM_005157	1	11	7	+	133750255	133750439
223605569	chr9	133750317	133750483	133750338	133750460	ABL1	NM_007313	2	11	7	+	133750255	133750439
223621703	chr9	133755837	133756009	133755858	133755988	ABL1	NM_005157	1	11	10	+	133755887	133756051
223621703	chr9	133755837	133756009	133755858	133755988	ABL1	NM_007313	2	11	10	+	133755887	133756051
224384454	chr9	133759522	133759674	133759541	133759656	ABL1	NM_005157	1	11	11	+	133759356	133763062
224384454	chr9	133759522	133759674	133759541	133759656	ABL1	NM_007313	2	11	11	+	133759356	133763062
224376366	chr9	133759910	133760070	133759934	133760049	ABL1	NM_005157	1	11	11	+	133759356	133763062
224376366	chr9	133759910	133760070	133759934	133760049	ABL1	NM_007313	2	11	11	+	133759356	133763062
224371825	chr9	133760285	133760419	133760304	133760401	ABL1	NM_005157	1	11	11	+	133759356	133763062
224371825	chr9	133760285	133760419	133760304	133760401	ABL1	NM_007313	2	11	11	+	133759356	133763062
224380515	chr9	133760667	133760832	133760685	133760815	ABL1	NM_005157	1	11	11	+	133759356	133763062
224380515	chr9	133760667	133760832	133760685	133760815	ABL1	NM_007313	2	11	11	+	133759356	133763062
238787110	chr9	134001002	134001153	134001023	134001130	NUP214	NM_005085	1	36	1	+	134000981	134001136
235093133	chr9	134002973	134003144	134002992	134003117	NUP214	NM_005085	1	36	2	+	134002911	134003106
241093629	chr9	134004675	134004810	134004698	134004788	NUP214	NM_005085	1	36	4	+	134004666	134004864
236296564	chr9	134007996	134008138	134008020	134008113	NUP214	NM_005085	1	36	6	+	134007983	134008046
236338744	chr9	134010294	134010421	134010321	134010401	NUP214	NM_005085	1	36	8	+	134010285	134010391

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237498725	chr9	134015828	134016001	134015853	134015978	NUP214	NM_005085	1	36	11	+	134015936	134016097
237094635	chr9	134019814	134019964	134019842	134019943	NUP214	NM_005085	1	36	12	+	134019667	134020141
235127840	chr9	134021516	134021684	134021538	134021663	NUP214	NM_005085	1	36	13	+	134021516	134021691
236731278	chr9	134025678	134025847	134025706	134025821	NUP214	NM_005085	1	36	15	+	134025711	134025797
236048289	chr9	134027175	134027345	134027195	134027319	NUP214	NM_005085	1	36	17	+	134027123	134027281
234917691	chr9	134039198	134039371	134039219	134039343	NUP214	NM_005085	1	36	20	+	134039257	134039342
236810767	chr9	134049519	134049688	134049541	134049665	NUP214	NM_005085	1	36	22	+	134049442	134049705
235495770	chr9	134053651	134053823	134053679	134053798	NUP214	NM_005085	1	36	24	+	134053698	134053797
235483117	chr9	134067523	134067692	134067551	134067665	NUP214	NM_005085	1	36	27	+	134067595	134067679
238021669	chr9	134072668	134072812	134072694	134072790	NUP214	NM_005085	1	36	29	+	134072603	134074402
234919866	chr9	134073042	134073201	134073063	134073176	NUP214	NM_005085	1	36	29	+	134072603	134074402
234947083	chr9	134073471	134073643	134073495	134073623	NUP214	NM_005085	1	36	29	+	134072603	134074402
238027284	chr9	134073921	134074086	134073941	134074066	NUP214	NM_005085	1	36	29	+	134072603	134074402
237151370	chr9	134077031	134077167	134077058	134077140	NUP214	NM_005085	1	36	30	+	134077034	134077104
236760309	chr9	134098249	134098400	134098269	134098374	NUP214	NM_005085	1	36	32	+	134098165	134098317
235660535	chr9	134106074	134106203	134106095	134106181	NUP214	NM_005085	1	36	34	+	134106017	134106156
265394942	chr9	135771721	135771883	135771742	135771861	TSC1	NM_000368	1	23	23	-	135766735	135772141
265394942	chr9	135771721	135771883	135771742	135771861	TSC1	NM_001162427	3	22	22	-	135766735	135772141
265394942	chr9	135771721	135771883	135771742	135771861	TSC1	NM_001162426	2	23	23	-	135766735	135772141
262322849	chr9	135772465	135772639	135772487	135772615	TSC1	NM_000368	1	23	22	-	135772571	135772732
262322849	chr9	135772465	135772639	135772487	135772615	TSC1	NM_001162427	3	22	21	-	135772571	135772732
262322849	chr9	135772465	135772639	135772487	135772615	TSC1	NM_001162426	2	23	22	-	135772571	135772732
242565948	chr9	135772932	135773094	135772956	135773066	TSC1	NM_000368	1	23	21	-	135772810	135772997
242565948	chr9	135772932	135773094	135772956	135773066	TSC1	NM_001162427	3	22	20	-	135772810	135772997
242565948	chr9	135772932	135773094	135772956	135773066	TSC1	NM_001162426	2	23	21	-	135772810	135772997
263245987	chr9	135777970	135778135	135777991	135778110	TSC1	NM_000368	1	23	18	-	135777992	135778174
263245987	chr9	135777970	135778135	135777991	135778110	TSC1	NM_001162427	3	22	17	-	135777992	135778174
263245987	chr9	135777970	135778135	135777991	135778110	TSC1	NM_001162426	2	23	18	-	135777992	135778174
242278796	chr9	135779765	135779917	135779788	135779889	TSC1	NM_000368	1	23	16	-	135779798	135779841
242278796	chr9	135779765	135779917	135779788	135779889	TSC1	NM_001162427	3	22	15	-	135779798	135779841
242278796	chr9	135779765	135779917	135779788	135779889	TSC1	NM_001162426	2	23	16	-	135779798	135779841
240601495	chr9	135781311	135781470	135781331	135781449	TSC1	NM_000368	1	23	15	-	135780968	135781526
240601495	chr9	135781311	135781470	135781331	135781449	TSC1	NM_001162427	3	22	14	-	135780968	135781526
240601495	chr9	135781311	135781470	135781331	135781449	TSC1	NM_001162426	2	23	15	-	135780968	135781526
239278102	chr9	135785939	135786109	135785957	135786082	TSC1	NM_000368	1	23	12	-	135785958	135786079
239278102	chr9	135785939	135786109	135785957	135786082	TSC1	NM_001162427	3	22	11	-	135785958	135786079
239278102	chr9	135785939	135786109	135785957	135786082	TSC1	NM_001162426	2	23	12	-	135785958	135786076
240219357	chr9	135787621	135787782	135787649	135787756	TSC1	NM_000368	1	23	9	-	135787669	135787844
240219357	chr9	135787621	135787782	135787649	135787756	TSC1	NM_001162427	3	22	8	-	135787669	135787844
240219357	chr9	135787621	135787782	135787649	135787756	TSC1	NM_001162426	2	23	9	-	135787669	135787844
239691764	chr9	135797109	135797268	135797133	135797240	TSC1	NM_000368	1	23	7	-	135797206	135797360

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239691764	chr9	135797109	135797268	135797133	135797240	TSC1	NM_001162427	3	22	6	-	135797206	135797360
239691764	chr9	135797109	135797268	135797133	135797240	TSC1	NM_001162426	2	23	7	-	135797206	135797360
262573009	chr9	135800892	135801035	135800915	135801010	TSC1	NM_000368	1	23	5	-	135800974	135801126
262573009	chr9	135800892	135801035	135800915	135801010	TSC1	NM_001162426	2	23	5	-	135800974	135801126
241686339	chr9	135804091	135804262	135804119	135804240	TSC1	NM_000368	1	23	3	-	135804154	135804339
241686339	chr9	135804091	135804262	135804119	135804240	TSC1	NM_001162427	3	22	3	-	135804154	135804339
241686339	chr9	135804091	135804262	135804119	135804240	TSC1	NM_001162426	2	23	3	-	135804154	135804339
273504119	chr9	135975632	135975805	135975654	135975783	RALGDS	NM_001042368	1	18	17	-	135975655	135975769
273504119	chr9	135975632	135975805	135975654	135975783	RALGDS	NM_006266	2	18	17	-	135975655	135975769
273259620	chr9	135977226	135977377	135977250	135977354	RALGDS	NM_001042368	1	18	15	-	135977325	135977526
273259620	chr9	135977226	135977377	135977250	135977354	RALGDS	NM_006266	2	18	15	-	135977325	135977526
272946083	chr9	135978134	135978299	135978153	135978281	RALGDS	NM_001042368	1	18	13	-	135978166	135978287
272946083	chr9	135978134	135978299	135978153	135978281	RALGDS	NM_006266	2	18	13	-	135978166	135978287
274229552	chr9	135979566	135979738	135979584	135979719	RALGDS	NM_001042368	1	18	10	-	135979650	135979718
274229552	chr9	135979566	135979738	135979584	135979719	RALGDS	NM_006266	2	18	10	-	135979650	135979718
273168323	chr9	135982418	135982590	135982442	135982568	RALGDS	NM_001042368	1	18	7	-	135982472	135982687
273168323	chr9	135982418	135982590	135982442	135982568	RALGDS	NM_006266	2	18	7	-	135982472	135982687
273173484	chr9	135983455	135983613	135983476	135983593	RALGDS	NM_001042368	1	18	6	-	135983375	135983793
273173484	chr9	135983455	135983613	135983476	135983593	RALGDS	NM_006266	2	18	6	-	135983375	135983793
273477760	chr9	135985659	135985788	135985677	135985771	RALGDS	NM_001042368	1	18	3	-	135985683	135985876
273477760	chr9	135985659	135985788	135985677	135985771	RALGDS	NM_006266	2	18	3	-	135985683	135985876
273885182	chr9	135996379	135996541	135996399	135996524	RALGDS	NM_006266	2	18	1	-	135996359	135996561
223261543	chr9	136899747	136899911	136899767	136899887	BRD3	NM_007371	1	12	11	-	136899823	136899951
223038330	chr9	136901332	136901494	136901353	136901472	BRD3	NM_007371	1	12	10	-	136901154	136901446
223282603	chr9	136906830	136906979	136906847	136906961	BRD3	NM_007371	1	12	8	-	136906882	136907073
222197871	chr9	136910454	136910606	136910481	136910585	BRD3	NM_007371	1	12	7	-	136910415	136910543
222650932	chr9	136913462	136913636	136913481	136913619	BRD3	NM_007371	1	12	6	-	136913205	136913576
222524510	chr9	136916709	136916853	136916729	136916831	BRD3	NM_007371	1	12	4	-	136916684	136916831
223872198	chr9	136918455	136918629	136918477	136918606	BRD3	NM_007371	1	12	2	-	136918387	136918712
240916946	chr9	139390703	139390841	139390721	139390824	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236043910	chr9	139391208	139391375	139391225	139391357	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
240923842	chr9	139391552	139391693	139391572	139391675	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236213226	chr9	139391954	139392091	139391972	139392068	NOTCH1	NM_017617	1	34	34	-	139388896	139392010
236194072	chr9	139394915	139395085	139394932	139395066	NOTCH1	NM_017617	1	34	31	-	139395004	139395299
237163908	chr9	139396317	139396478	139396336	139396456	NOTCH1	NM_017617	1	34	29	-	139396453	139396540
237163908	chr9	139396317	139396478	139396336	139396456	NOTCH1	NM_017617	1	34	30	-	139396200	139396365
238888040	chr9	139396783	139396913	139396803	139396895	NOTCH1	NM_017617	1	34	28	-	139396724	139396940
326921045	chr9	139399435	139399562	139399453	139399544	NOTCH1	NM_017617	1	34	26	-	139399125	139399556
235684100	chr9	139399935	139400095	139399953	139400073	NOTCH1	NM_017617	1	34	25	-	139399762	139400333
257696780	chr9	139400961	139401116	139400978	139401096	NOTCH1	NM_017617	1	34	24	-	139400979	139401091
239239668	chr9	139401338	139401503	139401358	139401485	NOTCH1	NM_017617	1	34	23	-	139401168	139401425

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236233222	chr9	139402466	139402627	139402484	139402608	NOTCH1	NM_017617	1	34	21	-	139402407	139402591
236358602	chr9	139403418	139403568	139403438	139403549	NOTCH1	NM_017617	1	34	19	-	139403322	139403523
238237084	chr9	139405001	139405152	139405020	139405134	NOTCH1	NM_017617	1	34	17	-	139405105	139405257
239890414	chr9	139405594	139405749	139405611	139405730	NOTCH1	NM_017617	1	34	16	-	139405604	139405723
242113770	chr9	139407916	139408077	139407940	139408057	NOTCH1	NM_017617	1	34	14	-	139407844	139407989
237197404	chr9	139409696	139409869	139409715	139409852	NOTCH1	NM_017617	1	34	12	-	139409742	139409852
239494401	chr9	139410363	139410527	139410384	139410507	NOTCH1	NM_017617	1	34	10	-	139410433	139410546
237693257	chr9	139412245	139412417	139412262	139412400	NOTCH1	NM_017617	1	34	8	-	139412204	139412389
242597787	chr9	139413136	139413301	139413155	139413283	NOTCH1	NM_017617	1	34	6	-	139413043	139413276
238630960	chr9	139417295	139417457	139417312	139417438	NOTCH1	NM_017617	1	34	4	-	139417302	139417640
237661409	chr9	139418080	139418221	139418098	139418203	NOTCH1	NM_017617	1	34	3	-	139418169	139418431
233330634	chr10	3823840	3824000	3823857	3823983	KLF6	NM_001160124	1	4	2	-	3823959	3824406
233330634	chr10	3823840	3824000	3823857	3823983	KLF6	NM_001300	3	4	2	-	3823833	3824406
233330634	chr10	3823840	3824000	3823857	3823983	KLF6	NM_001160125	2	3	2	-	3823833	3824406
233099997	chr10	3824288	3824434	3824312	3824411	KLF6	NM_001160124	1	4	2	-	3823959	3824406
233099997	chr10	3824288	3824434	3824312	3824411	KLF6	NR_027653	4	4	2	-	3823987	3824406
233099997	chr10	3824288	3824434	3824312	3824411	KLF6	NM_001300	3	4	2	-	3823833	3824406
233099997	chr10	3824288	3824434	3824312	3824411	KLF6	NM_001160125	2	3	2	-	3823833	3824406
227404538	chr10	8097705	8097846	8097723	8097828	GATA3	NM_002051	2	6	2	+	8097250	8097859
227404538	chr10	8097705	8097846	8097723	8097828	GATA3	NM_001002295	1	6	2	+	8097250	8097859
229538700	chr10	8100495	8100625	8100512	8100606	GATA3	NM_002051	2	6	3	+	8100268	8100804
229538700	chr10	8100495	8100625	8100512	8100606	GATA3	NM_001002295	1	6	3	+	8100268	8100804
228345756	chr10	8106047	8106218	8106073	8106197	GATA3	NM_002051	2	6	4	+	8105959	8106101
228345756	chr10	8106047	8106218	8106073	8106197	GATA3	NM_001002295	1	6	4	+	8105956	8106101
228225481	chr10	8115754	8115885	8115782	8115866	GATA3	NM_002051	2	6	6	+	8115702	8117164
228225481	chr10	8115754	8115885	8115782	8115866	GATA3	NM_001002295	1	6	6	+	8115702	8117164
233110243	chr10	21823603	21823750	21823623	21823731	MLLT10	NM_004641	5	24	2	+	21823574	21823733
233110243	chr10	21823603	21823750	21823623	21823731	MLLT10	NM_001195627	2	5	2	+	21823574	21823733
233110243	chr10	21823603	21823750	21823623	21823731	MLLT10	NM_001195626	1	22	1	+	21823574	21823733
233110243	chr10	21823603	21823750	21823623	21823731	MLLT10	NM_001195628	3	4	2	+	21823574	21823733
233110243	chr10	21823603	21823750	21823623	21823731	MLLT10	NM_001195630	4	4	2	+	21823574	21823733
231964182	chr10	21875124	21875294	21875152	21875271	MLLT10	NM_004641	5	24	4	+	21875223	21875277
231964182	chr10	21875124	21875294	21875152	21875271	MLLT10	NM_001195626	1	22	3	+	21875223	21875277
231113815	chr10	21901269	21901407	21901292	21901381	MLLT10	NM_004641	5	24	6	+	21901277	21901380
231113815	chr10	21901269	21901407	21901292	21901381	MLLT10	NM_001195626	1	22	5	+	21901277	21901380
233625577	chr10	21940479	21940651	21940508	21940629	MLLT10	NM_004641	5	24	9	+	21940602	21940697
233625577	chr10	21940479	21940651	21940508	21940629	MLLT10	NM_001195626	1	22	8	+	21940602	21940697
232526958	chr10	21959511	21959647	21959532	21959619	MLLT10	NM_004641	5	24	10	+	21959378	21959633
232526958	chr10	21959511	21959647	21959532	21959619	MLLT10	NM_001195626	1	22	9	+	21959378	21959633
234539199	chr10	21962383	21962542	21962407	21962514	MLLT10	NM_004641	5	24	11	+	21962279	21962848
234539199	chr10	21962383	21962542	21962407	21962514	MLLT10	NM_001195626	1	22	10	+	21962279	21962848

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
234832176	chr10	21970139	21970295	21970162	21970275	MLLT10	NM_004641	5	24	12	+	21970261	21970305
234832176	chr10	21970139	21970295	21970162	21970275	MLLT10	NM_001195626	1	22	11	+	21970261	21970305
233656845	chr10	22002747	22002919	22002770	22002893	MLLT10	NM_004641	5	24	15	+	22002701	22002879
233656845	chr10	22002747	22002919	22002770	22002893	MLLT10	NM_001195626	1	22	13	+	22002701	22002879
231551351	chr10	22019752	22019899	22019778	22019876	MLLT10	NM_004641	5	24	18	+	22019829	22019983
231551351	chr10	22019752	22019899	22019778	22019876	MLLT10	NM_001195626	1	22	16	+	22019829	22019983
232709749	chr10	22021975	22022140	22022003	22022109	MLLT10	NM_004641	5	24	19	+	22021828	22022016
232709749	chr10	22021975	22022140	22022003	22022109	MLLT10	NM_001195626	1	22	17	+	22021828	22022016
234680170	chr10	22022889	22023042	22022913	22023021	MLLT10	NM_004641	5	24	21	+	22022697	22023058
234680170	chr10	22022889	22023042	22022913	22023021	MLLT10	NM_001195626	1	22	19	+	22022697	22023058
233452984	chr10	22028909	22029083	22028930	22029057	MLLT10	NM_001195626	1	22	21	+	22028959	22029165
240733064	chr10	43595847	43595998	43595875	43595979	RET	NM_020630	1	19	2	+	43595907	43596170
240733064	chr10	43595847	43595998	43595875	43595979	RET	NM_020975	2	20	2	+	43595907	43596170
242208771	chr10	43597876	43598022	43597896	43598004	RET	NM_020630	1	19	3	+	43597790	43598077
242208771	chr10	43597876	43598022	43597896	43598004	RET	NM_020975	2	20	3	+	43597790	43598077
242044564	chr10	43600558	43600729	43600578	43600708	RET	NM_020630	1	19	4	+	43600400	43600641
242044564	chr10	43600558	43600729	43600578	43600708	RET	NM_020975	2	20	4	+	43600400	43600641
238129047	chr10	43604538	43604708	43604562	43604687	RET	NM_020630	1	19	6	+	43604479	43604678
238129047	chr10	43604538	43604708	43604562	43604687	RET	NM_020975	2	20	6	+	43604479	43604678
238725791	chr10	43606824	43606993	43606846	43606971	RET	NM_020630	1	19	7	+	43606655	43606913
238725791	chr10	43606824	43606993	43606846	43606971	RET	NM_020975	2	20	7	+	43606655	43606913
240421803	chr10	43609045	43609203	43609067	43609182	RET	NM_020630	1	19	10	+	43609004	43609123
240421803	chr10	43609045	43609203	43609067	43609182	RET	NM_020975	2	20	10	+	43609004	43609123
239565469	chr10	43611898	43612071	43611919	43612048	RET	NM_020630	1	19	12	+	43612032	43612179
239565469	chr10	43611898	43612071	43611919	43612048	RET	NM_020975	2	20	12	+	43612032	43612179
238824520	chr10	43613857	43614000	43613879	43613979	RET	NM_020630	1	19	13	+	43613821	43613928
238824520	chr10	43613857	43614000	43613879	43613979	RET	NM_020975	2	20	13	+	43613821	43613928
241626667	chr10	43615498	43615623	43615517	43615600	RET	NM_020630	1	19	15	+	43615529	43615651
241626667	chr10	43615498	43615623	43615517	43615600	RET	NM_020975	2	20	15	+	43615529	43615651
242451684	chr10	43619191	43619324	43619212	43619302	RET	NM_020630	1	19	17	+	43619119	43619256
242451684	chr10	43619191	43619324	43619212	43619302	RET	NM_020975	2	20	17	+	43619119	43619256
262763395	chr10	43623478	43623629	43623499	43623607	RET	NM_020975	2	20	20	+	43623560	43625797
295393510	chr10	49612774	49612947	49612798	49612922	MAPK8	NM_002750	1	11	2	+	49612895	49613024
295393510	chr10	49612774	49612947	49612798	49612922	MAPK8	NM_139049	4	11	2	+	49612895	49613024
295393510	chr10	49612774	49612947	49612798	49612922	MAPK8	NM_139046	2	11	2	+	49612895	49613024
295393510	chr10	49612774	49612947	49612798	49612922	MAPK8	NM_139047	3	11	2	+	49612895	49613024
293704592	chr10	49618019	49618167	49618044	49618139	MAPK8	NM_002750	1	11	4	+	49618073	49618211
293704592	chr10	49618019	49618167	49618044	49618139	MAPK8	NM_139049	4	11	4	+	49618073	49618211
293704592	chr10	49618019	49618167	49618044	49618139	MAPK8	NM_139046	2	11	4	+	49618073	49618211
293704592	chr10	49618019	49618167	49618044	49618139	MAPK8	NM_139047	3	11	4	+	49618073	49618211
294211985	chr10	49628333	49628470	49628353	49628442	MAPK8	NM_002750	1	11	5	+	49628198	49628363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
294211985	chr10	49628333	49628470	49628353	49628442	MAPK8	NM_139049	4	11	5	+	49628198	49628363
294211985	chr10	49628333	49628470	49628353	49628442	MAPK8	NM_139046	2	11	5	+	49628198	49628363
294211985	chr10	49628333	49628470	49628353	49628442	MAPK8	NM_139047	3	11	5	+	49628198	49628363
294680304	chr10	49633912	49634037	49633945	49634009	MAPK8	NM_002750	1	11	7	+	49633931	49634113
294680304	chr10	49633912	49634037	49633945	49634009	MAPK8	NM_139049	4	11	7	+	49633931	49634113
294680304	chr10	49633912	49634037	49633945	49634009	MAPK8	NM_139046	2	11	7	+	49633931	49634113
294680304	chr10	49633912	49634037	49633945	49634009	MAPK8	NM_139047	3	11	7	+	49633931	49634113
294343234	chr10	49634495	49634620	49634516	49634592	MAPK8	NM_002750	1	11	8	+	49634423	49634547
294343234	chr10	49634495	49634620	49634516	49634592	MAPK8	NM_139049	4	11	8	+	49634423	49634547
294343234	chr10	49634495	49634620	49634516	49634592	MAPK8	NM_139046	2	11	8	+	49634423	49634547
294343234	chr10	49634495	49634620	49634516	49634592	MAPK8	NM_139047	3	11	8	+	49634423	49634547
293713660	chr10	49642852	49642991	49642873	49642966	MAPK8	NM_002750	1	11	11	+	49642922	49643183
293713660	chr10	49642852	49642991	49642873	49642966	MAPK8	NM_139046	2	11	11	+	49642922	49643183
293713660	chr10	49642852	49642991	49642873	49642966	MAPK8	NM_139049	4	11	11	+	49642927	49643183
293713660	chr10	49642852	49642991	49642873	49642966	MAPK8	NM_139047	3	11	11	+	49642927	49643183
236199404	chr10	51579164	51579324	51579188	51579300	NCOA4	NM_001145261	2	11	3	+	51579128	51579282
236199404	chr10	51579164	51579324	51579188	51579300	NCOA4	NM_005437	5	10	2	+	51579128	51579282
236199404	chr10	51579164	51579324	51579188	51579300	NCOA4	NM_001145262	3	10	2	+	51579128	51579282
236199404	chr10	51579164	51579324	51579188	51579300	NCOA4	NM_001145263	4	10	2	+	51579128	51579282
236199404	chr10	51579164	51579324	51579188	51579300	NCOA4	NM_001145260	1	12	3	+	51579128	51579282
236470262	chr10	51580883	51581054	51580907	51581025	NCOA4	NM_001145261	2	11	5	+	51580880	51580968
236470262	chr10	51580883	51581054	51580907	51581025	NCOA4	NM_005437	5	10	4	+	51580880	51580968
236470262	chr10	51580883	51581054	51580907	51581025	NCOA4	NM_001145262	3	10	4	+	51580880	51580968
236470262	chr10	51580883	51581054	51580907	51581025	NCOA4	NM_001145263	4	10	4	+	51580880	51580968
236470262	chr10	51580883	51581054	51580907	51581025	NCOA4	NM_001145260	1	12	5	+	51580880	51580968
239228613	chr10	51582759	51582889	51582787	51582867	NCOA4	NM_001145261	2	11	8	+	51582796	51582939
239228613	chr10	51582759	51582889	51582787	51582867	NCOA4	NM_005437	5	10	7	+	51582796	51582939
239228613	chr10	51582759	51582889	51582787	51582867	NCOA4	NM_001145262	3	10	7	+	51582796	51582939
239228613	chr10	51582759	51582889	51582787	51582867	NCOA4	NM_001145263	4	10	7	+	51582796	51582939
239228613	chr10	51582759	51582889	51582787	51582867	NCOA4	NM_001145260	1	12	8	+	51582796	51582939
241419122	chr10	51584747	51584892	51584774	51584865	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
241419122	chr10	51584747	51584892	51584774	51584865	NCOA4	NM_005437	5	10	8	+	51584616	51585599
241419122	chr10	51584747	51584892	51584774	51584865	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
241419122	chr10	51584747	51584892	51584774	51584865	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
241419122	chr10	51584747	51584892	51584774	51584865	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
236607679	chr10	51585176	51585327	51585200	51585298	NCOA4	NM_001145261	2	11	9	+	51584616	51585599
236607679	chr10	51585176	51585327	51585200	51585298	NCOA4	NM_005437	5	10	8	+	51584616	51585599
236607679	chr10	51585176	51585327	51585200	51585298	NCOA4	NM_001145262	3	10	8	+	51584616	51585599
236607679	chr10	51585176	51585327	51585200	51585298	NCOA4	NM_001145263	4	10	8	+	51584616	51585599
236607679	chr10	51585176	51585327	51585200	51585298	NCOA4	NM_001145260	1	12	9	+	51584616	51585599
237308365	chr10	51586214	51586375	51586235	51586350	NCOA4	NM_001145261	2	11	10	+	51586271	51586411

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237308365	chr10	51586214	51586375	51586235	51586350	NCOA4	NM_005437	5	10	9	+	51586271	51586411
237308365	chr10	51586214	51586375	51586235	51586350	NCOA4	NM_001145262	3	10	9	+	51586271	51586411
237308365	chr10	51586214	51586375	51586235	51586350	NCOA4	NM_001145263	4	10	9	+	51586271	51586411
237308365	chr10	51586214	51586375	51586235	51586350	NCOA4	NM_001145260	1	12	10	+	51586271	51586411
262707737	chr10	70331961	70332134	70331989	70332111	TET1	NM_030625	1	12	2	+	70331974	70334009
262724139	chr10	70332374	70332518	70332396	70332490	TET1	NM_030625	1	12	2	+	70331974	70334009
262844720	chr10	70332795	70332963	70332820	70332936	TET1	NM_030625	1	12	2	+	70331974	70334009
262942459	chr10	70333270	70333440	70333293	70333414	TET1	NM_030625	1	12	2	+	70331974	70334009
262895190	chr10	70333680	70333854	70333702	70333829	TET1	NM_030625	1	12	2	+	70331974	70334009
262636340	chr10	70404396	70404564	70404429	70404537	TET1	NM_030625	1	12	4	+	70404455	70406762
262701792	chr10	70404773	70404942	70404800	70404918	TET1	NM_030625	1	12	4	+	70404455	70406762
262800778	chr10	70405225	70405387	70405249	70405362	TET1	NM_030625	1	12	4	+	70404455	70406762
262708254	chr10	70405567	70405718	70405595	70405692	TET1	NM_030625	1	12	4	+	70404455	70406762
262688650	chr10	70405946	70406101	70405967	70406075	TET1	NM_030625	1	12	4	+	70404455	70406762
262685175	chr10	70406393	70406548	70406414	70406526	TET1	NM_030625	1	12	4	+	70404455	70406762
241700476	chr10	70412183	70412316	70412206	70412287	TET1	NM_030625	1	12	6	+	70412258	70412351
240771526	chr10	70426987	70427132	70427008	70427104	TET1	NM_030625	1	12	7	+	70426802	70427013
241349010	chr10	70442566	70442739	70442591	70442713	TET1	NM_030625	1	12	10	+	70442593	70442730
238882482	chr10	70446212	70446386	70446233	70446359	TET1	NM_030625	1	12	11	+	70446113	70446464
239116087	chr10	70450683	70450837	70450704	70450816	TET1	NM_030625	1	12	12	+	70450565	70454239
239199100	chr10	70451114	70451287	70451138	70451265	TET1	NM_030625	1	12	12	+	70450565	70454239
238909628	chr10	70451524	70451685	70451546	70451659	TET1	NM_030625	1	12	12	+	70450565	70454239
312554684	chr10	76602845	76603012	76602865	76602984	KAT6B	NM_012330	3	18	3	+	76602358	76603236
312554684	chr10	76602845	76603012	76602865	76602984	KAT6B	NM_001256468	1	18	3	+	76602358	76603236
312554684	chr10	76602845	76603012	76602865	76602984	KAT6B	NM_001256469	2	18	3	+	76602358	76603236
312263466	chr10	76719738	76719895	76719766	76719868	KAT6B	NM_012330	3	18	4	+	76719728	76719836
312263466	chr10	76719738	76719895	76719766	76719868	KAT6B	NM_001256468	1	18	4	+	76719728	76719836
312263466	chr10	76719738	76719895	76719766	76719868	KAT6B	NM_001256469	2	18	4	+	76719728	76719836
312477596	chr10	76729813	76729947	76729838	76729923	KAT6B	NM_012330	3	18	6	+	76729778	76729859
312477596	chr10	76729813	76729947	76729838	76729923	KAT6B	NM_001256468	1	18	6	+	76729778	76729859
312477596	chr10	76729813	76729947	76729838	76729923	KAT6B	NM_001256469	2	18	6	+	76729778	76729859
312392429	chr10	76735128	76735254	76735159	76735231	KAT6B	NM_001256468	1	18	8	+	76735157	76735539
312392429	chr10	76735128	76735254	76735159	76735231	KAT6B	NM_001256469	2	18	8	+	76735157	76735212
312392429	chr10	76735128	76735254	76735159	76735231	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312438611	chr10	76735438	76735566	76735462	76735542	KAT6B	NM_001256468	1	18	8	+	76735157	76735539
312438611	chr10	76735438	76735566	76735462	76735542	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312439095	chr10	76735818	76735988	76735846	76735961	KAT6B	NM_012330	3	18	8	+	76735157	76736088
312510584	chr10	76738910	76739073	76738935	76739045	KAT6B	NM_012330	3	18	10	+	76738982	76739097
312510584	chr10	76738910	76739073	76738935	76739045	KAT6B	NM_001256468	1	18	10	+	76738982	76739097
312510584	chr10	76738910	76739073	76738935	76739045	KAT6B	NM_001256469	2	18	10	+	76738982	76739097
312390836	chr10	76744764	76744901	76744796	76744879	KAT6B	NM_012330	3	18	12	+	76744838	76744999

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312390836	chr10	76744764	76744901	76744796	76744879	KAT6B	NM_001256468	1	18	12	+	76744838	76744999
312390836	chr10	76744764	76744901	76744796	76744879	KAT6B	NM_001256469	2	18	12	+	76744838	76744999
312579661	chr10	76780286	76780446	76780307	76780424	KAT6B	NM_012330	3	18	14	+	76780340	76780571
312579661	chr10	76780286	76780446	76780307	76780424	KAT6B	NM_001256468	1	18	14	+	76780340	76780571
312579661	chr10	76780286	76780446	76780307	76780424	KAT6B	NM_001256469	2	18	14	+	76780340	76780571
312372501	chr10	76780918	76781056	76780941	76781028	KAT6B	NM_012330	3	18	15	+	76780884	76781043
312372501	chr10	76780918	76781056	76780941	76781028	KAT6B	NM_001256468	1	18	15	+	76780884	76781043
312372501	chr10	76780918	76781056	76780941	76781028	KAT6B	NM_001256469	2	18	15	+	76780884	76781043
312539458	chr10	76781806	76781976	76781832	76781956	KAT6B	NM_012330	3	18	16	+	76781639	76781989
312539458	chr10	76781806	76781976	76781832	76781956	KAT6B	NM_001256468	1	18	16	+	76781639	76781989
312539458	chr10	76781806	76781976	76781832	76781956	KAT6B	NM_001256469	2	18	16	+	76781639	76781989
312586053	chr10	76788185	76788359	76788210	76788337	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312586053	chr10	76788185	76788359	76788210	76788337	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312586053	chr10	76788185	76788359	76788210	76788337	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312654383	chr10	76788614	76788781	76788641	76788756	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312654383	chr10	76788614	76788781	76788641	76788756	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312654383	chr10	76788614	76788781	76788641	76788756	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312639371	chr10	76789076	76789237	76789097	76789214	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312639371	chr10	76789076	76789237	76789097	76789214	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312639371	chr10	76789076	76789237	76789097	76789214	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312660165	chr10	76789560	76789732	76789583	76789711	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312660165	chr10	76789560	76789732	76789583	76789711	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312660165	chr10	76789560	76789732	76789583	76789711	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312621257	chr10	76790034	76790183	76790060	76790160	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312621257	chr10	76790034	76790183	76790060	76790160	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312621257	chr10	76790034	76790183	76790060	76790160	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
312648822	chr10	76790516	76790658	76790542	76790637	KAT6B	NM_012330	3	18	18	+	76788247	76792380
312648822	chr10	76790516	76790658	76790542	76790637	KAT6B	NM_001256468	1	18	18	+	76788247	76792380
312648822	chr10	76790516	76790658	76790542	76790637	KAT6B	NM_001256469	2	18	18	+	76788247	76792380
223432807	chr10	88635799	88635925	88635828	88635899	BMPR1A	NM_004329	1	13	3	+	88635624	88635842
222180599	chr10	88651878	88652036	88651906	88652014	BMPR1A	NM_004329	1	13	5	+	88651884	88651986
222908297	chr10	88659790	88659943	88659813	88659916	BMPR1A	NM_004329	1	13	7	+	88659784	88659883
223169999	chr10	88676936	88677110	88676959	88677084	BMPR1A	NM_004329	1	13	9	+	88676891	88677083
223060116	chr10	88679099	88679243	88679124	88679223	BMPR1A	NM_004329	1	13	10	+	88678929	88679226
223000431	chr10	88683021	88683184	88683050	88683157	BMPR1A	NM_004329	1	13	12	+	88683133	88683263
237976051	chr10	89624184	89624346	89624208	89624322	PTEN	NM_000314	1	9	1	+	89623195	89624305
235012735	chr10	89692672	89692801	89692703	89692773	PTEN	NM_000314	1	9	5	+	89692770	89693008
236528189	chr10	89711782	89711956	89711803	89711928	PTEN	NM_000314	1	9	6	+	89711875	89712016
236178457	chr10	89717724	89717898	89717752	89717869	PTEN	NM_000314	1	9	7	+	89717610	89717776
238889133	chr10	89725029	89725175	89725059	89725147	PTEN	NM_000314	1	9	9	+	89725044	89728532
228708699	chr10	90767414	90767586	90767435	90767558	FAS	NM_152872	3	8	3	+	90767457	90767594

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228708699	chr10	90767414	90767586	90767435	90767558	FAS	NM_152871	2	8	3	+	90767457	90767594
228708699	chr10	90767414	90767586	90767435	90767558	FAS	NR_028036	7	8	3	+	90767457	90767594
228708699	chr10	90767414	90767586	90767435	90767558	FAS	NR_028033	4	7	3	+	90767457	90767594
228708699	chr10	90767414	90767586	90767435	90767558	FAS	NM_000043	1	9	3	+	90767457	90767594
232438424	chr10	90770393	90770560	90770415	90770535	FAS	NM_152872	3	8	6	+	90770510	90770572
232438424	chr10	90770393	90770560	90770415	90770535	FAS	NR_028036	7	8	5	+	90770510	90770572
232438424	chr10	90770393	90770560	90770415	90770535	FAS	NR_028035	6	7	4	+	90770510	90770572
232438424	chr10	90770393	90770560	90770415	90770535	FAS	NM_000043	1	9	6	+	90770510	90770572
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NM_152872	3	8	8	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NM_152871	2	8	8	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NR_028036	7	8	8	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NR_028035	6	7	7	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NR_028034	5	6	6	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NR_028033	4	7	7	+	90773876	90775542
231206950	chr10	90773900	90774036	90773923	90774011	FAS	NM_000043	1	9	9	+	90773876	90775542
286768824	chr10	96522363	96522518	96522388	96522491	CYP2C19	NM_000769	1	9	1	+	96522463	96522630
284949709	chr10	96534894	96535054	96534918	96535033	CYP2C19	NM_000769	1	9	2	+	96534815	96534977
286691724	chr10	96540127	96540285	96540156	96540263	CYP2C19	NM_000769	1	9	4	+	96540256	96540416
287472400	chr10	96541677	96541812	96541704	96541786	CYP2C19	NM_000769	1	9	5	+	96541578	96541754
287793603	chr10	96602660	96602828	96602680	96602801	CYP2C19	NM_000769	1	9	7	+	96602594	96602781
286704751	chr10	96612581	96612750	96612604	96612722	CYP2C19	NM_000769	1	9	9	+	96612490	96612671
294028623	chr10	97956659	97956803	97956686	97956783	BLNK	NM_013314	2	17	16	-	97956664	97956819
294028623	chr10	97956659	97956803	97956686	97956783	BLNK	NM_001114094	1	16	15	-	97956664	97956819
294612486	chr10	97960676	97960843	97960699	97960815	BLNK	NM_013314	2	17	14	-	97960738	97960814
294612486	chr10	97960676	97960843	97960699	97960815	BLNK	NM_001114094	1	16	13	-	97960738	97960814
293928765	chr10	97966725	97966872	97966751	97966845	BLNK	NM_013314	2	17	11	-	97966767	97966809
293928765	chr10	97966725	97966872	97966751	97966845	BLNK	NM_001114094	1	16	10	-	97966767	97966809
294433156	chr10	97975072	97975239	97975095	97975213	BLNK	NM_013314	2	17	8	-	97975077	97975145
293853138	chr10	97987090	97987257	97987109	97987236	BLNK	NM_013314	2	17	5	-	97987166	97987322
293853138	chr10	97987090	97987257	97987109	97987236	BLNK	NM_001114094	1	16	5	-	97987166	97987322
293814570	chr10	98006636	98006809	98006663	98006787	BLNK	NM_013314	2	17	2	-	98006740	98006805
293814570	chr10	98006636	98006809	98006663	98006787	BLNK	NM_001114094	1	16	2	-	98006740	98006805
264723004	chr10	102891383	102891537	102891400	102891516	TLX1	NM_005521	2	3	1	+	102891061	102891866
264723004	chr10	102891383	102891537	102891400	102891516	TLX1	NM_001195517	1	3	1	+	102891061	102891866
262941862	chr10	102893983	102894117	102894002	102894095	TLX1	NM_005521	2	3	2	+	102893932	102894133
262941862	chr10	102893983	102894117	102894002	102894095	TLX1	NM_001195517	1	3	2	+	102893932	102894133
266222728	chr10	102896554	102896696	102896571	102896677	TLX1	NM_001195517	1	3	3	+	102896425	102897546
266222728	chr10	102896554	102896696	102896571	102896677	TLX1	NM_005521	2	3	3	+	102896448	102897546
257868066	chr10	104156170	104156313	104156190	104156291	NFKB2	NM_002502	3	23	4	+	104156206	104156246
257868066	chr10	104156170	104156313	104156190	104156291	NFKB2	NM_001077494	2	23	4	+	104156206	104156246
257868066	chr10	104156170	104156313	104156190	104156291	NFKB2	NM_001077493	1	23	4	+	104156206	104156246

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236594430	chr10	104156951	104157118	104156973	104157090	NFKB2	NM_002502	3	23	7	+	104157059	104157165
236594430	chr10	104156951	104157118	104156973	104157090	NFKB2	NM_001077494	2	23	7	+	104157059	104157165
236594430	chr10	104156951	104157118	104156973	104157090	NFKB2	NM_001077493	1	23	7	+	104157059	104157165
235889035	chr10	104157690	104157862	104157711	104157842	NFKB2	NM_002502	3	23	9	+	104157738	104157842
235889035	chr10	104157690	104157862	104157711	104157842	NFKB2	NM_001077494	2	23	9	+	104157738	104157842
235889035	chr10	104157690	104157862	104157711	104157842	NFKB2	NM_001077493	1	23	9	+	104157738	104157842
237158839	chr10	104158450	104158621	104158474	104158602	NFKB2	NM_002502	3	23	12	+	104158496	104158621
237158839	chr10	104158450	104158621	104158474	104158602	NFKB2	NM_001077494	2	23	12	+	104158496	104158621
237158839	chr10	104158450	104158621	104158474	104158602	NFKB2	NM_001077493	1	23	12	+	104158496	104158621
239929896	chr10	104159245	104159406	104159265	104159387	NFKB2	NM_002502	3	23	14	+	104159334	104159475
239929896	chr10	104159245	104159406	104159265	104159387	NFKB2	NM_001077494	2	23	14	+	104159334	104159475
239929896	chr10	104159245	104159406	104159265	104159387	NFKB2	NM_001077493	1	23	14	+	104159334	104159475
241360432	chr10	104160009	104160150	104160028	104160130	NFKB2	NM_002502	3	23	16	+	104160035	104160248
241360432	chr10	104160009	104160150	104160028	104160130	NFKB2	NM_001077494	2	23	16	+	104160035	104160248
241360432	chr10	104160009	104160150	104160028	104160130	NFKB2	NM_001077493	1	23	16	+	104160035	104160248
257366070	chr10	104160662	104160826	104160682	104160807	NFKB2	NM_002502	3	23	18	+	104160704	104160806
257366070	chr10	104160662	104160826	104160682	104160807	NFKB2	NM_001077494	2	23	18	+	104160704	104160806
257366070	chr10	104160662	104160826	104160682	104160807	NFKB2	NM_001077493	1	23	18	+	104160704	104160806
257965684	chr10	104161478	104161651	104161501	104161630	NFKB2	NM_002502	3	23	21	+	104161502	104161674
257965684	chr10	104161478	104161651	104161501	104161630	NFKB2	NM_001077494	2	23	21	+	104161502	104161674
257965684	chr10	104161478	104161651	104161501	104161630	NFKB2	NM_001077493	1	23	21	+	104161502	104161674
237772923	chr10	104263863	104264025	104263883	104264006	SUFU	NM_016169	2	12	1	+	104263719	104264091
237772923	chr10	104263863	104264025	104263883	104264006	SUFU	NM_001178133	1	11	1	+	104263719	104264091
238592482	chr10	104309619	104309788	104309641	104309764	SUFU	NM_016169	2	12	3	+	104309727	104309863
238592482	chr10	104309619	104309788	104309641	104309764	SUFU	NM_001178133	1	11	3	+	104309727	104309863
260752233	chr10	104353349	104353499	104353370	104353478	SUFU	NM_016169	2	12	5	+	104353393	104353478
260752233	chr10	104353349	104353499	104353370	104353478	SUFU	NM_001178133	1	11	5	+	104353393	104353478
240590166	chr10	104359079	104359253	104359102	104359232	SUFU	NM_016169	2	12	8	+	104359190	104359301
240590166	chr10	104359079	104359253	104359102	104359232	SUFU	NM_001178133	1	11	8	+	104359190	104359301
238809192	chr10	104377024	104377197	104377046	104377176	SUFU	NM_016169	2	12	10	+	104377047	104377185
238809192	chr10	104377024	104377197	104377046	104377176	SUFU	NM_001178133	1	11	10	+	104377047	104377185
260714479	chr10	104389754	104389878	104389777	104389855	SUFU	NM_016169	2	12	12	+	104389823	104393214
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001146283	2	13	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198526	7	13	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_030756	13	14	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001146286	5	12	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001146285	4	13	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198530	11	11	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198529	10	13	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198525	6	15	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198531	12	13	1	+	114710009	114710704

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001146274	1	14	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198528	9	15	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001198527	8	15	1	+	114710009	114710704
274209126	chr10	114710645	114710784	114710674	114710760	TCF7L2	NM_001146284	3	13	1	+	114710009	114710704
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001146283	2	13	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198526	7	13	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_030756	13	14	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001146286	5	12	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001146285	4	13	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198529	10	13	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198525	6	15	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198531	12	13	5	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001146274	1	14	5	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198528	9	15	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001198527	8	15	4	+	114799784	114799885
273838365	chr10	114799681	114799808	114799705	114799787	TCF7L2	NM_001146284	3	13	4	+	114799784	114799885
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001146283	2	13	6	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198526	7	13	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_030756	13	14	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001146286	5	12	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001146285	4	13	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198530	11	11	4	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198529	10	13	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198525	6	15	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198531	12	13	6	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001146274	1	14	6	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198528	9	15	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001198527	8	15	5	+	114900943	114901075
272976878	chr10	114900908	114901051	114900931	114901029	TCF7L2	NM_001146284	3	13	5	+	114900943	114901075
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001146283	2	13	8	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198526	7	13	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_030756	13	14	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001146286	5	12	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001146285	4	13	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198530	11	11	6	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198529	10	13	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198525	6	15	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198531	12	13	8	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001146274	1	14	8	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198528	9	15	7	+	114905770	114905856
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001198527	8	15	7	+	114905770	114905856

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273266842	chr10	114905725	114905899	114905749	114905877	TCF7L2	NM_001146284	3	13	7	+	114905770	114905856
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001146283	2	13	10	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198526	7	13	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_030756	13	14	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001146286	5	12	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001146285	4	13	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198530	11	11	8	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198529	10	13	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198525	6	15	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198531	12	13	10	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001146274	1	14	10	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198528	9	15	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001198527	8	15	9	+	114911484	114911643
273612098	chr10	114911521	114911664	114911548	114911644	TCF7L2	NM_001146284	3	13	9	+	114911484	114911643
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_030756	13	14	12	+	114918426	114918476
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_001198529	10	13	12	+	114918426	114918476
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_001198525	6	15	12	+	114918426	114918476
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_001198528	9	15	12	+	114918426	114918476
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_001198527	8	15	12	+	114918426	114918476
273374911	chr10	114918442	114918586	114918467	114918556	TCF7L2	NM_001146284	3	13	12	+	114918426	114918476
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001146283	2	13	13	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198526	7	13	13	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_030756	13	14	14	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001146286	5	12	12	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001146285	4	13	13	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198530	11	11	11	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198529	10	13	13	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198525	6	15	15	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198531	12	13	13	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001146274	1	14	14	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198528	9	15	15	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001198527	8	15	15	+	114925314	114927436
274200063	chr10	114925202	114925345	114925223	114925320	TCF7L2	NM_001146284	3	13	13	+	114925314	114927436
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_001144915	4	17	17	-	123237844	123239184
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_001144918	7	16	16	-	123237844	123239535
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_000141	1	18	18	-	123237844	123239535
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_001144917	6	16	16	-	123237844	123239535
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_001144916	5	15	15	-	123237844	123239535
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_022970	9	18	18	-	123237844	123239535
230781525	chr10	123239072	123239207	123239090	123239181	FGFR2	NM_001144914	3	15	15	-	123237844	123239535
227820775	chr10	123241644	123241784	123241668	123241756	FGFR2	NM_001144913	2	17	17	-	123241367	123241691

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227820775	chr10	123241644	123241784	123241668	123241756	FGFR2	NM_001144919	8	17	17	-	123241367	123241691
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144913	2	17	15	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144918	7	16	14	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_000141	1	18	16	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144917	6	16	14	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144916	5	15	13	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_022970	9	18	16	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144914	3	15	13	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144915	4	17	15	-	123244909	123245046
228928425	chr10	123244903	123245071	123244925	123245049	FGFR2	NM_001144919	8	17	15	-	123244909	123245046
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144913	2	17	13	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144918	7	16	12	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_000141	1	18	14	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144917	6	16	12	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144916	5	15	11	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_022970	9	18	14	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144914	3	15	11	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144915	4	17	13	-	123247505	123247627
232242923	chr10	123247552	123247684	123247581	123247660	FGFR2	NM_001144919	8	17	13	-	123247505	123247627
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144913	2	17	10	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144918	7	16	9	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_000141	1	18	11	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144917	6	16	9	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144916	5	15	8	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_022970	9	18	11	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144914	3	15	8	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144915	4	17	10	-	123260340	123260461
227804434	chr10	123260264	123260436	123260288	123260415	FGFR2	NM_001144919	8	17	10	-	123260340	123260461
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144918	7	16	7	-	123274637	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144913	2	17	8	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_000141	1	18	9	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144916	5	15	6	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_022970	9	18	9	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144914	3	15	6	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144915	4	17	8	-	123274631	123274833
228049669	chr10	123274572	123274733	123274591	123274711	FGFR2	NM_001144919	8	17	8	-	123274631	123274833
232640301	chr10	123278099	123278256	123278120	123278232	FGFR2	NM_001144913	2	17	7	-	123278196	123278343
232640301	chr10	123278099	123278256	123278120	123278232	FGFR2	NM_022970	9	18	8	-	123278196	123278343
232640301	chr10	123278099	123278256	123278120	123278232	FGFR2	NM_001144919	8	17	7	-	123278196	123278343
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144913	2	17	5	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144918	7	16	4	-	123298106	123298229

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_000141	1	18	6	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144917	6	16	6	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144916	5	15	3	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_022970	9	18	6	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144914	3	15	5	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144915	4	17	5	-	123298106	123298229
232469173	chr10	123298004	123298138	123298031	123298115	FGFR2	NM_001144919	8	17	5	-	123298106	123298229
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_001144913	2	17	3	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_000141	1	18	4	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_001144917	6	16	4	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_022970	9	18	4	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_001144914	3	15	3	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_001144915	4	17	3	-	123324016	123324093
228652940	chr10	123323996	123324125	123324015	123324097	FGFR2	NM_001144919	8	17	3	-	123324016	123324093
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144916	5	15	1	-	123353223	123353772
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144913	2	17	1	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144918	7	16	2	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_000141	1	18	2	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144917	6	16	2	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_022970	9	18	2	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144914	3	15	1	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144915	4	17	2	-	123353223	123353481
227721433	chr10	123353123	123353265	123353149	123353241	FGFR2	NM_001144919	8	17	2	-	123353223	123353481
227387971	chr11	533461	533633	533480	533613	HRAS	NM_001130442	1	5	4	-	533453	533612
227387971	chr11	533461	533633	533480	533613	HRAS	NM_176795	3	6	4	-	533453	533612
227387971	chr11	533461	533633	533480	533613	HRAS	NM_005343	2	6	4	-	533453	533612
227444926	chr11	534140	534267	534159	534246	HRAS	NM_001130442	1	5	2	-	534212	534375
227444926	chr11	534140	534267	534159	534246	HRAS	NM_176795	3	6	2	-	534212	534375
227444926	chr11	534140	534267	534159	534246	HRAS	NM_005343	2	6	2	-	534212	534375
330093466	chr11	2154397	2154571	2154420	2154547	IGF2	NM_000612	1	4	4	-	2150347	2154453
330093466	chr11	2154397	2154571	2154420	2154547	IGF2	NM_001127598	3	5	5	-	2150347	2154453
330093466	chr11	2154397	2154571	2154420	2154547	IGF2	NM_001007139	2	5	5	-	2150347	2154453
330130572	chr11	2156654	2156789	2156672	2156772	IGF2	NM_000612	1	4	2	-	2156597	2156759
330130572	chr11	2156654	2156789	2156672	2156772	IGF2	NM_001127598	3	5	3	-	2156597	2156759
330130572	chr11	2156654	2156789	2156672	2156772	IGF2	NM_001007139	2	5	3	-	2156597	2156759
235781911	chr11	3697415	3697573	3697437	3697552	NUP98	NM_016320	2	33	33	-	3696240	3697606
235781911	chr11	3697415	3697573	3697437	3697552	NUP98	NM_139132	4	32	32	-	3696240	3697606
237216613	chr11	3700823	3700971	3700845	3700943	NUP98	NM_016320	2	33	31	-	3700784	3700938
237216613	chr11	3700823	3700971	3700845	3700943	NUP98	NM_139132	4	32	30	-	3700784	3700938
236040694	chr11	3707181	3707337	3707202	3707315	NUP98	NM_016320	2	33	29	-	3707203	3707424
240144463	chr11	3714385	3714538	3714405	3714511	NUP98	NM_016320	2	33	27	-	3714462	3714605

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240144463	chr11	3714385	3714538	3714405	3714511	NUP98	NM_139132	4	32	27	-	3714462	3714605
236067958	chr11	3720216	3720380	3720240	3720358	NUP98	NM_016320	2	33	25	-	3720312	3720578
236067958	chr11	3720216	3720380	3720240	3720358	NUP98	NM_139132	4	32	25	-	3720312	3720578
236639674	chr11	3721848	3722020	3721872	3721991	NUP98	NM_016320	2	33	24	-	3721840	3722069
236639674	chr11	3721848	3722020	3721872	3721991	NUP98	NM_139132	4	32	24	-	3721840	3722069
237347538	chr11	3723871	3724043	3723892	3724016	NUP98	NM_016320	2	33	23	-	3723693	3724122
237347538	chr11	3723871	3724043	3723892	3724016	NUP98	NM_139132	4	32	23	-	3723693	3724122
237660525	chr11	3727600	3727769	3727625	3727746	NUP98	NM_016320	2	33	21	-	3727675	3727857
237660525	chr11	3727600	3727769	3727625	3727746	NUP98	NM_139132	4	32	21	-	3727675	3727857
238856536	chr11	3734935	3735108	3734964	3735084	NUP98	NM_005387	1	20	19	-	3735048	3735225
238856536	chr11	3734935	3735108	3734964	3735084	NUP98	NM_139131	3	20	19	-	3735048	3735225
238856536	chr11	3734935	3735108	3734964	3735084	NUP98	NM_016320	2	33	19	-	3735048	3735225
238856536	chr11	3734935	3735108	3734964	3735084	NUP98	NM_139132	4	32	19	-	3735048	3735225
235172751	chr11	3741897	3742061	3741921	3742032	NUP98	NM_005387	1	20	17	-	3741942	3742055
235172751	chr11	3741897	3742061	3741921	3742032	NUP98	NM_139131	3	20	17	-	3741942	3742055
235172751	chr11	3741897	3742061	3741921	3742032	NUP98	NM_016320	2	33	17	-	3741942	3742055
235172751	chr11	3741897	3742061	3741921	3742032	NUP98	NM_139132	4	32	17	-	3741942	3742055
236522963	chr11	3746280	3746450	3746313	3746422	NUP98	NM_005387	1	20	15	-	3746333	3746449
236522963	chr11	3746280	3746450	3746313	3746422	NUP98	NM_139131	3	20	15	-	3746333	3746449
236522963	chr11	3746280	3746450	3746313	3746422	NUP98	NM_016320	2	33	15	-	3746333	3746449
236522963	chr11	3746280	3746450	3746313	3746422	NUP98	NM_139132	4	32	15	-	3746333	3746449
236961869	chr11	3756356	3756511	3756384	3756483	NUP98	NM_005387	1	20	13	-	3756421	3756554
236961869	chr11	3756356	3756511	3756384	3756483	NUP98	NM_139131	3	20	13	-	3756421	3756554
236961869	chr11	3756356	3756511	3756384	3756483	NUP98	NM_016320	2	33	13	-	3756421	3756554
236961869	chr11	3756356	3756511	3756384	3756483	NUP98	NM_139132	4	32	13	-	3756421	3756554
236009827	chr11	3774498	3774668	3774521	3774640	NUP98	NM_005387	1	20	11	-	3774546	3774638
236009827	chr11	3774498	3774668	3774521	3774640	NUP98	NM_139131	3	20	11	-	3774546	3774638
236009827	chr11	3774498	3774668	3774521	3774640	NUP98	NM_016320	2	33	11	-	3774546	3774638
236009827	chr11	3774498	3774668	3774521	3774640	NUP98	NM_139132	4	32	11	-	3774546	3774638
237791372	chr11	3784197	3784329	3784218	3784301	NUP98	NM_005387	1	20	9	-	3784132	3784269
237791372	chr11	3784197	3784329	3784218	3784301	NUP98	NM_139131	3	20	9	-	3784132	3784269
237791372	chr11	3784197	3784329	3784218	3784301	NUP98	NM_016320	2	33	9	-	3784132	3784269
237791372	chr11	3784197	3784329	3784218	3784301	NUP98	NM_139132	4	32	9	-	3784132	3784269
236106254	chr11	3793055	3793180	3793076	3793154	NUP98	NM_005387	1	20	7	-	3792978	3793158
236106254	chr11	3793055	3793180	3793076	3793154	NUP98	NM_139131	3	20	7	-	3792978	3793158
236106254	chr11	3793055	3793180	3793076	3793154	NUP98	NM_016320	2	33	7	-	3792978	3793158
236106254	chr11	3793055	3793180	3793076	3793154	NUP98	NM_139132	4	32	7	-	3792978	3793158
237224709	chr11	3797173	3797325	3797194	3797298	NUP98	NM_005387	1	20	5	-	3797112	3797251
237224709	chr11	3797173	3797325	3797194	3797298	NUP98	NM_139131	3	20	5	-	3797112	3797251
237224709	chr11	3797173	3797325	3797194	3797298	NUP98	NM_016320	2	33	5	-	3797112	3797251
237224709	chr11	3797173	3797325	3797194	3797298	NUP98	NM_139132	4	32	5	-	3797112	3797251

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
236418816	chr11	3800399	3800558	3800421	3800530	NUP98	NM_005387	1	20	3	-	3800386	3800487
236418816	chr11	3800399	3800558	3800421	3800530	NUP98	NM_139131	3	20	3	-	3800386	3800487
236418816	chr11	3800399	3800558	3800421	3800530	NUP98	NM_016320	2	33	3	-	3800386	3800487
236418816	chr11	3800399	3800558	3800421	3800530	NUP98	NM_139132	4	32	3	-	3800386	3800487
294187859	chr11	4123104	4123276	4123131	4123248	RRM1	NM_001033	1	19	2	+	4123223	4123311
294145451	chr11	4128555	4128729	4128581	4128711	RRM1	NM_001033	1	19	4	+	4128665	4128765
294679080	chr11	4133075	4133205	4133102	4133178	RRM1	NM_001033	1	19	7	+	4133130	4133292
295374367	chr11	4141033	4141186	4141053	4141158	RRM1	NM_001033	1	19	9	+	4141075	4141158
293967181	chr11	4143357	4143517	4143384	4143492	RRM1	NM_001033	1	19	11	+	4143371	4143450
294165497	chr11	4147834	4147979	4147855	4147954	RRM1	NM_001033	1	19	13	+	4147914	4148063
293963463	chr11	4148364	4148519	4148391	4148491	RRM1	NM_001033	1	19	14	+	4148265	4148486
294093373	chr11	4154724	4154874	4154751	4154848	RRM1	NM_001033	1	19	17	+	4154793	4154888
295413041	chr11	4156420	4156551	4156446	4156523	RRM1	NM_001033	1	19	18	+	4156312	4156500
232901991	chr11	22646142	22646300	22646167	22646276	FANCF	NM_022725	1	1	1	-	22644079	22647387
230647094	chr11	22646612	22646778	22646635	22646760	FANCF	NM_022725	1	1	1	-	22644079	22647387
230565239	chr11	22647083	22647240	22647101	22647221	FANCF	NM_022725	1	1	1	-	22644079	22647387
239558795	chr11	32410612	32410748	32410634	32410725	WT1	NM_000378	1	9	9	-	32409322	32410725
239558795	chr11	32410612	32410748	32410634	32410725	WT1	NM_001198552	3	9	9	-	32409322	32410725
239558795	chr11	32410612	32410748	32410634	32410725	WT1	NM_001198551	2	10	10	-	32409322	32410725
239558795	chr11	32410612	32410748	32410634	32410725	WT1	NM_024426	5	10	10	-	32409322	32410725
239558795	chr11	32410612	32410748	32410634	32410725	WT1	NM_024424	4	10	10	-	32409322	32410725
240673548	chr11	32417709	32417870	32417731	32417842	WT1	NM_000378	1	9	6	-	32417803	32417953
240673548	chr11	32417709	32417870	32417731	32417842	WT1	NM_001198552	3	9	6	-	32417803	32417953
240673548	chr11	32417709	32417870	32417731	32417842	WT1	NM_001198551	2	10	7	-	32417803	32417953
240673548	chr11	32417709	32417870	32417731	32417842	WT1	NM_024426	5	10	7	-	32417803	32417953
240673548	chr11	32417709	32417870	32417731	32417842	WT1	NM_024424	4	10	7	-	32417803	32417953
241663938	chr11	32437939	32438112	32437960	32438087	WT1	NM_001198551	2	10	5	-	32438036	32438086
241663938	chr11	32437939	32438112	32437960	32438087	WT1	NM_024426	5	10	5	-	32438036	32438086
241663938	chr11	32437939	32438112	32437960	32438087	WT1	NM_024424	4	10	5	-	32438036	32438086
238651096	chr11	32449491	32449631	32449510	32449609	WT1	NM_000378	1	9	3	-	32449502	32449604
238651096	chr11	32449491	32449631	32449510	32449609	WT1	NM_001198552	3	9	3	-	32449502	32449604
238651096	chr11	32449491	32449631	32449510	32449609	WT1	NM_001198551	2	10	3	-	32449502	32449604
238651096	chr11	32449491	32449631	32449510	32449609	WT1	NM_024426	5	10	3	-	32449502	32449604
238651096	chr11	32449491	32449631	32449510	32449609	WT1	NM_024424	4	10	3	-	32449502	32449604
262312722	chr11	32456177	32456306	32456197	32456287	WT1	NM_000378	1	9	1	-	32456246	32457081
262312722	chr11	32456177	32456306	32456197	32456287	WT1	NM_024426	5	10	1	-	32456246	32457081
262312722	chr11	32456177	32456306	32456197	32456287	WT1	NM_024424	4	10	1	-	32456246	32457081
262327761	chr11	32456672	32456823	32456689	32456805	WT1	NM_000378	1	9	1	-	32456246	32457081
262327761	chr11	32456672	32456823	32456689	32456805	WT1	NM_024426	5	10	1	-	32456246	32457081
262327761	chr11	32456672	32456823	32456689	32456805	WT1	NM_024424	4	10	1	-	32456246	32457081
230535354	chr11	44129173	44129347	44129201	44129321	EXT2	NM_000401	1	14	2	+	44129233	44129798

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230535354	chr11	44129173	44129347	44129201	44129321	EXT2	NM_001178083	2	15	2	+	44129233	44129798
230535354	chr11	44129173	44129347	44129201	44129321	EXT2	NM_207122	3	14	2	+	44129233	44129798
230572700	chr11	44129661	44129822	44129682	44129799	EXT2	NM_000401	1	14	2	+	44129233	44129798
230572700	chr11	44129661	44129822	44129682	44129799	EXT2	NM_001178083	2	15	2	+	44129233	44129798
230572700	chr11	44129661	44129822	44129682	44129799	EXT2	NM_207122	3	14	2	+	44129233	44129798
229271159	chr11	44135753	44135926	44135776	44135904	EXT2	NM_000401	1	14	4	+	44135735	44135851
229271159	chr11	44135753	44135926	44135776	44135904	EXT2	NM_001178083	2	15	4	+	44135735	44135851
229271159	chr11	44135753	44135926	44135776	44135904	EXT2	NM_207122	3	14	4	+	44135735	44135851
229909299	chr11	44148448	44148591	44148470	44148562	EXT2	NM_000401	1	14	6	+	44148366	44148505
229909299	chr11	44148448	44148591	44148470	44148562	EXT2	NM_001178083	2	15	6	+	44148366	44148505
229909299	chr11	44148448	44148591	44148470	44148562	EXT2	NM_207122	3	14	6	+	44148366	44148505
231054642	chr11	44193065	44193208	44193090	44193185	EXT2	NM_000401	1	14	8	+	44193161	44193292
231054642	chr11	44193065	44193208	44193090	44193185	EXT2	NM_207122	3	14	8	+	44193161	44193292
231607889	chr11	44228238	44228411	44228263	44228384	EXT2	NM_000401	1	14	10	+	44228343	44228509
231607889	chr11	44228238	44228411	44228263	44228384	EXT2	NM_001178083	2	15	11	+	44228343	44228509
231607889	chr11	44228238	44228411	44228263	44228384	EXT2	NM_207122	3	14	10	+	44228343	44228509
230438047	chr11	44253953	44254087	44253979	44254064	EXT2	NM_000401	1	14	11	+	44253903	44254046
230438047	chr11	44253953	44254087	44253979	44254064	EXT2	NM_001178083	2	15	12	+	44253903	44254046
230438047	chr11	44253953	44254087	44253979	44254064	EXT2	NM_207122	3	14	11	+	44253903	44254046
230851855	chr11	44265694	44265858	44265716	44265837	EXT2	NM_000401	1	14	14	+	44265699	44266980
230851855	chr11	44265694	44265858	44265716	44265837	EXT2	NM_001178083	2	15	15	+	44265699	44266980
230851855	chr11	44265694	44265858	44265716	44265837	EXT2	NM_207122	3	14	14	+	44265699	44266980
228074500	chr11	47237881	47238055	47237902	47238032	DDB2	NM_000107	1	10	2	+	47237887	47238023
229467224	chr11	47254326	47254456	47254348	47254434	DDB2	NM_000107	1	10	4	+	47254365	47254510
228691940	chr11	47256193	47256349	47256214	47256325	DDB2	NM_000107	1	10	6	+	47256308	47256485
228691940	chr11	47256193	47256349	47256214	47256325	DDB2	NM_000107	1	10	5	+	47256124	47256223
228823341	chr11	47256862	47257012	47256883	47256990	DDB2	NM_000107	1	10	7	+	47256821	47256963
232384922	chr11	47260291	47260424	47260312	47260403	DDB2	NM_000107	1	10	10	+	47260351	47260769
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130800	3	10	10	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130803	6	10	10	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130802	5	10	10	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130801	4	10	10	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130804	7	11	11	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_000244	1	10	10	-	64570986	64572288
234683375	chr11	64572125	64572285	64572142	64572267	MEN1	NM_130799	2	10	10	-	64570986	64572288
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130800	3	10	8	-	64573107	64573242
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130803	6	10	8	-	64573107	64573242
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130802	5	10	8	-	64573107	64573242
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130801	4	10	8	-	64573107	64573242
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130804	7	11	9	-	64573107	64573242
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_000244	1	10	8	-	64573107	64573242

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
231864044	chr11	64573009	64573180	64573030	64573160	MEN1	NM_130799	2	10	8	-	64573107	64573242
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130800	3	10	6	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130803	6	10	6	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130802	5	10	6	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130801	4	10	6	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130804	7	11	7	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_000244	1	10	6	-	64574483	64574570
232658748	chr11	64574432	64574597	64574453	64574571	MEN1	NM_130799	2	10	6	-	64574483	64574570
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130800	3	10	3	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130803	6	10	3	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130802	5	10	3	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130801	4	10	3	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130804	7	11	4	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_000244	1	10	3	-	64575363	64575571
233661958	chr11	64575435	64575608	64575454	64575584	MEN1	NM_130799	2	10	3	-	64575363	64575571
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130800	3	10	2	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130803	6	10	2	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130802	5	10	2	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130801	4	10	2	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130804	7	11	3	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_000244	1	10	2	-	64577122	64577604
231207881	chr11	64577417	64577566	64577435	64577547	MEN1	NM_130799	2	10	2	-	64577137	64577604
253642417	chr11	69456199	69456323	69456220	69456298	CCND1	NM_053056	1	5	1	+	69455873	69456279
226435281	chr11	69458578	69458702	69458596	69458683	CCND1	NM_053056	1	5	3	+	69458600	69458759
226971562	chr11	69465782	69465940	69465806	69465921	CCND1	NM_053056	1	5	5	+	69465886	69469242
237736714	chr11	71714913	71715064	71714932	71715043	NUMA1	NM_006185	1	27	26	-	71714933	71715145
236053538	chr11	71715736	71715906	71715753	71715883	NUMA1	NM_006185	1	27	24	-	71715686	71715862
236640700	chr11	71717171	71717345	71717193	71717321	NUMA1	NM_006185	1	27	22	-	71717081	71717309
237957637	chr11	71719685	71719856	71719707	71719835	NUMA1	NM_006185	1	27	20	-	71719734	71719891
238733857	chr11	71720180	71720333	71720202	71720310	NUMA1	NM_006185	1	27	19	-	71720013	71720231
237399437	chr11	71723384	71723531	71723405	71723507	NUMA1	NM_006185	1	27	16	-	71723447	71723488
258186555	chr11	71724244	71724408	71724264	71724391	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238450256	chr11	71724635	71724799	71724654	71724780	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258140673	chr11	71725020	71725170	71725041	71725152	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238404364	chr11	71725451	71725623	71725472	71725602	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258176544	chr11	71725917	71726059	71725938	71726037	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258234352	chr11	71726284	71726428	71726305	71726404	NUMA1	NM_006185	1	27	15	-	71723941	71727306
258224394	chr11	71726733	71726898	71726751	71726879	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238160056	chr11	71727224	71727390	71727246	71727367	NUMA1	NM_006185	1	27	15	-	71723941	71727306
238711791	chr11	71729107	71729256	71729132	71729233	NUMA1	NM_006185	1	27	12	-	71729229	71729346
236311791	chr11	71729815	71729948	71729835	71729926	NUMA1	NM_006185	1	27	10	-	71729869	71730026

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237757670	chr11	71732221	71732379	71732243	71732352	NUMA1	NM_006185	1	27	8	-	71732250	71732337
238461555	chr11	71740199	71740362	71740221	71740336	NUMA1	NM_006185	1	27	4	-	71740251	71740336
235535331	chr11	94163087	94163217	94163114	94163190	MRE11A	NM_005591	2	20	19	-	94163077	94163152
235535331	chr11	94163087	94163217	94163114	94163190	MRE11A	NM_005590	1	19	18	-	94163077	94163152
236770477	chr11	94178955	94179115	94178983	94179088	MRE11A	NM_005591	2	20	16	-	94178976	94179059
238877237	chr11	94192565	94192699	94192593	94192673	MRE11A	NM_005591	2	20	13	-	94192574	94192747
238877237	chr11	94192565	94192699	94192593	94192673	MRE11A	NM_005590	1	19	13	-	94192574	94192747
235717175	chr11	94197285	94197451	94197312	94197426	MRE11A	NM_005591	2	20	11	-	94197279	94197405
235717175	chr11	94197285	94197451	94197312	94197426	MRE11A	NM_005590	1	19	11	-	94197279	94197405
237412111	chr11	94203647	94203816	94203669	94203793	MRE11A	NM_005591	2	20	9	-	94203637	94203808
237412111	chr11	94203647	94203816	94203669	94203793	MRE11A	NM_005590	1	19	9	-	94203637	94203808
235380215	chr11	94209414	94209586	94209436	94209559	MRE11A	NM_005591	2	20	7	-	94209455	94209569
235380215	chr11	94209414	94209586	94209436	94209559	MRE11A	NM_005590	1	19	7	-	94209455	94209569
235914054	chr11	94212715	94212882	94212744	94212854	MRE11A	NM_005591	2	20	5	-	94212840	94212927
235914054	chr11	94212715	94212882	94212744	94212854	MRE11A	NM_005590	1	19	5	-	94212840	94212927
235309467	chr11	94223898	94224055	94223926	94224027	MRE11A	NM_005591	2	20	3	-	94223999	94224131
235309467	chr11	94223898	94224055	94223926	94224027	MRE11A	NM_005590	1	19	3	-	94223999	94224131
234482705	chr11	95712120	95712281	95712147	95712259	MAML2	NM_032427	1	5	5	-	95711440	95713127
234490968	chr11	95712575	95712740	95712597	95712714	MAML2	NM_032427	1	5	5	-	95711440	95713127
234496587	chr11	95713010	95713176	95713031	95713148	MAML2	NM_032427	1	5	5	-	95711440	95713127
233042373	chr11	95825017	95825185	95825043	95825165	MAML2	NM_032427	1	5	2	-	95825056	95826681
234516291	chr11	95825755	95825898	95825778	95825877	MAML2	NM_032427	1	5	2	-	95825056	95826681
234524686	chr11	95826208	95826379	95826232	95826356	MAML2	NM_032427	1	5	2	-	95825056	95826681
234511691	chr11	95826629	95826756	95826654	95826726	MAML2	NM_032427	1	5	2	-	95825056	95826681
233187793	chr11	96074943	96075093	96074962	96075072	MAML2	NM_032427	1	5	1	-	96074547	96076344
222391345	chr11	102195515	102195649	102195537	102195626	BIRC3	NM_182962	2	10	3	+	102195192	102196093
222391345	chr11	102195515	102195649	102195537	102195626	BIRC3	NM_001165	1	9	2	+	102192568	102196093
222474390	chr11	102195945	102196095	102195973	102196070	BIRC3	NM_182962	2	10	3	+	102195192	102196093
222474390	chr11	102195945	102196095	102195973	102196070	BIRC3	NM_001165	1	9	2	+	102192568	102196093
223939058	chr11	102198667	102198841	102198692	102198819	BIRC3	NM_182962	2	10	5	+	102198783	102198861
223939058	chr11	102198667	102198841	102198692	102198819	BIRC3	NM_001165	1	9	4	+	102198783	102198861
222996885	chr11	102201734	102201862	102201758	102201834	BIRC3	NM_182962	2	10	7	+	102201730	102201972
222996885	chr11	102201734	102201862	102201758	102201834	BIRC3	NM_001165	1	9	6	+	102201730	102201972
222723909	chr11	102206783	102206943	102206812	102206918	BIRC3	NM_182962	2	10	8	+	102206697	102206951
222723909	chr11	102206783	102206943	102206812	102206918	BIRC3	NM_001165	1	9	7	+	102206697	102206951
224050788	chr11	102207658	102207813	102207685	102207785	BIRC3	NM_182962	2	10	10	+	102207640	102210135
224050788	chr11	102207658	102207813	102207685	102207785	BIRC3	NM_001165	1	9	9	+	102207640	102210135
295146914	chr11	102220715	102220872	102220742	102220846	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294262511	chr11	102221150	102221297	102221178	102221273	BIRC2	NM_001166	1	9	2	+	102219329	102221480
294933106	chr11	102221463	102221615	102221491	102221591	BIRC2	NM_001166	1	9	3	+	102221575	102221674
294633037	chr11	102239134	102239304	102239161	102239283	BIRC2	NM_001166	1	9	6	+	102239037	102239279

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293816315	chr11	102248599	102248738	102248629	102248710	BIRC2	NM_001166	1	9	8	+	102248588	102248629
270133652	chr11	106558236	106558402	106558261	106558379	GUCY1A2	NM_000855	1	8	8	-	106544738	106558482
270133652	chr11	106558236	106558402	106558261	106558379	GUCY1A2	NM_001256424	2	9	9	-	106544738	106558482
271800930	chr11	106647039	106647210	106647060	106647186	GUCY1A2	NM_000855	1	8	6	-	106647165	106647308
271800930	chr11	106647039	106647210	106647060	106647186	GUCY1A2	NM_001256424	2	9	6	-	106647165	106647308
272141974	chr11	106680937	106681100	106680964	106681074	GUCY1A2	NM_000855	1	8	5	-	106680719	106681204
272141974	chr11	106680937	106681100	106680964	106681074	GUCY1A2	NM_001256424	2	9	5	-	106680719	106681204
272642351	chr11	106810162	106810336	106810187	106810313	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
272642351	chr11	106810162	106810336	106810187	106810313	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
271254661	chr11	106810654	106810814	106810678	106810792	GUCY1A2	NM_000855	1	8	4	-	106810186	106810904
271254661	chr11	106810654	106810814	106810678	106810792	GUCY1A2	NM_001256424	2	9	4	-	106810186	106810904
270178281	chr11	106856684	106856853	106856711	106856829	GUCY1A2	NM_000855	1	8	2	-	106856796	106856857
270178281	chr11	106856684	106856853	106856711	106856829	GUCY1A2	NM_001256424	2	9	2	-	106856796	106856857
270722096	chr11	106888746	106888878	106888765	106888858	GUCY1A2	NM_000855	1	8	1	-	106888479	106889171
270722096	chr11	106888746	106888878	106888765	106888858	GUCY1A2	NM_001256424	2	9	1	-	106888479	106889171
225134000	chr11	108099933	108100100	108099960	108100072	ATM	NM_000051	1	63	4	+	108099905	108100050
222536388	chr11	108114561	108114711	108114592	108114685	ATM	NM_000051	1	63	6	+	108114680	108114845
222991746	chr11	108115465	108115639	108115489	108115611	ATM	NM_000051	1	63	7	+	108115515	108115753
326891326	chr11	108117736	108117869	108117766	108117845	ATM	NM_000051	1	63	8	+	108117691	108117854
223526436	chr11	108121422	108121576	108121446	108121550	ATM	NM_000051	1	63	10	+	108121428	108121799
223259720	chr11	108122489	108122638	108122516	108122612	ATM	NM_000051	1	63	11	+	108122564	108122758
222803668	chr11	108123584	108123726	108123612	108123704	ATM	NM_000051	1	63	12	+	108123544	108123639
329548352	chr11	108126800	108126972	108126822	108126949	ATM	NM_000051	1	63	14	+	108126942	108127067
224419132	chr11	108128221	108128346	108128248	108128318	ATM	NM_000051	1	63	15	+	108128208	108128333
223649026	chr11	108139089	108139258	108139110	108139235	ATM	NM_000051	1	63	18	+	108139137	108139336
223505887	chr11	108141968	108142107	108141994	108142086	ATM	NM_000051	1	63	20	+	108141978	108142133
223777089	chr11	108143316	108143489	108143341	108143461	ATM	NM_000051	1	63	22	+	108143449	108143579
222424733	chr11	108150247	108150413	108150271	108150385	ATM	NM_000051	1	63	23	+	108150218	108150335
224357617	chr11	108154856	108155022	108154888	108154996	ATM	NM_000051	1	63	26	+	108154954	108155200
223782500	chr11	108158361	108158524	108158386	108158496	ATM	NM_000051	1	63	27	+	108158327	108158442
222738097	chr11	108160355	108160483	108160378	108160464	ATM	NM_000051	1	63	29	+	108160329	108160528
222325224	chr11	108163415	108163549	108163435	108163518	ATM	NM_000051	1	63	30	+	108163346	108163520
223690762	chr11	108170431	108170579	108170457	108170554	ATM	NM_000051	1	63	34	+	108170441	108170612
326881720	chr11	108173517	108173644	108173545	108173617	ATM	NM_000051	1	63	36	+	108173580	108173756
223038506	chr11	108175418	108175560	108175447	108175540	ATM	NM_000051	1	63	37	+	108175402	108175579
222602870	chr11	108180939	108181102	108180962	108181074	ATM	NM_000051	1	63	39	+	108180887	108181042
224718117	chr11	108186586	108186710	108186610	108186683	ATM	NM_000051	1	63	41	+	108186550	108186638
222239028	chr11	108188167	108188302	108188192	108188275	ATM	NM_000051	1	63	43	+	108188100	108188248
223463337	chr11	108196008	108196137	108196034	108196109	ATM	NM_000051	1	63	46	+	108196037	108196271
223561270	chr11	108196860	108196997	108196884	108196964	ATM	NM_000051	1	63	47	+	108196785	108196952
222354520	chr11	108199790	108199935	108199818	108199911	ATM	NM_000051	1	63	49	+	108199748	108199965

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222195404	chr11	108201072	108201199	108201099	108201174	ATM	NM_000051	1	63	50	+	108200941	108201148
222590775	chr11	108202628	108202756	108202656	108202733	ATM	NM_000051	1	63	52	+	108202606	108202764
222310655	chr11	108203558	108203684	108203585	108203658	ATM	NM_000051	1	63	53	+	108203489	108203627
224358740	chr11	108206448	108206620	108206469	108206598	ATM	NM_000051	1	63	56	+	108206572	108206688
223800280	chr11	108216502	108216626	108216526	108216602	ATM	NM_000051	1	63	58	+	108216470	108216635
223522631	chr11	108224377	108224539	108224404	108224514	ATM	NM_000051	1	63	60	+	108224493	108224607
223017601	chr11	108235827	108235972	108235851	108235945	ATM	NM_000051	1	63	62	+	108235809	108235945
239758603	chr11	111958509	111958641	111958537	111958619	SDHD	NM_003002	1	4	2	+	111958581	111958697
263830694	chr11	111965452	111965623	111965479	111965599	SDHD	NM_003002	1	4	4	+	111965529	111966518
234012656	chr11	118342278	118342425	118342301	118342403	MLL	NM_005933	2	36	3	+	118342377	118345030
234012656	chr11	118342278	118342425	118342301	118342403	MLL	NM_001197104	1	36	3	+	118342377	118345030
234023680	chr11	118342662	118342817	118342685	118342790	MLL	NM_005933	2	36	3	+	118342377	118345030
234023680	chr11	118342662	118342817	118342685	118342790	MLL	NM_001197104	1	36	3	+	118342377	118345030
231625192	chr11	118343063	118343198	118343088	118343170	MLL	NM_005933	2	36	3	+	118342377	118345030
231625192	chr11	118343063	118343198	118343088	118343170	MLL	NM_001197104	1	36	3	+	118342377	118345030
231684200	chr11	118343480	118343640	118343508	118343619	MLL	NM_005933	2	36	3	+	118342377	118345030
231684200	chr11	118343480	118343640	118343508	118343619	MLL	NM_001197104	1	36	3	+	118342377	118345030
234019867	chr11	118343903	118344063	118343923	118344038	MLL	NM_005933	2	36	3	+	118342377	118345030
234019867	chr11	118343903	118344063	118343923	118344038	MLL	NM_001197104	1	36	3	+	118342377	118345030
234017106	chr11	118344320	118344476	118344341	118344455	MLL	NM_005933	2	36	3	+	118342377	118345030
234017106	chr11	118344320	118344476	118344341	118344455	MLL	NM_001197104	1	36	3	+	118342377	118345030
234045781	chr11	118344681	118344838	118344706	118344815	MLL	NM_005933	2	36	3	+	118342377	118345030
234045781	chr11	118344681	118344838	118344706	118344815	MLL	NM_001197104	1	36	3	+	118342377	118345030
232242412	chr11	118347598	118347742	118347617	118347717	MLL	NM_005933	2	36	4	+	118347520	118347697
232242412	chr11	118347598	118347742	118347617	118347717	MLL	NM_001197104	1	36	4	+	118347520	118347697
232744466	chr11	118350930	118351075	118350952	118351047	MLL	NM_005933	2	36	6	+	118350889	118350953
232744466	chr11	118350930	118351075	118350952	118351047	MLL	NM_001197104	1	36	6	+	118350889	118350953
233135290	chr11	118352715	118352880	118352736	118352857	MLL	NM_005933	2	36	7	+	118352430	118352807
233135290	chr11	118352715	118352880	118352736	118352857	MLL	NM_001197104	1	36	7	+	118352430	118352807
233255121	chr11	118355547	118355714	118355573	118355690	MLL	NM_005933	2	36	10	+	118355577	118355690
233255121	chr11	118355547	118355714	118355573	118355690	MLL	NM_001197104	1	36	10	+	118355577	118355690
233396032	chr11	118360506	118360661	118360530	118360635	MLL	NM_005933	2	36	12	+	118360507	118360602
233396032	chr11	118360506	118360661	118360530	118360635	MLL	NM_001197104	1	36	12	+	118360507	118360602
233059855	chr11	118361921	118362055	118361949	118362026	MLL	NM_001197104	1	36	14	+	118361911	118362033
233059855	chr11	118361921	118362055	118361949	118362026	MLL	NM_005933	2	36	14	+	118361911	118362024
234513051	chr11	118363835	118363973	118363857	118363945	MLL	NM_005933	2	36	16	+	118363772	118363945
234513051	chr11	118363835	118363973	118363857	118363945	MLL	NM_001197104	1	36	16	+	118363772	118363945
232469591	chr11	118365396	118365533	118365424	118365509	MLL	NM_005933	2	36	18	+	118365409	118365482
232469591	chr11	118365396	118365533	118365424	118365509	MLL	NM_001197104	1	36	18	+	118365409	118365482
233122255	chr11	118366934	118367106	118366959	118367083	MLL	NM_005933	2	36	20	+	118366976	118367082
233122255	chr11	118366934	118367106	118366959	118367083	MLL	NM_001197104	1	36	20	+	118366976	118367082

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233402114	chr11	118369133	118369258	118369154	118369235	MLL	NM_005933	2	36	22	+	118369085	118369243
233402114	chr11	118369133	118369258	118369154	118369235	MLL	NM_001197104	1	36	22	+	118369085	118369243
233301990	chr11	118371605	118371775	118371626	118371750	MLL	NM_005933	2	36	25	+	118371702	118371862
233301990	chr11	118371605	118371775	118371626	118371750	MLL	NM_001197104	1	36	25	+	118371702	118371862
233070959	chr11	118372442	118372614	118372463	118372588	MLL	NM_005933	2	36	26	+	118372387	118372572
233070959	chr11	118372442	118372614	118372463	118372588	MLL	NM_001197104	1	36	26	+	118372387	118372572
231284497	chr11	118373381	118373547	118373404	118373524	MLL	NM_005933	2	36	27	+	118373113	118377361
231284497	chr11	118373381	118373547	118373404	118373524	MLL	NM_001197104	1	36	27	+	118373113	118377361
233882371	chr11	118373840	118374000	118373867	118373976	MLL	NM_005933	2	36	27	+	118373113	118377361
233882371	chr11	118373840	118374000	118373867	118373976	MLL	NM_001197104	1	36	27	+	118373113	118377361
231335168	chr11	118374282	118374426	118374305	118374404	MLL	NM_005933	2	36	27	+	118373113	118377361
231335168	chr11	118374282	118374426	118374305	118374404	MLL	NM_001197104	1	36	27	+	118373113	118377361
233868975	chr11	118374676	118374802	118374700	118374775	MLL	NM_005933	2	36	27	+	118373113	118377361
233868975	chr11	118374676	118374802	118374700	118374775	MLL	NM_001197104	1	36	27	+	118373113	118377361
233868115	chr11	118375051	118375199	118375074	118375171	MLL	NM_005933	2	36	27	+	118373113	118377361
233868115	chr11	118375051	118375199	118375074	118375171	MLL	NM_001197104	1	36	27	+	118373113	118377361
233893517	chr11	118375484	118375658	118375511	118375635	MLL	NM_005933	2	36	27	+	118373113	118377361
233893517	chr11	118375484	118375658	118375511	118375635	MLL	NM_001197104	1	36	27	+	118373113	118377361
233910575	chr11	118376000	118376150	118376021	118376127	MLL	NM_005933	2	36	27	+	118373113	118377361
233910575	chr11	118376000	118376150	118376021	118376127	MLL	NM_001197104	1	36	27	+	118373113	118377361
233930469	chr11	118376454	118376603	118376482	118376582	MLL	NM_005933	2	36	27	+	118373113	118377361
233930469	chr11	118376454	118376603	118376482	118376582	MLL	NM_001197104	1	36	27	+	118373113	118377361
233913755	chr11	118376814	118376968	118376836	118376946	MLL	NM_005933	2	36	27	+	118373113	118377361
233913755	chr11	118376814	118376968	118376836	118376946	MLL	NM_001197104	1	36	27	+	118373113	118377361
233915836	chr11	118377241	118377388	118377265	118377362	MLL	NM_005933	2	36	27	+	118373113	118377361
233915836	chr11	118377241	118377388	118377265	118377362	MLL	NM_001197104	1	36	27	+	118373113	118377361
230990667	chr11	118380708	118380859	118380730	118380833	MLL	NM_005933	2	36	30	+	118380663	118380833
230990667	chr11	118380708	118380859	118380730	118380833	MLL	NM_001197104	1	36	30	+	118380663	118380833
231706832	chr11	118390562	118390700	118390586	118390673	MLL	NM_005933	2	36	33	+	118390672	118390779
231706832	chr11	118390562	118390700	118390586	118390673	MLL	NM_001197104	1	36	33	+	118390672	118390779
230949266	chr11	118391909	118392077	118391933	118392054	MLL	NM_005933	2	36	35	+	118392003	118392132
230949266	chr11	118391909	118392077	118391933	118392054	MLL	NM_001197104	1	36	35	+	118392003	118392132
232575825	chr11	118392785	118392951	118392813	118392931	MLL	NM_005933	2	36	36	+	118392612	118397539
232575825	chr11	118392785	118392951	118392813	118392931	MLL	NM_001197104	1	36	36	+	118392612	118397539
226469509	chr11	119103103	119103231	119103128	119103203	CBL	NM_005188	1	16	2	+	119103158	119103405
226310120	chr11	119142426	119142578	119142451	119142555	CBL	NM_005188	1	16	3	+	119142445	119142591
226085386	chr11	119145433	119145575	119145460	119145554	CBL	NM_005188	1	16	5	+	119145542	119145663
226646276	chr11	119148443	119148602	119148466	119148573	CBL	NM_005188	1	16	7	+	119148467	119148554
226232414	chr11	119149185	119149315	119149213	119149295	CBL	NM_005188	1	16	9	+	119149220	119149423
225884344	chr11	119155842	119155995	119155868	119155974	CBL	NM_005188	1	16	11	+	119155899	119156276
226176170	chr11	119158444	119158603	119158467	119158580	CBL	NM_005188	1	16	12	+	119158562	119158656

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225399199	chr11	119168057	119168197	119168084	119168175	CBL	NM_005188	1	16	14	+	119168094	119168191
226349499	chr11	119170147	119170308	119170174	119170287	CBL	NM_005188	1	16	16	+	119170205	119178859
226458465	chr11	125497373	125497543	125497397	125497518	CHEK1	NM_001244846	3	12	3	+	125497502	125497725
226458465	chr11	125497373	125497543	125497397	125497518	CHEK1	NR_045205	6	13	3	+	125497502	125497725
226458465	chr11	125497373	125497543	125497397	125497518	CHEK1	NM_001114121	1	14	3	+	125497502	125497725
226458465	chr11	125497373	125497543	125497397	125497518	CHEK1	NM_001114122	2	13	3	+	125497502	125497725
226458465	chr11	125497373	125497543	125497397	125497518	CHEK1	NM_001274	4	13	3	+	125497502	125497725
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NM_001244846	3	12	4	+	125499127	125499191
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NR_045205	6	13	4	+	125499127	125499191
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NM_001114121	1	14	4	+	125499127	125499191
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NM_001114122	2	13	4	+	125499127	125499191
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NM_001274	4	13	4	+	125499127	125499191
226112184	chr11	125499016	125499184	125499039	125499159	CHEK1	NR_045204	5	12	3	+	125499127	125499191
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NM_001244846	3	12	6	+	125503058	125503246
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NR_045205	6	13	6	+	125503058	125503246
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NM_001114121	1	14	6	+	125503058	125503246
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NM_001114122	2	13	6	+	125503058	125503246
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NM_001274	4	13	6	+	125503058	125503246
225722132	chr11	125502940	125503100	125502968	125503077	CHEK1	NR_045204	5	12	5	+	125503058	125503246
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NM_001244846	3	12	7	+	125505324	125505428
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NR_045205	6	13	7	+	125505324	125505428
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NM_001114121	1	14	7	+	125505324	125505428
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NM_001114122	2	13	7	+	125505324	125505428
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NM_001274	4	13	7	+	125505324	125505428
226209376	chr11	125505301	125505469	125505329	125505441	CHEK1	NR_045204	5	12	6	+	125505324	125505428
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NM_001244846	3	12	10	+	125513986	125514163
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NR_045205	6	13	10	+	125513986	125514163
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NM_001114121	1	14	10	+	125513986	125514163
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NM_001114122	2	13	10	+	125513986	125514163
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NM_001274	4	13	10	+	125513986	125514163
225531955	chr11	125513894	125514020	125513919	125513997	CHEK1	NR_045204	5	12	9	+	125513986	125514163
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NM_001244846	3	12	11	+	125514407	125514538
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NR_045205	6	13	11	+	125514407	125514538
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NM_001114121	1	14	11	+	125514407	125514538
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NM_001114122	2	13	11	+	125514407	125514538
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NM_001274	4	13	11	+	125514407	125514538
253763316	chr11	125514415	125514543	125514436	125514515	CHEK1	NR_045204	5	12	10	+	125514407	125514538
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NM_001244846	3	12	12	+	125525120	125527042
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NR_045205	6	13	13	+	125525120	125527042
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NM_001114122	2	13	13	+	125525120	125527042
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NM_001274	4	13	13	+	125525120	125527042

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NR_045204	5	12	12	+	125525120	125527042
227077992	chr11	125525119	125525253	125525142	125525227	CHEK1	NM_001114121	1	14	13	+	125525120	125525242
294358911	chr11	128333339	128333463	128333361	128333439	ETS1	NM_005238	3	8	7	-	128333404	128333522
294358911	chr11	128333339	128333463	128333361	128333439	ETS1	NM_001143820	1	10	9	-	128333404	128333522
294358911	chr11	128333339	128333463	128333361	128333439	ETS1	NM_001162422	2	4	3	-	128333404	128333522
294059848	chr11	128350224	128350377	128350245	128350353	ETS1	NM_005238	3	8	6	-	128350086	128350346
294059848	chr11	128350224	128350377	128350245	128350353	ETS1	NM_001143820	1	10	8	-	128350086	128350346
294059848	chr11	128350224	128350377	128350245	128350353	ETS1	NM_001162422	2	4	2	-	128350086	128350346
293954686	chr11	128355908	128356072	128355935	128356043	ETS1	NM_005238	3	8	4	-	128355964	128356041
293954686	chr11	128355908	128356072	128355935	128356043	ETS1	NM_001143820	1	10	6	-	128355964	128356041
293978595	chr11	128360408	128360560	128360435	128360537	ETS1	NM_005238	3	8	2	-	128360352	128360471
293978595	chr11	128360408	128360560	128360435	128360537	ETS1	NM_001143820	1	10	4	-	128360352	128360471
294514999	chr11	128426252	128426387	128426277	128426359	ETS1	NM_001143820	1	10	3	-	128426186	128426330
227991950	chr11	128628025	128628193	128628043	128628173	FLI1	NM_002017	2	9	2	+	128628010	128628221
227991950	chr11	128628025	128628193	128628043	128628173	FLI1	NM_001167681	1	10	3	+	128628010	128628221
227137262	chr11	128642636	128642783	128642657	128642760	FLI1	NM_002017	2	9	4	+	128642677	128642880
227137262	chr11	128642636	128642783	128642657	128642760	FLI1	NM_001167681	1	10	5	+	128642677	128642880
229246162	chr11	128675206	128675369	128675228	128675342	FLI1	NM_002017	2	9	6	+	128675261	128675326
229246162	chr11	128675206	128675369	128675228	128675342	FLI1	NM_001167681	1	10	7	+	128675261	128675326
229095982	chr11	128680409	128680582	128680429	128680558	FLI1	NM_002017	2	9	9	+	128680354	128683162
229095982	chr11	128680409	128680582	128680429	128680558	FLI1	NM_001167681	1	10	10	+	128680354	128683162
226187758	chr12	4385103	4385241	4385130	4385221	CCND2	NM_001759	1	5	2	+	4385171	4385386
226677039	chr12	4387969	4388106	4387991	4388085	CCND2	NM_001759	1	5	3	+	4387926	4388085
226813041	chr12	4409082	4409215	4409102	4409191	CCND2	NM_001759	1	5	5	+	4409026	4414522
281160122	chr12	6761442	6761612	6761464	6761588	ING4	NM_001127584	3	8	6	-	6761437	6761584
281160122	chr12	6761442	6761612	6761464	6761588	ING4	NM_001127583	2	8	6	-	6761437	6761584
281160122	chr12	6761442	6761612	6761464	6761588	ING4	NM_016162	6	8	6	-	6761437	6761584
281160122	chr12	6761442	6761612	6761464	6761588	ING4	NM_001127582	1	8	6	-	6761437	6761584
281160122	chr12	6761442	6761612	6761464	6761588	ING4	NM_001127585	4	7	5	-	6761437	6761584
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_001127584	3	8	3	-	6762396	6762562
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_001127583	2	8	3	-	6762396	6762562
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_016162	6	8	3	-	6762396	6762562
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_001127582	1	8	3	-	6762396	6762562
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_001127586	5	7	3	-	6762396	6762562
279571291	chr12	6762306	6762464	6762329	6762443	ING4	NM_001127585	4	7	2	-	6762396	6762562
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_001127584	3	8	1	-	6772231	6772308
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_001127583	2	8	1	-	6772231	6772308
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_016162	6	8	1	-	6772231	6772308
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_001127582	1	8	1	-	6772231	6772308
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_001127586	5	7	1	-	6772231	6772308
280939198	chr12	6772131	6772296	6772152	6772272	ING4	NM_001127585	4	7	1	-	6772231	6772308

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240520917	chr12	6777230	6777404	6777249	6777377	ZNF384	NM_133476	3	10	10	-	6775643	6777281
240520917	chr12	6777230	6777404	6777249	6777377	ZNF384	NM_001135734	2	11	11	-	6775643	6777281
240520917	chr12	6777230	6777404	6777249	6777377	ZNF384	NM_001039920	1	9	9	-	6775643	6777281
261998692	chr12	6781430	6781588	6781448	6781569	ZNF384	NM_001135734	2	11	8	-	6781516	6781698
240081302	chr12	6782425	6782597	6782451	6782574	ZNF384	NM_133476	3	10	7	-	6782382	6782606
240081302	chr12	6782425	6782597	6782451	6782574	ZNF384	NM_001135734	2	11	7	-	6782382	6782606
240081302	chr12	6782425	6782597	6782451	6782574	ZNF384	NM_001039920	1	9	6	-	6782382	6782606
239083028	chr12	6787452	6787580	6787473	6787558	ZNF384	NM_133476	3	10	6	-	6787293	6787626
239083028	chr12	6787452	6787580	6787473	6787558	ZNF384	NM_001135734	2	11	6	-	6787293	6787626
239083028	chr12	6787452	6787580	6787473	6787558	ZNF384	NM_001039920	1	9	5	-	6787293	6787509
240617009	chr12	6788189	6788347	6788210	6788320	ZNF384	NM_133476	3	10	4	-	6788112	6788349
240617009	chr12	6788189	6788347	6788210	6788320	ZNF384	NM_001135734	2	11	4	-	6788112	6788349
240617009	chr12	6788189	6788347	6788210	6788320	ZNF384	NM_001039920	1	9	4	-	6788112	6788349
233356818	chr12	25368298	25368463	25368319	25368435	KRAS	NM_033360	2	6	5	-	25368371	25368494
326772204	chr12	25380138	25380262	25380169	25380240	KRAS	NM_004985	1	5	3	-	25380168	25380346
326772204	chr12	25380138	25380262	25380169	25380240	KRAS	NM_033360	2	6	3	-	25380168	25380346
281400409	chr12	43747901	43748045	43747927	43748021	ADAMTS20	NM_025003	1	39	39	-	43748012	43748101
284270179	chr12	43762994	43763125	43763026	43763101	ADAMTS20	NM_025003	1	39	37	-	43763093	43763184
283686868	chr12	43769778	43769952	43769804	43769924	ADAMTS20	NM_025003	1	39	35	-	43769860	43769951
282525511	chr12	43770228	43770395	43770254	43770367	ADAMTS20	NM_025003	1	39	33	-	43770327	43770456
281596219	chr12	43771242	43771416	43771263	43771388	ADAMTS20	NM_025003	1	39	32	-	43771168	43771365
283679808	chr12	43777516	43777685	43777544	43777665	ADAMTS20	NM_025003	1	39	30	-	43777607	43777780
283707673	chr12	43792922	43793046	43792947	43793020	ADAMTS20	NM_025003	1	39	29	-	43792869	43793036
283395824	chr12	43821016	43821157	43821049	43821140	ADAMTS20	NM_025003	1	39	27	-	43821111	43821272
281766357	chr12	43822143	43822288	43822168	43822263	ADAMTS20	NM_025003	1	39	26	-	43822044	43822334
282285486	chr12	43822541	43822681	43822564	43822653	ADAMTS20	NM_025003	1	39	25	-	43822438	43822602
283363328	chr12	43824032	43824195	43824056	43824171	ADAMTS20	NM_025003	1	39	23	-	43824155	43824274
282483637	chr12	43825241	43825369	43825264	43825343	ADAMTS20	NM_025003	1	39	22	-	43825135	43825299
284456717	chr12	43826241	43826377	43826261	43826348	ADAMTS20	NM_025003	1	39	21	-	43826107	43826271
283904448	chr12	43827937	43828099	43827964	43828073	ADAMTS20	NM_025003	1	39	19	-	43828048	43828174
282779880	chr12	43833483	43833651	43833509	43833618	ADAMTS20	NM_025003	1	39	18	-	43833425	43833554
328491631	chr12	43833783	43833947	43833811	43833914	ADAMTS20	NM_025003	1	39	17	-	43833700	43833872
282062707	chr12	43845957	43846118	43845983	43846092	ADAMTS20	NM_025003	1	39	14	-	43846077	43846213
282128968	chr12	43846297	43846437	43846324	43846413	ADAMTS20	NM_025003	1	39	13	-	43846317	43846498
284463504	chr12	43856663	43856828	43856690	43856806	ADAMTS20	NM_025003	1	39	11	-	43856698	43856802
283121653	chr12	43860496	43860664	43860523	43860631	ADAMTS20	NM_025003	1	39	9	-	43860455	43860598
281557168	chr12	43886249	43886376	43886271	43886351	ADAMTS20	NM_025003	1	39	6	-	43886308	43886432
283839618	chr12	43896016	43896189	43896044	43896163	ADAMTS20	NM_025003	1	39	4	-	43895955	43896208
283598411	chr12	43944722	43944884	43944742	43944865	ADAMTS20	NM_025003	1	39	2	-	43944712	43945073
272899388	chr12	46123567	46123729	46123589	46123712	ARID2	NM_152641	1	21	1	+	46123620	46123711
274083392	chr12	46125051	46125198	46125073	46125175	ARID2	NM_152641	1	21	3	+	46125000	46125097

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273378128	chr12	46211480	46211604	46211508	46211579	ARID2	NM_152641	1	21	5	+	46211453	46211671
273415698	chr12	46230291	46230439	46230318	46230412	ARID2	NM_152641	1	21	7	+	46230372	46230438
273659227	chr12	46230636	46230804	46230659	46230776	ARID2	NM_152641	1	21	8	+	46230524	46230774
273581895	chr12	46231375	46231501	46231400	46231473	ARID2	NM_152641	1	21	10	+	46231281	46231490
273456673	chr12	46240538	46240687	46240569	46240665	ARID2	NM_152641	1	21	12	+	46240639	46240720
273508156	chr12	46243243	46243405	46243270	46243380	ARID2	NM_152641	1	21	14	+	46243363	46243559
274418510	chr12	46243758	46243926	46243787	46243899	ARID2	NM_152641	1	21	15	+	46243819	46246679
274491731	chr12	46244202	46244375	46244227	46244350	ARID2	NM_152641	1	21	15	+	46243819	46246679
274518607	chr12	46244668	46244821	46244691	46244793	ARID2	NM_152641	1	21	15	+	46243819	46246679
274487647	chr12	46245094	46245268	46245114	46245246	ARID2	NM_152641	1	21	15	+	46243819	46246679
273572061	chr12	46245567	46245740	46245588	46245721	ARID2	NM_152641	1	21	15	+	46243819	46246679
273581612	chr12	46246005	46246147	46246033	46246120	ARID2	NM_152641	1	21	15	+	46243819	46246679
274451720	chr12	46246381	46246537	46246404	46246509	ARID2	NM_152641	1	21	15	+	46243819	46246679
272836461	chr12	46254597	46254731	46254619	46254707	ARID2	NM_152641	1	21	16	+	46254584	46254732
273979995	chr12	46285661	46285799	46285681	46285772	ARID2	NM_152641	1	21	17	+	46285563	46285701
273695315	chr12	46287222	46287352	46287244	46287328	ARID2	NM_152641	1	21	19	+	46287203	46287326
272957761	chr12	49415508	49415680	49415528	49415655	MLL2	NM_003482	1	54	54	-	49412758	49415655
273882982	chr12	49416414	49416588	49416435	49416567	MLL2	NM_003482	1	54	51	-	49416373	49416658
273559054	chr12	49418534	49418680	49418556	49418660	MLL2	NM_003482	1	54	49	-	49418593	49418729
273635667	chr12	49420147	49420315	49420171	49420293	MLL2	NM_003482	1	54	48	-	49419965	49421105
274610951	chr12	49420587	49420722	49420607	49420700	MLL2	NM_003482	1	54	48	-	49419965	49421105
273678567	chr12	49421038	49421162	49421060	49421138	MLL2	NM_003482	1	54	48	-	49419965	49421105
274158370	chr12	49422538	49422687	49422563	49422666	MLL2	NM_003482	1	54	45	-	49422611	49422741
273769864	chr12	49423135	49423299	49423155	49423275	MLL2	NM_003482	1	54	43	-	49423184	49423259
273425275	chr12	49424464	49424610	49424483	49424591	MLL2	NM_003482	1	54	41	-	49424384	49424551
274236587	chr12	49425057	49425208	49425077	49425188	MLL2	NM_003482	1	54	39	-	49424958	49427747
274230722	chr12	49425438	49425604	49425457	49425580	MLL2	NM_003482	1	54	39	-	49424958	49427747
273239626	chr12	49425863	49426014	49425884	49425996	MLL2	NM_003482	1	54	39	-	49424958	49427747
273261878	chr12	49426253	49426404	49426274	49426384	MLL2	NM_003482	1	54	39	-	49424958	49427747
273250529	chr12	49426841	49427012	49426865	49426991	MLL2	NM_003482	1	54	39	-	49424958	49427747
273259799	chr12	49427183	49427356	49427206	49427330	MLL2	NM_003482	1	54	39	-	49424958	49427747
273201154	chr12	49427615	49427768	49427634	49427748	MLL2	NM_003482	1	54	39	-	49424958	49427747
273091519	chr12	49428118	49428286	49428140	49428264	MLL2	NM_003482	1	54	37	-	49428193	49428259
274285742	chr12	49430971	49431136	49430990	49431118	MLL2	NM_003482	1	54	34	-	49430908	49432772
273266397	chr12	49431484	49431622	49431503	49431601	MLL2	NM_003482	1	54	34	-	49430908	49432772
273291202	chr12	49431890	49432041	49431913	49432021	MLL2	NM_003482	1	54	34	-	49430908	49432772
274256503	chr12	49432381	49432524	49432399	49432504	MLL2	NM_003482	1	54	34	-	49430908	49432772
273594826	chr12	49432883	49433038	49432910	49433018	MLL2	NM_003482	1	54	33	-	49433005	49433141
273592739	chr12	49433323	49433482	49433344	49433461	MLL2	NM_003482	1	54	32	-	49433218	49433400
274209251	chr12	49433799	49433955	49433822	49433933	MLL2	NM_003482	1	54	31	-	49433507	49435318
273179178	chr12	49434187	49434338	49434208	49434319	MLL2	NM_003482	1	54	31	-	49433507	49435318

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273149876	chr12	49434565	49434701	49434586	49434676	MLL2	NM_003482	1	54	31	-	49433507	49435318
273155983	chr12	49434941	49435087	49434962	49435066	MLL2	NM_003482	1	54	31	-	49433507	49435318
272916159	chr12	49435394	49435531	49435414	49435510	MLL2	NM_003482	1	54	30	-	49435438	49435488
273364186	chr12	49435993	49436145	49436010	49436128	MLL2	NM_003482	1	54	28	-	49435872	49436113
272759222	chr12	49436819	49436992	49436846	49436969	MLL2	NM_003482	1	54	25	-	49436859	49436969
273856047	chr12	49437453	49437607	49437475	49437584	MLL2	NM_003482	1	54	23	-	49437418	49437565
273362205	chr12	49438087	49438252	49438109	49438232	MLL2	NM_003482	1	54	20	-	49438186	49438305
274290336	chr12	49438677	49438838	49438697	49438813	MLL2	NM_003482	1	54	19	-	49438527	49438748
273197769	chr12	49440057	49440231	49440084	49440208	MLL2	NM_003482	1	54	16	-	49440043	49440207
273318054	chr12	49442406	49442577	49442427	49442552	MLL2	NM_003482	1	54	13	-	49442442	49442552
273757086	chr12	49443620	49443779	49443643	49443755	MLL2	NM_003482	1	54	11	-	49443465	49444573
273733346	chr12	49444062	49444216	49444081	49444196	MLL2	NM_003482	1	54	11	-	49443465	49444573
273729070	chr12	49444492	49444663	49444513	49444636	MLL2	NM_003482	1	54	11	-	49443465	49444573
273084527	chr12	49444965	49445092	49444987	49445073	MLL2	NM_003482	1	54	10	-	49444669	49446207
273134267	chr12	49445341	49445502	49445359	49445485	MLL2	NM_003482	1	54	10	-	49444669	49446207
273095802	chr12	49445689	49445833	49445710	49445809	MLL2	NM_003482	1	54	10	-	49444669	49446207
273105630	chr12	49446013	49446169	49446033	49446149	MLL2	NM_003482	1	54	10	-	49444669	49446207
272842645	chr12	49446676	49446805	49446697	49446783	MLL2	NM_003482	1	54	8	-	49446698	49446855
273573158	chr12	49447340	49447507	49447361	49447484	MLL2	NM_003482	1	54	6	-	49447259	49447424
273178971	chr12	49448195	49448356	49448217	49448336	MLL2	NM_003482	1	54	3	-	49448311	49448534
272953308	chr12	49448708	49448878	49448729	49448856	MLL2	NM_003482	1	54	2	-	49448683	49448809
224614765	chr12	51189643	51189817	51189666	51189792	ATF1	NM_005171	1	7	3	+	51189692	51189792
223268881	chr12	51207939	51208103	51207961	51208076	ATF1	NM_005171	1	7	6	+	51208063	51208222
223268881	chr12	51207939	51208103	51207961	51208076	ATF1	NM_005171	1	7	5	+	51207793	51207975
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NR_045039	7	5	5	-	54575239	54575431
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_001243791	5	4	4	-	54575239	54575431
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_001243790	4	5	5	-	54575239	54575431
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_001243789	3	6	6	-	54575239	54575431
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321896288	chr12	54575331	54575461	54575353	54575437	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NR_045039	7	5	4	-	54576288	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_001243791	5	4	3	-	54576288	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_001243790	4	5	4	-	54576288	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_001243789	3	6	5	-	54576288	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_014311	6	4	4	-	54574142	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_001243788	2	3	3	-	54574142	54576407
321954574	chr12	54576147	54576308	54576168	54576289	SMUG1	NM_001243787	1	4	4	-	54574142	54576407
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_014311	6	4	3	-	54577440	54577743
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NR_045039	7	5	3	-	54577440	54577743
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_001243791	5	4	2	-	54577440	54577743

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_001243790	4	5	3	-	54577440	54577743
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_001243789	3	6	4	-	54577440	54577743
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_001243788	2	3	2	-	54577440	54577743
321766166	chr12	54577606	54577769	54577626	54577747	SMUG1	NM_001243787	1	4	3	-	54577440	54577743
269971951	chr12	56478692	56478845	56478717	56478819	ERBB3	NM_001005915	1	3	3	+	56478779	56479401
269971951	chr12	56478692	56478845	56478717	56478819	ERBB3	NM_001982	2	28	3	+	56478779	56478965
271121170	chr12	56480290	56480464	56480313	56480441	ERBB3	NM_001982	2	28	4	+	56480315	56480440
270106305	chr12	56481846	56481970	56481867	56481948	ERBB3	NM_001982	2	28	7	+	56481805	56481946
271945643	chr12	56486742	56486887	56486763	56486862	ERBB3	NM_001982	2	28	11	+	56486770	56486860
270854537	chr12	56487611	56487745	56487632	56487723	ERBB3	NM_001982	2	28	13	+	56487548	56487680
271218662	chr12	56488944	56489118	56488969	56489094	ERBB3	NM_001982	2	28	16	+	56489041	56489094
269748813	chr12	56490486	56490656	56490510	56490630	ERBB3	NM_001982	2	28	19	+	56490532	56490630
271106666	chr12	56491625	56491780	56491645	56491759	ERBB3	NM_001982	2	28	21	+	56491569	56491724
271895145	chr12	56493377	56493551	56493401	56493529	ERBB3	NM_001982	2	28	24	+	56493432	56493529
270308946	chr12	56494790	56494964	56494819	56494943	ERBB3	NM_001982	2	28	27	+	56494845	56495145
269746437	chr12	56495338	56495489	56495360	56495464	ERBB3	NM_001982	2	28	28	+	56495313	56497291
269730311	chr12	56495756	56495886	56495778	56495864	ERBB3	NM_001982	2	28	28	+	56495313	56497291
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_001195055	3	4	4	-	57910371	57910963
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_001195054	2	4	4	-	57910371	57910963
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_001195053	1	4	4	-	57910371	57910963
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_001195057	5	4	4	-	57910371	57910963
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_001195056	4	3	3	-	57910371	57910963
231105420	chr12	57910831	57910992	57910850	57910964	DDIT3	NM_004083	6	4	4	-	57910371	57910963
226781087	chr12	58142257	58142428	58142279	58142406	CDK4	NM_000075	1	8	8	-	58141510	58142400
227114580	chr12	58144402	58144575	58144424	58144548	CDK4	NM_000075	1	8	5	-	58144439	58144548
253749736	chr12	58145020	58145156	58145042	58145128	CDK4	NM_000075	1	8	3	-	58144990	58145125
231810854	chr12	69202146	69202303	69202164	69202284	MDM2	NM_002392	1	11	1	+	69201971	69202271
230911493	chr12	69207371	69207495	69207397	69207474	MDM2	NM_002392	1	11	3	+	69207334	69207408
231180683	chr12	69218154	69218292	69218179	69218261	MDM2	NM_002392	1	11	6	+	69218143	69218210
234467767	chr12	69222674	69222832	69222698	69222804	MDM2	NM_002392	1	11	8	+	69222551	69222711
234776515	chr12	69233015	69233188	69233039	69233165	MDM2	NM_002392	1	11	11	+	69233054	69239212
234797841	chr12	69233443	69233612	69233465	69233584	MDM2	NM_002392	1	11	11	+	69233054	69239212
235873922	chr12	112888095	112888236	112888116	112888209	PTPN11	NM_002834	1	16	3	+	112888122	112888316
235035547	chr12	112892359	112892508	112892386	112892486	PTPN11	NM_002834	1	16	5	+	112892368	112892484
237509378	chr12	112910744	112910912	112910768	112910887	PTPN11	NM_002834	1	16	7	+	112910748	112910844
240073706	chr12	112919759	112919933	112919781	112919905	PTPN11	NM_002834	1	16	10	+	112919878	112920009
235680759	chr12	112926184	112926337	112926207	112926317	PTPN11	NM_002834	1	16	12	+	112926247	112926314
236449228	chr12	112942434	112942591	112942458	112942568	PTPN11	NM_002834	1	16	15	+	112942499	112942600
227192295	chr12	121416742	121416887	121416759	121416868	HNF1A	NM_000545	1	10	1	+	121416549	121416897
227540496	chr12	121426798	121426962	121426816	121426939	HNF1A	NM_000545	1	10	2	+	121426636	121426835
227613086	chr12	121431886	121432058	121431908	121432037	HNF1A	NM_000545	1	10	4	+	121431967	121432208

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227377050	chr12	121434099	121434273	121434120	121434250	HNF1A	NM_000545	1	10	5	+	121434065	121434216
227485480	chr12	121435372	121435543	121435390	121435525	HNF1A	NM_000545	1	10	7	+	121435277	121435468
229005560	chr12	121438839	121439000	121438859	121438979	HNF1A	NM_000545	1	10	10	+	121438868	121440314
280182409	chr12	123214000	123214171	123214028	123214146	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280143383	chr12	123214416	123214579	123214438	123214559	HCAR1	NM_032554	1	1	1	-	123212153	123215129
280135277	chr12	123214844	123214974	123214863	123214954	HCAR1	NM_032554	1	1	1	-	123212153	123215129
288129777	chr12	132445184	132445358	132445204	132445330	EP400	NM_015409	1	53	2	+	132445130	132446499
288137494	chr12	132446346	132446504	132446373	132446476	EP400	NM_015409	1	53	2	+	132445130	132446499
287501588	chr12	132466588	132466745	132466608	132466728	EP400	NM_015409	1	53	5	+	132466638	132467023
287544880	chr12	132470976	132471138	132470995	132471117	EP400	NM_015409	1	53	6	+	132471059	132471352
287825454	chr12	132472224	132472398	132472246	132472378	EP400	NM_015409	1	53	7	+	132472250	132472435
286306942	chr12	132475120	132475293	132475144	132475273	EP400	NM_015409	1	53	9	+	132475181	132475259
287665422	chr12	132489524	132489685	132489546	132489665	EP400	NM_015409	1	53	13	+	132489622	132489729
287325674	chr12	132491208	132491353	132491236	132491326	EP400	NM_015409	1	53	15	+	132491245	132491422
289157212	chr12	132497488	132497662	132497514	132497640	EP400	NM_015409	1	53	17	+	132497554	132497723
288334654	chr12	132498161	132498295	132498187	132498269	EP400	NM_015409	1	53	18	+	132498035	132498209
288503751	chr12	132502092	132502252	132502112	132502229	EP400	NM_015409	1	53	20	+	132502080	132502266
287893219	chr12	132504573	132504744	132504592	132504726	EP400	NM_015409	1	53	22	+	132504594	132504763
288761472	chr12	132505713	132505886	132505731	132505865	EP400	NM_015409	1	53	23	+	132505624	132505866
288743561	chr12	132510128	132510276	132510148	132510258	EP400	NM_015409	1	53	25	+	132510191	132510349
288230441	chr12	132512562	132512698	132512588	132512677	EP400	NM_015409	1	53	27	+	132512562	132512833
287414439	chr12	132514322	132514466	132514345	132514449	EP400	NM_015409	1	53	28	+	132514246	132514448
288635591	chr12	132516560	132516734	132516585	132516709	EP400	NM_015409	1	53	30	+	132516498	132516694
288953720	chr12	132527720	132527884	132527745	132527861	EP400	NM_015409	1	53	33	+	132527849	132528007
284839729	chr12	132528684	132528857	132528708	132528836	EP400	NM_015409	1	53	35	+	132528722	132528856
288401724	chr12	132529392	132529566	132529412	132529546	EP400	NM_015409	1	53	37	+	132529345	132529498
285912767	chr12	132530166	132530337	132530187	132530315	EP400	NM_015409	1	53	39	+	132530272	132530445
286226436	chr12	132535033	132535169	132535061	132535144	EP400	NM_015409	1	53	41	+	132535144	132535200
287241417	chr12	132539396	132539559	132539417	132539539	EP400	NM_015409	1	53	44	+	132539519	132539564
288155355	chr12	132546750	132546907	132546769	132546887	EP400	NM_015409	1	53	46	+	132546655	132546868
288804924	chr12	132549097	132549249	132549123	132549227	EP400	NM_015409	1	53	48	+	132549213	132549431
286528968	chr12	132551399	132551566	132551416	132551546	EP400	NM_015409	1	53	49	+	132551319	132551514
285577072	chr12	132554072	132554231	132554091	132554213	EP400	NM_015409	1	53	51	+	132554040	132554186
286163401	chr12	132562152	132562320	132562173	132562299	EP400	NM_015409	1	53	53	+	132561946	132565011
270023511	chr13	26923182	26923343	26923209	26923320	CDK8	NM_001260	1	13	3	+	26923209	26923319
270129627	chr13	26956975	26957130	26956993	26957102	CDK8	NM_001260	1	13	5	+	26956951	26957008
272642188	chr13	26967510	26967655	26967537	26967633	CDK8	NM_001260	1	13	7	+	26967504	26967647
269989212	chr13	26974540	26974713	26974567	26974687	CDK8	NM_001260	1	13	10	+	26974590	26974687
269710926	chr13	26977977	26978119	26978005	26978097	CDK8	NM_001260	1	13	13	+	26978093	26978569
227490842	chr13	28588463	28588622	28588486	28588599	FLT3	NM_004119	1	24	23	-	28588589	28588694
229375186	chr13	28592520	28592648	28592542	28592621	FLT3	NM_004119	1	24	20	-	28592604	28592726

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227134030	chr13	28598950	28599089	28598981	28599062	FLT3	NM_004119	1	24	18	-	28598998	28599080
230148893	chr13	28602363	28602520	28602384	28602492	FLT3	NM_004119	1	24	16	-	28602315	28602425
228137447	chr13	28608321	28608495	28608345	28608467	FLT3	NM_004119	1	24	14	-	28608219	28608351
228137447	chr13	28608321	28608495	28608345	28608467	FLT3	NM_004119	1	24	13	-	28608438	28608544
227607747	chr13	28610002	28610132	28610030	28610108	FLT3	NM_004119	1	24	11	-	28610072	28610180
229072319	chr13	28622342	28622508	28622362	28622485	FLT3	NM_004119	1	24	9	-	28622412	28622580
227874155	chr13	28623764	28623938	28623788	28623912	FLT3	NM_004119	1	24	7	-	28623772	28623911
227739551	chr13	28631449	28631598	28631472	28631570	FLT3	NM_004119	1	24	4	-	28631484	28631599
228786007	chr13	28636110	28636256	28636134	28636230	FLT3	NM_004119	1	24	3	-	28636004	28636206
228856206	chr13	28877287	28877435	28877311	28877418	FLT1	NM_002019	4	30	30	-	28874483	28877505
228900893	chr13	28882947	28883105	28882969	28883076	FLT1	NM_002019	4	30	28	-	28882980	28883064
227832178	chr13	28891509	28891668	28891534	28891644	FLT1	NM_002019	4	30	25	-	28891635	28891734
227524795	chr13	28895501	28895674	28895523	28895648	FLT1	NM_002019	4	30	23	-	28895600	28895722
227394335	chr13	28896880	28897014	28896906	28896992	FLT1	NM_002019	4	30	21	-	28896927	28897083
228796687	chr13	28903731	28903888	28903751	28903865	FLT1	NM_002019	4	30	19	-	28903752	28903865
227567194	chr13	28919634	28919785	28919655	28919761	FLT1	NM_002019	4	30	16	-	28919582	28919688
229306028	chr13	28959075	28959202	28959096	28959177	FLT1	NM_002019	4	30	14	-	28959022	28959168
229306028	chr13	28959075	28959202	28959096	28959177	FLT1	NM_001160030	2	15	14	-	28959022	28959168
227297552	chr13	28964086	28964236	28964114	28964210	FLT1	NM_001159920	1	13	13	-	28959688	28964241
227297552	chr13	28964086	28964236	28964114	28964210	FLT1	NM_002019	4	30	13	-	28963933	28964241
227297552	chr13	28964086	28964236	28964114	28964210	FLT1	NM_001160030	2	15	13	-	28963933	28964241
227412507	chr13	28979849	28979974	28979874	28979950	FLT1	NM_002019	4	30	11	-	28979917	28980031
227412507	chr13	28979849	28979974	28979874	28979950	FLT1	NM_001159920	1	13	11	-	28979917	28980031
227412507	chr13	28979849	28979974	28979874	28979950	FLT1	NM_001160031	3	12	11	-	28979917	28980031
227412507	chr13	28979849	28979974	28979874	28979950	FLT1	NM_001160030	2	15	11	-	28979917	28980031
227980669	chr13	29001833	29001977	29001860	29001949	FLT1	NM_002019	4	30	9	-	29001889	29002058
227980669	chr13	29001833	29001977	29001860	29001949	FLT1	NM_001159920	1	13	9	-	29001889	29002058
227980669	chr13	29001833	29001977	29001860	29001949	FLT1	NM_001160031	3	12	9	-	29001889	29002058
227980669	chr13	29001833	29001977	29001860	29001949	FLT1	NM_001160030	2	15	9	-	29001889	29002058
228407857	chr13	29005245	29005400	29005266	29005372	FLT1	NM_002019	4	30	7	-	29005273	29005447
228407857	chr13	29005245	29005400	29005266	29005372	FLT1	NM_001159920	1	13	7	-	29005273	29005447
228407857	chr13	29005245	29005400	29005266	29005372	FLT1	NM_001160031	3	12	7	-	29005273	29005447
228407857	chr13	29005245	29005400	29005266	29005372	FLT1	NM_001160030	2	15	7	-	29005273	29005447
228897936	chr13	29008146	29008273	29008171	29008248	FLT1	NM_002019	4	30	5	-	29008195	29008357
228897936	chr13	29008146	29008273	29008171	29008248	FLT1	NM_001159920	1	13	5	-	29008195	29008357
228897936	chr13	29008146	29008273	29008171	29008248	FLT1	NM_001160031	3	12	5	-	29008195	29008357
228897936	chr13	29008146	29008273	29008171	29008248	FLT1	NM_001160030	2	15	5	-	29008195	29008357
227415199	chr13	29040938	29041111	29040966	29041083	FLT1	NM_002019	4	30	3	-	29041040	29041266
227415199	chr13	29040938	29041111	29040966	29041083	FLT1	NM_001159920	1	13	3	-	29041040	29041266
227415199	chr13	29040938	29041111	29040966	29041083	FLT1	NM_001160031	3	12	3	-	29041040	29041266
227415199	chr13	29040938	29041111	29040966	29041083	FLT1	NM_001160030	2	15	3	-	29041040	29041266

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227389424	chr13	29041704	29041841	29041730	29041811	FLT1	NM_002019	4	30	2	-	29041658	29041754
227389424	chr13	29041704	29041841	29041730	29041811	FLT1	NM_001159920	1	13	2	-	29041658	29041754
227389424	chr13	29041704	29041841	29041730	29041811	FLT1	NM_001160031	3	12	2	-	29041658	29041754
227389424	chr13	29041704	29041841	29041730	29041811	FLT1	NM_001160030	2	15	2	-	29041658	29041754
230273779	chr13	41133716	41133844	41133743	41133823	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230250609	chr13	41134104	41134267	41134127	41134246	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230330912	chr13	41134524	41134651	41134548	41134628	FOXO1	NM_002015	1	3	2	-	41133646	41134997
230294694	chr13	41134911	41135052	41134935	41135025	FOXO1	NM_002015	1	3	2	-	41133646	41134997
229111677	chr13	41240115	41240264	41240134	41240245	FOXO1	NM_002015	1	3	1	-	41239720	41240734
264236629	chr13	48881419	48881554	48881447	48881526	RB1	NM_000321	1	27	2	+	48881416	48881542
241362320	chr13	48921939	48922105	48921970	48922078	RB1	NM_000321	1	27	5	+	48921961	48921999
262539419	chr13	48939074	48939234	48939103	48939210	RB1	NM_000321	1	27	9	+	48939030	48939107
241627155	chr13	48954293	48954456	48954321	48954437	RB1	NM_000321	1	27	16	+	48954301	48954377
326867722	chr13	49027174	49027308	49027198	49027280	RB1	NM_000321	1	27	18	+	49027129	49027247
242362523	chr13	49037731	49037903	49037759	49037878	RB1	NM_000321	1	27	21	+	49037867	49037971
238894549	chr13	49039237	49039409	49039258	49039384	RB1	NM_000321	1	27	23	+	49039341	49039504
239943702	chr13	49050866	49051011	49050888	49050984	RB1	NM_000321	1	27	25	+	49050837	49050979
232336130	chr13	103498550	103498724	103498571	103498704	ERCC5	NM_000123	1	15	1	+	103498191	103498704
230573040	chr13	103506127	103506300	103506148	103506275	ERCC5	NM_000123	1	15	3	+	103506107	103506222
231397839	chr13	103510654	103510782	103510680	103510758	ERCC5	NM_000123	1	15	6	+	103510625	103510768
227932117	chr13	103513994	103514144	103514016	103514116	ERCC5	NM_000123	1	15	7	+	103513857	103514064
227805115	chr13	103514660	103514822	103514686	103514794	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230995822	chr13	103515099	103515247	103515126	103515226	ERCC5	NM_000123	1	15	8	+	103514380	103515453
230610618	chr13	103518074	103518248	103518097	103518226	ERCC5	NM_000123	1	15	9	+	103518017	103518261
230531168	chr13	103518955	103519112	103518976	103519087	ERCC5	NM_000123	1	15	11	+	103518982	103519195
231227779	chr13	103520455	103520582	103520482	103520560	ERCC5	NM_000123	1	15	12	+	103520463	103520607
227785555	chr13	103524685	103524828	103524704	103524797	ERCC5	NM_000123	1	15	13	+	103524548	103524748
231467912	chr13	103527693	103527860	103527721	103527833	ERCC5	NM_000123	1	15	15	+	103527657	103528351
231469575	chr13	103528179	103528311	103528199	103528284	ERCC5	NM_000123	1	15	15	+	103527657	103528351
272382009	chr13	110434507	110434665	110434524	110434641	IRS2	NM_003749	1	2	1	-	110434389	110438914
272380270	chr13	110434928	110435097	110434945	110435080	IRS2	NM_003749	1	2	1	-	110434389	110438914
272381493	chr13	110435542	110435688	110435559	110435670	IRS2	NM_003749	1	2	1	-	110434389	110438914
272382984	chr13	110435928	110436064	110435946	110436046	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383532	chr13	110436234	110436385	110436251	110436364	IRS2	NM_003749	1	2	1	-	110434389	110438914
272387972	chr13	110436664	110436838	110436686	110436821	IRS2	NM_003749	1	2	1	-	110434389	110438914
272383762	chr13	110437322	110437494	110437339	110437474	IRS2	NM_003749	1	2	1	-	110434389	110438914
272389006	chr13	110437700	110437857	110437720	110437840	IRS2	NM_003749	1	2	1	-	110434389	110438914
272388122	chr13	110438144	110438307	110438162	110438290	IRS2	NM_003749	1	2	1	-	110434389	110438914
280065059	chr13	113965028	113965201	113965057	113965183	LAMP1	NM_005561	1	9	4	+	113965024	113965182
279386876	chr13	113974620	113974788	113974641	113974767	LAMP1	NM_005561	1	9	6	+	113974660	113974785
278141231	chr13	113975962	113976122	113975983	113976102	LAMP1	NM_005561	1	9	8	+	113975872	113976042

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269588483	chr14	23777210	23777355	23777229	23777334	BCL2L2	NM_004050	2	4	3	+	23776969	23777408
269588483	chr14	23777210	23777355	23777229	23777334	BCL2L2	NM_001199839	1	4	3	+	23776969	23777408
238984110	chr14	36986405	36986574	36986424	36986556	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
238984110	chr14	36986405	36986574	36986424	36986556	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
258662099	chr14	36987064	36987232	36987082	36987210	NKX2-1	NM_003317	2	2	2	-	36985604	36987225
258662099	chr14	36987064	36987232	36987082	36987210	NKX2-1	NM_001079668	1	3	3	-	36985604	36987225
237519534	chr14	36988345	36988515	36988362	36988494	NKX2-1	NM_003317	2	2	1	-	36988190	36988903
237519534	chr14	36988345	36988515	36988362	36988494	NKX2-1	NM_001079668	1	3	2	-	36988190	36988575
235812061	chr14	51190266	51190419	51190293	51190392	NIN	NM_020921	2	31	31	-	51186481	51190390
242113245	chr14	51194366	51194498	51194388	51194471	NIN	NM_182944	3	30	30	-	51193951	51194469
239350135	chr14	51202164	51202332	51202190	51202304	NIN	NM_016350	1	29	27	-	51202234	51202335
239350135	chr14	51202164	51202332	51202190	51202304	NIN	NM_182946	4	30	28	-	51202234	51202335
239350135	chr14	51202164	51202332	51202190	51202304	NIN	NM_182944	3	30	28	-	51202234	51202335
239350135	chr14	51202164	51202332	51202190	51202304	NIN	NM_020921	2	31	28	-	51202234	51202335
242087973	chr14	51206000	51206128	51206022	51206103	NIN	NM_016350	1	29	25	-	51206026	51206205
242087973	chr14	51206000	51206128	51206022	51206103	NIN	NM_182946	4	30	26	-	51206026	51206205
242087973	chr14	51206000	51206128	51206022	51206103	NIN	NM_182944	3	30	26	-	51206026	51206205
242087973	chr14	51206000	51206128	51206022	51206103	NIN	NM_020921	2	31	26	-	51206026	51206205
235804875	chr14	51210103	51210275	51210130	51210248	NIN	NM_016350	1	29	23	-	51210134	51210247
235804875	chr14	51210103	51210275	51210130	51210248	NIN	NM_182946	4	30	24	-	51210134	51210247
235804875	chr14	51210103	51210275	51210130	51210248	NIN	NM_182944	3	30	24	-	51210134	51210247
235804875	chr14	51210103	51210275	51210130	51210248	NIN	NM_020921	2	31	24	-	51210134	51210247
237099287	chr14	51214703	51214875	51214729	51214849	NIN	NM_016350	1	29	21	-	51214710	51214823
237099287	chr14	51214703	51214875	51214729	51214849	NIN	NM_182946	4	30	22	-	51214710	51214823
237099287	chr14	51214703	51214875	51214729	51214849	NIN	NM_182944	3	30	22	-	51214710	51214823
237099287	chr14	51214703	51214875	51214729	51214849	NIN	NM_020921	2	31	22	-	51214710	51214823
240800175	chr14	51223120	51223279	51223143	51223257	NIN	NM_182946	4	30	18	-	51223210	51225348
240800175	chr14	51223120	51223279	51223143	51223257	NIN	NM_182944	3	30	18	-	51223210	51225348
240800175	chr14	51223120	51223279	51223143	51223257	NIN	NM_020921	2	31	18	-	51223210	51225348
236020284	chr14	51224024	51224171	51224051	51224148	NIN	NM_182946	4	30	18	-	51223210	51225348
236020284	chr14	51224024	51224171	51224051	51224148	NIN	NM_182944	3	30	18	-	51223210	51225348
236020284	chr14	51224024	51224171	51224051	51224148	NIN	NM_020921	2	31	18	-	51223210	51225348
240881104	chr14	51224430	51224601	51224457	51224581	NIN	NM_182946	4	30	18	-	51223210	51225348
240881104	chr14	51224430	51224601	51224457	51224581	NIN	NM_182944	3	30	18	-	51223210	51225348
240881104	chr14	51224430	51224601	51224457	51224581	NIN	NM_020921	2	31	18	-	51223210	51225348
236135209	chr14	51224897	51225071	51224918	51225046	NIN	NM_182946	4	30	18	-	51223210	51225348
236135209	chr14	51224897	51225071	51224918	51225046	NIN	NM_182944	3	30	18	-	51223210	51225348
236135209	chr14	51224897	51225071	51224918	51225046	NIN	NM_020921	2	31	18	-	51223210	51225348
235447238	chr14	51226538	51226711	51226558	51226689	NIN	NM_016350	1	29	17	-	51226575	51227077
235447238	chr14	51226538	51226711	51226558	51226689	NIN	NM_182946	4	30	17	-	51226575	51227077
235447238	chr14	51226538	51226711	51226558	51226689	NIN	NM_182944	3	30	17	-	51226575	51227077

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235447238	chr14	51226538	51226711	51226558	51226689	NIN	NM_020921	2	31	17	-	51226575	51227077
235492806	chr14	51226972	51227108	51226996	51227086	NIN	NM_016350	1	29	17	-	51226575	51227077
235492806	chr14	51226972	51227108	51226996	51227086	NIN	NM_182946	4	30	17	-	51226575	51227077
235492806	chr14	51226972	51227108	51226996	51227086	NIN	NM_182944	3	30	17	-	51226575	51227077
235492806	chr14	51226972	51227108	51226996	51227086	NIN	NM_020921	2	31	17	-	51226575	51227077
236019764	chr14	51233033	51233171	51233058	51233151	NIN	NM_016350	1	29	14	-	51233025	51233114
236019764	chr14	51233033	51233171	51233058	51233151	NIN	NM_182946	4	30	14	-	51233025	51233114
236019764	chr14	51233033	51233171	51233058	51233151	NIN	NM_182944	3	30	14	-	51233025	51233114
236019764	chr14	51233033	51233171	51233058	51233151	NIN	NM_020921	2	31	14	-	51233025	51233114
236756004	chr14	51237146	51237307	51237174	51237280	NIN	NM_016350	1	29	12	-	51237106	51237280
236756004	chr14	51237146	51237307	51237174	51237280	NIN	NM_182946	4	30	12	-	51237106	51237280
236756004	chr14	51237146	51237307	51237174	51237280	NIN	NM_182944	3	30	12	-	51237106	51237280
236756004	chr14	51237146	51237307	51237174	51237280	NIN	NM_020921	2	31	12	-	51237106	51237280
236139599	chr14	51238090	51238214	51238112	51238187	NIN	NM_016350	1	29	10	-	51238050	51238186
236139599	chr14	51238090	51238214	51238112	51238187	NIN	NM_182946	4	30	10	-	51238050	51238186
236139599	chr14	51238090	51238214	51238112	51238187	NIN	NM_182944	3	30	10	-	51238050	51238186
236139599	chr14	51238090	51238214	51238112	51238187	NIN	NM_020921	2	31	10	-	51238050	51238186
239224564	chr14	51239669	51239818	51239692	51239790	NIN	NM_016350	1	29	8	-	51239667	51239813
239224564	chr14	51239669	51239818	51239692	51239790	NIN	NM_182946	4	30	8	-	51239667	51239813
239224564	chr14	51239669	51239818	51239692	51239790	NIN	NM_182944	3	30	8	-	51239667	51239813
239224564	chr14	51239669	51239818	51239692	51239790	NIN	NM_020921	2	31	8	-	51239667	51239813
237351262	chr14	51245391	51245550	51245412	51245523	NIN	NM_016350	1	29	6	-	51245483	51245522
237351262	chr14	51245391	51245550	51245412	51245523	NIN	NM_182946	4	30	6	-	51245483	51245522
237351262	chr14	51245391	51245550	51245412	51245523	NIN	NM_182944	3	30	6	-	51245483	51245522
237351262	chr14	51245391	51245550	51245412	51245523	NIN	NM_020921	2	31	6	-	51245483	51245522
236020792	chr14	51288556	51288685	51288576	51288664	NIN	NM_016350	1	29	3	-	51288592	51288795
236020792	chr14	51288556	51288685	51288576	51288664	NIN	NM_182946	4	30	3	-	51288592	51288795
236020792	chr14	51288556	51288685	51288576	51288664	NIN	NM_182944	3	30	3	-	51288592	51288795
236020792	chr14	51288556	51288685	51288576	51288664	NIN	NM_020921	2	31	3	-	51288592	51288795
278556741	chr14	62164577	62164740	62164604	62164715	HIF1A	NM_001243084	1	15	1	+	62164340	62164672
279179721	chr14	62188131	62188304	62188159	62188278	HIF1A	NM_001243084	1	15	3	+	62188227	62188372
279179721	chr14	62188131	62188304	62188159	62188278	HIF1A	NM_001530	2	15	3	+	62188227	62188372
279179721	chr14	62188131	62188304	62188159	62188278	HIF1A	NM_181054	3	14	3	+	62188227	62188372
279334346	chr14	62193304	62193465	62193330	62193443	HIF1A	NM_001243084	1	15	5	+	62193424	62193536
279334346	chr14	62193304	62193465	62193330	62193443	HIF1A	NM_001530	2	15	5	+	62193424	62193536
279334346	chr14	62193304	62193465	62193330	62193443	HIF1A	NM_181054	3	14	5	+	62193424	62193536
279953221	chr14	62194181	62194351	62194204	62194329	HIF1A	NM_001243084	1	15	6	+	62194171	62194373
279953221	chr14	62194181	62194351	62194204	62194329	HIF1A	NM_001530	2	15	6	+	62194171	62194373
279953221	chr14	62194181	62194351	62194204	62194329	HIF1A	NM_181054	3	14	6	+	62194171	62194373
280848182	chr14	62200757	62200911	62200785	62200890	HIF1A	NM_001243084	1	15	8	+	62200856	62201003
280848182	chr14	62200757	62200911	62200785	62200890	HIF1A	NM_001530	2	15	8	+	62200856	62201003

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
280848182	chr14	62200757	62200911	62200785	62200890	HIF1A	NM_181054	3	14	8	+	62200856	62201003
279032446	chr14	62203605	62203779	62203633	62203756	HIF1A	NM_001243084	1	15	9	+	62203607	62203827
279032446	chr14	62203605	62203779	62203633	62203756	HIF1A	NM_001530	2	15	9	+	62203607	62203827
279032446	chr14	62203605	62203779	62203633	62203756	HIF1A	NM_181054	3	14	9	+	62203607	62203827
280356584	chr14	62204959	62205097	62204987	62205073	HIF1A	NM_001243084	1	15	10	+	62204805	62205091
280356584	chr14	62204959	62205097	62204987	62205073	HIF1A	NM_001530	2	15	10	+	62204805	62205091
280356584	chr14	62204959	62205097	62204987	62205073	HIF1A	NM_181054	3	14	10	+	62204805	62205091
278387712	chr14	62207430	62207556	62207454	62207531	HIF1A	NM_001243084	1	15	12	+	62207473	62207906
278387712	chr14	62207430	62207556	62207454	62207531	HIF1A	NM_001530	2	15	12	+	62207473	62207906
278387712	chr14	62207430	62207556	62207454	62207531	HIF1A	NM_181054	3	14	12	+	62207473	62207906
278434184	chr14	62207850	62208021	62207876	62207993	HIF1A	NM_001243084	1	15	12	+	62207473	62207906
278434184	chr14	62207850	62208021	62207876	62207993	HIF1A	NM_001530	2	15	12	+	62207473	62207906
278434184	chr14	62207850	62208021	62207876	62207993	HIF1A	NM_181054	3	14	12	+	62207473	62207906
278367295	chr14	62212462	62212635	62212490	62212609	HIF1A	NM_001243084	1	15	14	+	62212409	62212535
278367295	chr14	62212462	62212635	62212490	62212609	HIF1A	NM_001530	2	15	14	+	62212409	62212535
263052808	chr14	81422116	81422282	81422136	81422257	TSHR	NM_001142626	3	9	1	+	81421869	81422194
263052808	chr14	81422116	81422282	81422136	81422257	TSHR	NM_000369	1	10	1	+	81421869	81422194
263052808	chr14	81422116	81422282	81422136	81422257	TSHR	NM_001018036	2	9	1	+	81421869	81422194
262042257	chr14	81534616	81534747	81534634	81534725	TSHR	NM_001142626	3	9	3	+	81534598	81534672
262042257	chr14	81534616	81534747	81534634	81534725	TSHR	NM_000369	1	10	3	+	81534598	81534672
262042257	chr14	81534616	81534747	81534634	81534725	TSHR	NM_001018036	2	9	3	+	81534598	81534672
263152168	chr14	81562934	81563077	81562955	81563051	TSHR	NM_001142626	3	9	7	+	81562983	81563051
263152168	chr14	81562934	81563077	81562955	81563051	TSHR	NM_000369	1	10	7	+	81562983	81563051
263152168	chr14	81562934	81563077	81562955	81563051	TSHR	NM_001018036	2	9	7	+	81562983	81563051
266387738	chr14	81605982	81606140	81606004	81606115	TSHR	NM_000369	1	10	9	+	81606023	81606211
262725402	chr14	81609488	81609660	81609510	81609632	TSHR	NM_000369	1	10	10	+	81609284	81612646
266489845	chr14	81609937	81610108	81609956	81610082	TSHR	NM_000369	1	10	10	+	81609284	81612646
262787059	chr14	81610406	81610580	81610430	81610552	TSHR	NM_000369	1	10	10	+	81609284	81612646
264382426	chr14	92436047	92436219	92436068	92436192	TRIP11	NM_004239	1	21	21	-	92434243	92436237
240726145	chr14	92441056	92441219	92441075	92441190	TRIP11	NM_004239	1	21	19	-	92440971	92441087
241319323	chr14	92460085	92460257	92460113	92460229	TRIP11	NM_004239	1	21	15	-	92460153	92460256
238376416	chr14	92465583	92465750	92465609	92465725	TRIP11	NM_004239	1	21	13	-	92465584	92465777
264843680	chr14	92466396	92466569	92466424	92466549	TRIP11	NM_004239	1	21	12	-	92466312	92466452
266131321	chr14	92469995	92470160	92470023	92470134	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266129093	chr14	92470407	92470568	92470432	92470540	TRIP11	NM_004239	1	21	11	-	92469763	92472792
242765384	chr14	92470786	92470954	92470814	92470931	TRIP11	NM_004239	1	21	11	-	92469763	92472792
262002097	chr14	92471161	92471290	92471189	92471262	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266148776	chr14	92471496	92471652	92471525	92471624	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266158982	chr14	92471820	92471947	92471845	92471920	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266164941	chr14	92472201	92472355	92472227	92472325	TRIP11	NM_004239	1	21	11	-	92469763	92472792
266170791	chr14	92472663	92472814	92472693	92472787	TRIP11	NM_004239	1	21	11	-	92469763	92472792

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240293972	chr14	92474077	92474247	92474105	92474221	TRIP11	NM_004239	1	21	10	-	92473984	92474196
264660059	chr14	92480506	92480649	92480534	92480620	TRIP11	NM_004239	1	21	7	-	92480559	92480921
263131013	chr14	92484061	92484212	92484088	92484188	TRIP11	NM_004239	1	21	5	-	92484026	92484094
265039407	chr14	92491534	92491695	92491567	92491667	TRIP11	NM_004239	1	21	3	-	92491654	92491764
266225755	chr14	92505805	92505950	92505826	92505923	TRIP11	NM_004239	1	21	1	-	92505891	92506403
230019503	chr14	95556911	95557084	95556939	95557062	DICER1	NM_177438	3	27	27	-	95552565	95557000
230019503	chr14	95556911	95557084	95556939	95557062	DICER1	NM_001195573	1	25	25	-	95552565	95557000
230019503	chr14	95556911	95557084	95556939	95557062	DICER1	NM_030621	2	28	28	-	95552565	95557000
230813954	chr14	95557515	95557668	95557541	95557643	DICER1	NM_177438	3	27	25	-	95557540	95557702
230813954	chr14	95557515	95557668	95557541	95557643	DICER1	NM_030621	2	28	26	-	95557540	95557702
229780257	chr14	95560416	95560541	95560437	95560516	DICER1	NM_177438	3	27	24	-	95560225	95560493
229780257	chr14	95560416	95560541	95560437	95560516	DICER1	NM_001195573	1	25	23	-	95560225	95560493
229780257	chr14	95560416	95560541	95560437	95560516	DICER1	NM_030621	2	28	25	-	95560225	95560493
233007649	chr14	95562395	95562520	95562420	95562497	DICER1	NM_177438	3	27	23	-	95562162	95563050
233007649	chr14	95562395	95562520	95562420	95562497	DICER1	NM_001195573	1	25	22	-	95562162	95563050
233007649	chr14	95562395	95562520	95562420	95562497	DICER1	NM_030621	2	28	24	-	95562162	95563050
230665165	chr14	95562805	95562964	95562830	95562942	DICER1	NM_177438	3	27	23	-	95562162	95563050
230665165	chr14	95562805	95562964	95562830	95562942	DICER1	NM_001195573	1	25	22	-	95562162	95563050
230665165	chr14	95562805	95562964	95562830	95562942	DICER1	NM_030621	2	28	24	-	95562162	95563050
232751710	chr14	95566195	95566334	95566219	95566310	DICER1	NM_177438	3	27	22	-	95566117	95566272
232751710	chr14	95566195	95566334	95566219	95566310	DICER1	NM_001195573	1	25	21	-	95566117	95566272
232751710	chr14	95566195	95566334	95566219	95566310	DICER1	NM_030621	2	28	23	-	95566117	95566272
228201032	chr14	95569980	95570154	95570008	95570129	DICER1	NM_177438	3	27	21	-	95569683	95570463
228201032	chr14	95569980	95570154	95570008	95570129	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228201032	chr14	95569980	95570154	95570008	95570129	DICER1	NM_030621	2	28	22	-	95569683	95570463
228141845	chr14	95570386	95570531	95570414	95570509	DICER1	NM_177438	3	27	21	-	95569683	95570463
228141845	chr14	95570386	95570531	95570414	95570509	DICER1	NM_001195573	1	25	20	-	95569683	95570463
228141845	chr14	95570386	95570531	95570414	95570509	DICER1	NM_030621	2	28	22	-	95569683	95570463
228741312	chr14	95572059	95572229	95572081	95572206	DICER1	NM_177438	3	27	19	-	95572015	95572120
228741312	chr14	95572059	95572229	95572081	95572206	DICER1	NM_001195573	1	25	18	-	95572015	95572120
228741312	chr14	95572059	95572229	95572081	95572206	DICER1	NM_030621	2	28	20	-	95572015	95572120
228398999	chr14	95573950	95574092	95573978	95574064	DICER1	NM_177438	3	27	17	-	95573945	95574098
228398999	chr14	95573950	95574092	95573978	95574064	DICER1	NM_001195573	1	25	16	-	95573945	95574098
228398999	chr14	95573950	95574092	95573978	95574064	DICER1	NM_030621	2	28	18	-	95573945	95574098
228812034	chr14	95574316	95574442	95574343	95574415	DICER1	NM_177438	3	27	16	-	95574217	95574430
228812034	chr14	95574316	95574442	95574343	95574415	DICER1	NM_001195573	1	25	15	-	95574217	95574430
228812034	chr14	95574316	95574442	95574343	95574415	DICER1	NM_030621	2	28	17	-	95574217	95574430
227742373	chr14	95577570	95577739	95577592	95577714	DICER1	NM_177438	3	27	14	-	95577654	95577793
227742373	chr14	95577570	95577739	95577592	95577714	DICER1	NM_001195573	1	25	13	-	95577654	95577793
227742373	chr14	95577570	95577739	95577592	95577714	DICER1	NM_030621	2	28	15	-	95577654	95577793
230403910	chr14	95579299	95579473	95579321	95579445	DICER1	NM_177438	3	27	12	-	95579429	95579561

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230403910	chr14	95579299	95579473	95579321	95579445	DICER1	NM_001195573	1	25	11	-	95579429	95579561
230403910	chr14	95579299	95579473	95579321	95579445	DICER1	NM_030621	2	28	13	-	95579429	95579561
230698106	chr14	95582754	95582924	95582775	95582896	DICER1	NM_177438	3	27	10	-	95582790	95583032
230698106	chr14	95582754	95582924	95582775	95582896	DICER1	NM_001195573	1	25	9	-	95582790	95583032
230698106	chr14	95582754	95582924	95582775	95582896	DICER1	NM_030621	2	28	11	-	95582790	95583032
229824845	chr14	95583964	95584130	95583991	95584102	DICER1	NM_177438	3	27	9	-	95583959	95584091
229824845	chr14	95583964	95584130	95583991	95584102	DICER1	NM_001195573	1	25	8	-	95583959	95584091
229824845	chr14	95583964	95584130	95583991	95584102	DICER1	NM_030621	2	28	10	-	95583959	95584091
232532142	chr14	95590825	95590997	95590853	95590977	DICER1	NM_177438	3	27	8	-	95590533	95591005
232532142	chr14	95590825	95590997	95590853	95590977	DICER1	NM_001195573	1	25	7	-	95590533	95591005
232532142	chr14	95590825	95590997	95590853	95590977	DICER1	NM_030621	2	28	9	-	95590533	95591005
227759354	chr14	95595887	95596048	95595916	95596020	DICER1	NM_177438	3	27	6	-	95595809	95595969
227759354	chr14	95595887	95596048	95595916	95596020	DICER1	NM_001195573	1	25	5	-	95595809	95595969
227759354	chr14	95595887	95596048	95595916	95596020	DICER1	NM_030621	2	28	7	-	95595809	95595969
230507676	chr14	95597884	95598053	95597912	95598025	DICER1	NM_177438	3	27	4	-	95597846	95597976
230507676	chr14	95597884	95598053	95597912	95598025	DICER1	NM_001195573	1	25	3	-	95597846	95597976
230507676	chr14	95597884	95598053	95597912	95598025	DICER1	NM_030621	2	28	5	-	95597846	95597976
231600663	chr14	95599622	95599748	95599647	95599728	DICER1	NM_177438	3	27	2	-	95599652	95599840
231600663	chr14	95599622	95599748	95599647	95599728	DICER1	NM_001195573	1	25	1	-	95599652	95599840
231600663	chr14	95599622	95599748	95599647	95599728	DICER1	NM_030621	2	28	3	-	95599652	95599840
239861023	chr14	96178596	96178766	96178617	96178741	TCL1A	NM_021966	2	4	2	-	96178557	96178733
239861023	chr14	96178596	96178766	96178617	96178741	TCL1A	NM_001098725	1	4	2	-	96178557	96178733
223918824	chr14	99640536	99640699	99640555	99640680	BCL11B	NM_138576	2	4	4	-	99635625	99642532
223918824	chr14	99640536	99640699	99640555	99640680	BCL11B	NM_022898	1	3	3	-	99635625	99642532
223927319	chr14	99641036	99641182	99641055	99641165	BCL11B	NM_138576	2	4	4	-	99635625	99642532
223927319	chr14	99641036	99641182	99641055	99641165	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225207431	chr14	99641728	99641896	99641745	99641877	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225207431	chr14	99641728	99641896	99641745	99641877	BCL11B	NM_022898	1	3	3	-	99635625	99642532
225211125	chr14	99642167	99642330	99642185	99642312	BCL11B	NM_138576	2	4	4	-	99635625	99642532
225211125	chr14	99642167	99642330	99642185	99642312	BCL11B	NM_022898	1	3	3	-	99635625	99642532
222195101	chr14	99697556	99697717	99697576	99697699	BCL11B	NM_138576	2	4	3	-	99697682	99697894
222965497	chr14	99723875	99724032	99723895	99724007	BCL11B	NM_138576	2	4	2	-	99723808	99724176
222965497	chr14	99723875	99724032	99723895	99724007	BCL11B	NM_022898	1	3	2	-	99723808	99724176
229817109	chr14	102548001	102548167	102548029	102548140	HSP90AA1	NM_005348	2	11	11	-	102547075	102548158
229817109	chr14	102548001	102548167	102548029	102548140	HSP90AA1	NM_001017963	1	12	12	-	102547075	102548158
227282151	chr14	102548622	102548796	102548646	102548769	HSP90AA1	NM_005348	2	11	10	-	102548448	102548781
227282151	chr14	102548622	102548796	102548646	102548769	HSP90AA1	NM_001017963	1	12	11	-	102548448	102548781
228122834	chr14	102549478	102549612	102549498	102549591	HSP90AA1	NM_005348	2	11	9	-	102549371	102549639
228122834	chr14	102549478	102549612	102549498	102549591	HSP90AA1	NM_001017963	1	12	10	-	102549371	102549639
227287895	chr14	102550019	102550192	102550047	102550167	HSP90AA1	NM_005348	2	11	7	-	102550130	102550320
227287895	chr14	102550019	102550192	102550047	102550167	HSP90AA1	NM_001017963	1	12	8	-	102550130	102550320

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227709923	chr14	102550820	102550975	102550847	102550950	HSP90AA1	NM_005348	2	11	6	-	102550736	102550901
227709923	chr14	102550820	102550975	102550847	102550950	HSP90AA1	NM_001017963	1	12	7	-	102550736	102550901
227317667	chr14	102551204	102551367	102551232	102551339	HSP90AA1	NM_005348	2	11	5	-	102551018	102551335
227317667	chr14	102551204	102551367	102551232	102551339	HSP90AA1	NM_001017963	1	12	6	-	102551018	102551335
227732313	chr14	102552087	102552261	102552107	102552240	HSP90AA1	NM_005348	2	11	3	-	102552095	102552461
227732313	chr14	102552087	102552261	102552107	102552240	HSP90AA1	NM_001017963	1	12	4	-	102552095	102552461
227242104	chr14	102552628	102552760	102552649	102552738	HSP90AA1	NM_005348	2	11	2	-	102552554	102552715
227242104	chr14	102552628	102552760	102552649	102552738	HSP90AA1	NM_001017963	1	12	3	-	102552554	102552715
229409963	chr14	102605499	102605673	102605524	102605653	HSP90AA1	NM_001017963	1	12	1	-	102605587	102606086
225033329	chr14	105237113	105237257	105237134	105237236	AKT1	NM_005163	3	14	13	-	105237082	105237184
225033329	chr14	105237113	105237257	105237134	105237236	AKT1	NM_001014432	2	15	14	-	105237082	105237184
225033329	chr14	105237113	105237257	105237134	105237236	AKT1	NM_001014431	1	14	13	-	105237082	105237184
223604918	chr14	105239294	105239468	105239317	105239449	AKT1	NM_005163	3	14	11	-	105239215	105239429
223604918	chr14	105239294	105239468	105239317	105239449	AKT1	NM_001014432	2	15	12	-	105239215	105239429
223604918	chr14	105239294	105239468	105239317	105239449	AKT1	NM_001014431	1	14	11	-	105239215	105239429
222372092	chr14	105240211	105240341	105240228	105240321	AKT1	NM_005163	3	14	8	-	105240249	105240317
222372092	chr14	105240211	105240341	105240228	105240321	AKT1	NM_001014432	2	15	9	-	105240249	105240317
222372092	chr14	105240211	105240341	105240228	105240321	AKT1	NM_001014431	1	14	8	-	105240249	105240317
224409287	chr14	105241511	105241666	105241532	105241647	AKT1	NM_005163	3	14	6	-	105241413	105241544
224409287	chr14	105241511	105241666	105241532	105241647	AKT1	NM_001014432	2	15	7	-	105241413	105241544
224409287	chr14	105241511	105241666	105241532	105241647	AKT1	NM_001014431	1	14	6	-	105241413	105241544
223791861	chr14	105242987	105243111	105243004	105243091	AKT1	NM_005163	3	14	4	-	105242996	105243107
223791861	chr14	105242987	105243111	105243004	105243091	AKT1	NM_001014432	2	15	5	-	105242996	105243107
223791861	chr14	105242987	105243111	105243004	105243091	AKT1	NM_001014431	1	14	4	-	105242996	105243107
223356244	chr14	105258916	105259078	105258934	105259056	AKT1	NM_005163	3	14	2	-	105258935	105259059
223356244	chr14	105258916	105259078	105258934	105259056	AKT1	NM_001014432	2	15	3	-	105258935	105259059
223356244	chr14	105258916	105259078	105258934	105259056	AKT1	NM_001014431	1	14	2	-	105258935	105259059
304181343	chr15	39874496	39874664	39874516	39874644	THBS1	NM_003246	1	22	3	+	39874394	39874953
302334585	chr15	39875774	39875932	39875794	39875904	THBS1	NM_003246	1	22	4	+	39875818	39875893
305797489	chr15	39876471	39876644	39876498	39876624	THBS1	NM_003246	1	22	6	+	39876501	39876623
301718257	chr15	39880152	39880316	39880174	39880293	THBS1	NM_003246	1	22	9	+	39880243	39880419
302141775	chr15	39881135	39881307	39881159	39881287	THBS1	NM_003246	1	22	11	+	39881160	39881287
303257458	chr15	39882080	39882246	39882100	39882225	THBS1	NM_003246	1	22	13	+	39882006	39882224
300918409	chr15	39883402	39883573	39883426	39883552	THBS1	NM_003246	1	22	15	+	39883392	39883551
299895996	chr15	39885097	39885264	39885119	39885243	THBS1	NM_003246	1	22	18	+	39885201	39885428
301624430	chr15	39885647	39885812	39885668	39885787	THBS1	NM_003246	1	22	19	+	39885598	39885869
305998873	chr15	39886495	39886669	39886517	39886644	THBS1	NM_003246	1	22	21	+	39886502	39886641
223307757	chr15	40457271	40457421	40457295	40457397	BUB1B	NM_001211	1	23	2	+	40457254	40457397
223916149	chr15	40468615	40468784	40468642	40468756	BUB1B	NM_001211	1	23	5	+	40468678	40468874
222289365	chr15	40476038	40476185	40476061	40476157	BUB1B	NM_001211	1	23	6	+	40475915	40476084
223784672	chr15	40477682	40477818	40477708	40477793	BUB1B	NM_001211	1	23	8	+	40477752	40477843

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224133794	chr15	40488813	40488938	40488838	40488912	BUB1B	NM_001211	1	23	9	+	40488746	40488975
224843784	chr15	40492332	40492491	40492359	40492463	BUB1B	NM_001211	1	23	11	+	40492445	40492560
223436077	chr15	40494761	40494899	40494789	40494872	BUB1B	NM_001211	1	23	14	+	40494790	40494895
222403638	chr15	40498496	40498630	40498524	40498606	BUB1B	NM_001211	1	23	15	+	40498385	40498659
223379060	chr15	40501831	40502005	40501853	40501981	BUB1B	NM_001211	1	23	17	+	40501836	40501976
222847305	chr15	40504784	40504911	40504811	40504884	BUB1B	NM_001211	1	23	19	+	40504700	40504849
223935120	chr15	40509725	40509898	40509753	40509870	BUB1B	NM_001211	1	23	21	+	40509697	40509868
224974483	chr15	40512869	40512995	40512894	40512974	BUB1B	NM_001211	1	23	23	+	40512765	40513337
225671791	chr15	40897320	40897449	40897342	40897426	CASC5	NM_144508	1	26	3	+	40897308	40897347
225671791	chr15	40897320	40897449	40897342	40897426	CASC5	NM_170589	2	27	3	+	40897308	40897347
227037134	chr15	40901038	40901168	40901066	40901139	CASC5	NM_144508	1	26	5	+	40901045	40901106
227037134	chr15	40901038	40901168	40901066	40901139	CASC5	NM_170589	2	27	5	+	40901045	40901106
225326289	chr15	40912724	40912892	40912749	40912869	CASC5	NM_144508	1	26	10	+	40912838	40917838
225326289	chr15	40912724	40912892	40912749	40912869	CASC5	NM_170589	2	27	11	+	40912838	40917838
225344247	chr15	40913068	40913207	40913096	40913178	CASC5	NM_144508	1	26	10	+	40912838	40917838
225344247	chr15	40913068	40913207	40913096	40913178	CASC5	NM_170589	2	27	11	+	40912838	40917838
226623971	chr15	40913429	40913590	40913456	40913562	CASC5	NM_144508	1	26	10	+	40912838	40917838
226623971	chr15	40913429	40913590	40913456	40913562	CASC5	NM_170589	2	27	11	+	40912838	40917838
226620190	chr15	40913770	40913906	40913798	40913878	CASC5	NM_144508	1	26	10	+	40912838	40917838
226620190	chr15	40913770	40913906	40913798	40913878	CASC5	NM_170589	2	27	11	+	40912838	40917838
226628425	chr15	40914090	40914257	40914115	40914235	CASC5	NM_144508	1	26	10	+	40912838	40917838
226628425	chr15	40914090	40914257	40914115	40914235	CASC5	NM_170589	2	27	11	+	40912838	40917838
226627956	chr15	40914483	40914646	40914511	40914619	CASC5	NM_144508	1	26	10	+	40912838	40917838
226627956	chr15	40914483	40914646	40914511	40914619	CASC5	NM_170589	2	27	11	+	40912838	40917838
226622394	chr15	40914824	40914973	40914845	40914946	CASC5	NM_144508	1	26	10	+	40912838	40917838
226622394	chr15	40914824	40914973	40914845	40914946	CASC5	NM_170589	2	27	11	+	40912838	40917838
225341116	chr15	40915330	40915464	40915357	40915439	CASC5	NM_144508	1	26	10	+	40912838	40917838
225341116	chr15	40915330	40915464	40915357	40915439	CASC5	NM_170589	2	27	11	+	40912838	40917838
225364666	chr15	40915721	40915853	40915748	40915828	CASC5	NM_144508	1	26	10	+	40912838	40917838
225364666	chr15	40915721	40915853	40915748	40915828	CASC5	NM_170589	2	27	11	+	40912838	40917838
225383787	chr15	40916079	40916253	40916104	40916230	CASC5	NM_144508	1	26	10	+	40912838	40917838
225383787	chr15	40916079	40916253	40916104	40916230	CASC5	NM_170589	2	27	11	+	40912838	40917838
226630807	chr15	40916451	40916595	40916476	40916567	CASC5	NM_144508	1	26	10	+	40912838	40917838
226630807	chr15	40916451	40916595	40916476	40916567	CASC5	NM_170589	2	27	11	+	40912838	40917838
226624450	chr15	40916899	40917040	40916924	40917011	CASC5	NM_144508	1	26	10	+	40912838	40917838
226624450	chr15	40916899	40917040	40916924	40917011	CASC5	NM_170589	2	27	11	+	40912838	40917838
226633253	chr15	40917200	40917359	40917220	40917331	CASC5	NM_144508	1	26	10	+	40912838	40917838
226633253	chr15	40917200	40917359	40917220	40917331	CASC5	NM_170589	2	27	11	+	40912838	40917838
226640199	chr15	40917526	40917675	40917549	40917647	CASC5	NM_144508	1	26	10	+	40912838	40917838
226640199	chr15	40917526	40917675	40917549	40917647	CASC5	NM_170589	2	27	11	+	40912838	40917838
226418226	chr15	40920198	40920365	40920228	40920343	CASC5	NM_144508	1	26	11	+	40920268	40920406

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226418226	chr15	40920198	40920365	40920228	40920343	CASC5	NM_170589	2	27	12	+	40920268	40920406
225879368	chr15	40920816	40920949	40920844	40920919	CASC5	NM_144508	1	26	12	+	40920809	40920876
225879368	chr15	40920816	40920949	40920844	40920919	CASC5	NM_170589	2	27	13	+	40920809	40920876
225984800	chr15	40937193	40937336	40937219	40937309	CASC5	NM_144508	1	26	15	+	40937195	40937285
225984800	chr15	40937193	40937336	40937219	40937309	CASC5	NM_170589	2	27	16	+	40937195	40937285
253655145	chr15	40939228	40939355	40939259	40939329	CASC5	NM_144508	1	26	17	+	40939185	40939272
253655145	chr15	40939228	40939355	40939259	40939329	CASC5	NM_170589	2	27	18	+	40939185	40939272
226565267	chr15	40943665	40943801	40943690	40943777	CASC5	NM_144508	1	26	20	+	40943669	40943770
226565267	chr15	40943665	40943801	40943690	40943777	CASC5	NM_170589	2	27	21	+	40943669	40943770
225803356	chr15	40951544	40951684	40951568	40951661	CASC5	NM_144508	1	26	25	+	40951537	40951659
225803356	chr15	40951544	40951684	40951568	40951661	CASC5	NM_170589	2	27	26	+	40951537	40951659
270748102	chr15	41796408	41796532	41796431	41796508	LTK	NM_001135685	1	18	18	-	41795840	41796442
270748102	chr15	41796408	41796532	41796431	41796508	LTK	NM_002344	2	20	20	-	41795840	41796442
270748102	chr15	41796408	41796532	41796431	41796508	LTK	NM_206961	3	19	19	-	41795840	41796442
270225241	chr15	41796830	41796999	41796852	41796975	LTK	NM_001135685	1	18	15	-	41796971	41797072
270225241	chr15	41796830	41796999	41796852	41796975	LTK	NM_002344	2	20	17	-	41796971	41797072
270225241	chr15	41796830	41796999	41796852	41796975	LTK	NM_206961	3	19	16	-	41796971	41797072
271144718	chr15	41797385	41797542	41797405	41797520	LTK	NM_001135685	1	18	13	-	41797406	41797503
271144718	chr15	41797385	41797542	41797405	41797520	LTK	NM_002344	2	20	15	-	41797406	41797503
271144718	chr15	41797385	41797542	41797405	41797520	LTK	NM_206961	3	19	14	-	41797406	41797503
271372163	chr15	41798091	41798230	41798112	41798209	LTK	NM_002344	2	20	12	-	41798113	41798203
271372163	chr15	41798091	41798230	41798112	41798209	LTK	NM_206961	3	19	11	-	41798113	41798203
269522045	chr15	41800244	41800393	41800265	41800373	LTK	NM_001135685	1	18	8	-	41800267	41800419
269522045	chr15	41800244	41800393	41800265	41800373	LTK	NM_002344	2	20	9	-	41800267	41800419
269522045	chr15	41800244	41800393	41800265	41800373	LTK	NM_206961	3	19	8	-	41800267	41800419
270258525	chr15	41803656	41803810	41803673	41803793	LTK	NM_001135685	1	18	6	-	41803620	41803776
270258525	chr15	41803656	41803810	41803673	41803793	LTK	NM_002344	2	20	6	-	41803620	41803776
270258525	chr15	41803656	41803810	41803673	41803793	LTK	NM_206961	3	19	6	-	41803620	41803776
270162015	chr15	41804319	41804475	41804336	41804457	LTK	NM_001135685	1	18	4	-	41804313	41804463
270162015	chr15	41804319	41804475	41804336	41804457	LTK	NM_002344	2	20	4	-	41804313	41804463
270162015	chr15	41804319	41804475	41804336	41804457	LTK	NM_206961	3	19	4	-	41804313	41804463
272210196	chr15	41805002	41805169	41805023	41805147	LTK	NM_001135685	1	18	3	-	41804905	41805076
272210196	chr15	41805002	41805169	41805023	41805147	LTK	NM_002344	2	20	3	-	41804905	41805076
272210196	chr15	41805002	41805169	41805023	41805147	LTK	NM_206961	3	19	3	-	41804905	41805076
295334985	chr15	43568577	43568708	43568600	43568684	TGM7	NM_052955	1	13	13	-	43568479	43568812
294724879	chr15	43571216	43571373	43571237	43571352	TGM7	NM_052955	1	13	11	-	43571315	43571475
294910146	chr15	43572043	43572186	43572064	43572165	TGM7	NM_052955	1	13	10	-	43571823	43572149
294339044	chr15	43574689	43574856	43574709	43574828	TGM7	NM_052955	1	13	8	-	43574715	43574818
294008465	chr15	43579571	43579744	43579592	43579722	TGM7	NM_052955	1	13	6	-	43579478	43579655
295275519	chr15	43584842	43585014	43584863	43584986	TGM7	NM_052955	1	13	3	-	43584907	43585152
294138303	chr15	43585684	43585855	43585702	43585836	TGM7	NM_052955	1	13	2	-	43585647	43585829

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261829633	chr15	57355835	57355995	57355855	57355973	TCF12	NM_207038	4	20	4	+	57355948	57356021
261829633	chr15	57355835	57355995	57355855	57355973	TCF12	NM_207036	2	21	4	+	57355948	57356021
261829633	chr15	57355835	57355995	57355855	57355973	TCF12	NM_003205	1	20	4	+	57355948	57356021
261829633	chr15	57355835	57355995	57355855	57355973	TCF12	NM_207037	3	21	4	+	57355948	57356021
239172825	chr15	57458523	57458679	57458552	57458651	TCF12	NM_207038	4	20	6	+	57458600	57458664
239172825	chr15	57458523	57458679	57458552	57458651	TCF12	NM_207036	2	21	6	+	57458600	57458664
239172825	chr15	57458523	57458679	57458552	57458651	TCF12	NM_003205	1	20	6	+	57458600	57458664
239172825	chr15	57458523	57458679	57458552	57458651	TCF12	NM_207037	3	21	6	+	57458600	57458664
241932108	chr15	57489967	57490091	57489989	57490064	TCF12	NM_207038	4	20	8	+	57489971	57490023
241932108	chr15	57489967	57490091	57489989	57490064	TCF12	NM_207036	2	21	8	+	57489971	57490023
241932108	chr15	57489967	57490091	57489989	57490064	TCF12	NM_003205	1	20	8	+	57489971	57490023
241932108	chr15	57489967	57490091	57489989	57490064	TCF12	NM_207037	3	21	8	+	57489971	57490023
241344438	chr15	57523356	57523489	57523380	57523461	TCF12	NM_207038	4	20	9	+	57523350	57523455
241344438	chr15	57523356	57523489	57523380	57523461	TCF12	NM_207036	2	21	9	+	57523350	57523455
241344438	chr15	57523356	57523489	57523380	57523461	TCF12	NM_003205	1	20	9	+	57523350	57523455
241344438	chr15	57523356	57523489	57523380	57523461	TCF12	NM_207037	3	21	9	+	57523350	57523455
241344438	chr15	57523356	57523489	57523380	57523461	TCF12	NM_207040	5	13	2	+	57523350	57523455
238766724	chr15	57524896	57525021	57524924	57525001	TCF12	NM_207038	4	20	11	+	57524910	57525054
238766724	chr15	57524896	57525021	57524924	57525001	TCF12	NM_207036	2	21	11	+	57524910	57525054
238766724	chr15	57524896	57525021	57524924	57525001	TCF12	NM_003205	1	20	11	+	57524910	57525054
238766724	chr15	57524896	57525021	57524924	57525001	TCF12	NM_207037	3	21	11	+	57524910	57525054
238766724	chr15	57524896	57525021	57524924	57525001	TCF12	NM_207040	5	13	4	+	57524910	57525054
241028034	chr15	57543519	57543687	57543540	57543659	TCF12	NM_207038	4	20	14	+	57543548	57543621
241028034	chr15	57543519	57543687	57543540	57543659	TCF12	NM_207036	2	21	14	+	57543548	57543621
241028034	chr15	57543519	57543687	57543540	57543659	TCF12	NM_003205	1	20	14	+	57543548	57543621
241028034	chr15	57543519	57543687	57543540	57543659	TCF12	NM_207037	3	21	14	+	57543548	57543621
241028034	chr15	57543519	57543687	57543540	57543659	TCF12	NM_207040	5	13	7	+	57543548	57543621
261810380	chr15	57545487	57545658	57545511	57545637	TCF12	NM_207038	4	20	15	+	57545460	57545666
261810380	chr15	57545487	57545658	57545511	57545637	TCF12	NM_207036	2	21	16	+	57545460	57545666
261810380	chr15	57545487	57545658	57545511	57545637	TCF12	NM_003205	1	20	15	+	57545460	57545666
261810380	chr15	57545487	57545658	57545511	57545637	TCF12	NM_207037	3	21	16	+	57545460	57545666
261810380	chr15	57545487	57545658	57545511	57545637	TCF12	NM_207040	5	13	8	+	57545460	57545666
238679589	chr15	57555188	57555344	57555214	57555317	TCF12	NM_207038	4	20	17	+	57555310	57555472
238679589	chr15	57555188	57555344	57555214	57555317	TCF12	NM_207036	2	21	18	+	57555310	57555472
238679589	chr15	57555188	57555344	57555214	57555317	TCF12	NM_003205	1	20	17	+	57555310	57555472
238679589	chr15	57555188	57555344	57555214	57555317	TCF12	NM_207037	3	21	18	+	57555310	57555472
238679589	chr15	57555188	57555344	57555214	57555317	TCF12	NM_207040	5	13	10	+	57555310	57555472
264063192	chr15	57565233	57565357	57565261	57565331	TCF12	NM_207038	4	20	18	+	57565228	57565460
264063192	chr15	57565233	57565357	57565261	57565331	TCF12	NM_207036	2	21	19	+	57565228	57565460
264063192	chr15	57565233	57565357	57565261	57565331	TCF12	NM_003205	1	20	18	+	57565228	57565460
264063192	chr15	57565233	57565357	57565261	57565331	TCF12	NM_207037	3	21	19	+	57565228	57565460

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
264063192	chr15	57565233	57565357	57565261	57565331	TCF12	NM_207040	5	13	11	+	57565228	57565460
233359364	chr15	66679655	66679783	66679674	66679765	MAP2K1	NM_002755	1	11	1	+	66679211	66679765
231150679	chr15	66729146	66729278	66729166	66729256	MAP2K1	NM_002755	1	11	3	+	66729084	66729230
233572030	chr15	66736983	66737110	66737010	66737082	MAP2K1	NM_002755	1	11	5	+	66736994	66737045
233384285	chr15	66777377	66777549	66777399	66777529	MAP2K1	NM_002755	1	11	7	+	66777328	66777529
234102457	chr15	66782804	66782976	66782827	66782953	MAP2K1	NM_002755	1	11	11	+	66782840	66783882
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033250	9	7	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033249	8	7	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033247	7	5	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033246	6	6	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033244	5	8	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033240	4	7	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033239	3	8	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_033238	2	9	2	+	74290345	74290817
237949874	chr15	74290415	74290557	74290433	74290539	PML	NM_002675	1	8	2	+	74290345	74290817
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033250	9	7	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033249	8	7	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033247	7	5	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033246	6	6	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033244	5	8	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033240	4	7	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033239	3	8	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_033238	2	9	3	+	74315169	74315749
239370527	chr15	74315110	74315268	74315138	74315248	PML	NM_002675	1	8	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033250	9	7	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033249	8	7	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033247	7	5	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033246	6	6	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033244	5	8	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033240	4	7	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033239	3	8	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_033238	2	9	3	+	74315169	74315749
239375395	chr15	74315484	74315621	74315503	74315601	PML	NM_002675	1	8	3	+	74315169	74315749
241276589	chr15	74324869	74325037	74324891	74325015	PML	NM_033244	5	8	5	+	74324913	74325056
241276589	chr15	74324869	74325037	74324891	74325015	PML	NM_033240	4	7	5	+	74324913	74325056
241276589	chr15	74324869	74325037	74324891	74325015	PML	NM_033239	3	8	5	+	74324913	74325056
241276589	chr15	74324869	74325037	74324891	74325015	PML	NM_033238	2	9	5	+	74324913	74325056
241276589	chr15	74324869	74325037	74324891	74325015	PML	NM_002675	1	8	5	+	74324913	74325056
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033250	9	7	5	+	74325497	74325755
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033249	8	7	5	+	74325497	74325755
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033240	4	7	6	+	74325497	74325755

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033239	3	8	6	+	74325497	74325755
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033238	2	9	6	+	74325497	74325755
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_002675	1	8	6	+	74325497	74325755
235486084	chr15	74325684	74325854	74325704	74325834	PML	NM_033244	5	8	6	+	74325497	74325763
235995878	chr15	74327635	74327808	74327653	74327790	PML	NM_033250	9	7	7	+	74327513	74328735
235995878	chr15	74327635	74327808	74327653	74327790	PML	NM_033244	5	8	8	+	74327513	74328735
235995878	chr15	74327635	74327808	74327653	74327790	PML	NM_033239	3	8	8	+	74327513	74328735
235995878	chr15	74327635	74327808	74327653	74327790	PML	NM_033240	4	7	7	+	74326819	74328735
234992496	chr15	74328030	74328202	74328052	74328180	PML	NM_033250	9	7	7	+	74327513	74328735
234992496	chr15	74328030	74328202	74328052	74328180	PML	NM_033244	5	8	8	+	74327513	74328735
234992496	chr15	74328030	74328202	74328052	74328180	PML	NM_033239	3	8	8	+	74327513	74328735
234992496	chr15	74328030	74328202	74328052	74328180	PML	NM_033240	4	7	7	+	74326819	74328735
236712519	chr15	74335407	74335545	74335427	74335521	PML	NM_033238	2	9	8	+	74335330	74335480
236712519	chr15	74335407	74335545	74335427	74335521	PML	NM_033249	8	7	7	+	74335330	74335717
236712519	chr15	74335407	74335545	74335427	74335521	PML	NM_033246	6	6	6	+	74335330	74335717
236712519	chr15	74335407	74335545	74335427	74335521	PML	NM_002675	1	8	8	+	74335330	74335717
239468216	chr15	74336876	74337034	74336896	74337013	PML	NM_033238	2	9	9	+	74336562	74340155
236319071	chr15	88420142	88420301	88420163	88420280	NTRK3	NM_002530	4	19	19	-	88419988	88420351
236319071	chr15	88420142	88420301	88420163	88420280	NTRK3	NM_001012338	2	20	20	-	88419988	88420351
236319071	chr15	88420142	88420301	88420163	88420280	NTRK3	NM_001243101	3	18	18	-	88419988	88420351
235917643	chr15	88472313	88472466	88472337	88472445	NTRK3	NM_002530	4	19	17	-	88472422	88472665
235917643	chr15	88472313	88472466	88472337	88472445	NTRK3	NM_001012338	2	20	17	-	88472422	88472665
235917643	chr15	88472313	88472466	88472337	88472445	NTRK3	NM_001243101	3	18	16	-	88472422	88472665
238755874	chr15	88476308	88476438	88476328	88476416	NTRK3	NM_002530	4	19	16	-	88476243	88476415
238755874	chr15	88476308	88476438	88476328	88476416	NTRK3	NM_001012338	2	20	16	-	88476243	88476415
238755874	chr15	88476308	88476438	88476328	88476416	NTRK3	NM_001243101	3	18	15	-	88476243	88476415
242184051	chr15	88522614	88522781	88522638	88522755	NTRK3	NM_001007156	1	16	16	-	88520596	88522694
238065039	chr15	88670314	88670485	88670342	88670460	NTRK3	NM_002530	4	19	12	-	88670393	88670457
238065039	chr15	88670314	88670485	88670342	88670460	NTRK3	NM_001007156	1	16	12	-	88670393	88670457
238065039	chr15	88670314	88670485	88670342	88670460	NTRK3	NM_001012338	2	20	12	-	88670393	88670457
238065039	chr15	88670314	88670485	88670342	88670460	NTRK3	NM_001243101	3	18	11	-	88670393	88670457
239330191	chr15	88678477	88678648	88678504	88678628	NTRK3	NM_002530	4	19	10	-	88678332	88678628
239330191	chr15	88678477	88678648	88678504	88678628	NTRK3	NM_001007156	1	16	10	-	88678332	88678628
239330191	chr15	88678477	88678648	88678504	88678628	NTRK3	NM_001012338	2	20	10	-	88678332	88678628
239330191	chr15	88678477	88678648	88678504	88678628	NTRK3	NM_001243101	3	18	10	-	88678332	88678628
237568846	chr15	88679721	88679875	88679742	88679853	NTRK3	NM_002530	4	19	8	-	88679698	88679840
237568846	chr15	88679721	88679875	88679742	88679853	NTRK3	NM_001007156	1	16	8	-	88679698	88679840
237568846	chr15	88679721	88679875	88679742	88679853	NTRK3	NM_001012338	2	20	8	-	88679698	88679840
237568846	chr15	88679721	88679875	88679742	88679853	NTRK3	NM_001243101	3	18	8	-	88679698	88679840
240829013	chr15	88726597	88726749	88726618	88726724	NTRK3	NM_002530	4	19	5	-	88726649	88726720
240829013	chr15	88726597	88726749	88726618	88726724	NTRK3	NM_001007156	1	16	5	-	88726649	88726720

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240829013	chr15	88726597	88726749	88726618	88726724	NTRK3	NM_001012338	2	20	5	-	88726649	88726720
240829013	chr15	88726597	88726749	88726618	88726724	NTRK3	NM_001243101	3	18	5	-	88726649	88726720
237396779	chr15	88799356	88799529	88799375	88799511	NTRK3	NM_002530	4	19	3	-	88799137	88799399
237396779	chr15	88799356	88799529	88799375	88799511	NTRK3	NM_001007156	1	16	3	-	88799137	88799399
237396779	chr15	88799356	88799529	88799375	88799511	NTRK3	NM_001012338	2	20	3	-	88799137	88799399
237396779	chr15	88799356	88799529	88799375	88799511	NTRK3	NM_001243101	3	18	3	-	88799137	88799399
227256116	chr15	90628440	90628579	90628459	90628557	IDH2	NM_002168	1	11	8	-	90628507	90628619
227660438	chr15	90630563	90630737	90630583	90630713	IDH2	NM_002168	1	11	6	-	90630671	90630807
229754607	chr15	90631785	90631948	90631805	90631924	IDH2	NM_002168	1	11	4	-	90631819	90631979
227267157	chr15	90633805	90633964	90633826	90633942	IDH2	NM_002168	1	11	3	-	90633711	90633876
223820599	chr15	91290573	91290745	91290600	91290720	BLM	NM_000057	1	22	2	+	91290619	91290720
222702138	chr15	91292891	91293054	91292917	91293027	BLM	NM_000057	1	22	3	+	91292597	91293297
223082408	chr15	91294956	91295130	91294983	91295104	BLM	NM_000057	1	22	4	+	91295017	91295176
222363725	chr15	91298137	91298274	91298159	91298247	BLM	NM_000057	1	22	5	+	91298041	91298168
225058042	chr15	91303883	91304055	91303906	91304034	BLM	NM_000057	1	22	7	+	91303824	91304485
225045615	chr15	91304287	91304449	91304313	91304424	BLM	NM_000057	1	22	7	+	91303824	91304485
222194340	chr15	91306319	91306444	91306345	91306418	BLM	NM_000057	1	22	8	+	91306196	91306387
222962576	chr15	91312282	91312445	91312308	91312420	BLM	NM_000057	1	22	11	+	91312363	91312461
223817361	chr15	91326048	91326182	91326076	91326158	BLM	NM_000057	1	22	13	+	91326052	91326158
223092791	chr15	91333942	91334098	91333967	91334075	BLM	NM_000057	1	22	15	+	91333879	91334074
222438400	chr15	91341289	91341463	91341311	91341436	BLM	NM_000057	1	22	17	+	91341420	91341567
222530791	chr15	91346754	91346924	91346782	91346901	BLM	NM_000057	1	22	18	+	91346751	91346950
224054474	chr15	91352306	91352432	91352330	91352405	BLM	NM_000057	1	22	20	+	91352367	91352489
223774806	chr15	91358232	91358405	91358253	91358384	BLM	NM_000057	1	22	22	+	91358332	91358686
269825104	chr15	99250695	99250864	99250720	99250844	IGF1R	NM_000875	1	21	2	+	99250791	99251336
269873503	chr15	99251136	99251300	99251158	99251274	IGF1R	NM_000875	1	21	2	+	99250791	99251336
270058596	chr15	99434752	99434901	99434771	99434883	IGF1R	NM_000875	1	21	3	+	99434554	99434866
269662169	chr15	99442787	99442925	99442810	99442900	IGF1R	NM_000875	1	21	5	+	99442706	99442850
269909812	chr15	99454577	99454704	99454599	99454681	IGF1R	NM_000875	1	21	7	+	99454544	99454670
270982751	chr15	99459132	99459305	99459161	99459281	IGF1R	NM_000875	1	21	9	+	99459193	99459360
272086695	chr15	99460048	99460200	99460070	99460177	IGF1R	NM_000875	1	21	10	+	99459901	99460105
269726604	chr15	99467060	99467186	99467081	99467164	IGF1R	NM_000875	1	21	12	+	99467105	99467241
272352854	chr15	99472734	99472906	99472760	99472880	IGF1R	NM_000875	1	21	14	+	99472787	99472889
269872257	chr15	99478015	99478189	99478042	99478169	IGF1R	NM_000875	1	21	16	+	99478053	99478282
272026579	chr15	99482327	99482501	99482350	99482481	IGF1R	NM_000875	1	21	18	+	99482430	99482589
269553606	chr15	99491751	99491896	99491775	99491876	IGF1R	NM_000875	1	21	20	+	99491803	99491937
272141861	chr15	99500387	99500548	99500408	99500529	IGF1R	NM_000875	1	21	21	+	99500290	99507759
242471288	chr16	2103296	2103470	2103318	2103453	TSC2	NM_000548	1	42	4	+	2103343	2103453
242471288	chr16	2103296	2103470	2103318	2103453	TSC2	NM_001077183	2	40	4	+	2103343	2103453
242471288	chr16	2103296	2103470	2103318	2103453	TSC2	NM_001114382	3	41	4	+	2103343	2103453
263024893	chr16	2105435	2105559	2105457	2105532	TSC2	NM_000548	1	42	6	+	2105403	2105520

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263024893	chr16	2105435	2105559	2105457	2105532	TSC2	NM_001077183	2	40	6	+	2105403	2105520
263024893	chr16	2105435	2105559	2105457	2105532	TSC2	NM_001114382	3	41	6	+	2105403	2105520
264509540	chr16	2108714	2108888	2108735	2108865	TSC2	NM_000548	1	42	10	+	2108748	2108874
264509540	chr16	2108714	2108888	2108735	2108865	TSC2	NM_001077183	2	40	10	+	2108748	2108874
264509540	chr16	2108714	2108888	2108735	2108865	TSC2	NM_001114382	3	41	10	+	2108748	2108874
240831716	chr16	2110765	2110895	2110787	2110873	TSC2	NM_000548	1	42	11	+	2110671	2110814
240831716	chr16	2110765	2110895	2110787	2110873	TSC2	NM_001077183	2	40	11	+	2110671	2110814
240831716	chr16	2110765	2110895	2110787	2110873	TSC2	NM_001114382	3	41	11	+	2110671	2110814
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_000548	1	42	15	+	2114273	2114428
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_001077183	2	40	15	+	2114273	2114428
240579169	chr16	2114192	2114347	2114214	2114327	TSC2	NM_001114382	3	41	15	+	2114273	2114428
264648339	chr16	2120502	2120666	2120522	2120647	TSC2	NM_000548	1	42	17	+	2120457	2120579
264648339	chr16	2120502	2120666	2120522	2120647	TSC2	NM_001077183	2	40	17	+	2120457	2120579
264648339	chr16	2120502	2120666	2120522	2120647	TSC2	NM_001114382	3	41	17	+	2120457	2120579
238414740	chr16	2121776	2121946	2121794	2121929	TSC2	NM_000548	1	42	19	+	2121785	2121935
238414740	chr16	2121776	2121946	2121794	2121929	TSC2	NM_001077183	2	40	19	+	2121785	2121935
238414740	chr16	2121776	2121946	2121794	2121929	TSC2	NM_001114382	3	41	19	+	2121785	2121935
262269542	chr16	2122818	2122977	2122840	2122948	TSC2	NM_000548	1	42	21	+	2122850	2122984
262269542	chr16	2122818	2122977	2122840	2122948	TSC2	NM_001077183	2	40	21	+	2122850	2122984
262269542	chr16	2122818	2122977	2122840	2122948	TSC2	NM_001114382	3	41	21	+	2122850	2122984
263178386	chr16	2125733	2125866	2125751	2125846	TSC2	NM_000548	1	42	23	+	2125800	2125893
263178386	chr16	2125733	2125866	2125751	2125846	TSC2	NM_001077183	2	40	23	+	2125800	2125893
263178386	chr16	2125733	2125866	2125751	2125846	TSC2	NM_001114382	3	41	23	+	2125800	2125893
241957860	chr16	2126552	2126694	2126573	2126673	TSC2	NM_000548	1	42	25	+	2126492	2126586
241957860	chr16	2126552	2126694	2126573	2126673	TSC2	NM_001077183	2	40	25	+	2126492	2126586
241957860	chr16	2126552	2126694	2126573	2126673	TSC2	NM_001114382	3	41	25	+	2126492	2126586
240068470	chr16	2129032	2129186	2129053	2129165	TSC2	NM_001077183	2	40	26	+	2129036	2129197
240068470	chr16	2129032	2129186	2129053	2129165	TSC2	NM_000548	1	42	27	+	2129033	2129197
240068470	chr16	2129032	2129186	2129053	2129165	TSC2	NM_001114382	3	41	27	+	2129033	2129197
264189430	chr16	2129533	2129677	2129554	2129658	TSC2	NM_000548	1	42	29	+	2129558	2129670
264189430	chr16	2129533	2129677	2129554	2129658	TSC2	NM_001077183	2	40	28	+	2129558	2129670
264189430	chr16	2129533	2129677	2129554	2129658	TSC2	NM_001114382	3	41	29	+	2129558	2129670
241054915	chr16	2131558	2131695	2131577	2131676	TSC2	NM_000548	1	42	31	+	2131596	2131799
241054915	chr16	2131558	2131695	2131577	2131676	TSC2	NM_001077183	2	40	30	+	2131596	2131799
241054915	chr16	2131558	2131695	2131577	2131676	TSC2	NM_001114382	3	41	31	+	2131596	2131799
262027693	chr16	2133672	2133836	2133689	2133818	TSC2	NM_000548	1	42	33	+	2133696	2133817
262027693	chr16	2133672	2133836	2133689	2133818	TSC2	NM_001077183	2	40	31	+	2133696	2133817
262027693	chr16	2133672	2133836	2133689	2133818	TSC2	NM_001114382	3	41	32	+	2133696	2133817
262619219	chr16	2134470	2134643	2134488	2134625	TSC2	NM_000548	1	42	34	+	2134229	2134716
262619219	chr16	2134470	2134643	2134488	2134625	TSC2	NM_001077183	2	40	32	+	2134229	2134716
262619219	chr16	2134470	2134643	2134488	2134625	TSC2	NM_001114382	3	41	33	+	2134229	2134716

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241390613	chr16	2135211	2135361	2135228	2135343	TSC2	NM_000548	1	42	36	+	2135231	2135323
241390613	chr16	2135211	2135361	2135228	2135343	TSC2	NM_001077183	2	40	34	+	2135231	2135323
241390613	chr16	2135211	2135361	2135228	2135343	TSC2	NM_001114382	3	41	35	+	2135231	2135323
262166401	chr16	2136682	2136848	2136699	2136826	TSC2	NM_000548	1	42	38	+	2136733	2136872
262166401	chr16	2136682	2136848	2136699	2136826	TSC2	NM_001077183	2	40	36	+	2136733	2136872
262166401	chr16	2136682	2136848	2136699	2136826	TSC2	NM_001114382	3	41	37	+	2136733	2136872
240855631	chr16	2138022	2138180	2138039	2138162	TSC2	NM_000548	1	42	40	+	2138049	2138140
240855631	chr16	2138022	2138180	2138039	2138162	TSC2	NM_001077183	2	40	38	+	2138049	2138140
240855631	chr16	2138022	2138180	2138039	2138162	TSC2	NM_001114382	3	41	39	+	2138049	2138140
225462845	chr16	3777678	3777841	3777703	3777821	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225462845	chr16	3777678	3777841	3777703	3777821	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225490780	chr16	3778126	3778260	3778145	3778242	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225490780	chr16	3778126	3778260	3778145	3778242	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225494740	chr16	3778484	3778638	3778507	3778620	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
225494740	chr16	3778484	3778638	3778507	3778620	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226721641	chr16	3778912	3779060	3778930	3779041	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226721641	chr16	3778912	3779060	3778930	3779041	CREBBP	NM_004380	2	31	31	-	3775056	3779875
226719940	chr16	3779404	3779578	3779423	3779560	CREBBP	NM_001079846	1	30	30	-	3775056	3779875
226719940	chr16	3779404	3779578	3779423	3779560	CREBBP	NM_004380	2	31	31	-	3775056	3779875
225887934	chr16	3781090	3781258	3781112	3781236	CREBBP	NM_001079846	1	30	29	-	3781193	3781474
225887934	chr16	3781090	3781258	3781112	3781236	CREBBP	NM_004380	2	31	30	-	3781193	3781474
225823750	chr16	3781800	3781961	3781821	3781942	CREBBP	NM_001079846	1	30	28	-	3781777	3781938
225823750	chr16	3781800	3781961	3781821	3781942	CREBBP	NM_004380	2	31	29	-	3781777	3781938
226456974	chr16	3786680	3786852	3786701	3786831	CREBBP	NM_001079846	1	30	26	-	3786651	3786816
226456974	chr16	3786680	3786852	3786701	3786831	CREBBP	NM_004380	2	31	27	-	3786651	3786816
225558520	chr16	3789647	3789771	3789669	3789746	CREBBP	NM_001079846	1	30	24	-	3789579	3789725
225558520	chr16	3789647	3789771	3789669	3789746	CREBBP	NM_004380	2	31	25	-	3789579	3789725
225964824	chr16	3795230	3795386	3795250	3795363	CREBBP	NM_001079846	1	30	21	-	3795278	3795355
225964824	chr16	3795230	3795386	3795250	3795363	CREBBP	NM_004380	2	31	22	-	3795278	3795355
226481864	chr16	3807704	3807853	3807728	3807833	CREBBP	NM_001079846	1	30	17	-	3807810	3808049
226481864	chr16	3807704	3807853	3807728	3807833	CREBBP	NM_004380	2	31	18	-	3807810	3808049
227031257	chr16	3808887	3809025	3808909	3809000	CREBBP	NM_001079846	1	30	16	-	3808855	3808973
227031257	chr16	3808887	3809025	3808909	3809000	CREBBP	NM_004380	2	31	17	-	3808855	3808973
226649437	chr16	3819114	3819266	3819136	3819246	CREBBP	NM_001079846	1	30	14	-	3819175	3819354
226649437	chr16	3819114	3819266	3819136	3819246	CREBBP	NM_004380	2	31	15	-	3819175	3819354
226569257	chr16	3820686	3820854	3820704	3820835	CREBBP	NM_001079846	1	30	13	-	3820571	3820987
226569257	chr16	3820686	3820854	3820704	3820835	CREBBP	NM_004380	2	31	14	-	3820571	3820987
225705662	chr16	3823810	3823971	3823831	3823949	CREBBP	NM_001079846	1	30	12	-	3823752	3823931
225705662	chr16	3823810	3823971	3823831	3823949	CREBBP	NM_004380	2	31	13	-	3823752	3823931
226139930	chr16	3827612	3827781	3827634	3827754	CREBBP	NM_001079846	1	30	10	-	3827614	3827658
226139930	chr16	3827612	3827781	3827634	3827754	CREBBP	NM_004380	2	31	11	-	3827614	3827658

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225339560	chr16	3828718	3828891	3828740	3828868	CREBBP	NM_001079846	1	30	8	-	3828701	3828818
225339560	chr16	3828718	3828891	3828740	3828868	CREBBP	NM_004380	2	31	9	-	3828701	3828818
226537231	chr16	3831217	3831388	3831238	3831361	CREBBP	NM_001079846	1	30	6	-	3831205	3831307
226537231	chr16	3831217	3831388	3831238	3831361	CREBBP	NM_004380	2	31	7	-	3831205	3831307
253743100	chr16	3841968	3842121	3841991	3842094	CREBBP	NM_004380	2	31	5	-	3841982	3842095
226376853	chr16	3860582	3860707	3860602	3860686	CREBBP	NM_001079846	1	30	3	-	3860604	3860780
226376853	chr16	3860582	3860707	3860602	3860686	CREBBP	NM_004380	2	31	3	-	3860604	3860780
226007401	chr16	3900482	3900652	3900506	3900632	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
226007401	chr16	3900482	3900652	3900506	3900632	CREBBP	NM_004380	2	31	2	-	3900298	3901010
227061426	chr16	3900912	3901059	3900933	3901031	CREBBP	NM_001079846	1	30	2	-	3900298	3901010
227061426	chr16	3900912	3901059	3900933	3901031	CREBBP	NM_004380	2	31	2	-	3900298	3901010
264716728	chr16	11348753	11348916	11348771	11348898	SOCS1	NM_003745	1	2	2	-	11348274	11349385
264730437	chr16	11349157	11349318	11349177	11349301	SOCS1	NM_003745	1	2	2	-	11348274	11349385
229995515	chr16	14014144	14014307	14014161	14014289	ERCC4	NM_005236	1	11	1	+	14014014	14014229
228004159	chr16	14020365	14020503	14020391	14020479	ERCC4	NM_005236	1	11	3	+	14020418	14020613
232852689	chr16	14021874	14022027	14021901	14021999	ERCC4	NM_005236	1	11	4	+	14021885	14022092
233012558	chr16	14024704	14024832	14024729	14024810	ERCC4	NM_005236	1	11	5	+	14024567	14024747
229502504	chr16	14028088	14028213	14028115	14028185	ERCC4	NM_005236	1	11	7	+	14028049	14028159
232160081	chr16	14029259	14029416	14029287	14029388	ERCC4	NM_005236	1	11	8	+	14029003	14029600
228834105	chr16	14031603	14031767	14031628	14031743	ERCC4	NM_005236	1	11	9	+	14031623	14031715
232525942	chr16	14041625	14041756	14041648	14041735	ERCC4	NM_005236	1	11	11	+	14041471	14046205
230343071	chr16	14042055	14042229	14042076	14042204	ERCC4	NM_005236	1	11	11	+	14041471	14046205
236539485	chr16	15808704	15808878	15808723	15808860	MYH11	NM_022844	4	42	40	-	15808766	15808938
236539485	chr16	15808704	15808878	15808723	15808860	MYH11	NM_002474	3	41	40	-	15808766	15808938
236539485	chr16	15808704	15808878	15808723	15808860	MYH11	NM_001040113	1	43	41	-	15808766	15808938
236539485	chr16	15808704	15808878	15808723	15808860	MYH11	NM_001040114	2	42	41	-	15808766	15808938
240643515	chr16	15810932	15811075	15810955	15811052	MYH11	NM_022844	4	42	38	-	15810997	15811205
240643515	chr16	15810932	15811075	15810955	15811052	MYH11	NM_002474	3	41	38	-	15810997	15811205
240643515	chr16	15810932	15811075	15810955	15811052	MYH11	NM_001040113	1	43	39	-	15810997	15811205
240643515	chr16	15810932	15811075	15810955	15811052	MYH11	NM_001040114	2	42	39	-	15810997	15811205
235711596	chr16	15812207	15812377	15812225	15812358	MYH11	NM_022844	4	42	37	-	15812172	15812295
235711596	chr16	15812207	15812377	15812225	15812358	MYH11	NM_002474	3	41	37	-	15812172	15812295
235711596	chr16	15812207	15812377	15812225	15812358	MYH11	NM_001040113	1	43	38	-	15812172	15812295
235711596	chr16	15812207	15812377	15812225	15812358	MYH11	NM_001040114	2	42	38	-	15812172	15812295
236513303	chr16	15814063	15814199	15814084	15814177	MYH11	NM_022844	4	42	34	-	15814008	15814169
236513303	chr16	15814063	15814199	15814084	15814177	MYH11	NM_002474	3	41	34	-	15814008	15814169
236513303	chr16	15814063	15814199	15814084	15814177	MYH11	NM_001040113	1	43	35	-	15814008	15814169
236513303	chr16	15814063	15814199	15814084	15814177	MYH11	NM_001040114	2	42	35	-	15814008	15814169
240398814	chr16	15815213	15815385	15815234	15815365	MYH11	NM_022844	4	42	32	-	15815279	15815491
240398814	chr16	15815213	15815385	15815234	15815365	MYH11	NM_002474	3	41	32	-	15815279	15815491
240398814	chr16	15815213	15815385	15815234	15815365	MYH11	NM_001040113	1	43	33	-	15815279	15815491

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240398814	chr16	15815213	15815385	15815234	15815365	MYH11	NM_001040114	2	42	33	-	15815279	15815491
235110912	chr16	15818154	15818286	15818173	15818266	MYH11	NM_022844	4	42	31	-	15818018	15818266
235110912	chr16	15818154	15818286	15818173	15818266	MYH11	NM_002474	3	41	31	-	15818018	15818266
235110912	chr16	15818154	15818286	15818173	15818266	MYH11	NM_001040113	1	43	32	-	15818018	15818266
235110912	chr16	15818154	15818286	15818173	15818266	MYH11	NM_001040114	2	42	32	-	15818018	15818266
237072724	chr16	15820641	15820778	15820660	15820759	MYH11	NM_022844	4	42	28	-	15820705	15820911
237072724	chr16	15820641	15820778	15820660	15820759	MYH11	NM_002474	3	41	28	-	15820705	15820911
237072724	chr16	15820641	15820778	15820660	15820759	MYH11	NM_001040113	1	43	29	-	15820705	15820911
237072724	chr16	15820641	15820778	15820660	15820759	MYH11	NM_001040114	2	42	29	-	15820705	15820911
235980602	chr16	15826471	15826596	15826493	15826574	MYH11	NM_022844	4	42	27	-	15826421	15826565
235980602	chr16	15826471	15826596	15826493	15826574	MYH11	NM_002474	3	41	27	-	15826421	15826565
235980602	chr16	15826471	15826596	15826493	15826574	MYH11	NM_001040113	1	43	28	-	15826421	15826565
235980602	chr16	15826471	15826596	15826493	15826574	MYH11	NM_001040114	2	42	28	-	15826421	15826565
238390829	chr16	15831228	15831398	15831247	15831379	MYH11	NM_022844	4	42	25	-	15831306	15831477
238390829	chr16	15831228	15831398	15831247	15831379	MYH11	NM_002474	3	41	25	-	15831306	15831477
238390829	chr16	15831228	15831398	15831247	15831379	MYH11	NM_001040113	1	43	26	-	15831306	15831477
238390829	chr16	15831228	15831398	15831247	15831379	MYH11	NM_001040114	2	42	26	-	15831306	15831477
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_022844	4	42	24	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_002474	3	41	24	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_001040113	1	43	25	-	15832422	15832545
235719601	chr16	15832507	15832675	15832534	15832644	MYH11	NM_001040114	2	42	25	-	15832422	15832545
235598597	chr16	15835395	15835519	15835419	15835496	MYH11	NM_022844	4	42	22	-	15835320	15835526
235598597	chr16	15835395	15835519	15835419	15835496	MYH11	NM_002474	3	41	22	-	15835320	15835526
235598597	chr16	15835395	15835519	15835419	15835496	MYH11	NM_001040113	1	43	23	-	15835320	15835526
235598597	chr16	15835395	15835519	15835419	15835496	MYH11	NM_001040114	2	42	23	-	15835320	15835526
241160235	chr16	15838901	15839062	15838923	15839037	MYH11	NM_022844	4	42	20	-	15838986	15839094
241160235	chr16	15838901	15839062	15838923	15839037	MYH11	NM_002474	3	41	20	-	15838986	15839094
241160235	chr16	15838901	15839062	15838923	15839037	MYH11	NM_001040113	1	43	21	-	15838986	15839094
241160235	chr16	15838901	15839062	15838923	15839037	MYH11	NM_001040114	2	42	21	-	15838986	15839094
235917102	chr16	15841652	15841824	15841672	15841800	MYH11	NM_022844	4	42	18	-	15841731	15841800
235917102	chr16	15841652	15841824	15841672	15841800	MYH11	NM_002474	3	41	18	-	15841731	15841800
235917102	chr16	15841652	15841824	15841672	15841800	MYH11	NM_001040113	1	43	19	-	15841731	15841800
235917102	chr16	15841652	15841824	15841672	15841800	MYH11	NM_001040114	2	42	19	-	15841731	15841800
238079347	chr16	15844106	15844256	15844127	15844234	MYH11	NM_022844	4	42	16	-	15843995	15844188
238079347	chr16	15844106	15844256	15844127	15844234	MYH11	NM_002474	3	41	16	-	15843995	15844188
238079347	chr16	15844106	15844256	15844127	15844234	MYH11	NM_001040113	1	43	17	-	15843995	15844188
238079347	chr16	15844106	15844256	15844127	15844234	MYH11	NM_001040114	2	42	17	-	15843995	15844188
239188133	chr16	15850192	15850344	15850215	15850324	MYH11	NM_022844	4	42	14	-	15850198	15850371
239188133	chr16	15850192	15850344	15850215	15850324	MYH11	NM_002474	3	41	14	-	15850198	15850371
239188133	chr16	15850192	15850344	15850215	15850324	MYH11	NM_001040113	1	43	15	-	15850198	15850371
239188133	chr16	15850192	15850344	15850215	15850324	MYH11	NM_001040114	2	42	15	-	15850198	15850371

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235868201	chr16	15853381	15853555	15853403	15853533	MYH11	NM_022844	4	42	12	-	15853433	15853585
235868201	chr16	15853381	15853555	15853403	15853533	MYH11	NM_002474	3	41	12	-	15853433	15853585
235868201	chr16	15853381	15853555	15853403	15853533	MYH11	NM_001040113	1	43	13	-	15853433	15853585
235868201	chr16	15853381	15853555	15853403	15853533	MYH11	NM_001040114	2	42	13	-	15853433	15853585
257621190	chr16	15865391	15865563	15865413	15865542	MYH11	NM_022844	4	42	9	-	15865426	15865569
257621190	chr16	15865391	15865563	15865413	15865542	MYH11	NM_002474	3	41	9	-	15865426	15865569
257621190	chr16	15865391	15865563	15865413	15865542	MYH11	NM_001040113	1	43	10	-	15865426	15865569
257621190	chr16	15865391	15865563	15865413	15865542	MYH11	NM_001040114	2	42	10	-	15865426	15865569
239342461	chr16	15876199	15876373	15876224	15876345	MYH11	NM_022844	4	42	6	-	15876242	15876334
239342461	chr16	15876199	15876373	15876224	15876345	MYH11	NM_002474	3	41	6	-	15876242	15876334
239342461	chr16	15876199	15876373	15876224	15876345	MYH11	NM_001040113	1	43	7	-	15876242	15876334
239342461	chr16	15876199	15876373	15876224	15876345	MYH11	NM_001040114	2	42	7	-	15876242	15876334
235266540	chr16	15917023	15917197	15917045	15917173	MYH11	NM_022844	4	42	3	-	15917112	15917268
235266540	chr16	15917023	15917197	15917045	15917173	MYH11	NM_002474	3	41	3	-	15917112	15917268
235266540	chr16	15917023	15917197	15917045	15917173	MYH11	NM_001040113	1	43	3	-	15917112	15917268
235266540	chr16	15917023	15917197	15917045	15917173	MYH11	NM_001040114	2	42	3	-	15917112	15917268
235118885	chr16	15931890	15932058	15931912	15932034	MYH11	NM_022844	4	42	2	-	15931765	15932126
235118885	chr16	15931890	15932058	15931912	15932034	MYH11	NM_002474	3	41	2	-	15931765	15932126
235118885	chr16	15931890	15932058	15931912	15932034	MYH11	NM_001040113	1	43	2	-	15931765	15932126
235118885	chr16	15931890	15932058	15931912	15932034	MYH11	NM_001040114	2	42	2	-	15931765	15932126
235983247	chr16	23614908	23615079	23614931	23615054	PALB2	NM_024675	1	13	13	-	23614483	23614990
234949586	chr16	23632712	23632846	23632733	23632820	PALB2	NM_024675	1	13	10	-	23632683	23632799
240223410	chr16	23635381	23635542	23635406	23635514	PALB2	NM_024675	1	13	8	-	23635330	23635415
236510532	chr16	23640887	23641043	23640915	23641014	PALB2	NM_024675	1	13	5	-	23640961	23641790
236613578	chr16	23641338	23641486	23641360	23641459	PALB2	NM_024675	1	13	5	-	23640961	23641790
238202758	chr16	23646104	23646254	23646128	23646228	PALB2	NM_024675	1	13	4	-	23646183	23647655
235056744	chr16	23646588	23646759	23646609	23646732	PALB2	NM_024675	1	13	4	-	23646183	23647655
235065617	chr16	23646922	23647061	23646949	23647036	PALB2	NM_024675	1	13	4	-	23646183	23647655
238235502	chr16	23647286	23647411	23647312	23647383	PALB2	NM_024675	1	13	4	-	23646183	23647655
236419237	chr16	23649265	23649435	23649282	23649409	PALB2	NM_024675	1	13	2	-	23649391	23649450
227421031	chr16	27414490	27414626	27414509	27414604	IL21R	NM_181079	3	10	2	+	27414401	27414541
228865671	chr16	27448890	27449048	27448913	27449028	IL21R	NM_181079	3	10	5	+	27448809	27449008
228865671	chr16	27448890	27449048	27448913	27449028	IL21R	NM_181078	2	9	4	+	27448809	27449008
228865671	chr16	27448890	27449048	27448913	27449028	IL21R	NM_021798	1	9	4	+	27448809	27449008
229433623	chr16	27455915	27456062	27455935	27456041	IL21R	NM_181079	3	10	7	+	27455863	27456040
229433623	chr16	27455915	27456062	27455935	27456041	IL21R	NM_181078	2	9	6	+	27455863	27456040
229433623	chr16	27455915	27456062	27455935	27456041	IL21R	NM_021798	1	9	6	+	27455863	27456040
228956773	chr16	27459807	27459948	27459829	27459929	IL21R	NM_181079	3	10	10	+	27459855	27463363
228956773	chr16	27459807	27459948	27459829	27459929	IL21R	NM_181078	2	9	9	+	27459855	27463363
228956773	chr16	27459807	27459948	27459829	27459929	IL21R	NM_021798	1	9	9	+	27459855	27463363
228966197	chr16	27460189	27460363	27460207	27460344	IL21R	NM_181079	3	10	10	+	27459855	27463363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228966197	chr16	27460189	27460363	27460207	27460344	IL21R	NM_181078	2	9	9	+	27459855	27463363
228966197	chr16	27460189	27460363	27460207	27460344	IL21R	NM_021798	1	9	9	+	27459855	27463363
225411627	chr16	50783491	50783655	50783513	50783629	CYLD	NM_015247	3	20	4	+	50783487	50784113
225411627	chr16	50783491	50783655	50783513	50783629	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225411627	chr16	50783491	50783655	50783513	50783629	CYLD	NM_001042412	2	18	3	+	50783487	50784113
225415004	chr16	50783897	50784023	50783925	50783999	CYLD	NM_015247	3	20	4	+	50783487	50784113
225415004	chr16	50783897	50784023	50783925	50783999	CYLD	NM_001042355	1	18	3	+	50783487	50784113
225415004	chr16	50783897	50784023	50783925	50783999	CYLD	NM_001042412	2	18	3	+	50783487	50784113
226597228	chr16	50785576	50785735	50785598	50785710	CYLD	NM_015247	3	20	5	+	50785515	50785817
226597228	chr16	50785576	50785735	50785598	50785710	CYLD	NM_001042355	1	18	4	+	50785515	50785817
226597228	chr16	50785576	50785735	50785598	50785710	CYLD	NM_001042412	2	18	4	+	50785515	50785817
226562213	chr16	50813578	50813703	50813600	50813675	CYLD	NM_015247	3	20	10	+	50813576	50813955
226562213	chr16	50813578	50813703	50813600	50813675	CYLD	NM_001042355	1	18	8	+	50813576	50813955
226562213	chr16	50813578	50813703	50813600	50813675	CYLD	NM_001042412	2	18	8	+	50813576	50813955
225886045	chr16	50815046	50815213	50815070	50815191	CYLD	NM_015247	3	20	11	+	50815157	50815322
225886045	chr16	50815046	50815213	50815070	50815191	CYLD	NM_001042355	1	18	9	+	50815157	50815322
225886045	chr16	50815046	50815213	50815070	50815191	CYLD	NM_001042412	2	18	9	+	50815157	50815322
225939326	chr16	50816299	50816423	50816327	50816397	CYLD	NM_015247	3	20	12	+	50816236	50816377
225939326	chr16	50816299	50816423	50816327	50816397	CYLD	NM_001042355	1	18	10	+	50816236	50816377
225939326	chr16	50816299	50816423	50816327	50816397	CYLD	NM_001042412	2	18	10	+	50816236	50816377
225520367	chr16	50820761	50820917	50820789	50820889	CYLD	NM_015247	3	20	14	+	50820766	50820857
225520367	chr16	50820761	50820917	50820789	50820889	CYLD	NM_001042355	1	18	12	+	50820766	50820857
225520367	chr16	50820761	50820917	50820789	50820889	CYLD	NM_001042412	2	18	12	+	50820766	50820857
225874019	chr16	50826392	50826554	50826416	50826529	CYLD	NM_015247	3	20	17	+	50826508	50826616
225874019	chr16	50826392	50826554	50826416	50826529	CYLD	NM_001042355	1	18	15	+	50826508	50826616
225874019	chr16	50826392	50826554	50826416	50826529	CYLD	NM_001042412	2	18	15	+	50826508	50826616
227057161	chr16	50828208	50828365	50828229	50828342	CYLD	NM_015247	3	20	19	+	50828123	50828339
227057161	chr16	50828208	50828365	50828229	50828342	CYLD	NM_001042355	1	18	17	+	50828123	50828339
227057161	chr16	50828208	50828365	50828229	50828342	CYLD	NM_001042412	2	18	17	+	50828123	50828339
292994096	chr16	55513482	55513616	55513502	55513595	MMP2	NM_004530	2	13	1	+	55513081	55513544
291492922	chr16	55517902	55518060	55517925	55518037	MMP2	NM_001127891	1	13	3	+	55517928	55518076
291492922	chr16	55517902	55518060	55517925	55518037	MMP2	NM_004530	2	13	3	+	55517928	55518076
291247110	chr16	55519423	55519593	55519445	55519569	MMP2	NM_001127891	1	13	5	+	55519516	55519689
291247110	chr16	55519423	55519593	55519445	55519569	MMP2	NM_004530	2	13	5	+	55519516	55519689
292520061	chr16	55522575	55522746	55522595	55522724	MMP2	NM_001127891	1	13	6	+	55522455	55522628
292520061	chr16	55522575	55522746	55522595	55522724	MMP2	NM_004530	2	13	6	+	55522455	55522628
290988450	chr16	55525787	55525936	55525807	55525915	MMP2	NM_001127891	1	13	8	+	55525713	55525868
290988450	chr16	55525787	55525936	55525807	55525915	MMP2	NM_004530	2	13	8	+	55525713	55525868
293218313	chr16	55530905	55531079	55530924	55531055	MMP2	NM_001127891	1	13	10	+	55530838	55530974
293218313	chr16	55530905	55531079	55530924	55531055	MMP2	NM_004530	2	13	10	+	55530838	55530974
293165293	chr16	55539153	55539285	55539174	55539260	MMP2	NM_001127891	1	13	13	+	55539251	55540586

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293165293	chr16	55539153	55539285	55539174	55539260	MMP2	NM_004530	2	13	13	+	55539251	55540586
226965718	chr16	64981652	64981822	64981673	64981800	CDH11	NM_001797	1	13	13	-	64980683	64982002
226576061	chr16	64984722	64984878	64984741	64984856	CDH11	NM_001797	1	13	12	-	64984670	64984921
226010029	chr16	65005710	65005868	65005736	65005846	CDH11	NM_001797	1	13	10	-	65005834	65005967
225499915	chr16	65015878	65016051	65015899	65016031	CDH11	NM_001797	1	13	8	-	65015951	65016204
225608075	chr16	65022075	65022240	65022097	65022218	CDH11	NM_001797	1	13	7	-	65022060	65022247
225984505	chr16	65026758	65026910	65026779	65026888	CDH11	NM_001797	1	13	5	-	65026818	65026937
253675711	chr16	65032620	65032745	65032641	65032717	CDH11	NM_001797	1	13	4	-	65032465	65032759
272535818	chr16	66413202	66413357	66413224	66413340	CDH5	NM_001795	1	12	2	+	66413222	66413450
270832010	chr16	66420921	66421079	66420944	66421057	CDH5	NM_001795	1	12	3	+	66420712	66421000
271159558	chr16	66424237	66424411	66424258	66424388	CDH5	NM_001795	1	12	6	+	66424306	66424493
270149876	chr16	66426201	66426325	66426223	66426297	CDH5	NM_001795	1	12	7	+	66426039	66426286
272043876	chr16	66431890	66432032	66431914	66432012	CDH5	NM_001795	1	12	9	+	66431885	66432009
271433400	chr16	66434829	66434962	66434852	66434940	CDH5	NM_001795	1	12	11	+	66434674	66434919
271664562	chr16	66436888	66437050	66436907	66437033	CDH5	NM_001795	1	12	12	+	66436555	66438689
226424948	chr16	68772254	68772378	68772274	68772357	CDH1	NM_004360	1	16	2	+	68772200	68772314
226160708	chr16	68842211	68842381	68842233	68842358	CDH1	NM_004360	1	16	4	+	68842327	68842470
226256825	chr16	68844038	68844173	68844060	68844149	CDH1	NM_004360	1	16	6	+	68844100	68844244
226007838	chr16	68845994	68846159	68846016	68846133	CDH1	NM_004360	1	16	8	+	68846038	68846166
225852873	chr16	68849392	68849543	68849420	68849520	CDH1	NM_004360	1	16	10	+	68849418	68849662
225771654	chr16	68853268	68853423	68853292	68853395	CDH1	NM_004360	1	16	11	+	68853183	68853328
226586445	chr16	68857259	68857426	68857280	68857405	CDH1	NM_004360	1	16	13	+	68857302	68857529
254157667	chr16	68863485	68863644	68863509	68863623	CDH1	NM_004360	1	16	15	+	68863557	68863700
232675728	chr16	79628281	79628406	79628303	79628385	MAF	NM_001031804	1	1	1	-	79627745	79634622
232675728	chr16	79628281	79628406	79628303	79628385	MAF	NM_005360	2	2	2	-	79627745	79628450
232463787	chr16	79632805	79632944	79632825	79632924	MAF	NM_001031804	1	1	1	-	79627745	79634622
232463787	chr16	79632805	79632944	79632825	79632924	MAF	NM_005360	2	2	1	-	79632682	79634622
233799225	chr16	79633534	79633707	79633551	79633685	MAF	NM_001031804	1	1	1	-	79627745	79634622
233799225	chr16	79633534	79633707	79633551	79633685	MAF	NM_005360	2	2	1	-	79632682	79634622
231341760	chr16	89805003	89805172	89805024	89805152	FANCA	NM_000135	1	43	43	-	89803959	89805116
229506673	chr16	89805814	89805981	89805834	89805961	FANCA	NM_000135	1	43	40	-	89805886	89805961
228888648	chr16	89809222	89809387	89809244	89809367	FANCA	NM_000135	1	43	37	-	89809208	89809346
229365652	chr16	89813155	89813329	89813177	89813301	FANCA	NM_000135	1	43	34	-	89813239	89813298
230457371	chr16	89818495	89818669	89818518	89818642	FANCA	NM_000135	1	43	31	-	89818546	89818630
228953917	chr16	89831195	89831351	89831215	89831329	FANCA	NM_000135	1	43	28	-	89831298	89831474
228500518	chr16	89833581	89833751	89833606	89833723	FANCA	NM_000135	1	43	27	-	89833549	89833645
230398944	chr16	89836874	89837035	89836894	89837015	FANCA	NM_000135	1	43	24	-	89836972	89837042
229673061	chr16	89839653	89839818	89839673	89839792	FANCA	NM_000135	1	43	22	-	89839679	89839792
232792596	chr16	89846241	89846392	89846261	89846370	FANCA	NM_000135	1	43	18	-	89846277	89846365
230160328	chr16	89857710	89857846	89857735	89857825	FANCA	NM_000135	1	43	14	-	89857811	89857944
230693004	chr16	89858840	89858991	89858860	89858963	FANCA	NM_000135	1	43	12	-	89858879	89858955

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230541989	chr16	89865506	89865678	89865531	89865654	FANCA	NM_000135	1	43	10	-	89865574	89865640
230541989	chr16	89865506	89865678	89865531	89865654	FANCA	NM_001018112	2	11	10	-	89865574	89865640
229932120	chr16	89874604	89874771	89874626	89874750	FANCA	NM_000135	1	43	6	-	89874702	89874775
229932120	chr16	89874604	89874771	89874626	89874750	FANCA	NM_001018112	2	11	6	-	89874702	89874775
230671200	chr16	89877266	89877435	89877292	89877414	FANCA	NM_000135	1	43	4	-	89877337	89877479
230671200	chr16	89877266	89877435	89877292	89877414	FANCA	NM_001018112	2	11	4	-	89877337	89877479
228470998	chr16	89882263	89882415	89882284	89882394	FANCA	NM_000135	1	43	2	-	89882285	89882394
228470998	chr16	89882263	89882415	89882284	89882394	FANCA	NM_001018112	2	11	2	-	89882285	89882394
240365375	chr17	5418279	5418426	5418301	5418405	NLRP1	NM_014922	2	16	16	-	5417438	5418393
240365375	chr17	5418279	5418426	5418301	5418405	NLRP1	NM_033007	5	15	15	-	5417438	5418393
240365375	chr17	5418279	5418426	5418301	5418405	NLRP1	NM_033006	4	16	16	-	5417438	5418393
240365375	chr17	5418279	5418426	5418301	5418405	NLRP1	NM_033004	3	17	17	-	5417438	5418393
236165362	chr17	5424077	5424251	5424102	5424229	NLRP1	NM_001033053	1	16	14	-	5424201	5424332
236165362	chr17	5424077	5424251	5424102	5424229	NLRP1	NM_033006	4	16	13	-	5424201	5424332
236165362	chr17	5424077	5424251	5424102	5424229	NLRP1	NM_033004	3	17	14	-	5424201	5424332
236777598	chr17	5424961	5425135	5424986	5425110	NLRP1	NM_014922	2	16	13	-	5424844	5425106
236777598	chr17	5424961	5425135	5424986	5425110	NLRP1	NM_001033053	1	16	13	-	5424844	5425106
236777598	chr17	5424961	5425135	5424986	5425110	NLRP1	NM_033007	5	15	12	-	5424844	5425106
236777598	chr17	5424961	5425135	5424986	5425110	NLRP1	NM_033006	4	16	12	-	5424844	5425106
236777598	chr17	5424961	5425135	5424986	5425110	NLRP1	NM_033004	3	17	13	-	5424844	5425106
235085500	chr17	5436138	5436273	5436164	5436253	NLRP1	NM_014922	2	16	11	-	5436142	5436304
235085500	chr17	5436138	5436273	5436164	5436253	NLRP1	NM_001033053	1	16	11	-	5436142	5436304
235085500	chr17	5436138	5436273	5436164	5436253	NLRP1	NM_033007	5	15	10	-	5436142	5436304
235085500	chr17	5436138	5436273	5436164	5436253	NLRP1	NM_033006	4	16	10	-	5436142	5436304
235085500	chr17	5436138	5436273	5436164	5436253	NLRP1	NM_033004	3	17	11	-	5436142	5436304
238956749	chr17	5442668	5442838	5442688	5442818	NLRP1	NM_014922	2	16	7	-	5442735	5442905
238956749	chr17	5442668	5442838	5442688	5442818	NLRP1	NM_001033053	1	16	7	-	5442735	5442905
238956749	chr17	5442668	5442838	5442688	5442818	NLRP1	NM_033007	5	15	7	-	5442735	5442905
238956749	chr17	5442668	5442838	5442688	5442818	NLRP1	NM_033006	4	16	7	-	5442735	5442905
238956749	chr17	5442668	5442838	5442688	5442818	NLRP1	NM_033004	3	17	7	-	5442735	5442905
238288038	chr17	5456668	5456828	5456690	5456806	NLRP1	NM_014922	2	16	5	-	5456706	5456876
238288038	chr17	5456668	5456828	5456690	5456806	NLRP1	NM_001033053	1	16	5	-	5456706	5456876
238288038	chr17	5456668	5456828	5456690	5456806	NLRP1	NM_033007	5	15	5	-	5456706	5456876
238288038	chr17	5456668	5456828	5456690	5456806	NLRP1	NM_033006	4	16	5	-	5456706	5456876
238288038	chr17	5456668	5456828	5456690	5456806	NLRP1	NM_033004	3	17	5	-	5456706	5456876
257604762	chr17	5461840	5462014	5461861	5461994	NLRP1	NM_014922	2	16	4	-	5461659	5463363
257604762	chr17	5461840	5462014	5461861	5461994	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
257604762	chr17	5461840	5462014	5461861	5461994	NLRP1	NM_033007	5	15	4	-	5461659	5463363
257604762	chr17	5461840	5462014	5461861	5461994	NLRP1	NM_033006	4	16	4	-	5461659	5463363
257604762	chr17	5461840	5462014	5461861	5461994	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237491009	chr17	5462347	5462520	5462370	5462495	NLRP1	NM_014922	2	16	4	-	5461659	5463363

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
237491009	chr17	5462347	5462520	5462370	5462495	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237491009	chr17	5462347	5462520	5462370	5462495	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237491009	chr17	5462347	5462520	5462370	5462495	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237491009	chr17	5462347	5462520	5462370	5462495	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237713225	chr17	5462759	5462926	5462779	5462902	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237713225	chr17	5462759	5462926	5462779	5462902	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237713225	chr17	5462759	5462926	5462779	5462902	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237713225	chr17	5462759	5462926	5462779	5462902	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237713225	chr17	5462759	5462926	5462779	5462902	NLRP1	NM_033004	3	17	4	-	5461659	5463363
237686202	chr17	5463216	5463390	5463237	5463364	NLRP1	NM_014922	2	16	4	-	5461659	5463363
237686202	chr17	5463216	5463390	5463237	5463364	NLRP1	NM_001033053	1	16	4	-	5461659	5463363
237686202	chr17	5463216	5463390	5463237	5463364	NLRP1	NM_033007	5	15	4	-	5461659	5463363
237686202	chr17	5463216	5463390	5463237	5463364	NLRP1	NM_033006	4	16	4	-	5461659	5463363
237686202	chr17	5463216	5463390	5463237	5463364	NLRP1	NM_033004	3	17	4	-	5461659	5463363
238275826	chr17	5486062	5486208	5486082	5486188	NLRP1	NM_014922	2	16	2	-	5485990	5486166
238275826	chr17	5486062	5486208	5486082	5486188	NLRP1	NM_001033053	1	16	2	-	5485990	5486166
238275826	chr17	5486062	5486208	5486082	5486188	NLRP1	NM_033007	5	15	2	-	5485990	5486166
238275826	chr17	5486062	5486208	5486082	5486188	NLRP1	NM_033006	4	16	2	-	5485990	5486166
238275826	chr17	5486062	5486208	5486082	5486188	NLRP1	NM_033004	3	17	2	-	5485990	5486166
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126117	7	8	8	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126116	6	8	8	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126113	3	12	12	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_000546	1	11	11	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126118	8	10	10	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126114	4	12	12	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126112	2	11	11	-	7571720	7573008
239769572	chr17	7572811	7572957	7572831	7572936	TP53	NM_001126115	5	7	7	-	7571720	7573008
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126117	7	8	5	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126116	6	8	5	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126113	3	12	9	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_000546	1	11	9	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126118	8	10	8	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126114	4	12	9	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126112	2	11	9	-	7576853	7576926
241066932	chr17	7576781	7576950	7576807	7576927	TP53	NM_001126115	5	7	5	-	7576853	7576926
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126117	7	8	3	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126116	6	8	3	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126113	3	12	7	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_000546	1	11	7	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126118	8	10	6	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126114	4	12	7	-	7577499	7577608

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126112	2	11	7	-	7577499	7577608
261746128	chr17	7577489	7577636	7577509	7577613	TP53	NM_001126115	5	7	3	-	7577499	7577608
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126113	3	12	5	-	7578371	7578554
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_000546	1	11	5	-	7578371	7578554
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126118	8	10	4	-	7578371	7578554
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126114	4	12	5	-	7578371	7578554
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126112	2	11	5	-	7578371	7578554
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126117	7	8	1	-	7578371	7578811
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126116	6	8	1	-	7578371	7578811
262610068	chr17	7578408	7578582	7578429	7578557	TP53	NM_001126115	5	7	1	-	7578371	7578811
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126113	3	12	3	-	7579700	7579721
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_000546	1	11	3	-	7579700	7579721
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126114	4	12	3	-	7579700	7579721
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126112	2	11	3	-	7579700	7579721
263209938	chr17	7579587	7579750	7579610	7579728	TP53	NM_001126118	8	10	2	-	7579700	7579940
239270819	chr17	8044559	8044717	8044578	8044697	PER1	NM_002616	1	23	23	-	8043788	8044658
240588445	chr17	8045637	8045811	8045657	8045792	PER1	NM_002616	1	23	21	-	8045587	8045776
237922146	chr17	8046646	8046805	8046663	8046786	PER1	NM_002616	1	23	19	-	8046584	8047194
237925161	chr17	8046986	8047160	8047008	8047140	PER1	NM_002616	1	23	19	-	8046584	8047194
237545172	chr17	8048182	8048355	8048199	8048332	PER1	NM_002616	1	23	18	-	8048069	8048311
236848499	chr17	8049770	8049928	8049792	8049907	PER1	NM_002616	1	23	16	-	8049690	8049820
239350990	chr17	8050503	8050628	8050525	8050607	PER1	NM_002616	1	23	13	-	8050568	8050699
236949611	chr17	8050985	8051116	8051007	8051096	PER1	NM_002616	1	23	11	-	8050992	8051145
235586113	chr17	8051471	8051604	8051493	8051583	PER1	NM_002616	1	23	9	-	8051499	8051577
237436378	chr17	8052681	8052854	8052705	8052833	PER1	NM_002616	1	23	6	-	8052780	8052981
237400814	chr17	8053091	8053231	8053111	8053209	PER1	NM_002616	1	23	5	-	8053073	8053194
235840214	chr17	8053587	8053758	8053608	8053735	PER1	NM_002616	1	23	3	-	8053537	8053635
270876121	chr17	8108162	8108329	8108180	8108310	AURKB	NM_004217	1	9	9	-	8108049	8108362
272129413	chr17	8108627	8108768	8108651	8108744	AURKB	NM_004217	1	9	8	-	8108534	8108708
270129371	chr17	8110099	8110265	8110122	8110238	AURKB	NM_004217	1	9	6	-	8110068	8110206
270444343	chr17	8110796	8110970	8110816	8110944	AURKB	NM_004217	1	9	4	-	8110889	8110943
234444604	chr17	11924179	11924333	11924196	11924316	MAP2K4	NM_003010	1	11	1	+	11924135	11924318
230926262	chr17	11984675	11984825	11984699	11984800	MAP2K4	NM_003010	1	11	3	+	11984673	11984847
232494379	chr17	12011106	12011241	12011129	12011215	MAP2K4	NM_003010	1	11	5	+	12011107	12011226
233549608	chr17	12016439	12016607	12016466	12016579	MAP2K4	NM_003010	1	11	7	+	12016550	12016677
232252230	chr17	12032509	12032636	12032535	12032609	MAP2K4	NM_003010	1	11	9	+	12032456	12032604
234227975	chr17	12044488	12044657	12044507	12044629	MAP2K4	NM_003010	1	11	11	+	12044464	12047051
228714017	chr17	17118346	17118483	17118367	17118457	FLCN	NM_144997	2	14	13	-	17118299	17118404
229789564	chr17	17119739	17119896	17119760	17119874	FLCN	NM_144997	2	14	11	-	17119694	17119817
229348225	chr17	17124634	17124772	17124657	17124752	FLCN	NM_144606	1	8	8	-	17124485	17124942
227491082	chr17	17125899	17126056	17125920	17126035	FLCN	NM_144997	2	14	7	-	17125815	17125975

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227491082	chr17	17125899	17126056	17125920	17126035	FLCN	NM_144606	1	8	7	-	17125815	17125975
227374060	chr17	17129448	17129616	17129466	17129596	FLCN	NM_144997	2	14	5	-	17129490	17129636
227374060	chr17	17129448	17129616	17129466	17129596	FLCN	NM_144606	1	8	5	-	17129490	17129636
227947597	chr17	17131381	17131534	17131401	17131510	FLCN	NM_144997	2	14	4	-	17131203	17131475
227947597	chr17	17131381	17131534	17131401	17131510	FLCN	NM_144606	1	8	4	-	17131203	17131475
237194048	chr17	29483021	29483175	29483046	29483152	NF1	NM_000267	1	57	2	+	29483001	29483144
237194048	chr17	29483021	29483175	29483046	29483152	NF1	NM_001128147	3	15	2	+	29483001	29483144
237194048	chr17	29483021	29483175	29483046	29483152	NF1	NM_001042492	2	58	2	+	29483001	29483144
235554666	chr17	29496980	29497118	29497008	29497090	NF1	NM_000267	1	57	5	+	29496909	29497015
235554666	chr17	29496980	29497118	29497008	29497090	NF1	NM_001128147	3	15	5	+	29496909	29497015
235554666	chr17	29496980	29497118	29497008	29497090	NF1	NM_001042492	2	58	5	+	29496909	29497015
237439469	chr17	29509465	29509631	29509491	29509602	NF1	NM_000267	1	57	8	+	29509526	29509683
237439469	chr17	29509465	29509631	29509491	29509602	NF1	NM_001128147	3	15	8	+	29509526	29509683
237439469	chr17	29509465	29509631	29509491	29509602	NF1	NM_001042492	2	58	8	+	29509526	29509683
235108616	chr17	29527496	29527622	29527518	29527596	NF1	NM_000267	1	57	9	+	29527440	29527613
235108616	chr17	29527496	29527622	29527518	29527596	NF1	NM_001128147	3	15	9	+	29527440	29527613
235108616	chr17	29527496	29527622	29527518	29527596	NF1	NM_001042492	2	58	9	+	29527440	29527613
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_000267	1	57	10	+	29528055	29528177
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_001128147	3	15	10	+	29528055	29528177
258513834	chr17	29528145	29528310	29528169	29528279	NF1	NM_001042492	2	58	10	+	29528055	29528177
236072329	chr17	29533260	29533425	29533281	29533398	NF1	NM_000267	1	57	12	+	29533258	29533389
236072329	chr17	29533260	29533425	29533281	29533398	NF1	NM_001128147	3	15	12	+	29533258	29533389
236072329	chr17	29533260	29533425	29533281	29533398	NF1	NM_001042492	2	58	12	+	29533258	29533389
237409001	chr17	29548905	29549072	29548928	29549042	NF1	NM_001128147	3	15	15	+	29548868	29549782
237409001	chr17	29548905	29549072	29548928	29549042	NF1	NM_000267	1	57	15	+	29548868	29548947
237409001	chr17	29548905	29549072	29548928	29549042	NF1	NM_001042492	2	58	15	+	29548868	29548947
236044556	chr17	29553417	29553556	29553444	29553536	NF1	NM_000267	1	57	18	+	29553453	29553702
236044556	chr17	29553417	29553556	29553444	29553536	NF1	NM_001042492	2	58	18	+	29553453	29553702
237283168	chr17	29554496	29554665	29554523	29554637	NF1	NM_000267	1	57	20	+	29554541	29554624
237283168	chr17	29554496	29554665	29554523	29554637	NF1	NM_001042492	2	58	20	+	29554541	29554624
236385605	chr17	29556239	29556393	29556262	29556365	NF1	NM_000267	1	57	21	+	29556043	29556483
236385605	chr17	29556239	29556393	29556262	29556365	NF1	NM_001042492	2	58	21	+	29556043	29556483
235501994	chr17	29557219	29557366	29557252	29557339	NF1	NM_000267	1	57	23	+	29557278	29557400
235501994	chr17	29557219	29557366	29557252	29557339	NF1	NM_001042492	2	58	23	+	29557278	29557400
236466406	chr17	29559149	29559308	29559171	29559283	NF1	NM_000267	1	57	25	+	29559091	29559207
236466406	chr17	29559149	29559308	29559171	29559283	NF1	NM_001042492	2	58	25	+	29559091	29559207
237082665	chr17	29559979	29560143	29560006	29560119	NF1	NM_000267	1	57	27	+	29560020	29560231
237082665	chr17	29559979	29560143	29560006	29560119	NF1	NM_001042492	2	58	27	+	29560020	29560231
236752957	chr17	29562855	29563028	29562876	29563004	NF1	NM_000267	1	57	29	+	29562936	29563039
236752957	chr17	29562855	29563028	29562876	29563004	NF1	NM_001042492	2	58	29	+	29562936	29563039
242724574	chr17	29576077	29576227	29576101	29576205	NF1	NM_000267	1	57	30	+	29576002	29576137

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242724574	chr17	29576077	29576227	29576101	29576205	NF1	NM_001042492	2	58	30	+	29576002	29576137
235375004	chr17	29585473	29585645	29585497	29585617	NF1	NM_000267	1	57	31	+	29585362	29585520
235375004	chr17	29585473	29585645	29585497	29585617	NF1	NM_001042492	2	58	32	+	29585362	29585520
235098163	chr17	29587464	29587635	29587489	29587607	NF1	NM_000267	1	57	33	+	29587387	29587533
235098163	chr17	29587464	29587635	29587489	29587607	NF1	NM_001042492	2	58	34	+	29587387	29587533
235390321	chr17	29592245	29592372	29592273	29592345	NF1	NM_000267	1	57	35	+	29592247	29592357
235390321	chr17	29592245	29592372	29592273	29592345	NF1	NM_001042492	2	58	36	+	29592247	29592357
239312901	chr17	29653019	29653184	29653047	29653159	NF1	NM_000267	1	57	36	+	29652838	29653270
239312901	chr17	29653019	29653184	29653047	29653159	NF1	NM_001042492	2	58	37	+	29652838	29653270
239838122	chr17	29654696	29654863	29654719	29654842	NF1	NM_000267	1	57	37	+	29654517	29654857
239838122	chr17	29654696	29654863	29654719	29654842	NF1	NM_001042492	2	58	38	+	29654517	29654857
257426404	chr17	29657370	29657511	29657394	29657482	NF1	NM_000267	1	57	38	+	29657314	29657516
257426404	chr17	29657370	29657511	29657394	29657482	NF1	NM_001042492	2	58	39	+	29657314	29657516
238334068	chr17	29663258	29663406	29663285	29663383	NF1	NM_000267	1	57	40	+	29663351	29663491
238334068	chr17	29663258	29663406	29663285	29663383	NF1	NM_001042492	2	58	41	+	29663351	29663491
240025344	chr17	29663695	29663850	29663724	29663829	NF1	NM_000267	1	57	41	+	29663653	29663932
240025344	chr17	29663695	29663850	29663724	29663829	NF1	NM_001042492	2	58	42	+	29663653	29663932
239220201	chr17	29664482	29664618	29664505	29664591	NF1	NM_000267	1	57	42	+	29664386	29664600
239220201	chr17	29664482	29664618	29664505	29664591	NF1	NM_001042492	2	58	43	+	29664386	29664600
237076660	chr17	29665705	29665870	29665732	29665844	NF1	NM_000267	1	57	45	+	29665722	29665823
237076660	chr17	29665705	29665870	29665732	29665844	NF1	NM_001042492	2	58	46	+	29665722	29665823
235874062	chr17	29670125	29670283	29670148	29670253	NF1	NM_000267	1	57	47	+	29670027	29670153
235874062	chr17	29670125	29670283	29670148	29670253	NF1	NM_001042492	2	58	48	+	29670027	29670153
239686717	chr17	29677178	29677323	29677200	29677295	NF1	NM_000267	1	57	49	+	29677201	29677336
239686717	chr17	29677178	29677323	29677200	29677295	NF1	NM_001042492	2	58	50	+	29677201	29677336
237994921	chr17	29679397	29679556	29679416	29679528	NF1	NM_000267	1	57	50	+	29679275	29679432
237994921	chr17	29679397	29679556	29679416	29679528	NF1	NM_001042492	2	58	51	+	29679275	29679432
241766339	chr17	29683921	29684085	29683947	29684057	NF1	NM_000267	1	57	52	+	29683978	29684108
241766339	chr17	29683921	29684085	29683947	29684057	NF1	NM_001042492	2	58	53	+	29683978	29684108
238959080	chr17	29685379	29685552	29685406	29685527	NF1	NM_000267	1	57	54	+	29685498	29685640
238959080	chr17	29685379	29685552	29685406	29685527	NF1	NM_001042492	2	58	55	+	29685498	29685640
235203153	chr17	29687617	29687789	29687638	29687763	NF1	NM_000267	1	57	56	+	29687505	29687721
235203153	chr17	29687617	29687789	29687638	29687763	NF1	NM_001042492	2	58	57	+	29687505	29687721
274609702	chr17	37618366	37618495	37618388	37618474	CDK12	NM_016507	2	14	1	+	37617739	37619370
274609702	chr17	37618366	37618495	37618388	37618474	CDK12	NM_015083	1	14	1	+	37617739	37619370
274638263	chr17	37618791	37618964	37618815	37618938	CDK12	NM_016507	2	14	1	+	37617739	37619370
274638263	chr17	37618791	37618964	37618815	37618938	CDK12	NM_015083	1	14	1	+	37617739	37619370
274622039	chr17	37619253	37619406	37619275	37619378	CDK12	NM_016507	2	14	1	+	37617739	37619370
274622039	chr17	37619253	37619406	37619275	37619378	CDK12	NM_015083	1	14	1	+	37617739	37619370
274422532	chr17	37627404	37627564	37627431	37627538	CDK12	NM_016507	2	14	2	+	37627132	37628016
274422532	chr17	37627404	37627564	37627431	37627538	CDK12	NM_015083	1	14	2	+	37627132	37628016

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
273530063	chr17	37627824	37627975	37627848	37627952	CDK12	NM_016507	2	14	2	+	37627132	37628016
273530063	chr17	37627824	37627975	37627848	37627952	CDK12	NM_015083	1	14	2	+	37627132	37628016
274357394	chr17	37648954	37649078	37648982	37649057	CDK12	NM_016507	2	14	4	+	37649004	37649143
274357394	chr17	37648954	37649078	37648982	37649057	CDK12	NM_015083	1	14	4	+	37649004	37649143
274588668	chr17	37657433	37657580	37657459	37657555	CDK12	NM_016507	2	14	6	+	37657503	37657692
274588668	chr17	37657433	37657580	37657459	37657555	CDK12	NM_015083	1	14	6	+	37657503	37657692
273543052	chr17	37667657	37667826	37667681	37667802	CDK12	NM_016507	2	14	8	+	37667782	37667883
273543052	chr17	37667657	37667826	37667681	37667802	CDK12	NM_015083	1	14	8	+	37667782	37667883
273414242	chr17	37673662	37673835	37673688	37673809	CDK12	NM_016507	2	14	10	+	37673693	37673809
273414242	chr17	37673662	37673835	37673688	37673809	CDK12	NM_015083	1	14	10	+	37673693	37673809
273080770	chr17	37681005	37681157	37681026	37681138	CDK12	NM_016507	2	14	12	+	37680927	37681138
273080770	chr17	37681005	37681157	37681026	37681138	CDK12	NM_015083	1	14	12	+	37680927	37681138
273943268	chr17	37682420	37682594	37682447	37682569	CDK12	NM_016507	2	14	13	+	37682117	37682569
273943268	chr17	37682420	37682594	37682447	37682569	CDK12	NM_015083	1	14	13	+	37682117	37682569
274052304	chr17	37687090	37687263	37687111	37687242	CDK12	NM_016507	2	14	14	+	37686857	37690800
274052304	chr17	37687090	37687263	37687111	37687242	CDK12	NM_015083	1	14	14	+	37686884	37690800
299265006	chr17	37829034	37829159	37829051	37829139	PGAP3	NM_033419	1	8	8	-	37827375	37829119
299080712	chr17	37829655	37829804	37829677	37829782	PGAP3	NM_033419	1	8	6	-	37829767	37829903
299232433	chr17	37830896	37831024	37830919	37831000	PGAP3	NM_033419	1	8	4	-	37830870	37830932
299065839	chr17	37844005	37844139	37844026	37844119	PGAP3	NM_033419	1	8	1	-	37844087	37844310
230008216	chr17	37863211	37863385	37863231	37863367	ERBB2	NM_004448	2	27	2	+	37863243	37863394
230008216	chr17	37863211	37863385	37863231	37863367	ERBB2	NM_001005862	1	30	5	+	37863243	37863394
231786701	chr17	37865536	37865663	37865557	37865639	ERBB2	NM_004448	2	27	4	+	37865571	37865705
231786701	chr17	37865536	37865663	37865557	37865639	ERBB2	NM_001005862	1	30	7	+	37865571	37865705
228212085	chr17	37866516	37866681	37866537	37866660	ERBB2	NM_004448	2	27	7	+	37866593	37866734
228212085	chr17	37866516	37866681	37866537	37866660	ERBB2	NM_001005862	1	30	10	+	37866593	37866734
231696523	chr17	37868511	37868664	37868530	37868642	ERBB2	NM_004448	2	27	9	+	37868575	37868701
231696523	chr17	37868511	37868664	37868530	37868642	ERBB2	NM_001005862	1	30	12	+	37868575	37868701
231206820	chr17	37871658	37871810	37871680	37871790	ERBB2	NM_004448	2	27	11	+	37871699	37871789
231206820	chr17	37871658	37871810	37871680	37871790	ERBB2	NM_001005862	1	30	14	+	37871699	37871789
227748141	chr17	37872743	37872893	37872763	37872875	ERBB2	NM_004448	2	27	14	+	37872768	37872858
227748141	chr17	37872743	37872893	37872763	37872875	ERBB2	NM_001005862	1	30	17	+	37872768	37872858
228515237	chr17	37879531	37879698	37879553	37879680	ERBB2	NM_004448	2	27	17	+	37879572	37879710
228515237	chr17	37879531	37879698	37879553	37879680	ERBB2	NM_001005862	1	30	20	+	37879572	37879710
229976976	chr17	37880130	37880304	37880156	37880283	ERBB2	NM_004448	2	27	19	+	37880165	37880263
229976976	chr17	37880130	37880304	37880156	37880283	ERBB2	NM_001005862	1	30	22	+	37880165	37880263
230483103	chr17	37881353	37881480	37881373	37881458	ERBB2	NM_004448	2	27	21	+	37881302	37881457
230483103	chr17	37881353	37881480	37881373	37881458	ERBB2	NM_001005862	1	30	24	+	37881302	37881457
229968094	chr17	37881944	37882114	37881966	37882094	ERBB2	NM_004448	2	27	23	+	37881960	37882106
229968094	chr17	37881944	37882114	37881966	37882094	ERBB2	NM_001005862	1	30	26	+	37881960	37882106
229042522	chr17	37882972	37883141	37882995	37883121	ERBB2	NM_004448	2	27	25	+	37883068	37883256

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229042522	chr17	37882972	37883141	37882995	37883121	ERBB2	NM_001005862	1	30	28	+	37883068	37883256
230202748	chr17	37883712	37883837	37883733	37883815	ERBB2	NM_004448	2	27	26	+	37883548	37883800
230202748	chr17	37883712	37883837	37883733	37883815	ERBB2	NM_001005862	1	30	29	+	37883548	37883800
242266370	chr17	38487440	38487577	38487460	38487557	RARA	NM_001145302	4	7	2	+	38487109	38487648
242266370	chr17	38487440	38487577	38487460	38487557	RARA	NM_001145301	3	9	2	+	38487109	38487648
242266370	chr17	38487440	38487577	38487460	38487557	RARA	NM_000964	1	9	2	+	38487109	38487648
241595689	chr17	38504510	38504678	38504533	38504656	RARA	NM_001145301	3	9	3	+	38504568	38504716
241595689	chr17	38504510	38504678	38504533	38504656	RARA	NM_000964	1	9	3	+	38504568	38504716
241595689	chr17	38504510	38504678	38504533	38504656	RARA	NM_001024809	2	8	2	+	38504568	38504716
241587222	chr17	38508124	38508294	38508142	38508274	RARA	NM_001145302	4	7	3	+	38508162	38508322
241587222	chr17	38508124	38508294	38508142	38508274	RARA	NM_001145301	3	9	5	+	38508162	38508322
241587222	chr17	38508124	38508294	38508142	38508274	RARA	NM_000964	1	9	5	+	38508162	38508322
241587222	chr17	38508124	38508294	38508142	38508274	RARA	NM_001024809	2	8	4	+	38508162	38508322
240645872	chr17	38510521	38510694	38510541	38510677	RARA	NM_001145302	4	7	5	+	38510554	38510758
240645872	chr17	38510521	38510694	38510541	38510677	RARA	NM_001145301	3	9	7	+	38510554	38510758
240645872	chr17	38510521	38510694	38510541	38510677	RARA	NM_000964	1	9	7	+	38510554	38510758
240645872	chr17	38510521	38510694	38510541	38510677	RARA	NM_001024809	2	8	6	+	38510554	38510758
262511146	chr17	38512236	38512369	38512254	38512351	RARA	NM_001145302	4	7	7	+	38512261	38513895
262511146	chr17	38512236	38512369	38512254	38512351	RARA	NM_001145301	3	9	9	+	38512261	38513895
262511146	chr17	38512236	38512369	38512254	38512351	RARA	NM_000964	1	9	9	+	38512261	38513895
262511146	chr17	38512236	38512369	38512254	38512351	RARA	NM_001024809	2	8	8	+	38512261	38513895
228486714	chr17	41606471	41606639	41606491	41606613	ETV4	NM_001986	2	13	12	-	41606503	41606604
228486714	chr17	41606471	41606639	41606491	41606613	ETV4	NM_001079675	1	13	12	-	41606503	41606604
230232136	chr17	41607433	41607581	41607452	41607559	ETV4	NM_001986	2	13	9	-	41607475	41607549
230232136	chr17	41607433	41607581	41607452	41607559	ETV4	NM_001079675	1	13	9	-	41607475	41607549
230745822	chr17	41610532	41610664	41610554	41610645	ETV4	NM_001986	2	13	7	-	41610555	41610716
230745822	chr17	41610532	41610664	41610554	41610645	ETV4	NM_001079675	1	13	7	-	41610555	41610716
228110050	chr17	41613703	41613876	41613727	41613851	ETV4	NM_001986	2	13	5	-	41613794	41613847
228110050	chr17	41613703	41613876	41613727	41613851	ETV4	NM_001079675	1	13	5	-	41613794	41613847
230671277	chr17	41622921	41623074	41622941	41623057	ETV4	NM_001986	2	13	2	-	41622926	41623036
230671277	chr17	41622921	41623074	41622941	41623057	ETV4	NM_001079675	1	13	2	-	41622926	41623036
278761968	chr17	45360780	45360945	45360801	45360925	ITGB3	NM_000212	1	15	3	+	45360720	45360915
278705665	chr17	45363517	45363685	45363537	45363665	ITGB3	NM_000212	1	15	5	+	45363626	45363788
278970516	chr17	45366961	45367119	45366984	45367091	ITGB3	NM_000212	1	15	7	+	45367047	45367142
278480890	chr17	45368350	45368497	45368371	45368475	ITGB3	NM_000212	1	15	9	+	45368320	45368454
279374287	chr17	45369847	45370014	45369868	45369990	ITGB3	NM_000212	1	15	10	+	45369505	45369934
278723481	chr17	45379974	45380143	45379996	45380116	ITGB3	NM_000212	1	15	13	+	45380087	45380206
279074864	chr17	45387442	45387604	45387464	45387578	ITGB3	NM_000212	1	15	15	+	45387505	45390077
226704161	chr17	48263152	48263302	48263173	48263280	COL1A1	NM_000088	1	51	50	-	48263139	48263381
226578332	chr17	48263951	48264118	48263970	48264099	COL1A1	NM_000088	1	51	48	-	48264001	48264283
226987709	chr17	48264370	48264522	48264393	48264500	COL1A1	NM_000088	1	51	47	-	48264376	48264483

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
226424468	chr17	48265400	48265543	48265422	48265521	COL1A1	NM_000088	1	51	44	-	48265457	48265510
226048161	chr17	48266471	48266641	48266492	48266620	COL1A1	NM_000088	1	51	40	-	48266529	48266636
253712561	chr17	48266945	48267118	48266966	48267093	COL1A1	NM_000088	1	51	38	-	48267040	48267093
226587590	chr17	48267606	48267771	48267627	48267742	COL1A1	NM_000088	1	51	35	-	48267688	48267741
225532195	chr17	48268657	48268803	48268680	48268782	COL1A1	NM_000088	1	51	32	-	48268744	48268851
227086461	chr17	48269748	48269910	48269772	48269890	COL1A1	NM_000088	1	51	29	-	48269836	48269889
225495517	chr17	48271271	48271424	48271292	48271402	COL1A1	NM_000088	1	51	25	-	48271304	48271402
225408463	chr17	48271839	48272013	48271862	48271994	COL1A1	NM_000088	1	51	22	-	48271934	48271987
225631412	chr17	48272567	48272738	48272588	48272718	COL1A1	NM_000088	1	51	19	-	48272593	48272691
226188436	chr17	48273451	48273605	48273473	48273583	COL1A1	NM_000088	1	51	15	-	48273516	48273560
227042352	chr17	48274341	48274465	48274364	48274442	COL1A1	NM_000088	1	51	11	-	48274371	48274424
225332276	chr17	48275455	48275610	48275476	48275588	COL1A1	NM_000088	1	51	7	-	48275522	48275566
226209611	chr17	48276846	48276998	48276869	48276977	COL1A1	NM_000088	1	51	3	-	48276917	48276951
227207963	chr17	53342729	53342902	53342750	53342882	HLF	NM_002126	1	4	1	+	53342321	53342960
227381998	chr17	53345262	53345434	53345289	53345412	HLF	NM_002126	1	4	2	+	53345112	53345447
230209475	chr17	53397919	53398071	53397938	53398049	HLF	NM_002126	1	4	4	+	53398025	53402426
223435409	chr17	59760678	59760848	59760705	59760820	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223439321	chr17	59760943	59761111	59760971	59761086	BRIP1	NM_032043	1	20	20	-	59756547	59761501
223459480	chr17	59761305	59761447	59761327	59761424	BRIP1	NM_032043	1	20	20	-	59756547	59761501
222200981	chr17	59763313	59763459	59763340	59763431	BRIP1	NM_032043	1	20	19	-	59763197	59763526
222791338	chr17	59793294	59793419	59793321	59793391	BRIP1	NM_032043	1	20	17	-	59793312	59793424
223194452	chr17	59821804	59821934	59821832	59821912	BRIP1	NM_032043	1	20	15	-	59821793	59821952
225122006	chr17	59857532	59857705	59857557	59857679	BRIP1	NM_032043	1	20	13	-	59857622	59857762
224705829	chr17	59861688	59861831	59861717	59861808	BRIP1	NM_032043	1	20	11	-	59861631	59861785
222619143	chr17	59876546	59876720	59876567	59876693	BRIP1	NM_032043	1	20	9	-	59876461	59876660
223666210	chr17	59885707	59885870	59885737	59885843	BRIP1	NM_032043	1	20	7	-	59885828	59886118
223625846	chr17	59924448	59924615	59924475	59924587	BRIP1	NM_032043	1	20	6	-	59924462	59924581
223416464	chr17	59934487	59934661	59934513	59934632	BRIP1	NM_032043	1	20	4	-	59934419	59934592
222484346	chr17	59938807	59938973	59938833	59938945	BRIP1	NM_032043	1	20	2	-	59938808	59938930
226783603	chr17	62007053	62007214	62007073	62007190	CD79B	NM_000626	1	6	4	-	62007130	62007248
226783603	chr17	62007053	62007214	62007073	62007190	CD79B	NM_021602	3	5	3	-	62007130	62007248
226783603	chr17	62007053	62007214	62007073	62007190	CD79B	NM_001039933	2	6	4	-	62007130	62007248
227075151	chr17	62007556	62007717	62007579	62007695	CD79B	NM_000626	1	6	3	-	62007434	62007745
227075151	chr17	62007556	62007717	62007579	62007695	CD79B	NM_001039933	2	6	3	-	62007434	62007745
236768155	chr17	66511432	66511606	66511461	66511583	PRKAR1A	NM_002734	1	11	2	+	66511535	66511717
236768155	chr17	66511432	66511606	66511461	66511583	PRKAR1A	NM_212472	3	11	2	+	66511535	66511717
236768155	chr17	66511432	66511606	66511461	66511583	PRKAR1A	NM_212471	2	11	2	+	66511535	66511717
237619351	chr17	66518944	66519116	66518969	66519095	PRKAR1A	NM_002734	1	11	3	+	66518897	66519067
237619351	chr17	66518944	66519116	66518969	66519095	PRKAR1A	NM_212472	3	11	3	+	66518897	66519067
237619351	chr17	66518944	66519116	66518969	66519095	PRKAR1A	NM_212471	2	11	3	+	66518897	66519067
235785665	chr17	66520939	66521112	66520965	66521085	PRKAR1A	NM_002734	1	11	6	+	66521053	66521099

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235785665	chr17	66520939	66521112	66520965	66521085	PRKAR1A	NM_212472	3	11	6	+	66521053	66521099
235785665	chr17	66520939	66521112	66520965	66521085	PRKAR1A	NM_212471	2	11	6	+	66521053	66521099
237759237	chr17	66521980	66522105	66522002	66522073	PRKAR1A	NM_002734	1	11	7	+	66521895	66522053
237759237	chr17	66521980	66522105	66522002	66522073	PRKAR1A	NM_212472	3	11	7	+	66521895	66522053
237759237	chr17	66521980	66522105	66522002	66522073	PRKAR1A	NM_212471	2	11	7	+	66521895	66522053
238114052	chr17	66526024	66526198	66526050	66526171	PRKAR1A	NM_002734	1	11	10	+	66526061	66526142
238114052	chr17	66526024	66526198	66526050	66526171	PRKAR1A	NM_212472	3	11	10	+	66526061	66526142
238114052	chr17	66526024	66526198	66526050	66526171	PRKAR1A	NM_212471	2	11	10	+	66526061	66526142
239407307	chr17	75303188	75303330	75303210	75303309	SEPT9	NM_001113492	2	12	2	+	75303223	75303279
239407307	chr17	75303188	75303330	75303210	75303309	SEPT9	NM_001113491	1	12	2	+	75303223	75303279
264708743	chr17	75398170	75398314	75398190	75398293	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264708743	chr17	75398170	75398314	75398190	75398293	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264708743	chr17	75398170	75398314	75398190	75398293	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264708743	chr17	75398170	75398314	75398190	75398293	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264708743	chr17	75398170	75398314	75398190	75398293	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
264698791	chr17	75398618	75398770	75398640	75398751	SEPT9	NM_006640	7	11	2	+	75398141	75398785
264698791	chr17	75398618	75398770	75398640	75398751	SEPT9	NM_001113494	4	11	2	+	75398141	75398785
264698791	chr17	75398618	75398770	75398640	75398751	SEPT9	NM_001113493	3	11	2	+	75398141	75398785
264698791	chr17	75398618	75398770	75398640	75398751	SEPT9	NM_001113492	2	12	3	+	75398141	75398785
264698791	chr17	75398618	75398770	75398640	75398751	SEPT9	NM_001113491	1	12	3	+	75398141	75398785
260716363	chr17	75471710	75471883	75471729	75471865	SEPT9	NM_001113495	5	10	1	+	75471325	75471985
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_006640	7	11	4	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113496	6	10	3	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113495	5	10	3	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113494	4	11	4	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113493	3	11	4	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113492	2	12	5	+	75483506	75483634
264248305	chr17	75483390	75483549	75483411	75483523	SEPT9	NM_001113491	1	12	5	+	75483506	75483634
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_006640	7	11	6	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113496	6	10	5	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113495	5	10	5	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113494	4	11	6	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113493	3	11	6	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113492	2	12	7	+	75484809	75484946
242363876	chr17	75484694	75484858	75484715	75484835	SEPT9	NM_001113491	1	12	7	+	75484809	75484946
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_006640	7	11	9	+	75489062	75489158
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113496	6	10	8	+	75489062	75489158
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113495	5	10	8	+	75489062	75489158
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113494	4	11	9	+	75489062	75489158
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113493	3	11	9	+	75489062	75489158
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113492	2	12	10	+	75489062	75489158

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240232017	chr17	75489021	75489159	75489042	75489138	SEPT9	NM_001113491	1	12	10	+	75489062	75489158
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_006640	7	11	11	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113496	6	10	10	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113495	5	10	10	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113494	4	11	11	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113493	3	11	11	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113492	2	12	12	+	75494605	75496678
241900387	chr17	75494662	75494790	75494680	75494771	SEPT9	NM_001113491	1	12	12	+	75494605	75496678
295397769	chr17	76212684	76212819	76212705	76212792	BIRC5	NM_001168	3	4	3	+	76212745	76212862
295397769	chr17	76212684	76212819	76212705	76212792	BIRC5	NM_001012271	2	5	4	+	76212745	76212862
242353642	chr17	78237352	78237520	78237375	78237498	RNF213	NM_020954	2	17	2	+	78237373	78237577
242353642	chr17	78237352	78237520	78237375	78237498	RNF213	NM_001256071	1	68	2	+	78237373	78237577
263740247	chr17	78261701	78261870	78261723	78261853	RNF213	NM_020954	2	17	4	+	78261614	78262162
263740247	chr17	78261701	78261870	78261723	78261853	RNF213	NM_001256071	1	68	4	+	78261614	78262162
240554407	chr17	78262386	78262559	78262406	78262542	RNF213	NM_020954	2	17	5	+	78262432	78262554
240554407	chr17	78262386	78262559	78262406	78262542	RNF213	NM_001256071	1	68	5	+	78262432	78262554
237785195	chr17	78264321	78264445	78264342	78264419	RNF213	NM_020954	2	17	7	+	78264369	78264527
237785195	chr17	78264321	78264445	78264342	78264419	RNF213	NM_001256071	1	68	7	+	78264369	78264527
238562983	chr17	78265544	78265703	78265568	78265684	RNF213	NM_020954	2	17	8	+	78265427	78265626
238562983	chr17	78265544	78265703	78265568	78265684	RNF213	NM_001256071	1	68	8	+	78265427	78265626
242399640	chr17	78269318	78269486	78269341	78269463	RNF213	NM_020954	2	17	10	+	78269357	78269613
242399640	chr17	78269318	78269486	78269341	78269463	RNF213	NM_001256071	1	68	10	+	78269357	78269613
238999868	chr17	78272201	78272374	78272221	78272349	RNF213	NM_020954	2	17	11	+	78272121	78272318
238999868	chr17	78272201	78272374	78272221	78272349	RNF213	NM_001256071	1	68	11	+	78272121	78272318
261106648	chr17	78282703	78282870	78282727	78282847	RNF213	NM_020954	2	17	14	+	78282818	78282971
261106648	chr17	78282703	78282870	78282727	78282847	RNF213	NM_001256071	1	68	14	+	78282818	78282971
261949816	chr17	78290937	78291108	78290957	78291087	RNF213	NM_020954	2	17	16	+	78290988	78291077
261949816	chr17	78290937	78291108	78290957	78291087	RNF213	NM_001256071	1	68	16	+	78290988	78291077
242063723	chr17	78298741	78298913	78298770	78298888	RNF213	NM_001256071	1	68	18	+	78298830	78298998
238144974	chr17	78302057	78302184	78302081	78302163	RNF213	NM_001256071	1	68	20	+	78302128	78302277
263975593	chr17	78305937	78306100	78305959	78306078	RNF213	NM_001256071	1	68	21	+	78305806	78306431
238586183	chr17	78307833	78307991	78307854	78307969	RNF213	NM_001256071	1	68	22	+	78307905	78308070
264530127	chr17	78310101	78310264	78310125	78310243	RNF213	NM_001256071	1	68	23	+	78309961	78310178
238284235	chr17	78311700	78311827	78311726	78311806	RNF213	NM_001256071	1	68	25	+	78311633	78311797
263938063	chr17	78313340	78313514	78313363	78313491	RNF213	NM_001256071	1	68	26	+	78313001	78314156
263869423	chr17	78313830	78313971	78313849	78313952	RNF213	NM_001256071	1	68	26	+	78313001	78314156
240522554	chr17	78317003	78317177	78317027	78317156	RNF213	NM_001256071	1	68	27	+	78316932	78317125
238986016	chr17	78318482	78318653	78318502	78318625	RNF213	NM_001256071	1	68	29	+	78318478	78322086
238955987	chr17	78318961	78319126	78318982	78319106	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239116303	chr17	78319403	78319542	78319425	78319520	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262432715	chr17	78319871	78320045	78319893	78320023	RNF213	NM_001256071	1	68	29	+	78318478	78322086

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
239143980	chr17	78320379	78320548	78320403	78320530	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262260924	chr17	78320890	78321027	78320911	78321001	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262389373	chr17	78321293	78321456	78321316	78321434	RNF213	NM_001256071	1	68	29	+	78318478	78322086
262420854	chr17	78321761	78321917	78321781	78321895	RNF213	NM_001256071	1	68	29	+	78318478	78322086
239950912	chr17	78323640	78323811	78323660	78323791	RNF213	NM_001256071	1	68	30	+	78323570	78323706
242371116	chr17	78326711	78326878	78326730	78326861	RNF213	NM_001256071	1	68	33	+	78326740	78326859
241566768	chr17	78327896	78328050	78327914	78328028	RNF213	NM_001256071	1	68	35	+	78327819	78327966
241611179	chr17	78332148	78332302	78332169	78332280	RNF213	NM_001256071	1	68	37	+	78332088	78332279
239730565	chr17	78335546	78335718	78335568	78335692	RNF213	NM_001256071	1	68	39	+	78335534	78335688
237857475	chr17	78337387	78337523	78337404	78337505	RNF213	NM_001256071	1	68	41	+	78337409	78337590
240904645	chr17	78341715	78341879	78341737	78341858	RNF213	NM_001256071	1	68	44	+	78341761	78341943
238998048	chr17	78343330	78343501	78343351	78343476	RNF213	NM_001256071	1	68	45	+	78343302	78343471
241798612	chr17	78346215	78346389	78346241	78346365	RNF213	NM_001256071	1	68	48	+	78346321	78346534
239780944	chr17	78346847	78346972	78346864	78346951	RNF213	NM_001256071	1	68	49	+	78346775	78346965
238797056	chr17	78349973	78350147	78349999	78350124	RNF213	NM_001256071	1	68	52	+	78350101	78350343
239906792	chr17	78351469	78351633	78351492	78351612	RNF213	NM_001256071	1	68	54	+	78351562	78351596
240207799	chr17	78355282	78355431	78355305	78355411	RNF213	NM_001256071	1	68	57	+	78355347	78355527
263463824	chr17	78357477	78357644	78357502	78357618	RNF213	NM_001256071	1	68	59	+	78357477	78357728
240355096	chr17	78359295	78359459	78359319	78359438	RNF213	NM_001256071	1	68	61	+	78359338	78359421
241964125	chr17	78360508	78360653	78360530	78360633	RNF213	NM_001256071	1	68	63	+	78360490	78360691
261562283	chr17	78363022	78363195	78363042	78363171	RNF213	NM_001256071	1	68	65	+	78362973	78363167
241466854	chr17	78363846	78364020	78363867	78363997	RNF213	NM_001256071	1	68	67	+	78363812	78363996
238379074	chr18	22671792	22671948	22671817	22671928	ZNF521	NM_015461	1	8	6	-	22671914	22672045
241232803	chr18	22804258	22804432	22804280	22804409	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241294377	chr18	22804722	22804881	22804743	22804855	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265161744	chr18	22805145	22805308	22805166	22805287	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265141815	chr18	22805597	22805758	22805618	22805736	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265102577	chr18	22806076	22806230	22806100	22806202	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265057178	chr18	22806473	22806619	22806495	22806591	ZNF521	NM_015461	1	8	4	-	22804309	22807661
265032170	chr18	22806895	22807038	22806918	22807017	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241241894	chr18	22807377	22807538	22807401	22807518	ZNF521	NM_015461	1	8	4	-	22804309	22807661
241452361	chr18	22902080	22902241	22902101	22902213	ZNF521	NM_015461	1	8	3	-	22901972	22902151
271834954	chr18	25532244	25532383	25532265	25532356	CDH2	NM_001792	1	16	16	-	25530930	25532323
272089384	chr18	25562895	25563043	25562914	25563019	CDH2	NM_001792	1	16	14	-	25562908	25563047
270753116	chr18	25565409	25565555	25565439	25565527	CDH2	NM_001792	1	16	12	-	25565492	25565725
270736181	chr18	25568483	25568607	25568511	25568579	CDH2	NM_001792	1	16	11	-	25568488	25568630
270544430	chr18	25570230	25570366	25570252	25570339	CDH2	NM_001792	1	16	10	-	25570061	25570314
270222997	chr18	25573529	25573691	25573552	25573663	CDH2	NM_001792	1	16	8	-	25573464	25573601
270873211	chr18	25585698	25585855	25585725	25585834	CDH2	NM_001792	1	16	6	-	25585813	25585957
271545350	chr18	25589747	25589913	25589773	25589892	CDH2	NM_001792	1	16	5	-	25589681	25589836
271858911	chr18	25593712	25593882	25593734	25593854	CDH2	NM_001792	1	16	3	-	25593647	25593873

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272408578	chr18	45368107	45368273	45368133	45368252	SMAD2	NM_005901	3	11	11	-	45359466	45368321
272408578	chr18	45368107	45368273	45368133	45368252	SMAD2	NM_001135937	2	10	10	-	45359466	45368321
272408578	chr18	45368107	45368273	45368133	45368252	SMAD2	NM_001003652	1	11	11	-	45359466	45368321
271189801	chr18	45371810	45371965	45371833	45371937	SMAD2	NM_005901	3	11	10	-	45371711	45371855
271189801	chr18	45371810	45371965	45371833	45371937	SMAD2	NM_001135937	2	10	9	-	45371711	45371855
271189801	chr18	45371810	45371965	45371833	45371937	SMAD2	NM_001003652	1	11	10	-	45371711	45371855
271241475	chr18	45374869	45375031	45374890	45375003	SMAD2	NM_005901	3	11	8	-	45374846	45375058
271241475	chr18	45374869	45375031	45374890	45375003	SMAD2	NM_001135937	2	10	7	-	45374846	45375058
271241475	chr18	45374869	45375031	45374890	45375003	SMAD2	NM_001003652	1	11	8	-	45374846	45375058
270522154	chr18	45391315	45391480	45391340	45391455	SMAD2	NM_005901	3	11	6	-	45391430	45391504
270522154	chr18	45391315	45391480	45391340	45391455	SMAD2	NM_001135937	2	10	5	-	45391430	45391504
270522154	chr18	45391315	45391480	45391340	45391455	SMAD2	NM_001003652	1	11	6	-	45391430	45391504
272555064	chr18	45395520	45395646	45395547	45395620	SMAD2	NM_005901	3	11	4	-	45395614	45395807
272555064	chr18	45395520	45395646	45395547	45395620	SMAD2	NM_001135937	2	10	3	-	45395614	45395807
272555064	chr18	45395520	45395646	45395547	45395620	SMAD2	NM_001003652	1	11	4	-	45395614	45395807
269485586	chr18	45422862	45423030	45422890	45423007	SMAD2	NM_005901	3	11	2	-	45422892	45423180
269485586	chr18	45422862	45423030	45422890	45423007	SMAD2	NM_001135937	2	10	2	-	45422892	45423180
269485586	chr18	45422862	45423030	45422890	45423007	SMAD2	NM_001003652	1	11	2	-	45422892	45423180
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_001204137	2	17	17	-	47797412	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_001204140	5	16	16	-	47797412	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_001204138	3	17	17	-	47797412	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_015846	13	17	16	-	47797839	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_015844	11	16	15	-	47797839	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_015847	14	16	15	-	47797839	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_001204151	9	13	13	-	47797839	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_002384	10	15	14	-	47797839	47797910
312373278	chr18	47797765	47797937	47797785	47797914	MBD1	NM_001204139	4	17	16	-	47797839	47797910
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_015846	13	17	13	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204137	2	17	14	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204136	1	16	13	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_015844	11	16	12	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_015847	14	16	12	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204141	6	15	12	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204140	5	16	13	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204139	4	17	13	-	47799704	47799841
312405699	chr18	47799723	47799877	47799745	47799856	MBD1	NM_001204138	3	17	14	-	47799704	47799841
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_015846	13	17	11	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204137	2	17	12	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204136	1	16	11	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_015845	12	14	10	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_015847	14	16	10	-	47800556	47800723

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204151	9	13	9	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204142	7	14	11	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204139	4	17	11	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204138	3	17	12	-	47800556	47800723
312166453	chr18	47800517	47800669	47800537	47800651	MBD1	NM_001204141	6	15	10	-	47800556	47800720
312408211	chr18	47801697	47801866	47801716	47801845	MBD1	NM_001204137	2	17	9	-	47801740	47801814
312408211	chr18	47801697	47801866	47801716	47801845	MBD1	NM_001204140	5	16	9	-	47801740	47801814
312408211	chr18	47801697	47801866	47801716	47801845	MBD1	NM_001204138	3	17	9	-	47801740	47801814
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_015846	13	17	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204137	2	17	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204136	1	16	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_015845	12	14	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_015844	11	16	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204151	9	13	6	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_002384	10	15	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204142	7	14	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204140	5	16	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204139	4	17	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204138	3	17	7	-	47802205	47802351
312370322	chr18	47802232	47802381	47802253	47802361	MBD1	NM_001204143	8	14	7	-	47802205	47802351
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_015846	13	17	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204137	2	17	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204136	1	16	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_015845	12	14	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_015844	11	16	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_015847	14	16	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204151	9	13	3	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_002384	10	15	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204142	7	14	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204141	6	15	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204140	5	16	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204139	4	17	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204138	3	17	4	-	47803202	47803368
312242703	chr18	47803266	47803411	47803287	47803389	MBD1	NM_001204143	8	14	4	-	47803202	47803368
242737916	chr18	48573459	48573618	48573480	48573590	SMAD4	NM_005359	1	12	2	+	48573290	48573665
263539942	chr18	48575531	48575704	48575557	48575677	SMAD4	NM_005359	1	12	4	+	48575665	48575694
326754327	chr18	48584461	48584598	48584491	48584574	SMAD4	NM_005359	1	12	6	+	48584495	48584614
239529723	chr18	48586224	48586348	48586248	48586321	SMAD4	NM_005359	1	12	8	+	48586236	48586286
239063567	chr18	48593381	48593506	48593405	48593479	SMAD4	NM_005359	1	12	10	+	48593389	48593557
261631832	chr18	48604587	48604760	48604608	48604732	SMAD4	NM_005359	1	12	12	+	48604626	48611411
287183000	chr18	50278393	50278565	50278419	50278540	DCC	NM_005215	1	29	2	+	50278424	50278744

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
286131790	chr18	50432461	50432629	50432483	50432608	DCC	NM_005215	1	29	3	+	50432414	50432698
288215387	chr18	50451501	50451665	50451527	50451638	DCC	NM_005215	1	29	5	+	50451604	50451740
286188511	chr18	50592293	50592453	50592315	50592431	DCC	NM_005215	1	29	7	+	50592416	50592536
286778448	chr18	50705241	50705415	50705265	50705392	DCC	NM_005215	1	29	9	+	50705332	50705486
288785574	chr18	50734023	50734188	50734050	50734164	DCC	NM_005215	1	29	11	+	50734049	50734187
286831282	chr18	50831982	50832115	50832010	50832090	DCC	NM_005215	1	29	13	+	50831948	50832089
286509190	chr18	50866123	50866292	50866145	50866264	DCC	NM_005215	1	29	15	+	50866083	50866277
286283103	chr18	50917918	50918090	50917944	50918070	DCC	NM_005215	1	29	17	+	50918025	50918257
287554957	chr18	50923679	50923844	50923708	50923819	DCC	NM_005215	1	29	18	+	50923678	50923816
287057746	chr18	50936954	50937128	50936978	50937104	DCC	NM_005215	1	29	20	+	50936822	50937016
287797189	chr18	50976902	50977056	50976923	50977033	DCC	NM_005215	1	29	23	+	50976870	50977032
285480821	chr18	50994233	50994405	50994256	50994380	DCC	NM_005215	1	29	25	+	50994264	50994380
286790941	chr18	51025542	51025708	51025566	51025688	DCC	NM_005215	1	29	27	+	51025668	51025880
287741458	chr18	51053007	51053170	51053029	51053142	DCC	NM_005215	1	29	28	+	51052987	51053129
232263267	chr18	56338870	56339021	56338887	56339004	MALT1	NM_173844	2	16	1	+	56338618	56339084
232263267	chr18	56338870	56339021	56338887	56339004	MALT1	NM_006785	1	17	1	+	56338618	56339084
231394623	chr18	56367624	56367780	56367649	56367752	MALT1	NM_173844	2	16	4	+	56367673	56367823
231394623	chr18	56367624	56367780	56367649	56367752	MALT1	NM_006785	1	17	4	+	56367673	56367823
233264683	chr18	56376688	56376816	56376713	56376789	MALT1	NM_173844	2	16	5	+	56376610	56376788
233264683	chr18	56376688	56376816	56376713	56376789	MALT1	NM_006785	1	17	5	+	56376610	56376788
234679711	chr18	56381208	56381356	56381236	56381330	MALT1	NM_173844	2	16	7	+	56381315	56381341
234679711	chr18	56381208	56381356	56381236	56381330	MALT1	NM_006785	1	17	8	+	56381315	56381341
232174467	chr18	56390339	56390464	56390362	56390438	MALT1	NM_173844	2	16	9	+	56390280	56390483
232174467	chr18	56390339	56390464	56390362	56390438	MALT1	NM_006785	1	17	10	+	56390280	56390483
233685948	chr18	56401459	56401587	56401492	56401561	MALT1	NM_173844	2	16	11	+	56401539	56401613
233685948	chr18	56401459	56401587	56401492	56401561	MALT1	NM_006785	1	17	12	+	56401539	56401613
233150560	chr18	56409128	56409265	56409156	56409241	MALT1	NM_173844	2	16	13	+	56409097	56409246
233150560	chr18	56409128	56409265	56409156	56409241	MALT1	NM_006785	1	17	14	+	56409097	56409246
232729313	chr18	56412921	56413094	56412945	56413065	MALT1	NM_173844	2	16	15	+	56412898	56413023
232729313	chr18	56412921	56413094	56412945	56413065	MALT1	NM_006785	1	17	16	+	56412898	56413023
232752186	chr18	56414882	56415020	56414907	56414991	MALT1	NM_173844	2	16	16	+	56414637	56417370
232752186	chr18	56414882	56415020	56414907	56414991	MALT1	NM_006785	1	17	17	+	56414637	56417370
271406385	chr18	59157894	59158060	59157917	59158034	CDH20	NM_031891	1	11	1	+	59157775	59158032
271283454	chr18	59167551	59167719	59167574	59167696	CDH20	NM_031891	1	11	3	+	59167616	59167735
270170327	chr18	59174564	59174732	59174588	59174705	CDH20	NM_031891	1	11	5	+	59174606	59174793
271429300	chr18	59195341	59195502	59195363	59195476	CDH20	NM_031891	1	11	6	+	59195200	59195453
269616440	chr18	59206272	59206414	59206296	59206394	CDH20	NM_031891	1	11	8	+	59206257	59206378
272629616	chr18	59221389	59221562	59221414	59221544	CDH20	NM_031891	1	11	11	+	59221423	59222365
271227257	chr18	59221841	59221973	59221862	59221952	CDH20	NM_031891	1	11	11	+	59221423	59222365
222778166	chr18	60985295	60985463	60985316	60985440	BCL2	NM_000633	1	3	2	-	60985315	60986185
222778166	chr18	60985295	60985463	60985316	60985440	BCL2	NM_000657	2	2	2	-	60985187	60986185

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
224515944	chr18	60985712	60985873	60985729	60985847	BCL2	NM_000633	1	3	2	-	60985315	60986185
224515944	chr18	60985712	60985873	60985729	60985847	BCL2	NM_000657	2	2	2	-	60985187	60986185
238829899	chr19	1218360	1218512	1218380	1218484	STK11	NM_000455	1	10	2	+	1218416	1218499
237773994	chr19	1220277	1220420	1220296	1220402	STK11	NM_000455	1	10	4	+	1220372	1220504
238653132	chr19	1221189	1221342	1221210	1221321	STK11	NM_000455	1	10	6	+	1221212	1221339
264064519	chr19	1222912	1223086	1222931	1223065	STK11	NM_000455	1	10	8	+	1222984	1223171
240471636	chr19	1226469	1226627	1226488	1226610	STK11	NM_000455	1	10	9	+	1226453	1226662
239987086	chr19	1612135	1612305	1612153	1612285	TCF3	NM_001136139	1	19	17	-	1612206	1612432
240580071	chr19	1615285	1615427	1615303	1615410	TCF3	NM_003200	2	19	18	-	1615284	1615519
239427009	chr19	1619096	1619270	1619117	1619253	TCF3	NM_001136139	1	19	15	-	1619110	1619233
239427009	chr19	1619096	1619270	1619117	1619253	TCF3	NM_003200	2	19	16	-	1619110	1619233
262197189	chr19	1619709	1619874	1619729	1619856	TCF3	NM_001136139	1	19	13	-	1619779	1619852
262197189	chr19	1619709	1619874	1619729	1619856	TCF3	NM_003200	2	19	14	-	1619779	1619852
262586114	chr19	1621793	1621959	1621811	1621939	TCF3	NM_001136139	1	19	10	-	1621837	1621969
262586114	chr19	1621793	1621959	1621811	1621939	TCF3	NM_003200	2	19	11	-	1621837	1621969
242044298	chr19	1622188	1622349	1622206	1622331	TCF3	NM_001136139	1	19	8	-	1622312	1622414
242044298	chr19	1622188	1622349	1622206	1622331	TCF3	NM_003200	2	19	9	-	1622312	1622414
242044298	chr19	1622188	1622349	1622206	1622331	TCF3	NM_001136139	1	19	9	-	1622053	1622222
242044298	chr19	1622188	1622349	1622206	1622331	TCF3	NM_003200	2	19	10	-	1622053	1622222
240443752	chr19	1625624	1625795	1625645	1625775	TCF3	NM_001136139	1	19	6	-	1625575	1625707
240443752	chr19	1625624	1625795	1625645	1625775	TCF3	NM_003200	2	19	7	-	1625575	1625707
264382579	chr19	1646289	1646414	1646312	1646395	TCF3	NM_001136139	1	19	2	-	1646354	1646426
264382579	chr19	1646289	1646414	1646312	1646395	TCF3	NM_003200	2	19	3	-	1646354	1646426
274025845	chr19	3110065	3110228	3110084	3110208	GNA11	NM_002067	1	7	2	+	3110147	3110331
273019483	chr19	3113385	3113554	3113407	3113536	GNA11	NM_002067	1	7	3	+	3113328	3113482
272887045	chr19	3118946	3119115	3118964	3119098	GNA11	NM_002067	1	7	5	+	3118922	3119051
274413113	chr19	3121052	3121211	3121076	3121193	GNA11	NM_002067	1	7	7	+	3120987	3121454
299172709	chr19	3525957	3526087	3525975	3526070	FZR1	NM_016263	3	14	3	+	3525866	3525991
299172709	chr19	3525957	3526087	3525975	3526070	FZR1	NM_001136197	1	11	2	+	3525866	3525991
299172709	chr19	3525957	3526087	3525975	3526070	FZR1	NM_001136198	2	13	2	+	3525866	3525991
298955681	chr19	3527573	3527746	3527593	3527725	FZR1	NM_016263	3	14	7	+	3527629	3527812
298955681	chr19	3527573	3527746	3527593	3527725	FZR1	NM_001136198	2	13	6	+	3527629	3527812
299086528	chr19	3531827	3531980	3531844	3531961	FZR1	NM_016263	3	14	10	+	3531909	3532093
299086528	chr19	3531827	3531980	3531844	3531961	FZR1	NM_001136197	1	11	7	+	3531909	3532093
299086528	chr19	3531827	3531980	3531844	3531961	FZR1	NM_001136198	2	13	9	+	3531909	3532093
299042105	chr19	3532422	3532581	3532443	3532561	FZR1	NM_016263	3	14	11	+	3532415	3532648
299042105	chr19	3532422	3532581	3532443	3532561	FZR1	NM_001136197	1	11	8	+	3532415	3532648
299042105	chr19	3532422	3532581	3532443	3532561	FZR1	NM_001136198	2	13	10	+	3532415	3532648
299087524	chr19	3534759	3534916	3534777	3534896	FZR1	NM_016263	3	14	14	+	3534793	3536755
299087524	chr19	3534759	3534916	3534777	3534896	FZR1	NM_001136197	1	11	11	+	3534793	3536755
299087524	chr19	3534759	3534916	3534777	3534896	FZR1	NM_001136198	2	13	13	+	3534793	3536755

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270455843	chr19	4097257	4097382	4097280	4097365	MAP2K2	NM_030662	1	11	8	-	4097277	4097341
271294520	chr19	4101040	4101189	4101059	4101172	MAP2K2	NM_030662	1	11	6	-	4101017	4101141
269760417	chr19	4110443	4110596	4110465	4110576	MAP2K2	NM_030662	1	11	3	-	4110507	4110653
270004075	chr19	4117515	4117679	4117535	4117657	MAP2K2	NM_030662	1	11	2	-	4117417	4117627
294377806	chr19	10599814	10599973	10599836	10599953	KEAP1	NM_012289	1	6	5	-	10599868	10600044
294377806	chr19	10599814	10599973	10599836	10599953	KEAP1	NM_203500	2	6	5	-	10599868	10600044
293889780	chr19	10600406	10600564	10600425	10600540	KEAP1	NM_012289	1	6	4	-	10600324	10600529
293889780	chr19	10600406	10600564	10600425	10600540	KEAP1	NM_203500	2	6	4	-	10600324	10600529
294565410	chr19	10602538	10602697	10602558	10602680	KEAP1	NM_012289	1	6	3	-	10602253	10602938
294565410	chr19	10602538	10602697	10602558	10602680	KEAP1	NM_203500	2	6	3	-	10602253	10602938
294865610	chr19	10610024	10610158	10610045	10610139	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294865610	chr19	10610024	10610158	10610045	10610139	KEAP1	NM_203500	2	6	2	-	10610071	10610756
294856943	chr19	10610496	10610653	10610515	10610634	KEAP1	NM_012289	1	6	2	-	10610071	10610756
294856943	chr19	10610496	10610653	10610515	10610634	KEAP1	NM_203500	2	6	2	-	10610071	10610756
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128845	2	33	1	+	11094828	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128847	4	33	1	+	11094828	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128846	3	33	1	+	11094828	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128848	5	33	1	+	11094828	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128844	1	36	3	+	11094797	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_003072	7	35	2	+	11094797	11095049
262130001	chr19	11095014	11095165	11095034	11095144	SMARCA4	NM_001128849	6	36	2	+	11094797	11095049
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128844	1	36	5	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_003072	7	35	4	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128845	2	33	3	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128849	6	36	4	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128847	4	33	3	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128846	3	33	3	+	11096865	11097269
242521245	chr19	11096915	11097086	11096932	11097067	SMARCA4	NM_001128848	5	33	3	+	11096865	11097269
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128844	1	36	7	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_003072	7	35	6	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128845	2	33	5	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128849	6	36	6	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128847	4	33	5	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128846	3	33	5	+	11098342	11098600
240432777	chr19	11098321	11098473	11098338	11098456	SMARCA4	NM_001128848	5	33	5	+	11098342	11098600
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128844	1	36	8	+	11099993	11100119
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_003072	7	35	7	+	11099993	11100119
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128845	2	33	6	+	11099993	11100119
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128849	6	36	7	+	11099993	11100119
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128847	4	33	6	+	11099993	11100119
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128846	3	33	6	+	11099993	11100119

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
263363234	chr19	11099871	11100045	11099893	11100023	SMARCA4	NM_001128848	5	33	6	+	11099993	11100119
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128844	1	36	10	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_003072	7	35	9	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128845	2	33	8	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128849	6	36	9	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128847	4	33	8	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128846	3	33	8	+	11105504	11105677
240066636	chr19	11105467	11105591	11105488	11105568	SMARCA4	NM_001128848	5	33	8	+	11105504	11105677
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128844	1	36	12	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_003072	7	35	11	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128845	2	33	10	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128849	6	36	11	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128847	4	33	10	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128846	3	33	10	+	11107170	11107220
241640254	chr19	11107142	11107266	11107163	11107241	SMARCA4	NM_001128848	5	33	10	+	11107170	11107220
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128844	1	36	15	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_003072	7	35	14	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128845	2	33	13	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128849	6	36	14	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128847	4	33	13	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128846	3	33	13	+	11118578	11118699
239824520	chr19	11118545	11118718	11118566	11118699	SMARCA4	NM_001128848	5	33	13	+	11118578	11118699
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128844	1	36	17	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_003072	7	35	16	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128845	2	33	15	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128849	6	36	16	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128847	4	33	15	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128846	3	33	15	+	11123625	11123788
241747361	chr19	11123638	11123805	11123657	11123788	SMARCA4	NM_001128848	5	33	15	+	11123625	11123788
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128844	1	36	20	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_003072	7	35	19	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128845	2	33	18	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128849	6	36	19	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128847	4	33	18	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128846	3	33	18	+	11132401	11132643
261096127	chr19	11132472	11132617	11132492	11132595	SMARCA4	NM_001128848	5	33	18	+	11132401	11132643
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128844	1	36	22	+	11135007	11135114
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_003072	7	35	21	+	11135007	11135114
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128845	2	33	20	+	11135007	11135114
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128849	6	36	21	+	11135007	11135114
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128847	4	33	20	+	11135007	11135114

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128846	3	33	20	+	11135007	11135114
241395251	chr19	11135047	11135214	11135066	11135192	SMARCA4	NM_001128848	5	33	20	+	11135007	11135114
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128844	1	36	25	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_003072	7	35	24	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128845	2	33	23	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128849	6	36	24	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128847	4	33	23	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128846	3	33	23	+	11138460	11138626
264351153	chr19	11138476	11138647	11138500	11138626	SMARCA4	NM_001128848	5	33	23	+	11138460	11138626
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128844	1	36	27	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_003072	7	35	26	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128845	2	33	25	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128849	6	36	26	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128847	4	33	25	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128846	3	33	25	+	11143966	11144193
239995827	chr19	11144068	11144242	11144089	11144224	SMARCA4	NM_001128848	5	33	25	+	11143966	11144193
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128844	1	36	31	+	11151983	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_003072	7	35	30	+	11151983	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128849	6	36	31	+	11151983	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128847	4	33	28	+	11151983	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128848	5	33	28	+	11151983	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128845	2	33	28	+	11151974	11152236
238841446	chr19	11151943	11152067	11151961	11152050	SMARCA4	NM_001128846	3	33	28	+	11151974	11152236
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128844	1	36	33	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_003072	7	35	32	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128845	2	33	30	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128849	6	36	33	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128847	4	33	30	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128846	3	33	30	+	11169464	11169565
242329242	chr19	11169426	11169550	11169447	11169529	SMARCA4	NM_001128848	5	33	30	+	11169464	11169565
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128844	1	36	35	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_003072	7	35	34	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128845	2	33	32	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128849	6	36	35	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128847	4	33	32	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128846	3	33	32	+	11170721	11170863
237936877	chr19	11170681	11170850	11170703	11170828	SMARCA4	NM_001128848	5	33	32	+	11170721	11170863
234650497	chr19	17937556	17937718	17937578	17937697	JAK3	NM_000215	1	24	24	-	17935593	17937719
233079040	chr19	17941322	17941468	17941343	17941446	JAK3	NM_000215	1	24	22	-	17941312	17941429
232256745	chr19	17942488	17942629	17942512	17942608	JAK3	NM_000215	1	24	20	-	17942483	17942607
231803662	chr19	17943621	17943781	17943644	17943761	JAK3	NM_000215	1	24	18	-	17943599	17943738

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
233513228	chr19	17945690	17945845	17945712	17945824	JAK3	NM_000215	1	24	16	-	17945661	17945812
234212609	chr19	17947878	17948050	17947900	17948028	JAK3	NM_000215	1	24	13	-	17947938	17948022
234725896	chr19	17950349	17950511	17950367	17950492	JAK3	NM_000215	1	24	10	-	17950286	17950472
232173602	chr19	17952352	17952483	17952370	17952461	JAK3	NM_000215	1	24	7	-	17952449	17952571
233108744	chr19	17953256	17953422	17953277	17953402	JAK3	NM_000215	1	24	6	-	17953125	17953419
234204966	chr19	17954119	17954287	17954139	17954265	JAK3	NM_000215	1	24	4	-	17954189	17954300
233378654	chr19	17955021	17955195	17955042	17955176	JAK3	NM_000215	1	24	2	-	17955043	17955239
294964045	chr19	18266772	18266926	18266791	18266905	PIK3R2	NM_005027	1	16	2	+	18266267	18267011
294127269	chr19	18271686	18271845	18271707	18271822	PIK3R2	NM_005027	1	16	4	+	18271729	18271779
294028836	chr19	18272977	18273131	18272999	18273108	PIK3R2	NM_005027	1	16	8	+	18273012	18273120
294700374	chr19	18273845	18273999	18273865	18273982	PIK3R2	NM_005027	1	16	10	+	18273777	18273957
294113796	chr19	18276999	18277165	18277027	18277144	PIK3R2	NM_005027	1	16	12	+	18276970	18277112
294997101	chr19	18279591	18279764	18279612	18279742	PIK3R2	NM_005027	1	16	15	+	18279536	18279706
225474364	chr19	18853758	18853928	18853778	18853906	CRTC1	NM_015321	2	14	2	+	18853720	18853836
225474364	chr19	18853758	18853928	18853778	18853906	CRTC1	NM_001098482	1	15	2	+	18853720	18853836
226099940	chr19	18856740	18856903	18856757	18856883	CRTC1	NM_015321	2	14	3	+	18856633	18856770
226099940	chr19	18856740	18856903	18856757	18856883	CRTC1	NM_001098482	1	15	4	+	18856633	18856770
225777077	chr19	18864298	18864456	18864319	18864433	CRTC1	NM_015321	2	14	6	+	18864310	18864395
225777077	chr19	18864298	18864456	18864319	18864433	CRTC1	NM_001098482	1	15	7	+	18864310	18864395
226131374	chr19	18876190	18876347	18876213	18876328	CRTC1	NM_015321	2	14	9	+	18876214	18876338
226131374	chr19	18876190	18876347	18876213	18876328	CRTC1	NM_001098482	1	15	10	+	18876214	18876338
226135820	chr19	18882163	18882314	18882180	18882296	CRTC1	NM_015321	2	14	11	+	18882252	18882356
226135820	chr19	18882163	18882314	18882180	18882296	CRTC1	NM_001098482	1	15	12	+	18882252	18882356
226272414	chr19	18886507	18886640	18886528	18886621	CRTC1	NM_015321	2	14	13	+	18886451	18886631
226272414	chr19	18886507	18886640	18886528	18886621	CRTC1	NM_001098482	1	15	14	+	18886451	18886631
254000374	chr19	18888126	18888290	18888145	18888273	CRTC1	NM_015321	2	14	14	+	18887981	18893143
254000374	chr19	18888126	18888290	18888145	18888273	CRTC1	NM_001098482	1	15	15	+	18887981	18893143
270690834	chr19	30303863	30304014	30303888	30303993	CCNE1	NM_001238	1	12	4	+	30303876	30303944
271362473	chr19	30308374	30308519	30308398	30308491	CCNE1	NM_001238	1	12	6	+	30308313	30308448
269571036	chr19	30312819	30312957	30312840	30312934	CCNE1	NM_001238	1	12	9	+	30312903	30313037
271446284	chr19	30313378	30313551	30313401	30313526	CCNE1	NM_001238	1	12	11	+	30313353	30313510
226691978	chr19	33792253	33792386	33792271	33792367	CEBPA	NM_004364	1	1	1	-	33790840	33793430
225391089	chr19	33792771	33792897	33792790	33792880	CEBPA	NM_004364	1	1	1	-	33790840	33793430
223015469	chr19	40740866	40741018	40740888	40740994	AKT2	NM_001626	3	14	13	-	40740952	40741054
223015469	chr19	40740866	40741018	40740888	40740994	AKT2	NM_001243028	2	13	12	-	40740952	40741054
223015469	chr19	40740866	40741018	40740888	40740994	AKT2	NM_001243027	1	14	13	-	40740952	40741054
223746080	chr19	40741684	40741832	40741703	40741811	AKT2	NM_001626	3	14	11	-	40741797	40742011
223746080	chr19	40741684	40741832	40741703	40741811	AKT2	NM_001243028	2	13	10	-	40741797	40742011
223746080	chr19	40741684	40741832	40741703	40741811	AKT2	NM_001243027	1	14	11	-	40741797	40742011
222668951	chr19	40742247	40742404	40742270	40742384	AKT2	NM_001626	3	14	10	-	40742164	40742292
222668951	chr19	40742247	40742404	40742270	40742384	AKT2	NM_001243028	2	13	9	-	40742164	40742292

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
222668951	chr19	40742247	40742404	40742270	40742384	AKT2	NM_001243027	1	14	10	-	40742164	40742292
222840891	chr19	40745869	40746039	40745894	40746021	AKT2	NM_001626	3	14	7	-	40745952	40746017
222840891	chr19	40745869	40746039	40745894	40746021	AKT2	NM_001243028	2	13	6	-	40745952	40746017
222840891	chr19	40745869	40746039	40745894	40746021	AKT2	NM_001243027	1	14	7	-	40745952	40746017
223149212	chr19	40748459	40748618	40748477	40748600	AKT2	NM_001626	3	14	5	-	40748441	40748594
223149212	chr19	40748459	40748618	40748477	40748600	AKT2	NM_001243028	2	13	4	-	40748441	40748594
223149212	chr19	40748459	40748618	40748477	40748600	AKT2	NM_001243027	1	14	5	-	40748441	40748594
222417293	chr19	40771085	40771213	40771106	40771194	AKT2	NM_001626	3	14	2	-	40771129	40771258
222417293	chr19	40771085	40771213	40771106	40771194	AKT2	NM_001243027	1	14	2	-	40771166	40771258
281445291	chr19	41726663	41726821	41726683	41726800	AXL	NM_021913	2	20	2	+	41726541	41726763
281445291	chr19	41726663	41726821	41726683	41726800	AXL	NM_001699	1	19	2	+	41726541	41726763
282095462	chr19	41727831	41727994	41727851	41727973	AXL	NM_021913	2	20	4	+	41727785	41727961
282095462	chr19	41727831	41727994	41727851	41727973	AXL	NM_001699	1	19	4	+	41727785	41727961
281299447	chr19	41743910	41744080	41743928	41744060	AXL	NM_021913	2	20	7	+	41743849	41744059
281299447	chr19	41743910	41744080	41743928	41744060	AXL	NM_001699	1	19	7	+	41743849	41744059
281834804	chr19	41745080	41745241	41745102	41745220	AXL	NM_021913	2	20	9	+	41745069	41745219
281834804	chr19	41745080	41745241	41745102	41745220	AXL	NM_001699	1	19	9	+	41745069	41745219
281573775	chr19	41749434	41749558	41749455	41749536	AXL	NM_021913	2	20	12	+	41749521	41749612
281573775	chr19	41749434	41749558	41749455	41749536	AXL	NM_001699	1	19	11	+	41749521	41749612
283892392	chr19	41758224	41758383	41758245	41758361	AXL	NM_021913	2	20	15	+	41758256	41758348
283892392	chr19	41758224	41758383	41758245	41758361	AXL	NM_001699	1	19	14	+	41758256	41758348
283313013	chr19	41762331	41762482	41762354	41762458	AXL	NM_021913	2	20	18	+	41762357	41762516
283313013	chr19	41762331	41762482	41762354	41762458	AXL	NM_001699	1	19	17	+	41762357	41762516
284488710	chr19	41765437	41765607	41765457	41765586	AXL	NM_021913	2	20	20	+	41765458	41767671
284488710	chr19	41765437	41765607	41765457	41765586	AXL	NM_001699	1	19	19	+	41765458	41767671
225841991	chr19	42383010	42383169	42383031	42383148	CD79A	NM_021601	2	5	2	+	42383060	42383245
225841991	chr19	42383010	42383169	42383031	42383148	CD79A	NM_001783	1	5	2	+	42383060	42383359
225531462	chr19	42384665	42384825	42384689	42384805	CD79A	NM_001783	1	5	4	+	42384737	42384805
225531462	chr19	42384665	42384825	42384689	42384805	CD79A	NM_021601	2	5	4	+	42384737	42384805
226647836	chr19	42790903	42791077	42790922	42791056	CIC	NM_015125	1	20	2	+	42790923	42791072
225727055	chr19	42791362	42791536	42791385	42791517	CIC	NM_015125	1	20	3	+	42791158	42791392
225727055	chr19	42791362	42791536	42791385	42791517	CIC	NM_015125	1	20	4	+	42791472	42791601
227048776	chr19	42791775	42791948	42791796	42791929	CIC	NM_015125	1	20	5	+	42791697	42791879
226131433	chr19	42793011	42793184	42793031	42793165	CIC	NM_015125	1	20	7	+	42793040	42793242
225618062	chr19	42793342	42793511	42793361	42793488	CIC	NM_015125	1	20	8	+	42793333	42793558
225866345	chr19	42794469	42794599	42794488	42794580	CIC	NM_015125	1	20	10	+	42794385	42795618
225867560	chr19	42794814	42794986	42794832	42794967	CIC	NM_015125	1	20	10	+	42794385	42795618
225876733	chr19	42795244	42795416	42795265	42795399	CIC	NM_015125	1	20	10	+	42794385	42795618
226528688	chr19	42795769	42795934	42795789	42795911	CIC	NM_015125	1	20	11	+	42795710	42795897
253710385	chr19	42796679	42796839	42796702	42796817	CIC	NM_015125	1	20	14	+	42796718	42797011
226103103	chr19	42797185	42797314	42797202	42797294	CIC	NM_015125	1	20	15	+	42797108	42797433

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227045837	chr19	42797844	42798002	42797861	42797983	CIC	NM_015125	1	20	16	+	42797744	42797988
226162760	chr19	42798297	42798452	42798319	42798430	CIC	NM_015125	1	20	18	+	42798325	42798456
253755754	chr19	42798946	42799098	42798964	42799081	CIC	NM_015125	1	20	20	+	42798976	42799949
223556325	chr19	45254563	45254697	45254583	45254676	BCL3	NM_005178	1	9	2	+	45254484	45254637
223262074	chr19	45260317	45260477	45260334	45260457	BCL3	NM_005178	1	9	4	+	45260274	45260478
222171016	chr19	45260942	45261115	45260965	45261095	BCL3	NM_005178	1	9	6	+	45260903	45260980
222929181	chr19	45261952	45262121	45261972	45262100	BCL3	NM_005178	1	9	8	+	45261981	45262098
290448455	chr19	45762303	45762468	45762320	45762450	MARK4	NM_031417	2	18	2	+	45762247	45762447
290448455	chr19	45762303	45762468	45762320	45762450	MARK4	NM_001199867	1	17	2	+	45762247	45762447
289332169	chr19	45767964	45768123	45767986	45768100	MARK4	NM_031417	2	18	6	+	45768098	45768168
289332169	chr19	45767964	45768123	45767986	45768100	MARK4	NM_001199867	1	17	6	+	45768098	45768168
289332169	chr19	45767964	45768123	45767986	45768100	MARK4	NM_031417	2	18	5	+	45767942	45768007
289332169	chr19	45767964	45768123	45767986	45768100	MARK4	NM_001199867	1	17	5	+	45767942	45768007
290668320	chr19	45769493	45769656	45769520	45769633	MARK4	NM_031417	2	18	7	+	45769483	45769539
290668320	chr19	45769493	45769656	45769520	45769633	MARK4	NM_001199867	1	17	7	+	45769483	45769539
292108769	chr19	45781148	45781304	45781168	45781281	MARK4	NM_031417	2	18	9	+	45781181	45781300
292108769	chr19	45781148	45781304	45781168	45781281	MARK4	NM_001199867	1	17	9	+	45781181	45781300
293657085	chr19	45783656	45783829	45783681	45783807	MARK4	NM_031417	2	18	11	+	45783632	45783741
293657085	chr19	45783656	45783829	45783681	45783807	MARK4	NM_001199867	1	17	11	+	45783632	45783741
290997370	chr19	45797495	45797661	45797518	45797639	MARK4	NM_031417	2	18	14	+	45797607	45797710
290997370	chr19	45797495	45797661	45797518	45797639	MARK4	NM_001199867	1	17	14	+	45797607	45797710
292312757	chr19	45801118	45801287	45801136	45801266	MARK4	NM_031417	2	18	15	+	45800934	45801212
292312757	chr19	45801118	45801287	45801136	45801266	MARK4	NM_001199867	1	17	15	+	45800934	45801212
292526173	chr19	45805538	45805662	45805561	45805641	MARK4	NM_031417	2	18	18	+	45805632	45808541
292526173	chr19	45805538	45805662	45805561	45805641	MARK4	NM_001199867	1	17	17	+	45805632	45808541
292532939	chr19	45805938	45806108	45805956	45806087	MARK4	NM_031417	2	18	18	+	45805632	45808541
292532939	chr19	45805938	45806108	45805956	45806087	MARK4	NM_001199867	1	17	17	+	45805632	45808541
230790587	chr19	45855704	45855865	45855725	45855839	ERCC2	NM_000400	1	23	21	-	45855764	45855907
232732580	chr19	45856429	45856582	45856450	45856559	ERCC2	NM_000400	1	23	18	-	45856500	45856592
229917685	chr19	45858871	45859014	45858893	45858992	ERCC2	NM_000400	1	23	16	-	45858923	45858986
230845062	chr19	45864698	45864859	45864719	45864839	ERCC2	NM_000400	1	23	12	-	45864782	45864900
230845062	chr19	45864698	45864859	45864719	45864839	ERCC2	NM_001130867	2	12	11	-	45864782	45864900
230441803	chr19	45867238	45867401	45867255	45867383	ERCC2	NM_000400	1	23	10	-	45867244	45867377
230441803	chr19	45867238	45867401	45867255	45867383	ERCC2	NM_001130867	2	12	9	-	45867244	45867377
230584347	chr19	45867689	45867836	45867707	45867818	ERCC2	NM_000400	1	23	8	-	45867682	45867805
230584347	chr19	45867689	45867836	45867707	45867818	ERCC2	NM_001130867	2	12	7	-	45867682	45867805
227689332	chr19	45871816	45871988	45871837	45871960	ERCC2	NM_000400	1	23	5	-	45871888	45872001
227689332	chr19	45871816	45871988	45871837	45871960	ERCC2	NM_001130867	2	12	4	-	45871888	45872001
231121598	chr19	45873284	45873449	45873304	45873428	ERCC2	NM_000400	1	23	2	-	45873391	45873490
231121598	chr19	45873284	45873449	45873304	45873428	ERCC2	NM_001130867	2	12	1	-	45873391	45873845
293863977	chr19	45916863	45917024	45916887	45917003	ERCC1	NM_202001	3	8	8	-	45916692	45917003

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
293863977	chr19	45916863	45917024	45916887	45917003	ERCC1	NM_001983	2	10	9	-	45916935	45917003
293863977	chr19	45916863	45917024	45916887	45917003	ERCC1	NM_001166049	1	9	8	-	45916935	45917003
293947636	chr19	45920026	45920194	45920045	45920166	ERCC1	NM_202001	3	8	5	-	45920079	45920155
293947636	chr19	45920026	45920194	45920045	45920166	ERCC1	NM_001983	2	10	6	-	45920079	45920155
293947636	chr19	45920026	45920194	45920045	45920166	ERCC1	NM_001166049	1	9	6	-	45920079	45920155
293821678	chr19	45923609	45923740	45923632	45923716	ERCC1	NM_202001	3	8	3	-	45923582	45923685
293821678	chr19	45923609	45923740	45923632	45923716	ERCC1	NM_001983	2	10	4	-	45923582	45923685
293821678	chr19	45923609	45923740	45923632	45923716	ERCC1	NM_001166049	1	9	4	-	45923582	45923685
294400710	chr19	45926507	45926652	45926527	45926632	ERCC1	NM_202001	3	8	1	-	45926528	45926820
294400710	chr19	45926507	45926652	45926527	45926632	ERCC1	NM_001983	2	10	2	-	45926528	45926639
294400710	chr19	45926507	45926652	45926527	45926632	ERCC1	NM_001166049	1	9	2	-	45926528	45926639
236800945	chr19	52714478	52714603	52714499	52714583	PPP2R1A	NR_033500	2	14	3	+	52714513	52714745
236800945	chr19	52714478	52714603	52714499	52714583	PPP2R1A	NM_014225	1	15	4	+	52714513	52714745
238709653	chr19	52716004	52716169	52716023	52716148	PPP2R1A	NR_033500	2	14	4	+	52715939	52716086
238709653	chr19	52716004	52716169	52716023	52716148	PPP2R1A	NM_014225	1	15	5	+	52715939	52716086
237761719	chr19	52719047	52719217	52719067	52719196	PPP2R1A	NR_033500	2	14	6	+	52719032	52719146
237761719	chr19	52719047	52719217	52719067	52719196	PPP2R1A	NM_014225	1	15	7	+	52719032	52719146
237339717	chr19	52722838	52723008	52722861	52722988	PPP2R1A	NR_033500	2	14	9	+	52722944	52723117
237339717	chr19	52722838	52723008	52722861	52722988	PPP2R1A	NM_014225	1	15	10	+	52722944	52723117
237785329	chr19	52724176	52724301	52724201	52724281	PPP2R1A	NR_033500	2	14	11	+	52724232	52724386
237785329	chr19	52724176	52724301	52724201	52724281	PPP2R1A	NM_014225	1	15	12	+	52724232	52724386
235211457	chr19	52728945	52729084	52728966	52729063	PPP2R1A	NR_033500	2	14	13	+	52728970	52729061
235211457	chr19	52728945	52729084	52728966	52729063	PPP2R1A	NM_014225	1	15	14	+	52728970	52729061
294146122	chr19	57743094	57743229	57743115	57743206	AURKC	NM_001015879	2	7	2	+	57743110	57743155
294146122	chr19	57743094	57743229	57743115	57743206	AURKC	NM_001015878	1	7	2	+	57743110	57743155
294146122	chr19	57743094	57743229	57743115	57743206	AURKC	NM_003160	3	7	2	+	57743110	57743155
294994210	chr19	57743955	57744098	57743976	57744076	AURKC	NM_001015879	2	7	4	+	57743910	57744048
294994210	chr19	57743955	57744098	57743976	57744076	AURKC	NM_001015878	1	7	4	+	57743910	57744048
294994210	chr19	57743955	57744098	57743976	57744076	AURKC	NM_003160	3	7	4	+	57743910	57744048
294855254	chr19	57746278	57746452	57746299	57746431	AURKC	NM_001015879	2	7	6	+	57746252	57746426
294855254	chr19	57746278	57746452	57746299	57746431	AURKC	NM_001015878	1	7	6	+	57746252	57746426
294855254	chr19	57746278	57746452	57746299	57746431	AURKC	NM_003160	3	7	6	+	57746252	57746426
271645780	chr20	30309520	30309666	30309539	30309638	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
269636126	chr20	30309939	30310066	30309966	30310043	BCL2L1	NM_001191	1	3	2	-	30309647	30310151
269636126	chr20	30309939	30310066	30309966	30310043	BCL2L1	NM_138578	2	3	2	-	30309458	30310151
223982445	chr20	31015903	31016077	31015925	31016052	ASXL1	NM_015338	2	12	4	+	31015931	31016051
222665635	chr20	31017691	31017860	31017710	31017842	ASXL1	NM_015338	2	12	7	+	31017704	31017856
222876091	chr20	31019229	31019398	31019252	31019378	ASXL1	NM_015338	2	12	8	+	31019124	31019287
225123165	chr20	31021040	31021179	31021061	31021157	ASXL1	NM_015338	2	12	11	+	31021087	31021720
225166839	chr20	31021438	31021588	31021461	31021562	ASXL1	NM_015338	2	12	11	+	31021087	31021720
223989334	chr20	31022232	31022394	31022259	31022377	ASXL1	NM_015338	2	12	12	+	31022235	31027122

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
225258408	chr20	31022704	31022851	31022727	31022829	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225249715	chr20	31023140	31023313	31023169	31023291	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225324192	chr20	31023608	31023773	31023633	31023752	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225312335	chr20	31024045	31024208	31024068	31024180	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225310638	chr20	31024499	31024668	31024521	31024645	ASXL1	NM_015338	2	12	12	+	31022235	31027122
225305180	chr20	31024961	31025131	31024982	31025108	ASXL1	NM_015338	2	12	12	+	31022235	31027122
263447769	chr20	36014488	36014662	36014509	36014641	SRC	NM_198291	2	14	5	+	36014478	36014577
263447769	chr20	36014488	36014662	36014509	36014641	SRC	NM_005417	1	14	5	+	36014478	36014577
239935048	chr20	36024601	36024773	36024620	36024754	SRC	NM_198291	2	14	8	+	36024565	36024714
239935048	chr20	36024601	36024773	36024620	36024754	SRC	NM_005417	1	14	8	+	36024565	36024714
240384360	chr20	36028621	36028781	36028642	36028756	SRC	NM_198291	2	14	10	+	36028518	36028697
240384360	chr20	36028621	36028781	36028642	36028756	SRC	NM_005417	1	14	10	+	36028518	36028697
238915636	chr20	36031125	36031295	36031145	36031273	SRC	NM_198291	2	14	13	+	36031152	36031283
238915636	chr20	36031125	36031295	36031145	36031273	SRC	NM_005417	1	14	13	+	36031152	36031283
234399762	chr20	39316393	39316546	39316415	39316529	MAFB	NM_005461	1	1	1	-	39314517	39317876
234398985	chr20	39316777	39316947	39316795	39316930	MAFB	NM_005461	1	1	1	-	39314517	39317876
232722614	chr20	39317202	39317334	39317224	39317317	MAFB	NM_005461	1	1	1	-	39314517	39317876
261686408	chr20	39689982	39690154	39690008	39690130	TOP1	NM_003286	1	21	3	+	39690034	39690130
239540037	chr20	39708687	39708824	39708709	39708802	TOP1	NM_003286	1	21	6	+	39708725	39708820
242184044	chr20	39721090	39721262	39721115	39721240	TOP1	NM_003286	1	21	9	+	39721112	39721227
264585728	chr20	39726890	39727021	39726918	39726995	TOP1	NM_003286	1	21	11	+	39726855	39726977
241262201	chr20	39729846	39730016	39729869	39729993	TOP1	NM_003286	1	21	13	+	39729849	39729993
242518778	chr20	39742673	39742826	39742693	39742798	TOP1	NM_003286	1	21	15	+	39742610	39742795
241955285	chr20	39746792	39746966	39746817	39746938	TOP1	NM_003286	1	21	18	+	39746809	39746936
240246146	chr20	39751785	39751959	39751806	39751937	TOP1	NM_003286	1	21	21	+	39751835	39753126
271824929	chr20	39788483	39788625	39788505	39788603	PLCG1	NM_002660	1	32	3	+	39788510	39788603
271824929	chr20	39788483	39788625	39788505	39788603	PLCG1	NM_182811	2	32	3	+	39788510	39788603
271564759	chr20	39791317	39791484	39791337	39791462	PLCG1	NM_002660	1	32	6	+	39791282	39791365
271564759	chr20	39791317	39791484	39791337	39791462	PLCG1	NM_182811	2	32	6	+	39791282	39791365
270153612	chr20	39792320	39792453	39792343	39792431	PLCG1	NM_002660	1	32	10	+	39792355	39792473
270153612	chr20	39792320	39792453	39792343	39792431	PLCG1	NM_182811	2	32	10	+	39792355	39792473
271321210	chr20	39792691	39792861	39792711	39792842	PLCG1	NM_002660	1	32	12	+	39792721	39792841
271321210	chr20	39792691	39792861	39792711	39792842	PLCG1	NM_182811	2	32	12	+	39792721	39792841
269694019	chr20	39793928	39794101	39793954	39794079	PLCG1	NM_002660	1	32	14	+	39793885	39794007
269694019	chr20	39793928	39794101	39793954	39794079	PLCG1	NM_182811	2	32	14	+	39793885	39794007
270252193	chr20	39794742	39794915	39794763	39794890	PLCG1	NM_002660	1	32	17	+	39794834	39795034
270252193	chr20	39794742	39794915	39794763	39794890	PLCG1	NM_182811	2	32	17	+	39794834	39795034
271224741	chr20	39795285	39795441	39795307	39795417	PLCG1	NM_002660	1	32	19	+	39795319	39795499
271224741	chr20	39795285	39795441	39795307	39795417	PLCG1	NM_182811	2	32	19	+	39795319	39795499
271200723	chr20	39797638	39797789	39797661	39797766	PLCG1	NM_002660	1	32	22	+	39797719	39797815
271200723	chr20	39797638	39797789	39797661	39797766	PLCG1	NM_182811	2	32	22	+	39797719	39797815

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
269477748	chr20	39798781	39798934	39798804	39798912	PLCG1	NM_002660	1	32	24	+	39798752	39798909
269477748	chr20	39798781	39798934	39798804	39798912	PLCG1	NM_182811	2	32	24	+	39798752	39798909
272232230	chr20	39801076	39801242	39801095	39801220	PLCG1	NM_002660	1	32	26	+	39801061	39801285
272232230	chr20	39801076	39801242	39801095	39801220	PLCG1	NM_182811	2	32	26	+	39801061	39801285
269984737	chr20	39802037	39802199	39802058	39802177	PLCG1	NM_002660	1	32	28	+	39802060	39802174
269984737	chr20	39802037	39802199	39802058	39802177	PLCG1	NM_182811	2	32	28	+	39802060	39802174
272686798	chr20	39802563	39802734	39802587	39802709	PLCG1	NM_002660	1	32	30	+	39802563	39802651
272686798	chr20	39802563	39802734	39802587	39802709	PLCG1	NM_182811	2	32	30	+	39802563	39802651
298168761	chr20	40709428	40709582	40709448	40709555	PTPRT	NM_007050	1	31	31	-	40701392	40709572
298168761	chr20	40709428	40709582	40709448	40709555	PTPRT	NM_133170	2	32	32	-	40701392	40709572
295540805	chr20	40713356	40713515	40713378	40713494	PTPRT	NM_007050	1	31	29	-	40713322	40713485
295540805	chr20	40713356	40713515	40713378	40713494	PTPRT	NM_133170	2	32	30	-	40713322	40713485
297053607	chr20	40730711	40730879	40730737	40730855	PTPRT	NM_007050	1	31	26	-	40730764	40730937
297053607	chr20	40730711	40730879	40730737	40730855	PTPRT	NM_133170	2	32	27	-	40730764	40730937
296934176	chr20	40735388	40735538	40735409	40735517	PTPRT	NM_007050	1	31	24	-	40735426	40735561
296934176	chr20	40735388	40735538	40735409	40735517	PTPRT	NM_133170	2	32	25	-	40735426	40735561
295534270	chr20	40743785	40743925	40743806	40743901	PTPRT	NM_007050	1	31	22	-	40743839	40743955
295534270	chr20	40743785	40743925	40743806	40743901	PTPRT	NM_133170	2	32	23	-	40743839	40743955
297151302	chr20	40757329	40757497	40757352	40757474	PTPRT	NM_007050	1	31	19	-	40757394	40757470
297151302	chr20	40757329	40757497	40757352	40757474	PTPRT	NM_133170	2	32	20	-	40757394	40757470
295755375	chr20	40827752	40827926	40827775	40827898	PTPRT	NM_007050	1	31	16	-	40827880	40828028
295755375	chr20	40827752	40827926	40827775	40827898	PTPRT	NM_133170	2	32	17	-	40827880	40828028
297709835	chr20	40877408	40877545	40877429	40877517	PTPRT	NM_007050	1	31	14	-	40877327	40877462
297709835	chr20	40877408	40877545	40877429	40877517	PTPRT	NM_133170	2	32	15	-	40877327	40877462
295669960	chr20	40944371	40944536	40944393	40944514	PTPRT	NM_007050	1	31	12	-	40944363	40944636
295669960	chr20	40944371	40944536	40944393	40944514	PTPRT	NM_133170	2	32	12	-	40944363	40944636
296979899	chr20	40980698	40980867	40980726	40980845	PTPRT	NM_007050	1	31	10	-	40980724	40980925
296979899	chr20	40980698	40980867	40980726	40980845	PTPRT	NM_133170	2	32	10	-	40980724	40980925
297203310	chr20	41100928	41101099	41100948	41101078	PTPRT	NM_007050	1	31	8	-	41100906	41101202
297203310	chr20	41100928	41101099	41100948	41101078	PTPRT	NM_133170	2	32	8	-	41100906	41101202
297699282	chr20	41306664	41306830	41306685	41306802	PTPRT	NM_007050	1	31	7	-	41306506	41306799
297699282	chr20	41306664	41306830	41306685	41306802	PTPRT	NM_133170	2	32	7	-	41306506	41306799
297837128	chr20	41408818	41408984	41408839	41408958	PTPRT	NM_007050	1	31	4	-	41408858	41408939
297837128	chr20	41408818	41408984	41408839	41408958	PTPRT	NM_133170	2	32	4	-	41408858	41408939
296522444	chr20	41419994	41420141	41420020	41420119	PTPRT	NM_007050	1	31	3	-	41419835	41420106
296522444	chr20	41419994	41420141	41420020	41420119	PTPRT	NM_133170	2	32	3	-	41419835	41420106
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_003600	1	9	9	-	54944445	54945396
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_198435	4	9	9	-	54944445	54945396
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_198436	5	10	10	-	54944445	54945396
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_198434	3	10	10	-	54944445	54945396
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_198433	2	11	11	-	54944445	54945396

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271235727	chr20	54945240	54945413	54945268	54945385	AURKA	NM_198437	6	9	9	-	54944445	54945396
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_003600	1	9	7	-	54948464	54948612
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_198435	4	9	7	-	54948464	54948612
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_198436	5	10	8	-	54948464	54948612
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_198434	3	10	8	-	54948464	54948612
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_198433	2	11	9	-	54948464	54948612
270904696	chr20	54948427	54948588	54948455	54948560	AURKA	NM_198437	6	9	7	-	54948464	54948612
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_003600	1	9	5	-	54958041	54958232
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_198435	4	9	5	-	54958041	54958232
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_198436	5	10	6	-	54958041	54958232
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_198434	3	10	6	-	54958041	54958232
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_198433	2	11	7	-	54958041	54958232
270078455	chr20	54957993	54958148	54958014	54958122	AURKA	NM_198437	6	9	5	-	54958041	54958232
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_003600	1	9	3	-	54961313	54961589
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_198435	4	9	3	-	54961313	54961589
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_198436	5	10	4	-	54961313	54961589
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_198434	3	10	4	-	54961313	54961589
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_198433	2	11	5	-	54961313	54961589
270798180	chr20	54961217	54961386	54961242	54961364	AURKA	NM_198437	6	9	3	-	54961313	54961589
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_003600	1	9	2	-	54963212	54963258
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_198435	4	9	2	-	54963212	54963258
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_198436	5	10	3	-	54963212	54963258
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_198434	3	10	3	-	54963212	54963258
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_198433	2	11	4	-	54963212	54963258
269799570	chr20	54963149	54963300	54963170	54963272	AURKA	NM_198437	6	9	2	-	54963212	54963258
228099466	chr20	57415511	57415673	57415531	57415655	GNAS	NM_016592	5	13	1	+	57414795	57415941
227530063	chr20	57428274	57428398	57428294	57428378	GNAS	NM_001077490	4	13	1	+	57428036	57430388
227530063	chr20	57428274	57428398	57428294	57428378	GNAS	NM_080425	6	13	1	+	57428036	57430388
229439280	chr20	57428719	57428875	57428737	57428854	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229439280	chr20	57428719	57428875	57428737	57428854	GNAS	NM_080425	6	13	1	+	57428036	57430388
229431636	chr20	57429171	57429321	57429191	57429304	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229431636	chr20	57429171	57429321	57429191	57429304	GNAS	NM_080425	6	13	1	+	57428036	57430388
229440665	chr20	57429884	57430033	57429903	57430016	GNAS	NM_001077490	4	13	1	+	57428036	57430388
229440665	chr20	57429884	57430033	57429903	57430016	GNAS	NM_080425	6	13	1	+	57428036	57430388
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_016592	5	13	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_001077488	2	13	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NR_003259	8	13	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_001077490	4	13	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_080426	7	12	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_080425	6	13	2	+	57470667	57470739
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_001077489	3	12	2	+	57470667	57470739

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
227519289	chr20	57470605	57470762	57470625	57470739	GNAS	NM_000516	1	13	2	+	57470667	57470739
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_016592	5	13	5	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_001077488	2	13	5	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NR_003259	8	13	5	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_001077490	4	13	5	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_080426	7	12	4	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_080425	6	13	5	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_001077489	3	12	4	+	57478727	57478846
227956808	chr20	57478696	57478835	57478717	57478813	GNAS	NM_000516	1	13	5	+	57478727	57478846
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_016592	5	13	8	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_001077488	2	13	8	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NR_003259	8	13	8	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_001077490	4	13	8	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_080426	7	12	7	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_080425	6	13	8	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_001077489	3	12	7	+	57484405	57484478
227369383	chr20	57484358	57484532	57484379	57484504	GNAS	NM_000516	1	13	8	+	57484405	57484478
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_016592	5	13	12	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_001077488	2	13	12	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NR_003259	8	13	12	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_001077490	4	13	12	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_080426	7	12	11	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_080425	6	13	12	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_001077489	3	12	11	+	57485389	57485456
227722141	chr20	57485307	57485481	57485330	57485457	GNAS	NM_000516	1	13	12	+	57485389	57485456
242440737	chr21	36164729	36164860	36164747	36164843	RUNX1	NM_001754	3	9	9	-	36160098	36164907
242440737	chr21	36164729	36164860	36164747	36164843	RUNX1	NM_001001890	1	6	6	-	36160098	36164907
239694874	chr21	36193856	36194028	36193878	36194006	RUNX1	NM_001122607	2	5	5	-	36193574	36193993
238032241	chr21	36231744	36231913	36231764	36231885	RUNX1	NM_001754	3	9	6	-	36231771	36231875
238032241	chr21	36231744	36231913	36231764	36231885	RUNX1	NM_001122607	2	5	3	-	36231771	36231875
238032241	chr21	36231744	36231913	36231764	36231885	RUNX1	NM_001001890	1	6	3	-	36231771	36231875
241651493	chr21	36259245	36259399	36259263	36259381	RUNX1	NM_001122607	2	5	1	-	36259140	36260987
241651493	chr21	36259245	36259399	36259263	36259381	RUNX1	NM_001001890	1	6	1	-	36259140	36260987
241651493	chr21	36259245	36259399	36259263	36259381	RUNX1	NM_001754	3	9	4	-	36259140	36259393
240538425	chr21	36421055	36421221	36421076	36421199	RUNX1	NM_001754	3	9	2	-	36421139	36421255
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_001136154	1	12	12	-	39751950	39755845
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_001136155	2	9	9	-	39751950	39755845
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_004449	6	11	11	-	39751950	39755845
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_182918	7	10	10	-	39751950	39755845
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_001243429	4	9	9	-	39751950	39755845
232712495	chr21	39755618	39755792	39755642	39755772	ERG	NM_001243428	3	12	12	-	39751950	39755845

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_001136154	1	12	10	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_001136155	2	9	7	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_004449	6	11	9	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_182918	7	10	8	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_001243432	5	12	10	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_001243429	4	9	7	-	39763581	39763637
230614465	chr21	39763527	39763686	39763548	39763658	ERG	NM_001243428	3	12	10	-	39763581	39763637
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_001136154	1	12	7	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_001136155	2	9	4	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_004449	6	11	7	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_182918	7	10	5	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_001243432	5	12	7	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_001243429	4	9	5	-	39774479	39774559
227764265	chr21	39774504	39774631	39774532	39774600	ERG	NM_001243428	3	12	7	-	39774479	39774559
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_001136154	1	12	5	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_001136155	2	9	2	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_004449	6	11	5	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_182918	7	10	3	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_001243432	5	12	5	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_001243429	4	9	3	-	39795332	39795483
230691015	chr21	39795392	39795541	39795412	39795517	ERG	NM_001243428	3	12	5	-	39795332	39795483
232145904	chr21	39947482	39947650	39947502	39947627	ERG	NM_001136154	1	12	3	-	39947586	39947671
232145904	chr21	39947482	39947650	39947502	39947627	ERG	NM_004449	6	11	3	-	39947586	39947671
232145904	chr21	39947482	39947650	39947502	39947627	ERG	NM_001243432	5	12	3	-	39947586	39947671
232145904	chr21	39947482	39947650	39947502	39947627	ERG	NM_001243429	4	9	2	-	39947586	39947671
232145904	chr21	39947482	39947650	39947502	39947627	ERG	NM_001243428	3	12	3	-	39947586	39947671
280291358	chr21	46308504	46308646	46308526	46308625	ITGB2	NM_000211	1	16	14	-	46308608	46308810
280291358	chr21	46308504	46308646	46308526	46308625	ITGB2	NM_001127491	2	16	14	-	46308608	46308810
279439320	chr21	46309175	46309346	46309193	46309327	ITGB2	NM_000211	1	16	13	-	46309191	46309410
279439320	chr21	46309175	46309346	46309193	46309327	ITGB2	NM_001127491	2	16	13	-	46309191	46309410
279313588	chr21	46310029	46310195	46310053	46310175	ITGB2	NM_000211	1	16	12	-	46309893	46310137
279313588	chr21	46310029	46310195	46310053	46310175	ITGB2	NM_001127491	2	16	12	-	46309893	46310137
279206785	chr21	46313218	46313360	46313236	46313342	ITGB2	NM_000211	1	16	10	-	46313319	46313459
279206785	chr21	46313218	46313360	46313236	46313342	ITGB2	NM_001127491	2	16	10	-	46313319	46313459
278022257	chr21	46320121	46320275	46320144	46320254	ITGB2	NM_000211	1	16	7	-	46320235	46320390
278022257	chr21	46320121	46320275	46320144	46320254	ITGB2	NM_001127491	2	16	7	-	46320235	46320390
279988150	chr21	46321495	46321639	46321518	46321620	ITGB2	NM_000211	1	16	6	-	46321407	46321648
279988150	chr21	46321495	46321639	46321518	46321620	ITGB2	NM_001127491	2	16	6	-	46321407	46321648
280496861	chr21	46326715	46326873	46326734	46326855	ITGB2	NM_000211	1	16	4	-	46326830	46327010
280496861	chr21	46326715	46326873	46326734	46326855	ITGB2	NM_001127491	2	16	4	-	46326830	46327010
279726929	chr21	46330225	46330372	46330244	46330350	ITGB2	NM_000211	1	16	3	-	46330199	46330287

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
279726929	chr21	46330225	46330372	46330244	46330350	ITGB2	NM_001127491	2	16	3	-	46330199	46330287
271519242	chr22	21288002	21288173	21288024	21288151	CRKL	NM_005207	1	3	2	+	21288067	21288532
271566381	chr22	21288484	21288649	21288510	21288621	CRKL	NM_005207	1	3	2	+	21288067	21288532
293890506	chr22	22123539	22123694	22123564	22123667	MAPK1	NM_002745	1	9	8	-	22123484	22123609
293890506	chr22	22123539	22123694	22123564	22123667	MAPK1	NM_138957	2	8	8	-	22123319	22123609
294294702	chr22	22142860	22143018	22142888	22142994	MAPK1	NM_138957	2	8	5	-	22142983	22143097
294294702	chr22	22142860	22143018	22142888	22142994	MAPK1	NM_002745	1	9	5	-	22142983	22143097
294304679	chr22	22160021	22160186	22160047	22160166	MAPK1	NM_138957	2	8	3	-	22160139	22160328
294304679	chr22	22160021	22160186	22160047	22160166	MAPK1	NM_002745	1	9	3	-	22160139	22160328
294653237	chr22	22162010	22162172	22162031	22162145	MAPK1	NM_138957	2	8	2	-	22161953	22162135
294653237	chr22	22162010	22162172	22162031	22162145	MAPK1	NM_002745	1	9	2	-	22161953	22162135
224667734	chr22	23523237	23523372	23523256	23523355	BCR	NM_004327	1	23	1	+	23522552	23524426
224667734	chr22	23523237	23523372	23523256	23523355	BCR	NM_021574	2	22	1	+	23522552	23524426
223050670	chr22	23523605	23523735	23523625	23523712	BCR	NM_004327	1	23	1	+	23522552	23524426
223050670	chr22	23523605	23523735	23523625	23523712	BCR	NM_021574	2	22	1	+	23522552	23524426
224667524	chr22	23524041	23524173	23524059	23524155	BCR	NM_004327	1	23	1	+	23522552	23524426
224667524	chr22	23524041	23524173	23524059	23524155	BCR	NM_021574	2	22	1	+	23522552	23524426
222178746	chr22	23595931	23596093	23595954	23596074	BCR	NM_004327	1	23	2	+	23595986	23596167
222178746	chr22	23595931	23596093	23595954	23596074	BCR	NM_021574	2	22	2	+	23595986	23596167
224083543	chr22	23603613	23603745	23603637	23603727	BCR	NM_004327	1	23	4	+	23603542	23603727
224083543	chr22	23603613	23603745	23603637	23603727	BCR	NM_021574	2	22	4	+	23603542	23603727
223973563	chr22	23615776	23615923	23615797	23615900	BCR	NM_004327	1	23	8	+	23615821	23615961
223973563	chr22	23615776	23615923	23615797	23615900	BCR	NM_021574	2	22	8	+	23615821	23615961
222485418	chr22	23627270	23627434	23627292	23627413	BCR	NM_004327	1	23	10	+	23627220	23627388
222485418	chr22	23627270	23627434	23627292	23627413	BCR	NM_021574	2	22	10	+	23627220	23627388
224709902	chr22	23631673	23631837	23631695	23631818	BCR	NM_004327	1	23	13	+	23631704	23631808
224709902	chr22	23631673	23631837	23631695	23631818	BCR	NM_021574	2	22	13	+	23631704	23631808
222505386	chr22	23637238	23637395	23637261	23637373	BCR	NM_004327	1	23	16	+	23637211	23637342
222694002	chr22	23656710	23656880	23656727	23656858	BCR	NM_004327	1	23	22	+	23656739	23656901
222694002	chr22	23656710	23656880	23656727	23656858	BCR	NM_021574	2	22	21	+	23656739	23656901
241659859	chr22	24129306	24129453	24129324	24129434	SMARCB1	NM_001007468	1	9	1	+	24129150	24129449
241659859	chr22	24129306	24129453	24129324	24129434	SMARCB1	NM_003073	2	9	1	+	24129150	24129449
239148283	chr22	24143090	24143253	24143114	24143233	SMARCB1	NM_001007468	1	9	4	+	24143131	24143268
239148283	chr22	24143090	24143253	24143114	24143233	SMARCB1	NM_003073	2	9	4	+	24143131	24143268
263887200	chr22	24158854	24159028	24158874	24159008	SMARCB1	NM_001007468	1	9	6	+	24158957	24159123
263887200	chr22	24158854	24159028	24158874	24159008	SMARCB1	NM_003073	2	9	6	+	24158957	24159123
261451075	chr22	24175712	24175874	24175740	24175854	SMARCB1	NM_001007468	1	9	8	+	24175759	24175890
261451075	chr22	24175712	24175874	24175740	24175854	SMARCB1	NM_003073	2	9	8	+	24175759	24175890
240602625	chr22	28146906	28147030	28146926	28147011	MN1	NM_002430	1	2	2	-	28144265	28147084
235349131	chr22	28192937	28193087	28192955	28193067	MN1	NM_002430	1	2	1	-	28192751	28197486
240187529	chr22	28193397	28193529	28193416	28193511	MN1	NM_002430	1	2	1	-	28192751	28197486

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
240197591	chr22	28193824	28193997	28193842	28193974	MN1	NM_002430	1	2	1	-	28192751	28197486
240205811	chr22	28194414	28194579	28194432	28194562	MN1	NM_002430	1	2	1	-	28192751	28197486
240214997	chr22	28194711	28194875	28194730	28194855	MN1	NM_002430	1	2	1	-	28192751	28197486
240228884	chr22	28195055	28195214	28195072	28195197	MN1	NM_002430	1	2	1	-	28192751	28197486
235394591	chr22	28195517	28195689	28195536	28195668	MN1	NM_002430	1	2	1	-	28192751	28197486
240239955	chr22	28195848	28196011	28195866	28195990	MN1	NM_002430	1	2	1	-	28192751	28197486
235501300	chr22	28196372	28196535	28196393	28196512	MN1	NM_002430	1	2	1	-	28192751	28197486
225797753	chr22	29090019	29090180	29090036	29090152	CHEK2	NM_145862	3	14	12	-	29090020	29090105
225797753	chr22	29090019	29090180	29090036	29090152	CHEK2	NM_007194	2	15	13	-	29090020	29090105
225797753	chr22	29090019	29090180	29090036	29090152	CHEK2	NM_001005735	1	16	14	-	29090020	29090105
226445640	chr22	29092841	29092998	29092868	29092976	CHEK2	NM_007194	2	15	10	-	29092889	29092975
226445640	chr22	29092841	29092998	29092868	29092976	CHEK2	NM_001005735	1	16	11	-	29092889	29092975
225436956	chr22	29107856	29108005	29107883	29107986	CHEK2	NM_145862	3	14	6	-	29107897	29108005
225436956	chr22	29107856	29108005	29107883	29107986	CHEK2	NM_007194	2	15	6	-	29107897	29108005
225436956	chr22	29107856	29108005	29107883	29107986	CHEK2	NM_001005735	1	16	7	-	29107897	29108005
253753394	chr22	29120888	29121023	29120915	29120997	CHEK2	NM_145862	3	14	4	-	29120965	29121112
253753394	chr22	29120888	29121023	29120915	29120997	CHEK2	NM_007194	2	15	4	-	29120965	29121112
253753394	chr22	29120888	29121023	29120915	29120997	CHEK2	NM_001005735	1	16	5	-	29120965	29121112
226114572	chr22	29121210	29121384	29121237	29121356	CHEK2	NM_145862	3	14	3	-	29121231	29121355
226114572	chr22	29121210	29121384	29121237	29121356	CHEK2	NM_007194	2	15	3	-	29121231	29121355
226114572	chr22	29121210	29121384	29121237	29121356	CHEK2	NM_001005735	1	16	4	-	29121231	29121355
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_016418	2	17	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_000268	1	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181833	9	5	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181832	8	17	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181828	4	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181825	3	16	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181831	7	15	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181830	6	15	1	+	29999545	30000101
258245320	chr22	29999928	30000063	29999949	30000043	NF2	NM_181829	5	16	1	+	29999545	30000101
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_016418	2	17	3	+	30035079	30035201
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_000268	1	16	3	+	30035079	30035201
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_181833	9	5	3	+	30035079	30035201
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_181832	8	17	3	+	30035079	30035201
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_181828	4	16	2	+	30035079	30035201
239059105	chr22	30035024	30035148	30035045	30035121	NF2	NM_181825	3	16	3	+	30035079	30035201
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_016418	2	17	6	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_000268	1	16	6	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181832	8	17	6	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181828	4	16	5	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181825	3	16	6	+	30051583	30051665

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181831	7	15	4	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181830	6	15	4	+	30051583	30051665
235098976	chr22	30051521	30051653	30051550	30051635	NF2	NM_181829	5	16	5	+	30051583	30051665
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_016418	2	17	8	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_000268	1	16	8	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181832	8	17	8	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181828	4	16	7	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181825	3	16	8	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181831	7	15	6	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181830	6	15	6	+	30057194	30057328
237951243	chr22	30057274	30057447	30057295	30057420	NF2	NM_181829	5	16	7	+	30057194	30057328
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_016418	2	17	10	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_000268	1	16	10	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181832	8	17	10	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181828	4	16	9	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181825	3	16	10	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181831	7	15	8	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181830	6	15	8	+	30064322	30064435
236025900	chr22	30064313	30064462	30064334	30064436	NF2	NM_181829	5	16	9	+	30064322	30064435
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_016418	2	17	13	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_000268	1	16	13	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181832	8	17	13	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181828	4	16	12	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181825	3	16	13	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181831	7	15	11	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181830	6	15	11	+	30070825	30070930
241505752	chr22	30070760	30070910	30070781	30070888	NF2	NM_181829	5	16	12	+	30070825	30070930
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_016418	2	17	15	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_000268	1	16	15	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181832	8	17	15	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181828	4	16	14	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181825	3	16	15	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181831	7	15	13	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181830	6	15	13	+	30077428	30077590
241344217	chr22	30077372	30077511	30077392	30077486	NF2	NM_181829	5	16	14	+	30077428	30077590
321788972	chr22	33197981	33198121	33197998	33198102	TIMP3	NM_000362	1	5	1	+	33196802	33198108
321697249	chr22	33255132	33255304	33255152	33255286	TIMP3	NM_000362	1	5	5	+	33255167	33259028
236003482	chr22	36680042	36680207	36680062	36680190	MYH9	NM_002473	1	41	40	-	36680139	36680311
237845317	chr22	36681159	36681295	36681180	36681271	MYH9	NM_002473	1	41	38	-	36681167	36681375
241075551	chr22	36681884	36682035	36681902	36682014	MYH9	NM_002473	1	41	36	-	36681911	36681999
237901881	chr22	36684319	36684490	36684337	36684466	MYH9	NM_002473	1	41	34	-	36684298	36684459

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
235695451	chr22	36685063	36685206	36685083	36685188	MYH9	NM_002473	1	41	32	-	36685131	36685343
236554257	chr22	36688124	36688284	36688143	36688266	MYH9	NM_002473	1	41	31	-	36688032	36688280
237045698	chr22	36689772	36689944	36689791	36689922	MYH9	NM_002473	1	41	29	-	36689805	36689909
242134062	chr22	36690955	36691116	36690972	36691097	MYH9	NM_002473	1	41	27	-	36690978	36691122
235727263	chr22	36692784	36692954	36692807	36692937	MYH9	NM_002473	1	41	25	-	36692889	36693060
235503357	chr22	36696101	36696233	36696120	36696212	MYH9	NM_002473	1	41	23	-	36696173	36696310
237103071	chr22	36696985	36697135	36697013	36697112	MYH9	NM_002473	1	41	22	-	36696897	36697103
238063591	chr22	36700020	36700190	36700040	36700169	MYH9	NM_002473	1	41	19	-	36700041	36700201
239251089	chr22	36701989	36702163	36702009	36702139	MYH9	NM_002473	1	41	17	-	36701976	36702097
236227221	chr22	36705224	36705394	36705245	36705372	MYH9	NM_002473	1	41	15	-	36705327	36705441
238455935	chr22	36708192	36708352	36708211	36708333	MYH9	NM_002473	1	41	14	-	36708094	36708267
238939266	chr22	36712582	36712755	36712604	36712733	MYH9	NM_002473	1	41	12	-	36712562	36712714
237158015	chr22	36716230	36716402	36716250	36716382	MYH9	NM_002473	1	41	9	-	36716265	36716408
236876743	chr22	36718348	36718504	36718370	36718481	MYH9	NM_002473	1	41	6	-	36718474	36718566
235206695	chr22	36737390	36737531	36737409	36737508	MYH9	NM_002473	1	41	3	-	36737415	36737571
236953598	chr22	36745053	36745200	36745077	36745180	MYH9	NM_002473	1	41	2	-	36744949	36745300
237774165	chr22	39626197	39626356	39626218	39626337	PDGFB	NM_033016	2	7	5	-	39626089	39626233
237774165	chr22	39626197	39626356	39626218	39626337	PDGFB	NM_002608	1	7	5	-	39626089	39626233
236386925	chr22	39629391	39629556	39629411	39629533	PDGFB	NM_033016	2	7	3	-	39629440	39629529
236386925	chr22	39629391	39629556	39629411	39629533	PDGFB	NM_002608	1	7	3	-	39629440	39629529
235303894	chr22	39639856	39640022	39639878	39640005	PDGFB	NM_002608	1	7	1	-	39639906	39640957
231334380	chr22	41513352	41513504	41513375	41513482	EP300	NM_001429	1	31	2	+	41513191	41513825
230168148	chr22	41521763	41521928	41521791	41521903	EP300	NM_001429	1	31	3	+	41521868	41522044
233030995	chr22	41523579	41523728	41523599	41523702	EP300	NM_001429	1	31	4	+	41523491	41523752
229583064	chr22	41527378	41527506	41527406	41527480	EP300	NM_001429	1	31	6	+	41527392	41527637
229226368	chr22	41533583	41533741	41533611	41533717	EP300	NM_001429	1	31	8	+	41533657	41533794
230715631	chr22	41536988	41537124	41537011	41537096	EP300	NM_001429	1	31	10	+	41537052	41537226
230724801	chr22	41543805	41543962	41543833	41543939	EP300	NM_001429	1	31	12	+	41543841	41543950
229950067	chr22	41545722	41545892	41545750	41545872	EP300	NM_001429	1	31	14	+	41545765	41546202
229967121	chr22	41546154	41546285	41546174	41546261	EP300	NM_001429	1	31	14	+	41545765	41546202
227915089	chr22	41548250	41548381	41548278	41548359	EP300	NM_001429	1	31	16	+	41548210	41548354
230508812	chr22	41553210	41553382	41553238	41553356	EP300	NM_001429	1	31	18	+	41553173	41553412
228093614	chr22	41558654	41558820	41558678	41558795	EP300	NM_001429	1	31	21	+	41558727	41558783
230431041	chr22	41564461	41564634	41564485	41564605	EP300	NM_001429	1	31	24	+	41564453	41564603
230724079	chr22	41565525	41565682	41565550	41565657	EP300	NM_001429	1	31	26	+	41565507	41565620
228835894	chr22	41568531	41568691	41568559	41568666	EP300	NM_001429	1	31	28	+	41568503	41568667
227883715	chr22	41572335	41572506	41572356	41572485	EP300	NM_001429	1	31	30	+	41572251	41572532
231281127	chr22	41572900	41573044	41572920	41573022	EP300	NM_001429	1	31	31	+	41572777	41576081
227969917	chr22	41573353	41573527	41573373	41573506	EP300	NM_001429	1	31	31	+	41572777	41576081
228046539	chr22	41573848	41574005	41573874	41573981	EP300	NM_001429	1	31	31	+	41572777	41576081
228132817	chr22	41574311	41574437	41574332	41574412	EP300	NM_001429	1	31	31	+	41572777	41576081

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
228175276	chr22	41574733	41574865	41574754	41574845	EP300	NM_001429	1	31	31	+	41572777	41576081
289128153	chr22	42523539	42523707	42523560	42523686	CYP2D6	NM_000106	1	9	7	-	42523449	42523636
289128153	chr22	42523539	42523707	42523560	42523686	CYP2D6	NM_001025161	2	8	6	-	42523449	42523636
287897749	chr22	42524247	42524418	42524268	42524399	CYP2D6	NM_000106	1	9	5	-	42524176	42524352
287897749	chr22	42524247	42524418	42524268	42524399	CYP2D6	NM_001025161	2	8	4	-	42524176	42524352
286427116	chr22	42525701	42525863	42525722	42525845	CYP2D6	NM_000106	1	9	2	-	42525740	42525911
286427116	chr22	42525701	42525863	42525722	42525845	CYP2D6	NM_001025161	2	8	2	-	42525740	42525911
286249837	chr22	42526689	42526814	42526706	42526792	CYP2D6	NM_000106	1	9	1	-	42526614	42526883
286249837	chr22	42526689	42526814	42526706	42526792	CYP2D6	NM_001025161	2	8	1	-	42526614	42526883
270682057	chrX	40990641	40990768	40990669	40990741	USP9X	NM_001039590	1	45	4	+	40990710	40990789
270682057	chrX	40990641	40990768	40990669	40990741	USP9X	NM_001039591	2	45	4	+	40990710	40990789
270094420	chrX	40996013	40996141	40996040	40996113	USP9X	NM_001039590	1	45	6	+	40996057	40996275
270094420	chrX	40996013	40996141	40996040	40996113	USP9X	NM_001039591	2	45	6	+	40996057	40996275
270210081	chrX	40999891	41000064	40999917	41000038	USP9X	NM_001039590	1	45	7	+	40999909	41000024
270210081	chrX	40999891	41000064	40999917	41000038	USP9X	NM_001039591	2	45	7	+	40999909	41000024
270260255	chrX	41000350	41000508	41000377	41000477	USP9X	NM_001039590	1	45	8	+	41000219	41000470
270260255	chrX	41000350	41000508	41000377	41000477	USP9X	NM_001039591	2	45	8	+	41000219	41000470
272244687	chrX	41002529	41002692	41002561	41002667	USP9X	NM_001039590	1	45	10	+	41002544	41002696
272244687	chrX	41002529	41002692	41002561	41002667	USP9X	NM_001039591	2	45	10	+	41002544	41002696
271299871	chrX	41007502	41007669	41007528	41007643	USP9X	NM_001039590	1	45	12	+	41007622	41007828
271299871	chrX	41007502	41007669	41007528	41007643	USP9X	NM_001039591	2	45	12	+	41007622	41007828
270299257	chrX	41010247	41010387	41010272	41010359	USP9X	NM_001039590	1	45	13	+	41010174	41010310
270299257	chrX	41010247	41010387	41010272	41010359	USP9X	NM_001039591	2	45	13	+	41010174	41010310
270981453	chrX	41022043	41022217	41022069	41022190	USP9X	NM_001039590	1	45	15	+	41022043	41022130
270981453	chrX	41022043	41022217	41022069	41022190	USP9X	NM_001039591	2	45	15	+	41022043	41022130
272447032	chrX	41025345	41025507	41025372	41025479	USP9X	NM_001039590	1	45	16	+	41025125	41025467
272447032	chrX	41025345	41025507	41025372	41025479	USP9X	NM_001039591	2	45	16	+	41025125	41025467
271854941	chrX	41027343	41027484	41027370	41027458	USP9X	NM_001039590	1	45	18	+	41027260	41027471
271854941	chrX	41027343	41027484	41027370	41027458	USP9X	NM_001039591	2	45	18	+	41027260	41027471
270090404	chrX	41029769	41029894	41029793	41029866	USP9X	NM_001039590	1	45	20	+	41029723	41029872
270090404	chrX	41029769	41029894	41029793	41029866	USP9X	NM_001039591	2	45	20	+	41029723	41029872
271319549	chrX	41043244	41043382	41043270	41043355	USP9X	NM_001039590	1	45	22	+	41043251	41043381
271319549	chrX	41043244	41043382	41043270	41043355	USP9X	NM_001039591	2	45	22	+	41043251	41043381
269643913	chrX	41043868	41044038	41043888	41044012	USP9X	NM_001039590	1	45	23	+	41043650	41043928
269643913	chrX	41043868	41044038	41043888	41044012	USP9X	NM_001039591	2	45	23	+	41043650	41043928
269800873	chrX	41048449	41048617	41048470	41048594	USP9X	NM_001039590	1	45	26	+	41048562	41048728
269800873	chrX	41048449	41048617	41048470	41048594	USP9X	NM_001039591	2	45	26	+	41048562	41048728
270701686	chrX	41055520	41055694	41055545	41055666	USP9X	NM_001039590	1	45	27	+	41055504	41055612
270701686	chrX	41055520	41055694	41055545	41055666	USP9X	NM_001039591	2	45	27	+	41055504	41055612
269947325	chrX	41057744	41057875	41057775	41057854	USP9X	NM_001039590	1	45	30	+	41057781	41058003
269947325	chrX	41057744	41057875	41057775	41057854	USP9X	NM_001039591	2	45	30	+	41057781	41058003

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
270042987	chrX	41060393	41060545	41060417	41060519	USP9X	NM_001039590	1	45	31	+	41060313	41060533
270042987	chrX	41060393	41060545	41060417	41060519	USP9X	NM_001039591	2	45	31	+	41060313	41060533
271400719	chrX	41064676	41064841	41064701	41064814	USP9X	NM_001039590	1	45	32	+	41064556	41064746
271400719	chrX	41064676	41064841	41064701	41064814	USP9X	NM_001039591	2	45	32	+	41064556	41064746
270376873	chrX	41073820	41073971	41073848	41073944	USP9X	NM_001039590	1	45	34	+	41073821	41073962
270376873	chrX	41073820	41073971	41073848	41073944	USP9X	NM_001039591	2	45	34	+	41073821	41073962
270934119	chrX	41075269	41075414	41075292	41075390	USP9X	NM_001039590	1	45	35	+	41075152	41075905
270934119	chrX	41075269	41075414	41075292	41075390	USP9X	NM_001039591	2	45	35	+	41075152	41075905
272451401	chrX	41075732	41075900	41075753	41075873	USP9X	NM_001039590	1	45	35	+	41075152	41075905
272451401	chrX	41075732	41075900	41075753	41075873	USP9X	NM_001039591	2	45	35	+	41075152	41075905
270128573	chrX	41077503	41077676	41077526	41077651	USP9X	NM_001039590	1	45	37	+	41077625	41077850
270128573	chrX	41077503	41077676	41077526	41077651	USP9X	NM_001039591	2	45	37	+	41077625	41077850
272554089	chrX	41082386	41082545	41082408	41082516	USP9X	NM_001039590	1	45	39	+	41082470	41082655
272554089	chrX	41082386	41082545	41082408	41082516	USP9X	NM_001039591	2	45	39	+	41082470	41082655
269706673	chrX	41084134	41084306	41084158	41084279	USP9X	NM_001039590	1	45	40	+	41083995	41084215
269706673	chrX	41084134	41084306	41084158	41084279	USP9X	NM_001039591	2	45	40	+	41083995	41084215
269637793	chrX	41088616	41088750	41088644	41088722	USP9X	NM_001039590	1	45	42	+	41088506	41088662
269637793	chrX	41088616	41088750	41088644	41088722	USP9X	NM_001039591	2	45	42	+	41088506	41088662
271026363	chrX	41089014	41089177	41089039	41089150	USP9X	NM_001039590	1	45	43	+	41088820	41089080
270075827	chrX	41091650	41091820	41091672	41091800	USP9X	NM_001039590	1	45	45	+	41091640	41095832
270075827	chrX	41091650	41091820	41091672	41091800	USP9X	NM_001039591	2	45	45	+	41091640	41095832
233405873	chrX	44820429	44820591	44820454	44820563	KDM6A	NM_021140	1	29	3	+	44820529	44820637
234424339	chrX	44879774	44879901	44879801	44879876	KDM6A	NM_021140	1	29	6	+	44879855	44879975
232096992	chrX	44896877	44897044	44896901	44897016	KDM6A	NM_021140	1	29	8	+	44896900	44896934
233443884	chrX	44913120	44913252	44913148	44913221	KDM6A	NM_021140	1	29	10	+	44913074	44913200
234516140	chrX	44918440	44918565	44918464	44918539	KDM6A	NM_021140	1	29	12	+	44918492	44918711
233038392	chrX	44919321	44919471	44919343	44919443	KDM6A	NM_021140	1	29	13	+	44919267	44919401
232193379	chrX	44921960	44922110	44921987	44922077	KDM6A	NM_021140	1	29	15	+	44921892	44921993
231336583	chrX	44922942	44923109	44922966	44923080	KDM6A	NM_021140	1	29	16	+	44922667	44923062
232868391	chrX	44929159	44929291	44929180	44929269	KDM6A	NM_021140	1	29	17	+	44928824	44929602
231532480	chrX	44935828	44935995	44935850	44935967	KDM6A	NM_021140	1	29	18	+	44935942	44936071
234693612	chrX	44937690	44937825	44937713	44937802	KDM6A	NM_021140	1	29	19	+	44937645	44937750
230953583	chrX	44938565	44938689	44938584	44938657	KDM6A	NM_021140	1	29	20	+	44938391	44938596
231374061	chrX	44942752	44942926	44942776	44942897	KDM6A	NM_021140	1	29	23	+	44942705	44942853
231830822	chrX	44949042	44949176	44949069	44949151	KDM6A	NM_021140	1	29	25	+	44948988	44949175
233082598	chrX	44966560	44966710	44966588	44966686	KDM6A	NM_021140	1	29	27	+	44966655	44966781
232874671	chrX	44969418	44969553	44969443	44969530	KDM6A	NM_021140	1	29	28	+	44969324	44969494
262255709	chrX	48117925	48118059	48117949	48118032	SSX1	NM_005635	1	8	4	+	48117971	48118066
239697470	chrX	48542171	48542345	48542193	48542327	WAS	NM_000377	1	12	1	+	48542186	48542374
242072133	chrX	48543858	48544018	48543879	48543997	WAS	NM_000377	1	12	3	+	48543936	48544022
240629784	chrX	48544366	48544540	48544389	48544520	WAS	NM_000377	1	12	6	+	48544470	48544523

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
242203356	chrX	48546631	48546802	48546653	48546776	WAS	NM_000377	1	12	9	+	48546689	48546842
262402469	chrX	48547135	48547262	48547153	48547243	WAS	NM_000377	1	12	10	+	48547049	48547455
228116434	chrX	48649482	48649647	48649502	48649628	GATA1	NM_002049	1	6	2	+	48649498	48649736
227553840	chrX	48650387	48650559	48650407	48650537	GATA1	NM_002049	1	6	3	+	48650251	48650628
227705522	chrX	48651539	48651713	48651557	48651696	GATA1	NM_002049	1	6	5	+	48651579	48651704
227651008	chrX	48652432	48652597	48652449	48652579	GATA1	NM_002049	1	6	6	+	48652200	48652717
265479047	chrX	48887934	48888066	48887952	48888047	TFE3	NM_006521	1	10	10	-	48886242	48888112
263736118	chrX	48890902	48891076	48890926	48891055	TFE3	NM_006521	1	10	8	-	48890980	48891055
262026988	chrX	48895568	48895694	48895589	48895668	TFE3	NM_006521	1	10	5	-	48895535	48895639
241264888	chrX	48896570	48896712	48896593	48896692	TFE3	NM_006521	1	10	3	-	48896632	48896935
241392505	chrX	48897881	48898041	48897903	48898019	TFE3	NM_006521	1	10	2	-	48897982	48898095
262449287	chrX	48900720	48900885	48900738	48900867	TFE3	NM_006521	1	10	1	-	48900637	48900990
232721303	chrX	53222143	53222306	53222163	53222288	KDM5C	NM_004187	2	26	26	-	53220503	53222514
233190057	chrX	53222673	53222840	53222694	53222819	KDM5C	NM_004187	2	26	25	-	53222619	53222818
233190057	chrX	53222673	53222840	53222694	53222819	KDM5C	NM_001146702	1	24	23	-	53222680	53222818
233918757	chrX	53223443	53223588	53223468	53223568	KDM5C	NM_004187	2	26	23	-	53223321	53223920
233918757	chrX	53223443	53223588	53223468	53223568	KDM5C	NM_001146702	1	24	21	-	53223321	53223920
233467509	chrX	53224055	53224206	53224080	53224187	KDM5C	NM_004187	2	26	22	-	53224113	53224250
233467509	chrX	53224055	53224206	53224080	53224187	KDM5C	NM_001146702	1	24	20	-	53224113	53224250
234428678	chrX	53225020	53225193	53225043	53225172	KDM5C	NM_004187	2	26	20	-	53225098	53225236
234428678	chrX	53225020	53225193	53225043	53225172	KDM5C	NM_001146702	1	24	18	-	53225098	53225236
232604202	chrX	53225997	53226165	53226015	53226146	KDM5C	NM_004187	2	26	19	-	53225868	53226226
232604202	chrX	53225997	53226165	53226015	53226146	KDM5C	NM_001146702	1	24	17	-	53225868	53226226
234206466	chrX	53227728	53227866	53227752	53227838	KDM5C	NM_004187	2	26	17	-	53227672	53227819
234206466	chrX	53227728	53227866	53227752	53227838	KDM5C	NM_001146702	1	24	15	-	53227672	53227819
232131275	chrX	53228247	53228394	53228267	53228366	KDM5C	NM_004187	2	26	15	-	53228159	53228340
232131275	chrX	53228247	53228394	53228267	53228366	KDM5C	NM_001146702	1	24	13	-	53228159	53228340
234422584	chrX	53239531	53239698	53239553	53239674	KDM5C	NM_004187	2	26	12	-	53239596	53239758
234422584	chrX	53239531	53239698	53239553	53239674	KDM5C	NM_001146702	1	24	10	-	53239596	53239758
233179522	chrX	53240654	53240796	53240679	53240768	KDM5C	NM_004187	2	26	10	-	53240679	53240837
233179522	chrX	53240654	53240796	53240679	53240768	KDM5C	NM_001146702	1	24	8	-	53240679	53240837
232627176	chrX	53243928	53244068	53243949	53244041	KDM5C	NM_004187	2	26	8	-	53243871	53244029
232627176	chrX	53243928	53244068	53243949	53244041	KDM5C	NM_001146702	1	24	6	-	53243871	53244029
234222125	chrX	53246286	53246457	53246311	53246429	KDM5C	NM_004187	2	26	5	-	53246325	53246459
234222125	chrX	53246286	53246457	53246311	53246429	KDM5C	NM_001146702	1	24	3	-	53246325	53246459
231153938	chrX	53247432	53247606	53247455	53247581	KDM5C	NM_004187	2	26	3	-	53247458	53247580
229260883	chrX	63409729	63409877	63409750	63409857	FAM123B	NM_152424	1	2	2	-	63404997	63413264
231990223	chrX	63410168	63410338	63410192	63410314	FAM123B	NM_152424	1	2	2	-	63404997	63413264
228892223	chrX	63410583	63410714	63410608	63410692	FAM123B	NM_152424	1	2	2	-	63404997	63413264
231983618	chrX	63411009	63411161	63411033	63411140	FAM123B	NM_152424	1	2	2	-	63404997	63413264
229405671	chrX	63411446	63411608	63411470	63411584	FAM123B	NM_152424	1	2	2	-	63404997	63413264

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
229475225	chrX	63411886	63412049	63411908	63412026	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232055656	chrX	63412284	63412438	63412308	63412416	FAM123B	NM_152424	1	2	2	-	63404997	63413264
232024822	chrX	63412690	63412857	63412713	63412836	FAM123B	NM_152424	1	2	2	-	63404997	63413264
264312633	chrX	66765442	66765600	66765461	66765579	AR	NM_000044	1	8	1	+	66763874	66766604
264338487	chrX	66765911	66766048	66765934	66766028	AR	NM_000044	1	8	1	+	66763874	66766604
264326647	chrX	66766407	66766561	66766424	66766537	AR	NM_000044	1	8	1	+	66763874	66766604
264967340	chrX	66863128	66863271	66863155	66863249	AR	NM_001011645	2	8	2	+	66863098	66863249
264967340	chrX	66863128	66863271	66863155	66863249	AR	NM_000044	1	8	2	+	66863098	66863249
257507147	chrX	66931330	66931470	66931352	66931449	AR	NM_001011645	2	8	4	+	66931244	66931531
257507147	chrX	66931330	66931470	66931352	66931449	AR	NM_000044	1	8	4	+	66931244	66931531
260993146	chrX	66941565	66941739	66941588	66941717	AR	NM_001011645	2	8	6	+	66941675	66941805
260993146	chrX	66941565	66941739	66941588	66941717	AR	NM_000044	1	8	6	+	66941675	66941805
264961066	chrX	66943481	66943648	66943503	66943626	AR	NM_001011645	2	8	8	+	66943528	66950461
264961066	chrX	66943481	66943648	66943503	66943626	AR	NM_000044	1	8	8	+	66943528	66950461
303260558	chrX	70586259	70586405	70586280	70586384	TAF1	NM_138923	2	38	1	+	70586114	70586344
303260558	chrX	70586259	70586405	70586280	70586384	TAF1	NM_004606	1	38	1	+	70586114	70586344
305599079	chrX	70595027	70595170	70595055	70595143	TAF1	NM_138923	2	38	4	+	70595017	70595136
305599079	chrX	70595027	70595170	70595055	70595143	TAF1	NM_004606	1	38	4	+	70595017	70595136
302156155	chrX	70597397	70597571	70597422	70597550	TAF1	NM_138923	2	38	6	+	70597453	70597671
302156155	chrX	70597397	70597571	70597422	70597550	TAF1	NM_004606	1	38	6	+	70597453	70597671
305110972	chrX	70598618	70598792	70598641	70598771	TAF1	NM_138923	2	38	8	+	70598674	70598881
305110972	chrX	70598618	70598792	70598641	70598771	TAF1	NM_004606	1	38	8	+	70598674	70598881
301123512	chrX	70602314	70602467	70602340	70602439	TAF1	NM_138923	2	38	10	+	70602386	70602513
301123512	chrX	70602314	70602467	70602340	70602439	TAF1	NM_004606	1	38	10	+	70602386	70602513
301097724	chrX	70602764	70602936	70602788	70602915	TAF1	NM_138923	2	38	12	+	70602841	70603014
301097724	chrX	70602764	70602936	70602788	70602915	TAF1	NM_004606	1	38	12	+	70602841	70603014
305896794	chrX	70603947	70604096	70603968	70604071	TAF1	NM_138923	2	38	13	+	70603812	70603985
305896794	chrX	70603947	70604096	70603968	70604071	TAF1	NM_004606	1	38	13	+	70603812	70603985
300426621	chrX	70607119	70607290	70607144	70607266	TAF1	NM_138923	2	38	15	+	70607111	70607311
300426621	chrX	70607119	70607290	70607144	70607266	TAF1	NM_004606	1	38	15	+	70607111	70607311
301918910	chrX	70608479	70608620	70608499	70608598	TAF1	NM_138923	2	38	17	+	70608588	70608718
301918910	chrX	70608479	70608620	70608499	70608598	TAF1	NM_004606	1	38	17	+	70608588	70608718
303106616	chrX	70612613	70612783	70612635	70612761	TAF1	NM_138923	2	38	20	+	70612725	70612844
303106616	chrX	70612613	70612783	70612635	70612761	TAF1	NM_004606	1	38	20	+	70612725	70612844
302874292	chrX	70613291	70613423	70613313	70613397	TAF1	NM_138923	2	38	21	+	70613151	70613326
302874292	chrX	70613291	70613423	70613313	70613397	TAF1	NM_004606	1	38	21	+	70613151	70613326
303458813	chrX	70617178	70617340	70617198	70617312	TAF1	NM_138923	2	38	23	+	70617103	70617316
303458813	chrX	70617178	70617340	70617198	70617312	TAF1	NM_004606	1	38	23	+	70617103	70617316
304821234	chrX	70621465	70621613	70621486	70621589	TAF1	NM_138923	2	38	25	+	70621378	70621589
304821234	chrX	70621465	70621613	70621486	70621589	TAF1	NM_004606	1	38	25	+	70621378	70621589
302940836	chrX	70627876	70628028	70627898	70628001	TAF1	NM_138923	2	38	28	+	70627824	70628001

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
302940836	chrX	70627876	70628028	70627898	70628001	TAF1	NM_004606	1	38	28	+	70627824	70628001
305583982	chrX	70643748	70643919	70643773	70643891	TAF1	NM_138923	2	38	31	+	70643824	70643916
305583982	chrX	70643748	70643919	70643773	70643891	TAF1	NM_004606	1	38	31	+	70643824	70643916
300287654	chrX	70674628	70674784	70674652	70674759	TAF1	NM_138923	2	38	34	+	70674591	70674707
300287654	chrX	70674628	70674784	70674652	70674759	TAF1	NM_004606	1	38	34	+	70674591	70674707
303069847	chrX	70679414	70679580	70679438	70679558	TAF1	NM_138923	2	38	36	+	70679402	70679558
303069847	chrX	70679414	70679580	70679438	70679558	TAF1	NM_004606	1	38	36	+	70679402	70679558
300081778	chrX	70683692	70683859	70683712	70683836	TAF1	NM_138923	2	38	38	+	70683674	70685855
300081778	chrX	70683692	70683859	70683712	70683836	TAF1	NM_004606	1	38	38	+	70683674	70685855
274087077	chrX	76763934	76764069	76763961	76764047	ATRX	NM_000489	1	35	35	-	76760356	76764107
274087077	chrX	76763934	76764069	76763961	76764047	ATRX	NM_138270	2	34	34	-	76760356	76764107
273161997	chrX	76776828	76776965	76776850	76776937	ATRX	NM_000489	1	35	33	-	76776881	76776976
273161997	chrX	76776828	76776965	76776850	76776937	ATRX	NM_138270	2	34	32	-	76776881	76776976
274254359	chrX	76777822	76777967	76777847	76777940	ATRX	NM_000489	1	35	32	-	76777741	76777866
274254359	chrX	76777822	76777967	76777847	76777940	ATRX	NM_138270	2	34	31	-	76777741	76777866
273147101	chrX	76812969	76813129	76812997	76813101	ATRX	NM_000489	1	35	30	-	76812922	76813116
273147101	chrX	76812969	76813129	76812997	76813101	ATRX	NM_138270	2	34	29	-	76812922	76813116
273198417	chrX	76814220	76814344	76814242	76814311	ATRX	NM_000489	1	35	29	-	76814140	76814317
273198417	chrX	76814220	76814344	76814242	76814311	ATRX	NM_138270	2	34	28	-	76814140	76814317
274054673	chrX	76845279	76845408	76845308	76845386	ATRX	NM_000489	1	35	27	-	76845304	76845410
274054673	chrX	76845279	76845408	76845308	76845386	ATRX	NM_138270	2	34	26	-	76845304	76845410
272779969	chrX	76854778	76854929	76854806	76854903	ATRX	NM_000489	1	35	25	-	76854880	76855049
272779969	chrX	76854778	76854929	76854806	76854903	ATRX	NM_138270	2	34	24	-	76854880	76855049
274368103	chrX	76855217	76855391	76855243	76855365	ATRX	NM_000489	1	35	24	-	76855201	76855289
274368103	chrX	76855217	76855391	76855243	76855365	ATRX	NM_138270	2	34	23	-	76855201	76855289
273069038	chrX	76872129	76872272	76872156	76872244	ATRX	NM_000489	1	35	22	-	76872081	76872198
273069038	chrX	76872129	76872272	76872156	76872244	ATRX	NM_138270	2	34	21	-	76872081	76872198
273949908	chrX	76875865	76875990	76875895	76875962	ATRX	NM_000489	1	35	20	-	76875863	76876000
273949908	chrX	76875865	76875990	76875895	76875962	ATRX	NM_138270	2	34	19	-	76875863	76876000
272769579	chrX	76888832	76888957	76888854	76888930	ATRX	NM_000489	1	35	19	-	76888695	76888872
272769579	chrX	76888832	76888957	76888854	76888930	ATRX	NM_138270	2	34	18	-	76888695	76888872
273039038	chrX	76890054	76890195	76890083	76890170	ATRX	NM_000489	1	35	17	-	76890085	76890194
273039038	chrX	76890054	76890195	76890083	76890170	ATRX	NM_138270	2	34	16	-	76890085	76890194
273629636	chrX	76907599	76907738	76907626	76907710	ATRX	NM_000489	1	35	15	-	76907604	76907843
273629636	chrX	76907599	76907738	76907626	76907710	ATRX	NM_138270	2	34	14	-	76907604	76907843
273886790	chrX	76911988	76912112	76912013	76912085	ATRX	NM_000489	1	35	13	-	76912050	76912143
273886790	chrX	76911988	76912112	76912013	76912085	ATRX	NM_138270	2	34	12	-	76912050	76912143
272932646	chrX	76920124	76920273	76920143	76920245	ATRX	NM_000489	1	35	11	-	76920134	76920267
272932646	chrX	76920124	76920273	76920143	76920245	ATRX	NM_138270	2	34	10	-	76920134	76920267
273989940	chrX	76936907	76937044	76936939	76937017	ATRX	NM_000489	1	35	9	-	76937012	76940085
273989940	chrX	76936907	76937044	76936939	76937017	ATRX	NM_138270	2	34	8	-	76937012	76940085

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
274015843	chrX	76937281	76937443	76937308	76937415	ATRX	NM_000489	1	35	9	-	76937012	76940085
274015843	chrX	76937281	76937443	76937308	76937415	ATRX	NM_138270	2	34	8	-	76937012	76940085
273999563	chrX	76937542	76937716	76937570	76937689	ATRX	NM_000489	1	35	9	-	76937012	76940085
273999563	chrX	76937542	76937716	76937570	76937689	ATRX	NM_138270	2	34	8	-	76937012	76940085
273992254	chrX	76937950	76938120	76937977	76938092	ATRX	NM_000489	1	35	9	-	76937012	76940085
273992254	chrX	76937950	76938120	76937977	76938092	ATRX	NM_138270	2	34	8	-	76937012	76940085
274001506	chrX	76938512	76938655	76938534	76938628	ATRX	NM_000489	1	35	9	-	76937012	76940085
274001506	chrX	76938512	76938655	76938534	76938628	ATRX	NM_138270	2	34	8	-	76937012	76940085
272770409	chrX	76938929	76939103	76938954	76939080	ATRX	NM_000489	1	35	9	-	76937012	76940085
272770409	chrX	76938929	76939103	76938954	76939080	ATRX	NM_138270	2	34	8	-	76937012	76940085
272809684	chrX	76939344	76939492	76939373	76939467	ATRX	NM_000489	1	35	9	-	76937012	76940085
272809684	chrX	76939344	76939492	76939373	76939467	ATRX	NM_138270	2	34	8	-	76937012	76940085
274023876	chrX	76939711	76939883	76939737	76939854	ATRX	NM_000489	1	35	9	-	76937012	76940085
274023876	chrX	76939711	76939883	76939737	76939854	ATRX	NM_138270	2	34	8	-	76937012	76940085
273792447	chrX	76944315	76944452	76944342	76944424	ATRX	NM_000489	1	35	7	-	76944311	76944420
273792447	chrX	76944315	76944452	76944342	76944424	ATRX	NM_138270	2	34	6	-	76944311	76944420
273141468	chrX	76952111	76952250	76952139	76952223	ATRX	NM_000489	1	35	5	-	76952065	76952192
273141468	chrX	76952111	76952250	76952139	76952223	ATRX	NM_138270	2	34	5	-	76952065	76952192
273600893	chrX	76972513	76972641	76972544	76972620	ATRX	NM_000489	1	35	2	-	76972608	76972720
273600893	chrX	76972513	76972641	76972544	76972620	ATRX	NM_138270	2	34	2	-	76972608	76972720
270178706	chrX	79277828	79278001	79277856	79277981	TBX22	NM_016954	3	8	1	+	79277742	79277943
270178706	chrX	79277828	79278001	79277856	79277981	TBX22	NM_001109879	2	9	2	+	79277767	79277943
270178706	chrX	79277828	79278001	79277856	79277981	TBX22	NM_001109878	1	9	2	+	79277767	79277943
270139699	chrX	79281007	79281179	79281030	79281150	TBX22	NM_016954	3	8	4	+	79281102	79281276
270139699	chrX	79281007	79281179	79281030	79281150	TBX22	NM_001109879	2	9	5	+	79281102	79281276
270139699	chrX	79281007	79281179	79281030	79281150	TBX22	NM_001109878	1	9	5	+	79281102	79281276
270316619	chrX	79282682	79282842	79282708	79282818	TBX22	NM_016954	3	8	6	+	79282755	79282819
270316619	chrX	79282682	79282842	79282708	79282818	TBX22	NM_001109879	2	9	7	+	79282755	79282819
270316619	chrX	79282682	79282842	79282708	79282818	TBX22	NM_001109878	1	9	7	+	79282755	79282819
271659821	chrX	79286056	79286225	79286083	79286202	TBX22	NM_016954	3	8	8	+	79285997	79287268
271659821	chrX	79286056	79286225	79286083	79286202	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271659821	chrX	79286056	79286225	79286083	79286202	TBX22	NM_001109878	1	9	9	+	79285997	79287268
271640782	chrX	79286540	79286707	79286566	79286679	TBX22	NM_016954	3	8	8	+	79285997	79287268
271640782	chrX	79286540	79286707	79286566	79286679	TBX22	NM_001109879	2	9	9	+	79285997	79287268
271640782	chrX	79286540	79286707	79286566	79286679	TBX22	NM_001109878	1	9	9	+	79285997	79287268
254198832	chrX	100608754	100608892	100608782	100608868	BTK	NM_000061	1	19	17	-	100608858	100608976
265700190	chrX	100611138	100611281	100611160	100611256	BTK	NM_000061	1	19	15	-	100611040	100611256
263835681	chrX	100613157	100613331	100613182	100613306	BTK	NM_000061	1	19	12	-	100613298	100613425
256744700	chrX	100615025	100615162	100615048	100615139	BTK	NM_000061	1	19	9	-	100615076	100615138
264499296	chrX	100617086	100617258	100617111	100617231	BTK	NM_000061	1	19	7	-	100617161	100617228
262533692	chrX	100626559	100626733	100626584	100626705	BTK	NM_000061	1	19	4	-	100626621	100626689

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_001128172	4	15	1	+	110366305	110366506
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_001128168	3	16	1	+	110366305	110366506
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_001128173	5	15	1	+	110366305	110366506
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_001128166	1	16	3	+	110366305	110366506
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_001128167	2	15	2	+	110366305	110366506
271302276	chrX	110366251	110366411	110366277	110366387	PAK3	NM_002578	6	18	5	+	110366305	110366506
269816666	chrX	110388050	110388213	110388078	110388187	PAK3	NM_001128172	4	15	3	+	110388088	110388150
269816666	chrX	110388050	110388213	110388078	110388187	PAK3	NM_001128168	3	16	3	+	110388088	110388150
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_001128172	4	15	5	+	110395638	110395675
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_001128168	3	16	6	+	110395638	110395675
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_001128173	5	15	5	+	110395638	110395675
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_001128166	1	16	6	+	110395638	110395675
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_001128167	2	15	5	+	110395638	110395675
270823721	chrX	110395566	110395718	110395592	110395693	PAK3	NM_002578	6	18	8	+	110395638	110395675
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_001128172	4	15	7	+	110406790	110406955
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_001128168	3	16	8	+	110406790	110406955
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_001128173	5	15	7	+	110406790	110406955
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_001128166	1	16	8	+	110406790	110406955
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_001128167	2	15	7	+	110406790	110406955
271053099	chrX	110406721	110406861	110406748	110406839	PAK3	NM_002578	6	18	10	+	110406790	110406955
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_001128172	4	15	9	+	110435355	110435403
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_001128168	3	16	10	+	110435355	110435403
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_001128173	5	15	9	+	110435355	110435403
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_001128166	1	16	10	+	110435355	110435403
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_001128167	2	15	9	+	110435355	110435403
270241826	chrX	110435350	110435482	110435371	110435458	PAK3	NM_002578	6	18	12	+	110435355	110435403
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_001128172	4	15	11	+	110437529	110437646
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_001128168	3	16	12	+	110437529	110437646
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_001128173	5	15	11	+	110437529	110437646
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_001128166	1	16	12	+	110437529	110437646
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_001128167	2	15	11	+	110437529	110437646
270515896	chrX	110437518	110437680	110437544	110437652	PAK3	NM_002578	6	18	14	+	110437529	110437646
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_001128172	4	15	13	+	110439672	110439868
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_001128168	3	16	14	+	110439672	110439868
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_001128173	5	15	13	+	110439672	110439868
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_001128166	1	16	14	+	110439672	110439868
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_001128167	2	15	13	+	110439672	110439868
270768040	chrX	110439755	110439902	110439778	110439874	PAK3	NM_002578	6	18	16	+	110439672	110439868
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_001128172	4	15	15	+	110463586	110464173
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_001128168	3	16	16	+	110463586	110464173
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_001128173	5	15	15	+	110463586	110464173

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_001128166	1	16	16	+	110463586	110464173
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_001128167	2	15	15	+	110463586	110464173
272592175	chrX	110463571	110463745	110463594	110463718	PAK3	NM_002578	6	18	18	+	110463586	110464173
299080185	chrX	123503947	123504119	123503971	123504093	SH2D1A	NM_002351	2	4	3	+	123504026	123504170
299080185	chrX	123503947	123504119	123503971	123504093	SH2D1A	NM_001114937	1	4	3	+	123504026	123504161
295139298	chrX	152482143	152482304	152482168	152482282	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
295144058	chrX	152482555	152482725	152482576	152482702	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
294214787	chrX	152482967	152483133	152482986	152483109	MAGEA1	NM_004988	1	3	3	-	152481522	152483075
298909430	chrX	153760426	153760580	153760447	153760559	G6PD	NM_001042351	2	13	12	-	153760403	153760495
298909430	chrX	153760426	153760580	153760447	153760559	G6PD	NM_000402	1	13	12	-	153760403	153760495
299077514	chrX	153761136	153761302	153761154	153761284	G6PD	NM_001042351	2	13	9	-	153761157	153761343
299077514	chrX	153761136	153761302	153761154	153761284	G6PD	NM_000402	1	13	9	-	153761157	153761343
298994600	chrX	153762162	153762335	153762184	153762315	G6PD	NM_001042351	2	13	7	-	153762250	153762375
298994600	chrX	153762162	153762335	153762184	153762315	G6PD	NM_000402	1	13	7	-	153762250	153762375
298963808	chrX	153763305	153763441	153763326	153763424	G6PD	NM_001042351	2	13	5	-	153763383	153763600
298963808	chrX	153763305	153763441	153763326	153763424	G6PD	NM_000402	1	13	5	-	153763383	153763600
299075599	chrX	153764206	153764368	153764226	153764347	G6PD	NM_001042351	2	13	4	-	153764152	153764260
299075599	chrX	153764206	153764368	153764226	153764347	G6PD	NM_000402	1	13	4	-	153764152	153764260
298942621	chrX	153774892	153775065	153774913	153775048	G6PD	NM_000402	1	13	1	-	153775004	153775233
343115165	chr10	89720663	89720774	89720696	89720747	PTEN	NM_000314	1	9	8	+	89720651	89720875
343115166	chr11	108173586	108173694	108173614	108173666	ATM	NM_000051	1	63	36	+	108173580	108173756
343115167	chr11	108180901	108181025	108180929	108180995	ATM	NM_000051	1	63	39	+	108180887	108181042
343115168	chr11	108204603	108204717	108204635	108204684	ATM	NM_000051	1	63	54	+	108204613	108204695
343115169	chr13	48919199	48919324	48919232	48919296	RB1	NM_000321	1	27	4	+	48919216	48919335
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126117	7	8	7	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126116	6	8	7	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126113	3	12	11	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_000546	1	11	10	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126118	8	10	9	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126114	4	12	11	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126112	2	11	10	-	7573927	7574033
343115170	chr17	7573976	7574097	7573998	7574069	TP53	NM_001126115	5	7	6	-	7573927	7574033
343115171	chr3	178927906	178928013	178927932	178927986	PIK3CA	NM_006218	1	21	8	+	178927974	178928126
343115173	chr4	55140963	55141091	55140989	55141063	PDGFRA	NM_006206	1	23	12	+	55141008	55141140
343115174	chr4	55593558	55593712	55593583	55593689	KIT	NM_000222	1	21	11	+	55593582	55593708
343115174	chr4	55593558	55593712	55593583	55593689	KIT	NM_001093772	2	21	11	+	55593582	55593708
343115175	chr5	112175561	112175714	112175582	112175690	APC	NM_000038	1	16	16	+	112173250	112181936
343115175	chr5	112175561	112175714	112175582	112175690	APC	NM_001127510	2	17	17	+	112173250	112181936
343115175	chr5	112175561	112175714	112175582	112175690	APC	NM_001127511	3	14	14	+	112173250	112181936
326727246	chr3	41265929	41266165	41265956	41266142	CTNNB1	NM_001904	3	15	3	+	41266017	41266244
326727246	chr3	41265929	41266165	41265956	41266142	CTNNB1	NM_001098209	1	16	3	+	41266017	41266244

TABLE 18

Amplicon ID	Amplicon Chr	Amplicon Start	Amplicon End	Amplicon Insert Start	Amplicon Insert End	Gene Symbol	Accession	Transcript #	Number of Exons	Exon #	Strand	Exon Start	Exon End
32672724	chr3	41265929	41266165	41265956	41266142	CTNNB1	NM_001098210	2	16	3	+	41266017	41266244

TABLE 19

SEQ ID NO		
103122	AMP_114F_deoxyI_GSP	CCTGCAA/ideoxyI/TAATTT/ideoxyI/AAGAGTT/ideoxyI/T
103123	AMP_114R_deoxyI_GSP	TGGCAAC/ideoxyI/ACATTCA/ideoxyI/TTATTTAATT/ideoxyI/G
103124	AMP_135F_deoxyI_GSP	GAAGG/ideoxyI/TGTTGA/ideoxyI/GCAAC/ideoxyI/G
103125	AMP_135R_deoxyI_GSP	ACAAC/ideoxyI/GGCAAAC/ideoxyI/GATG/ideoxyI/CA
103126	AMP_170F_deoxyI_GSP	GACTGTA/ideoxyI/CCTGGA/ideoxyI/ATTATTCTT/ideoxyI/T
103127	AMP_170R_deoxyI_GSP	TCT/ideoxyI/TCAA/ideoxyI/ACAACACACAAAC/ideoxyI/CT
103128	AMP_185F_deoxyI_GSP	ATGAT/ideoxyI/CTGGAGT/ideoxyI/TTCATGTG/ideoxyI/T
103129	AMP_185R_deoxyI_GSP	TCTTCT/ideoxyI/TCACTAC/ideoxyI/GCCAGTAA/ideoxyI/T
103130	AMP_206F_deoxyI_GSP	GCATAA/ideoxyI/AATAGG/ideoxyI/ATAGCTTCC/ideoxyI/G
103131	AMP_206R_deoxyI_GSP	TGATA/ideoxyI/ACAGCAACA/ideoxyI/CTCTCTT/ideoxyI/G
103132	AMP_411F_deoxyI_GSP	ACATCA/ideoxyI/CTACAGT/ideoxyI/CCTCATG/ideoxyI/A
103133	AMP_411R_deoxyI_GSP	GCG/ideoxyI/GGT/ideoxyI/CCA/ideoxyI/CCC
103134	AMP_550F_deoxyI_GSP	AAAGAA/ideoxyI/GGCAGAC/ideoxyI/GACAG/ideoxyI/T
103135	AMP_550R_deoxyI_GSP	TGACT/ideoxyI/ATTTT/ideoxyI/ACCAAGAGT/ideoxyI/CA
103136	AMP_576F_deoxyI_GSP	TCTGTTT/ideoxyI/ATGTTT/ideoxyI/CATTCTTG/ideoxyI/G
103137	AMP_576R_deoxyI_GSP	GAACA/ideoxyI/TCTGG/ideoxyI/TGGAAT/ideoxyI/G
103138	AMP_650F_deoxyI_GSP	TTCAAG/ideoxyI/GAGTGG/ideoxyI/AGCAG/ideoxyI/A
103139	AMP_650R_deoxyI_GSP	TTTTAAAAAA/ideoxyI/TTCTCTC/ideoxyI/TATGCTT/ideoxyI/C
103140	AMP_84F_deoxyI_GSP	GCAG/ideoxyI/CGTTCACAA/ideoxyI/GT/ideoxyI/CAT
103141	AMP_84R_deoxyI_GSP	AACA/ideoxyI/CCAAACAACAGTG/ideoxyI/G
103142	AMP_86F_deoxyI_GSP	ACAAGAA/ideoxyI/TAGCCA/ideoxyI/AAGAACA/ideoxyI/G
103143	AMP_86R_deoxyI_GSP	AAAAG/ideoxyI/ATAAGTT/ideoxyI/CCAACTGTT/ideoxyI/AT

“ideoxyI” denotes location of inosine within target-specific primer

CLAIMS

We claim:

1. A method for amplifying a plurality of different target sequences within a sample, comprising:

amplifying within a single amplification reaction mixture at least one hundred different target sequences from a sample including a plurality of different target sequences, wherein the amplifying includes contacting at least some portion of the sample with a plurality of target-specific primers, and a polymerase under amplification conditions, thereby producing at least one hundred different amplified target sequences, wherein at least two of the different amplified target sequences are less than 50% complementary to each other and wherein at least one of the plurality of target-specific primers and at least one of the amplified target sequences includes a cleavable group;

cleaving a cleavable group of at least one amplified target sequence;

ligating at least one adapter to at least one amplified target sequence in a blunt-ended ligation reaction, thereby producing one or more adapter-ligated amplified target sequences, and

reamplifying at least one of the adapter-ligated amplified target sequences.

2. The method of claim 1, wherein one or more of the at least one adapter is not substantially complementary to at least one amplified target sequence.

3. The method of claim 1, wherein the reamplifying includes contacting the at least one adapter-ligated amplified target sequence with one or more primers including a sequence that is complementary to at least one of the adapters or their complement, and a polymerase under amplification conditions, thereby producing at least one reamplified adapter-ligated amplified target sequence.

4. The method of claim 3, wherein at least one of the one or more adapters or their complements is not substantially complementary to at least one amplified target sequence.

5. The method of claim 1, wherein at least one target-specific primer is substantially complementary to at least a portion of a corresponding target sequence in the sample.

6. The method of claim 1, wherein an adapter that is ligated to at least one of the amplified target sequences is susceptible to exonuclease digestion.

7. The method of claim 1, wherein an adapter that is ligated to at least one of the amplified target sequences does not include a protecting group.

8. The method of claim 1, wherein the ligating includes contacting at least one amplified target sequence having a 3' end and a 5'end with a ligation reaction mixture including one or more adapters and a ligase under ligation conditions, wherein none of the adapters in the ligation reaction mixture includes, prior to the ligating, a target-specific sequence.

9. The method of claim 8, wherein the ligating includes contacting at least one amplified target sequence with a ligation reaction mixture including one or more adapters and a ligase under ligation conditions, wherein the ligation reaction mixture does not include one or more additional oligonucleotide adapters prior to ligating the one or more adapters to at least one amplified target sequence.

10. The method of claim 1, wherein the amplifying further includes a digestion step prior to the ligating, thereby producing a plurality of blunt-end amplified target sequences possessing a 5' phosphate group.

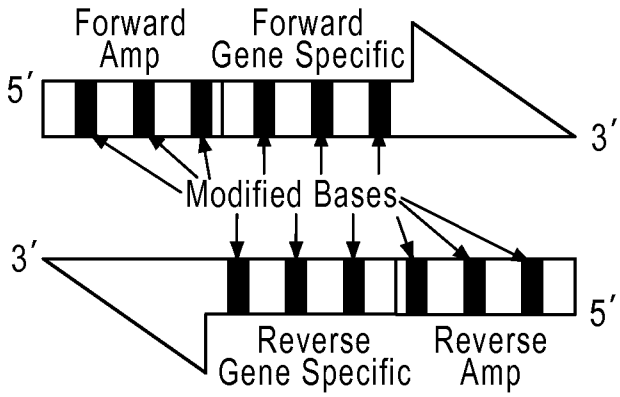


FIG. 1A

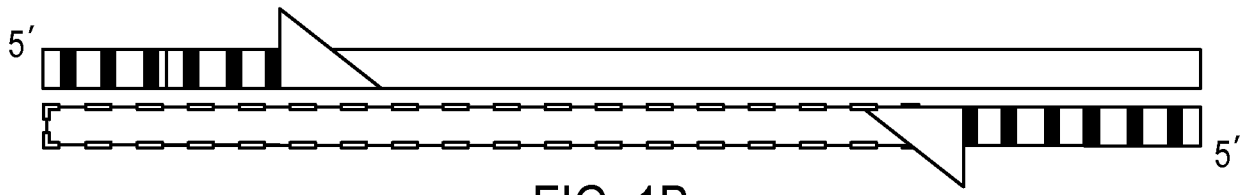


FIG. 1B1

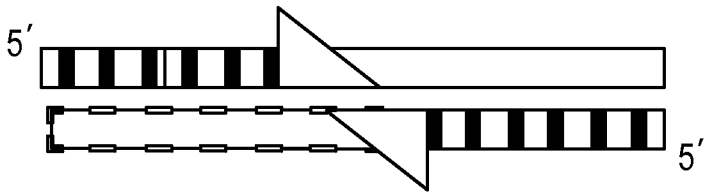


FIG. 1B2

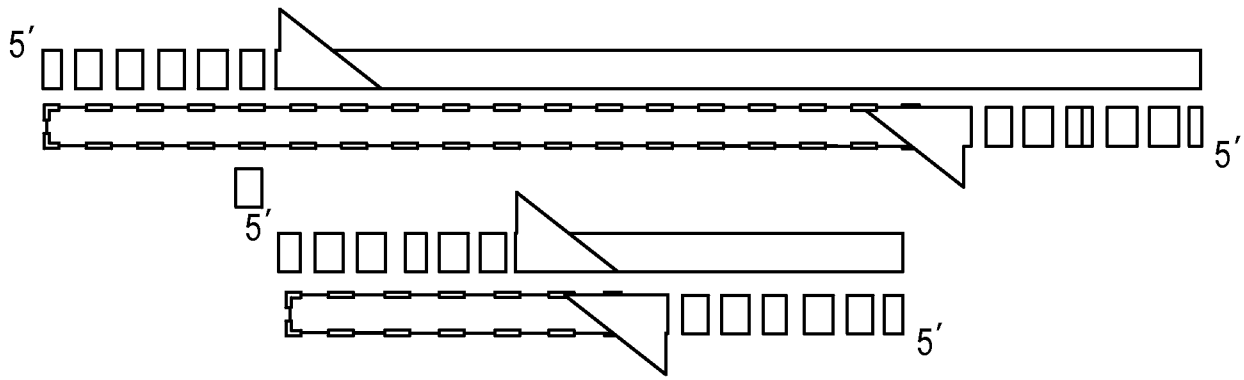


FIG. 1C1

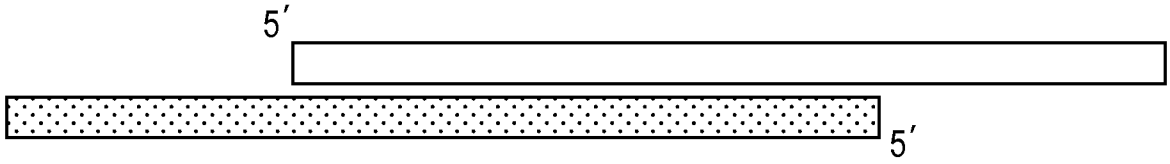


FIG. 1D1

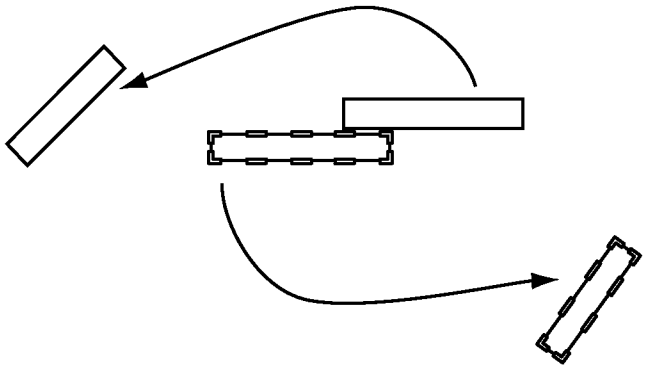


FIG. 1D2

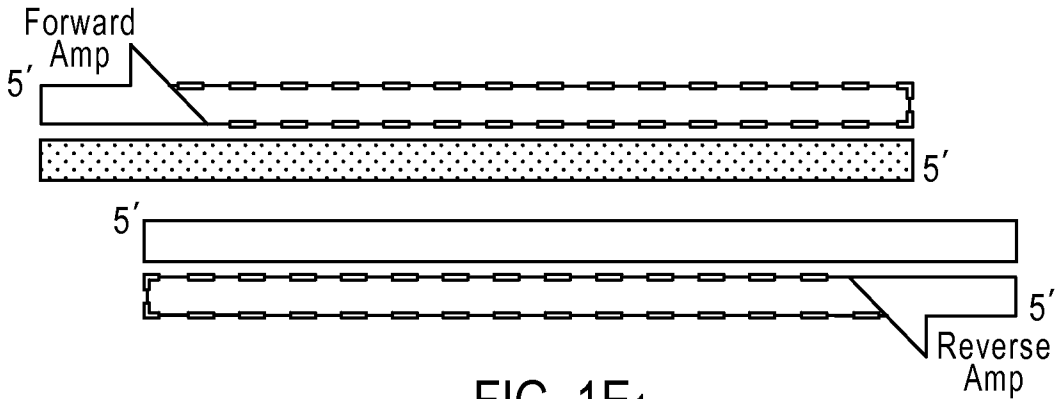


FIG. 1E1

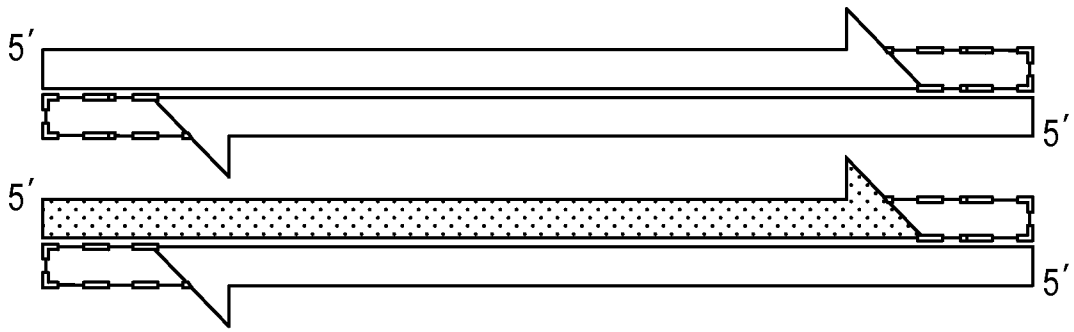


FIG. 1E1i

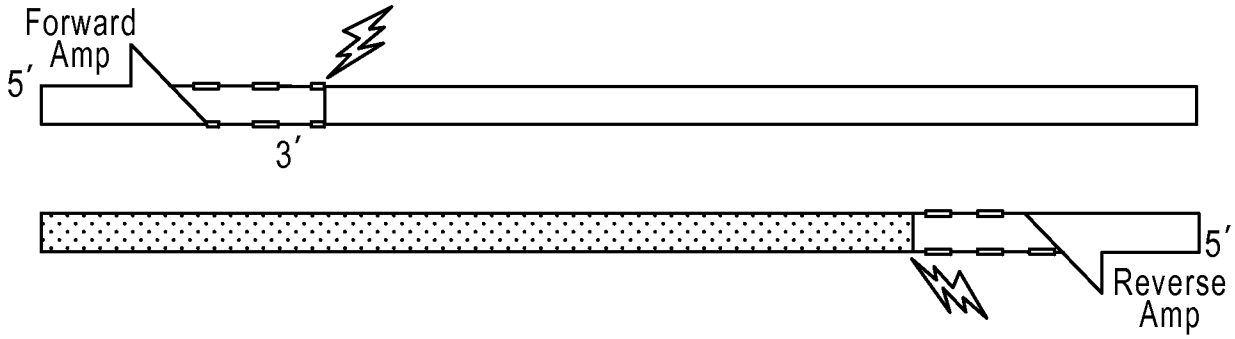


FIG. 1E2

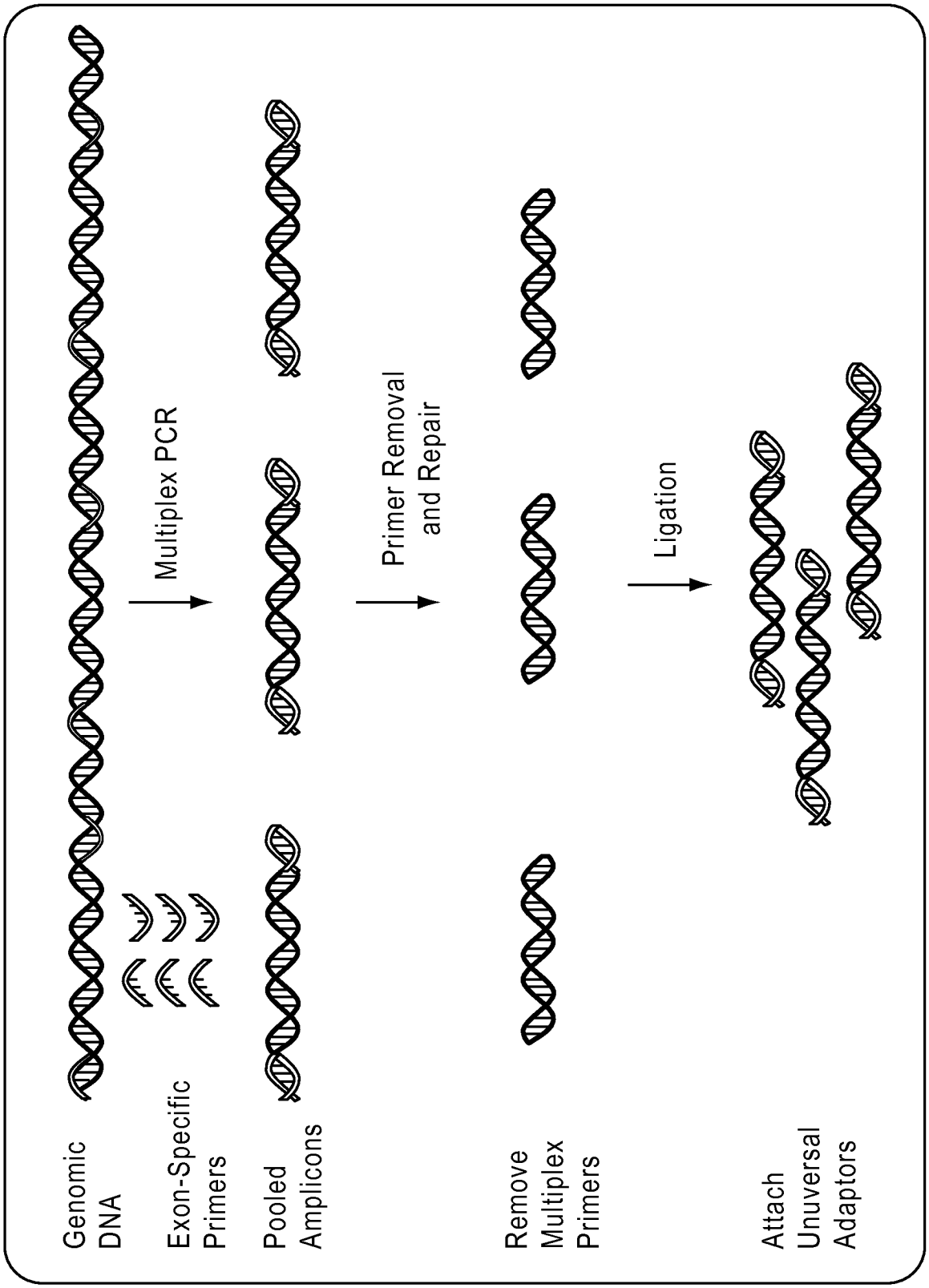

Genomic DNA
Exon-Specific Primers
Multiplex PCR
Pooled Amplicons
Primer Removal and Repair
Remove Multiplex Primers
Ligation
Attach Unuversal Adaptors

FIG. 2

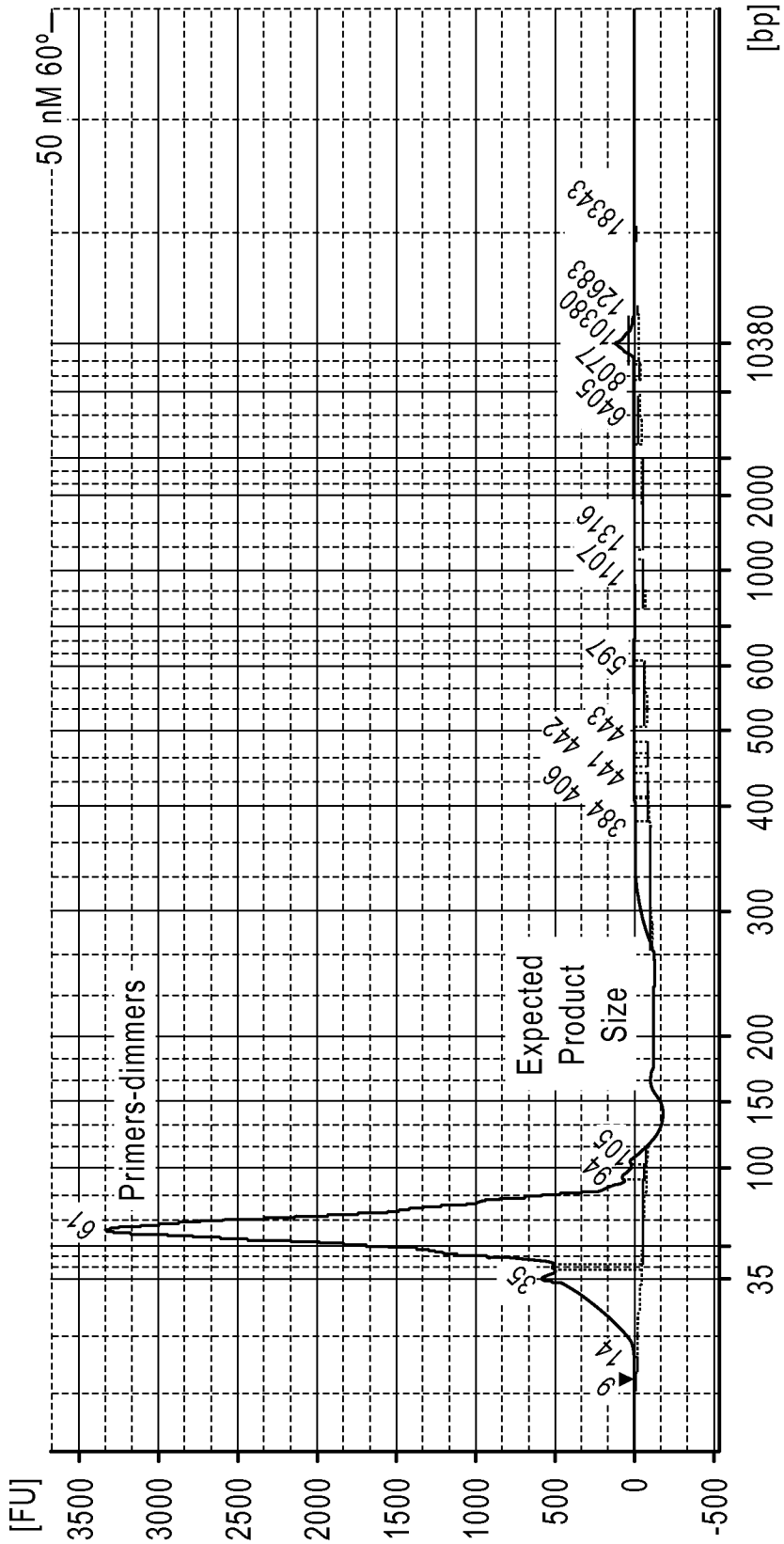

50 nM 60°
[FU]
3500
3000
2500
2000
1500
1000
500
0
-500
[bp]
35
100
150
200
300
400
500
600
1000
2000
10380
Primers-dimmers
Expected Product Size
67
35
9
14
94
105
384
406
441
442
443
597
1107
1316
6405
8077
10380
12683
18343

FIG. 3A

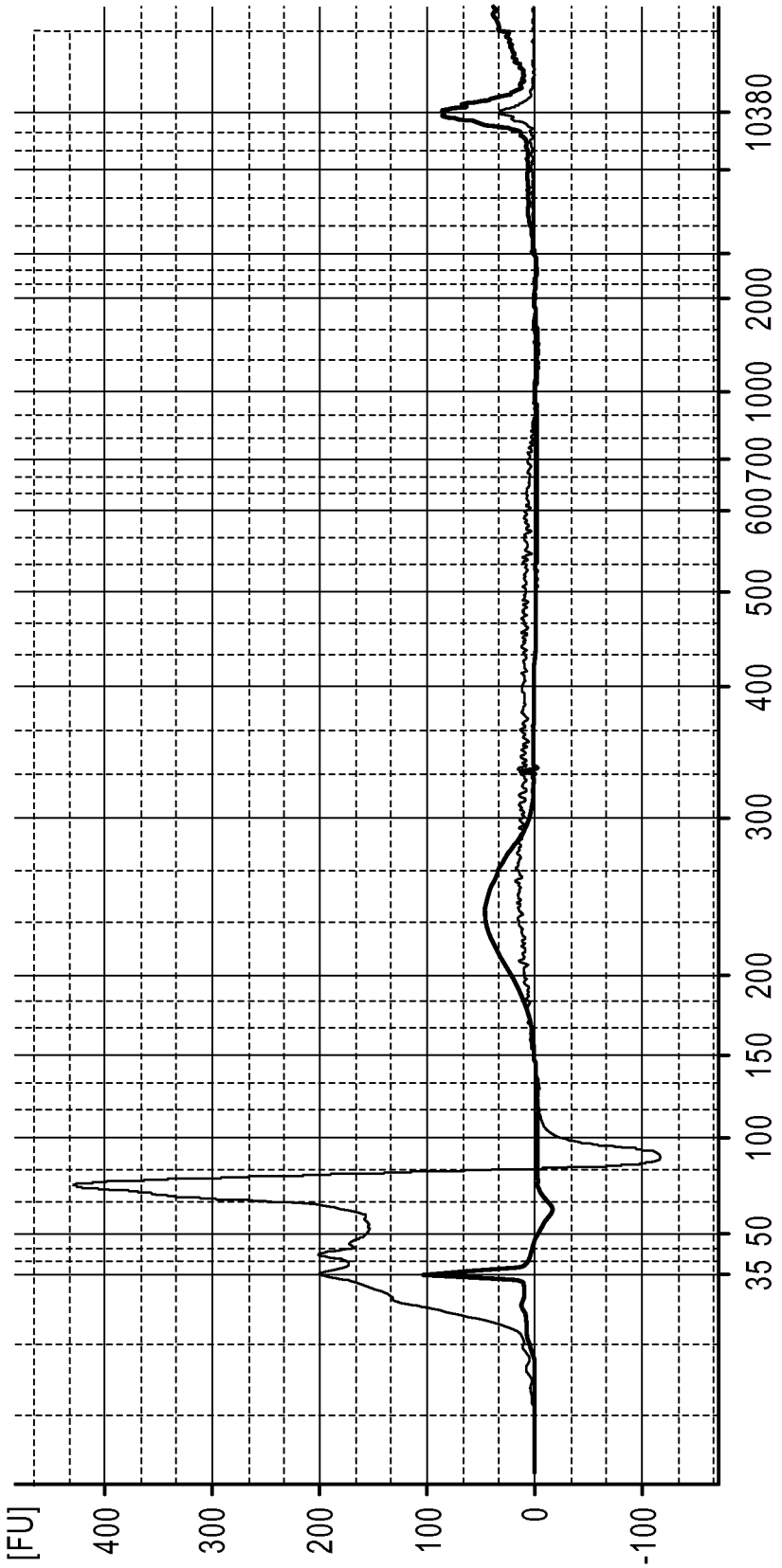

[FU]
400
300
200
100
0
-100
35 50 100 150 200 300 400 500 600 700 1000 2000 10380

FIG. 3B

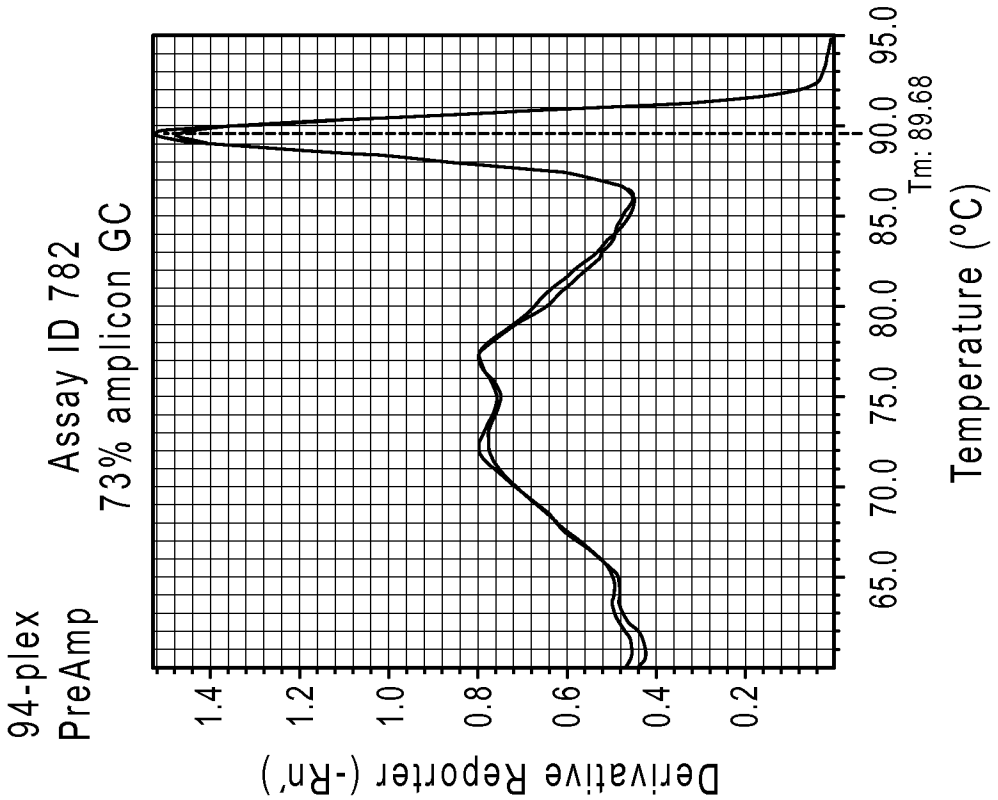

94-plex
PreAmp
Assay ID 782
73% amplicon GC
Derivative Reporter (-Rn')
1.4
1.2
1.0
0.8
0.6
0.4
0.2
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 89.68
Temperature (°C)

FIG. 4B

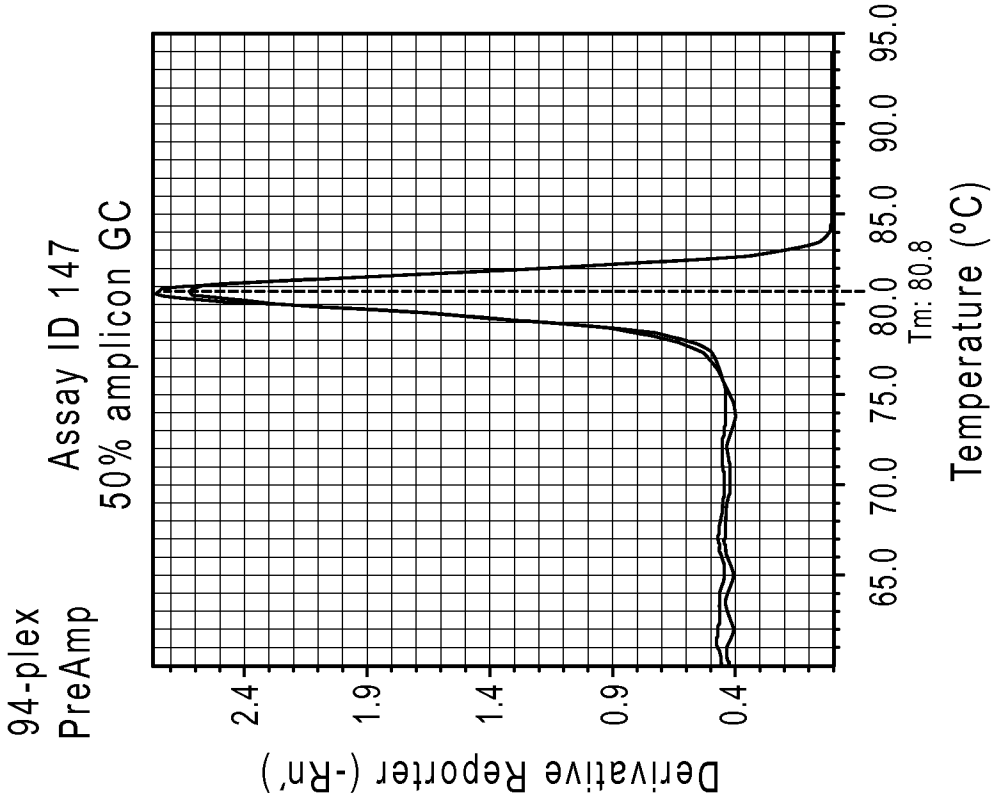

94-plex
PreAmp
Assay ID 147
50% amplicon GC
Derivative Reporter (-Rn')
2.4
1.9
1.4
0.9
0.4
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 80.8
Temperature (°C)

FIG. 4A

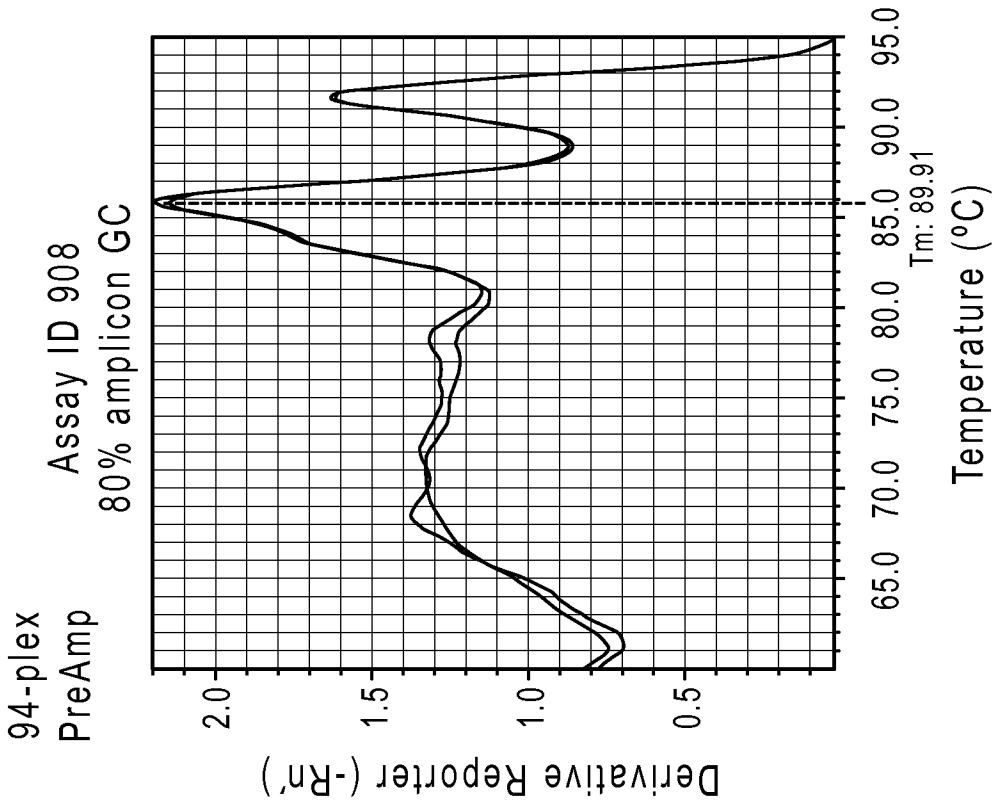

94-plex
PreAmp
Assay ID 908
80% amplicon GC
Derivative Reporter (-Rn')
2.0
1.5
1.0
0.5
65.0
70.0
75.0
80.0
85.0
90.0
95.0
Tm: 89.91
Temperature (°C)

FIG. 4D

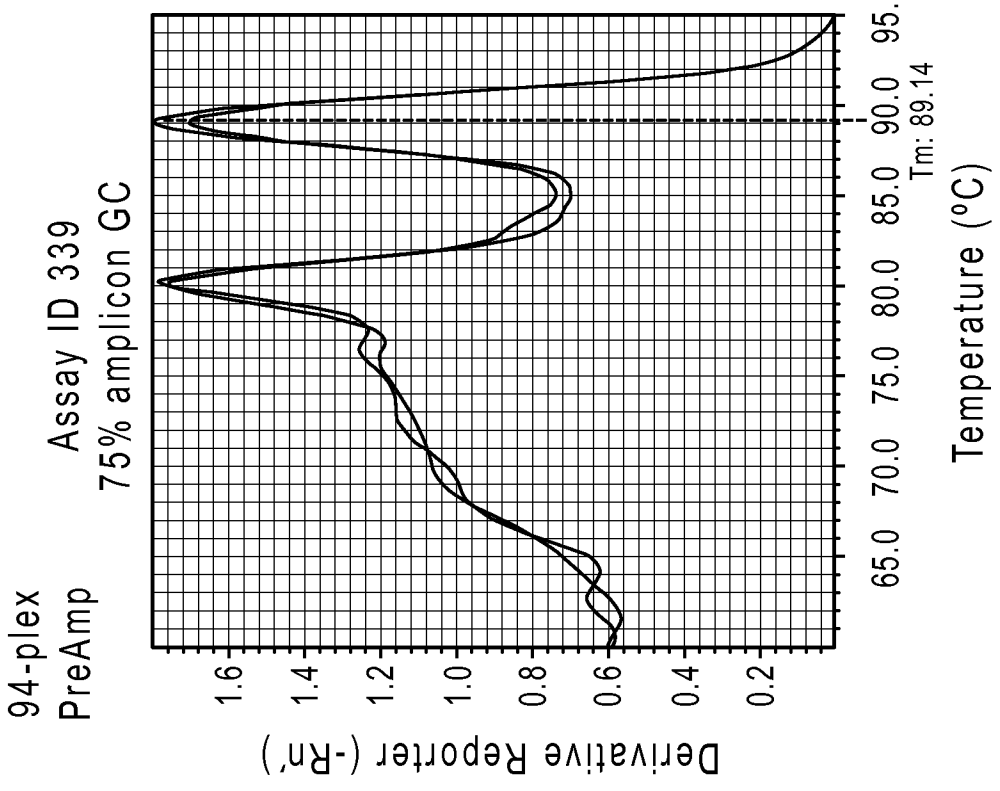

94-plex
PreAmp
Assay ID 339
75% amplicon GC
Derivative Reporter (-Rn')
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
65.0
70.0
75.0
80.0
85.0
90.0
95.0
Tm: 89.14
Temperature (°C)

FIG. 4C

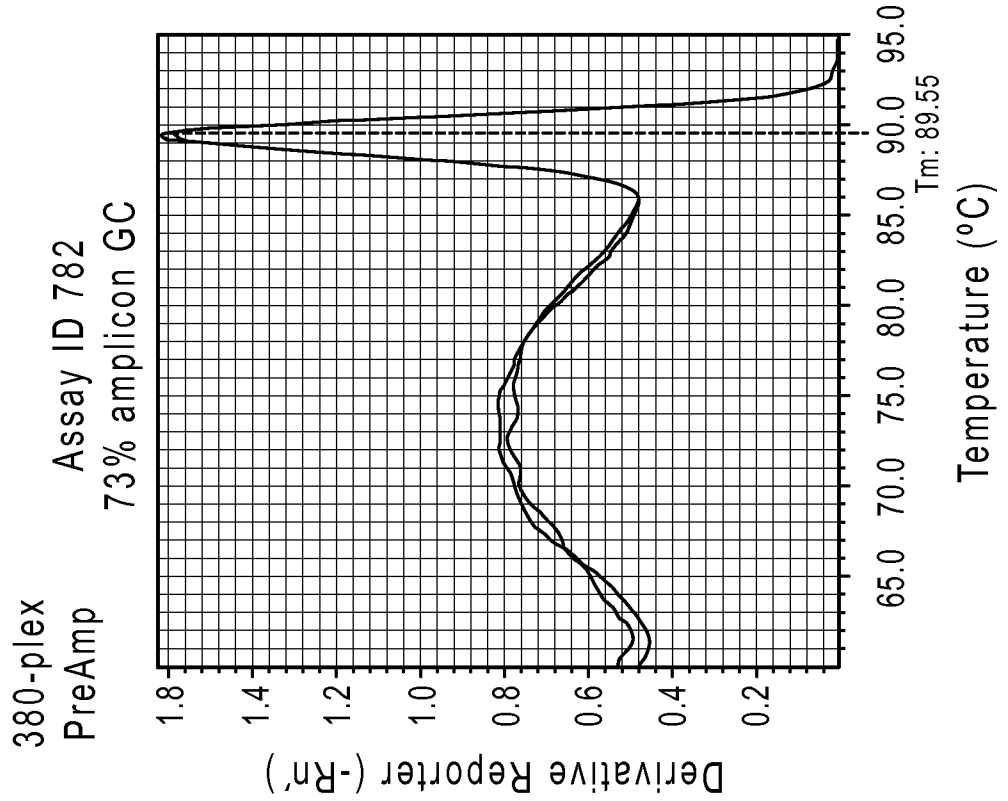

380-plex
PreAmp
Assay ID 782
73% amplicon GC
Derivative Reporter (-Rn')
1.8
1.4
1.2
1.0
0.8
0.6
0.4
0.2
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 89.55
Temperature (°C)

FIG. 4F

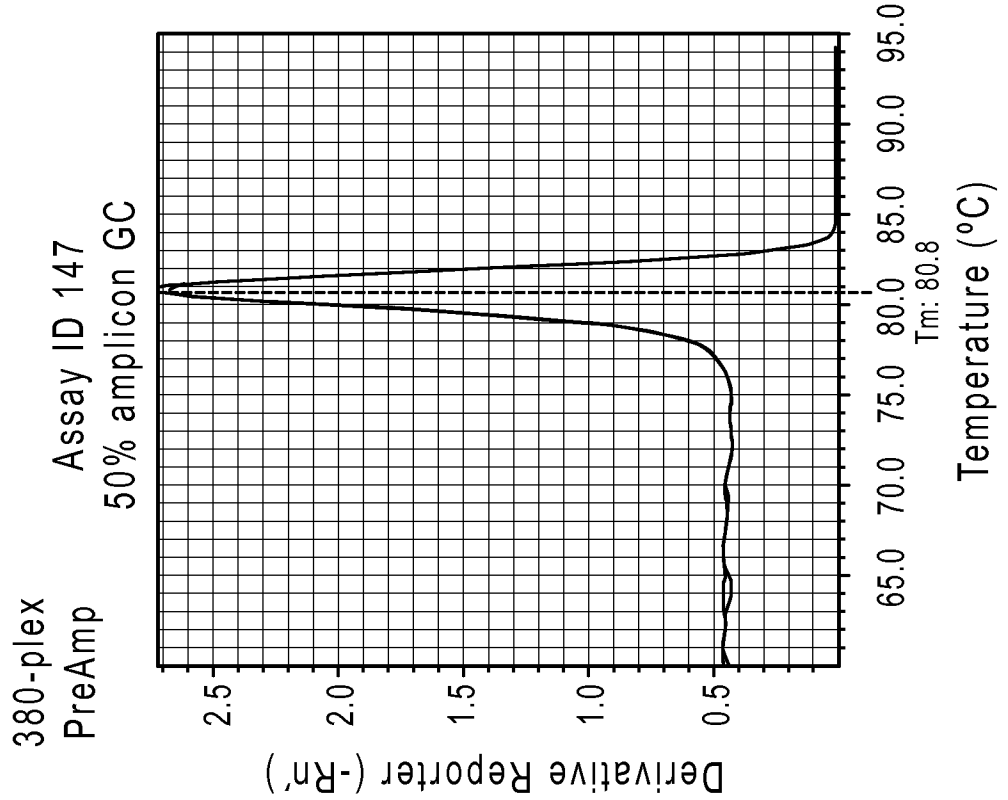

380-plex
PreAmp
Assay ID 147
50% amplicon GC
Derivative Reporter (-Rn')
2.5
2.0
1.5
1.0
0.5
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 80.8
Temperature (°C)

FIG. 4E

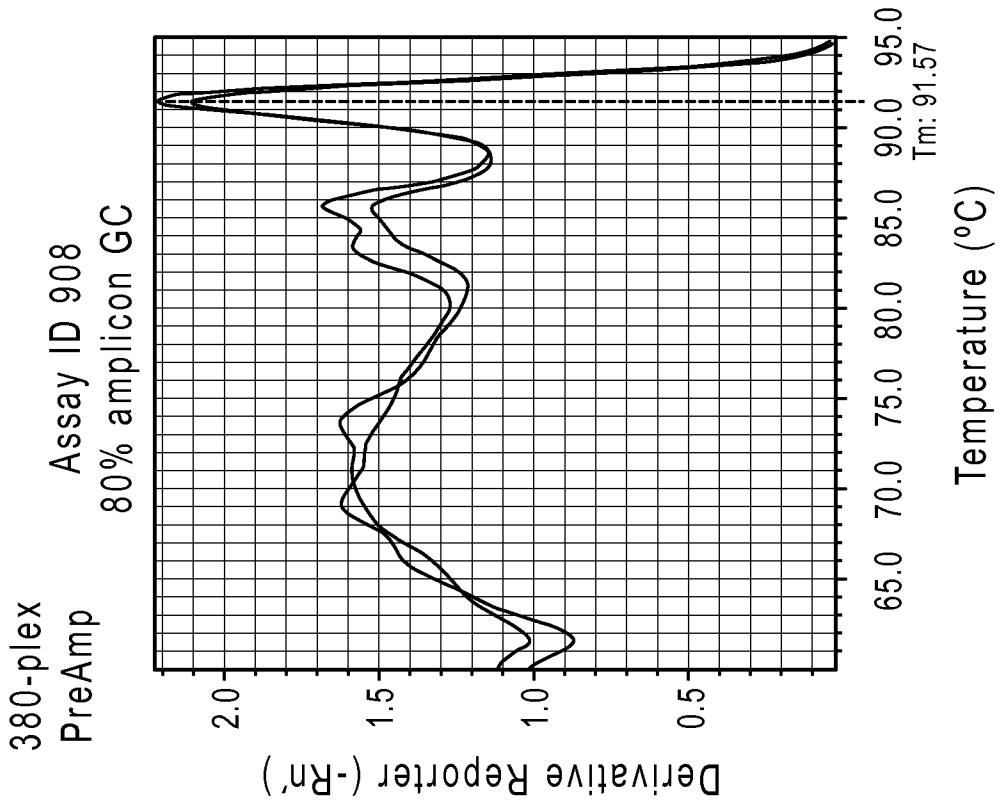

380-plex
PreAmp
Assay ID 908
80% amplicon GC
Derivative Reporter (-Rn')
2.0
1.5
1.0
0.5
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 91.57
Temperature (°C)

FIG. 4H

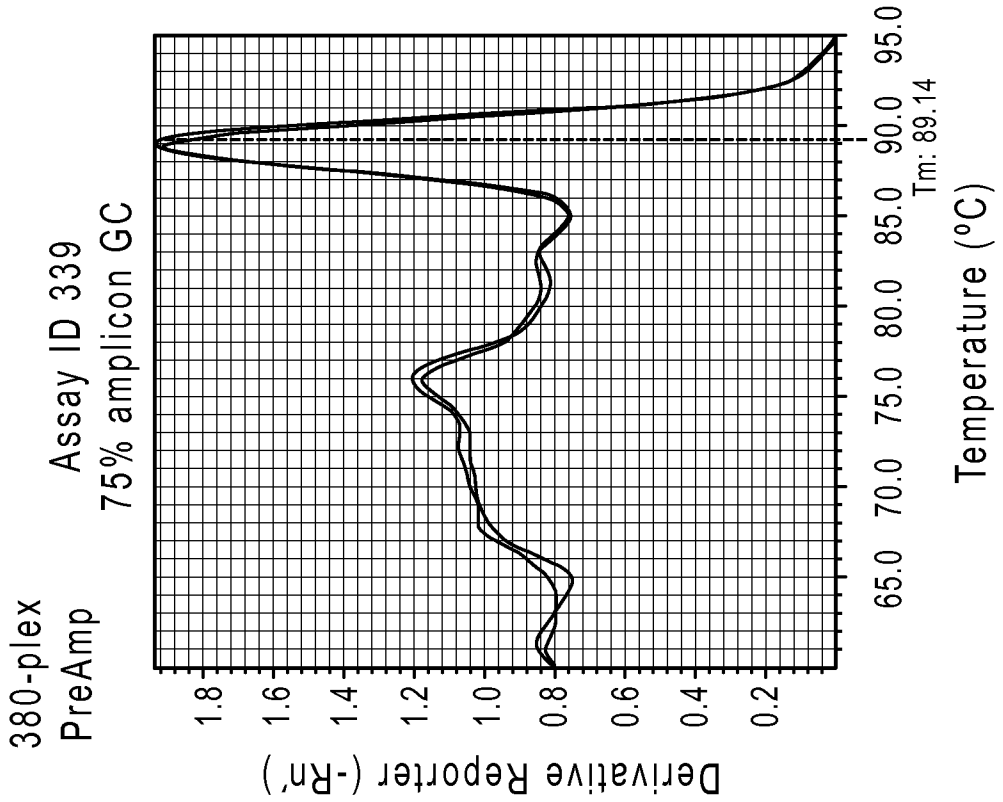

380-plex
PreAmp
Assay ID 339
75% amplicon GC
Derivative Reporter (-Rn')
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
65.0 70.0 75.0 80.0 85.0 90.0 95.0
Tm: 89.14
Temperature (°C)

FIG. 4G

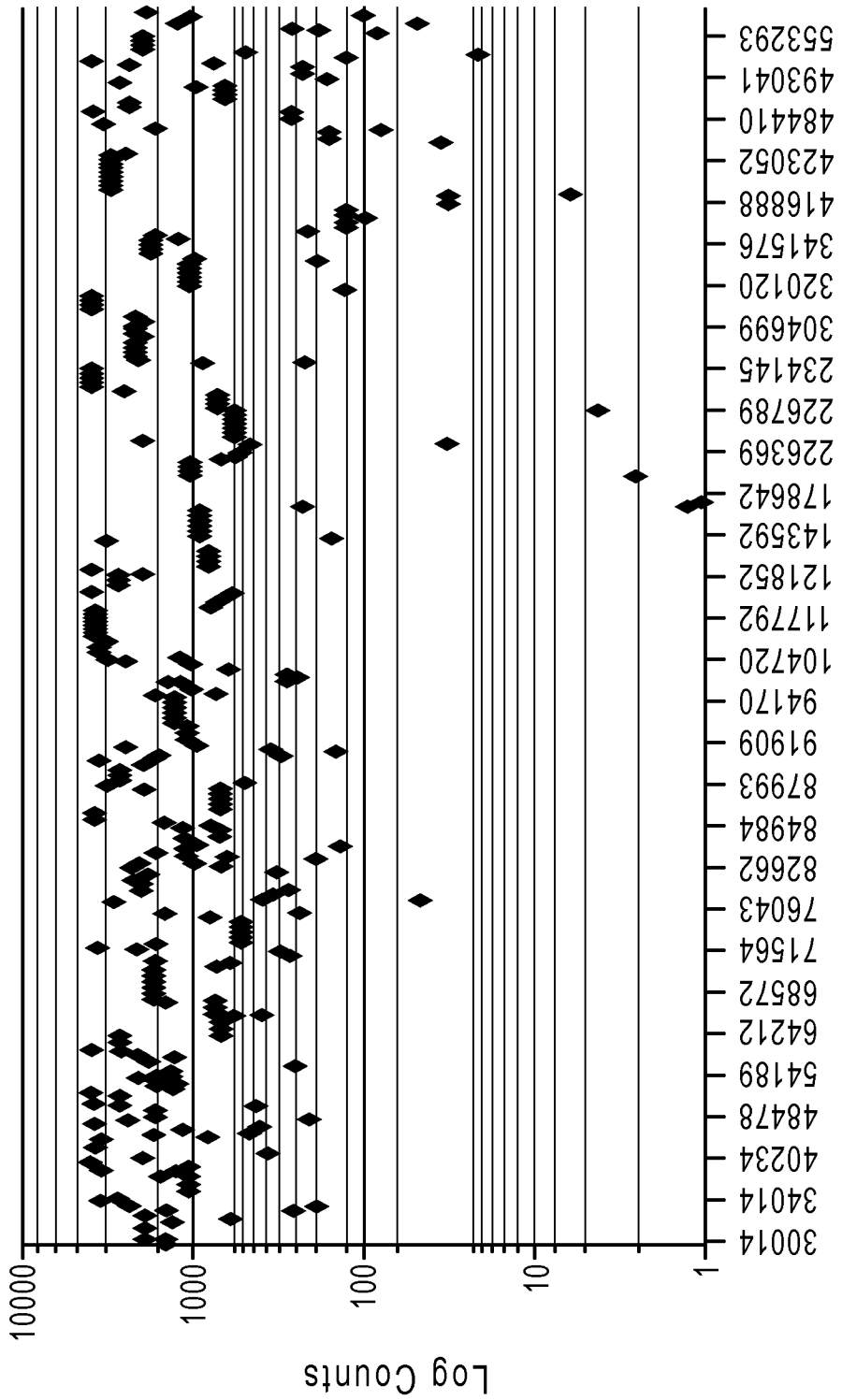

Log Counts
10000
1000
100
10
1
300 14
340 14
402 34
484 78
541 89
642 12
685 72
715 64
760 43
826 62
849 84
879 93
919 09
941 70
1047 20
1177 92
1218 52
1435 92
1786 42
2263 69
2267 89
2341 45
3046 99
3201 20
3415 76
4168 88
4230 52
4844 10
4930 41
5532 93

FIG. 5

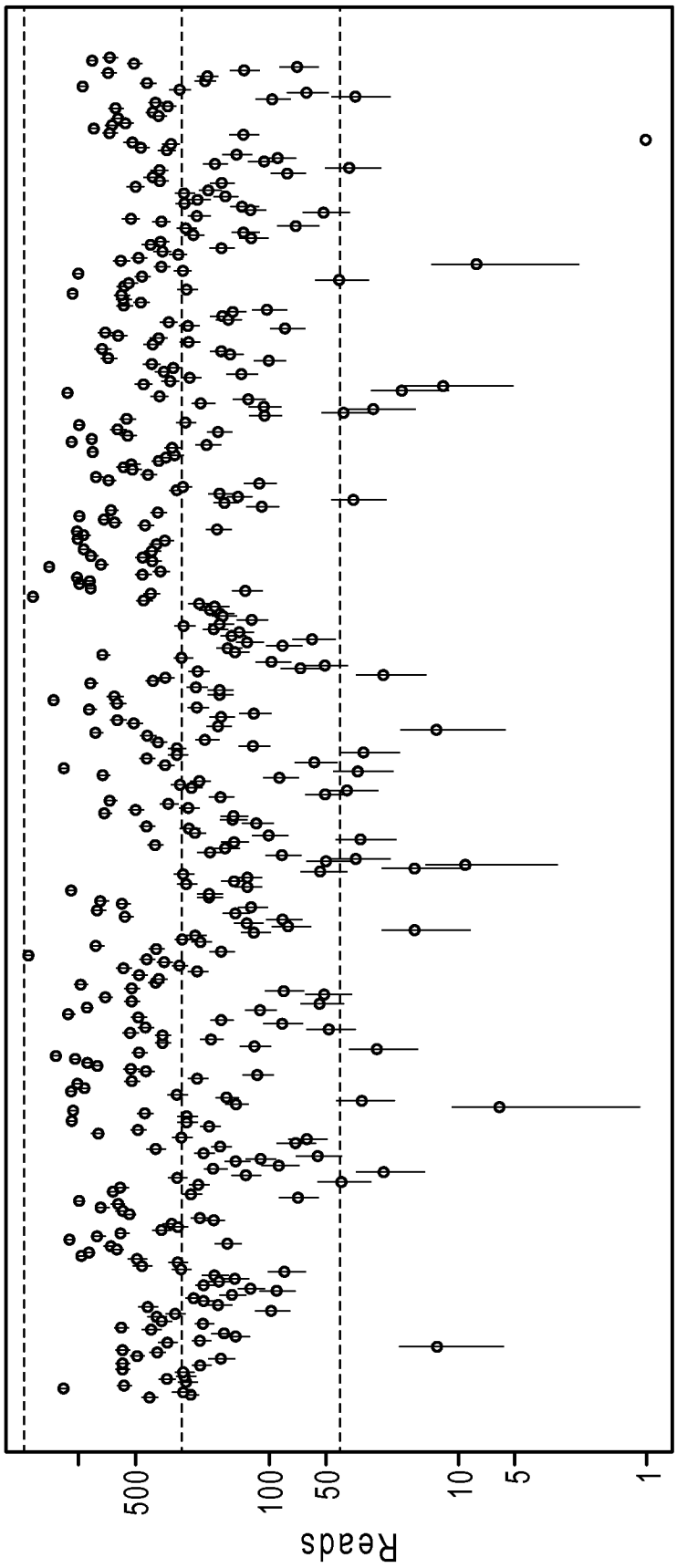


FIG. 6A

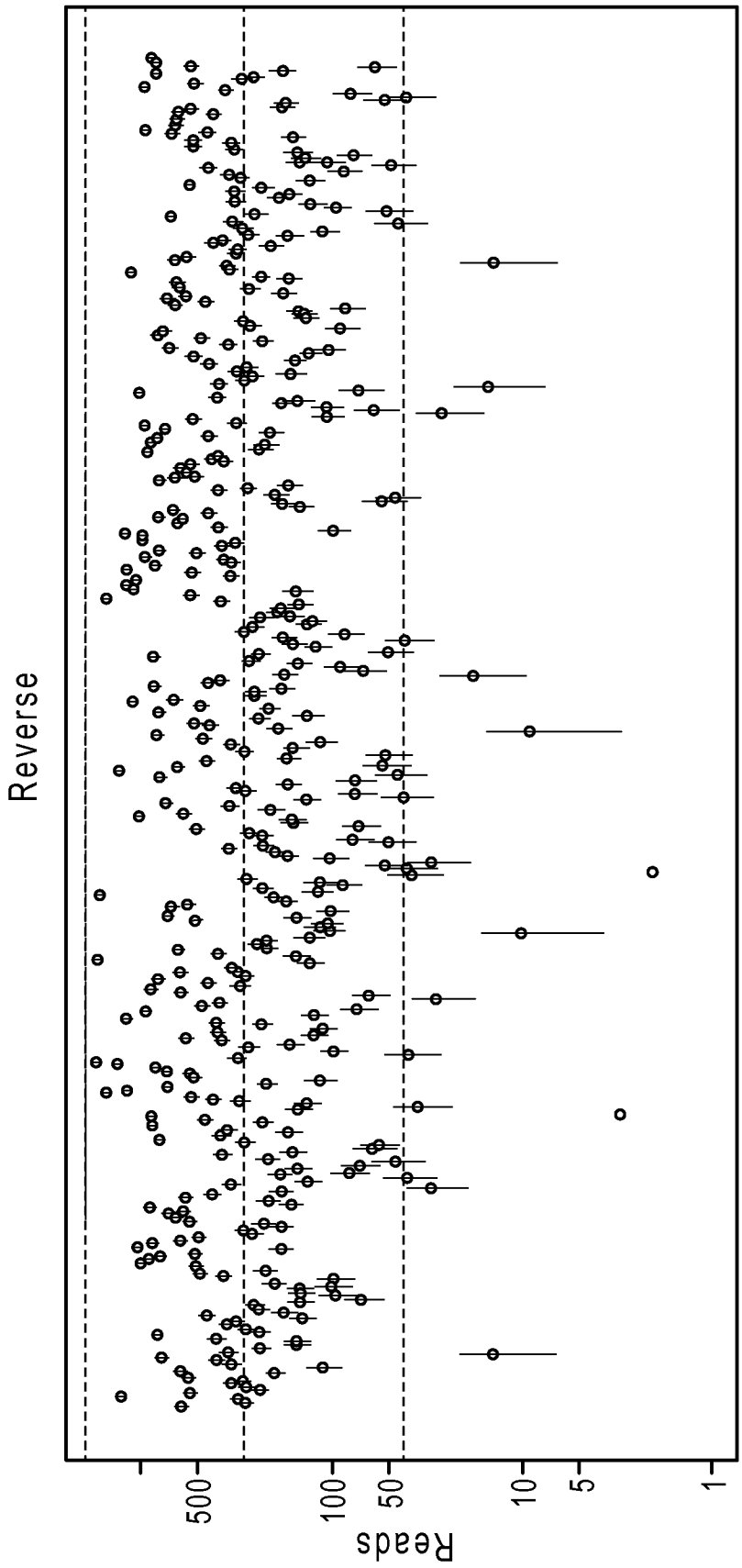


FIG. 6B

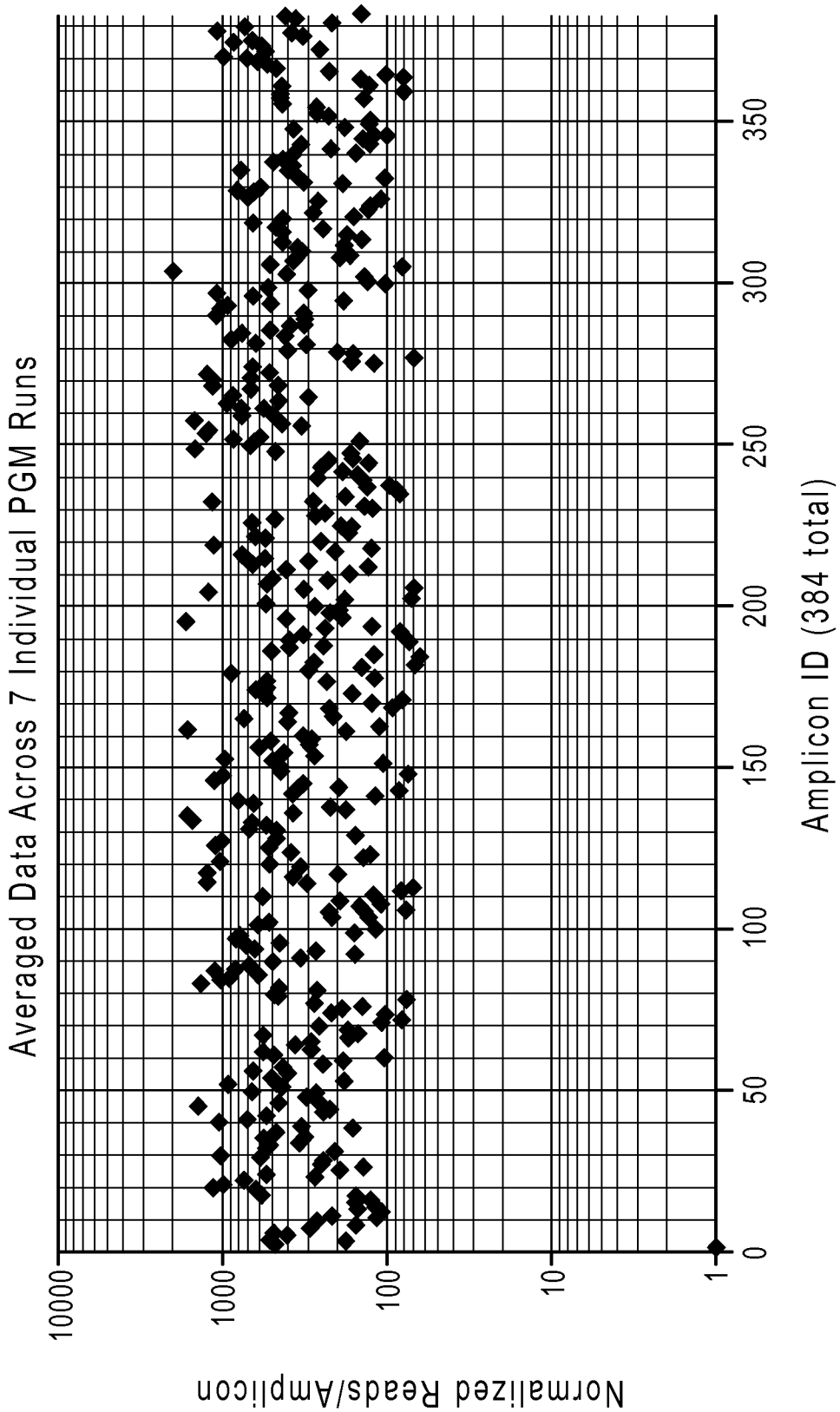

Averaged Data Across 7 Individual PGM Runs
Normalized Reads/Amplicon
10000
1000
100
10
1
0
50
100
150
200
250
300
350
Amplicon ID (384 total)

FIG. 7

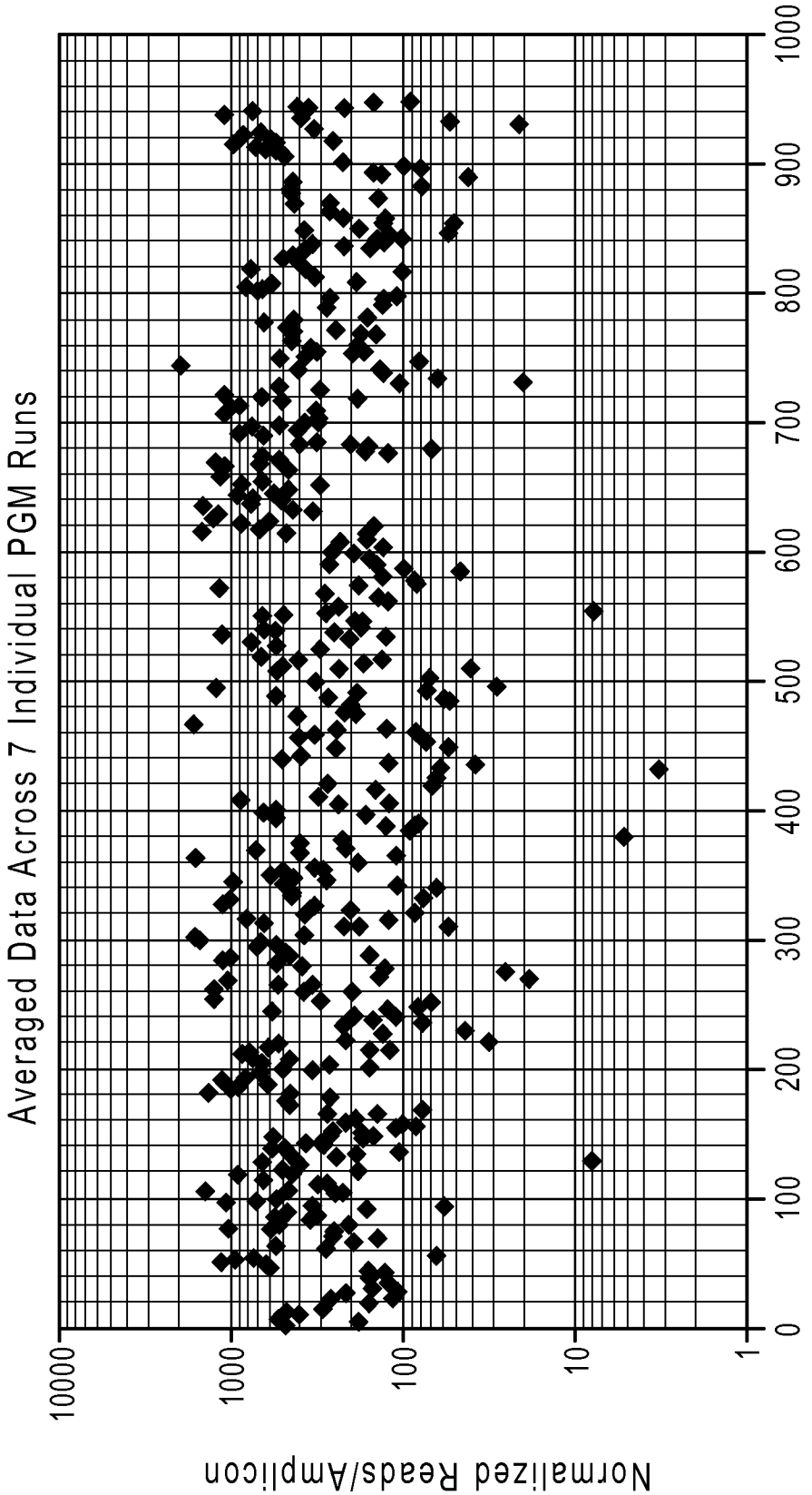

Averaged Data Across 7 Individual PGM Runs
Normalized Reads/Amplicon
10000
1000
100
10
1
0
100
200
300
400
500
600
700
800
900
1000
Amplicon ID (411 total)

FIG. 8

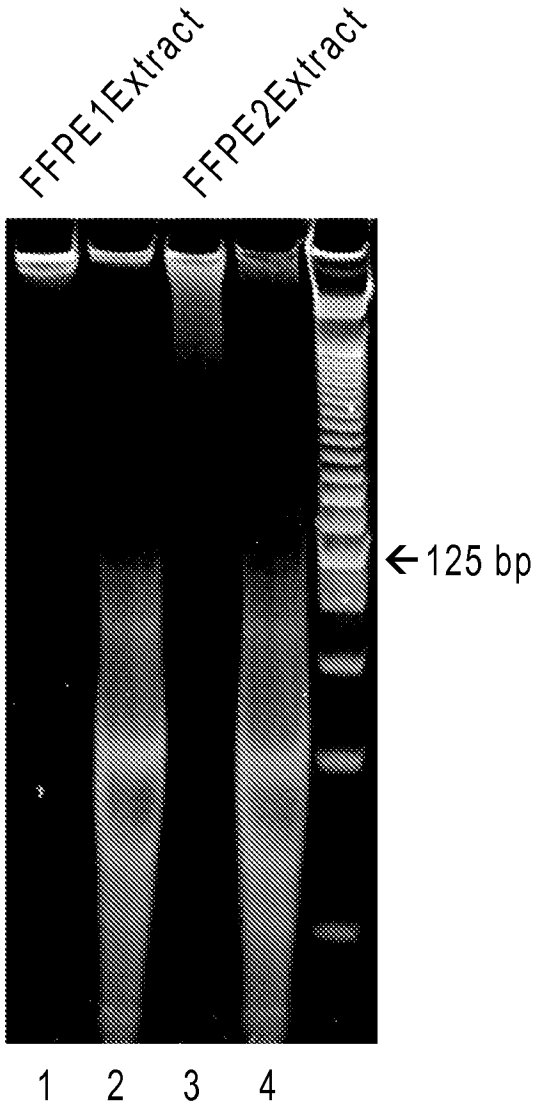


FIG. 9

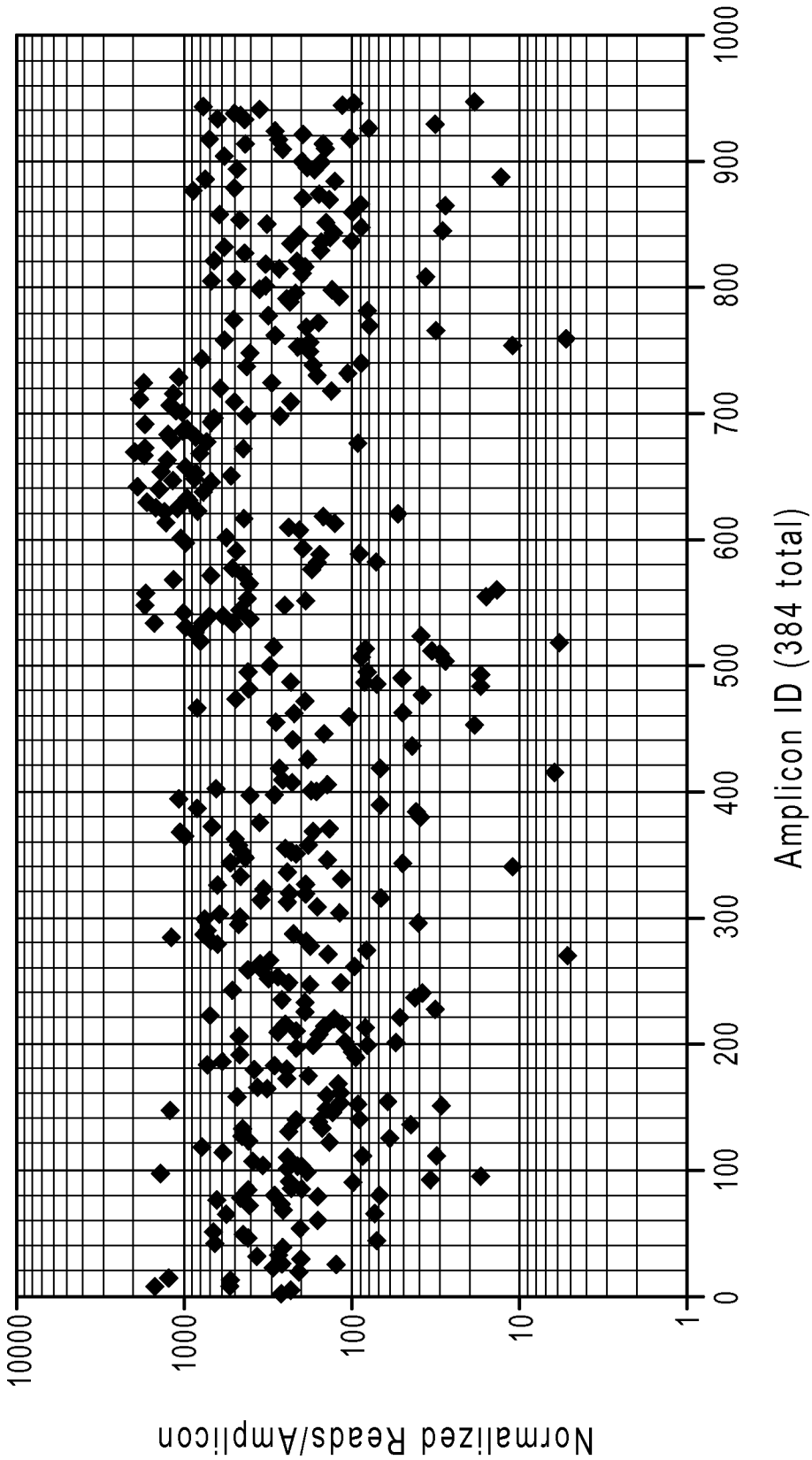

Normalized Reads/Amplicon
10000
1000
100
10
1
Amplicon ID (384 total)
0
100
200
300
400
500
600
700
800
900
1000

FIG. 10

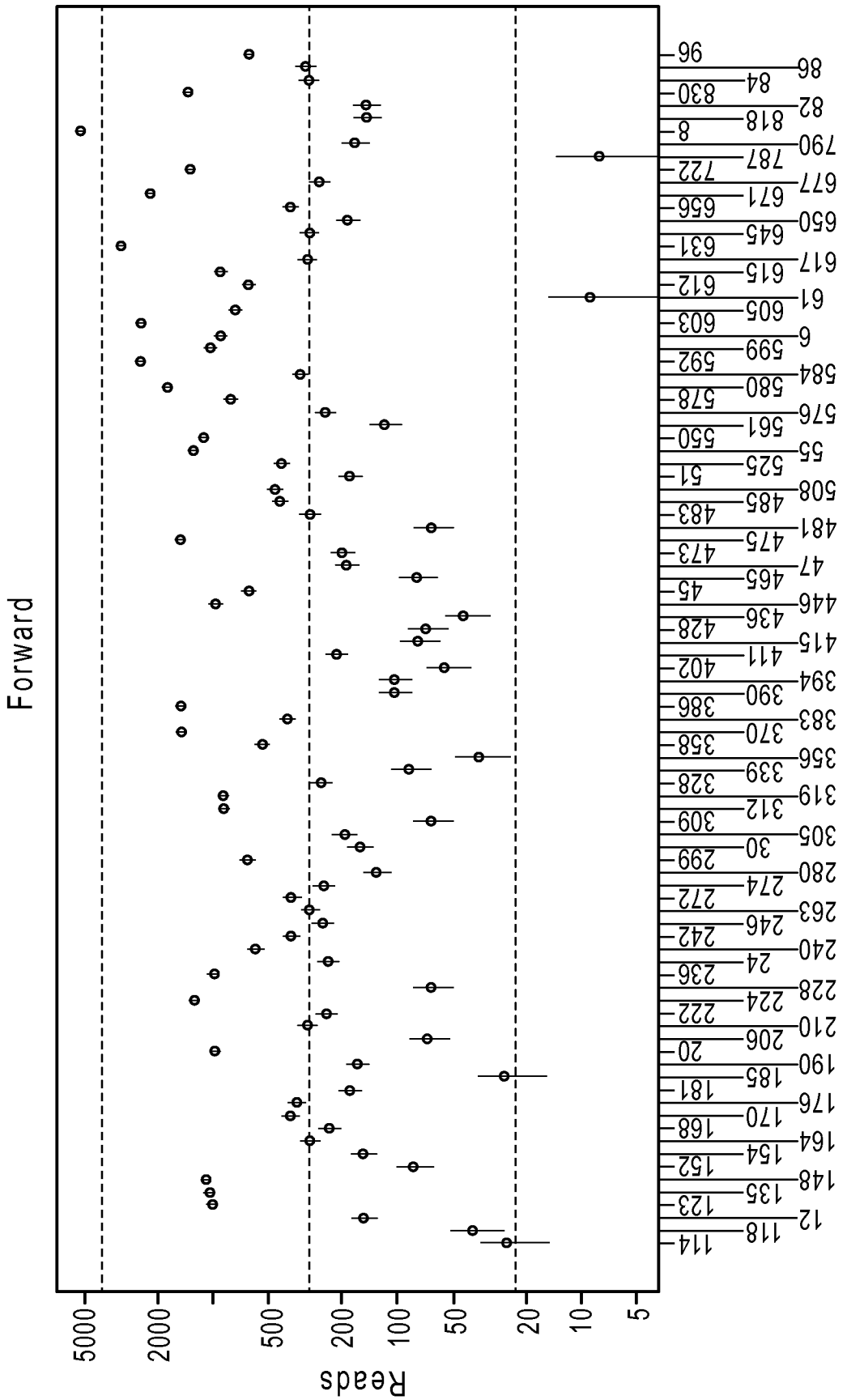

Forward
Reads
5000
2000
500
200
100
50
20
10
5
96
86
84
830
82
818
8
790
787
722
677
671
656
650
645
631
617
615
612
61
605
603
6
599
592
584
580
578
576
561
550
55
525
51
508
485
483
481
475
473
47
465
45
446
436
428
415
411
402
394
390
386
383
370
358
356
339
328
319
312
309
305
30
299
280
274
272
263
246
242
240
24
236
228
224
222
210
206
20
190
185
181
176
170
168
164
154
152
148
135
123
12
118
114

FIG. 11A

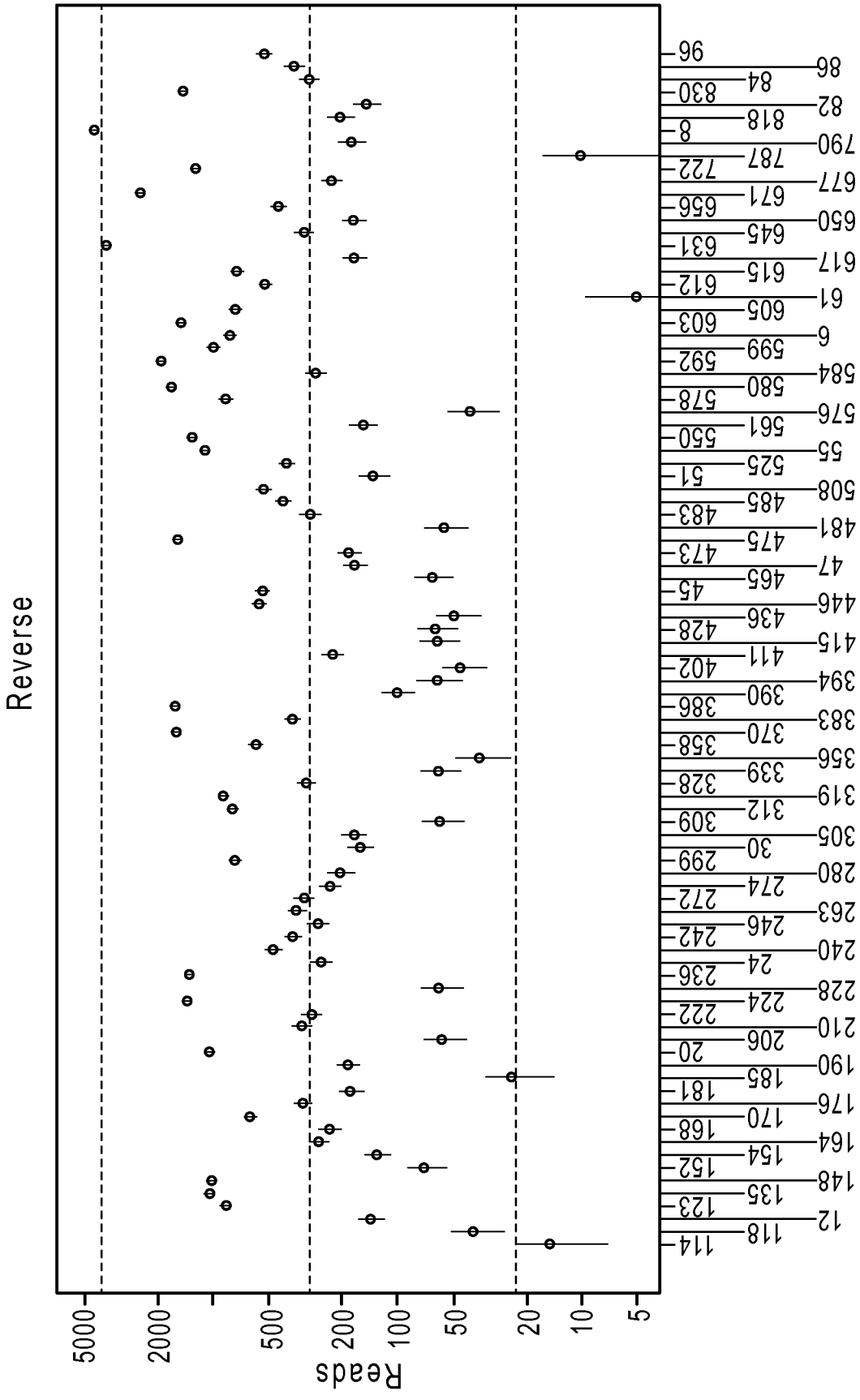

Reverse
Reads
5000
2000
500
200
100
50
20
10
5
96
86
84
830
82
818
8
790
787
722
677
671
656
650
645
631
617
615
612
61
605
603
6
599
592
584
580
578
576
561
550
55
525
51
508
485
483
481
475
473
47
465
45
446
436
428
415
411
402
394
390
386
383
370
358
356
339
328
319
312
309
305
30
299
280
274
272
263
246
242
240
24
236
228
224
222
210
206
20
190
185
181
176
170
168
164
154
152
148
135
123
12
118
114

FIG. 11B

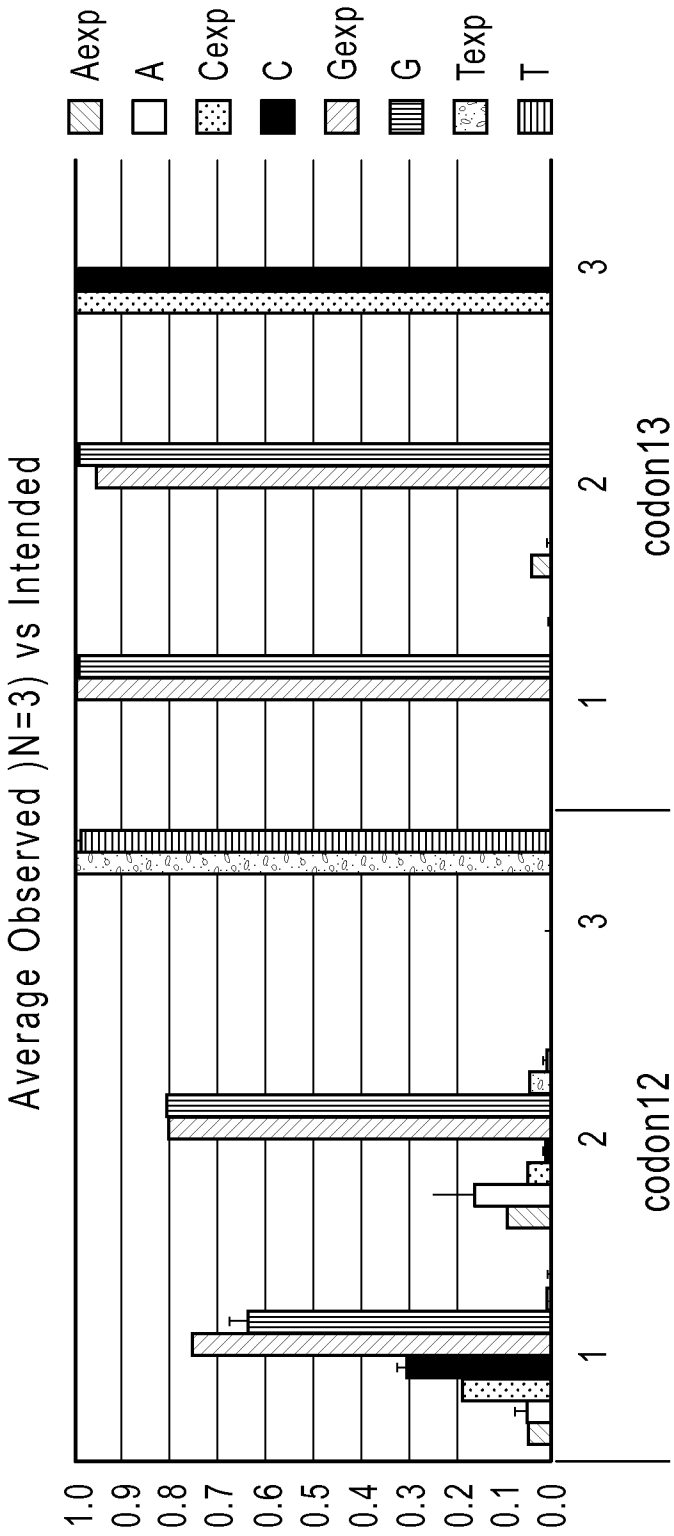

Aexp
A
Cexp
C
Gexp
G
Texp
T
Average Observed)N=3) vs Intended
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
1
2
3
codon12
1
2
3
codon13

FIG. 12

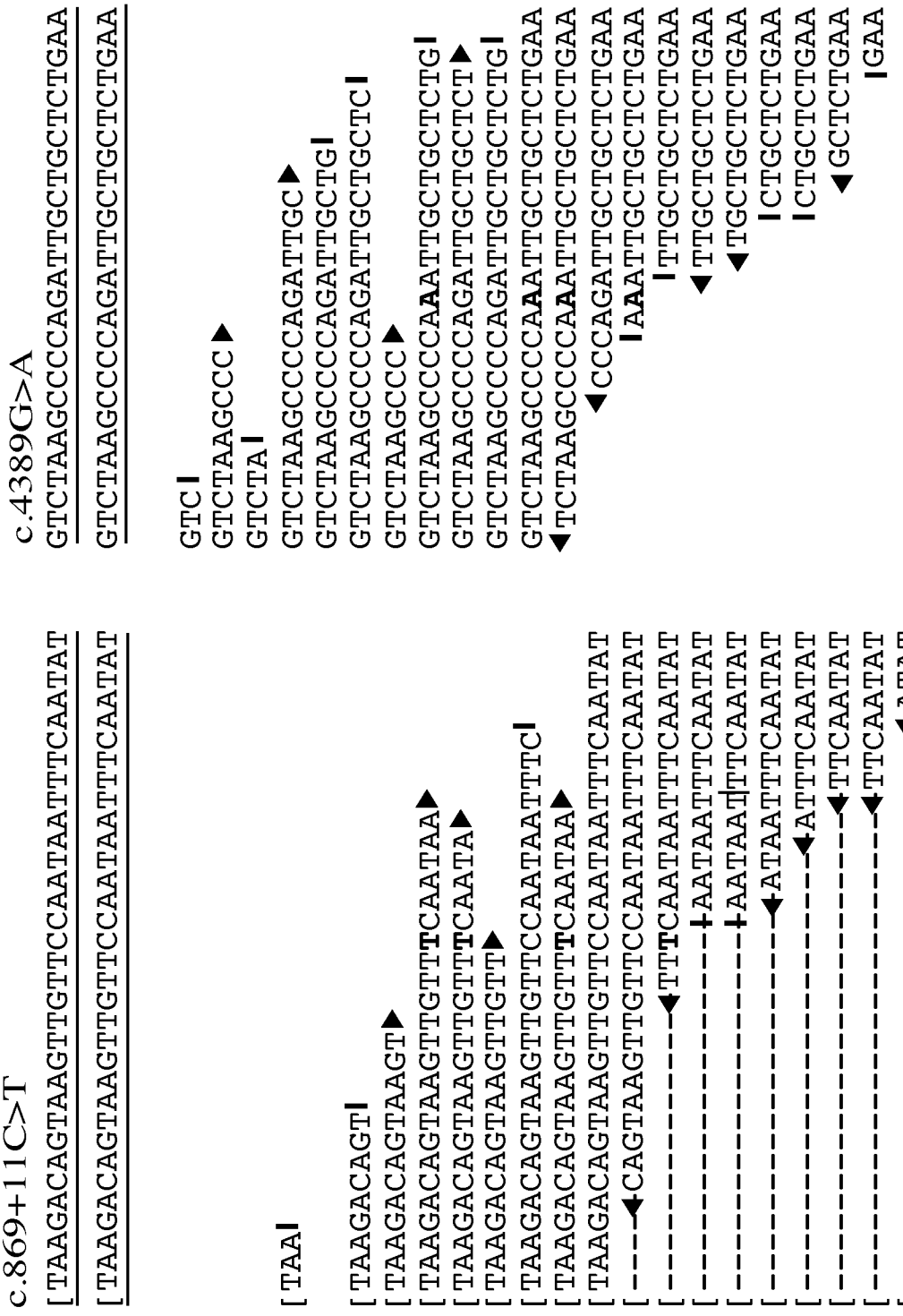


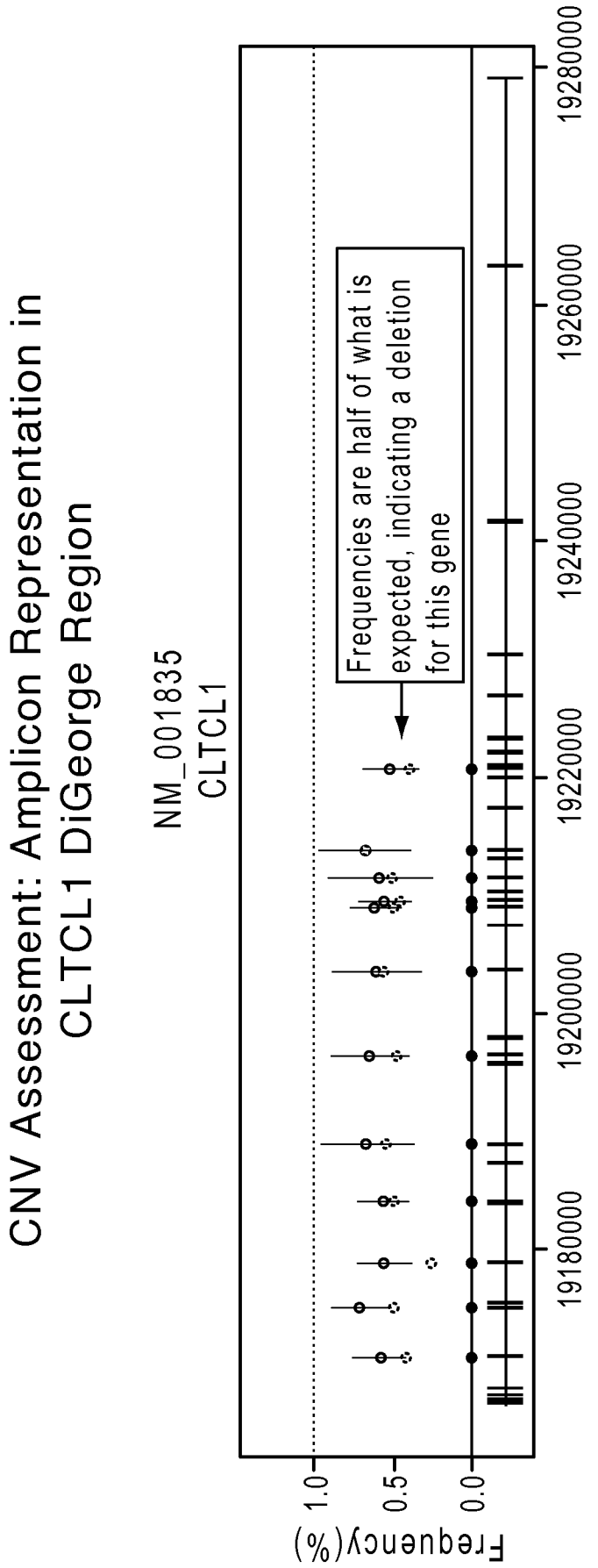
FIG. 13 (Part 1)

ΔF508
CACCATTAAAGAAAATATCATCTTTGGTGTTTCCTATGATGAAT
CACCATTAAAGAAAATATCATCTTTGGTGTTTCCTATGATGAAT
c.2562T>G
CGATATATTACTGTCCACAAGAGCTTA
CGATATATTACTGTCCACAAGAGCTTA

FIG. 13 (Part 2)

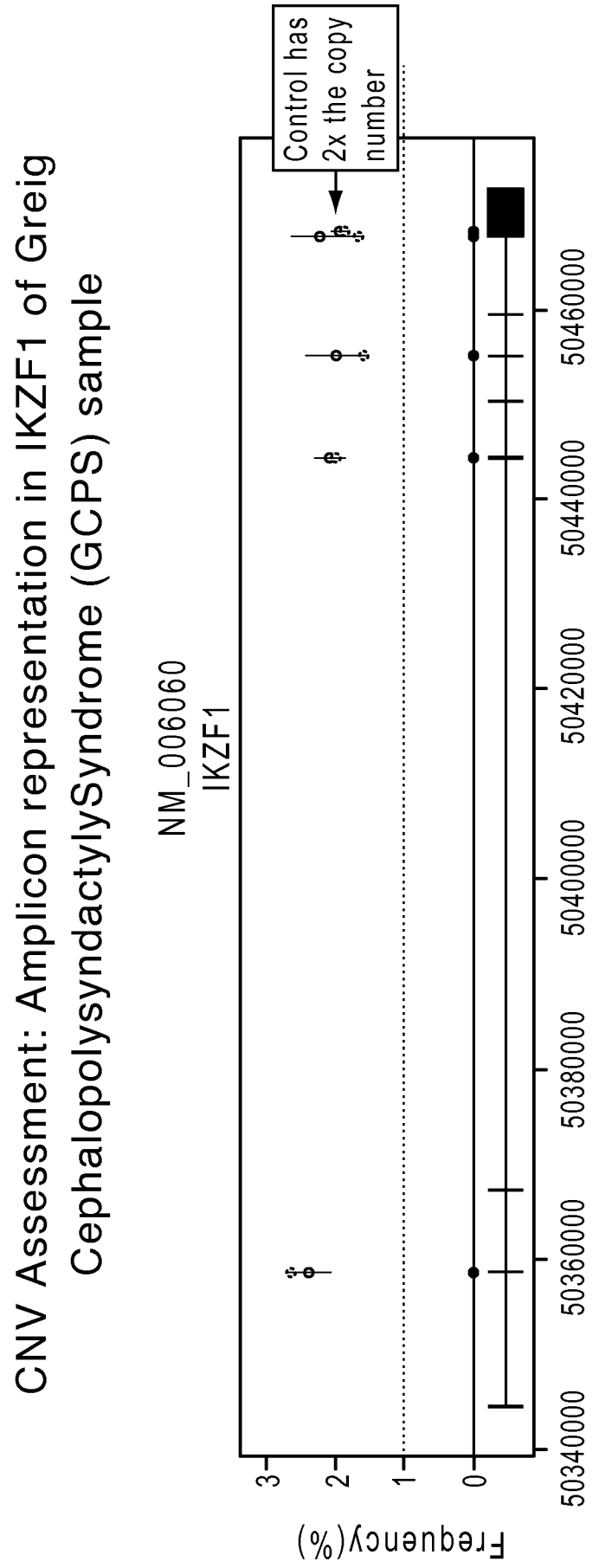
c.1408G>A
TCACTTCTAATGGTGATTATGGGAGA
TCACTTCTAATGGTGATTATGGGAGA
c.1-8G>C
GGACCCCAGCGCCCCGAGACCATGCAGAGGTCC
GGACCCCAGCGCCCCGAGACCATGCAGAGGTCC
TC
TCACTTCTAATGATGAT
TCACTTCTAATGATGAT
TCACTTCTAATGATGATTATGGGAGA
TCACTTCTAATG
CACTTCTAATGATGATTATGGGAGA
CTTCTAATGATGATTATGGGAGA
TCTAATGATGATTATGGGAGA
GATGATTATGGGAGA
TGATTATGGGAGA
ATTATGGGAGA
TATGGGAGA
TATGGGAGA
TATGGGAGA
AGA
GGACCCCAGCGCCCCGAGACCAT
GGACCCCAGCGCCCCGAGA
GGACCCCAGCGCCCCCAGAGACC
CCCCAGAGACCATGCAGAGGTCC
ATGCAGAGGTCC
AGAGGTCC

FIG. 13 (Part 3)



- Grey circles with error bars representing average ratio of percent total reads filtered for (four) DiGeorgesamples compared to control sample
- Red circles are data points for one DiGeorgeindividual
- Blue circles designate amplicons covered target-specific primer pairs

FIG. 14



•Ratios in this case had the control (numerator) compared to the diseased GCPS sample (denominator), control/GCPS

•Since GCPS only has one copy of this gene, the control has two times more amplicons represented with respect to GCPS, as would be expected

FIG. 15

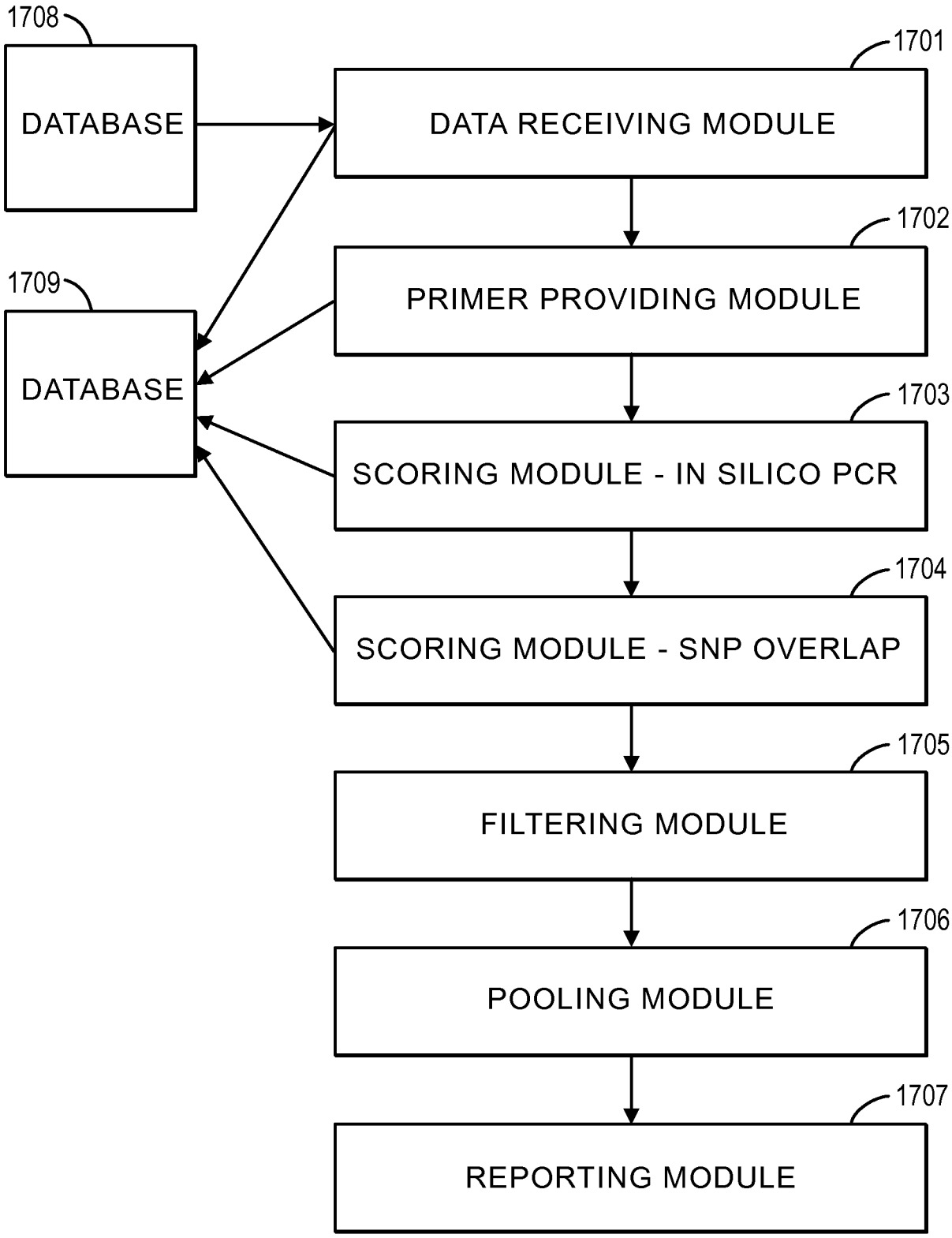

1708
DATABASE
1709
DATABASE
1701
DATA RECEIVING MODULE
1702
PRIMER PROVIDING MODULE
1703
SCORING MODULE - IN SILICO PCR
1704
SCORING MODULE - SNP OVERLAP
1705
FILTERING MODULE
1706
POOLING MODULE
1707
REPORTING MODULE

FIG. 17

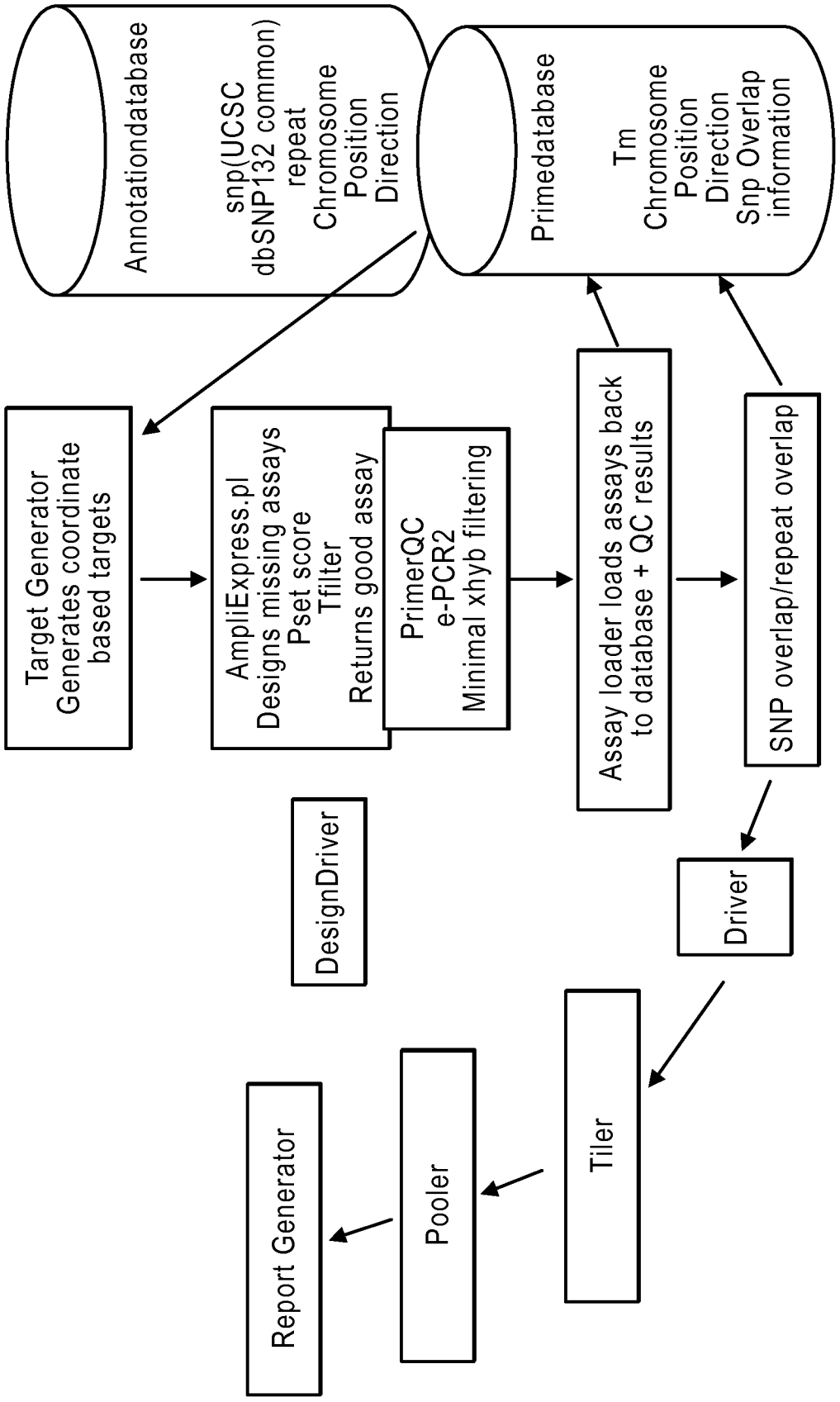

Annotationdatabase
snp(UCSC dbSNP132 common)
repeat
Chromosome
Position
Direction
Primedatabase
Tm
Chromosome
Position
Direction
Snp Overlap information
Target Generator
Generates coordinate based targets
AmpliExpress.pl
Designs missing assays
Pset score
Tfilter
Returns good assay
PrimerQC
e-PCR2
Minimal xhyb filtering
Assay loader loads assays back to database + QC results
SNP overlap/repeat overlap
DesignDriver
Driver
Tiler
Pooler
Report Generator

FIG. 18

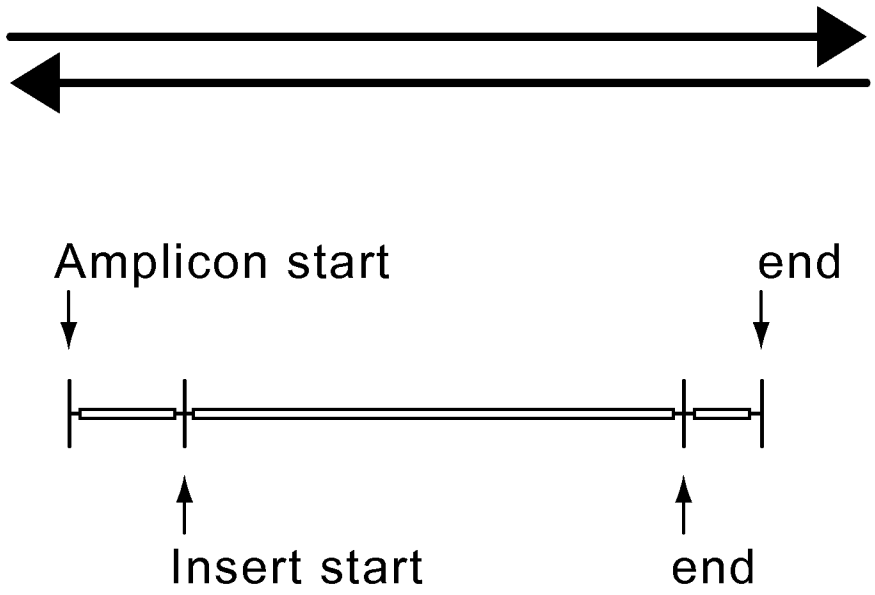
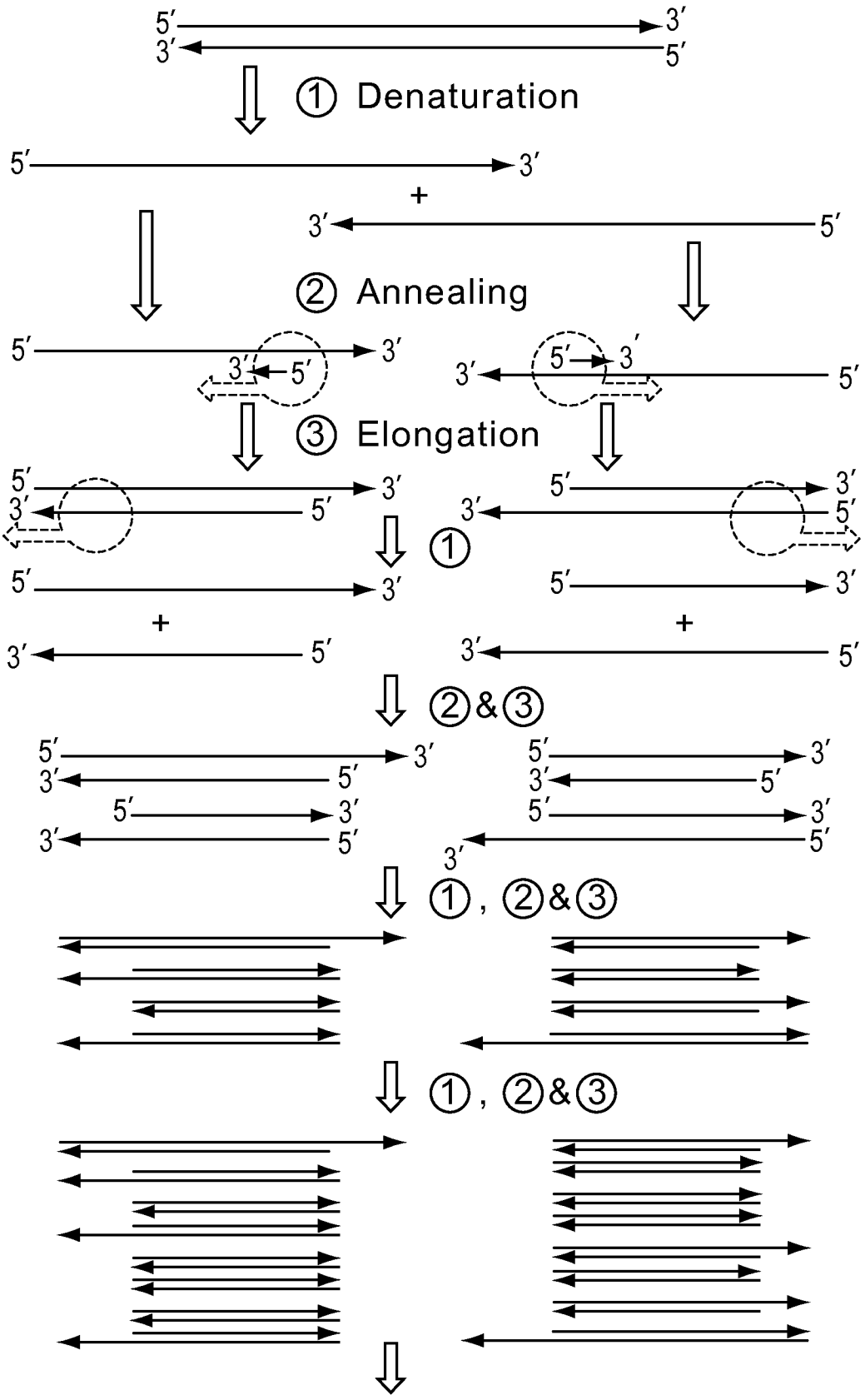


FIG. 19



Exponential growth of short product

FIG. 20

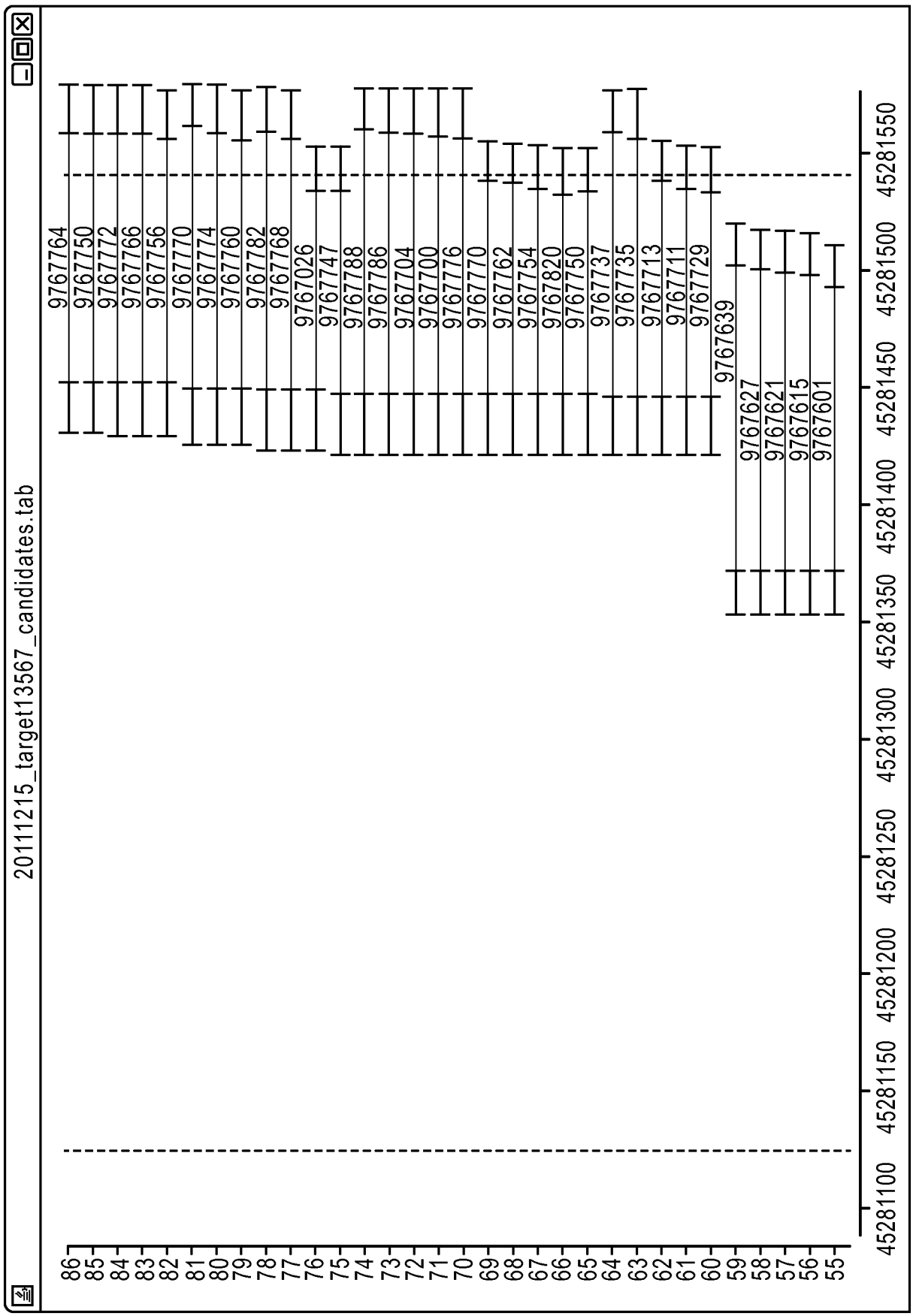

20111215_target13567_candidates.tab
9767764
9767750
9767772
9767766
9767756
9767770
9767774
9767760
9767782
9767768
9767026
9767747
9767788
9767786
9767704
9767700
9767776
9767770
9767762
9767754
9767820
9767750
9767737
9767735
9767713
9767711
9767729
9767639
9767627
9767621
9767615
9767601
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550
86
85
84
83
82
81
80
79
78
77
76
75
74
73
72
71
70
69
68
67
66
65
64
63
62
61
60
59
58
57
56
55

FIG. 21 (Part 1)

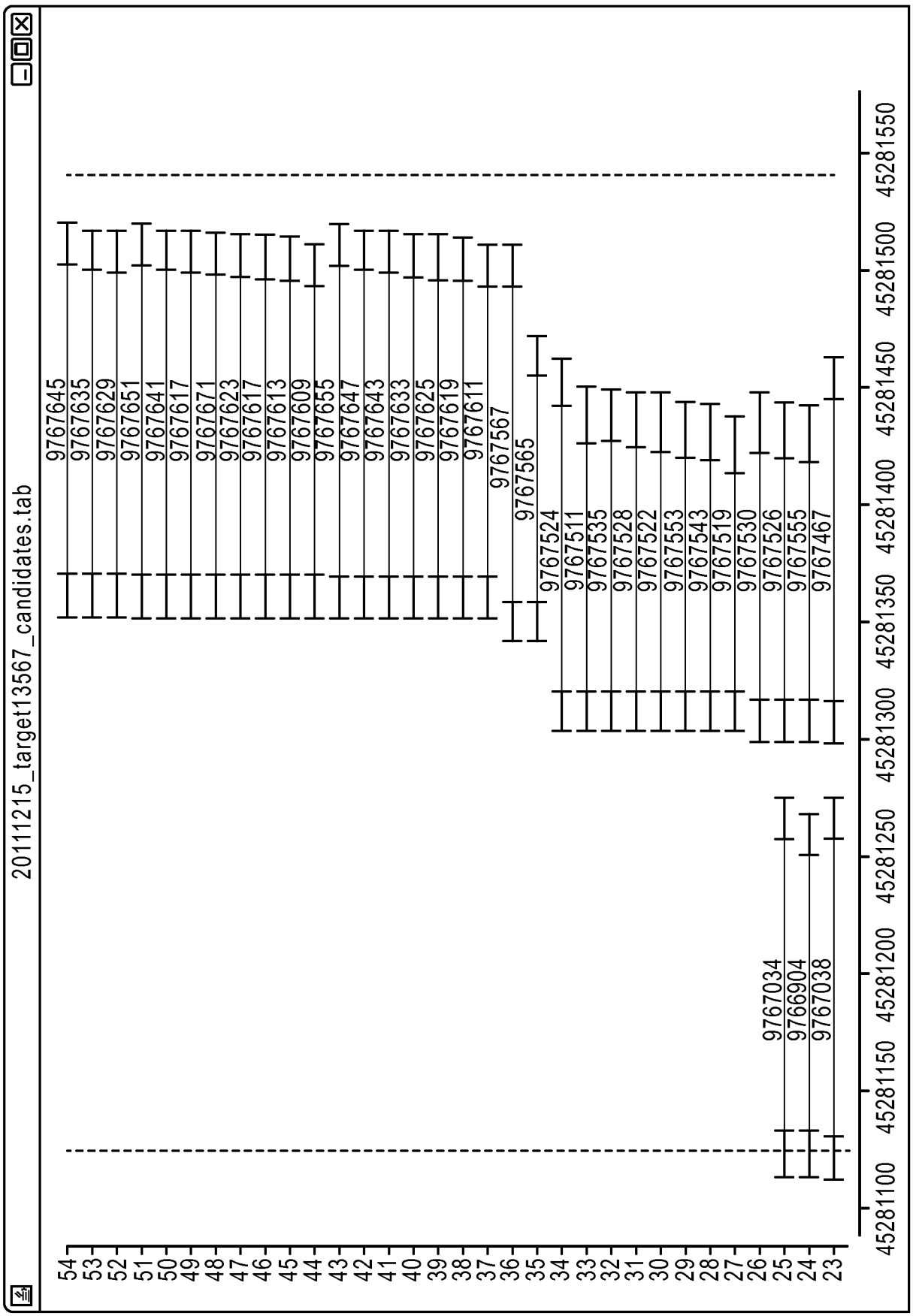

20111215_target13567_candidates.tab
9767645
9767635
9767629
9767651
9767641
9767617
9767671
9767623
9767617
9767613
9767609
9767655
9767647
9767643
9767633
9767625
9767619
9767611
9767567
9767565
9767524
9767511
9767535
9767528
9767522
9767553
9767543
9767519
9767530
9767526
9767555
9767467
9767034
9766904
9767038
54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23
45281100 45281150 45281200 45281250 45281300 45281350 45281400 45281450 45281500 45281550

FIG. 21 (Part 2)

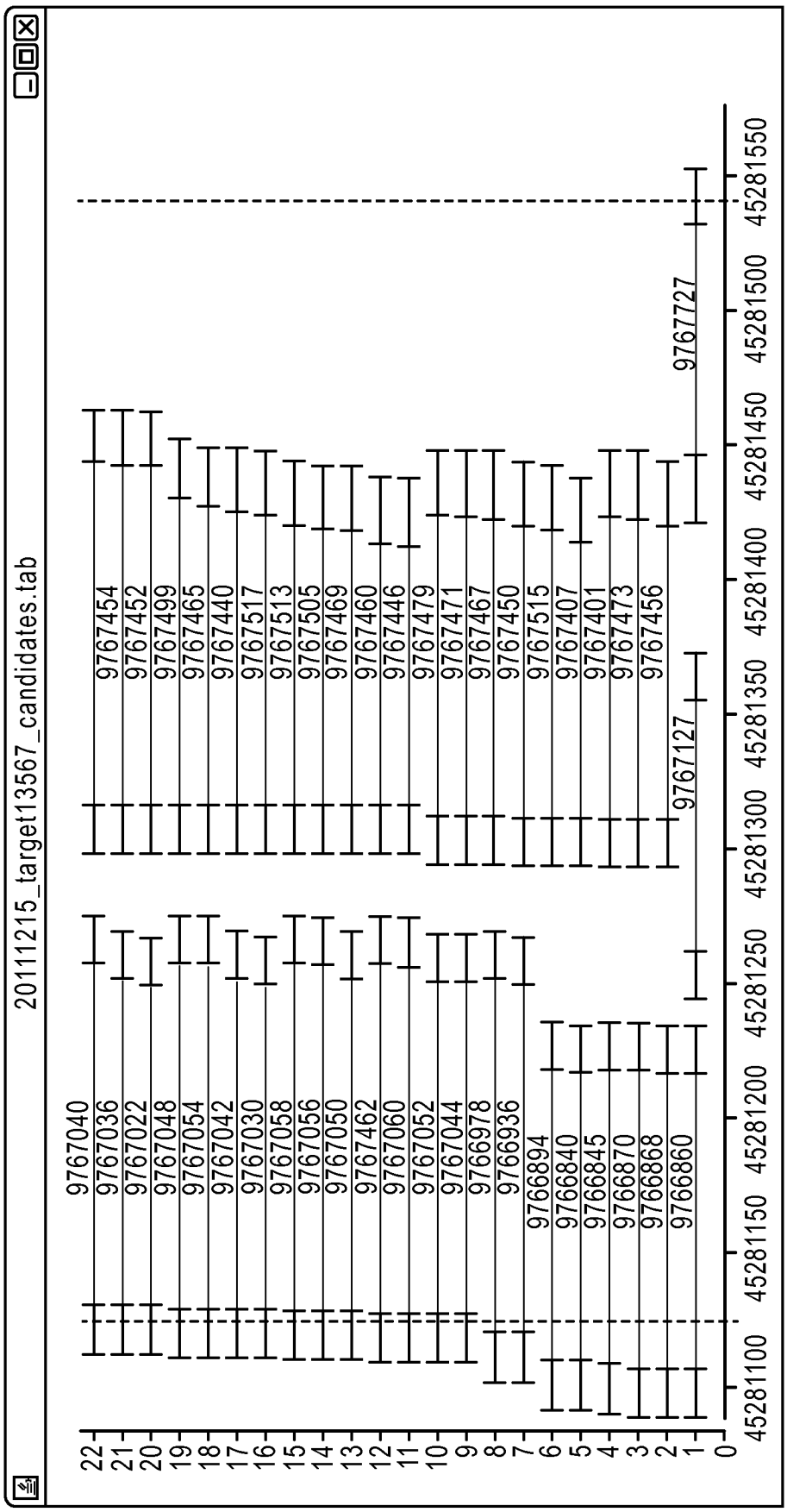

20111215_target13567_candidates.tab
9767040
9767036
9767022
9767048
9767054
9767042
9767030
9767058
9767056
9767050
9767462
9767060
9767052
9767044
9766978
9766936
9766894
9766840
9766845
9766870
9766868
9766860
9767454
9767452
9767499
9767465
9767440
9767517
9767513
9767505
9767469
9767460
9767446
9767479
9767471
9767467
9767450
9767515
9767407
9767401
9767473
9767456
9767127
9767727
22
21
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550

FIG. 21 (Part 3)

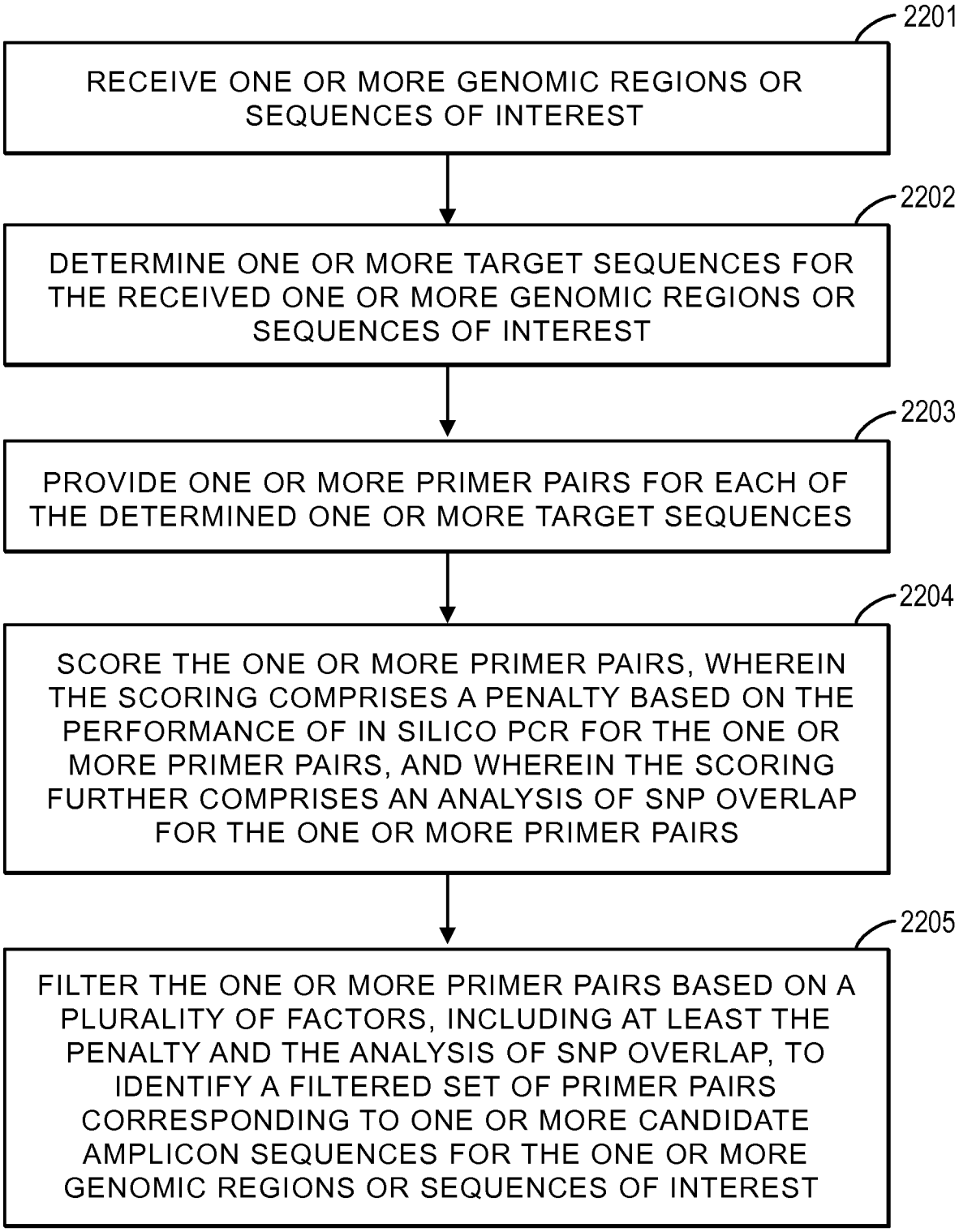

2201
RECEIVE ONE OR MORE GENOMIC REGIONS OR SEQUENCES OF INTEREST
2202
DETERMINE ONE OR MORE TARGET SEQUENCES FOR THE RECEIVED ONE OR MORE GENOMIC REGIONS OR SEQUENCES OF INTEREST
2203
PROVIDE ONE OR MORE PRIMER PAIRS FOR EACH OF THE DETERMINED ONE OR MORE TARGET SEQUENCES
2204
SCORE THE ONE OR MORE PRIMER PAIRS, WHEREIN THE SCORING COMPRISES A PENALTY BASED ON THE PERFORMANCE OF IN SILICO PCR FOR THE ONE OR MORE PRIMER PAIRS, AND WHEREIN THE SCORING FURTHER COMPRISES AN ANALYSIS OF SNP OVERLAP FOR THE ONE OR MORE PRIMER PAIRS
2205
FILTER THE ONE OR MORE PRIMER PAIRS BASED ON A PLURALITY OF FACTORS, INCLUDING AT LEAST THE PENALTY AND THE ANALYSIS OF SNP OVERLAP, TO IDENTIFY A FILTERED SET OF PRIMER PAIRS CORRESPONDING TO ONE OR MORE CANDIDATE AMPLICON SEQUENCES FOR THE ONE OR MORE GENOMIC REGIONS OR SEQUENCES OF INTEREST

FIG. 22

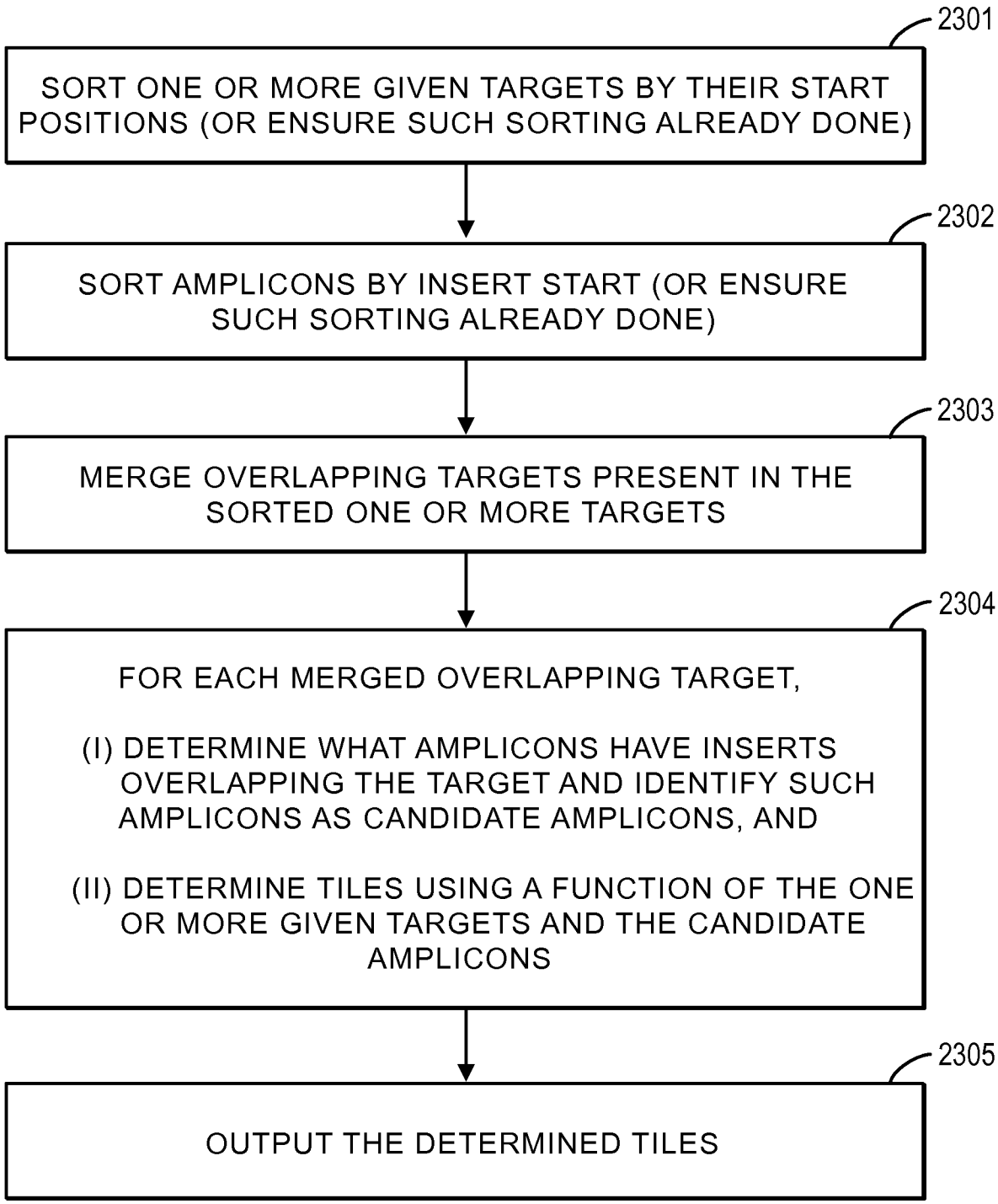

2301
SORT ONE OR MORE GIVEN TARGETS BY THEIR START POSITIONS (OR ENSURE SUCH SORTING ALREADY DONE)
2302
SORT AMPLICONS BY INSERT START (OR ENSURE SUCH SORTING ALREADY DONE)
2303
MERGE OVERLAPPING TARGETS PRESENT IN THE SORTED ONE OR MORE TARGETS
2304
FOR EACH MERGED OVERLAPPING TARGET,
(I) DETERMINE WHAT AMPLICONS HAVE INSERTS OVERLAPPING THE TARGET AND IDENTIFY SUCH AMPLICONS AS CANDIDATE AMPLICONS, AND
(II) DETERMINE TILES USING A FUNCTION OF THE ONE OR MORE GIVEN TARGETS AND THE CANDIDATE AMPLICONS
2305
OUTPUT THE DETERMINED TILES

FIG. 23

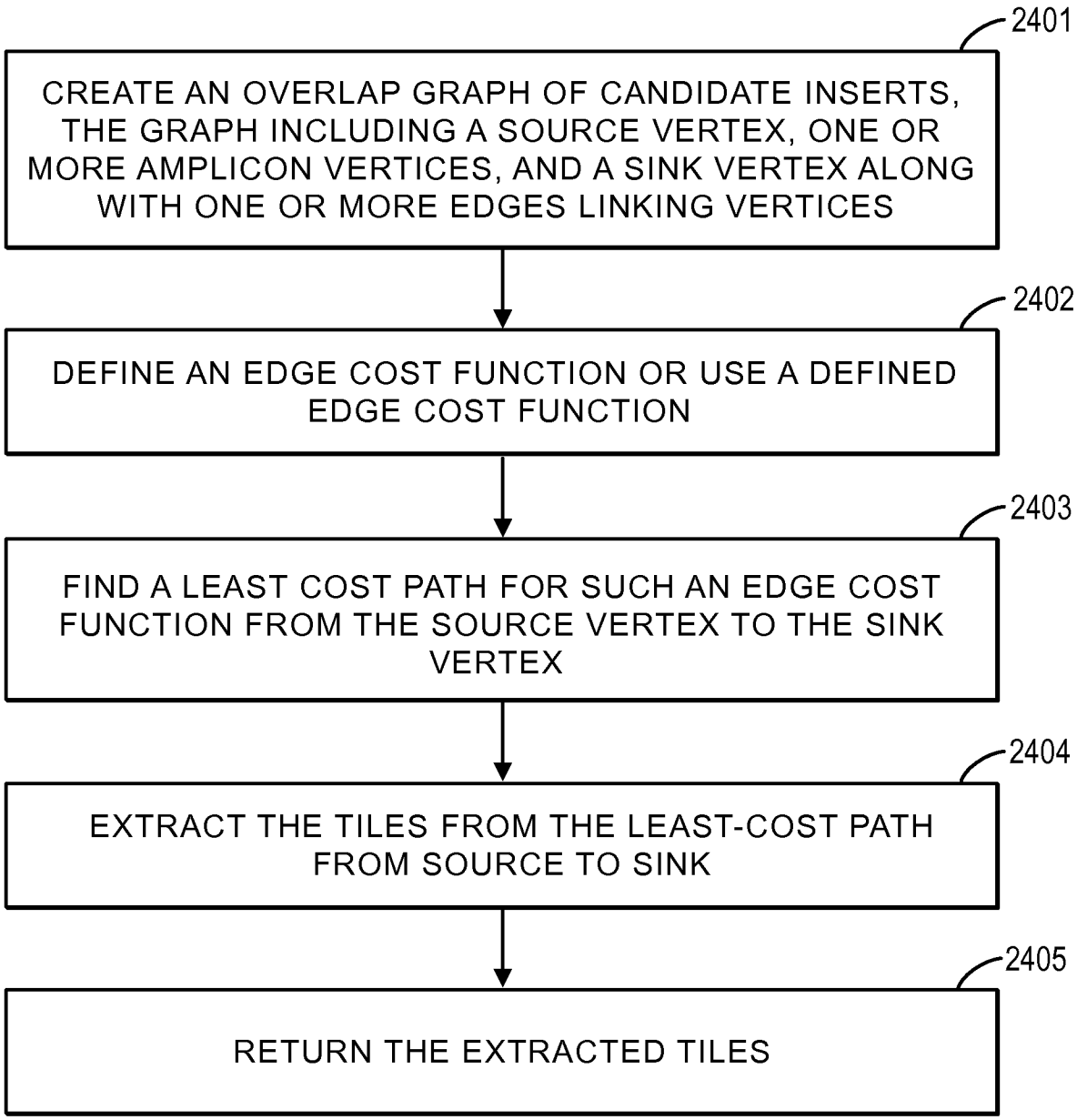

2401
CREATE AN OVERLAP GRAPH OF CANDIDATE INSERTS, THE GRAPH INCLUDING A SOURCE VERTEX, ONE OR MORE AMPLICON VERTICES, AND A SINK VERTEX ALONG WITH ONE OR MORE EDGES LINKING VERTICES
2402
DEFINE AN EDGE COST FUNCTION OR USE A DEFINED EDGE COST FUNCTION
2403
FIND A LEAST COST PATH FOR SUCH AN EDGE COST FUNCTION FROM THE SOURCE VERTEX TO THE SINK VERTEX
2404
EXTRACT THE TILES FROM THE LEAST-COST PATH FROM SOURCE TO SINK
2405
RETURN THE EXTRACTED TILES

FIG. 24

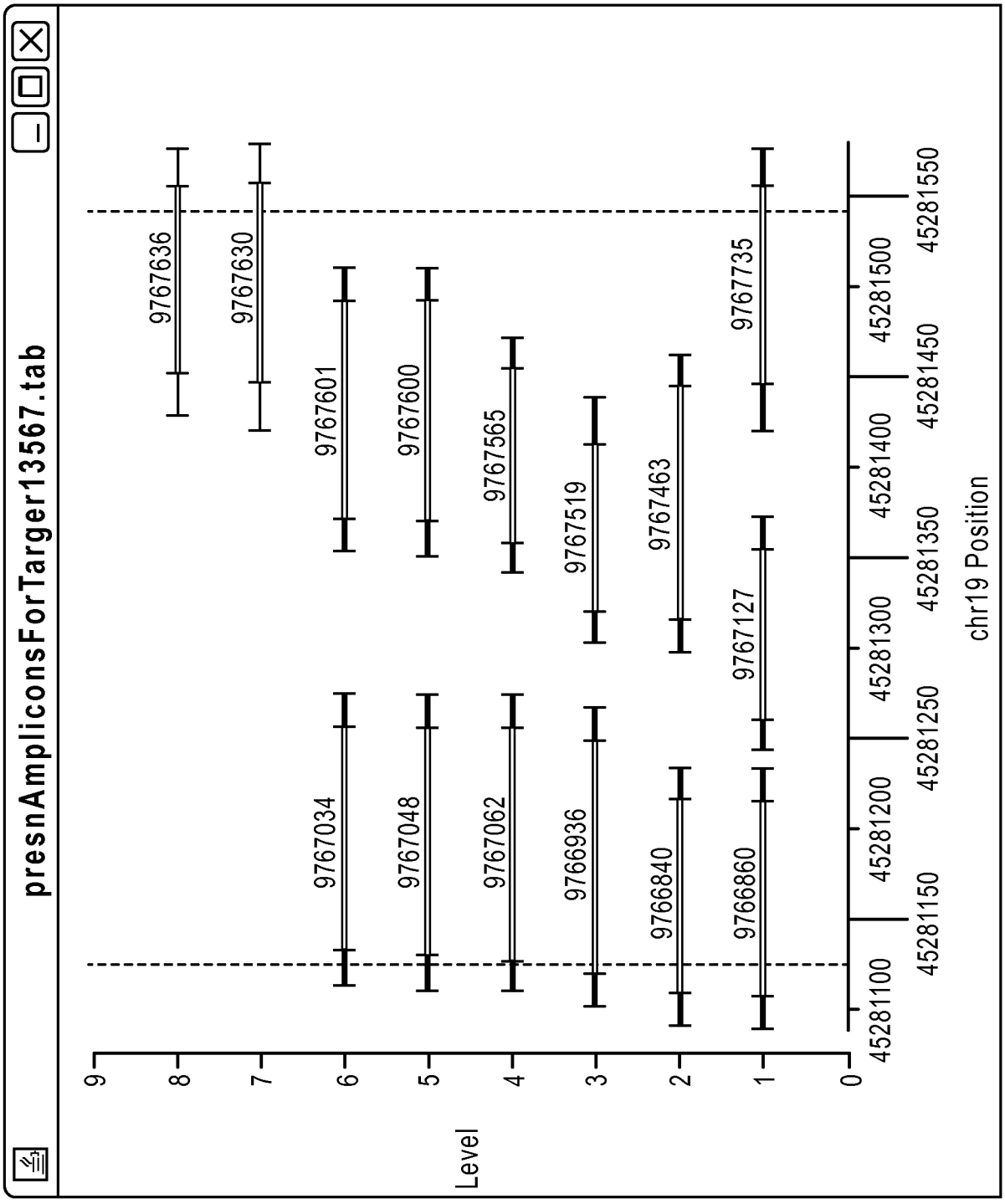

presnAmpliconsForTarger13567.tab
Level
chr19 Position
9
8
7
6
5
4
3
2
1
0
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550
9767636
9767630
9767601
9767600
9767565
9767519
9767463
9767735
9767127
9767034
9767048
9767062
9766936
9766840
9766860

FIG. 25A

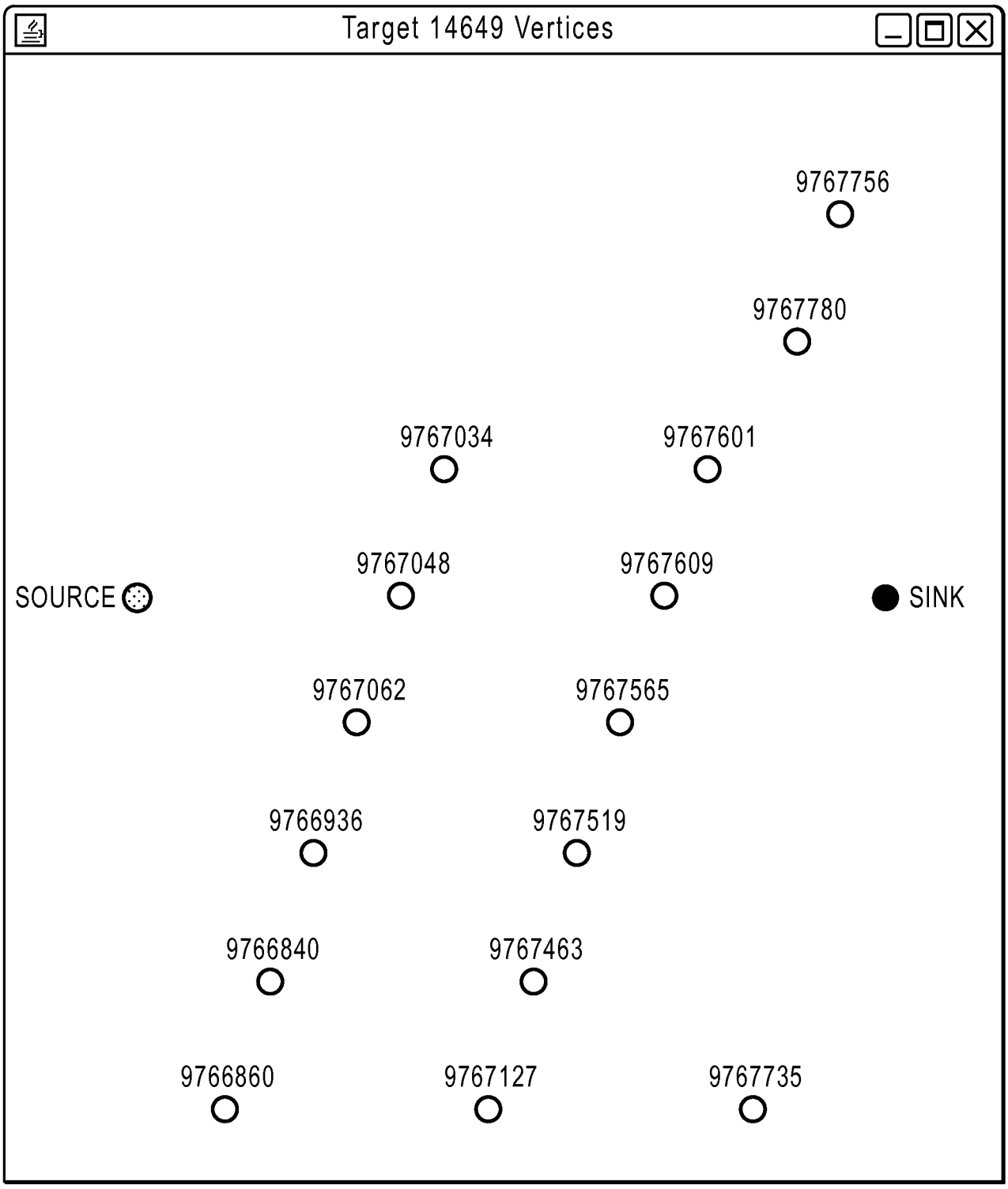

Target 14649 Vertices
9767756
9767780
9767034
9767601
9767048
9767609
SOURCE
SINK
9767062
9767565
9766936
9767519
9766840
9767463
9766860
9767127
9767735

FIG. 25B

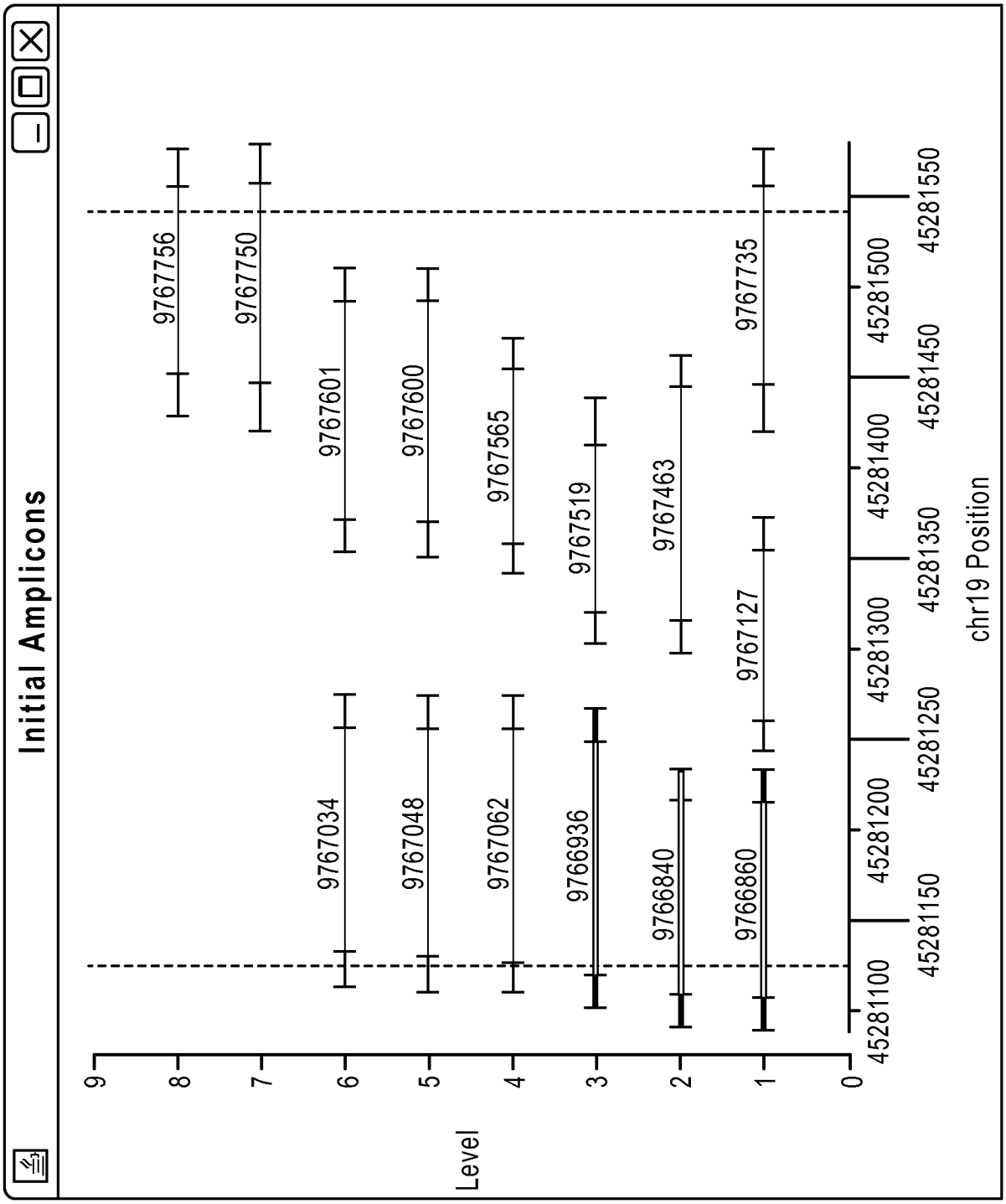

Initial Amplicons
Level
chr19 Position
9767756
9767750
9767601
9767600
9767565
9767519
9767463
9767735
9767034
9767048
9767062
9766936
9766840
9766860
9767127
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550

FIG. 26A

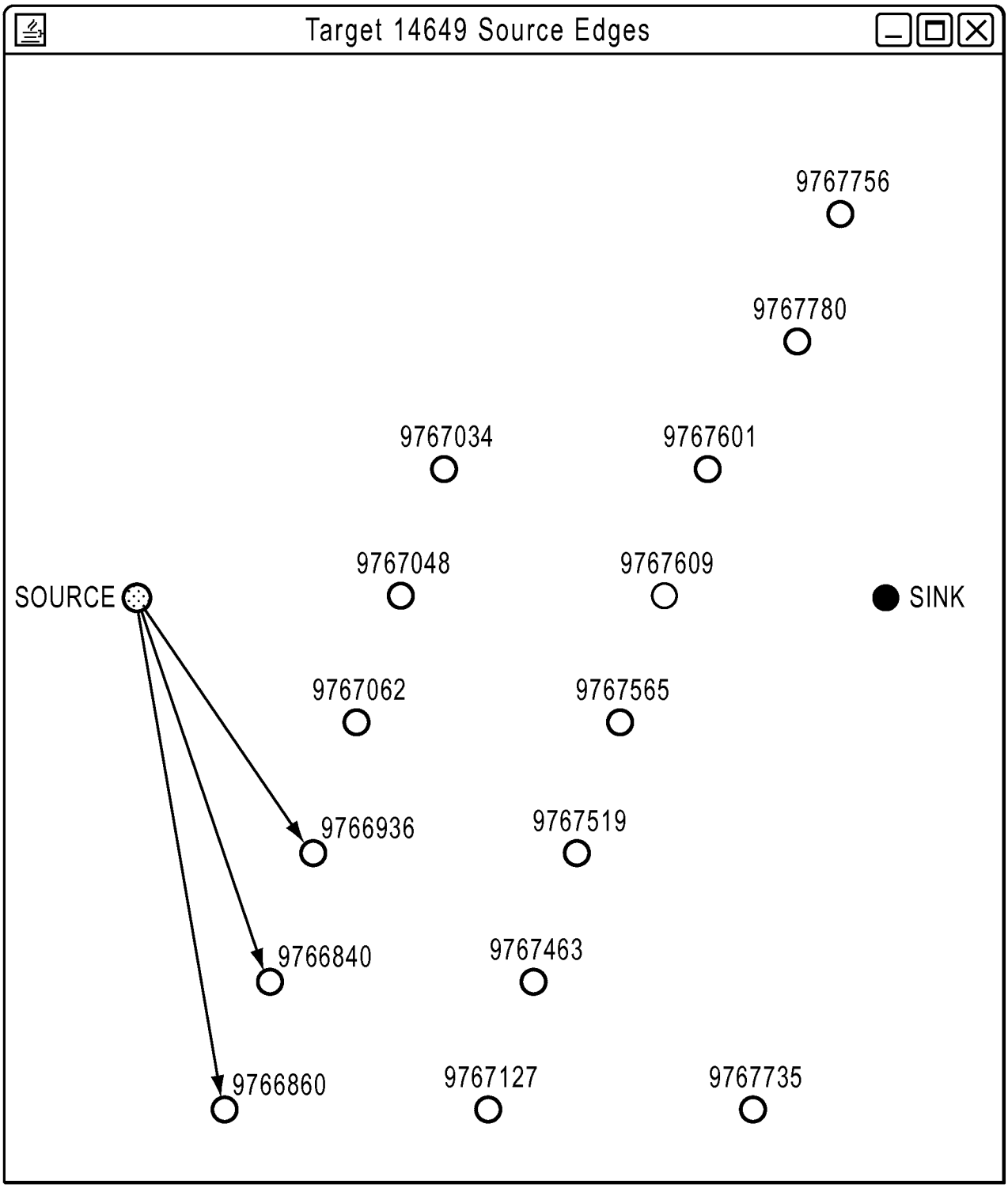

Target 14649 Source Edges
9767756
9767780
9767034
9767601
9767048
9767609
SOURCE
SINK
9767062
9767565
9766936
9767519
9766840
9767463
9766860
9767127
9767735

FIG. 26B

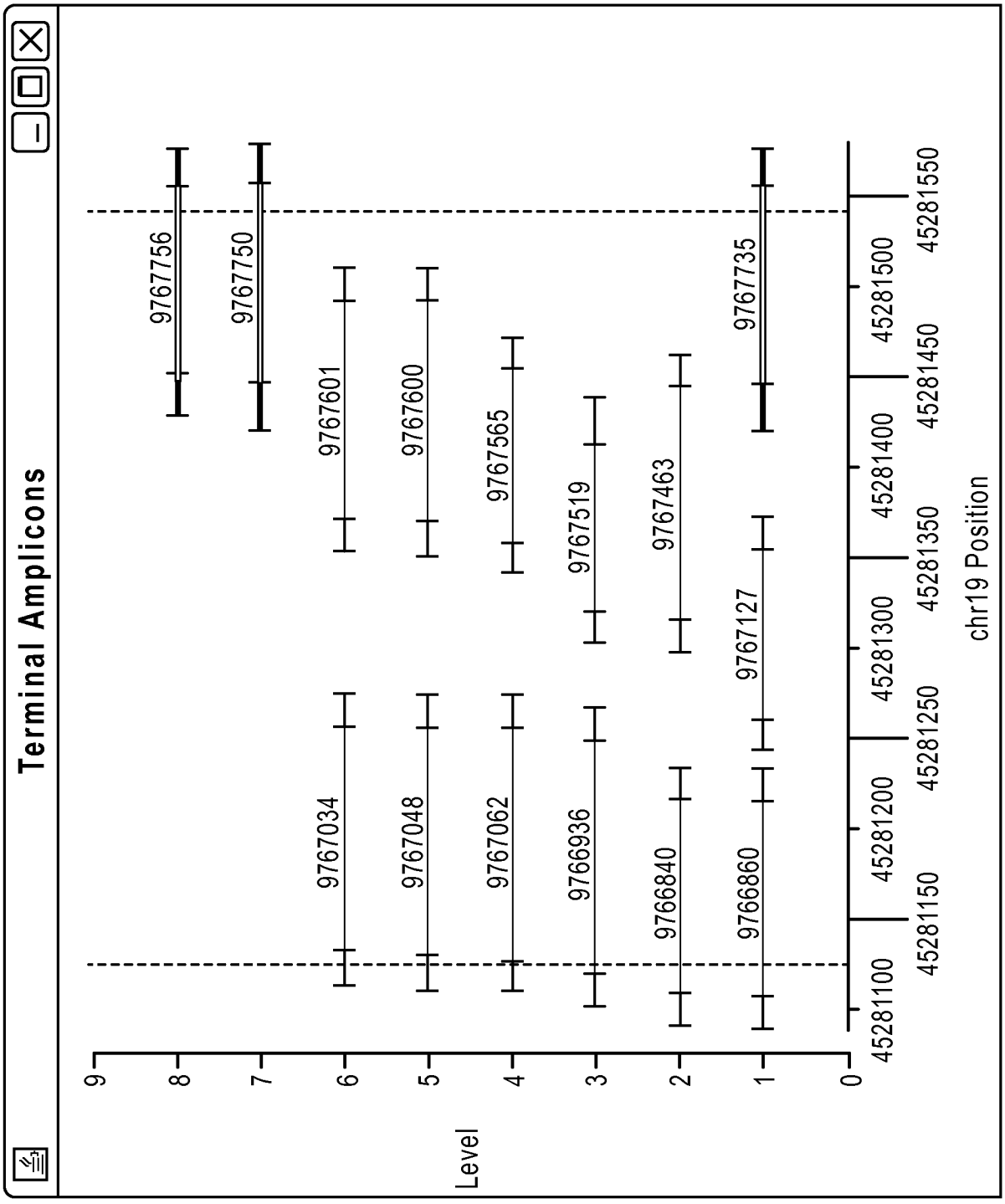

Terminal Amplicons
Level
chr19 Position
9767756
9767750
9767601
9767600
9767565
9767519
9767463
9767735
9767034
9767048
9767062
9766936
9766840
9766860
9767127
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550

FIG. 27A

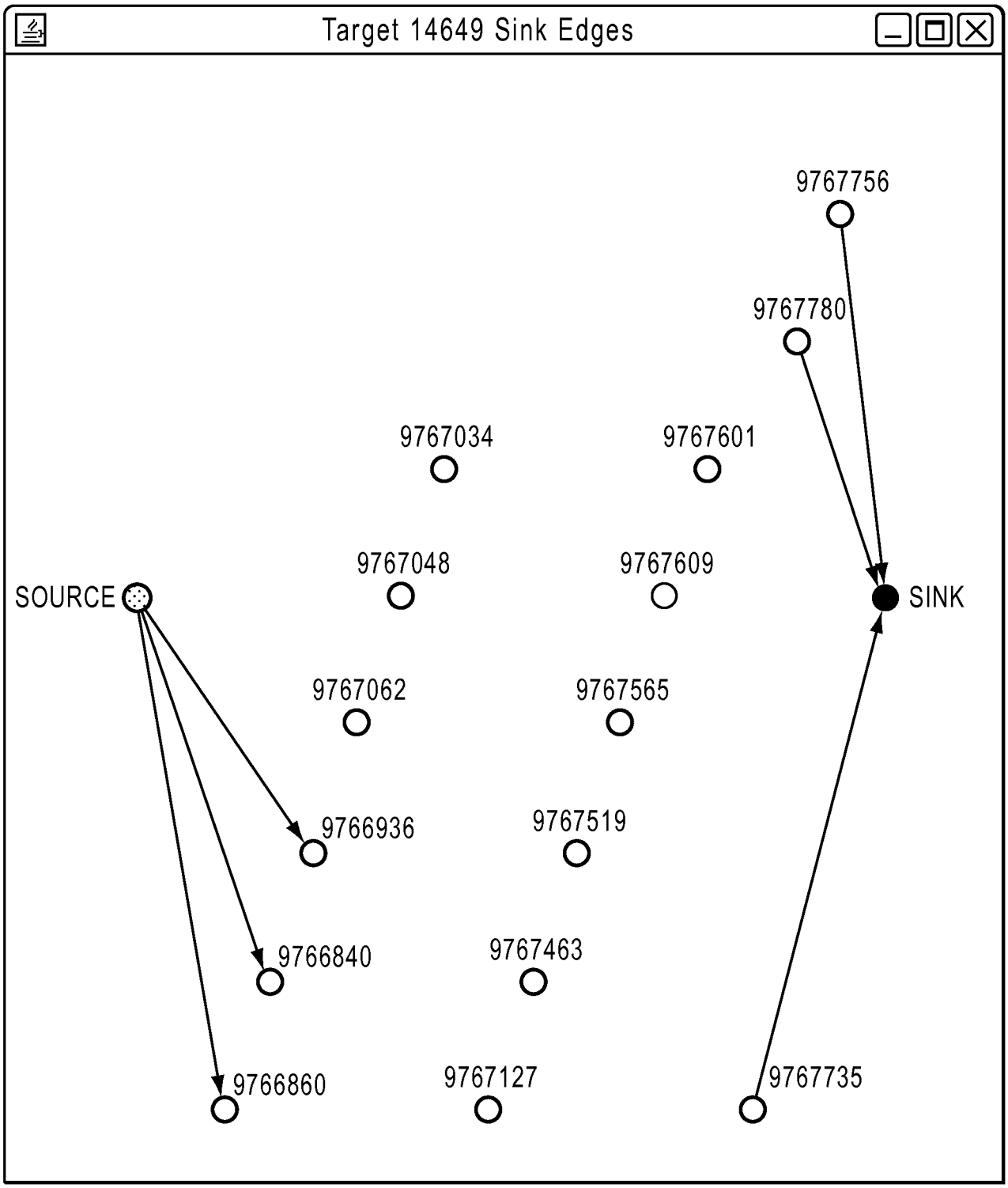

Target 14649 Sink Edges
9767756
9767780
9767034
9767601
9767048
9767609
SOURCE
SINK
9767062
9767565
9766936
9767519
9766840
9767463
9766860
9767127
9767735

FIG. 27B

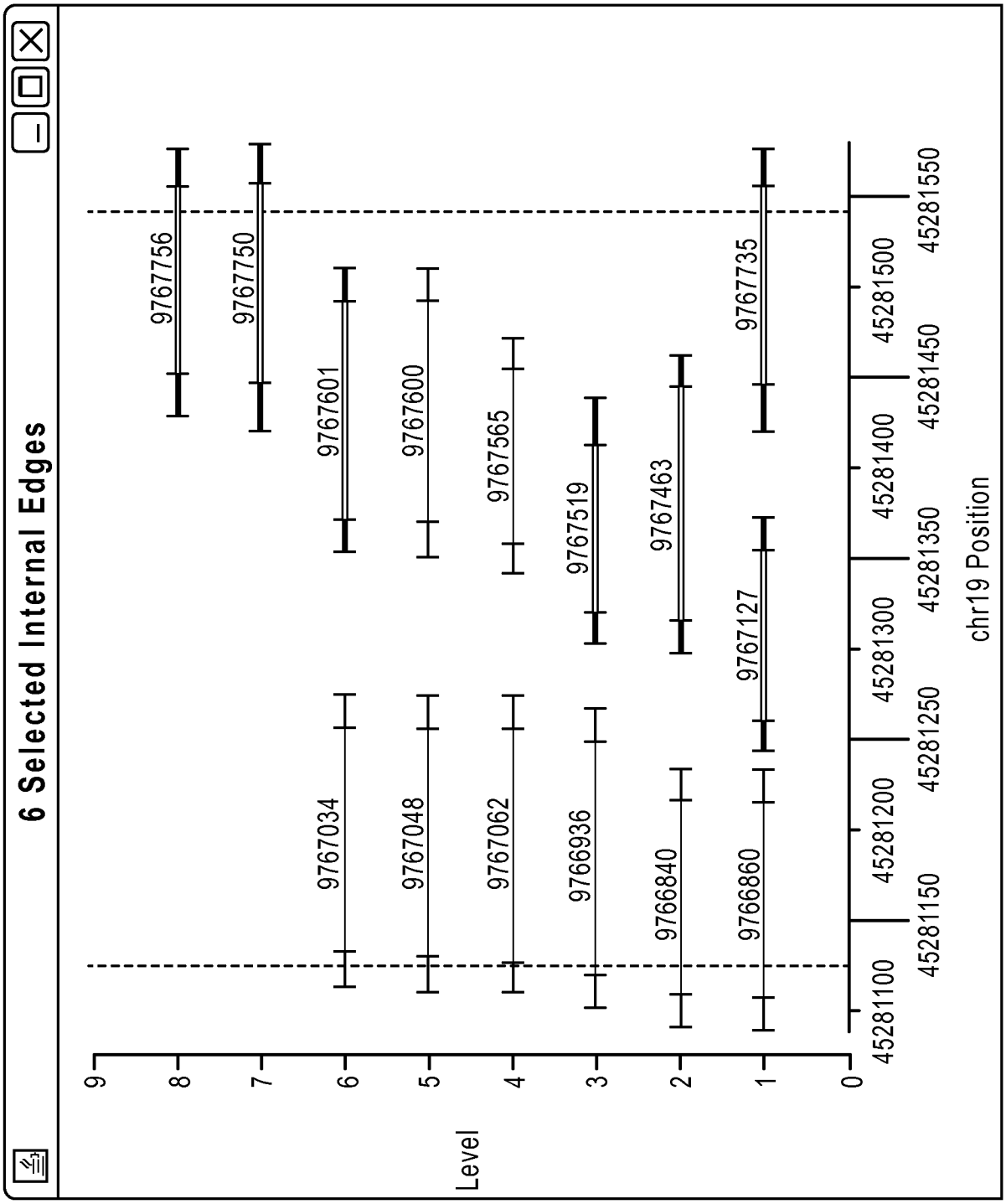

6 Selected Internal Edges
9767756
9767750
9767601
9767600
9767565
9767519
9767463
9767735
9767034
9767048
9767062
9766936
9766840
9766860
9767127
Level
9
8
7
6
5
4
3
2
1
0
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550
chr19 Position

FIG. 28A

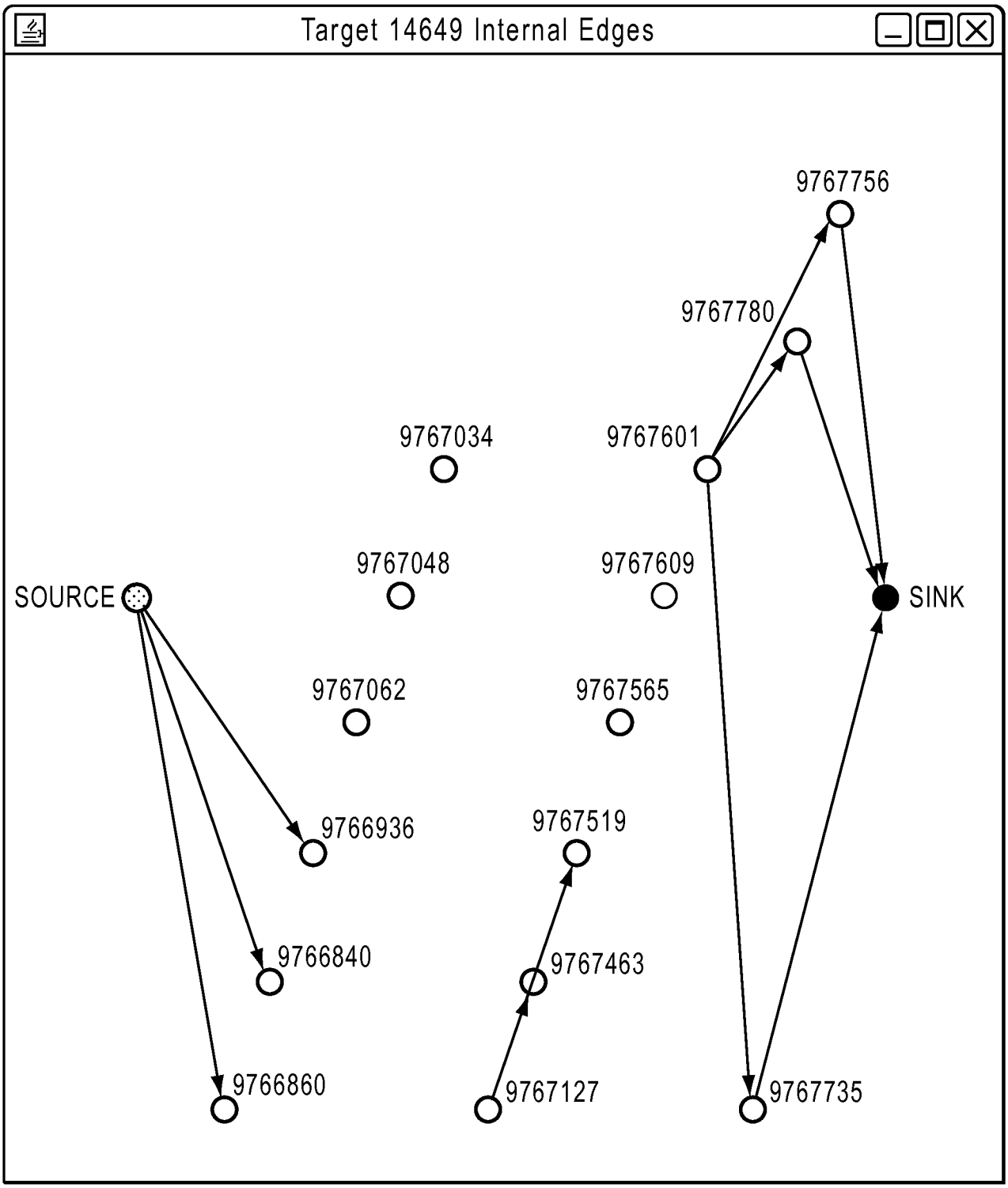

Target 14649 Internal Edges
9767756
9767780
9767034
9767601
9767048
9767609
SOURCE
SINK
9767062
9767565
9766936
9767519
9766840
9767463
9766860
9767127
9767735

FIG. 28B

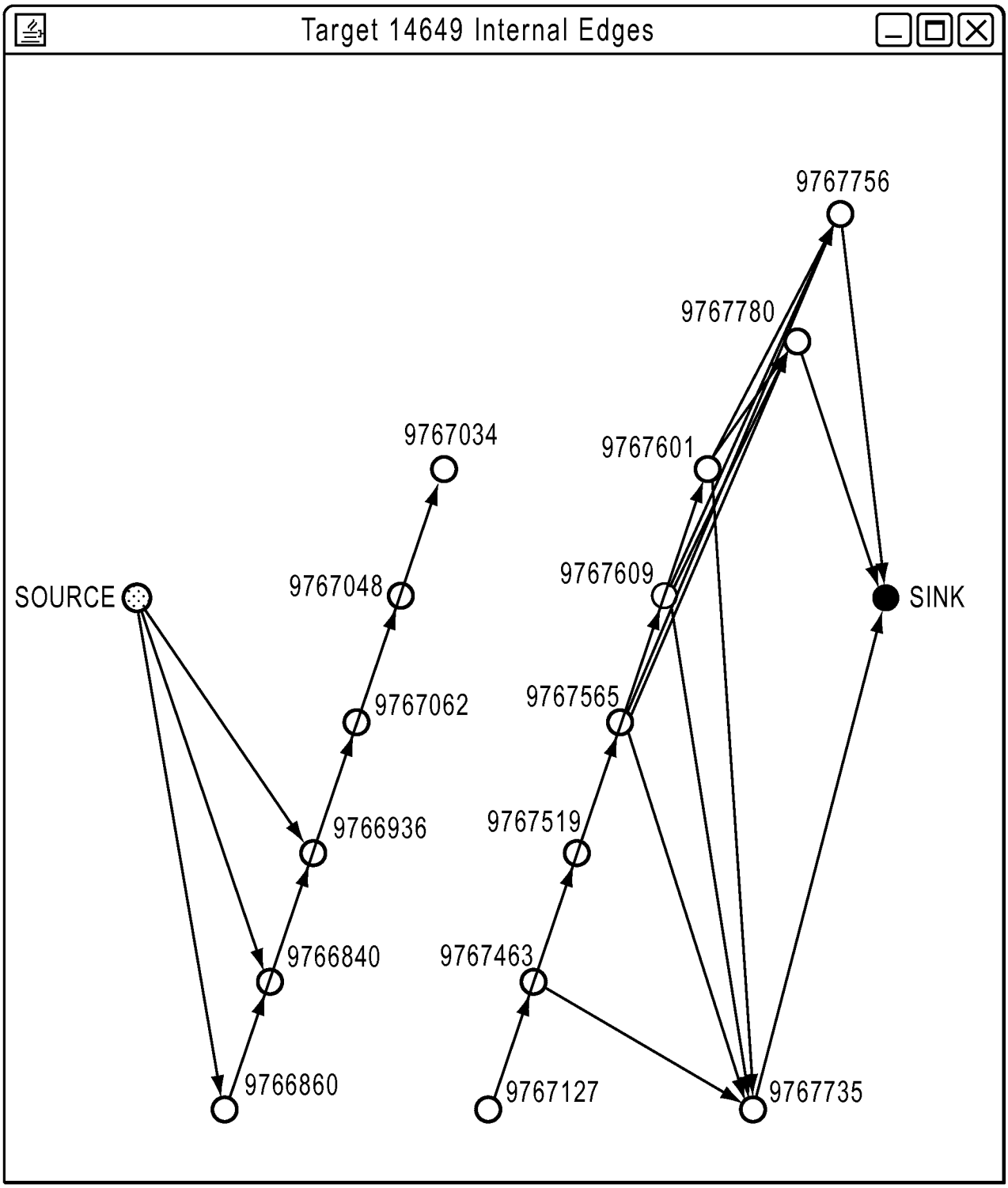

Target 14649 Internal Edges
9767756
9767780
9767034
9767601
SOURCE
9767048
9767609
SINK
9767062
9767565
9766936
9767519
9766840
9767463
9766860
9767127
9767735

FIG. 29A

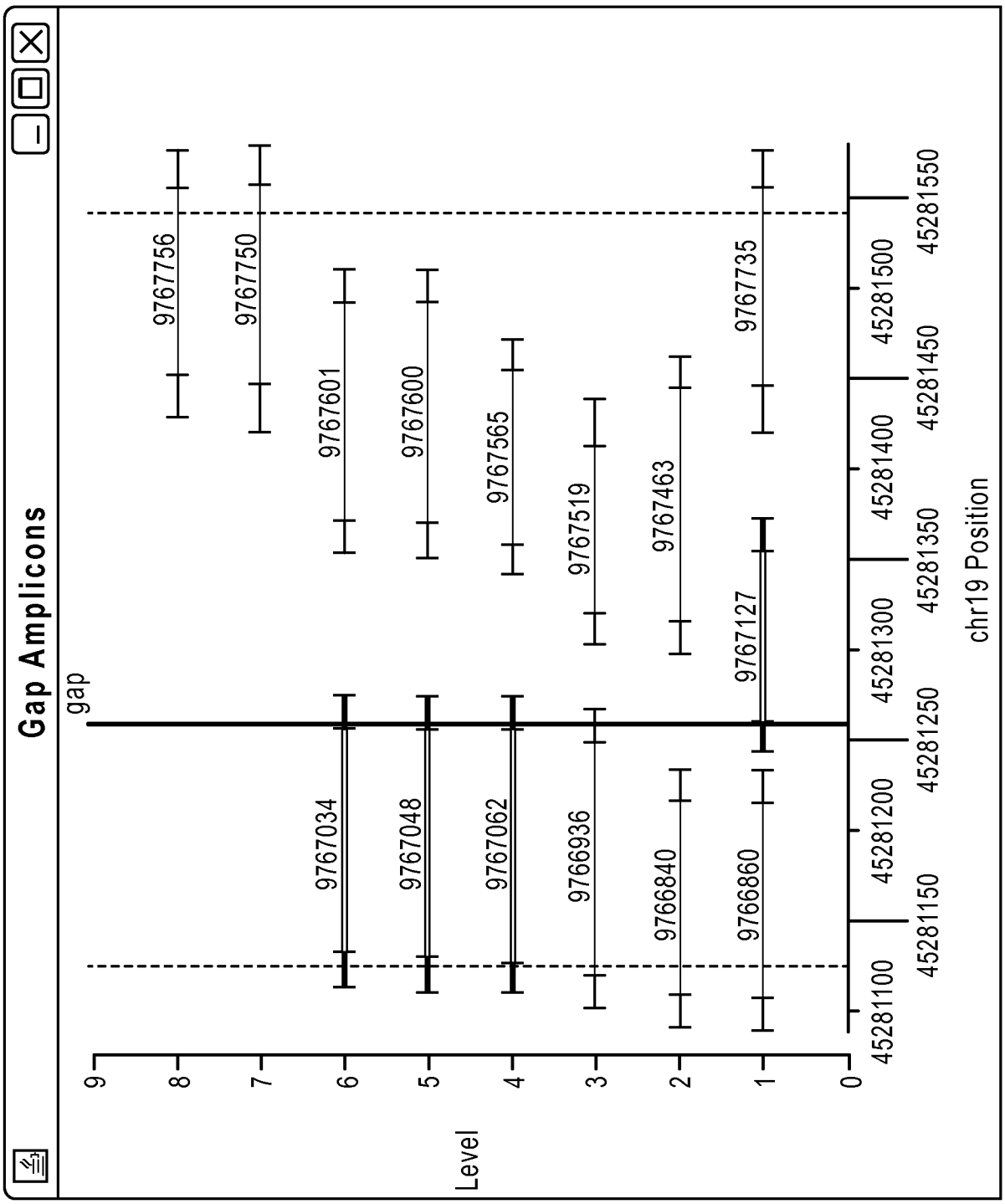

Gap Amplicons
gap
9767756
9767750
9767601
9767600
9767565
9767519
9767463
9767735
9767034
9767048
9767062
9766936
9766840
9766860
9767127
Level
9
8
7
6
5
4
3
2
1
0
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550
chr19 Position

FIG. 29B

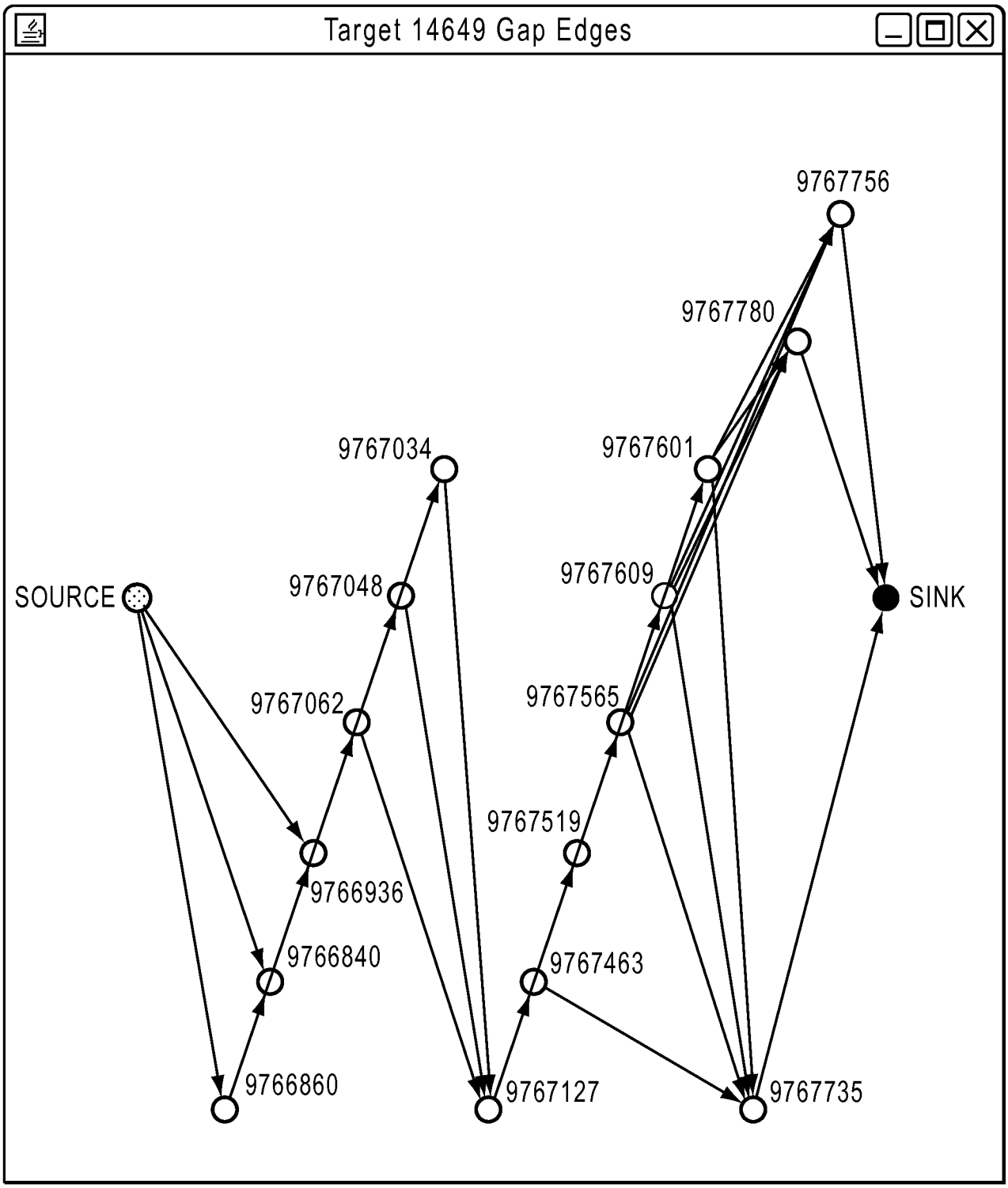

Target 14649 Gap Edges
9767756
9767780
9767034
9767601
SOURCE
9767048
9767609
SINK
9767062
9767565
9767519
9766936
9766840
9767463
9766860
9767127
9767735

FIG. 30A

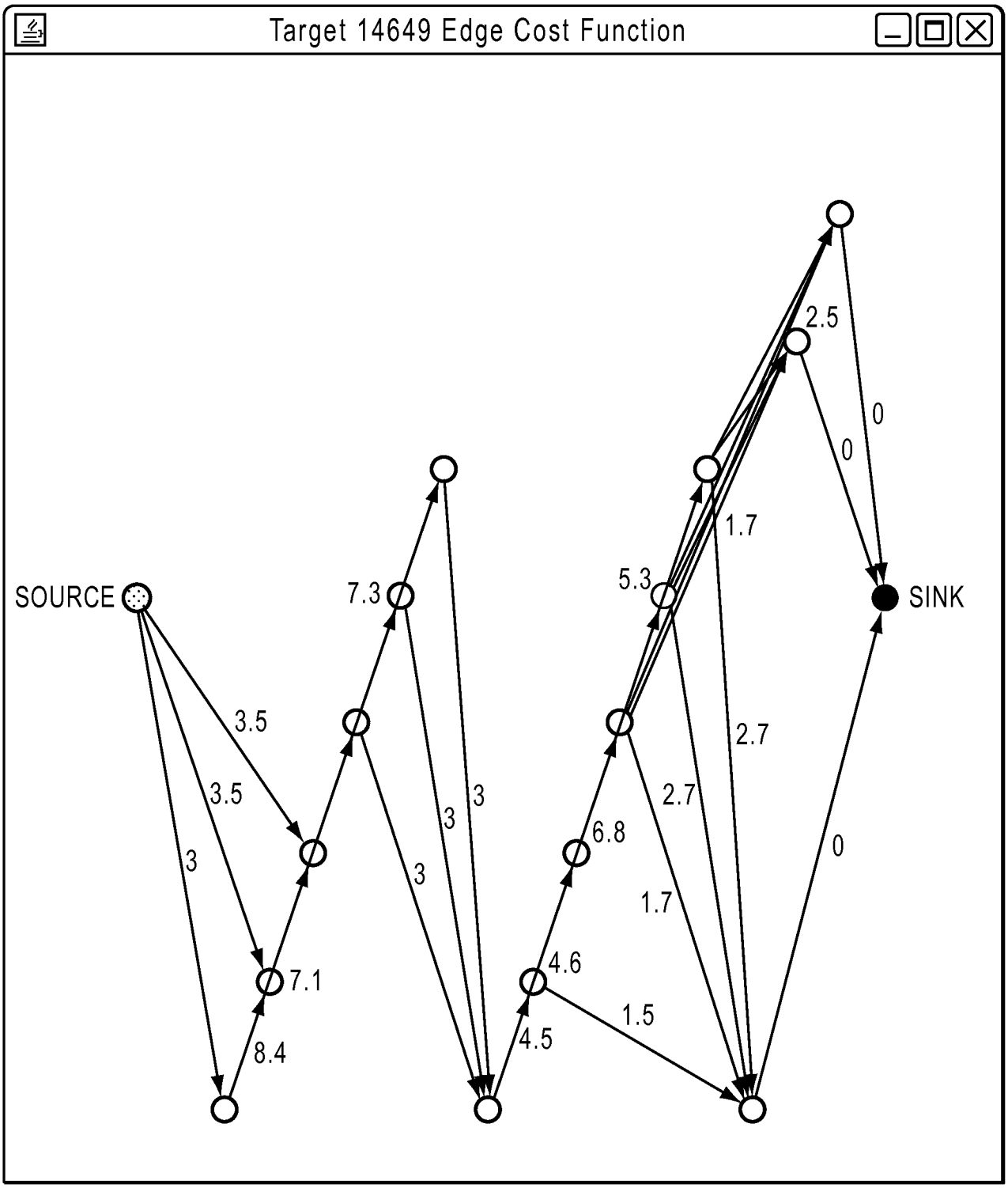

Target 14649 Edge Cost Function
SOURCE
SINK
3.5
3.5
3
7.1
8.4
7.3
3
3
3
4.5
4.6
1.5
6.8
1.7
5.3
2.7
2.7
1.7
2.5
0
0
0

FIG. 30B

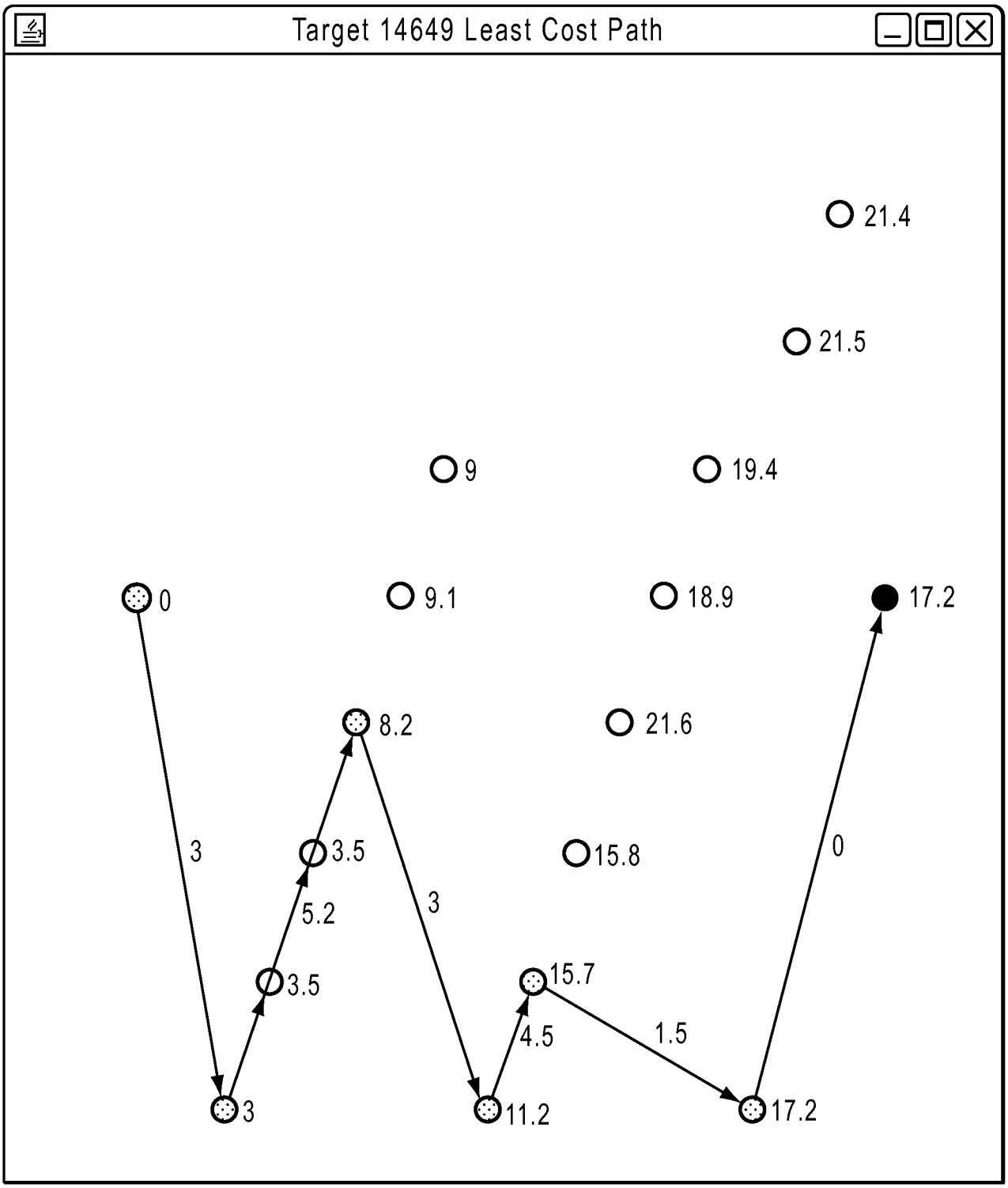

Target 14649 Least Cost Path
21.4
21.5
9
19.4
0
9.1
18.9
17.2
8.2
21.6
3
3.5
15.8
0
5.2
3
3.5
15.7
4.5
1.5
3
11.2
17.2

FIG. 30C

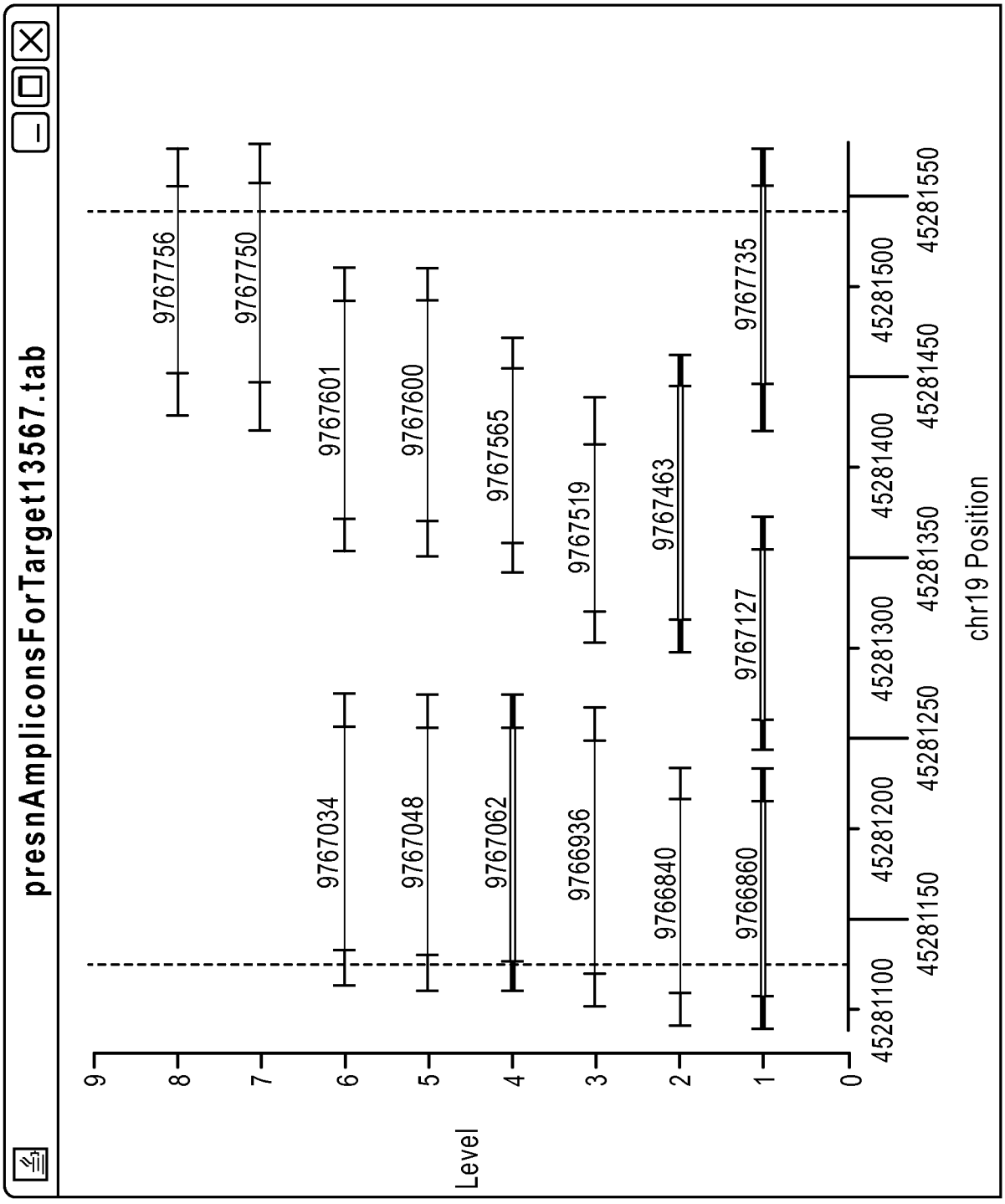

presnAmpliconsForTarget13567.tab
Level
chr19 Position
9767756
9767750
9767601
9767600
9767565
9767519
9767463
9767735
9767034
9767048
9767062
9766936
9766840
9766860
9767127
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550

FIG. 31

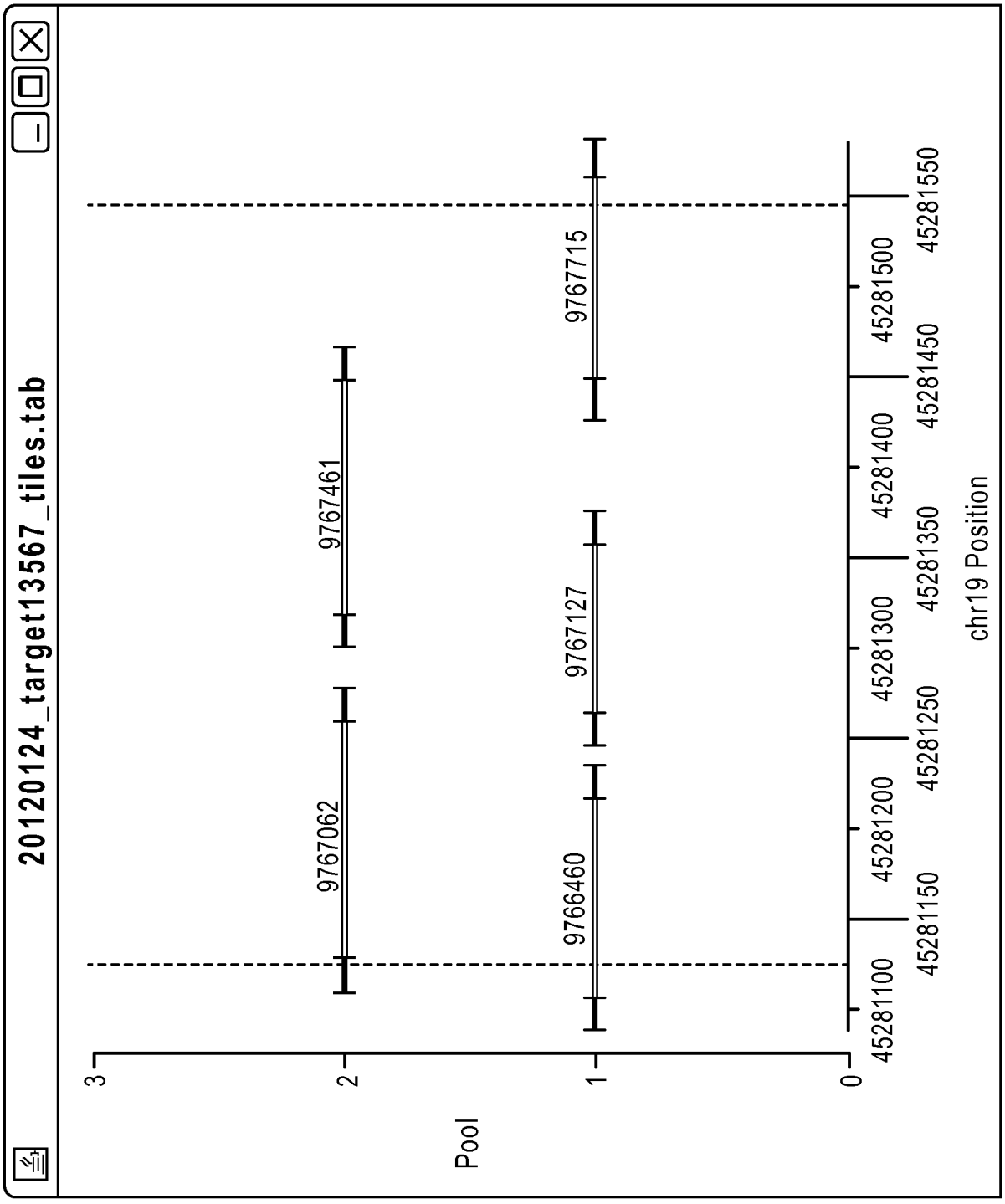

20120124_target13567_tiles.tab
Pool
3
2
1
0
9767062
9767461
9766460
9767127
9767715
45281100
45281150
45281200
45281250
45281300
45281350
45281400
45281450
45281500
45281550
chr19 Position

FIG. 32

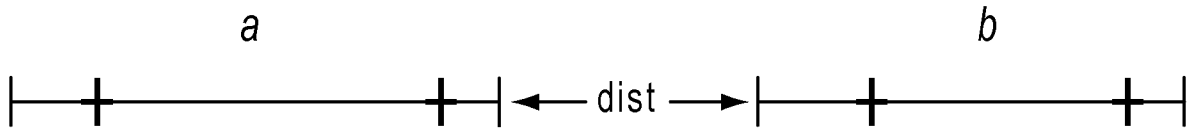


FIG. 33A

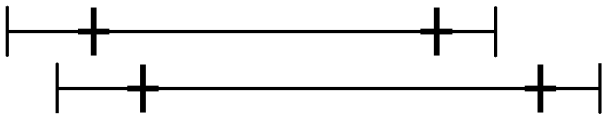


FIG. 33B

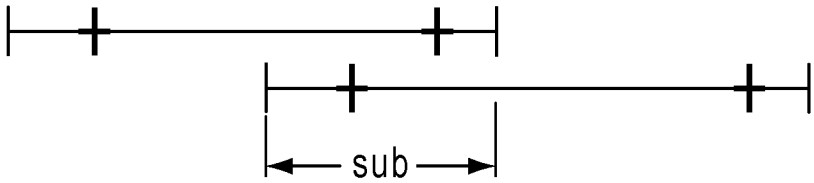


FIG. 33C

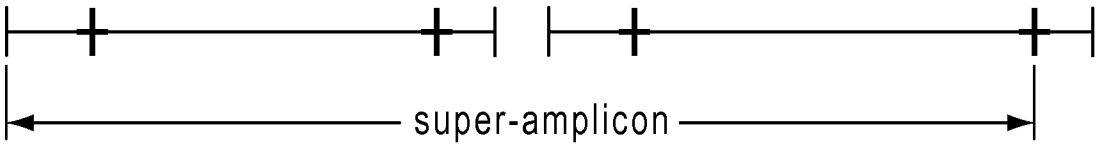


FIG. 33D

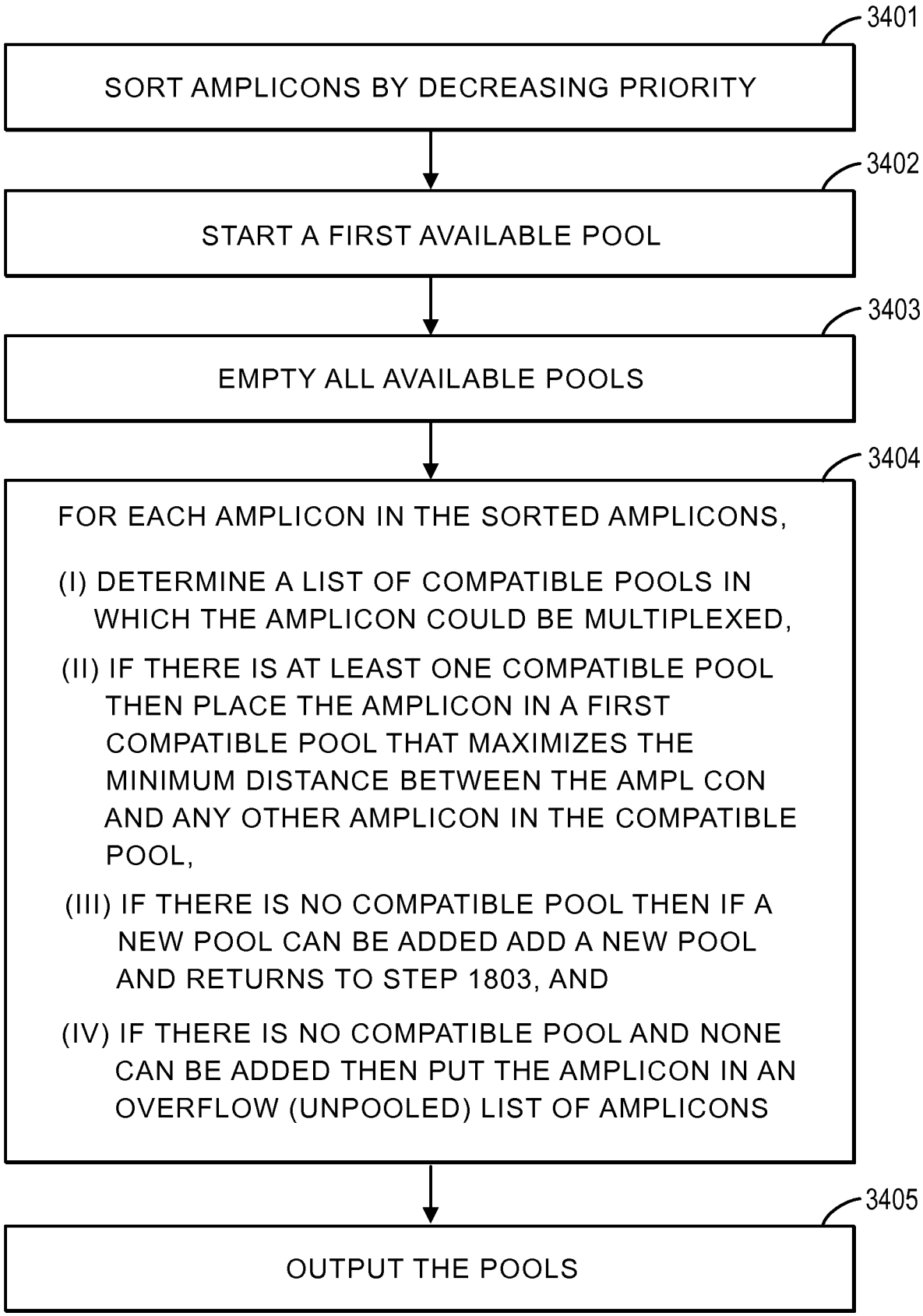

3401
SORT AMPLICONS BY DECREASING PRIORITY
3402
START A FIRST AVAILABLE POOL
3403
EMPTY ALL AVAILABLE POOLS
3404
FOR EACH AMPLICON IN THE SORTED AMPLICONS,
(I) DETERMINE A LIST OF COMPATIBLE POOLS IN WHICH THE AMPLICON COULD BE MULTIPLEXED,
(II) IF THERE IS AT LEAST ONE COMPATIBLE POOL THEN PLACE THE AMPLICON IN A FIRST COMPATIBLE POOL THAT MAXIMIZES THE MINIMUM DISTANCE BETWEEN THE AMPL CON AND ANY OTHER AMPLICON IN THE COMPATIBLE POOL,
(III) IF THERE IS NO COMPATIBLE POOL THEN IF A NEW POOL CAN BE ADDED ADD A NEW POOL AND RETURNS TO STEP 1803, AND
(IV) IF THERE IS NO COMPATIBLE POOL AND NONE CAN BE ADDED THEN PUT THE AMPLICON IN AN OVERFLOW (UNPOOLED) LIST OF AMPLICONS
3405
OUTPUT THE POOLS

FIG. 34

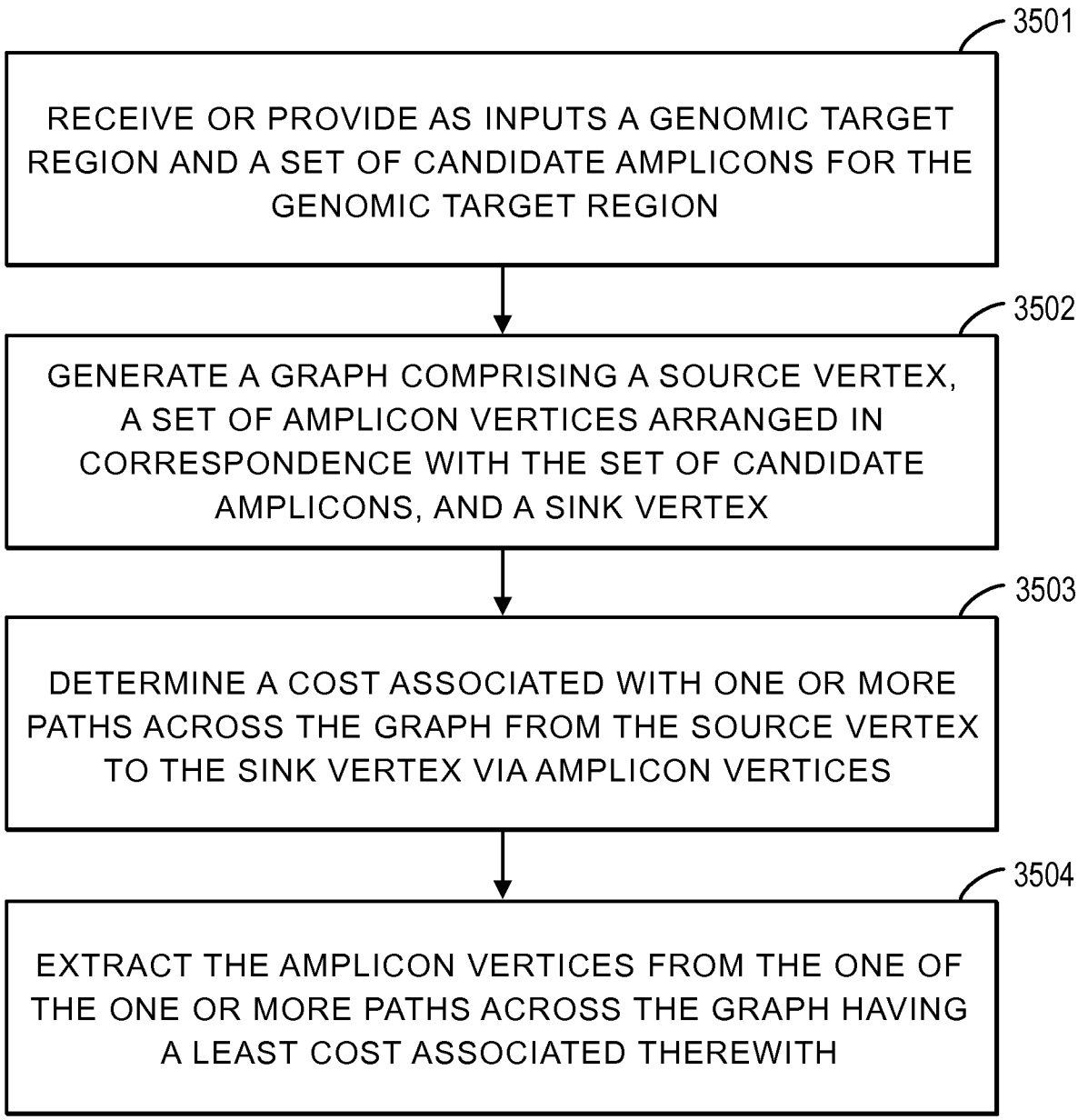

3501
RECEIVE OR PROVIDE AS INPUTS A GENOMIC TARGET REGION AND A SET OF CANDIDATE AMPLICONS FOR THE GENOMIC TARGET REGION
3502
GENERATE A GRAPH COMPRISING A SOURCE VERTEX, A SET OF AMPLICON VERTICES ARRANGED IN CORRESPONDENCE WITH THE SET OF CANDIDATE AMPLICONS, AND A SINK VERTEX
3503
DETERMINE A COST ASSOCIATED WITH ONE OR MORE PATHS ACROSS THE GRAPH FROM THE SOURCE VERTEX TO THE SINK VERTEX VIA AMPLICON VERTICES
3504
EXTRACT THE AMPLICON VERTICES FROM THE ONE OF THE ONE OR MORE PATHS ACROSS THE GRAPH HAVING A LEAST COST ASSOCIATED THEREWITH

FIG. 35

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2012/035612

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VARLEY KATHERINE ELENA ET AL: "Nested Patch PCR enables highly multiplexed mutation discovery in candidate genes", GENOME RESEARCH, vol. 18, no. 11, November 2008 (2008-11), pages 1844-1850, XP002678933, ISSN: 1088-9051 figure 1 -----	1-10
A	US 2008/293589 A1 (SHAPERO MICHAEL H [US]) 27 November 2008 (2008-11-27) paragraph [0087] - paragraph [0093] -----	1-10

☐ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
29 June 2012	25/07/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Aslund, Fredrik

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2012/035612

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2008293589 A1	27-11-2008	NONE	